

Package ‘curatedTCGAData’

March 6, 2025

Type Package

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

Version 1.29.2

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

License Artistic-2.0

BugReports <https://github.com/waldronlab/curatedTCGAData/issues>

Depends R (>= 4.5.0), MultiAssayExperiment

Imports AnnotationHub, ExperimentHub, HDF5Array, methods, S4Vectors, stats, SummarizedExperiment, utils

Suggests BiocStyle, knitr, RaggedExperiment, readr, rmarkdown, TCGAutils, testthat

VignetteBuilder knitr

biocViews Homo_sapiens_Data, ReproducibleResearch, CancerData, ExperimentHub

Encoding UTF-8

RoxygenNote 7.3.2

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 curatedTCGAData-package

curatedTCGAData-package

Description

The curatedTCGAData package provides a convenient and user-friendly interface for The Cancer Genome Atlas data from the Firehose GDAC Pipeline. Please note that `_most_` of the data from the GDAC Firehose pipeline uses the ‘hg19’ reference genome (except for a few cancers; refer to <https://confluence.broadinstitute.org/display/GDAC/FAQ>).

It is highly recommended to use the ‘TCGAutils’ companion package. It provides convenience functions for manipulating curatedTCGAData objects. See package for more details (<http://bioconductor.org/packages/TCGAutils>).

diseaseCodes

The following are the TCGA disease codes and full names as posted on the official website (<https://gdc.cancer.gov/resources-tcga-users/tcga-code-tables/tcga-study-abbreviations>).

| | 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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- Martin Morgan <martin.morgan@roswellpark.org> [contributor]

See Also

Useful links:

- Report bugs at <https://github.com/waldronlab/curatedTCGAData/issues>

Examples

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

 ACC

Adrenocortical carcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( ACC )
ExperimentList class object of length 10:
 [1] ACC_CNASNP-20160128: RaggedExperiment with 79861 rows and 180 columns
 [2] ACC_CNVSNP-20160128: RaggedExperiment with 21052 rows and 180 columns
 [3] ACC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 90 columns
 [4] ACC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 42 rows and 90 columns
 [5] ACC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 90 columns
 [6] ACC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 80 columns
 [7] ACC_Mutation-20160128: RaggedExperiment with 20166 rows and 90 columns
 [8] ACC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 79 columns
 [9] ACC_RPPAArray-20160128: SummarizedExperiment with 192 rows and 46 columns
 [10] ACC_Methylation-20160128: SummarizedExperiment with 485577 rows and 80 columns

> rownames( ACC )
CharacterList of length 10
[["ACC_CNASNP-20160128"]] character(0)
[["ACC_CNVSNP-20160128"]] character(0)
[["ACC_GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["ACC_GISTIC_Peaks-20160128"]] chr1:8403012-8925111 ...
[["ACC_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["ACC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["ACC_Mutation-20160128"]] character(0)
[["ACC_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 TAKR
[["ACC_RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363
[["ACC_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873

> colnames( ACC )
CharacterList of length 10
[["ACC_CNASNP-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["ACC_CNVSNP-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["ACC_GISTIC_AllByGene-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["ACC_GISTIC_Peaks-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["ACC_GISTIC_ThresholdedByGene-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["ACC_miRNASeqGene-20160128"]] TCGA-OR-A5J1-01A-11R-A29W-13 ...
```

```

[["ACC_Mutation-20160128"]] TCGA-OR-A5J1-01A-11D-A29I-10 ...
[["ACC_RNASeq2GeneNorm-20160128"]] TCGA-OR-A5J1-01A-11R-A29S-07 ...
[["ACC_RPPAArray-20160128"]] TCGA-OR-A5J2-01A-21-A39K-20 ...
[["ACC_Methylation-20160128"]] TCGA-OR-A5J1-01A-11D-A29J-05 ...

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|---------------------------------------|---------------|
| 1 | ACC_CNASNP-20160128 | 2.2 Mb |
| 2 | ACC_CNVSNP-20160128 | 0.6 Mb |
| 3 | ACC_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | ACC_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | ACC_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | ACC_miRNASeqGene-20160128 | 0.1 Mb |
| 7 | ACC_Mutation-20160128 | 12.6 Mb |
| 8 | ACC_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 9 | ACC_RPPAArray-20160128 | 0 Mb |
| 10 | ACC_Methylation-20160128 | 75 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 | 78 |
| NA's | |
| 11 | |

ethnicity:

| | | |
|--------------------|------------------------|------|
| hispanic or latino | not hispanic or latino | NA's |
| 8 | 40 | 44 |

Including an additional 806 columns

See Also

[ACC-v2.0.1](#)

ACC-v2.0.1

Adrenocortical carcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( ACC )
ExperimentList class object of length 11:
 [1] ACC_CNASNP-20160128: RaggedExperiment with 79861 rows and 180 columns
 [2] ACC_CNVSNP-20160128: RaggedExperiment with 21052 rows and 180 columns
 [3] ACC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 90 columns
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 [6] ACC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 80 columns
 [7] ACC_Mutation-20160128: RaggedExperiment with 20166 rows and 90 columns
 [8] ACC_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 79 columns
 [9] ACC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 79 columns
 [10] ACC_RPPAArray-20160128: SummarizedExperiment with 192 rows and 46 columns
 [11] ACC_Methylation-20160128: SummarizedExperiment with 485577 rows and 80 columns

> rownames( ACC )
CharacterList of length 11
[["ACC_CNASNP-20160128"]] character(0)
[["ACC_CNVSNP-20160128"]] character(0)
[["ACC_GISTIC_AllByGene-20160128"]] character(0)
[["ACC_GISTIC_Peaks-20160128"]] 19 1 20 21 22 2 24 ... 41 42 14 15 16 43 44
[["ACC_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["ACC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["ACC_Mutation-20160128"]] character(0)
```

```

[["ACC_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["ACC_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["ACC_RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363
...
<1 more element>

```

```

> colnames( ACC )
CharacterList of length 11
[["ACC_CNASNP-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["ACC_CNVSNP-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["ACC_GISTIC_AllByGene-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["ACC_GISTIC_Peaks-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["ACC_GISTIC_ThresholdedByGene-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["ACC_miRNASeqGene-20160128"]] TCGA-OR-A5J1-01A-11R-A29W-13 ...
[["ACC_Mutation-20160128"]] TCGA-OR-A5J1-01A-11D-A29I-10 ...
[["ACC_RNASeq2Gene-20160128"]] TCGA-OR-A5J1-01A-11R-A29S-07 ...
[["ACC_RNASeq2GeneNorm-20160128"]] TCGA-OR-A5J1-01A-11R-A29S-07 ...
[["ACC_RPPAArray-20160128"]] TCGA-OR-A5J2-01A-21-A39K-20 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|---------------------------------------|---------------|
| 1 | ACC_CNASNP-20160128 | 2.2 Mb |
| 2 | ACC_CNVSNP-20160128 | 0.6 Mb |
| 3 | ACC_GISTIC_AllByGene-20160128 | 20.5 Mb |
| 4 | ACC_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | ACC_GISTIC_ThresholdedByGene-20160128 | 20.4 Mb |
| 6 | ACC_miRNASeqGene-20160128 | 0.8 Mb |
| 7 | ACC_Mutation-20160128 | 12.6 Mb |
| 8 | ACC_RNASeq2Gene-20160128 | 14.9 Mb |
| 9 | ACC_RNASeq2GeneNorm-20160128 | 14.9 Mb |
| 10 | ACC_RPPAArray-20160128 | 0.1 Mb |
| 11 | ACC_Methylation-20160128 | 75 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

```

 ACC-v2.1.0

Adrenocortical carcinoma

Description

A document describing the TCGA cancer code

Details

```

> experiments( ACC )
ExperimentList class object of length 11:
 [1] ACC_CNASNP-20160128: RaggedExperiment with 79861 rows and 180 columns
 [2] ACC_CNVSNP-20160128: RaggedExperiment with 21052 rows and 180 columns
 [3] ACC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 90 columns
 [4] ACC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 42 rows and 90 columns
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 [7] ACC_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 79 columns
 [8] ACC_RPPAArray-20160128: SummarizedExperiment with 192 rows and 46 columns

```

```
[9] ACC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 80 columns
[10] ACC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 17716 rows and 79 columns
[11] ACC_Methylation-20160128: SummarizedExperiment with 485577 rows and 80 columns
```

```
> rownames( ACC )
CharacterList of length 11
[["ACC_CNASNP-20160128"]] character(0)
[["ACC_CNVSNP-20160128"]] character(0)
[["ACC_GISTIC_AllByGene-20160128"]] character(0)
[["ACC_GISTIC_Peaks-20160128"]] 19 1 20 21 22 2 24 ... 41 42 14 15 16 43 44
[["ACC_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["ACC_Mutation-20160128"]] character(0)
[["ACC_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE2 tAKR
[["ACC_RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363
[["ACC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["ACC_RNASeq2GeneNorm-20160128"]] A1BG A2BP1 A2LD1 ... ZZEF1 ZZZ3 psiTPTE2
...
<1 more element>
```

```
> colnames( ACC )
CharacterList of length 11
[["ACC_CNASNP-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["ACC_CNVSNP-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["ACC_GISTIC_AllByGene-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["ACC_GISTIC_Peaks-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["ACC_GISTIC_ThresholdedByGene-20160128"]] TCGA-OR-A5J1-01A-11D-A29H-01 ...
[["ACC_Mutation-20160128"]] TCGA-OR-A5J1-01A-11D-A29I-10 ...
[["ACC_RNASeq2Gene-20160128"]] TCGA-OR-A5J1-01A-11R-A29S-07 ...
[["ACC_RPPAArray-20160128"]] TCGA-OR-A5J2-01A-21-A39K-20 ...
[["ACC_miRNASeqGene-20160128"]] TCGA-OR-A5J1-01A-11R-A29W-13 ...
[["ACC_RNASeq2GeneNorm-20160128"]] TCGA-OR-A5J1-01 ... TCGA-PK-A5HB-01
...
<1 more element>
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|---------------------------------------|---------------|
| 1 | ACC_CNASNP-20160128 | 2.2 Mb |
| 2 | ACC_CNVSNP-20160128 | 0.6 Mb |
| 3 | ACC_GISTIC_AllByGene-20160128 | 20.5 Mb |
| 4 | ACC_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | ACC_GISTIC_ThresholdedByGene-20160128 | 20.4 Mb |
| 6 | ACC_Mutation-20160128 | 12.6 Mb |
| 7 | ACC_RNASeq2Gene-20160128 | 14.9 Mb |
| 8 | ACC_RPPAArray-20160128 | 0.1 Mb |
| 9 | ACC_miRNASeqGene-20160128 | 0.8 Mb |
| 10 | ACC_RNASeq2GeneNorm-20160128 | 12.9 Mb |
| 11 | ACC_Methylation-20160128 | 75 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
[1,] 34 34 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 12:
 [1] BLCA_CNASeq-20160128: RaggedExperiment with 35692 rows and 232 columns
 [2] BLCA_CNASNP-20160128: RaggedExperiment with 479978 rows and 806 columns
 [3] BLCA_CNVSNP-20160128: RaggedExperiment with 104349 rows and 797 columns
 [4] BLCA_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 408 columns
 [5] BLCA_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 71 rows and 408 columns
 [6] BLCA_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 408 columns
 [7] BLCA_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 429 columns
 [8] BLCA_Mutation-20160128: RaggedExperiment with 39312 rows and 130 columns
 [9] BLCA_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 427 columns
[10] BLCA_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 67 columns
[11] BLCA_RPPAArray-20160128: SummarizedExperiment with 208 rows and 344 columns
[12] BLCA_Methylation-20160128: SummarizedExperiment with 485577 rows and 434 columns

> rownames( BLCA )
CharacterList of length 12
[["BLCA_CNASeq-20160128"]] character(0)
[["BLCA_CNASNP-20160128"]] character(0)
[["BLCA_CNVSNP-20160128"]] character(0)
[["BLCA_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["BLCA_GISTIC_Peaks-20160128"]] chr1:26963410-27155421 ...
[["BLCA_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["BLCA_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["BLCA_Mutation-20160128"]] character(0)
[["BLCA_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["BLCA_RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
...
<2 more elements>

> colnames( BLCA )
CharacterList of length 12
[["BLCA_CNASeq-20160128"]] TCGA-BL-A0C8-01A-11D-A10R-02 ...
[["BLCA_CNASNP-20160128"]] TCGA-2F-A9KO-01A-11D-A38F-01 ...
[["BLCA_CNVSNP-20160128"]] TCGA-2F-A9KO-01A-11D-A38F-01 ...
[["BLCA_GISTIC_AllByGene-20160128"]] TCGA-2F-A9KO-01A-11D-A38F-01 ...
[["BLCA_GISTIC_Peaks-20160128"]] TCGA-2F-A9KO-01A-11D-A38F-01 ...
[["BLCA_GISTIC_ThresholdedByGene-20160128"]] TCGA-2F-A9KO-01A-11D-A38F-01 ...
[["BLCA_miRNASeqGene-20160128"]] TCGA-2F-A9KO-01A-11R-A38M-13 ...
[["BLCA_Mutation-20160128"]] TCGA-BL-A0C8-01A-11D-A10S-08 ...
[["BLCA_RNASeq2GeneNorm-20160128"]] TCGA-2F-A9KO-01A-11R-A38B-07 ...
[["BLCA_RNASeqGene-20160128"]] TCGA-BL-A0C8-01A-11R-A10U-07 ...
...
<2 more elements>

```

Sizes of each ExperimentList element:

| | | assay | size.Mb |
|----|--|----------------------|---------|
| 1 | | BLCA_CNASeq-20160128 | 1 Mb |
| 2 | | BLCA_CNASNP-20160128 | 13.1 Mb |
| 3 | | BLCA_CNVSNP-20160128 | 3 Mb |
| 4 | BLCA_GISTIC_AllByGene-20160128 | | 4.9 Mb |
| 5 | BLCA_GISTIC_Peaks-20160128 | | 0.1 Mb |
| 6 | BLCA_GISTIC_ThresholdedByGene-20160128 | | 4.9 Mb |
| 7 | BLCA_miRNASeqGene-20160128 | | 0.1 Mb |
| 8 | BLCA_Mutation-20160128 | | 56.1 Mb |
| 9 | BLCA_RNASeq2GeneNorm-20160128 | | 1.3 Mb |
| 10 | BLCA_RNASeqGene-20160128 | | 1.3 Mb |
| 11 | BLCA_RPPAArray-20160128 | | 0 Mb |
| 12 | BLCA_Methylation-20160128 | | 75.1 Mb |

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

See Also

[BLCA-v2.0.1](#)

BLCA-v2.0.1

Bladder Urothelial Carcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( BLCA )
ExperimentList class object of length 13:
 [1] BLCA_CNASeq-20160128: RaggedExperiment with 35692 rows and 232 columns
 [2] BLCA_CNASNP-20160128: RaggedExperiment with 479978 rows and 806 columns
 [3] BLCA_CNVSNP-20160128: RaggedExperiment with 104349 rows and 797 columns
 [4] BLCA_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 408 columns
 [5] BLCA_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 71 rows and 408 columns
 [6] BLCA_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 408 columns
 [7] BLCA_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 429 columns
 [8] BLCA_Mutation-20160128: RaggedExperiment with 39312 rows and 130 columns
 [9] BLCA_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 427 columns
 [10] BLCA_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 427 columns
 [11] BLCA_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 67 columns
 [12] BLCA_RPPAArray-20160128: SummarizedExperiment with 208 rows and 344 columns
 [13] BLCA_Methylation-20160128: SummarizedExperiment with 485577 rows and 434 columns

> rownames( BLCA )
CharacterList of length 13
[["BLCA_CNASeq-20160128"]] character(0)
[["BLCA_CNASNP-20160128"]] character(0)
[["BLCA_CNVSNP-20160128"]] character(0)
[["BLCA_GISTIC_AllByGene-20160128"]] character(0)
[["BLCA_GISTIC_Peaks-20160128"]] 38 1 2 3 39 4 40 41 ... 69 70 34 35 36 37 71
[["BLCA_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["BLCA_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["BLCA_Mutation-20160128"]] character(0)
[["BLCA_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["BLCA_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
```

```

...
<3 more elements>

> colnames( BLCA )
CharacterList of length 13
[["BLCA_CNASeq-20160128"]] TCGA-BL-A0C8-01A-11D-A10R-02 ...
[["BLCA_CNASNP-20160128"]] TCGA-2F-A9KO-01A-11D-A38F-01 ...
[["BLCA_CNVSNP-20160128"]] TCGA-2F-A9KO-01A-11D-A38F-01 ...
[["BLCA_GISTIC_AllByGene-20160128"]] TCGA-2F-A9KO-01A-11D-A38F-01 ...
[["BLCA_GISTIC_Peaks-20160128"]] TCGA-2F-A9KO-01A-11D-A38F-01 ...
[["BLCA_GISTIC_ThresholdedByGene-20160128"]] TCGA-2F-A9KO-01A-11D-A38F-01 ...
[["BLCA_miRNASeqGene-20160128"]] TCGA-2F-A9KO-01A-11R-A38M-13 ...
[["BLCA_Mutation-20160128"]] TCGA-BL-A0C8-01A-11D-A10S-08 ...
[["BLCA_RNASeq2Gene-20160128"]] TCGA-2F-A9KO-01A-11R-A38B-07 ...
[["BLCA_RNASeq2GeneNorm-20160128"]] TCGA-2F-A9KO-01A-11R-A38B-07 ...
...
<3 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | BLCA_CNASeq-20160128 | 1 Mb |
| 2 | BLCA_CNASNP-20160128 | 13.1 Mb |
| 3 | BLCA_CNVSNP-20160128 | 3 Mb |
| 4 | BLCA_GISTIC_AllByGene-20160128 | 80.7 Mb |
| 5 | BLCA_GISTIC_Peaks-20160128 | 0.4 Mb |
| 6 | BLCA_GISTIC_ThresholdedByGene-20160128 | 80.5 Mb |
| 7 | BLCA_miRNASeqGene-20160128 | 3.6 Mb |
| 8 | BLCA_Mutation-20160128 | 56.1 Mb |
| 9 | BLCA_RNASeq2Gene-20160128 | 69.4 Mb |
| 10 | BLCA_RNASeq2GeneNorm-20160128 | 69.4 Mb |
| 11 | BLCA_RNASeqGene-20160128 | 13 Mb |
| 12 | BLCA_RPPAArray-20160128 | 0.6 Mb |
| 13 | BLCA_Methylation-20160128 | 75.1 Mb |

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

BLCA-v2.1.0

Bladder Urothelial Carcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( BLCA )
```

```
ExperimentList class object of length 13:
```

- [1] BLCA_CNASeq-20160128: RaggedExperiment with 35692 rows and 232 columns
- [2] BLCA_CNASNP-20160128: RaggedExperiment with 479978 rows and 806 columns
- [3] BLCA_CNVSNP-20160128: RaggedExperiment with 104349 rows and 797 columns
- [4] BLCA_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 408 columns
- [5] BLCA_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 71 rows and 408 columns
- [6] BLCA_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 408 columns
- [7] BLCA_Mutation-20160128: RaggedExperiment with 39312 rows and 130 columns
- [8] BLCA_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 427 columns
- [9] BLCA_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 67 columns

```
[10] BLCA_RPPAArray-20160128: SummarizedExperiment with 208 rows and 344 columns
[11] BLCA_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 429 columns
[12] BLCA_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18205 rows and 427 columns
[13] BLCA_Methylation-20160128: SummarizedExperiment with 485577 rows and 434 columns
```

```
> rownames( BLCA )
CharacterList of length 13
[["BLCA_CNASeq-20160128"]] character(0)
[["BLCA_CNASNP-20160128"]] character(0)
[["BLCA_CNVSNP-20160128"]] character(0)
[["BLCA_GISTIC_AllByGene-20160128"]] character(0)
[["BLCA_GISTIC_Peaks-20160128"]] 38 1 2 3 39 4 40 41 ... 69 70 34 35 36 37 71
[["BLCA_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["BLCA_Mutation-20160128"]] character(0)
[["BLCA_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["BLCA_RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["BLCA_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<3 more elements>
```

```
> colnames( BLCA )
CharacterList of length 13
[["BLCA_CNASeq-20160128"]] TCGA-BL-A0C8-01A-11D-A10R-02 ...
[["BLCA_CNASNP-20160128"]] TCGA-2F-A9K0-01A-11D-A38F-01 ...
[["BLCA_CNVSNP-20160128"]] TCGA-2F-A9K0-01A-11D-A38F-01 ...
[["BLCA_GISTIC_AllByGene-20160128"]] TCGA-2F-A9K0-01A-11D-A38F-01 ...
[["BLCA_GISTIC_Peaks-20160128"]] TCGA-2F-A9K0-01A-11D-A38F-01 ...
[["BLCA_GISTIC_ThresholdedByGene-20160128"]] TCGA-2F-A9K0-01A-11D-A38F-01 ...
[["BLCA_Mutation-20160128"]] TCGA-BL-A0C8-01A-11D-A10S-08 ...
[["BLCA_RNASeq2Gene-20160128"]] TCGA-2F-A9K0-01A-11R-A38B-07 ...
[["BLCA_RNASeqGene-20160128"]] TCGA-BL-A0C8-01A-11R-A10U-07 ...
[["BLCA_RPPAArray-20160128"]] TCGA-2F-A9K0-01A-21-A459-20 ...
...
<3 more elements>
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | BLCA_CNASeq-20160128 | 1 Mb |
| 2 | BLCA_CNASNP-20160128 | 13.1 Mb |
| 3 | BLCA_CNVSNP-20160128 | 3 Mb |
| 4 | BLCA_GISTIC_AllByGene-20160128 | 80.7 Mb |
| 5 | BLCA_GISTIC_Peaks-20160128 | 0.4 Mb |
| 6 | BLCA_GISTIC_ThresholdedByGene-20160128 | 80.5 Mb |
| 7 | BLCA_Mutation-20160128 | 56.1 Mb |
| 8 | BLCA_RNASeq2Gene-20160128 | 69.4 Mb |
| 9 | BLCA_RNASeqGene-20160128 | 13 Mb |
| 10 | BLCA_RPPAArray-20160128 | 0.6 Mb |

```

11          BLCA_miRNASeqGene-20160128  3.6 Mb
12          BLCA_RNASeq2GeneNorm-20160128 61.6 Mb
13          BLCA_Methylation-20160128 75.1 Mb

```

```

-----
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
[1,] 180    180    1.12    0.992    1.33

```

```

-----
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

44

23

white

327

NA's

18

ethnicity:

hispanic or latino not hispanic or latino

9

371

NA's

32

Including an additional 1695 columns

Description

A document describing the TCGA cancer code

Details

```
> experiments( BRCA )
ExperimentList class object of length 14:
 [1] BRCA_CNASeq-20160128: RaggedExperiment with 5298 rows and 38 columns
 [2] BRCA_CNASNP-20160128: RaggedExperiment with 1132786 rows and 2209 columns
 [3] BRCA_CNVSNP-20160128: RaggedExperiment with 284458 rows and 2199 columns
 [4] BRCA_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 1080 columns
 [5] BRCA_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 70 rows and 1080 columns
 [6] BRCA_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 1080 columns
 [7] BRCA_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 849 columns
 [8] BRCA_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 590 columns
 [9] BRCA_Mutation-20160128: RaggedExperiment with 90490 rows and 993 columns
[10] BRCA_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 1212 columns
[11] BRCA_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 878 columns
[12] BRCA_RPPAArray-20160128: SummarizedExperiment with 226 rows and 937 columns
[13] BRCA_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 343 columns
[14] BRCA_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 885 columns

> rownames( BRCA )
CharacterList of length 14
[["BRCA_CNASeq-20160128"]] character(0)
[["BRCA_CNASNP-20160128"]] character(0)
[["BRCA_CNVSNP-20160128"]] character(0)
[["BRCA_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["BRCA_GISTIC_Peaks-20160128"]] chr1:12675879-21133098 ...
[["BRCA_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["BRCA_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["BRCA_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["BRCA_Mutation-20160128"]] character(0)
[["BRCA_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
...
<4 more elements>

> colnames( BRCA )
CharacterList of length 14
[["BRCA_CNASeq-20160128"]] TCGA-A2-A0EU-01A-22D-A060-02 ...
[["BRCA_CNASNP-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["BRCA_CNVSNP-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["BRCA_GISTIC_AllByGene-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["BRCA_GISTIC_Peaks-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["BRCA_GISTIC_ThresholdedByGene-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["BRCA_miRNASeqGene-20160128"]] TCGA-3C-AAAU-01A-11R-A41G-13 ...
[["BRCA_mRNAArray-20160128"]] TCGA-A1-A0SD-01A-11R-A115-07 ...
[["BRCA_Mutation-20160128"]] TCGA-A1-A0SB-01A-11D-A142-09 ...
```

```
[[ "BRCA_RNASeq2GeneNorm-20160128" ]] TCGA-3C-AAAU-01A-11R-A41B-07 ...
...
<4 more elements>
```

Sizes of each ExperimentList element:

| | | assay | size.Mb |
|----|--|----------------------------|---------|
| 1 | | BRCA_CNASeq-20160128 | 0.2 Mb |
| 2 | | BRCA_CNASNP-20160128 | 30.9 Mb |
| 3 | | BRCA_CNVSNP-20160128 | 8.2 Mb |
| 4 | BRCA_GISTIC_AllByGene-20160128 | | 5 Mb |
| 5 | | BRCA_GISTIC_Peaks-20160128 | 0.2 Mb |
| 6 | BRCA_GISTIC_ThresholdedByGene-20160128 | | 5 Mb |
| 7 | | BRCA_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | | BRCA_mRNAArray-20160128 | 1.2 Mb |
| 9 | | BRCA_Mutation-20160128 | 67.4 Mb |
| 10 | BRCA_RNASeq2GeneNorm-20160128 | | 1.4 Mb |
| 11 | | BRCA_RNASeqGene-20160128 | 1.4 Mb |
| 12 | | BRCA_RPPAArray-20160128 | 0.1 Mb |
| 13 | BRCA_Methylation_methyl27-20160128 | | 4.9 Mb |
| 14 | BRCA_Methylation_methyl450-20160128 | | 75.1 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

See Also

[BRCA-v2.0.1](#)

 BRCA-v2.0.1

Breast invasive carcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( BRCA )
ExperimentList class object of length 15:
 [1] BRCA_CNASeq-20160128: RaggedExperiment with 5298 rows and 38 columns
 [2] BRCA_CNASNP-20160128: RaggedExperiment with 1132786 rows and 2209 columns
 [3] BRCA_CNVSNP-20160128: RaggedExperiment with 284458 rows and 2199 columns
 [4] BRCA_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 1080 columns
 [5] BRCA_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 70 rows and 1080 columns
 [6] BRCA_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 1080 columns
 [7] BRCA_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 849 columns
 [8] BRCA_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 590 columns
 [9] BRCA_Mutation-20160128: RaggedExperiment with 90490 rows and 993 columns
[10] BRCA_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 1212 columns
[11] BRCA_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 1212 columns
[12] BRCA_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 878 columns
[13] BRCA_RPPAArray-20160128: SummarizedExperiment with 226 rows and 937 columns
[14] BRCA_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 343 columns
[15] BRCA_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 885 columns

> rownames( BRCA )
CharacterList of length 15
[["BRCA_CNASeq-20160128"]] character(0)
[["BRCA_CNASNP-20160128"]] character(0)
[["BRCA_CNVSNP-20160128"]] character(0)
[["BRCA_GISTIC_AllByGene-20160128"]] character(0)
[["BRCA_GISTIC_Peaks-20160128"]] 29 30 1 2 31 3 32 4 ... 66 27 67 28 68 69 70
[["BRCA_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["BRCA_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["BRCA_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["BRCA_Mutation-20160128"]] character(0)
[["BRCA_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
```

```

...
<5 more elements>

> colnames( BRCA )
CharacterList of length 15
[["BRCA_CNASeq-20160128"]] TCGA-A2-A0EU-01A-22D-A060-02 ...
[["BRCA_CNASNP-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["BRCA_CNVSNP-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["BRCA_GISTIC_AllByGene-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["BRCA_GISTIC_Peaks-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["BRCA_GISTIC_ThresholdedByGene-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["BRCA_miRNASeqGene-20160128"]] TCGA-3C-AAAU-01A-11R-A41G-13 ...
[["BRCA_mRNAArray-20160128"]] TCGA-A1-A0SD-01A-11R-A115-07 ...
[["BRCA_Mutation-20160128"]] TCGA-A1-A0SB-01A-11D-A142-09 ...
[["BRCA_RNASeq2Gene-20160128"]] TCGA-3C-AAAU-01A-11R-A41B-07 ...
...
<5 more elements>

```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|----|--|----------|
| 1 | BRCA_CNASeq-20160128 | 0.2 Mb |
| 2 | BRCA_CNASNP-20160128 | 30.9 Mb |
| 3 | BRCA_CNVSNP-20160128 | 8.2 Mb |
| 4 | BRCA_GISTIC_AllByGene-20160128 | 207.9 Mb |
| 5 | BRCA_GISTIC_Peaks-20160128 | 0.8 Mb |
| 6 | BRCA_GISTIC_ThresholdedByGene-20160128 | 207.7 Mb |
| 7 | BRCA_miRNASeqGene-20160128 | 7.1 Mb |
| 8 | BRCA_mRNAArray-20160128 | 82.5 Mb |
| 9 | BRCA_Mutation-20160128 | 67.4 Mb |
| 10 | BRCA_RNASeq2Gene-20160128 | 192.3 Mb |
| 11 | BRCA_RNASeq2GeneNorm-20160128 | 192.3 Mb |
| 12 | BRCA_RNASeqGene-20160128 | 140 Mb |
| 13 | BRCA_RPPAArray-20160128 | 1.8 Mb |
| 14 | BRCA_Methylation_methyl27-20160128 | 4.9 Mb |
| 15 | BRCA_Methylation_methyl450-20160128 | 75.1 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

BRCA-v2.1.0

Breast invasive carcinoma

Description

A document describing the TCGA cancer code

Details

```

> experiments( BRCA )
ExperimentList class object of length 15:
 [1] BRCA_CNASeq-20160128: RaggedExperiment with 5298 rows and 38 columns
 [2] BRCA_CNASNP-20160128: RaggedExperiment with 1132786 rows and 2209 columns
 [3] BRCA_CNVSNP-20160128: RaggedExperiment with 284458 rows and 2199 columns
 [4] BRCA_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 1080 columns
 [5] BRCA_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 70 rows and 1080 columns
 [6] BRCA_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 1080 columns
 [7] BRCA_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 590 columns
 [8] BRCA_Mutation-20160128: RaggedExperiment with 90490 rows and 993 columns
 [9] BRCA_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 1212 columns
 [10] BRCA_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 878 columns
 [11] BRCA_RPPAArray-20160128: SummarizedExperiment with 226 rows and 937 columns
 [12] BRCA_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 849 columns
 [13] BRCA_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18300 rows and 1212 columns
 [14] BRCA_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 343 columns
 [15] BRCA_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 885 columns

> rownames( BRCA )

```



```

CharacterList of length 15
[["BRCA_CNASeq-20160128"]] character(0)
[["BRCA_CNASNP-20160128"]] character(0)
[["BRCA_CNVSNP-20160128"]] character(0)
[["BRCA_GISTIC_AllByGene-20160128"]] character(0)
[["BRCA_GISTIC_Peaks-20160128"]] 29 30 1 2 31 3 32 4 ... 66 27 67 28 68 69 70
[["BRCA_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["BRCA_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["BRCA_Mutation-20160128"]] character(0)
[["BRCA_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["BRCA_RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
...
<5 more elements>

```

```

> colnames( BRCA )
CharacterList of length 15
[["BRCA_CNASeq-20160128"]] TCGA-A2-A0EU-01A-22D-A060-02 ...
[["BRCA_CNASNP-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["BRCA_CNVSNP-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["BRCA_GISTIC_AllByGene-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["BRCA_GISTIC_Peaks-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["BRCA_GISTIC_ThresholdedByGene-20160128"]] TCGA-3C-AAAU-01A-11D-A41E-01 ...
[["BRCA_mRNAArray-20160128"]] TCGA-A1-A0SD-01A-11R-A115-07 ...
[["BRCA_Mutation-20160128"]] TCGA-A1-A0SB-01A-11D-A142-09 ...
[["BRCA_RNASeq2Gene-20160128"]] TCGA-3C-AAAU-01A-11R-A41B-07 ...
[["BRCA_RNASeqGene-20160128"]] TCGA-A1-A0SB-01A-11R-A144-07 ...
...
<5 more elements>

```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|----|--|----------|
| 1 | BRCA_CNASeq-20160128 | 0.2 Mb |
| 2 | BRCA_CNASNP-20160128 | 30.9 Mb |
| 3 | BRCA_CNVSNP-20160128 | 8.2 Mb |
| 4 | BRCA_GISTIC_AllByGene-20160128 | 207.9 Mb |
| 5 | BRCA_GISTIC_Peaks-20160128 | 0.8 Mb |
| 6 | BRCA_GISTIC_ThresholdedByGene-20160128 | 207.7 Mb |
| 7 | BRCA_mRNAArray-20160128 | 82.5 Mb |
| 8 | BRCA_Mutation-20160128 | 67.4 Mb |
| 9 | BRCA_RNASeq2Gene-20160128 | 192.3 Mb |
| 10 | BRCA_RNASeqGene-20160128 | 140 Mb |
| 11 | BRCA_RPPAArray-20160128 | 1.8 Mb |
| 12 | BRCA_miRNASeqGene-20160128 | 7.1 Mb |
| 13 | BRCA_RNASeq2GeneNorm-20160128 | 171.7 Mb |
| 14 | BRCA_Methylation_methyl27-20160128 | 4.9 Mb |
| 15 | BRCA_Methylation_methyl450-20160128 | 75.1 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
[1,] 151 151 3.48 2.83 4.5
```

```
-----
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 | 1 | asian | 61 |
| black or african american | 183 | white | 757 |
| NA's | 96 | | |

ethnicity:

| | | | | | |
|--------------------|----|------------------------|-----|------|-----|
| hispanic or latino | 39 | not hispanic or latino | 884 | NA's | 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 11:
 [1] CESC_CNASeq-20160128: RaggedExperiment with 7834 rows and 100 columns
 [2] CESC_CNASNP-20160128: RaggedExperiment with 267855 rows and 586 columns
 [3] CESC_CNVSNP-20160128: RaggedExperiment with 59450 rows and 586 columns
 [4] CESC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 295 columns
 [5] CESC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 60 rows and 295 columns
 [6] CESC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 295 columns
```

```
[7] CESC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 312 columns
[8] CESC_Mutation-20160128: RaggedExperiment with 46547 rows and 194 columns
[9] CESC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 309 columns
[10] CESC_RPPAArray-20160128: SummarizedExperiment with 192 rows and 173 columns
[11] CESC_Methylation-20160128: SummarizedExperiment with 485577 rows and 312 columns
```

```
> rownames( CESC )
CharacterList of length 11
[["CESC_CNASeq-20160128"]] character(0)
[["CESC_CNASNP-20160128"]] character(0)
[["CESC_CNVSNP-20160128"]] character(0)
[["CESC_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["CESC_GISTIC_Peaks-20160128"]] chr1:1-28840301 ... chr22:48668582-51304566
[["CESC_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["CESC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["CESC_Mutation-20160128"]] character(0)
[["CESC_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["CESC_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<1 more element>
```

```
> colnames( CESC )
CharacterList of length 11
[["CESC_CNASeq-20160128"]] TCGA-C5-A1BQ-01C-11D-A20X-26 ...
[["CESC_CNASNP-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["CESC_CNVSNP-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["CESC_GISTIC_AllByGene-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["CESC_GISTIC_Peaks-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["CESC_GISTIC_ThresholdedByGene-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["CESC_miRNASeqGene-20160128"]] TCGA-2W-A8YY-01A-11R-A37P-13 ...
[["CESC_Mutation-20160128"]] TCGA-BI-A0VR-01A-11D-A10S-08 ...
[["CESC_RNASeq2GeneNorm-20160128"]] TCGA-2W-A8YY-01A-11R-A370-07 ...
[["CESC_RPPAArray-20160128"]] TCGA-2W-A8YY-01A-21-A40H-20 ...
...
<1 more element>
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|---|--|---------------|
| 1 | CESC_CNASeq-20160128 | 0.3 Mb |
| 2 | CESC_CNASNP-20160128 | 7.3 Mb |
| 3 | CESC_CNVSNP-20160128 | 1.8 Mb |
| 4 | CESC_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | CESC_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | CESC_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | CESC_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | CESC_Mutation-20160128 | 32.9 Mb |
| 9 | CESC_RNASeq2GeneNorm-20160128 | 1.3 Mb |

```

10          CESC_RPPAArray-20160128    0 Mb
11          CESC_Methylation-20160128  75 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

24

171

NA's

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

See Also

[CESC-v2.0.1](#)

CESC-v2.0.1

Cervical squamous cell carcinoma and endocervical adenocarcinoma

Description

A document describing the TCGA cancer code

Details

```

> experiments( CESC )
ExperimentList class object of length 12:
 [1] CESC_CNASeq-20160128: RaggedExperiment with 7834 rows and 100 columns
 [2] CESC_CNASNP-20160128: RaggedExperiment with 267855 rows and 586 columns
 [3] CESC_CNVSNP-20160128: RaggedExperiment with 59450 rows and 586 columns
 [4] CESC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 295 columns
 [5] CESC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 60 rows and 295 columns
 [6] CESC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 295 columns
 [7] CESC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 312 columns
 [8] CESC_Mutation-20160128: RaggedExperiment with 46547 rows and 194 columns
 [9] CESC_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 309 columns
 [10] CESC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 309 columns
 [11] CESC_RPPAArray-20160128: SummarizedExperiment with 192 rows and 173 columns
 [12] CESC_Methylation-20160128: SummarizedExperiment with 485577 rows and 312 columns

> rownames( CESC )
CharacterList of length 12
[["CESC_CNASeq-20160128"]] character(0)
[["CESC_CNASNP-20160128"]] character(0)
[["CESC_CNVSNP-20160128"]] character(0)

```

```

[["CESC_GISTIC_AllByGene-20160128"]] character(0)
[["CESC_GISTIC_Peaks-20160128"]] 27 1 28 2 3 29 4 30 ... 23 58 59 24 60 25 61
[["CESC_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["CESC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["CESC_Mutation-20160128"]] character(0)
[["CESC_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["CESC_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
...
<2 more elements>

```

```

> colnames( CESC )
CharacterList of length 12
[["CESC_CNASeq-20160128"]] TCGA-C5-A1BQ-01C-11D-A20X-26 ...
[["CESC_CNASNP-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["CESC_CNVSNP-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["CESC_GISTIC_AllByGene-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["CESC_GISTIC_Peaks-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["CESC_GISTIC_ThresholdedByGene-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["CESC_miRNASeqGene-20160128"]] TCGA-2W-A8YY-01A-11R-A37P-13 ...
[["CESC_Mutation-20160128"]] TCGA-BI-A0VR-01A-11D-A10S-08 ...
[["CESC_RNASeq2Gene-20160128"]] TCGA-2W-A8YY-01A-11R-A370-07 ...
[["CESC_RNASeq2GeneNorm-20160128"]] TCGA-2W-A8YY-01A-11R-A370-07 ...
...
<2 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | CESC_CNASeq-20160128 | 0.3 Mb |
| 2 | CESC_CNASNP-20160128 | 7.3 Mb |
| 3 | CESC_CNVSNP-20160128 | 1.8 Mb |
| 4 | CESC_GISTIC_AllByGene-20160128 | 59.3 Mb |
| 5 | CESC_GISTIC_Peaks-20160128 | 0.3 Mb |
| 6 | CESC_GISTIC_ThresholdedByGene-20160128 | 59.1 Mb |
| 7 | CESC_miRNASeqGene-20160128 | 2.7 Mb |
| 8 | CESC_Mutation-20160128 | 32.9 Mb |
| 9 | CESC_RNASeq2Gene-20160128 | 50.9 Mb |
| 10 | CESC_RNASeq2GeneNorm-20160128 | 50.9 Mb |
| 11 | CESC_RPPAArray-20160128 | 0.3 Mb |
| 12 | CESC_Methylation-20160128 | 75 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 |

agebeganmokinginyears:

| 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

| 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

| current user | former user | never used | NA's |
|--------------|-------------|------------|------|
| 15 | 54 | 90 | 148 |

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

| absent | present | NA's |
|--------|---------|------|
| 99 | 19 | 189 |

| carboplatin | cisplatin | other | NA's |
|-------------|-----------|-------|------|
| 7 | 104 | 2 | 194 |

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

| cardiopulmonary arrest | lung cancer | renal failure |
|------------------------|-------------|---------------|
| 1 | 1 | 1 |
| NA's | | |
| 304 | | |

| 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

CESC-v2.1.0

Cervical squamous cell carcinoma and endocervical adenocarcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( CESC )
ExperimentList class object of length 12:
 [1] CESC_CNASeq-20160128: RaggedExperiment with 7834 rows and 100 columns
 [2] CESC_CNASNP-20160128: RaggedExperiment with 267855 rows and 586 columns
 [3] CESC_CNVSNP-20160128: RaggedExperiment with 59450 rows and 586 columns
 [4] CESC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 295 columns
 [5] CESC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 60 rows and 295 columns
 [6] CESC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 295 columns
 [7] CESC_Mutation-20160128: RaggedExperiment with 46547 rows and 194 columns
 [8] CESC_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 309 columns
 [9] CESC_RPPAArray-20160128: SummarizedExperiment with 192 rows and 173 columns
 [10] CESC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 312 columns
 [11] CESC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18162 rows and 309 columns
 [12] CESC_Methylation-20160128: SummarizedExperiment with 485577 rows and 312 columns

> rownames( CESC )
CharacterList of length 12
[["CESC_CNASeq-20160128"]] character(0)
[["CESC_CNASNP-20160128"]] character(0)
[["CESC_CNVSNP-20160128"]] character(0)
[["CESC_GISTIC_AllByGene-20160128"]] character(0)
[["CESC_GISTIC_Peaks-20160128"]] 27 1 28 2 3 29 4 30 ... 23 58 59 24 60 25 61
[["CESC_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["CESC_Mutation-20160128"]] character(0)
[["CESC_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["CESC_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["CESC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
...
<2 more elements>

> colnames( CESC )
CharacterList of length 12
[["CESC_CNASeq-20160128"]] TCGA-C5-A1BQ-01C-11D-A20X-26 ...
[["CESC_CNASNP-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
```

```

[["CESC_CNVSNP-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["CESC_GISTIC_AllByGene-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["CESC_GISTIC_Peaks-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["CESC_GISTIC_ThresholdedByGene-20160128"]] TCGA-2W-A8YY-01A-11D-A37M-01 ...
[["CESC_Mutation-20160128"]] TCGA-BI-A0VR-01A-11D-A10S-08 ...
[["CESC_RNASeq2Gene-20160128"]] TCGA-2W-A8YY-01A-11R-A370-07 ...
[["CESC_RPPAArray-20160128"]] TCGA-2W-A8YY-01A-21-A40H-20 ...
[["CESC_miRNASeqGene-20160128"]] TCGA-2W-A8YY-01A-11R-A37P-13 ...
...
<2 more elements>

```

Sizes of each ExperimentList element:

| | | assay | size.Mb |
|----|--|----------------------------|---------|
| 1 | | CESC_CNASeq-20160128 | 0.3 Mb |
| 2 | | CESC_CNASNP-20160128 | 7.3 Mb |
| 3 | | CESC_CNVSNP-20160128 | 1.8 Mb |
| 4 | CESC_GISTIC_AllByGene-20160128 | | 59.3 Mb |
| 5 | | CESC_GISTIC_Peaks-20160128 | 0.3 Mb |
| 6 | CESC_GISTIC_ThresholdedByGene-20160128 | | 59.1 Mb |
| 7 | | CESC_Mutation-20160128 | 32.9 Mb |
| 8 | | CESC_RNASeq2Gene-20160128 | 50.9 Mb |
| 9 | | CESC_RPPAArray-20160128 | 0.3 Mb |
| 10 | | CESC_miRNASeqGene-20160128 | 2.7 Mb |
| 11 | CESC_RNASeq2GeneNorm-20160128 | | 45.1 Mb |
| 12 | | CESC_Methylation-20160128 | 75 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
[1,] 72      72      1.7      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 |
| agebeganmokinginyears: | | | | | | |
| 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
                             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 10:
 [1] CHOL_CNASNP-20160128: RaggedExperiment with 39698 rows and 85 columns
 [2] CHOL_CNVSNP-20160128: RaggedExperiment with 7570 rows and 85 columns
 [3] CHOL_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 36 columns
 [4] CHOL_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 19 rows and 36 columns
 [5] CHOL_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 36 columns
 [6] CHOL_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 45 columns
 [7] CHOL_Mutation-20160128: RaggedExperiment with 6755 rows and 35 columns
 [8] CHOL_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 45 columns
 [9] CHOL_RPPAArray-20160128: SummarizedExperiment with 192 rows and 30 columns
 [10] CHOL_Methylation-20160128: SummarizedExperiment with 485577 rows and 45 columns

> rownames( CHOL )
CharacterList of length 10
[["CHOL_CNASNP-20160128"]] character(0)
[["CHOL_CNVSNP-20160128"]] character(0)
[["CHOL_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["CHOL_GISTIC_Peaks-20160128"]] chr1:7829287-29140747 ... chr16:1-90354753
[["CHOL_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["CHOL_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["CHOL_Mutation-20160128"]] character(0)
[["CHOL_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["CHOL_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["CHOL_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873

> colnames( CHOL )
CharacterList of length 10
[["CHOL_CNASNP-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["CHOL_CNVSNP-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["CHOL_GISTIC_AllByGene-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["CHOL_GISTIC_Peaks-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["CHOL_GISTIC_ThresholdedByGene-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["CHOL_miRNASeqGene-20160128"]] TCGA-3X-AAV9-01A-72R-A41D-13 ...
[["CHOL_Mutation-20160128"]] TCGA-3X-AAV9-01A-72D-A417-09 ...
[["CHOL_RNASeq2GeneNorm-20160128"]] TCGA-3X-AAV9-01A-72R-A41I-07 ...
[["CHOL_RPPAArray-20160128"]] TCGA-3X-AAV9-01A-81-A45N-20 ...
[["CHOL_Methylation-20160128"]] TCGA-3X-AAV9-01A-72D-A418-05 ...

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|---|--|---------------|
| 1 | CHOL_CNASNP-20160128 | 1.1 Mb |
| 2 | CHOL_CNVSNP-20160128 | 0.2 Mb |
| 3 | CHOL_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | CHOL_GISTIC_Peaks-20160128 | 0 Mb |
| 5 | CHOL_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |

| | | |
|----|-------------------------------|--------|
| 6 | CHOL_miRNASeqGene-20160128 | 0.1 Mb |
| 7 | CHOL_Mutation-20160128 | 4.6 Mb |
| 8 | CHOL_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 9 | CHOL_RPPAArray-20160128 | 0 Mb |
| 10 | CHOL_Methylation-20160128 | 75 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

See Also

[CHOL-v2.0.1](#)

Description

A document describing the TCGA cancer code

Details

```
> experiments( CHOL )
ExperimentList class object of length 11:
 [1] CHOL_CNASNP-20160128: RaggedExperiment with 39698 rows and 85 columns
 [2] CHOL_CNVSNP-20160128: RaggedExperiment with 7570 rows and 85 columns
 [3] CHOL_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 36 columns
 [4] CHOL_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 19 rows and 36 columns
 [5] CHOL_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 36 columns
 [6] CHOL_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 45 columns
 [7] CHOL_Mutation-20160128: RaggedExperiment with 6755 rows and 35 columns
 [8] CHOL_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 45 columns
 [9] CHOL_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 45 columns
 [10] CHOL_RPPAArray-20160128: SummarizedExperiment with 192 rows and 30 columns
 [11] CHOL_Methylation-20160128: SummarizedExperiment with 485577 rows and 45 columns

> rownames( CHOL )
CharacterList of length 11
[["CHOL_CNASNP-20160128"]] character(0)
[["CHOL_CNVSNP-20160128"]] character(0)
[["CHOL_GISTIC_AllByGene-20160128"]] character(0)
[["CHOL_GISTIC_Peaks-20160128"]] 4 1 5 6 7 8 9 10 ... 13 3 14 15 18 16 17 20
[["CHOL_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["CHOL_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["CHOL_Mutation-20160128"]] character(0)
[["CHOL_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["CHOL_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["CHOL_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<1 more element>

> colnames( CHOL )
CharacterList of length 11
[["CHOL_CNASNP-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["CHOL_CNVSNP-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["CHOL_GISTIC_AllByGene-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["CHOL_GISTIC_Peaks-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["CHOL_GISTIC_ThresholdedByGene-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["CHOL_miRNASeqGene-20160128"]] TCGA-3X-AAV9-01A-72R-A41D-13 ...
[["CHOL_Mutation-20160128"]] TCGA-3X-AAV9-01A-72D-A417-09 ...
[["CHOL_RNASeq2Gene-20160128"]] TCGA-3X-AAV9-01A-72R-A41I-07 ...
[["CHOL_RNASeq2GeneNorm-20160128"]] TCGA-3X-AAV9-01A-72R-A41I-07 ...
[["CHOL_RPPAArray-20160128"]] TCGA-3X-AAV9-01A-81-A45N-20 ...
...
<1 more element>
```


Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | CHOL_CNASNP-20160128 | 1.1 Mb |
| 2 | CHOL_CNVSNP-20160128 | 0.2 Mb |
| 3 | CHOL_GISTIC_AllByGene-20160128 | 10.2 Mb |
| 4 | CHOL_GISTIC_Peaks-20160128 | 0 Mb |
| 5 | CHOL_GISTIC_ThresholdedByGene-20160128 | 10.1 Mb |
| 6 | CHOL_miRNASeqGene-20160128 | 0.5 Mb |
| 7 | CHOL_Mutation-20160128 | 4.6 Mb |
| 8 | CHOL_RNASeq2Gene-20160128 | 9.6 Mb |
| 9 | CHOL_RNASeq2GeneNorm-20160128 | 9.6 Mb |
| 10 | CHOL_RPPAArray-20160128 | 0.1 Mb |
| 11 | CHOL_Methylation-20160128 | 75 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

```

CHOL-v2.1.0

*Cholangiocarcinoma***Description**

A document describing the TCGA cancer code

Details

```

> experiments( CHOL )
ExperimentList class object of length 11:
 [1] CHOL_CNASNP-20160128: RaggedExperiment with 39698 rows and 85 columns
 [2] CHOL_CNVSNP-20160128: RaggedExperiment with 7570 rows and 85 columns
 [3] CHOL_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 36 columns
 [4] CHOL_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 19 rows and 36 columns
 [5] CHOL_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 36 columns
 [6] CHOL_Mutation-20160128: RaggedExperiment with 6755 rows and 35 columns
 [7] CHOL_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 45 columns
 [8] CHOL_RPPAArray-20160128: SummarizedExperiment with 192 rows and 30 columns
 [9] CHOL_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 45 columns
[10] CHOL_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18002 rows and 45 columns
[11] CHOL_Methylation-20160128: SummarizedExperiment with 485577 rows and 45 columns

> rownames( CHOL )
CharacterList of length 11
[["CHOL_CNASNP-20160128"]] character(0)
[["CHOL_CNVSNP-20160128"]] character(0)
[["CHOL_GISTIC_AllByGene-20160128"]] character(0)
[["CHOL_GISTIC_Peaks-20160128"]] 4 1 5 6 7 8 9 10 ... 13 3 14 15 18 16 17 20
[["CHOL_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["CHOL_Mutation-20160128"]] character(0)
[["CHOL_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["CHOL_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["CHOL_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["CHOL_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
...
<1 more element>

> colnames( CHOL )
CharacterList of length 11
[["CHOL_CNASNP-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["CHOL_CNVSNP-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["CHOL_GISTIC_AllByGene-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["CHOL_GISTIC_Peaks-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["CHOL_GISTIC_ThresholdedByGene-20160128"]] TCGA-3X-AAV9-01A-72D-A416-01 ...
[["CHOL_Mutation-20160128"]] TCGA-3X-AAV9-01A-72D-A417-09 ...
[["CHOL_RNASeq2Gene-20160128"]] TCGA-3X-AAV9-01A-72R-A41I-07 ...

```

```

[["CHOL_RPPAArray-20160128"]] TCGA-3X-AAV9-01A-81-A45N-20 ...
[["CHOL_miRNASeqGene-20160128"]] TCGA-3X-AAV9-01A-72R-A41D-13 ...
[["CHOL_RNASeq2GeneNorm-20160128"]] TCGA-3X-AAV9-01 ... TCGA-ZU-A8S4-01
...
<1 more element>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | CHOL_CNASNP-20160128 | 1.1 Mb |
| 2 | CHOL_CNVSNP-20160128 | 0.2 Mb |
| 3 | CHOL_GISTIC_AllByGene-20160128 | 10.2 Mb |
| 4 | CHOL_GISTIC_Peaks-20160128 | 0 Mb |
| 5 | CHOL_GISTIC_ThresholdedByGene-20160128 | 10.1 Mb |
| 6 | CHOL_Mutation-20160128 | 4.6 Mb |
| 7 | CHOL_RNASeq2Gene-20160128 | 9.6 Mb |
| 8 | CHOL_RPPAArray-20160128 | 0.1 Mb |
| 9 | CHOL_miRNASeqGene-20160128 | 0.5 Mb |
| 10 | CHOL_RNASeq2GeneNorm-20160128 | 8.4 Mb |
| 11 | CHOL_Methylation-20160128 | 75 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
[1,] 18 18 1.37 0.742 2.53

```

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 |

histological_type:

| | |
|-------------------------------------|----|
| cholangiocarcinoma; distal | 2 |
| cholangiocarcinoma; hilar/perihilar | 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 | <i>Colon adenocarcinoma</i> |
|------|-----------------------------|

Description

A document describing the TCGA cancer code

Details

```
> experiments( COAD )
ExperimentList class object of length 14:
 [1] COAD_CNASeq-20160128: RaggedExperiment with 40530 rows and 136 columns
 [2] COAD_CNASNP-20160128: RaggedExperiment with 459490 rows and 914 columns
 [3] COAD_CNVSNP-20160128: RaggedExperiment with 90534 rows and 914 columns
 [4] COAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 449 columns
 [5] COAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 66 rows and 449 columns
 [6] COAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 449 columns
 [7] COAD_miRNASeqGene-20160128: SummarizedExperiment with 705 rows and 221 columns
 [8] COAD_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 172 columns
 [9] COAD_Mutation-20160128: RaggedExperiment with 62530 rows and 154 columns
 [10] COAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 191 columns
 [11] COAD_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 10 columns
 [12] COAD_RPPAArray-20160128: SummarizedExperiment with 208 rows and 360 columns
 [13] COAD_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 202 columns
 [14] COAD_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 333 columns

> rownames( COAD )
CharacterList of length 14
[["COAD_CNASeq-20160128"]] character(0)
[["COAD_CNASNP-20160128"]] character(0)
[["COAD_CNVSNP-20160128"]] character(0)
[["COAD_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["COAD_GISTIC_Peaks-20160128"]] chr1:26527443-27650365 ...
[["COAD_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["COAD_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["COAD_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["COAD_Mutation-20160128"]] character(0)
[["COAD_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
...
<4 more elements>
```

```

> colnames( COAD )
CharacterList of length 14
[["COAD_CNASeq-20160128"]] TCGA-A6-2671-01A-01D-1405-02 ...
[["COAD_CNASNP-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["COAD_CNVSNP-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["COAD_GISTIC_AllByGene-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["COAD_GISTIC_Peaks-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["COAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["COAD_miRNASeqGene-20160128"]] TCGA-A6-2675-01A-02T-1722-13 ...
[["COAD_mRNAArray-20160128"]] TCGA-A6-2671-11A-01R-1758-07 ...
[["COAD_Mutation-20160128"]] TCGA-A6-2672-01A-01W-0833-10 ...
[["COAD_RNASeq2GeneNorm-20160128"]] TCGA-A6-2671-01A-01R-1410-07 ...
...
<4 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | COAD_CNASeq-20160128 | 1.1 Mb |
| 2 | COAD_CNASNP-20160128 | 12.5 Mb |
| 3 | COAD_CNVSNP-20160128 | 2.7 Mb |
| 4 | COAD_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | COAD_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | COAD_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | COAD_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | COAD_mRNAArray-20160128 | 1.1 Mb |
| 9 | COAD_Mutation-20160128 | 23.6 Mb |
| 10 | COAD_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 11 | COAD_RNASeqGene-20160128 | 1.3 Mb |
| 12 | COAD_RPPAArray-20160128 | 0 Mb |
| 13 | COAD_Methylation_methyl27-20160128 | 4.9 Mb |
| 14 | COAD_Methylation_methyl450-20160128 | 75 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

See Also

[COAD-v2.0.1](#)

COAD-v2.0.1

Colon adenocarcinoma

Description

A document describing the TCGA cancer code

Details

```

> experiments( COAD )
ExperimentList class object of length 16:
 [1] COAD_CNASeq-20160128: RaggedExperiment with 40530 rows and 136 columns
 [2] COAD_CNASNP-20160128: RaggedExperiment with 459490 rows and 914 columns
 [3] COAD_CNVSNP-20160128: RaggedExperiment with 90534 rows and 914 columns
 [4] COAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 449 columns

```



```

[5] COAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 66 rows and 449 columns
[6] COAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 449 columns
[7] COAD_miRNASeqGene-20160128: SummarizedExperiment with 705 rows and 221 columns
[8] COAD_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 172 columns
[9] COAD_Mutation-20160128: RaggedExperiment with 62530 rows and 154 columns
[10] COAD_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 326 columns
[11] COAD_RNASeq2GeneNorm_illumina-20160128: SummarizedExperiment with 20501 rows and 191 columns
[12] COAD_RNASeq2GeneNorm_illuminahisec-20160128: SummarizedExperiment with 20501 rows and 326 columns
[13] COAD_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 10 columns
[14] COAD_RPPAArray-20160128: SummarizedExperiment with 208 rows and 360 columns
[15] COAD_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 202 columns
[16] COAD_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 333 columns

```

```

> rownames( COAD )
CharacterList of length 16
[["COAD_CNASeq-20160128"]] character(0)
[["COAD_CNASNP-20160128"]] character(0)
[["COAD_CNVSNP-20160128"]] character(0)
[["COAD_GISTIC_AllByGene-20160128"]] character(0)
[["COAD_GISTIC_Peaks-20160128"]] 23 24 25 26 27 1 28 ... 18 19 20 21 22 65 66
[["COAD_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["COAD_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["COAD_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["COAD_Mutation-20160128"]] character(0)
[["COAD_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
...
<6 more elements>

```

```

> colnames( COAD )
CharacterList of length 16
[["COAD_CNASeq-20160128"]] TCGA-A6-2671-01A-01D-1405-02 ...
[["COAD_CNASNP-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["COAD_CNVSNP-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["COAD_GISTIC_AllByGene-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["COAD_GISTIC_Peaks-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["COAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["COAD_miRNASeqGene-20160128"]] TCGA-A6-2675-01A-02T-1722-13 ...
[["COAD_mRNAArray-20160128"]] TCGA-A6-2671-11A-01R-1758-07 ...
[["COAD_Mutation-20160128"]] TCGA-A6-2672-01A-01W-0833-10 ...
[["COAD_RNASeq2Gene-20160128"]] TCGA-3L-AA1B-01A-11R-A37K-07 ...
...
<6 more elements>

```

Sizes of each ExperimentList element:

| | assay size.Mb |
|---|------------------------------|
| 1 | COAD_CNASeq-20160128 1.1 Mb |
| 2 | COAD_CNASNP-20160128 12.5 Mb |

| | | |
|----|---|---------|
| 3 | COAD_CNVSNP-20160128 | 2.7 Mb |
| 4 | COAD_GISTIC_AllByGene-20160128 | 88.5 Mb |
| 5 | COAD_GISTIC_Peaks-20160128 | 0.4 Mb |
| 6 | COAD_GISTIC_ThresholdedByGene-20160128 | 88.3 Mb |
| 7 | COAD_miRNASeqGene-20160128 | 1.3 Mb |
| 8 | COAD_mRNAArray-20160128 | 25.6 Mb |
| 9 | COAD_Mutation-20160128 | 23.6 Mb |
| 10 | COAD_RNASeq2Gene-20160128 | 53.6 Mb |
| 11 | COAD_RNASeq2GeneNorm_illumina-20160128 | 32.5 Mb |
| 12 | COAD_RNASeq2GeneNorm_illuminahisec-20160128 | 53.6 Mb |
| 13 | COAD_RNASeqGene-20160128 | 4.1 Mb |
| 14 | COAD_RPPAArray-20160128 | 0.7 Mb |
| 15 | COAD_Methylation_methyl27-20160128 | 4.9 Mb |
| 16 | COAD_Methylation_methyl450-20160128 | 75 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 | 1 | asian | 11 |
| black or african american | | white | |

```

59
NA's
173

```

```

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

```

Including an additional 2604 columns

COAD-v2.1.0 *Colon adenocarcinoma*

Description

A document describing the TCGA cancer code

Details

```

> experiments( COAD )
ExperimentList class object of length 17:
 [1] COAD_CNASeq-20160128: RaggedExperiment with 40530 rows and 136 columns
 [2] COAD_CNASNP-20160128: RaggedExperiment with 459490 rows and 914 columns
 [3] COAD_CNVSNP-20160128: RaggedExperiment with 90534 rows and 914 columns
 [4] COAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 449 columns
 [5] COAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 66 rows and 449 columns
 [6] COAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 449 columns
 [7] COAD_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 172 columns
 [8] COAD_Mutation-20160128: RaggedExperiment with 62530 rows and 154 columns
 [9] COAD_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 326 columns
[10] COAD_RNASeq2GeneNorm_illumina-20160128: SummarizedExperiment with 20501 rows and 191 columns
[11] COAD_RNASeq2GeneNorm_illumina-hiseq-20160128: SummarizedExperiment with 20501 rows and 326 columns
[12] COAD_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 10 columns
[13] COAD_RPPAArray-20160128: SummarizedExperiment with 208 rows and 360 columns
[14] COAD_miRNASeqGene-20160128: SummarizedExperiment with 705 rows and 221 columns
[15] COAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18025 rows and 498 columns
[16] COAD_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 202 columns
[17] COAD_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 333 columns

> rownames( COAD )
CharacterList of length 17
[["COAD_CNASeq-20160128"]] character(0)
[["COAD_CNASNP-20160128"]] character(0)
[["COAD_CNVSNP-20160128"]] character(0)
[["COAD_GISTIC_AllByGene-20160128"]] character(0)
[["COAD_GISTIC_Peaks-20160128"]] 23 24 25 26 27 1 28 ... 18 19 20 21 22 65 66
[["COAD_GISTIC_ThresholdedByGene-20160128"]] character(0)

```

```

[["COAD_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["COAD_Mutation-20160128"]] character(0)
[["COAD_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
[["COAD_RNASeq2GeneNorm_illumina-20160128"]] A1BG A1CF ... psiTPTE22 TAKR
...
<7 more elements>

```

```

> colnames( COAD )
CharacterList of length 17
[["COAD_CNASeq-20160128"]] TCGA-A6-2671-01A-01D-1405-02 ...
[["COAD_CNASNP-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["COAD_CNVSNP-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["COAD_GISTIC_AllByGene-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["COAD_GISTIC_Peaks-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["COAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-3L-AA1B-01A-11D-A36W-01 ...
[["COAD_mRNAArray-20160128"]] TCGA-A6-2671-11A-01R-1758-07 ...
[["COAD_Mutation-20160128"]] TCGA-A6-2672-01A-01W-0833-10 ...
[["COAD_RNASeq2Gene-20160128"]] TCGA-3L-AA1B-01A-11R-A37K-07 ...
[["COAD_RNASeq2GeneNorm_illumina-20160128"]] TCGA-A6-2671-01A-01R-1410-07...
...
<7 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|---|---------------|
| 1 | COAD_CNASeq-20160128 | 1.1 Mb |
| 2 | COAD_CNASNP-20160128 | 12.5 Mb |
| 3 | COAD_CNVSNP-20160128 | 2.7 Mb |
| 4 | COAD_GISTIC_AllByGene-20160128 | 88.5 Mb |
| 5 | COAD_GISTIC_Peaks-20160128 | 0.4 Mb |
| 6 | COAD_GISTIC_ThresholdedByGene-20160128 | 88.3 Mb |
| 7 | COAD_mRNAArray-20160128 | 25.6 Mb |
| 8 | COAD_Mutation-20160128 | 23.6 Mb |
| 9 | COAD_RNASeq2Gene-20160128 | 53.6 Mb |
| 10 | COAD_RNASeq2GeneNorm_illumina-20160128 | 32.5 Mb |
| 11 | COAD_RNASeq2GeneNorm_illuminahisec-20160128 | 53.6 Mb |
| 12 | COAD_RNASeqGene-20160128 | 4.1 Mb |
| 13 | COAD_RPPAArray-20160128 | 0.7 Mb |
| 14 | COAD_miRNASeqGene-20160128 | 1.3 Mb |
| 15 | COAD_RNASeq2GeneNorm-20160128 | 70.8 Mb |
| 16 | COAD_Methylation_methyl27-20160128 | 4.9 Mb |
| 17 | COAD_Methylation_methyl450-20160128 | 75 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

curatedTCGAData assembles data on-the-fly from ExperimentHub to provide cohesive [MultiAssayExperiment](#) container objects. All the user has to do is to provide TCGA disease code(s) and assay types. It is highly recommended to use the companion package TCGAutils, developed to work with TCGA data specifically from curatedTCGAData and some flat files.

Usage

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

Arguments

| | | |
|-------------|--------------|--|
| diseaseCode | character() | A vector of TCGA cancer cohort codes (e.g., COAD) |
| assays | character() | A vector of TCGA assays, glob matches allowed; see below for more details |
| version | character(1) | One of 1.1.38, 2.0.1, 2.1.0, or 2.1.1 indicating the data version to obtain from ExperimentHub. Version 2.1.1 includes various improvements as well as the addition of the RNASeq2Gene assay and subtype updates. See version section details. |
| dry.run | logical(1) | Whether to return the dataset names before actual download (default TRUE) |
| verbose | logical(1) | Whether to show the dataset currently being (down)loaded (default TRUE) |
| ... | | Additional arguments passed on to the ExperimentHub constructor |

Details

This function will check against available resources in ExperimentHub. Only the latest runDate ("2016-01-28") is supported. Use the `dry.run = FALSE` to download remote datasets and build an integrative [MultiAssayExperiment](#) object. For a list of 'diseaseCodes', see the [curatedTCGAData-package](#) help page.

Value

a [MultiAssayExperiment](#) of the specified assays and cancer codes or informative data.frame of resources when `dry.run` is TRUE

Available Assays

Below is a list of partial ExperimentList assay names and their respective description. These assays can be entered as part of the assays argument in the main function. Partial glob matches are allowed such as: 'CN*' for "CNASeq", "CNASNP", "CNVSNP" assays. Credit: Ludwig G.

| ExperimentList data types | Description |
|---------------------------|-------------|
|---------------------------|-------------|

SummarizedExperiment*

| | |
|---|--|
| RNASeqGene | Gene expression values |
| RNASeq2Gene | RSEM TPM gene expression values |
| RNASeq2GeneNorm | Upper quartile log2 normalized RSEM TPM gene expression values |
| miRNAArray | Probe-level miRNA expression values |
| miRNASeqGene | Gene-level log2 RPM miRNA expression values |
| mRNAArray | Unified gene-level mRNA expression values |
| mRNAArray_huex | Gene-level mRNA expression values from Affymetrix Human Exon Array |
| mRNAArray_TX_g4502a | Gene-level mRNA expression values from Agilent 244K Array |
| mRNAArray_TX_ht_hg_u133a | Gene-level mRNA expression values from Affymetrix Human Genome U133 Array |
| GISTIC_AllByGene | Gene-level GISTIC2 copy number values |
| GISTIC_ThresholdedByGene | Gene-level GISTIC2 thresholded discrete copy number values |
| RPPAArray | Reverse Phase Protein Array normalized protein expression values |
| RangedSummarizedExperiment | |
| GISTIC_Peaks | GISTIC2 thresholded discrete copy number values in recurrent peak regions |
| SummarizedExperiment with HDF5Array DelayedMatrix | |
| Methylation_methyl27 | Probe-level methylation beta values from Illumina HumanMethylation 27K BeadChip |
| Methylation_methyl450 | Probe-level methylation beta values from Infinium HumanMethylation 450K BeadChip |
| RaggedExperiment | |
| CNASNP | Segmented somatic Copy Number Alteration calls from SNP array |
| CNVSNP | Segmented germline Copy Number Variant calls from SNP Array |
| CNASeq | Segmented somatic Copy Number Alteration calls from low pass DNA Sequencing |
| Mutation* | Somatic mutations calls |
| CNACGH_CGH_hg_244a | Segmented somatic Copy Number Alteration calls from CGH Agilent Microarray 244A |
| CNACGH_CGH_hg_415k_g4124a | Segmented somatic Copy Number Alteration calls from CGH Agilent Microarray 415K |

* All can be converted to RangedSummarizedExperiment (except RPPAArray) with TCGAutils

version

Version 2.1.1 provides a couple of corrections to the colData for ovarian cancer (OV) and skin cancer (SKCM). In these new data, the cancer subtype variables are fully available. One get obtain the mapping of columns to subtypes in the colData with the getSubtypeMap function in TCGAutils.

Version 2.1.0 provides gene-level log2 RPM miRNA expression values for miRNASeqGene data

log2 normalized RSEM for RNASeq2GeneNorm assays. Previously, the data provided were read counts and normalized counts, respectively. See issue [#53 on GitHub](#) for additional details.

The new version 2.0.1 includes various improvements including an additional assay that provides RNASeq2Gene data as RSEM TPM gene expression values (issue #38). Additional changes include genomic information for RaggedExperiment type data objects where '37' is now 'GRCh37' as reported in issue #40. Datasets (e.g., OV, GBM) that contain multiple assays that could be merged are now provided as merged assays (issue #27). We corrected an issue where mRNAArray assays were returning DataFrames instead of matrix type data (issue #31). Version 1.1.38 provides the original run of curatedTCGAData and is provided due to legacy reasons.

See Also

curatedTCGAData-package

Examples

```
curatedTCGAData(
  diseaseCode = c("GBM", "ACC"), assays = "CNASNP", version = "2.0.1"
)

curatedTCGAData("BRCA", "GISTIC*", "2.0.1")
```

DLBC

Lymphoid Neoplasm Diffuse Large B-cell Lymphoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( DLBC )
ExperimentList class object of length 10:
 [1] DLBC_CNASNP-20160128: RaggedExperiment with 44725 rows and 94 columns
 [2] DLBC_CNVSNP-20160128: RaggedExperiment with 9343 rows and 94 columns
 [3] DLBC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 48 columns
 [4] DLBC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 39 rows and 48 columns
 [5] DLBC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 48 columns
 [6] DLBC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 47 columns
 [7] DLBC_Mutation-20160128: RaggedExperiment with 16918 rows and 48 columns
 [8] DLBC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 48 columns
 [9] DLBC_RPPAArray-20160128: SummarizedExperiment with 192 rows and 33 columns
 [10] DLBC_Methylation-20160128: SummarizedExperiment with 485577 rows and 48 columns

> rownames( DLBC )
CharacterList of length 10
```



```

[["DLBC_CNASNP-20160128"]] character(0)
[["DLBC_CNVSNP-20160128"]] character(0)
[["DLBC_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["DLBC_GISTIC_Peaks-20160128"]] chr1:1-48649489 ... chr22:41635693-51304566
[["DLBC_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["DLBC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["DLBC_Mutation-20160128"]] character(0)
[["DLBC_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["DLBC_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["DLBC_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873

```

```

> colnames( DLBC )
CharacterList of length 10
[["DLBC_CNASNP-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["DLBC_CNVSNP-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["DLBC_GISTIC_AllByGene-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["DLBC_GISTIC_Peaks-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["DLBC_GISTIC_ThresholdedByGene-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["DLBC_miRNASeqGene-20160128"]] TCGA-FA-8693-01A-11R-2401-13 ...
[["DLBC_Mutation-20160128"]] TCGA-FA-8693-01A-11D-2397-10 ...
[["DLBC_RNASeq2GeneNorm-20160128"]] TCGA-FA-8693-01A-11R-2404-07 ...
[["DLBC_RPPAArray-20160128"]] TCGA-FA-8693-01A-21-A45K-20 ...
[["DLBC_Methylation-20160128"]] TCGA-FA-8693-01A-11D-2399-05 ...

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | DLBC_CNASNP-20160128 | 1.2 Mb |
| 2 | DLBC_CNVSNP-20160128 | 0.3 Mb |
| 3 | DLBC_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | DLBC_GISTIC_Peaks-20160128 | 0 Mb |
| 5 | DLBC_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | DLBC_miRNASeqGene-20160128 | 0.1 Mb |
| 7 | DLBC_Mutation-20160128 | 12.6 Mb |
| 8 | DLBC_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 9 | DLBC_RPPAArray-20160128 | 0 Mb |
| 10 | DLBC_Methylation-20160128 | 75 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 | 29 |

ethnicity:

hispanic or latino not hispanic or latino
 12 36

Including an additional 607 columns

See Also

[DLBC-v2.0.1](#)

DLBC-v2.0.1

Lymphoid Neoplasm Diffuse Large B-cell Lymphoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( DLBC )
ExperimentList class object of length 11:
 [1] DLBC_CNASNP-20160128: RaggedExperiment with 44725 rows and 94 columns
 [2] DLBC_CNVSNP-20160128: RaggedExperiment with 9343 rows and 94 columns
 [3] DLBC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 48 columns
 [4] DLBC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 39 rows and 48 columns
 [5] DLBC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 48 columns
 [6] DLBC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 47 columns
 [7] DLBC_Mutation-20160128: RaggedExperiment with 16918 rows and 48 columns
 [8] DLBC_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 48 columns
 [9] DLBC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 48 columns
 [10] DLBC_RPPAArray-20160128: SummarizedExperiment with 192 rows and 33 columns
 [11] DLBC_Methylation-20160128: SummarizedExperiment with 485577 rows and 48 columns

> rownames( DLBC )
CharacterList of length 11
[["DLBC_CNASNP-20160128"]] character(0)
[["DLBC_CNVSNP-20160128"]] character(0)
[["DLBC_GISTIC_AllByGene-20160128"]] character(0)
[["DLBC_GISTIC_Peaks-20160128"]] 15 17 16 1 2 18 19 ... 36 37 12 38 39 13 40
[["DLBC_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["DLBC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["DLBC_Mutation-20160128"]] character(0)
[["DLBC_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["DLBC_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["DLBC_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<1 more element>
```

```
> colnames( DLBC )
CharacterList of length 11
[["DLBC_CNASNP-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["DLBC_CNVSNP-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["DLBC_GISTIC_AllByGene-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["DLBC_GISTIC_Peaks-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["DLBC_GISTIC_ThresholdedByGene-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["DLBC_miRNASeqGene-20160128"]] TCGA-FA-8693-01A-11R-2401-13 ...
[["DLBC_Mutation-20160128"]] TCGA-FA-8693-01A-11D-2397-10 ...
[["DLBC_RNASeq2Gene-20160128"]] TCGA-FA-8693-01A-11R-2404-07 ...
[["DLBC_RNASeq2GeneNorm-20160128"]] TCGA-FA-8693-01A-11R-2404-07 ...
[["DLBC_RPPAArray-20160128"]] TCGA-FA-8693-01A-21-A45K-20 ...
...
<1 more element>
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | DLBC_CNASNP-20160128 | 1.2 Mb |
| 2 | DLBC_CNVSNP-20160128 | 0.3 Mb |
| 3 | DLBC_GISTIC_AllByGene-20160128 | 12.5 Mb |
| 4 | DLBC_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | DLBC_GISTIC_ThresholdedByGene-20160128 | 12.4 Mb |
| 6 | DLBC_miRNASeqGene-20160128 | 0.5 Mb |
| 7 | DLBC_Mutation-20160128 | 12.6 Mb |
| 8 | DLBC_RNASeq2Gene-20160128 | 10.1 Mb |
| 9 | DLBC_RNASeq2GeneNorm-20160128 | 10.1 Mb |
| 10 | DLBC_RPPAArray-20160128 | 0.1 Mb |
| 11 | DLBC_Methylation-20160128 | 75 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

18 1

white

29

ethnicity:

hispanic or latino not hispanic or latino

12 36

Including an additional 607 columns

Description

A document describing the TCGA cancer code

Details

```

> experiments( DLBC )
ExperimentList class object of length 11:
 [1] DLBC_CNASNP-20160128: RaggedExperiment with 44725 rows and 94 columns
 [2] DLBC_CNVSNP-20160128: RaggedExperiment with 9343 rows and 94 columns
 [3] DLBC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 48 columns
 [4] DLBC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 39 rows and 48 columns
 [5] DLBC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 48 columns
 [6] DLBC_Mutation-20160128: RaggedExperiment with 16918 rows and 48 columns
 [7] DLBC_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 48 columns
 [8] DLBC_RPPAArray-20160128: SummarizedExperiment with 192 rows and 33 columns
 [9] DLBC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 47 columns
[10] DLBC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 17665 rows and 48 columns
[11] DLBC_Methylation-20160128: SummarizedExperiment with 485577 rows and 48 columns

> rownames( DLBC )
CharacterList of length 11
[["DLBC_CNASNP-20160128"]] character(0)
[["DLBC_CNVSNP-20160128"]] character(0)
[["DLBC_GISTIC_AllByGene-20160128"]] character(0)
[["DLBC_GISTIC_Peaks-20160128"]] 15 17 16 1 2 18 19 ... 36 37 12 38 39 13 40
[["DLBC_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["DLBC_Mutation-20160128"]] character(0)
[["DLBC_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["DLBC_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["DLBC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["DLBC_RNASeq2GeneNorm-20160128"]] A1BG A2LD1 A2ML1 ... ZZEF1 ZZZ3 psiTPTE22
...
<1 more element>

> colnames( DLBC )
CharacterList of length 11
[["DLBC_CNASNP-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["DLBC_CNVSNP-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["DLBC_GISTIC_AllByGene-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["DLBC_GISTIC_Peaks-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["DLBC_GISTIC_ThresholdedByGene-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["DLBC_Mutation-20160128"]] TCGA-FA-8693-01A-11D-2397-10 ...
[["DLBC_RNASeq2Gene-20160128"]] TCGA-FA-8693-01A-11R-2404-07 ...
[["DLBC_RPPAArray-20160128"]] TCGA-FA-8693-01A-21-A45K-20 ...
[["DLBC_miRNASeqGene-20160128"]] TCGA-FA-8693-01A-11R-2401-13 ...
[["DLBC_RNASeq2GeneNorm-20160128"]] TCGA-FA-8693-01 ... TCGA-VB-A8QN-01
...
<1 more element>

```

Sizes of each ExperimentList element:

| | | assay | size.Mb |
|----|--|-------|---------|
| 1 | DLBC_CNASNP-20160128 | | 1.2 Mb |
| 2 | DLBC_CNVSNP-20160128 | | 0.3 Mb |
| 3 | DLBC_GISTIC_AllByGene-20160128 | | 12.5 Mb |
| 4 | DLBC_GISTIC_Peaks-20160128 | | 0.1 Mb |
| 5 | DLBC_GISTIC_ThresholdedByGene-20160128 | | 12.4 Mb |
| 6 | DLBC_Mutation-20160128 | | 12.6 Mb |
| 7 | DLBC_RNASeq2Gene-20160128 | | 10.1 Mb |
| 8 | DLBC_RPPAArray-20160128 | | 0.1 Mb |
| 9 | DLBC_miRNASeqGene-20160128 | | 0.5 Mb |
| 10 | DLBC_RNASeq2GeneNorm-20160128 | | 8.7 Mb |
| 11 | DLBC_Methylation-20160128 | | 75 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
[1,] 9 9 1.63 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
                                     18                                     1
                                                                                                     white
                                                                                                     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 12:
 [1] ESCA_CNASeq-20160128: RaggedExperiment with 17059 rows and 104 columns
 [2] ESCA_CNASNP-20160128: RaggedExperiment with 203186 rows and 373 columns
 [3] ESCA_CNVSNP-20160128: RaggedExperiment with 60803 rows and 373 columns
 [4] ESCA_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [5] ESCA_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 77 rows and 184 columns

```



```
[6] ESCA_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
[7] ESCA_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 198 columns
[8] ESCA_Mutation-20160128: RaggedExperiment with 58602 rows and 185 columns
[9] ESCA_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 196 columns
[10] ESCA_RNASeqGene-20160128: SummarizedExperiment with 26120 rows and 198 columns
[11] ESCA_RPPAArray-20160128: SummarizedExperiment with 192 rows and 126 columns
[12] ESCA_Methylation-20160128: SummarizedExperiment with 485577 rows and 202 columns
```

```
> rownames( ESCA )
CharacterList of length 12
[["ESCA_CNASeq-20160128"]] character(0)
[["ESCA_CNASNP-20160128"]] character(0)
[["ESCA_CNVSNP-20160128"]] character(0)
[["ESCA_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["ESCA_GISTIC_Peaks-20160128"]] chr1:23960869-31653987 ... chr22:1-18218209
[["ESCA_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["ESCA_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["ESCA_Mutation-20160128"]] character(0)
[["ESCA_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1... ZZZ3 psiTPTE22 tAKR
[["ESCA_RNASeqGene-20160128"]] AADACL3 AADACL4 AB007962 ... VCY XKRY ZFY
...
<2 more elements>
```

```
> colnames( ESCA )
CharacterList of length 12
[["ESCA_CNASeq-20160128"]] TCGA-IG-A3I8-01A-11D-A248-26 ...
[["ESCA_CNASNP-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["ESCA_CNVSNP-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["ESCA_GISTIC_AllByGene-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["ESCA_GISTIC_Peaks-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["ESCA_GISTIC_ThresholdedByGene-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["ESCA_miRNASeqGene-20160128"]] TCGA-2H-A9GF-01A-11R-A37J-13 ...
[["ESCA_Mutation-20160128"]] TCGA-2H-A9GF-01A-11D-A37C-09 ...
[["ESCA_RNASeq2GeneNorm-20160128"]] TCGA-2H-A9GF-01A-11R-A37I-31 ...
[["ESCA_RNASeqGene-20160128"]] TCGA-2H-A9GF-01A-11R-A37I-31 ...
...
<2 more elements>
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|---|--|---------------|
| 1 | ESCA_CNASeq-20160128 | 0.5 Mb |
| 2 | ESCA_CNASNP-20160128 | 5.5 Mb |
| 3 | ESCA_CNVSNP-20160128 | 1.7 Mb |
| 4 | ESCA_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | ESCA_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | ESCA_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | ESCA_miRNASeqGene-20160128 | 0.1 Mb |

| | | |
|----|-------------------------------|--------|
| 8 | ESCA_Mutation-20160128 | 45 Mb |
| 9 | ESCA_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 10 | ESCA_RNASeqGene-20160128 | 1.7 Mb |
| 11 | ESCA_RPPAArray-20160128 | 0 Mb |
| 12 | ESCA_Methylation-20160128 | 75 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
                                46                                5
                                NA's
                                20
                                white
                                114

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

```

Including an additional 940 columns

See Also

[ESCA-v2.0.1](#)

 ESCA-v2.0.1

Esophageal carcinoma

Description

A document describing the TCGA cancer code

Details

```

> experiments( ESCA )
ExperimentList class object of length 13:
 [1] ESCA_CNASeq-20160128: RaggedExperiment with 17059 rows and 104 columns
 [2] ESCA_CNASNP-20160128: RaggedExperiment with 203186 rows and 373 columns
 [3] ESCA_CNVSNP-20160128: RaggedExperiment with 60803 rows and 373 columns
 [4] ESCA_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [5] ESCA_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 77 rows and 184 columns
 [6] ESCA_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [7] ESCA_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 198 columns
 [8] ESCA_Mutation-20160128: RaggedExperiment with 58602 rows and 185 columns
 [9] ESCA_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 196 columns
 [10] ESCA_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 196 columns
 [11] ESCA_RNASeqGene-20160128: SummarizedExperiment with 26120 rows and 198 columns
 [12] ESCA_RPPAArray-20160128: SummarizedExperiment with 192 rows and 126 columns
 [13] ESCA_Methylation-20160128: SummarizedExperiment with 485577 rows and 202 columns

> rownames( ESCA )
CharacterList of length 13
[["ESCA_CNASeq-20160128"]] character(0)
[["ESCA_CNASNP-20160128"]] character(0)
[["ESCA_CNVSNP-20160128"]] character(0)
[["ESCA_GISTIC_AllByGene-20160128"]] character(0)
[["ESCA_GISTIC_Peaks-20160128"]] 31 1 32 2 3 33 4 34 ... 73 74 29 75 76 77 78
[["ESCA_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["ESCA_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["ESCA_Mutation-20160128"]] character(0)
[["ESCA_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["ESCA_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
...
<3 more elements>

> colnames( ESCA )
CharacterList of length 13
[["ESCA_CNASeq-20160128"]] TCGA-IG-A3I8-01A-11D-A248-26 ...
[["ESCA_CNASNP-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["ESCA_CNVSNP-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["ESCA_GISTIC_AllByGene-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["ESCA_GISTIC_Peaks-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...

```

```

[["ESCA_GISTIC_ThresholdedByGene-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["ESCA_miRNASeqGene-20160128"]] TCGA-2H-A9GF-01A-11R-A37J-13 ...
[["ESCA_Mutation-20160128"]] TCGA-2H-A9GF-01A-11D-A37C-09 ...
[["ESCA_RNASeq2Gene-20160128"]] TCGA-2H-A9GF-01A-11R-A37I-31 ...
[["ESCA_RNASeq2GeneNorm-20160128"]] TCGA-2H-A9GF-01A-11R-A37I-31 ...
...
<3 more elements>

```

Sizes of each ExperimentList element:

| | | assay | size.Mb |
|----|--|----------------------------|---------|
| 1 | | ESCA_CNASeq-20160128 | 0.5 Mb |
| 2 | | ESCA_CNASNP-20160128 | 5.5 Mb |
| 3 | | ESCA_CNVSNP-20160128 | 1.7 Mb |
| 4 | ESCA_GISTIC_AllByGene-20160128 | | 38.3 Mb |
| 5 | | ESCA_GISTIC_Peaks-20160128 | 0.2 Mb |
| 6 | ESCA_GISTIC_ThresholdedByGene-20160128 | | 38.1 Mb |
| 7 | | ESCA_miRNASeqGene-20160128 | 1.8 Mb |
| 8 | | ESCA_Mutation-20160128 | 45 Mb |
| 9 | | ESCA_RNASeq2Gene-20160128 | 33.2 Mb |
| 10 | ESCA_RNASeq2GeneNorm-20160128 | | 33.2 Mb |
| 11 | | ESCA_RNASeqGene-20160128 | 42.8 Mb |
| 12 | | ESCA_RPPAArray-20160128 | 0.2 Mb |
| 13 | | ESCA_Methylation-20160128 | 75 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 | 89 | esophagus squamous cell carcinoma | 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

ESCA-v2.1.0

Esophageal carcinoma

Description

A document describing the TCGA cancer code

Details

```

> experiments( ESCA )
ExperimentList class object of length 13:
 [1] ESCA_CNASeq-20160128: RaggedExperiment with 17059 rows and 104 columns
 [2] ESCA_CNASNP-20160128: RaggedExperiment with 203186 rows and 373 columns
 [3] ESCA_CNVSNP-20160128: RaggedExperiment with 60803 rows and 373 columns
 [4] ESCA_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [5] ESCA_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 77 rows and 184 columns
 [6] ESCA_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [7] ESCA_Mutation-20160128: RaggedExperiment with 58602 rows and 185 columns
 [8] ESCA_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 196 columns
 [9] ESCA_RNASeqGene-20160128: SummarizedExperiment with 26120 rows and 198 columns
[10] ESCA_RPPAArray-20160128: SummarizedExperiment with 192 rows and 126 columns
[11] ESCA_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 198 columns
[12] ESCA_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18730 rows and 196 columns
[13] ESCA_Methylation-20160128: SummarizedExperiment with 485577 rows and 202 columns

> rownames( ESCA )
CharacterList of length 13
[["ESCA_CNASeq-20160128"]] character(0)
[["ESCA_CNASNP-20160128"]] character(0)
[["ESCA_CNVSNP-20160128"]] character(0)
[["ESCA_GISTIC_AllByGene-20160128"]] character(0)

```

```

[["ESCA_GISTIC_Peaks-20160128"]] 31 1 32 2 3 33 4 34 ... 73 74 29 75 76 77 78
[["ESCA_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["ESCA_Mutation-20160128"]] character(0)
[["ESCA_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["ESCA_RNASeqGene-20160128"]] AADACL3 AADACL4 AB007962 ... VCY XKRY ZFY
[["ESCA_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<3 more elements>

```

```

> colnames( ESCA )
CharacterList of length 13
[["ESCA_CNASeq-20160128"]] TCGA-IG-A3I8-01A-11D-A248-26 ...
[["ESCA_CNASNP-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["ESCA_CNVSNP-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["ESCA_GISTIC_AllByGene-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["ESCA_GISTIC_Peaks-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["ESCA_GISTIC_ThresholdedByGene-20160128"]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[["ESCA_Mutation-20160128"]] TCGA-2H-A9GF-01A-11D-A37C-09 ...
[["ESCA_RNASeq2Gene-20160128"]] TCGA-2H-A9GF-01A-11R-A37I-31 ...
[["ESCA_RNASeqGene-20160128"]] TCGA-2H-A9GF-01A-11R-A37I-31 ...
[["ESCA_RPPAArray-20160128"]] TCGA-2H-A9GF-01A-21-A41Y-20 ...
...
<3 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | ESCA_CNASeq-20160128 | 0.5 Mb |
| 2 | ESCA_CNASNP-20160128 | 5.5 Mb |
| 3 | ESCA_CNVSNP-20160128 | 1.7 Mb |
| 4 | ESCA_GISTIC_AllByGene-20160128 | 38.3 Mb |
| 5 | ESCA_GISTIC_Peaks-20160128 | 0.2 Mb |
| 6 | ESCA_GISTIC_ThresholdedByGene-20160128 | 38.1 Mb |
| 7 | ESCA_Mutation-20160128 | 45 Mb |
| 8 | ESCA_RNASeq2Gene-20160128 | 33.2 Mb |
| 9 | ESCA_RNASeqGene-20160128 | 42.8 Mb |
| 10 | ESCA_RPPAArray-20160128 | 0.2 Mb |
| 11 | ESCA_miRNASeqGene-20160128 | 1.8 Mb |
| 12 | ESCA_RNASeq2GeneNorm-20160128 | 30.4 Mb |
| 13 | ESCA_Methylation-20160128 | 75 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
 [1,] 77 77 0.962 0.677 1.35

 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 | 46 | 5 | white |
| NA's | 20 | | 114 |

ethnicity:

| | | | |
|---|---|----|------|
| hispanic or latino not hispanic or latino | 6 | 88 | NA's |
| | | | 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 18:
[1] GBM_CNACGH_CGH_hg_244a-20160128: RaggedExperiment with 81512 rows and 438 columns
[2] GBM_CNACGH_CGH_hg_415k_g4124a-20160128: RaggedExperiment with 57975 rows and 338 columns
[3] GBM_CNASNP-20160128: RaggedExperiment with 602338 rows and 1104 columns
[4] GBM_CNVSNP-20160128: RaggedExperiment with 146852 rows and 1104 columns
```

```

[5] GBM_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 577 columns
[6] GBM_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 68 rows and 577 columns
[7] GBM_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 577 columns
[8] GBM_miRNAArray-20160128: SummarizedExperiment with 534 rows and 565 columns
[9] GBM_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 0 columns
[10] GBM_mRNAArray_huex-20160128: SummarizedExperiment with 18632 rows and 431 columns
[11] GBM_mRNAArray_TX_g4502a_1-20160128: SummarizedExperiment with 17814 rows and 401 columns
[12] GBM_mRNAArray_TX_g4502a-20160128: SummarizedExperiment with 17814 rows and 101 columns
[13] GBM_mRNAArray_TX_ht_hg_u133a-20160128: SummarizedExperiment with 12042 rows and 528 columns
[14] GBM_Mutation-20160128: RaggedExperiment with 22073 rows and 290 columns
[15] GBM_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 166 columns
[16] GBM_RPPAArray-20160128: SummarizedExperiment with 208 rows and 244 columns
[17] GBM_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 285 columns
[18] GBM_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 154 columns

```

```

> rownames( GBM )
CharacterList of length 18
[["GBM_CNACGH_CGH_hg_244a-20160128"]] character(0)
[["GBM_CNACGH_CGH_hg_415k_g4124a-20160128"]] character(0)
[["GBM_CNASNP-20160128"]] character(0)
[["GBM_CNVSNP-20160128"]] character(0)
[["GBM_GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GBM_GISTIC_Peaks-20160128"]] chr1:3394251-6475685 ...
[["GBM_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["GBM_miRNAArray-20160128"]] ebv-miR-BART1-3p ... kshv-miR-K12-9*
[["GBM_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["GBM_mRNAArray_huex-20160128"]] C9orf152 ELM02 RPS11 ... SLC39A6 CTSC AQP7
...
<8 more elements>

```

```

> colnames( GBM )
CharacterList of length 18
[["GBM_CNACGH_CGH_hg_244a-20160128"]] TCGA-02-0001-01C-01D-0185-02 ...
[["GBM_CNACGH_CGH_hg_415k_g4124a-20160128"]] TCGA-02-2466-01A-01D-0787-02 ...
[["GBM_CNASNP-20160128"]] TCGA-02-0001-01C-01D-0182-01 ...
[["GBM_CNVSNP-20160128"]] TCGA-02-0001-01C-01D-0182-01 ...
[["GBM_GISTIC_AllByGene-20160128"]] TCGA-02-0001-01C-01D-0182-01 ...
[["GBM_GISTIC_Peaks-20160128"]] TCGA-02-0001-01C-01D-0182-01 ...
[["GBM_GISTIC_ThresholdedByGene-20160128"]] TCGA-02-0001-01C-01D-0182-01 ...
[["GBM_miRNAArray-20160128"]] TCGA-02-0001-01C-01T-0179-07 ...
[["GBM_miRNASeqGene-20160128"]] character(0)
[["GBM_mRNAArray_huex-20160128"]] TCGA-02-0001-01C-01R-0178-03 ...
...
<8 more elements>

```

Sizes of each ExperimentList element:

assay size.Mb

| | | |
|----|--|---------|
| 1 | GBM_CNACGH_CGH_hg_244a-20160128 | 2.3 Mb |
| 2 | GBM_CNACGH_CGH_hg_415k_g4124a-20160128 | 1.7 Mb |
| 3 | GBM_CNASNP-20160128 | 16.4 Mb |
| 4 | GBM_CNVSNP-20160128 | 4.2 Mb |
| 5 | GBM_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 6 | GBM_GISTIC_Peaks-20160128 | 0.1 Mb |
| 7 | GBM_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 8 | GBM_miRNAArray-20160128 | 0.1 Mb |
| 9 | GBM_miRNASeqGene-20160128 | 0.1 Mb |
| 10 | GBM_mRNAArray_huex-20160128 | 1.2 Mb |
| 11 | GBM_mRNAArray_TX_g4502a_1-20160128 | 1.1 Mb |
| 12 | GBM_mRNAArray_TX_g4502a-20160128 | 1.1 Mb |
| 13 | GBM_mRNAArray_TX_ht_hg_u133a-20160128 | 0.8 Mb |
| 14 | GBM_Mutation-20160128 | 31 Mb |
| 15 | GBM_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 16 | GBM_RPPAArray-20160128 | 0 Mb |
| 17 | GBM_Methylation_methyl27-20160128 | 4.9 Mb |
| 18 | GBM_Methylation_methyl450-20160128 | 75 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

See Also

[GBM-v2.0.1](#)

Description

A document describing the TCGA cancer code

Details

```
> experiments( GBM )
ExperimentList class object of length 18:
 [1] GBM_CNACGH_CGH_hg_244a-20160128: RaggedExperiment with 81512 rows and 438 columns
 [2] GBM_CNACGH_CGH_hg_415k_g4124a-20160128: RaggedExperiment with 57975 rows and 338 columns
 [3] GBM_CNASNP-20160128: RaggedExperiment with 602338 rows and 1104 columns
 [4] GBM_CNVSNP-20160128: RaggedExperiment with 146852 rows and 1104 columns
 [5] GBM_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 577 columns
 [6] GBM_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 68 rows and 577 columns
 [7] GBM_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 577 columns
 [8] GBM_miRNAArray-20160128: SummarizedExperiment with 534 rows and 565 columns
 [9] GBM_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 0 columns
[10] GBM_mRNAArray_huex-20160128: SummarizedExperiment with 18632 rows and 431 columns
[11] GBM_mRNAArray_TX_g4502a-20160128: SummarizedExperiment with 17814 rows and 502 columns
[12] GBM_mRNAArray_TX_ht_hg_u133a-20160128: SummarizedExperiment with 12042 rows and 528 columns
[13] GBM_Mutation-20160128: RaggedExperiment with 22073 rows and 290 columns
[14] GBM_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 166 columns
[15] GBM_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 166 columns
[16] GBM_RPPAArray-20160128: SummarizedExperiment with 208 rows and 244 columns
[17] GBM_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 285 columns
[18] GBM_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 154 columns

> rownames( GBM )
CharacterList of length 18
[["GBM_CNACGH_CGH_hg_244a-20160128"]] character(0)
[["GBM_CNACGH_CGH_hg_415k_g4124a-20160128"]] character(0)
[["GBM_CNASNP-20160128"]] character(0)
[["GBM_CNVSNP-20160128"]] character(0)
[["GBM_GISTIC_AllByGene-20160128"]] character(0)
[["GBM_GISTIC_Peaks-20160128"]] 25 26 1 27 28 2 29 3 ... 65 22 23 66 67 24 68
[["GBM_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["GBM_miRNAArray-20160128"]] ebv-miR-BART1-3p ... kshv-miR-K12-9*
[["GBM_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["GBM_mRNAArray_huex-20160128"]] C9orf152 ELM02 RPS11 ... SLC39A6 CTSC AQP7
...
<8 more elements>

> colnames( GBM )
CharacterList of length 18
[["GBM_CNACGH_CGH_hg_244a-20160128"]] TCGA-02-0001-01C-01D-0185-02 ...
[["GBM_CNACGH_CGH_hg_415k_g4124a-20160128"]] TCGA-02-2466-01A-01D-0787-02 ...
[["GBM_CNASNP-20160128"]] TCGA-02-0001-01C-01D-0182-01 ...
[["GBM_CNVSNP-20160128"]] TCGA-02-0001-01C-01D-0182-01 ...
[["GBM_GISTIC_AllByGene-20160128"]] TCGA-02-0001-01C-01D-0182-01 ...
```

```

[["GBM_GISTIC_Peaks-20160128"]] TCGA-02-0001-01C-01D-0182-01 ...
[["GBM_GISTIC_ThresholdedByGene-20160128"]] TCGA-02-0001-01C-01D-0182-01 ...
[["GBM_miRNAArray-20160128"]] TCGA-02-0001-01C-01T-0179-07 ...
[["GBM_miRNASeqGene-20160128"]] character(0)
[["GBM_mRNAArray_huex-20160128"]] TCGA-02-0001-01C-01R-0178-03 ...
...
<8 more elements>

```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|----|--|----------|
| 1 | GBM_CNACGH_CGH_hg_244a-20160128 | 2.3 Mb |
| 2 | GBM_CNACGH_CGH_hg_415k_g4124a-20160128 | 1.7 Mb |
| 3 | GBM_CNASNP-20160128 | 16.4 Mb |
| 4 | GBM_CNVSNP-20160128 | 4.2 Mb |
| 5 | GBM_GISTIC_AllByGene-20160128 | 112.7 Mb |
| 6 | GBM_GISTIC_Peaks-20160128 | 0.5 Mb |
| 7 | GBM_GISTIC_ThresholdedByGene-20160128 | 112.5 Mb |
| 8 | GBM_miRNAArray-20160128 | 2.5 Mb |
| 9 | GBM_miRNASeqGene-20160128 | 0.2 Mb |
| 10 | GBM_mRNAArray_huex-20160128 | 63.7 Mb |
| 11 | GBM_mRNAArray_TX_g4502a-20160128 | 70.5 Mb |
| 12 | GBM_mRNAArray_TX_ht_hg_u133a-20160128 | 50.1 Mb |
| 13 | GBM_Mutation-20160128 | 31 Mb |
| 14 | GBM_RNASeq2Gene-20160128 | 28.5 Mb |
| 15 | GBM_RNASeq2GeneNorm-20160128 | 28.5 Mb |
| 16 | GBM_RPPAArray-20160128 | 0.5 Mb |
| 17 | GBM_Methylation_methyl27-20160128 | 4.9 Mb |
| 18 | GBM_Methylation_methyl450-20160128 | 75 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

 GBM-v2.1.0

Glioblastoma multiforme

Description

A document describing the TCGA cancer code

Details

```

> experiments( GBM )
ExperimentList class object of length 18:
 [1] GBM_CNACGH_CGH_hg_244a-20160128: RaggedExperiment with 81512 rows and 438 columns
 [2] GBM_CNACGH_CGH_hg_415k_g4124a-20160128: RaggedExperiment with 57975 rows and 338 columns
 [3] GBM_CNASNP-20160128: RaggedExperiment with 602338 rows and 1104 columns
 [4] GBM_CNVSNP-20160128: RaggedExperiment with 146852 rows and 1104 columns
 [5] GBM_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 577 columns
 [6] GBM_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 68 rows and 577 columns
 [7] GBM_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 577 columns
 [8] GBM_miRNAArray-20160128: SummarizedExperiment with 534 rows and 565 columns
 [9] GBM_mRNAArray_huex-20160128: SummarizedExperiment with 18632 rows and 431 columns
[10] GBM_mRNAArray_TX_g4502a-20160128: SummarizedExperiment with 17814 rows and 502 columns
[11] GBM_mRNAArray_TX_ht_hg_u133a-20160128: SummarizedExperiment with 12042 rows and 528 columns
[12] GBM_Mutation-20160128: RaggedExperiment with 22073 rows and 290 columns
[13] GBM_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 166 columns
[14] GBM_RPPAArray-20160128: SummarizedExperiment with 208 rows and 244 columns
[15] GBM_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 0 columns
[16] GBM_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18199 rows and 166 columns
[17] GBM_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 285 columns
[18] GBM_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 154 columns

> rownames( GBM )
CharacterList of length 18
[["GBM_CNACGH_CGH_hg_244a-20160128"]] character(0)
[["GBM_CNACGH_CGH_hg_415k_g4124a-20160128"]] character(0)
[["GBM_CNASNP-20160128"]] character(0)
[["GBM_CNVSNP-20160128"]] character(0)
[["GBM_GISTIC_AllByGene-20160128"]] character(0)
[["GBM_GISTIC_Peaks-20160128"]] 25 26 1 27 28 2 29 3 ... 65 22 23 66 67 24 68
[["GBM_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["GBM_miRNAArray-20160128"]] ebv-miR-BART1-3p ... kshv-miR-K12-9*
[["GBM_mRNAArray_huex-20160128"]] C9orf152 ELM02 RPS11 ... SLC39A6 CTSC AQP7
[["GBM_mRNAArray_TX_g4502a-20160128"]] 15E1.2 2'-PDE ... tcag7.23 tcag7.350
...

```

```
<8 more elements>
```

```
> colnames( GBM )
```

```
CharacterList of length 18
```

```
[[ "GBM_CNACGH_CGH_hg_244a-20160128" ]] TCGA-02-0001-01C-01D-0185-02 ...
[[ "GBM_CNACGH_CGH_hg_415k_g4124a-20160128" ]] TCGA-02-2466-01A-01D-0787-02 ...
[[ "GBM_CNASNP-20160128" ]] TCGA-02-0001-01C-01D-0182-01 ...
[[ "GBM_CNVSNP-20160128" ]] TCGA-02-0001-01C-01D-0182-01 ...
[[ "GBM_GISTIC_AllByGene-20160128" ]] TCGA-02-0001-01C-01D-0182-01 ...
[[ "GBM_GISTIC_Peaks-20160128" ]] TCGA-02-0001-01C-01D-0182-01 ...
[[ "GBM_GISTIC_ThresholdedByGene-20160128" ]] TCGA-02-0001-01C-01D-0182-01 ...
[[ "GBM_miRNAArray-20160128" ]] TCGA-02-0001-01C-01T-0179-07 ...
[[ "GBM_mRNAArray_huex-20160128" ]] TCGA-02-0001-01C-01R-0178-03 ...
[[ "GBM_mRNAArray_TX_g4502a-20160128" ]] TCGA-02-0001-01C-01R-0179-07 ...
```

```
...
```

```
<8 more elements>
```

```
Sizes of each ExperimentList element:
```

| | assay | size.Mb |
|----|--|----------|
| 1 | GBM_CNACGH_CGH_hg_244a-20160128 | 2.3 Mb |
| 2 | GBM_CNACGH_CGH_hg_415k_g4124a-20160128 | 1.7 Mb |
| 3 | GBM_CNASNP-20160128 | 16.4 Mb |
| 4 | GBM_CNVSNP-20160128 | 4.2 Mb |
| 5 | GBM_GISTIC_AllByGene-20160128 | 112.7 Mb |
| 6 | GBM_GISTIC_Peaks-20160128 | 0.5 Mb |
| 7 | GBM_GISTIC_ThresholdedByGene-20160128 | 112.5 Mb |
| 8 | GBM_miRNAArray-20160128 | 2.5 Mb |
| 9 | GBM_mRNAArray_huex-20160128 | 63.7 Mb |
| 10 | GBM_mRNAArray_TX_g4502a-20160128 | 70.5 Mb |
| 11 | GBM_mRNAArray_TX_ht_hg_u133a-20160128 | 50.1 Mb |
| 12 | GBM_Mutation-20160128 | 31 Mb |
| 13 | GBM_RNASeq2Gene-20160128 | 28.5 Mb |
| 14 | GBM_RPPAArray-20160128 | 0.5 Mb |
| 15 | GBM_miRNASeqGene-20160128 | 0.2 Mb |
| 16 | GBM_RNASeq2GeneNorm-20160128 | 25.3 Mb |
| 17 | GBM_Methylation_methyl27-20160128 | 4.9 Mb |
| 18 | GBM_Methylation_methyl450-20160128 | 75 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
```

[1,] 490 490 1.05 0.981 1.16

 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 12:
 [1] HNSC_CNASeq-20160128: RaggedExperiment with 32905 rows and 225 columns
 [2] HNSC_CNASNP-20160128: RaggedExperiment with 499142 rows and 1090 columns
 [3] HNSC_CNVSNP-20160128: RaggedExperiment with 110289 rows and 1089 columns
 [4] HNSC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 522 columns
 [5] HNSC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 72 rows and 522 columns
 [6] HNSC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 522 columns
 [7] HNSC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 532 columns
 [8] HNSC_Mutation-20160128: RaggedExperiment with 51799 rows and 279 columns
 [9] HNSC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 566 columns
[10] HNSC_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 294 columns
[11] HNSC_RPPAArray-20160128: SummarizedExperiment with 160 rows and 212 columns
[12] HNSC_Methylation-20160128: SummarizedExperiment with 485577 rows and 580 columns

> rownames( HNSC )
CharacterList of length 12
[["HNSC_CNASeq-20160128"]] character(0)
[["HNSC_CNASNP-20160128"]] character(0)
[["HNSC_CNVSNP-20160128"]] character(0)
[["HNSC_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["HNSC_GISTIC_Peaks-20160128"]] chr1:1-27864255 ... chr21:41298805-43485528
[["HNSC_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["HNSC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["HNSC_Mutation-20160128"]] character(0)

```

```

[["HNSC_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["HNSC_RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
...
<2 more elements>

```

```

> colnames( HNSC )
CharacterList of length 12
[["HNSC_CNASeq-20160128"]] TCGA-BA-4074-01A-01D-1431-02 ...
[["HNSC_CNASNP-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["HNSC_CNVSNP-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["HNSC_GISTIC_AllByGene-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["HNSC_GISTIC_Peaks-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["HNSC_GISTIC_ThresholdedByGene-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["HNSC_miRNASeqGene-20160128"]] TCGA-4P-AA8J-01A-11R-A39B-13 ...
[["HNSC_Mutation-20160128"]] TCGA-BA-4074-01A-01D-1434-08 ...
[["HNSC_RNASeq2GeneNorm-20160128"]] TCGA-4P-AA8J-01A-11R-A39I-07 ...
[["HNSC_RNASeqGene-20160128"]] TCGA-BA-4074-01A-01R-1436-07 ...
...
<2 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | HNSC_CNASeq-20160128 | 1 Mb |
| 2 | HNSC_CNASNP-20160128 | 13.6 Mb |
| 3 | HNSC_CNVSNP-20160128 | 3.3 Mb |
| 4 | HNSC_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | HNSC_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | HNSC_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | HNSC_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | HNSC_Mutation-20160128 | 68.9 Mb |
| 9 | HNSC_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 10 | HNSC_RNASeqGene-20160128 | 1.3 Mb |
| 11 | HNSC_RPPAArray-20160128 | 0 Mb |
| 12 | HNSC_Methylation-20160128 | 75.1 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                                          37

```

Including an additional 1426 columns

See Also

[HNSC-v2.0.1](#)

HNSC-v2.0.1

Head and Neck squamous cell carcinoma

Description

A document describing the TCGA cancer code

Details

```

> experiments( HNSC )
ExperimentList class object of length 13:
 [1] HNSC_CNASeq-20160128: RaggedExperiment with 32905 rows and 225 columns
 [2] HNSC_CNASNP-20160128: RaggedExperiment with 499142 rows and 1090 columns
 [3] HNSC_CNVSNP-20160128: RaggedExperiment with 110289 rows and 1089 columns
 [4] HNSC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 522 columns
 [5] HNSC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 72 rows and 522 columns
 [6] HNSC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 522 columns
 [7] HNSC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 532 columns
 [8] HNSC_Mutation-20160128: RaggedExperiment with 51799 rows and 279 columns
 [9] HNSC_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 566 columns
[10] HNSC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 566 columns
[11] HNSC_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 294 columns
[12] HNSC_RPPAArray-20160128: SummarizedExperiment with 160 rows and 212 columns
[13] HNSC_Methylation-20160128: SummarizedExperiment with 485577 rows and 580 columns

> rownames( HNSC )
CharacterList of length 13
[["HNSC_CNASeq-20160128"]] character(0)
[["HNSC_CNASNP-20160128"]] character(0)
[["HNSC_CNVSNP-20160128"]] character(0)
[["HNSC_GISTIC_AllByGene-20160128"]] character(0)
[["HNSC_GISTIC_Peaks-20160128"]] 29 30 31 1 32 33 2 ... 25 26 70 71 72 27 73
[["HNSC_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["HNSC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["HNSC_Mutation-20160128"]] character(0)
[["HNSC_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["HNSC_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
...
<3 more elements>

> colnames( HNSC )
CharacterList of length 13
[["HNSC_CNASeq-20160128"]] TCGA-BA-4074-01A-01D-1431-02 ...
[["HNSC_CNASNP-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["HNSC_CNVSNP-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["HNSC_GISTIC_AllByGene-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["HNSC_GISTIC_Peaks-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["HNSC_GISTIC_ThresholdedByGene-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["HNSC_miRNASeqGene-20160128"]] TCGA-4P-AA8J-01A-11R-A39B-13 ...
[["HNSC_Mutation-20160128"]] TCGA-BA-4074-01A-01D-1434-08 ...
[["HNSC_RNASeq2Gene-20160128"]] TCGA-4P-AA8J-01A-11R-A39I-07 ...
[["HNSC_RNASeq2GeneNorm-20160128"]] TCGA-4P-AA8J-01A-11R-A39I-07 ...
...
<3 more elements>

Sizes of each ExperimentList element:

```


| | assay | size.Mb |
|----|--|----------|
| 1 | HNSC_CNASeq-20160128 | 1 Mb |
| 2 | HNSC_CNASNP-20160128 | 13.6 Mb |
| 3 | HNSC_CNVSNP-20160128 | 3.3 Mb |
| 4 | HNSC_GISTIC_AllByGene-20160128 | 102.3 Mb |
| 5 | HNSC_GISTIC_Peaks-20160128 | 0.5 Mb |
| 6 | HNSC_GISTIC_ThresholdedByGene-20160128 | 102.1 Mb |
| 7 | HNSC_miRNASeqGene-20160128 | 4.5 Mb |
| 8 | HNSC_Mutation-20160128 | 68.9 Mb |
| 9 | HNSC_RNASeq2Gene-20160128 | 91.2 Mb |
| 10 | HNSC_RNASeq2GeneNorm-20160128 | 91.2 Mb |
| 11 | HNSC_RNASeqGene-20160128 | 48.6 Mb |
| 12 | HNSC_RPPAArray-20160128 | 0.3 Mb |
| 13 | HNSC_Methylation-20160128 | 75.1 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 | 2 | asian | 11 |
| black or african american | 48 | white | 452 |
| NA's | 15 | | |
| ethnicity: | | | |
| hispanic or latino | 26 | not hispanic or latino | 465 |
| | | NA's | 37 |

Including an additional 1426 columns

HNSC-v2.1.0

Head and Neck squamous cell carcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( HNSC )
ExperimentList class object of length 13:
 [1] HNSC_CNASeq-20160128: RaggedExperiment with 32905 rows and 225 columns
 [2] HNSC_CNASNP-20160128: RaggedExperiment with 499142 rows and 1090 columns
 [3] HNSC_CNVSNP-20160128: RaggedExperiment with 110289 rows and 1089 columns
 [4] HNSC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 522 columns
 [5] HNSC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 72 rows and 522 columns
 [6] HNSC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 522 columns
 [7] HNSC_Mutation-20160128: RaggedExperiment with 51799 rows and 279 columns
 [8] HNSC_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 566 columns
 [9] HNSC_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 294 columns
 [10] HNSC_RPPAArray-20160128: SummarizedExperiment with 160 rows and 212 columns
 [11] HNSC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 532 columns
 [12] HNSC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18361 rows and 566 columns
 [13] HNSC_Methylation-20160128: SummarizedExperiment with 485577 rows and 580 columns

> rownames( HNSC )
CharacterList of length 13
[["HNSC_CNASeq-20160128"]] character(0)
[["HNSC_CNASNP-20160128"]] character(0)
[["HNSC_CNVSNP-20160128"]] character(0)
[["HNSC_GISTIC_AllByGene-20160128"]] character(0)
[["HNSC_GISTIC_Peaks-20160128"]] 29 30 31 1 32 33 2 ... 25 26 70 71 72 27 73
[["HNSC_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["HNSC_Mutation-20160128"]] character(0)
```

```

[["HNSC_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["HNSC_RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["HNSC_RPPAArray-20160128"]] 14-3-3_epsilon 4E-BP1 ... p90RSK_pT359_S363
...

```

```
<3 more elements>
```

```
> colnames( HNSC )
```

```
CharacterList of length 13
```

```

[["HNSC_CNASeq-20160128"]] TCGA-BA-4074-01A-01D-1431-02 ...
[["HNSC_CNASNP-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["HNSC_CNVSNP-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["HNSC_GISTIC_AllByGene-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["HNSC_GISTIC_Peaks-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["HNSC_GISTIC_ThresholdedByGene-20160128"]] TCGA-4P-AA8J-01A-11D-A390-01 ...
[["HNSC_Mutation-20160128"]] TCGA-BA-4074-01A-01D-1434-08 ...
[["HNSC_RNASeq2Gene-20160128"]] TCGA-4P-AA8J-01A-11R-A39I-07 ...
[["HNSC_RNASeqGene-20160128"]] TCGA-BA-4074-01A-01R-1436-07 ...
[["HNSC_RPPAArray-20160128"]] TCGA-BA-4074-01A-21-2072-20 ...
...

```

```
<3 more elements>
```

```
Sizes of each ExperimentList element:
```

| | assay | size.Mb |
|----|--|----------|
| 1 | HNSC_CNASeq-20160128 | 1 Mb |
| 2 | HNSC_CNASNP-20160128 | 13.6 Mb |
| 3 | HNSC_CNVSNP-20160128 | 3.3 Mb |
| 4 | HNSC_GISTIC_AllByGene-20160128 | 102.3 Mb |
| 5 | HNSC_GISTIC_Peaks-20160128 | 0.5 Mb |
| 6 | HNSC_GISTIC_ThresholdedByGene-20160128 | 102.1 Mb |
| 7 | HNSC_Mutation-20160128 | 68.9 Mb |
| 8 | HNSC_RNASeq2Gene-20160128 | 91.2 Mb |
| 9 | HNSC_RNASeqGene-20160128 | 48.6 Mb |
| 10 | HNSC_RPPAArray-20160128 | 0.3 Mb |
| 11 | HNSC_miRNASeqGene-20160128 | 4.5 Mb |
| 12 | HNSC_RNASeq2GeneNorm-20160128 | 81.6 Mb |
| 13 | HNSC_Methylation-20160128 | 75.1 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
[1,] 223 223 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
                                     2
                                     asian
                                     11
    black or african american
                                     48
                                     white
                                     452
                                     NA's
                                     15

ethnicity:
    hispanic or latino not hispanic or latino
                                     26
                                     NA's
                                     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 10:
 [1] KICH_CNASNP-20160128: RaggedExperiment with 57729 rows and 132 columns

```

```

[2] KICH_CNVSNP-20160128: RaggedExperiment with 10164 rows and 132 columns
[3] KICH_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 66 columns
[4] KICH_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 2 rows and 66 columns
[5] KICH_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 66 columns
[6] KICH_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 91 columns
[7] KICH_Mutation-20160128: RaggedExperiment with 7559 rows and 66 columns
[8] KICH_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 91 columns
[9] KICH_RPPAArray-20160128: SummarizedExperiment with 193 rows and 63 columns
[10] KICH_Methylation-20160128: SummarizedExperiment with 485577 rows and 66 columns

```

```
> rownames( KICH )
```

```
CharacterList of length 10
```

```

[["KICH_CNASNP-20160128"]] character(0)
[["KICH_CNVSNP-20160128"]] character(0)
[["KICH_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["KICH_GISTIC_Peaks-20160128"]] chr8:116272008-117149163 chr15:1-66482794
[["KICH_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["KICH_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["KICH_Mutation-20160128"]] character(0)
[["KICH_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["KICH_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["KICH_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873

```

```
> colnames( KICH )
```

```
CharacterList of length 10
```

```

[["KICH_CNASNP-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["KICH_CNVSNP-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["KICH_GISTIC_AllByGene-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["KICH_GISTIC_Peaks-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["KICH_GISTIC_ThresholdedByGene-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["KICH_miRNASeqGene-20160128"]] TCGA-KL-8323-01A-21R-2314-13 ...
[["KICH_Mutation-20160128"]] TCGA-KL-8323-01A-21D-2310-10 ...
[["KICH_RNASeq2GeneNorm-20160128"]] TCGA-KL-8323-01A-21R-2315-07 ...
[["KICH_RPPAArray-20160128"]] TCGA-KL-8324-01A-21-A421-20 ...
[["KICH_Methylation-20160128"]] TCGA-KL-8323-01A-21D-2312-05 ...

```

```
Sizes of each ExperimentList element:
```

| | | assay size.Mb |
|---|--|---------------|
| 1 | KICH_CNASNP-20160128 | 1.6 Mb |
| 2 | KICH_CNVSNP-20160128 | 0.3 Mb |
| 3 | KICH_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | KICH_GISTIC_Peaks-20160128 | 0 Mb |
| 5 | KICH_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | KICH_miRNASeqGene-20160128 | 0.1 Mb |
| 7 | KICH_Mutation-20160128 | 2.6 Mb |
| 8 | KICH_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 9 | KICH_RPPAArray-20160128 | 0 Mb |

10 KICH_Methylation-20160128 75 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

See Also

[KICH-v2.0.1](#)

KICH-v2.0.1

*Kidney Chromophobe***Description**

A document describing the TCGA cancer code

Details

```

> experiments( KICH )
ExperimentList class object of length 11:
 [1] KICH_CNASNP-20160128: RaggedExperiment with 57729 rows and 132 columns
 [2] KICH_CNVSNP-20160128: RaggedExperiment with 10164 rows and 132 columns
 [3] KICH_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 66 columns
 [4] KICH_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 2 rows and 66 columns
 [5] KICH_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 66 columns
 [6] KICH_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 91 columns
 [7] KICH_Mutation-20160128: RaggedExperiment with 7559 rows and 66 columns
 [8] KICH_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 91 columns
 [9] KICH_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 91 columns
 [10] KICH_RPPAArray-20160128: SummarizedExperiment with 193 rows and 63 columns
 [11] KICH_Methylation-20160128: SummarizedExperiment with 485577 rows and 66 columns

> rownames( KICH )
CharacterList of length 11
[["KICH_CNASNP-20160128"]] character(0)
[["KICH_CNVSNP-20160128"]] character(0)
[["KICH_GISTIC_AllByGene-20160128"]] character(0)
[["KICH_GISTIC_Peaks-20160128"]] 1 2
[["KICH_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["KICH_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["KICH_Mutation-20160128"]] character(0)
[["KICH_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["KICH_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["KICH_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<1 more element>

> colnames( KICH )
CharacterList of length 11
[["KICH_CNASNP-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["KICH_CNVSNP-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["KICH_GISTIC_AllByGene-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["KICH_GISTIC_Peaks-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["KICH_GISTIC_ThresholdedByGene-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["KICH_miRNASeqGene-20160128"]] TCGA-KL-8323-01A-21R-2314-13 ...
[["KICH_Mutation-20160128"]] TCGA-KL-8323-01A-21D-2310-10 ...

```

```

[["KICH_RNASeq2Gene-20160128"]] TCGA-KL-8323-01A-21R-2315-07 ...
[["KICH_RNASeq2GeneNorm-20160128"]] TCGA-KL-8323-01A-21R-2315-07 ...
[["KICH_RPPAArray-20160128"]] TCGA-KL-8324-01A-21-A421-20 ...

```

```
...
```

```
<1 more element>
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | KICH_CNASNP-20160128 | 1.6 Mb |
| 2 | KICH_CNVSNP-20160128 | 0.3 Mb |
| 3 | KICH_GISTIC_AllByGene-20160128 | 15.9 Mb |
| 4 | KICH_GISTIC_Peaks-20160128 | 0 Mb |
| 5 | KICH_GISTIC_ThresholdedByGene-20160128 | 15.8 Mb |
| 6 | KICH_miRNASeqGene-20160128 | 0.9 Mb |
| 7 | KICH_Mutation-20160128 | 2.6 Mb |
| 8 | KICH_RNASeq2Gene-20160128 | 16.8 Mb |
| 9 | KICH_RNASeq2GeneNorm-20160128 | 16.8 Mb |
| 10 | KICH_RPPAArray-20160128 | 0.1 Mb |
| 11 | KICH_Methylation-20160128 | 75 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

KICH-v2.1.0

*Kidney Chromophobe***Description**

A document describing the TCGA cancer code

Details

```
> experiments( KICH )
ExperimentList class object of length 11:
 [1] KICH_CNASNP-20160128: RaggedExperiment with 57729 rows and 132 columns
 [2] KICH_CNVSNP-20160128: RaggedExperiment with 10164 rows and 132 columns
 [3] KICH_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 66 columns
 [4] KICH_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 2 rows and 66 columns
 [5] KICH_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 66 columns
 [6] KICH_Mutation-20160128: RaggedExperiment with 7559 rows and 66 columns
 [7] KICH_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 91 columns
 [8] KICH_RPPAArray-20160128: SummarizedExperiment with 193 rows and 63 columns
 [9] KICH_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 91 columns
 [10] KICH_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18122 rows and 91 columns
 [11] KICH_Methylation-20160128: SummarizedExperiment with 485577 rows and 66 columns

> rownames( KICH )
CharacterList of length 11
[["KICH_CNASNP-20160128"]] character(0)
[["KICH_CNVSNP-20160128"]] character(0)
[["KICH_GISTIC_AllByGene-20160128"]] character(0)
[["KICH_GISTIC_Peaks-20160128"]] 1 2
[["KICH_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["KICH_Mutation-20160128"]] character(0)
[["KICH_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["KICH_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
```

```

[["KICH_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["KICH_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 TAKR
...
<1 more element>

```

```

> colnames( KICH )
CharacterList of length 11
[["KICH_CNASNP-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["KICH_CNVSNP-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["KICH_GISTIC_AllByGene-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["KICH_GISTIC_Peaks-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["KICH_GISTIC_ThresholdedByGene-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["KICH_Mutation-20160128"]] TCGA-KL-8323-01A-21D-2310-10 ...
[["KICH_RNASeq2Gene-20160128"]] TCGA-KL-8323-01A-21R-2315-07 ...
[["KICH_RPPAArray-20160128"]] TCGA-KL-8324-01A-21-A421-20 ...
[["KICH_miRNASeqGene-20160128"]] TCGA-KL-8323-01A-21R-2314-13 ...
[["KICH_RNASeq2GeneNorm-20160128"]] TCGA-KL-8323-01 ... TCGA-KO-8417-01
...
<1 more element>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | KICH_CNASNP-20160128 | 1.6 Mb |
| 2 | KICH_CNVSNP-20160128 | 0.3 Mb |
| 3 | KICH_GISTIC_AllByGene-20160128 | 15.9 Mb |
| 4 | KICH_GISTIC_Peaks-20160128 | 0 Mb |
| 5 | KICH_GISTIC_ThresholdedByGene-20160128 | 15.8 Mb |
| 6 | KICH_Mutation-20160128 | 2.6 Mb |
| 7 | KICH_RNASeq2Gene-20160128 | 16.8 Mb |
| 8 | KICH_RPPAArray-20160128 | 0.1 Mb |
| 9 | KICH_miRNASeqGene-20160128 | 0.9 Mb |
| 10 | KICH_RNASeq2GeneNorm-20160128 | 14.8 Mb |
| 11 | KICH_Methylation-20160128 | 75 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
[1,] 9 9 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 13:

- [1] KIRC_CNASNP-20160128: RaggedExperiment with 488691 rows and 1059 columns
- [2] KIRC_CNVSNP-20160128: RaggedExperiment with 85036 rows and 1059 columns
- [3] KIRC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 528 columns
- [4] KIRC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 26 rows and 528 columns
- [5] KIRC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 528 columns
- [6] KIRC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 326 columns
- [7] KIRC_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 72 columns
- [8] KIRC_Mutation-20160128: RaggedExperiment with 26369 rows and 437 columns


```

[9] KIRC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 606 columns
[10] KIRC_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 537 columns
[11] KIRC_RPPAArray-20160128: SummarizedExperiment with 217 rows and 478 columns
[12] KIRC_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 418 columns
[13] KIRC_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 480 columns

```

```

> rownames( KIRC )
CharacterList of length 13
[["KIRC_CNASNP-20160128"]] character(0)
[["KIRC_CNVSNP-20160128"]] character(0)
[["KIRC_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["KIRC_GISTIC_Peaks-20160128"]] chr1:1-31345223 ... chr14:56181301-107349540
[["KIRC_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["KIRC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["KIRC_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["KIRC_Mutation-20160128"]] character(0)
[["KIRC_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["KIRC_RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
...
<3 more elements>

```

```

> colnames( KIRC )
CharacterList of length 13
[["KIRC_CNASNP-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["KIRC_CNVSNP-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["KIRC_GISTIC_AllByGene-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["KIRC_GISTIC_Peaks-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["KIRC_GISTIC_ThresholdedByGene-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["KIRC_miRNASeqGene-20160128"]] TCGA-3Z-A93Z-01A-11R-A37P-13 ...
[["KIRC_mRNAArray-20160128"]] TCGA-A3-3306-01A-01R-0864-07 ...
[["KIRC_Mutation-20160128"]] TCGA-A3-3308-01A-01D-0966-08 ...
[["KIRC_RNASeq2GeneNorm-20160128"]] TCGA-3Z-A93Z-01A-11R-A370-07 ...
[["KIRC_RNASeqGene-20160128"]] TCGA-A3-3306-01A-01R-0864-07 ...
...
<3 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|---|--|---------------|
| 1 | KIRC_CNASNP-20160128 | 13.4 Mb |
| 2 | KIRC_CNVSNP-20160128 | 2.6 Mb |
| 3 | KIRC_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | KIRC_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | KIRC_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | KIRC_miRNASeqGene-20160128 | 0.1 Mb |
| 7 | KIRC_mRNAArray-20160128 | 1.1 Mb |
| 8 | KIRC_Mutation-20160128 | 8.2 Mb |
| 9 | KIRC_RNASeq2GeneNorm-20160128 | 1.3 Mb |

```

10          KIRC_RNASeqGene-20160128  1.3 Mb
11          KIRC_RPPAArray-20160128  0.1 Mb
12  KIRC_Methylation_methyl27-20160128  4.9 Mb
13  KIRC_Methylation_methyl450-20160128 75.1 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

See Also

[KIRC-v2.0.1](#)

KIRC-v2.0.1

Kidney renal clear cell carcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( KIRC )
ExperimentList class object of length 14:
 [1] KIRC_CNASNP-20160128: RaggedExperiment with 488691 rows and 1059 columns
 [2] KIRC_CNVSNP-20160128: RaggedExperiment with 85036 rows and 1059 columns
 [3] KIRC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 528 columns
 [4] KIRC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 26 rows and 528 columns
 [5] KIRC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 528 columns
 [6] KIRC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 326 columns
 [7] KIRC_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 72 columns
 [8] KIRC_Mutation-20160128: RaggedExperiment with 26369 rows and 437 columns
 [9] KIRC_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 606 columns
 [10] KIRC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 606 columns
 [11] KIRC_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 537 columns
 [12] KIRC_RPPAArray-20160128: SummarizedExperiment with 217 rows and 478 columns
 [13] KIRC_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 418 columns
 [14] KIRC_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 480 columns

> rownames( KIRC )
CharacterList of length 14
[["KIRC_CNASNP-20160128"]] character(0)
[["KIRC_CNVSNP-20160128"]] character(0)
[["KIRC_GISTIC_AllByGene-20160128"]] character(0)
[["KIRC_GISTIC_Peaks-20160128"]] 11 12 1 2 13 14 15 16 ... 7 25 26 8 27 28 29
[["KIRC_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["KIRC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["KIRC_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["KIRC_Mutation-20160128"]] character(0)
[["KIRC_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["KIRC_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
...
<4 more elements>
```

```
> colnames( KIRC )
CharacterList of length 14
[["KIRC_CNASNP-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["KIRC_CNVSNP-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["KIRC_GISTIC_AllByGene-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["KIRC_GISTIC_Peaks-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["KIRC_GISTIC_ThresholdedByGene-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["KIRC_miRNASeqGene-20160128"]] TCGA-3Z-A93Z-01A-11R-A37P-13 ...
[["KIRC_mRNAArray-20160128"]] TCGA-A3-3306-01A-01R-0864-07 ...
[["KIRC_Mutation-20160128"]] TCGA-A3-3308-01A-01D-0966-08 ...
[["KIRC_RNASeq2Gene-20160128"]] TCGA-3Z-A93Z-01A-11R-A370-07 ...
[["KIRC_RNASeq2GeneNorm-20160128"]] TCGA-3Z-A93Z-01A-11R-A370-07 ...
...
<4 more elements>
```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|----|--|----------|
| 1 | KIRC_CNASNP-20160128 | 13.4 Mb |
| 2 | KIRC_CNVSNP-20160128 | 2.6 Mb |
| 3 | KIRC_GISTIC_AllByGene-20160128 | 103.4 Mb |
| 4 | KIRC_GISTIC_Peaks-20160128 | 0.2 Mb |
| 5 | KIRC_GISTIC_ThresholdedByGene-20160128 | 103.2 Mb |
| 6 | KIRC_miRNASeqGene-20160128 | 2.8 Mb |
| 7 | KIRC_mRNAArray-20160128 | 12 Mb |
| 8 | KIRC_Mutation-20160128 | 8.2 Mb |
| 9 | KIRC_RNASeq2Gene-20160128 | 97.4 Mb |
| 10 | KIRC_RNASeq2GeneNorm-20160128 | 97.4 Mb |
| 11 | KIRC_RNASeqGene-20160128 | 86.6 Mb |
| 12 | KIRC_RPPAArray-20160128 | 0.9 Mb |
| 13 | KIRC_Methylation_methyl27-20160128 | 4.9 Mb |
| 14 | KIRC_Methylation_methyl450-20160128 | 75.1 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

KIRC-v2.1.0

Kidney renal clear cell carcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( KIRC )
```

ExperimentList class object of length 14:

- [1] KIRC_CNASNP-20160128: RaggedExperiment with 488691 rows and 1059 columns
- [2] KIRC_CNVSNP-20160128: RaggedExperiment with 85036 rows and 1059 columns
- [3] KIRC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 528 columns
- [4] KIRC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 26 rows and 528 columns
- [5] KIRC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 528 columns
- [6] KIRC_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 72 columns

```

[7] KIRC_Mutation-20160128: RaggedExperiment with 26369 rows and 437 columns
[8] KIRC_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 606 columns
[9] KIRC_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 537 columns
[10] KIRC_RPPAArray-20160128: SummarizedExperiment with 217 rows and 478 columns
[11] KIRC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 326 columns
[12] KIRC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18292 rows and 606 columns
[13] KIRC_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 418 columns
[14] KIRC_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 480 columns

```

```

> rownames( KIRC )
CharacterList of length 14
[["KIRC_CNASNP-20160128"]] character(0)
[["KIRC_CNVSNP-20160128"]] character(0)
[["KIRC_GISTIC_AllByGene-20160128"]] character(0)
[["KIRC_GISTIC_Peaks-20160128"]] 11 12 1 2 13 14 15 16 ... 7 25 26 8 27 28 29
[["KIRC_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["KIRC_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["KIRC_Mutation-20160128"]] character(0)
[["KIRC_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["KIRC_RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["KIRC_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<4 more elements>

```

```

> colnames( KIRC )
CharacterList of length 14
[["KIRC_CNASNP-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["KIRC_CNVSNP-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["KIRC_GISTIC_AllByGene-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["KIRC_GISTIC_Peaks-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["KIRC_GISTIC_ThresholdedByGene-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["KIRC_mRNAArray-20160128"]] TCGA-A3-3306-01A-01R-0864-07 ...
[["KIRC_Mutation-20160128"]] TCGA-A3-3308-01A-01D-0966-08 ...
[["KIRC_RNASeq2Gene-20160128"]] TCGA-3Z-A93Z-01A-11R-A370-07 ...
[["KIRC_RNASeqGene-20160128"]] TCGA-A3-3306-01A-01R-0864-07 ...
[["KIRC_RPPAArray-20160128"]] TCGA-3Z-A93Z-01A-21-A45H-20 ...
...
<4 more elements>

```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|---|--|----------|
| 1 | KIRC_CNASNP-20160128 | 13.4 Mb |
| 2 | KIRC_CNVSNP-20160128 | 2.6 Mb |
| 3 | KIRC_GISTIC_AllByGene-20160128 | 103.4 Mb |
| 4 | KIRC_GISTIC_Peaks-20160128 | 0.2 Mb |
| 5 | KIRC_GISTIC_ThresholdedByGene-20160128 | 103.2 Mb |
| 6 | KIRC_mRNAArray-20160128 | 12 Mb |

| | | |
|----|-------------------------------------|---------|
| 7 | KIRC_Mutation-20160128 | 8.2 Mb |
| 8 | KIRC_RNASeq2Gene-20160128 | 97.4 Mb |
| 9 | KIRC_RNASeqGene-20160128 | 86.6 Mb |
| 10 | KIRC_RPPAArray-20160128 | 0.9 Mb |
| 11 | KIRC_miRNASeqGene-20160128 | 2.8 Mb |
| 12 | KIRC_RNASeq2GeneNorm-20160128 | 86.9 Mb |
| 13 | KIRC_Methylation_methyl27-20160128 | 4.9 Mb |
| 14 | KIRC_Methylation_methyl450-20160128 | 75.1 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
[1,] 177 177 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 | <i>Kidney renal papillary cell carcinoma</i> |
|------|--|

Description

A document describing the TCGA cancer code

Details

```
> experiments( KIRP )
ExperimentList class object of length 13:
 [1] KIRP_CNASNP-20160128: RaggedExperiment with 300681 rows and 593 columns
 [2] KIRP_CNVSNP-20160128: RaggedExperiment with 46914 rows and 590 columns
 [3] KIRP_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 288 columns
 [4] KIRP_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 28 rows and 288 columns
 [5] KIRP_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 288 columns
 [6] KIRP_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 326 columns
 [7] KIRP_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 16 columns
 [8] KIRP_Mutation-20160128: RaggedExperiment with 15585 rows and 161 columns
 [9] KIRP_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 323 columns
 [10] KIRP_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 14 columns
 [11] KIRP_RPPAArray-20160128: SummarizedExperiment with 195 rows and 216 columns
 [12] KIRP_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 21 columns
 [13] KIRP_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 321 columns

> rownames( KIRP )
CharacterList of length 13
[["KIRP_CNASNP-20160128"]] character(0)
[["KIRP_CNVSNP-20160128"]] character(0)
[["KIRP_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["KIRP_GISTIC_Peaks-20160128"]] chr1:1-29472434 ... chr22:29969457-30128393
[["KIRP_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["KIRP_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["KIRP_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["KIRP_Mutation-20160128"]] character(0)
[["KIRP_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["KIRP_RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
...
<3 more elements>

> colnames( KIRP )
```

```

CharacterList of length 13
[["KIRP_CNASNP-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["KIRP_CNVSNP-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["KIRP_GISTIC_AllByGene-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["KIRP_GISTIC_Peaks-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["KIRP_GISTIC_ThresholdedByGene-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["KIRP_miRNASeqGene-20160128"]] TCGA-2K-A9WE-01A-11R-A38N-13 ...
[["KIRP_mRNAArray-20160128"]] TCGA-AL-3466-01A-01R-1193-07 ...
[["KIRP_Mutation-20160128"]] TCGA-A4-7286-01A-11D-2136-08 ...
[["KIRP_RNASeq2GeneNorm-20160128"]] TCGA-2K-A9WE-01A-11R-A38C-07 ...
[["KIRP_RNASeqGene-20160128"]] TCGA-AL-3466-01A-02R-1351-07 ...
...
<3 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | KIRP_CNASNP-20160128 | 8.2 Mb |
| 2 | KIRP_CNVSNP-20160128 | 1.4 Mb |
| 3 | KIRP_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | KIRP_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | KIRP_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | KIRP_miRNASeqGene-20160128 | 0.1 Mb |
| 7 | KIRP_mRNAArray-20160128 | 1.1 Mb |
| 8 | KIRP_Mutation-20160128 | 10.6 Mb |
| 9 | KIRP_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 10 | KIRP_RNASeqGene-20160128 | 1.3 Mb |
| 11 | KIRP_RPPAArray-20160128 | 0 Mb |
| 12 | KIRP_Methylation_methyl27-20160128 | 4.9 Mb |
| 13 | KIRP_Methylation_methyl450-20160128 | 75 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

See Also

[KIRP-v2.0.1](#)

KIRP-v2.0.1

Kidney renal papillary cell carcinoma

Description

A document describing the TCGA cancer code

Details

```

> experiments( KIRP )
ExperimentList class object of length 14:
 [1] KIRP_CNASNP-20160128: RaggedExperiment with 300681 rows and 593 columns
 [2] KIRP_CNVSNP-20160128: RaggedExperiment with 46914 rows and 590 columns

```

```

[3] KIRP_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 288 columns
[4] KIRP_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 28 rows and 288 columns
[5] KIRP_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 288 columns
[6] KIRP_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 326 columns
[7] KIRP_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 16 columns
[8] KIRP_Mutation-20160128: RaggedExperiment with 15585 rows and 161 columns
[9] KIRP_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 323 columns
[10] KIRP_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 323 columns
[11] KIRP_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 14 columns
[12] KIRP_RPPAArray-20160128: SummarizedExperiment with 195 rows and 216 columns
[13] KIRP_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 21 columns
[14] KIRP_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 321 columns

```

```
> rownames( KIRP )
```

```
CharacterList of length 14
```

```

[["KIRP_CNASNP-20160128"]] character(0)
[["KIRP_CNVSNP-20160128"]] character(0)
[["KIRP_GISTIC_AllByGene-20160128"]] character(0)
[["KIRP_GISTIC_Peaks-20160128"]] 8 9 1 10 2 11 12 3... 22 24 25 7 26 27 28
[["KIRP_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["KIRP_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["KIRP_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["KIRP_Mutation-20160128"]] character(0)
[["KIRP_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["KIRP_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR

```

```
...
```

```
<4 more elements>
```

```
> colnames( KIRP )
```

```
CharacterList of length 14
```

```

[["KIRP_CNASNP-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["KIRP_CNVSNP-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["KIRP_GISTIC_AllByGene-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["KIRP_GISTIC_Peaks-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["KIRP_GISTIC_ThresholdedByGene-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["KIRP_miRNASeqGene-20160128"]] TCGA-2K-A9WE-01A-11R-A38N-13 ...
[["KIRP_mRNAArray-20160128"]] TCGA-AL-3466-01A-01R-1193-07 ...
[["KIRP_Mutation-20160128"]] TCGA-A4-7286-01A-11D-2136-08 ...
[["KIRP_RNASeq2Gene-20160128"]] TCGA-2K-A9WE-01A-11R-A38C-07 ...
[["KIRP_RNASeq2GeneNorm-20160128"]] TCGA-2K-A9WE-01A-11R-A38C-07 ...

```

```
...
```

```
<4 more elements>
```

```
Sizes of each ExperimentList element:
```

| | | assay size.Mb |
|---|----------------------|---------------|
| 1 | KIRP_CNASNP-20160128 | 8.2 Mb |
| 2 | KIRP_CNVSNP-20160128 | 1.4 Mb |

```

3      KIRP_GISTIC_AllByGene-20160128  58 Mb
4      KIRP_GISTIC_Peaks-20160128    0.2 Mb
5  KIRP_GISTIC_ThresholdedByGene-20160128 57.8 Mb
6      KIRP_miRNASeqGene-20160128    2.8 Mb
7      KIRP_mRNAArray-20160128       4.4 Mb
8      KIRP_Mutation-20160128        10.6 Mb
9      KIRP_RNASeq2Gene-20160128     53.1 Mb
10     KIRP_RNASeq2GeneNorm-20160128  53.1 Mb
11     KIRP_RNASeqGene-20160128      4.7 Mb
12     KIRP_RPPAArray-20160128       0.4 Mb
13     KIRP_Methylation_methyl27-20160128 4.9 Mb
14     KIRP_Methylation_methyl450-20160128 75 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

KIRP-v2.1.0

Kidney renal papillary cell carcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( KIRP )
ExperimentList class object of length 14:
 [1] KIRP_CNASNP-20160128: RaggedExperiment with 300681 rows and 593 columns
 [2] KIRP_CNVSNP-20160128: RaggedExperiment with 46914 rows and 590 columns
 [3] KIRP_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 288 columns
 [4] KIRP_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 28 rows and 288 columns
 [5] KIRP_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 288 columns
 [6] KIRP_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 16 columns
 [7] KIRP_Mutation-20160128: RaggedExperiment with 15585 rows and 161 columns
 [8] KIRP_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 323 columns
 [9] KIRP_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 14 columns
 [10] KIRP_RPPAArray-20160128: SummarizedExperiment with 195 rows and 216 columns
 [11] KIRP_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 326 columns
 [12] KIRP_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18059 rows and 323 columns
 [13] KIRP_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 21 columns
 [14] KIRP_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 321 columns

> rownames( KIRP )
CharacterList of length 14
[["KIRP_CNASNP-20160128"]] character(0)
[["KIRP_CNVSNP-20160128"]] character(0)
[["KIRP_GISTIC_AllByGene-20160128"]] character(0)
[["KIRP_GISTIC_Peaks-20160128"]] 8 9 1 10 2 11 12 3 ... 22 24 25 7 26 27 28
[["KIRP_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["KIRP_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["KIRP_Mutation-20160128"]] character(0)
```

```

[["KIRP_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["KIRP_RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["KIRP_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<4 more elements>

```

```

> colnames( KIRP )
CharacterList of length 14
[["KIRP_CNASNP-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["KIRP_CNVSNP-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["KIRP_GISTIC_AllByGene-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["KIRP_GISTIC_Peaks-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["KIRP_GISTIC_ThresholdedByGene-20160128"]] TCGA-2K-A9WE-01A-11D-A381-01 ...
[["KIRP_mRNAArray-20160128"]] TCGA-AL-3466-01A-01R-1193-07 ...
[["KIRP_Mutation-20160128"]] TCGA-A4-7286-01A-11D-2136-08 ...
[["KIRP_RNASeq2Gene-20160128"]] TCGA-2K-A9WE-01A-11R-A38C-07 ...
[["KIRP_RNASeqGene-20160128"]] TCGA-AL-3466-01A-02R-1351-07 ...
[["KIRP_RPPAArray-20160128"]] TCGA-2K-A9WE-01A-21-A39N-20 ...
...
<4 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | KIRP_CNASNP-20160128 | 8.2 Mb |
| 2 | KIRP_CNVSNP-20160128 | 1.4 Mb |
| 3 | KIRP_GISTIC_AllByGene-20160128 | 58 Mb |
| 4 | KIRP_GISTIC_Peaks-20160128 | 0.2 Mb |
| 5 | KIRP_GISTIC_ThresholdedByGene-20160128 | 57.8 Mb |
| 6 | KIRP_mRNAArray-20160128 | 4.4 Mb |
| 7 | KIRP_Mutation-20160128 | 10.6 Mb |
| 8 | KIRP_RNASeq2Gene-20160128 | 53.1 Mb |
| 9 | KIRP_RNASeqGene-20160128 | 4.7 Mb |
| 10 | KIRP_RPPAArray-20160128 | 0.4 Mb |
| 11 | KIRP_miRNASeqGene-20160128 | 2.8 Mb |
| 12 | KIRP_RNASeq2GeneNorm-20160128 | 46.8 Mb |
| 13 | KIRP_Methylation_methyl27-20160128 | 4.9 Mb |
| 14 | KIRP_Methylation_methyl450-20160128 | 75 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

```

[1,] 44 44 1.76 1.35 3.6

 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 | 2 | asian | 6 |
| black or african american | 61 | white | 207 |
| NA's | 15 | | |

ethnicity:

| | | | | | |
|--------------------|----|------------------------|-----|------|----|
| hispanic or latino | 12 | not hispanic or latino | 243 | NA's | 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 10:
 [1] LAML_CNASNP-20160128: RaggedExperiment with 874897 rows and 392 columns
 [2] LAML_CNVSNP-20160128: RaggedExperiment with 28324 rows and 380 columns
 [3] LAML_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 191 columns
 [4] LAML_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 16 rows and 191 columns
 [5] LAML_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 191 columns
 [6] LAML_Mutation-20160128: RaggedExperiment with 2585 rows and 197 columns
 [7] LAML_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 173 columns
 [8] LAML_RNASeqGene-20160128: SummarizedExperiment with 19990 rows and 179 columns
 [9] LAML_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 194 columns
 [10] LAML_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 194 columns

> rownames( LAML )
CharacterList of length 10
[["LAML_CNASNP-20160128"]] character(0)
[["LAML_CNVSNP-20160128"]] character(0)
[["LAML_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["LAML_GISTIC_Peaks-20160128"]] chr1:47516423-47533836 ...
[["LAML_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["LAML_Mutation-20160128"]] character(0)
[["LAML_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["LAML_RNASeqGene-20160128"]] AADACL3 AADACL4 ABCA4 ... XGPY2 XKRY2 ZFY
[["LAML_Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["LAML_Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873

> colnames( LAML )
CharacterList of length 10
[["LAML_CNASNP-20160128"]] TCGA-AB-2802-03A-01D-0756-21 ...
[["LAML_CNVSNP-20160128"]] TCGA-AB-2803-03A-01D-0756-21 ...
[["LAML_GISTIC_AllByGene-20160128"]] TCGA-AB-2803-03A-01D-0756-21 ...
[["LAML_GISTIC_Peaks-20160128"]] TCGA-AB-2803-03A-01D-0756-21 ...
[["LAML_GISTIC_ThresholdedByGene-20160128"]] TCGA-AB-2803-03A-01D-0756-21 ...
[["LAML_Mutation-20160128"]] TCGA-AB-2802-03B-01W-0728-08 ...
[["LAML_RNASeq2GeneNorm-20160128"]] TCGA-AB-2803-03A-01T-0734-13 ...
[["LAML_RNASeqGene-20160128"]] TCGA-AB-2803-03A-01T-0734-13 ...
[["LAML_Methylation_methyl27-20160128"]] TCGA-AB-2802-03A-01D-0741-05 ...
[["LAML_Methylation_methyl450-20160128"]] TCGA-AB-2802-03A-01D-0741-05 ...

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|---|--|---------------|
| 1 | LAML_CNASNP-20160128 | 23.5 Mb |
| 2 | LAML_CNVSNP-20160128 | 0.9 Mb |
| 3 | LAML_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | LAML_GISTIC_Peaks-20160128 | 0 Mb |
| 5 | LAML_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |

| | | |
|----|-------------------------------------|--------|
| 6 | LAML_Mutation-20160128 | 2.8 Mb |
| 7 | LAML_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 8 | LAML_RNASeqGene-20160128 | 1.3 Mb |
| 9 | LAML_Methylation_methyl27-20160128 | 4.9 Mb |
| 10 | LAML_Methylation_methyl450-20160128 | 75 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

See Also

[LAML-v2.0.1](#)

LAML-v2.0.1

Acute Myeloid Leukemia

Description

A document describing the TCGA cancer code

Details

```
> experiments( LAML )
ExperimentList class object of length 11:
 [1] LAML_CNASNP-20160128: RaggedExperiment with 874897 rows and 392 columns
 [2] LAML_CNVSNP-20160128: RaggedExperiment with 28324 rows and 380 columns
 [3] LAML_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 191 columns
 [4] LAML_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 16 rows and 191 columns
 [5] LAML_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 191 columns
 [6] LAML_Mutation-20160128: RaggedExperiment with 2585 rows and 197 columns
 [7] LAML_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 173 columns
 [8] LAML_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 173 columns
 [9] LAML_RNASeqGene-20160128: SummarizedExperiment with 19990 rows and 179 columns
 [10] LAML_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 194 columns
 [11] LAML_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 194 columns

> rownames( LAML )
CharacterList of length 11
[["LAML_CNASNP-20160128"]] character(0)
[["LAML_CNVSNP-20160128"]] character(0)
[["LAML_GISTIC_AllByGene-20160128"]] character(0)
[["LAML_GISTIC_Peaks-20160128"]] 1 5 6 7 8 9 2 10 11 12 13 14 15 3 16 4
```



```

[["LAML_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["LAML_Mutation-20160128"]] character(0)
[["LAML_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["LAML_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["LAML_RNASeqGene-20160128"]] AADACL3 AADACL4 ABCA4 ... XGPY2 XKRY2 ZFY
[["LAML_Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
...
<1 more element>

```

```

> colnames( LAML )
CharacterList of length 11
[["LAML_CNASNP-20160128"]] TCGA-AB-2802-03A-01D-0756-21 ...
[["LAML_CNVSNP-20160128"]] TCGA-AB-2803-03A-01D-0756-21 ...
[["LAML_GISTIC_AllByGene-20160128"]] TCGA-AB-2803-03A-01D-0756-21 ...
[["LAML_GISTIC_Peaks-20160128"]] TCGA-AB-2803-03A-01D-0756-21 ...
[["LAML_GISTIC_ThresholdedByGene-20160128"]] TCGA-AB-2803-03A-01D-0756-21 ...
[["LAML_Mutation-20160128"]] TCGA-AB-2802-03B-01W-0728-08 ...
[["LAML_RNASeq2Gene-20160128"]] TCGA-AB-2803-03A-01T-0734-13 ...
[["LAML_RNASeq2GeneNorm-20160128"]] TCGA-AB-2803-03A-01T-0734-13 ...
[["LAML_RNASeqGene-20160128"]] TCGA-AB-2803-03A-01T-0734-13 ...
[["LAML_Methylation_methyl27-20160128"]] TCGA-AB-2802-03A-01D-0741-05 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | LAML_CNASNP-20160128 | 23.5 Mb |
| 2 | LAML_CNVSNP-20160128 | 0.9 Mb |
| 3 | LAML_GISTIC_AllByGene-20160128 | 39.5 Mb |
| 4 | LAML_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | LAML_GISTIC_ThresholdedByGene-20160128 | 39.5 Mb |
| 6 | LAML_Mutation-20160128 | 2.8 Mb |
| 7 | LAML_RNASeq2Gene-20160128 | 29.6 Mb |
| 8 | LAML_RNASeq2GeneNorm-20160128 | 29.6 Mb |
| 9 | LAML_RNASeqGene-20160128 | 29.8 Mb |
| 10 | LAML_Methylation_methyl27-20160128 | 4.9 Mb |
| 11 | LAML_Methylation_methyl450-20160128 | 75 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

Description

A document describing the TCGA cancer code

Details

```
> experiments( LAML )
ExperimentList class object of length 11:
 [1] LAML_CNASNP-20160128: RaggedExperiment with 874897 rows and 392 columns
 [2] LAML_CNVSNP-20160128: RaggedExperiment with 28324 rows and 380 columns
 [3] LAML_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 191 columns
 [4] LAML_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 16 rows and 191 columns
 [5] LAML_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 191 columns
 [6] LAML_Mutation-20160128: RaggedExperiment with 2585 rows and 197 columns
 [7] LAML_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 173 columns
 [8] LAML_RNASeqGene-20160128: SummarizedExperiment with 19990 rows and 179 columns
 [9] LAML_RNASeq2GeneNorm-20160128: SummarizedExperiment with 17258 rows and 173 columns
 [10] LAML_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 194 columns
 [11] LAML_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 194 columns

> rownames( LAML )
CharacterList of length 11
[["LAML_CNASNP-20160128"]] character(0)
[["LAML_CNVSNP-20160128"]] character(0)
[["LAML_GISTIC_AllByGene-20160128"]] character(0)
[["LAML_GISTIC_Peaks-20160128"]] 1 5 6 7 8 9 2 10 11 12 13 14 15 3 16 4
[["LAML_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["LAML_Mutation-20160128"]] character(0)
[["LAML_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["LAML_RNASeqGene-20160128"]] AADACL3 AADACL4 ABCA4 ... XGPY2 XKRY2 ZFY
[["LAML_RNASeq2GeneNorm-20160128"]] A1BG A2LD1 A2ML1 ... ZZZ3 psiTPTE22 tAKR
[["LAML_Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
...
<1 more element>

> colnames( LAML )
CharacterList of length 11
[["LAML_CNASNP-20160128"]] TCGA-AB-2802-03A-01D-0756-21 ...
[["LAML_CNVSNP-20160128"]] TCGA-AB-2803-03A-01D-0756-21 ...
[["LAML_GISTIC_AllByGene-20160128"]] TCGA-AB-2803-03A-01D-0756-21 ...
[["LAML_GISTIC_Peaks-20160128"]] TCGA-AB-2803-03A-01D-0756-21 ...
[["LAML_GISTIC_ThresholdedByGene-20160128"]] TCGA-AB-2803-03A-01D-0756-21 ...
[["LAML_Mutation-20160128"]] TCGA-AB-2802-03B-01W-0728-08 ...
[["LAML_RNASeq2Gene-20160128"]] TCGA-AB-2803-03A-01T-0734-13 ...
```

```

[["LAML_RNASeqGene-20160128"]] TCGA-AB-2803-03A-01T-0734-13 ...
[["LAML_RNASeq2GeneNorm-20160128"]] TCGA-AB-2803-03 ... TCGA-AB-3012-03
[["LAML_Methylation_methyl27-20160128"]] TCGA-AB-2802-03A-01D-0741-05 ...
...

```

<1 more element>

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | LAML_CNASNP-20160128 | 23.5 Mb |
| 2 | LAML_CNVSNP-20160128 | 0.9 Mb |
| 3 | LAML_GISTIC_AllByGene-20160128 | 39.5 Mb |
| 4 | LAML_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | LAML_GISTIC_ThresholdedByGene-20160128 | 39.5 Mb |
| 6 | LAML_Mutation-20160128 | 2.8 Mb |
| 7 | LAML_RNASeq2Gene-20160128 | 29.6 Mb |
| 8 | LAML_RNASeqGene-20160128 | 29.8 Mb |
| 9 | LAML_RNASeq2GeneNorm-20160128 | 24.9 Mb |
| 10 | LAML_Methylation_methyl27-20160128 | 4.9 Mb |
| 11 | LAML_Methylation_methyl450-20160128 | 75 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
[1,] 120    120  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 12:
 [1] LGG_CNASeq-20160128: RaggedExperiment with 6360 rows and 104 columns
 [2] LGG_CNASNP-20160128: RaggedExperiment with 411918 rows and 1015 columns
 [3] LGG_CNVSNP-20160128: RaggedExperiment with 79791 rows and 1015 columns
 [4] LGG_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 513 columns
 [5] LGG_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 46 rows and 513 columns
 [6] LGG_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 513 columns
 [7] LGG_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 526 columns

```

```
[8] LGG_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 27 columns
[9] LGG_Mutation-20160128: RaggedExperiment with 9885 rows and 286 columns
[10] LGG_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 530 columns
[11] LGG_RPPAArray-20160128: SummarizedExperiment with 201 rows and 435 columns
[12] LGG_Methylation-20160128: SummarizedExperiment with 485577 rows and 530 columns
```

```
> rownames( LGG )
```

```
CharacterList of length 12
```

```
[[ "LGG_CNASeq-20160128" ]] character(0)
[[ "LGG_CNASNP-20160128" ]] character(0)
[[ "LGG_CNVSNP-20160128" ]] character(0)
[[ "LGG_GISTIC_AllByGene-20160128" ]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[[ "LGG_GISTIC_Peaks-20160128" ]] chr1:3814904-5625565 ...
[[ "LGG_GISTIC_ThresholdedByGene-20160128" ]] ACAP3 ...
[[ "LGG_miRNASeqGene-20160128" ]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[[ "LGG_mRNAArray-20160128" ]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[[ "LGG_Mutation-20160128" ]] character(0)
[[ "LGG_RNASeq2GeneNorm-20160128" ]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
...
<2 more elements>
```

```
> colnames( LGG )
```

```
CharacterList of length 12
```

```
[[ "LGG_CNASeq-20160128" ]] TCGA-CS-4938-01B-11D-1891-02 ...
[[ "LGG_CNASNP-20160128" ]] TCGA-CS-4938-01B-11D-1892-01 ...
[[ "LGG_CNVSNP-20160128" ]] TCGA-CS-4938-01B-11D-1892-01 ...
[[ "LGG_GISTIC_AllByGene-20160128" ]] TCGA-CS-4938-01B-11D-1892-01 ...
[[ "LGG_GISTIC_Peaks-20160128" ]] TCGA-CS-4938-01B-11D-1892-01 ...
[[ "LGG_GISTIC_ThresholdedByGene-20160128" ]] TCGA-CS-4938-01B-11D-1892-01 ...
[[ "LGG_miRNASeqGene-20160128" ]] TCGA-CS-4938-01B-11R-1895-13 ...
[[ "LGG_mRNAArray-20160128" ]] TCGA-CS-4942-01A-01R-1470-07 ...
[[ "LGG_Mutation-20160128" ]] TCGA-CS-4938-01B-11D-1893-08 ...
[[ "LGG_RNASeq2GeneNorm-20160128" ]] TCGA-CS-4938-01B-11R-1896-07 ...
...
<2 more elements>
```

```
Sizes of each ExperimentList element:
```

| | | assay size.Mb |
|---|---------------------------------------|---------------|
| 1 | LGG_CNASeq-20160128 | 0.2 Mb |
| 2 | LGG_CNASNP-20160128 | 11.3 Mb |
| 3 | LGG_CNVSNP-20160128 | 2.4 Mb |
| 4 | LGG_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | LGG_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | LGG_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | LGG_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | LGG_mRNAArray-20160128 | 1.1 Mb |
| 9 | LGG_Mutation-20160128 | 4.2 Mb |

```

10      LGG_RNASeq2GeneNorm-20160128  1.3 Mb
11      LGG_RPPAArray-20160128    0.1 Mb
12      LGG_Methylation-20160128  75.1 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 | 1 | asian | 8 |
| black or african american | 21 | white | 475 |
| NA's | 11 | | |

ethnicity:

| | | | | | |
|--------------------|----|------------------------|-----|------|----|
| hispanic or latino | 32 | not hispanic or latino | 449 | NA's | 35 |
|--------------------|----|------------------------|-----|------|----|

Including an additional 1764 columns

See Also

[LGG-v2.0.1](#)

LGG-v2.0.1

Brain Lower Grade Glioma

Description

A document describing the TCGA cancer code

Details

```
> experiments( LGG )
```

ExperimentList class object of length 13:

- [1] LGG_CNASeq-20160128: RaggedExperiment with 6360 rows and 104 columns
- [2] LGG_CNASNP-20160128: RaggedExperiment with 411918 rows and 1015 columns
- [3] LGG_CNVSNP-20160128: RaggedExperiment with 79791 rows and 1015 columns
- [4] LGG_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 513 columns
- [5] LGG_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 46 rows and 513 columns
- [6] LGG_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 513 columns


```
[7] LGG_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 526 columns
[8] LGG_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 27 columns
[9] LGG_Mutation-20160128: RaggedExperiment with 9885 rows and 286 columns
[10] LGG_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 530 columns
[11] LGG_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 530 columns
[12] LGG_RPPAArray-20160128: SummarizedExperiment with 201 rows and 435 columns
[13] LGG_Methylation-20160128: SummarizedExperiment with 485577 rows and 530 columns
```

```
> rownames( LGG )
CharacterList of length 13
[["LGG_CNASeq-20160128"]] character(0)
[["LGG_CNASNP-20160128"]] character(0)
[["LGG_CNVSNP-20160128"]] character(0)
[["LGG_GISTIC_AllByGene-20160128"]] character(0)
[["LGG_GISTIC_Peaks-20160128"]] 21 22 1 2 23 3 24 25 ... 45 16 17 46 18 47 48
[["LGG_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["LGG_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["LGG_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["LGG_Mutation-20160128"]] character(0)
[["LGG_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
...
<3 more elements>
```

```
> colnames( LGG )
CharacterList of length 13
[["LGG_CNASeq-20160128"]] TCGA-CS-4938-01B-11D-1891-02 ...
[["LGG_CNASNP-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["LGG_CNVSNP-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["LGG_GISTIC_AllByGene-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["LGG_GISTIC_Peaks-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["LGG_GISTIC_ThresholdedByGene-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["LGG_miRNASeqGene-20160128"]] TCGA-CS-4938-01B-11R-1895-13 ...
[["LGG_mRNAArray-20160128"]] TCGA-CS-4942-01A-01R-1470-07 ...
[["LGG_Mutation-20160128"]] TCGA-CS-4938-01B-11D-1893-08 ...
[["LGG_RNASeq2Gene-20160128"]] TCGA-CS-4938-01B-11R-1896-07 ...
...
<3 more elements>
```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|---|---------------------------------------|----------|
| 1 | LGG_CNASeq-20160128 | 0.2 Mb |
| 2 | LGG_CNASNP-20160128 | 11.3 Mb |
| 3 | LGG_CNVSNP-20160128 | 2.4 Mb |
| 4 | LGG_GISTIC_AllByGene-20160128 | 100.5 Mb |
| 5 | LGG_GISTIC_Peaks-20160128 | 0.3 Mb |
| 6 | LGG_GISTIC_ThresholdedByGene-20160128 | 100.4 Mb |
| 7 | LGG_miRNASeqGene-20160128 | 4.4 Mb |

| | | |
|----|------------------------------|---------|
| 8 | LGG_mRNAArray-20160128 | 5.9 Mb |
| 9 | LGG_Mutation-20160128 | 4.2 Mb |
| 10 | LGG_RNASeq2Gene-20160128 | 85.5 Mb |
| 11 | LGG_RNASeq2GeneNorm-20160128 | 85.5 Mb |
| 12 | LGG_RPPAArray-20160128 | 0.8 Mb |
| 13 | LGG_Methylation-20160128 | 75.1 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

LGG-v2.1.0

Brain Lower Grade Glioma

Description

A document describing the TCGA cancer code

Details

```
> experiments( LGG )
ExperimentList class object of length 13:
 [1] LGG_CNASeq-20160128: RaggedExperiment with 6360 rows and 104 columns
 [2] LGG_CNASNP-20160128: RaggedExperiment with 411918 rows and 1015 columns
 [3] LGG_CNVSNP-20160128: RaggedExperiment with 79791 rows and 1015 columns
 [4] LGG_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 513 columns
 [5] LGG_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 46 rows and 513 columns
 [6] LGG_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 513 columns
 [7] LGG_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 27 columns
```

```
[8] LGG_Mutation-20160128: RaggedExperiment with 9885 rows and 286 columns
[9] LGG_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 530 columns
[10] LGG_RPPAArray-20160128: SummarizedExperiment with 201 rows and 435 columns
[11] LGG_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 526 columns
[12] LGG_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18311 rows and 530 columns
[13] LGG_Methylation-20160128: SummarizedExperiment with 485577 rows and 530 columns
```

```
> rownames( LGG )
CharacterList of length 13
[["LGG_CNASeq-20160128"]] character(0)
[["LGG_CNASNP-20160128"]] character(0)
[["LGG_CNVSNP-20160128"]] character(0)
[["LGG_GISTIC_AllByGene-20160128"]] character(0)
[["LGG_GISTIC_Peaks-20160128"]] 21 22 1 2 23 3 24 25 ... 45 16 17 46 18 47 48
[["LGG_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["LGG_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["LGG_Mutation-20160128"]] character(0)
[["LGG_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["LGG_RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363
...
<3 more elements>
```

```
> colnames( LGG )
CharacterList of length 13
[["LGG_CNASeq-20160128"]] TCGA-CS-4938-01B-11D-1891-02 ...
[["LGG_CNASNP-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["LGG_CNVSNP-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["LGG_GISTIC_AllByGene-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["LGG_GISTIC_Peaks-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["LGG_GISTIC_ThresholdedByGene-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["LGG_mRNAArray-20160128"]] TCGA-CS-4942-01A-01R-1470-07 ...
[["LGG_Mutation-20160128"]] TCGA-CS-4938-01B-11D-1893-08 ...
[["LGG_RNASeq2Gene-20160128"]] TCGA-CS-4938-01B-11R-1896-07 ...
[["LGG_RPPAArray-20160128"]] TCGA-CS-4938-01B-11-A300-20 ...
...
<3 more elements>
```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|---|---------------------------------------|----------|
| 1 | LGG_CNASeq-20160128 | 0.2 Mb |
| 2 | LGG_CNASNP-20160128 | 11.3 Mb |
| 3 | LGG_CNVSNP-20160128 | 2.4 Mb |
| 4 | LGG_GISTIC_AllByGene-20160128 | 100.5 Mb |
| 5 | LGG_GISTIC_Peaks-20160128 | 0.3 Mb |
| 6 | LGG_GISTIC_ThresholdedByGene-20160128 | 100.4 Mb |
| 7 | LGG_mRNAArray-20160128 | 5.9 Mb |
| 8 | LGG_Mutation-20160128 | 4.2 Mb |

| | | |
|----|------------------------------|---------|
| 9 | LGG_RNASeq2Gene-20160128 | 85.5 Mb |
| 10 | LGG_RPPAArray-20160128 | 0.8 Mb |
| 11 | LGG_miRNASeqGene-20160128 | 4.4 Mb |
| 12 | LGG_RNASeq2GeneNorm-20160128 | 76.4 Mb |
| 13 | LGG_Methylation-20160128 | 75.1 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
[1,] 125 125 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 | 186 | 296 | 34 | | | | |
| yes | | | | | | | |
| NA's | | | | | | | |
| karnofsky_performance_score: | | | | | | | |
| Min. | 40.00 | 80.00 | 90.00 | 86.64 | 100.00 | 100.00 | 209 |
| 1st Qu. | | | | | | | |
| Median | | | | | | | |
| Mean | | | | | | | |
| 3rd Qu. | | | | | | | |
| Max. | | | | | | | |
| NA's | | | | | | | |
| histological_type: | | | | | | | |
| astrocytoma | 194 | | | | | | |
| oligoastrocytoma | | | | 130 | | | |
| oligodendroglioma | | | | | 191 | | |
| NA's | | | | | | | 1 |
| race: | | | | | | | |
| american indian or alaska native | | | | 1 | | | asian |
| black or african american | | | | 21 | | | white |
| NA's | | | | 11 | | | 475 |
| ethnicity: | | | | | | | |
| hispanic or latino | | 32 | | | | | NA's |
| not hispanic or latino | | | | | 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 11:
 [1] LIHC_CNASNP-20160128: RaggedExperiment with 363628 rows and 760 columns
 [2] LIHC_CNVSNP-20160128: RaggedExperiment with 93328 rows and 760 columns
 [3] LIHC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 370 columns
 [4] LIHC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 59 rows and 370 columns
 [5] LIHC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 370 columns
 [6] LIHC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 424 columns
 [7] LIHC_Mutation-20160128: RaggedExperiment with 27892 rows and 198 columns
 [8] LIHC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 423 columns
```

```
[9] LIHC_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 26 columns
[10] LIHC_RPPAArray-20160128: SummarizedExperiment with 219 rows and 184 columns
[11] LIHC_Methylation-20160128: SummarizedExperiment with 485577 rows and 429 columns
```

```
> rownames( LIHC )
CharacterList of length 11
[["LIHC_CNASNP-20160128"]] character(0)
[["LIHC_CNVSNP-20160128"]] character(0)
[["LIHC_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["LIHC_GISTIC_Peaks-20160128"]] chr1:1-6847369 ... chr22:44205320-51304566
[["LIHC_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["LIHC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["LIHC_Mutation-20160128"]] character(0)
[["LIHC_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["LIHC_RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["LIHC_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<1 more element>
```

```
> colnames( LIHC )
CharacterList of length 11
[["LIHC_CNASNP-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["LIHC_CNVSNP-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["LIHC_GISTIC_AllByGene-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["LIHC_GISTIC_Peaks-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["LIHC_GISTIC_ThresholdedByGene-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["LIHC_miRNASeqGene-20160128"]] TCGA-2V-A95S-01A-11R-A37G-13 ...
[["LIHC_Mutation-20160128"]] TCGA-BC-4073-01B-02D-A12Z-10 ...
[["LIHC_RNASeq2GeneNorm-20160128"]] TCGA-2V-A95S-01A-11R-A37K-07 ...
[["LIHC_RNASeqGene-20160128"]] TCGA-BC-4073-01B-02R-A131-07 ...
[["LIHC_RPPAArray-20160128"]] TCGA-BC-4072-01B-21-A40L-20 ...
...
<1 more element>
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | LIHC_CNASNP-20160128 | 9.9 Mb |
| 2 | LIHC_CNVSNP-20160128 | 2.7 Mb |
| 3 | LIHC_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | LIHC_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | LIHC_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | LIHC_miRNASeqGene-20160128 | 0.1 Mb |
| 7 | LIHC_Mutation-20160128 | 16.8 Mb |
| 8 | LIHC_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 9 | LIHC_RNASeqGene-20160128 | 1.3 Mb |
| 10 | LIHC_RPPAArray-20160128 | 0 Mb |
| 11 | LIHC_Methylation-20160128 | 75 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

See Also

[LIHC-v2.0.1](#)

LIHC-v2.0.1

Liver hepatocellular carcinoma

Description

A document describing the TCGA cancer code

Details

```

> experiments( LIHC )
ExperimentList class object of length 12:
 [1] LIHC_CNASNP-20160128: RaggedExperiment with 363628 rows and 760 columns
 [2] LIHC_CNVSNP-20160128: RaggedExperiment with 93328 rows and 760 columns
 [3] LIHC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 370 columns
 [4] LIHC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 59 rows and 370 columns
 [5] LIHC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 370 columns
 [6] LIHC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 424 columns
 [7] LIHC_Mutation-20160128: RaggedExperiment with 27892 rows and 198 columns
 [8] LIHC_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 423 columns
 [9] LIHC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 423 columns
[10] LIHC_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 26 columns
[11] LIHC_RPPAArray-20160128: SummarizedExperiment with 219 rows and 184 columns
[12] LIHC_Methylation-20160128: SummarizedExperiment with 485577 rows and 429 columns

> rownames( LIHC )
CharacterList of length 12
[["LIHC_CNASNP-20160128"]] character(0)
[["LIHC_CNVSNP-20160128"]] character(0)
[["LIHC_GISTIC_AllByGene-20160128"]] character(0)
[["LIHC_GISTIC_Peaks-20160128"]] 28 29 1 2 3 30 4 31 ... 23 24 58 25 26 59 60
[["LIHC_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["LIHC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["LIHC_Mutation-20160128"]] character(0)
[["LIHC_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["LIHC_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["LIHC_RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
...
<2 more elements>

> colnames( LIHC )
CharacterList of length 12
[["LIHC_CNASNP-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["LIHC_CNVSNP-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["LIHC_GISTIC_AllByGene-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["LIHC_GISTIC_Peaks-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["LIHC_GISTIC_ThresholdedByGene-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["LIHC_miRNASeqGene-20160128"]] TCGA-2V-A95S-01A-11R-A37G-13 ...
[["LIHC_Mutation-20160128"]] TCGA-BC-4073-01B-02D-A12Z-10 ...
[["LIHC_RNASeq2Gene-20160128"]] TCGA-2V-A95S-01A-11R-A37K-07 ...
[["LIHC_RNASeq2GeneNorm-20160128"]] TCGA-2V-A95S-01A-11R-A37K-07 ...
[["LIHC_RNASeqGene-20160128"]] TCGA-BC-4073-01B-02R-A131-07 ...
...
<2 more elements>

```

Sizes of each ExperimentList element:

| | | assay | size.Mb |
|----|--|--|---------|
| 1 | | LIHC_CNASNP-20160128 | 9.9 Mb |
| 2 | | LIHC_CNVSNP-20160128 | 2.7 Mb |
| 3 | | LIHC_GISTIC_AllByGene-20160128 | 73.5 Mb |
| 4 | | LIHC_GISTIC_Peaks-20160128 | 0.3 Mb |
| 5 | | LIHC_GISTIC_ThresholdedByGene-20160128 | 73.3 Mb |
| 6 | | LIHC_miRNASeqGene-20160128 | 3.6 Mb |
| 7 | | LIHC_Mutation-20160128 | 16.8 Mb |
| 8 | | LIHC_RNASeq2Gene-20160128 | 68.8 Mb |
| 9 | | LIHC_RNASeq2GeneNorm-20160128 | 68.8 Mb |
| 10 | | LIHC_RNASeqGene-20160128 | 6.6 Mb |
| 11 | | LIHC_RPPAArray-20160128 | 0.4 Mb |
| 12 | | LIHC_Methylation-20160128 | 75.1 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

LIHC-v2.1.0

*Liver hepatocellular carcinoma***Description**

A document describing the TCGA cancer code

Details

```

> experiments( LIHC )
ExperimentList class object of length 12:
 [1] LIHC_CNASNP-20160128: RaggedExperiment with 363628 rows and 760 columns
 [2] LIHC_CNVSNP-20160128: RaggedExperiment with 93328 rows and 760 columns
 [3] LIHC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 370 columns
 [4] LIHC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 59 rows and 370 columns
 [5] LIHC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 370 columns
 [6] LIHC_Mutation-20160128: RaggedExperiment with 27892 rows and 198 columns
 [7] LIHC_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 423 columns
 [8] LIHC_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 26 columns
 [9] LIHC_RPPAArray-20160128: SummarizedExperiment with 219 rows and 184 columns
 [10] LIHC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 424 columns
 [11] LIHC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 17690 rows and 423 columns
 [12] LIHC_Methylation-20160128: SummarizedExperiment with 485577 rows and 429 columns

> rownames( LIHC )
CharacterList of length 12
[["LIHC_CNASNP-20160128"]] character(0)
[["LIHC_CNVSNP-20160128"]] character(0)
[["LIHC_GISTIC_AllByGene-20160128"]] character(0)
[["LIHC_GISTIC_Peaks-20160128"]] 28 29 1 2 3 30 4 31 ... 23 24 58 25 26 59 60
[["LIHC_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["LIHC_Mutation-20160128"]] character(0)
[["LIHC_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["LIHC_RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["LIHC_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["LIHC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
...
<2 more elements>

> colnames( LIHC )
CharacterList of length 12
[["LIHC_CNASNP-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["LIHC_CNVSNP-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["LIHC_GISTIC_AllByGene-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["LIHC_GISTIC_Peaks-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["LIHC_GISTIC_ThresholdedByGene-20160128"]] TCGA-2V-A95S-01A-11D-A36W-01 ...
[["LIHC_Mutation-20160128"]] TCGA-BC-4073-01B-02D-A12Z-10 ...

```

```

[["LIHC_RNASeq2Gene-20160128"]] TCGA-2V-A95S-01A-11R-A37K-07 ...
[["LIHC_RNASeqGene-20160128"]] TCGA-BC-4073-01B-02R-A131-07 ...
[["LIHC_RPPAArray-20160128"]] TCGA-BC-4072-01B-21-A40L-20 ...
[["LIHC_miRNASeqGene-20160128"]] TCGA-2V-A95S-01A-11R-A37G-13 ...
...
<2 more elements>

```

Sizes of each ExperimentList element:

| | | assay | size.Mb |
|----|--|--|---------|
| 1 | | LIHC_CNASNP-20160128 | 9.9 Mb |
| 2 | | LIHC_CNVSNP-20160128 | 2.7 Mb |
| 3 | | LIHC_GISTIC_AllByGene-20160128 | 73.5 Mb |
| 4 | | LIHC_GISTIC_Peaks-20160128 | 0.3 Mb |
| 5 | | LIHC_GISTIC_ThresholdedByGene-20160128 | 73.3 Mb |
| 6 | | LIHC_Mutation-20160128 | 16.8 Mb |
| 7 | | LIHC_RNASeq2Gene-20160128 | 68.8 Mb |
| 8 | | LIHC_RNASeqGene-20160128 | 6.6 Mb |
| 9 | | LIHC_RPPAArray-20160128 | 0.4 Mb |
| 10 | | LIHC_miRNASeqGene-20160128 | 3.6 Mb |
| 11 | | LIHC_RNASeq2GeneNorm-20160128 | 59.3 Mb |
| 12 | | LIHC_Methylation-20160128 | 75.1 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
[1,] 132    132   1.14   0.956   1.63

```

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: | | | NA's |
| hispanic or latino not hispanic or latino | 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 14:
 [1] LUAD_CNASeq-20160128: RaggedExperiment with 399592 rows and 249 columns
 [2] LUAD_CNASNP-20160128: RaggedExperiment with 501475 rows and 1095 columns
 [3] LUAD_CNVSNP-20160128: RaggedExperiment with 115836 rows and 1095 columns
 [4] LUAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 516 columns
 [5] LUAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 73 rows and 516 columns
 [6] LUAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 516 columns
 [7] LUAD_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 498 columns
 [8] LUAD_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 32 columns
 [9] LUAD_Mutation-20160128: RaggedExperiment with 72541 rows and 230 columns
[10] LUAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 576 columns
[11] LUAD_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 162 columns
[12] LUAD_RPPAArray-20160128: SummarizedExperiment with 223 rows and 365 columns
[13] LUAD_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 89 columns
[14] LUAD_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 492 columns

> rownames( LUAD )
CharacterList of length 14
[["LUAD_CNASeq-20160128"]] character(0)
[["LUAD_CNASNP-20160128"]] character(0)
[["LUAD_CNVSNP-20160128"]] character(0)
[["LUAD_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["LUAD_GISTIC_Peaks-20160128"]] chr1:1-32049393 ... chr22:46723702-51304566
[["LUAD_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["LUAD_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["LUAD_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["LUAD_Mutation-20160128"]] character(0)
[["LUAD_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
```



```

...
<4 more elements>

> colnames( LUAD )
CharacterList of length 14
[["LUAD_CNASeq-20160128"]] TCGA-05-4249-01A-01D-1103-02 ...
[["LUAD_CNASNP-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["LUAD_CNVSNP-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["LUAD_GISTIC_AllByGene-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["LUAD_GISTIC_Peaks-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["LUAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["LUAD_miRNASeqGene-20160128"]] TCGA-05-4384-01A-01T-1754-13 ...
[["LUAD_mRNAArray-20160128"]] TCGA-05-4244-01A-01R-1107-07 ...
[["LUAD_Mutation-20160128"]] TCGA-05-4249-01A-01D-1105-08 ...
[["LUAD_RNASeq2GeneNorm-20160128"]] TCGA-05-4244-01A-01R-1107-07 ...
...
<4 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | LUAD_CNASeq-20160128 | 10.8 Mb |
| 2 | LUAD_CNASNP-20160128 | 13.7 Mb |
| 3 | LUAD_CNVSNP-20160128 | 3.4 Mb |
| 4 | LUAD_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | LUAD_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | LUAD_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | LUAD_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | LUAD_mRNAArray-20160128 | 1.1 Mb |
| 9 | LUAD_Mutation-20160128 | 92.9 Mb |
| 10 | LUAD_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 11 | LUAD_RNASeqGene-20160128 | 1.3 Mb |
| 12 | LUAD_RPPAArray-20160128 | 0.1 Mb |
| 13 | LUAD_Methylation_methyl27-20160128 | 4.9 Mb |
| 14 | LUAD_Methylation_methyl450-20160128 | 75.1 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

See Also

[LUAD-v2.0.1](#)

LUAD-v2.0.1

Lung adenocarcinoma

Description

A document describing the TCGA cancer code

Details

```

> experiments( LUAD )
ExperimentList class object of length 15:
 [1] LUAD_CNASeq-20160128: RaggedExperiment with 399592 rows and 249 columns
 [2] LUAD_CNASNP-20160128: RaggedExperiment with 501475 rows and 1095 columns
 [3] LUAD_CNVSNP-20160128: RaggedExperiment with 115836 rows and 1095 columns
 [4] LUAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 516 columns
 [5] LUAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 73 rows and 516 columns

```

```

[6] LUAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 516 columns
[7] LUAD_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 498 columns
[8] LUAD_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 32 columns
[9] LUAD_Mutation-20160128: RaggedExperiment with 72541 rows and 230 columns
[10] LUAD_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 576 columns
[11] LUAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 576 columns
[12] LUAD_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 162 columns
[13] LUAD_RPPAArray-20160128: SummarizedExperiment with 223 rows and 365 columns
[14] LUAD_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 89 columns
[15] LUAD_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 492 columns

```

```

> rownames( LUAD )
CharacterList of length 15
[["LUAD_CNASeq-20160128"]] character(0)
[["LUAD_CNASNP-20160128"]] character(0)
[["LUAD_CNVSNP-20160128"]] character(0)
[["LUAD_GISTIC_AllByGene-20160128"]] character(0)
[["LUAD_GISTIC_Peaks-20160128"]] 30 1 31 2 32 33 34 ... 71 26 72 27 73 28 74
[["LUAD_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["LUAD_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["LUAD_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["LUAD_Mutation-20160128"]] character(0)
[["LUAD_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
...
<5 more elements>

```

```

> colnames( LUAD )
CharacterList of length 15
[["LUAD_CNASeq-20160128"]] TCGA-05-4249-01A-01D-1103-02 ...
[["LUAD_CNASNP-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["LUAD_CNVSNP-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["LUAD_GISTIC_AllByGene-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["LUAD_GISTIC_Peaks-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["LUAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["LUAD_miRNASeqGene-20160128"]] TCGA-05-4384-01A-01T-1754-13 ...
[["LUAD_mRNAArray-20160128"]] TCGA-05-4244-01A-01R-1107-07 ...
[["LUAD_Mutation-20160128"]] TCGA-05-4249-01A-01D-1105-08 ...
[["LUAD_RNASeq2Gene-20160128"]] TCGA-05-4244-01A-01R-1107-07 ...
...
<5 more elements>

```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|---|--------------------------------|----------|
| 1 | LUAD_CNASeq-20160128 | 10.8 Mb |
| 2 | LUAD_CNASNP-20160128 | 13.7 Mb |
| 3 | LUAD_CNVSNP-20160128 | 3.4 Mb |
| 4 | LUAD_GISTIC_AllByGene-20160128 | 101.2 Mb |

| | | |
|----|--|---------|
| 5 | LUAD_GISTIC_Peaks-20160128 | 0.5 Mb |
| 6 | LUAD_GISTIC_ThresholdedByGene-20160128 | 101 Mb |
| 7 | LUAD_miRNASeqGene-20160128 | 4.2 Mb |
| 8 | LUAD_mRNAArray-20160128 | 6.6 Mb |
| 9 | LUAD_Mutation-20160128 | 92.9 Mb |
| 10 | LUAD_RNASeq2Gene-20160128 | 92.7 Mb |
| 11 | LUAD_RNASeq2GeneNorm-20160128 | 92.7 Mb |
| 12 | LUAD_RNASeqGene-20160128 | 27.9 Mb |
| 13 | LUAD_RPPAArray-20160128 | 0.7 Mb |
| 14 | LUAD_Methylation_methyl27-20160128 | 4.9 Mb |
| 15 | LUAD_Methylation_methyl450-20160128 | 75.1 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 | 1 | asian | 8 |
| black or african american | 53 | white | 392 |
| NA's | 66 | | |

ethnicity:

| | | |
|--------------------|------------------------|------|
| hispanic or latino | not hispanic or latino | NA's |
| 7 | 388 | 125 |

Including an additional 2607 columns

LUAD-v2.1.0

Lung adenocarcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( LUAD )
ExperimentList class object of length 15:
 [1] LUAD_CNASeq-20160128: RaggedExperiment with 399592 rows and 249 columns
 [2] LUAD_CNASNP-20160128: RaggedExperiment with 501475 rows and 1095 columns
 [3] LUAD_CNVSNP-20160128: RaggedExperiment with 115836 rows and 1095 columns
 [4] LUAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 516 columns
 [5] LUAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 73 rows and 516 columns
 [6] LUAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 516 columns
 [7] LUAD_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 32 columns
 [8] LUAD_Mutation-20160128: RaggedExperiment with 72541 rows and 230 columns
 [9] LUAD_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 576 columns
 [10] LUAD_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 162 columns
 [11] LUAD_RPPAArray-20160128: SummarizedExperiment with 223 rows and 365 columns
 [12] LUAD_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 498 columns
 [13] LUAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18289 rows and 576 columns
 [14] LUAD_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 89 columns
 [15] LUAD_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 492 columns

> rownames( LUAD )
CharacterList of length 15
[["LUAD_CNASeq-20160128"]] character(0)
[["LUAD_CNASNP-20160128"]] character(0)
[["LUAD_CNVSNP-20160128"]] character(0)
[["LUAD_GISTIC_AllByGene-20160128"]] character(0)
[["LUAD_GISTIC_Peaks-20160128"]] 30 1 31 2 32 33 34 ... 71 26 72 27 73 28 74
[["LUAD_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["LUAD_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["LUAD_Mutation-20160128"]] character(0)
[["LUAD_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["LUAD_RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
...
<5 more elements>

> colnames( LUAD )
CharacterList of length 15
```

```

[["LUAD_CNASeq-20160128"]] TCGA-05-4249-01A-01D-1103-02 ...
[["LUAD_CNASNP-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["LUAD_CNVSNP-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["LUAD_GISTIC_AllByGene-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["LUAD_GISTIC_Peaks-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["LUAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["LUAD_mRNAArray-20160128"]] TCGA-05-4244-01A-01R-1107-07 ...
[["LUAD_Mutation-20160128"]] TCGA-05-4249-01A-01D-1105-08 ...
[["LUAD_RNASeq2Gene-20160128"]] TCGA-05-4244-01A-01R-1107-07 ...
[["LUAD_RNASeqGene-20160128"]] TCGA-05-4244-01A-01R-1107-07 ...

```

...

<5 more elements>

Sizes of each ExperimentList element:

| | assay | size.Mb |
|----|--|----------|
| 1 | LUAD_CNASeq-20160128 | 10.8 Mb |
| 2 | LUAD_CNASNP-20160128 | 13.7 Mb |
| 3 | LUAD_CNVSNP-20160128 | 3.4 Mb |
| 4 | LUAD_GISTIC_AllByGene-20160128 | 101.2 Mb |
| 5 | LUAD_GISTIC_Peaks-20160128 | 0.5 Mb |
| 6 | LUAD_GISTIC_ThresholdedByGene-20160128 | 101 Mb |
| 7 | LUAD_mRNAArray-20160128 | 6.6 Mb |
| 8 | LUAD_Mutation-20160128 | 92.9 Mb |
| 9 | LUAD_RNASeq2Gene-20160128 | 92.7 Mb |
| 10 | LUAD_RNASeqGene-20160128 | 27.9 Mb |
| 11 | LUAD_RPPAArray-20160128 | 0.7 Mb |
| 12 | LUAD_miRNASeqGene-20160128 | 4.2 Mb |
| 13 | LUAD_RNASeq2GeneNorm-20160128 | 82.7 Mb |
| 14 | LUAD_Methylation_methyl27-20160128 | 4.9 Mb |
| 15 | LUAD_Methylation_methyl450-20160128 | 75.1 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
[1,] 184 184 1.7 1.37 2

```

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 16:
 [1] LUSC_CNACGH-20160128: RaggedExperiment with 87417 rows and 407 columns
 [2] LUSC_CNASNP-20160128: RaggedExperiment with 543091 rows and 1035 columns
 [3] LUSC_CNVSNP-20160128: RaggedExperiment with 134864 rows and 1032 columns
 [4] LUSC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 501 columns
 [5] LUSC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 78 rows and 501 columns
 [6] LUSC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 501 columns
 [7] LUSC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 387 columns
 [8] LUSC_mRNAArray_huex-20160128: SummarizedExperiment with 18632 rows and 112 columns
 [9] LUSC_mRNAArray_TX_g4502a-20160128: SummarizedExperiment with 17814 rows and 154 columns
[10] LUSC_mRNAArray_TX_ht_hg_u133a-20160128: SummarizedExperiment with 12042 rows and 133 columns
[11] LUSC_Mutation-20160128: RaggedExperiment with 65305 rows and 178 columns
[12] LUSC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 552 columns
[13] LUSC_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 240 columns

```

```
[14] LUSC_RPPAArray-20160128: SummarizedExperiment with 223 rows and 328 columns
[15] LUSC_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 160 columns
[16] LUSC_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 412 columns
```

```
> rownames( LUSC )
CharacterList of length 16
[["LUSC_CNACGH-20160128"]] character(0)
[["LUSC_CNASNP-20160128"]] character(0)
[["LUSC_CNVSNP-20160128"]] character(0)
[["LUSC_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["LUSC_GISTIC_Peaks-20160128"]] chr1:1-31262836 ... chr22:45736500-51304566
[["LUSC_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["LUSC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["LUSC_mRNAArray_huex-20160128"]] C9orf152 ELMO2 RPS11 ... SLC39A6 CTSC AQP7
[["LUSC_mRNAArray_TX_g4502a-20160128"]] ELMO2 CREB3L1 RPS11 ... AQP7 CTSC
[["LUSC_mRNAArray_TX_ht_hg_u133a-20160128"]] AACS FSTL1 ELMO2 ... CTSC AQP7
...
<6 more elements>
```

```
> colnames( LUSC )
CharacterList of length 16
[["LUSC_CNACGH-20160128"]] TCGA-18-3406-01A-01D-1519-02 ...
[["LUSC_CNASNP-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_CNVSNP-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_GISTIC_AllByGene-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_GISTIC_Peaks-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_GISTIC_ThresholdedByGene-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_miRNASeqGene-20160128"]] TCGA-18-5592-01A-01T-1634-13 ...
[["LUSC_mRNAArray_huex-20160128"]] TCGA-18-3406-01A-01R-1030-03 ...
[["LUSC_mRNAArray_TX_g4502a-20160128"]] TCGA-18-3406-01A-01R-0980-07 ...
[["LUSC_mRNAArray_TX_ht_hg_u133a-20160128"]] TCGA-18-3406-01A-01R-1031-01 ...
...
<6 more elements>
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | LUSC_CNACGH-20160128 | 2.5 Mb |
| 2 | LUSC_CNASNP-20160128 | 14.8 Mb |
| 3 | LUSC_CNVSNP-20160128 | 3.9 Mb |
| 4 | LUSC_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | LUSC_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | LUSC_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | LUSC_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | LUSC_mRNAArray_huex-20160128 | 1.2 Mb |
| 9 | LUSC_mRNAArray_TX_g4502a-20160128 | 1.1 Mb |
| 10 | LUSC_mRNAArray_TX_ht_hg_u133a-20160128 | 0.8 Mb |
| 11 | LUSC_Mutation-20160128 | 81 Mb |

```

12      LUSC_RNASeq2GeneNorm-20160128  1.3 Mb
13      LUSC_RNASeqGene-20160128     1.3 Mb
14      LUSC_RPPAArray-20160128      0 Mb
15      LUSC_Methylation_methyl27-20160128  4.9 Mb
16      LUSC_Methylation_methyl450-20160128  75 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 carcinoma | 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 |
| NA's | 351 |
| 113 | |

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

Including an additional 2238 columns

See Also

[LUSC-v2.0.1](#)

LUSC-v2.0.1

Lung squamous cell carcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( LUSC )
ExperimentList class object of length 17:
 [1] LUSC_CNACGH-20160128: RaggedExperiment with 87417 rows and 407 columns
 [2] LUSC_CNASNP-20160128: RaggedExperiment with 543091 rows and 1035 columns
 [3] LUSC_CNVSNP-20160128: RaggedExperiment with 134864 rows and 1032 columns
 [4] LUSC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 501 columns
 [5] LUSC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 78 rows and 501 columns
 [6] LUSC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 501 columns
 [7] LUSC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 387 columns
 [8] LUSC_mRNAArray_huex-20160128: SummarizedExperiment with 18632 rows and 112 columns
 [9] LUSC_mRNAArray_TX_g4502a-20160128: SummarizedExperiment with 17814 rows and 154 columns
 [10] LUSC_mRNAArray_TX_ht_hg_u133a-20160128: SummarizedExperiment with 12042 rows and 133 columns
 [11] LUSC_Mutation-20160128: RaggedExperiment with 65305 rows and 178 columns
 [12] LUSC_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 552 columns
 [13] LUSC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 552 columns
 [14] LUSC_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 240 columns
 [15] LUSC_RPPAArray-20160128: SummarizedExperiment with 223 rows and 328 columns
 [16] LUSC_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 160 columns
 [17] LUSC_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 412 columns

> rownames( LUSC )
CharacterList of length 17
[["LUSC_CNACGH-20160128"]] character(0)
[["LUSC_CNASNP-20160128"]] character(0)
[["LUSC_CNVSNP-20160128"]] character(0)
[["LUSC_GISTIC_AllByGene-20160128"]] character(0)
[["LUSC_GISTIC_Peaks-20160128"]] 31 32 1 33 2 34 3 ... 27 28 76 77 78 29 79
```

```

[["LUSC_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["LUSC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["LUSC_mRNAArray_huex-20160128"]] C9orf152 ELMO2 RPS11 ... SLC39A6 CTSC AQP7
[["LUSC_mRNAArray_TX_g4502a-20160128"]] ELMO2 CREB3L1 RPS11 ... AQP7 CTSC
[["LUSC_mRNAArray_TX_ht_hg_u133a-20160128"]] AACS FSTL1 ELMO2 ... CTSC AQP7
...
<7 more elements>

```

```

> colnames( LUSC )
CharacterList of length 17
[["LUSC_CNACGH-20160128"]] TCGA-18-3406-01A-01D-1519-02 ...
[["LUSC_CNASNP-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_CNVSNP-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_GISTIC_AllByGene-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_GISTIC_Peaks-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_GISTIC_ThresholdedByGene-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_miRNASeqGene-20160128"]] TCGA-18-5592-01A-01T-1634-13 ...
[["LUSC_mRNAArray_huex-20160128"]] TCGA-18-3406-01A-01R-1030-03 ...
[["LUSC_mRNAArray_TX_g4502a-20160128"]] TCGA-18-3406-01A-01R-0980-07 ...
[["LUSC_mRNAArray_TX_ht_hg_u133a-20160128"]] TCGA-18-3406-01A-01R-1031-01 ...
...
<7 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | LUSC_CNACGH-20160128 | 2.5 Mb |
| 2 | LUSC_CNASNP-20160128 | 14.8 Mb |
| 3 | LUSC_CNVSNP-20160128 | 3.9 Mb |
| 4 | LUSC_GISTIC_AllByGene-20160128 | 98.3 Mb |
| 5 | LUSC_GISTIC_Peaks-20160128 | 0.5 Mb |
| 6 | LUSC_GISTIC_ThresholdedByGene-20160128 | 98.1 Mb |
| 7 | LUSC_miRNASeqGene-20160128 | 3.3 Mb |
| 8 | LUSC_mRNAArray_huex-20160128 | 18.3 Mb |
| 9 | LUSC_mRNAArray_TX_g4502a-20160128 | 23.2 Mb |
| 10 | LUSC_mRNAArray_TX_ht_hg_u133a-20160128 | 13.7 Mb |
| 11 | LUSC_Mutation-20160128 | 81 Mb |
| 12 | LUSC_RNASeq2Gene-20160128 | 89 Mb |
| 13 | LUSC_RNASeq2GeneNorm-20160128 | 89 Mb |
| 14 | LUSC_RNASeqGene-20160128 | 40.1 Mb |
| 15 | LUSC_RPPAArray-20160128 | 0.6 Mb |
| 16 | LUSC_Methylation_methyl27-20160128 | 4.9 Mb |
| 17 | LUSC_Methylation_methyl450-20160128 | 75.1 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 carcinoma | 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 |
| NA's | 351 |
| 113 | |

ethnicity:

| | | |
|--------------------|------------------------|------|
| hispanic or latino | not hispanic or latino | NA's |
| 8 | 319 | 177 |

Including an additional 2238 columns

Description

A document describing the TCGA cancer code

Details

```

> experiments( LUSC )
ExperimentList class object of length 17:
 [1] LUSC_CNACGH-20160128: RaggedExperiment with 87417 rows and 407 columns
 [2] LUSC_CNASNP-20160128: RaggedExperiment with 543091 rows and 1035 columns
 [3] LUSC_CNVSNP-20160128: RaggedExperiment with 134864 rows and 1032 columns
 [4] LUSC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 501 columns
 [5] LUSC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 78 rows and 501 columns
 [6] LUSC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 501 columns
 [7] LUSC_mRNAArray_huex-20160128: SummarizedExperiment with 18632 rows and 112 columns
 [8] LUSC_mRNAArray_TX_g4502a-20160128: SummarizedExperiment with 17814 rows and 154 columns
 [9] LUSC_mRNAArray_TX_ht_hg_u133a-20160128: SummarizedExperiment with 12042 rows and 133 columns
 [10] LUSC_Mutation-20160128: RaggedExperiment with 65305 rows and 178 columns
 [11] LUSC_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 552 columns
 [12] LUSC_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 240 columns
 [13] LUSC_RPPAArray-20160128: SummarizedExperiment with 223 rows and 328 columns
 [14] LUSC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 387 columns
 [15] LUSC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18520 rows and 552 columns
 [16] LUSC_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 160 columns
 [17] LUSC_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 412 columns

> rownames( LUSC )
CharacterList of length 17
[["LUSC_CNACGH-20160128"]] character(0)
[["LUSC_CNASNP-20160128"]] character(0)
[["LUSC_CNVSNP-20160128"]] character(0)
[["LUSC_GISTIC_AllByGene-20160128"]] character(0)
[["LUSC_GISTIC_Peaks-20160128"]] 31 32 1 33 2 34 3 ... 27 28 76 77 78 29 79
[["LUSC_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["LUSC_mRNAArray_huex-20160128"]] C9orf152 ELMO2 RPS11 ... SLC39A6 CTSC AQP7
[["LUSC_mRNAArray_TX_g4502a-20160128"]] ELMO2 CREB3L1 RPS11 ... AQP7 CTSC
[["LUSC_mRNAArray_TX_ht_hg_u133a-20160128"]] AACS FSTL1 ELMO2 ... CTSC AQP7
[["LUSC_Mutation-20160128"]] character(0)
...
<7 more elements>

> colnames( LUSC )
CharacterList of length 17
[["LUSC_CNACGH-20160128"]] TCGA-18-3406-01A-01D-1519-02 ...
[["LUSC_CNASNP-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_CNVSNP-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_GISTIC_AllByGene-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_GISTIC_Peaks-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_GISTIC_ThresholdedByGene-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...

```

```

[["LUSC_mRNAArray_huex-20160128"]] TCGA-18-3406-01A-01R-1030-03 ...
[["LUSC_mRNAArray_TX_g4502a-20160128"]] TCGA-18-3406-01A-01R-0980-07 ...
[["LUSC_mRNAArray_TX_ht_hg_u133a-20160128"]] TCGA-18-3406-01A-01R-1031-01 ...
[["LUSC_Mutation-20160128"]] TCGA-18-3406-01A-01D-0983-08 ...
...
<7 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | LUSC_CNACGH-20160128 | 2.5 Mb |
| 2 | LUSC_CNASNP-20160128 | 14.8 Mb |
| 3 | LUSC_CNVSNP-20160128 | 3.9 Mb |
| 4 | LUSC_GISTIC_AllByGene-20160128 | 98.3 Mb |
| 5 | LUSC_GISTIC_Peaks-20160128 | 0.5 Mb |
| 6 | LUSC_GISTIC_ThresholdedByGene-20160128 | 98.1 Mb |
| 7 | LUSC_mRNAArray_huex-20160128 | 18.3 Mb |
| 8 | LUSC_mRNAArray_TX_g4502a-20160128 | 23.2 Mb |
| 9 | LUSC_mRNAArray_TX_ht_hg_u133a-20160128 | 13.7 Mb |
| 10 | LUSC_Mutation-20160128 | 81 Mb |
| 11 | LUSC_RNASeq2Gene-20160128 | 89 Mb |
| 12 | LUSC_RNASeqGene-20160128 | 40.1 Mb |
| 13 | LUSC_RPPAArray-20160128 | 0.6 Mb |
| 14 | LUSC_miRNASeqGene-20160128 | 3.3 Mb |
| 15 | LUSC_RNASeq2GeneNorm-20160128 | 80.4 Mb |
| 16 | LUSC_Methylation_methyl27-20160128 | 4.9 Mb |
| 17 | LUSC_Methylation_methyl450-20160128 | 75.1 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
[1,] 215    215    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 carcinoma
                                           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 9:
 [1] MESO_CNASNP-20160128: RaggedExperiment with 90003 rows and 173 columns
 [2] MESO_CNVSNP-20160128: RaggedExperiment with 18335 rows and 172 columns
 [3] MESO_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 87 columns
 [4] MESO_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 21 rows and 87 columns
 [5] MESO_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 87 columns
 [6] MESO_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 87 columns
 [7] MESO_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 87 columns

```

```
[8] MESO_RPPAArray-20160128: SummarizedExperiment with 193 rows and 63 columns
[9] MESO_Methylation-20160128: SummarizedExperiment with 485577 rows and 87 columns
```

```
> rownames( MESO )
CharacterList of length 9
[["MESO_CNASNP-20160128"]] character(0)
[["MESO_CNVSNP-20160128"]] character(0)
[["MESO_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["MESO_GISTIC_Peaks-20160128"]] chr1:1-31262836 ... chr22:29969457-30128393
[["MESO_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["MESO_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["MESO_RNASeqGeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["MESO_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["MESO_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
```

```
> colnames( MESO )
CharacterList of length 9
[["MESO_CNASNP-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_CNVSNP-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_GISTIC_AllByGene-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_GISTIC_Peaks-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_GISTIC_ThresholdedByGene-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_miRNASeqGene-20160128"]] TCGA-3H-AB3K-01A-11R-A404-13 ...
[["MESO_RNASeqGeneNorm-20160128"]] TCGA-3H-AB3K-01A-11R-A40A-07 ...
[["MESO_RPPAArray-20160128"]] TCGA-3H-AB3K-01A-21-A450-20 ...
[["MESO_Methylation-20160128"]] TCGA-3H-AB3K-01A-11D-A39S-05 ...
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|---|--|---------------|
| 1 | MESO_CNASNP-20160128 | 2.5 Mb |
| 2 | MESO_CNVSNP-20160128 | 0.6 Mb |
| 3 | MESO_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | MESO_GISTIC_Peaks-20160128 | 0 Mb |
| 5 | MESO_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | MESO_miRNASeqGene-20160128 | 0.1 Mb |
| 7 | MESO_RNASeqGeneNorm-20160128 | 1.3 Mb |
| 8 | MESO_RPPAArray-20160128 | 0 Mb |
| 9 | MESO_Methylation-20160128 | 75 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

See Also

[MESO-v2.0.1](#)

MESO-v2.0.1

Mesothelioma

Description

A document describing the TCGA cancer code

Details

```
> experiments( MESO )
```

ExperimentList class object of length 10:

- [1] MESO_CNASNP-20160128: RaggedExperiment with 90003 rows and 173 columns
- [2] MESO_CNVSNP-20160128: RaggedExperiment with 18335 rows and 172 columns
- [3] MESO_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 87 columns
- [4] MESO_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 21 rows and 87 columns
- [5] MESO_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 87 columns
- [6] MESO_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 87 columns


```

[7] MESO_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 87 columns
[8] MESO_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 87 columns
[9] MESO_RPPAArray-20160128: SummarizedExperiment with 193 rows and 63 columns
[10] MESO_Methylation-20160128: SummarizedExperiment with 485577 rows and 87 columns

```

```

> rownames( MESO )
CharacterList of length 10
[["MESO_CNASNP-20160128"]] character(0)
[["MESO_CNVSNP-20160128"]] character(0)
[["MESO_GISTIC_AllByGene-20160128"]] character(0)
[["MESO_GISTIC_Peaks-20160128"]] 1 2 3 4 5 6 7 8 ... 14 15 16 17 18 19 20 21
[["MESO_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["MESO_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["MESO_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["MESO_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["MESO_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["MESO_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873

> colnames( MESO )
CharacterList of length 10
[["MESO_CNASNP-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_CNVSNP-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_GISTIC_AllByGene-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_GISTIC_Peaks-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_GISTIC_ThresholdedByGene-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_miRNASeqGene-20160128"]] TCGA-3H-AB3K-01A-11R-A404-13 ...
[["MESO_RNASeq2Gene-20160128"]] TCGA-3H-AB3K-01A-11R-A40A-07 ...
[["MESO_RNASeq2GeneNorm-20160128"]] TCGA-3H-AB3K-01A-11R-A40A-07 ...
[["MESO_RPPAArray-20160128"]] TCGA-3H-AB3K-01A-21-A450-20 ...
[["MESO_Methylation-20160128"]] TCGA-3H-AB3K-01A-11D-A39S-05 ...

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | MESO_CNASNP-20160128 | 2.5 Mb |
| 2 | MESO_CNVSNP-20160128 | 0.6 Mb |
| 3 | MESO_GISTIC_AllByGene-20160128 | 19.9 Mb |
| 4 | MESO_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | MESO_GISTIC_ThresholdedByGene-20160128 | 19.8 Mb |
| 6 | MESO_miRNASeqGene-20160128 | 0.9 Mb |
| 7 | MESO_RNASeq2Gene-20160128 | 16.2 Mb |
| 8 | MESO_RNASeq2GeneNorm-20160128 | 16.2 Mb |
| 9 | MESO_RPPAArray-20160128 | 0.1 Mb |
| 10 | MESO_Methylation-20160128 | 75 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

 MESO-v2.1.0

Mesothelioma

Description

A document describing the TCGA cancer code

Details

```
> experiments( MESO )
ExperimentList class object of length 10:
 [1] MESO_CNASNP-20160128: RaggedExperiment with 90003 rows and 173 columns
 [2] MESO_CNVSNP-20160128: RaggedExperiment with 18335 rows and 172 columns
 [3] MESO_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 87 columns
 [4] MESO_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 21 rows and 87 columns
 [5] MESO_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 87 columns
```

```
[6] MESO_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 87 columns
[7] MESO_RPPAArray-20160128: SummarizedExperiment with 193 rows and 63 columns
[8] MESO_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 87 columns
[9] MESO_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18192 rows and 87 columns
[10] MESO_Methylation-20160128: SummarizedExperiment with 485577 rows and 87 columns
```

```
> rownames( MESO )
CharacterList of length 10
[["MESO_CNASNP-20160128"]] character(0)
[["MESO_CNVSNP-20160128"]] character(0)
[["MESO_GISTIC_AllByGene-20160128"]] character(0)
[["MESO_GISTIC_Peaks-20160128"]] 1 2 3 4 5 6 7 8 ... 14 15 16 17 18 19 20 21
[["MESO_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["MESO_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
[["MESO_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["MESO_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["MESO_RNASeq2GeneNorm-20160128"]] A1BG A2BP1 A2LD1 ... ZZEF1 ZZZ3 psiTPTE22
[["MESO_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
```

```
> colnames( MESO )
CharacterList of length 10
[["MESO_CNASNP-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_CNVSNP-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_GISTIC_AllByGene-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_GISTIC_Peaks-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_GISTIC_ThresholdedByGene-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_RNASeq2Gene-20160128"]] TCGA-3H-AB3K-01A-11R-A40A-07 ...
[["MESO_RPPAArray-20160128"]] TCGA-3H-AB3K-01A-21-A450-20 ...
[["MESO_miRNASeqGene-20160128"]] TCGA-3H-AB3K-01A-11R-A404-13 ...
[["MESO_RNASeq2GeneNorm-20160128"]] TCGA-3H-AB3K-01 ... TCGA-ZN-A9VW-01
[["MESO_Methylation-20160128"]] TCGA-3H-AB3K-01A-11D-A39S-05 ...
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | MESO_CNASNP-20160128 | 2.5 Mb |
| 2 | MESO_CNVSNP-20160128 | 0.6 Mb |
| 3 | MESO_GISTIC_AllByGene-20160128 | 19.9 Mb |
| 4 | MESO_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | MESO_GISTIC_ThresholdedByGene-20160128 | 19.8 Mb |
| 6 | MESO_RNASeq2Gene-20160128 | 16.2 Mb |
| 7 | MESO_RPPAArray-20160128 | 0.1 Mb |
| 8 | MESO_miRNASeqGene-20160128 | 0.9 Mb |
| 9 | MESO_RNASeq2GeneNorm-20160128 | 14.3 Mb |
| 10 | MESO_Methylation-20160128 | 75 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
[1,] 73      73   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 19:
[1] OV_CNACGH_CGH_hg_244a-20160128: RaggedExperiment with 128946 rows and 472 columns
[2] OV_CNACGH_CGH_hg_415k_g4124a-20160128: RaggedExperiment with 245847 rows and 674 columns
[3] OV_CNASNP-20160128: RaggedExperiment with 907765 rows and 1145 columns
[4] OV_CNVSNP-20160128: RaggedExperiment with 261680 rows and 1141 columns

```

```

[5] OV_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 573 columns
[6] OV_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 70 rows and 573 columns
[7] OV_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 573 columns
[8] OV_miRNAArray-20160128: SummarizedExperiment with 821 rows and 573 columns
[9] OV_miRNASeqGene-20160128: SummarizedExperiment with 705 rows and 461 columns
[10] OV_mRNAArray_huex-20160128: SummarizedExperiment with 18632 rows and 575 columns
[11] OV_mRNAArray_TX_g4502a_1-20160128: SummarizedExperiment with 17814 rows and 546 columns
[12] OV_mRNAArray_TX_g4502a-20160128: SummarizedExperiment with 17814 rows and 31 columns
[13] OV_mRNAArray_TX_ht_hg_u133a-20160128: SummarizedExperiment with 12042 rows and 524 columns
[14] OV_Mutation-20160128: RaggedExperiment with 20219 rows and 316 columns
[15] OV_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 307 columns
[16] OV_RNASeqGene-20160128: SummarizedExperiment with 19990 rows and 299 columns
[17] OV_RPPAArray-20160128: SummarizedExperiment with 208 rows and 427 columns
[18] OV_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 591 columns
[19] OV_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 10 columns

```

```
> rownames( OV )
```

```
CharacterList of length 19
```

```

[["OV_CNACGH_CGH_hg_244a-20160128"]] character(0)
[["OV_CNACGH_CGH_hg_415k_g4124a-20160128"]] character(0)
[["OV_CNASNP-20160128"]] character(0)
[["OV_CNVSNP-20160128"]] character(0)
[["OV_GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["OV_GISTIC_Peaks-20160128"]] chr1:26963410-27570286 ...
[["OV_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["OV_miRNAArray-20160128"]] DarkCorner dmr_285 ... NegativeControl SCorner3
[["OV_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["OV_mRNAArray_huex-20160128"]] C9orf152 ELM02 RPS11 ... SLC39A6 CTSC AQP7
...
<9 more elements>

```

```
> colnames( OV )
```

```
CharacterList of length 19
```

```

[["OV_CNACGH_CGH_hg_244a-20160128"]] TCGA-04-1331-01A-01D-0431-02 ...
[["OV_CNACGH_CGH_hg_415k_g4124a-20160128"]] TCGA-04-1353-01A-01D-1046-02 ...
[["OV_CNASNP-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_CNVSNP-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_GISTIC_AllByGene-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_GISTIC_Peaks-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_GISTIC_ThresholdedByGene-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_miRNAArray-20160128"]] TCGA-04-1331-01A-01T-0438-07 ...
[["OV_miRNASeqGene-20160128"]] TCGA-04-1331-01A-01R-1569-13 ...
[["OV_mRNAArray_huex-20160128"]] TCGA-04-1331-01A-01R-0435-03 ...
...
<9 more elements>

```

```
Sizes of each ExperimentList element:
```

| | | assay | size.Mb |
|----|---------------------------------------|--------------------------------|---------|
| 1 | | OV_CNACGH_CGH_hg_244a-20160128 | 3.6 Mb |
| 2 | OV_CNACGH_CGH_hg_415k_g4124a-20160128 | | 6.8 Mb |
| 3 | | OV_CNASNP-20160128 | 24.6 Mb |
| 4 | | OV_CNVSNP-20160128 | 7.3 Mb |
| 5 | | OV_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 6 | | OV_GISTIC_Peaks-20160128 | 0.1 Mb |
| 7 | OV_GISTIC_ThresholdedByGene-20160128 | | 4.9 Mb |
| 8 | | OV_miRNAArray-20160128 | 0.1 Mb |
| 9 | | OV_miRNASeqGene-20160128 | 0.1 Mb |
| 10 | | OV_mRNAArray_huex-20160128 | 1.2 Mb |
| 11 | OV_mRNAArray_TX_g4502a_1-20160128 | | 1.2 Mb |
| 12 | OV_mRNAArray_TX_g4502a-20160128 | | 1.1 Mb |
| 13 | OV_mRNAArray_TX_ht_hg_u133a-20160128 | | 0.8 Mb |
| 14 | | OV_Mutation-20160128 | 10.3 Mb |
| 15 | | OV_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 16 | | OV_RNASeqGene-20160128 | 1.3 Mb |
| 17 | | OV_RPPAArray-20160128 | 0.1 Mb |
| 18 | OV_Methylation_methyl27-20160128 | | 4.9 Mb |
| 19 | OV_Methylation_methyl450-20160128 | | 75 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

See Also

[OV-v2.0.1](#)

Description

A document describing the TCGA cancer code

Details

```

> experiments( OV )
ExperimentList class object of length 19:
 [1] OV_CNACGH_CGH_hg_244a-20160128: RaggedExperiment with 128946 rows and 472 columns
 [2] OV_CNACGH_CGH_hg_415k_g4124a-20160128: RaggedExperiment with 245847 rows and 674 columns
 [3] OV_CNASNP-20160128: RaggedExperiment with 907765 rows and 1145 columns
 [4] OV_CNVSNP-20160128: RaggedExperiment with 261680 rows and 1141 columns
 [5] OV_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 573 columns
 [6] OV_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 70 rows and 573 columns
 [7] OV_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 573 columns
 [8] OV_miRNAArray-20160128: SummarizedExperiment with 821 rows and 573 columns
 [9] OV_miRNASeqGene-20160128: SummarizedExperiment with 705 rows and 461 columns
 [10] OV_mRNAArray_huex-20160128: SummarizedExperiment with 18632 rows and 575 columns
 [11] OV_mRNAArray_TX_g4502a-20160128: SummarizedExperiment with 17814 rows and 577 columns
 [12] OV_mRNAArray_TX_ht_hg_u133a-20160128: SummarizedExperiment with 12042 rows and 524 columns
 [13] OV_Mutation-20160128: RaggedExperiment with 20219 rows and 316 columns
 [14] OV_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 307 columns
 [15] OV_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 307 columns
 [16] OV_RNASeqGene-20160128: SummarizedExperiment with 19990 rows and 299 columns
 [17] OV_RPPAArray-20160128: SummarizedExperiment with 208 rows and 427 columns
 [18] OV_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 591 columns
 [19] OV_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 10 columns

> rownames( OV )
CharacterList of length 19
[["OV_CNACGH_CGH_hg_244a-20160128"]] character(0)
[["OV_CNACGH_CGH_hg_415k_g4124a-20160128"]] character(0)
[["OV_CNASNP-20160128"]] character(0)
[["OV_CNVSNP-20160128"]] character(0)
[["OV_GISTIC_AllByGene-20160128"]] character(0)
[["OV_GISTIC_Peaks-20160128"]] 34 1 2 35 3 36 4 37 ... 70 28 29 30 71 31 72
[["OV_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["OV_miRNAArray-20160128"]] DarkCorner dmr_285 ... NegativeControl SCorner3
[["OV_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["OV_mRNAArray_huex-20160128"]] C9orf152 ELM02 RPS11 ... SLC39A6 CTSC AQP7
...
<9 more elements>

> colnames( OV )
CharacterList of length 19
[["OV_CNACGH_CGH_hg_244a-20160128"]] TCGA-04-1331-01A-01D-0431-02 ...
[["OV_CNACGH_CGH_hg_415k_g4124a-20160128"]] TCGA-04-1353-01A-01D-1046-02 ...
[["OV_CNASNP-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_CNVSNP-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...

```

```

[[ "OV_GISTIC_AllByGene-20160128" ]] TCGA-04-1331-01A-01D-0428-01 ...
[[ "OV_GISTIC_Peaks-20160128" ]] TCGA-04-1331-01A-01D-0428-01 ...
[[ "OV_GISTIC_ThresholdedByGene-20160128" ]] TCGA-04-1331-01A-01D-0428-01 ...
[[ "OV_miRNAArray-20160128" ]] TCGA-04-1331-01A-01T-0438-07 ...
[[ "OV_miRNASeqGene-20160128" ]] TCGA-04-1331-01A-01R-1569-13 ...
[[ "OV_mRNAArray_huex-20160128" ]] TCGA-04-1331-01A-01R-0435-03 ...
...
<9 more elements>

```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|----|---------------------------------------|----------|
| 1 | OV_CNACGH_CGH_hg_244a-20160128 | 3.6 Mb |
| 2 | OV_CNACGH_CGH_hg_415k_g4124a-20160128 | 6.8 Mb |
| 3 | OV_CNASNP-20160128 | 24.6 Mb |
| 4 | OV_CNVSNP-20160128 | 7.3 Mb |
| 5 | OV_GISTIC_AllByGene-20160128 | 112 Mb |
| 6 | OV_GISTIC_Peaks-20160128 | 0.5 Mb |
| 7 | OV_GISTIC_ThresholdedByGene-20160128 | 111.7 Mb |
| 8 | OV_miRNAArray-20160128 | 3.8 Mb |
| 9 | OV_miRNASeqGene-20160128 | 2.7 Mb |
| 10 | OV_mRNAArray_huex-20160128 | 84.2 Mb |
| 11 | OV_mRNAArray_TX_g4502a-20160128 | 80.7 Mb |
| 12 | OV_mRNAArray_TX_ht_hg_u133a-20160128 | 49.7 Mb |
| 13 | OV_Mutation-20160128 | 10.3 Mb |
| 14 | OV_RNASeq2Gene-20160128 | 50.6 Mb |
| 15 | OV_RNASeq2GeneNorm-20160128 | 50.6 Mb |
| 16 | OV_RNASeqGene-20160128 | 48.1 Mb |
| 17 | OV_RPPAArray-20160128 | 0.8 Mb |
| 18 | OV_Methylation_methyl27-20160128 | 4.9 Mb |
| 19 | OV_Methylation_methyl450-20160128 | 75 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

OV-v2.1.0

Ovarian serous cystadenocarcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( OV )
ExperimentList class object of length 19:
 [1] OV_CNACGH_CGH_hg_244a-20160128: RaggedExperiment with 128946 rows and 472 columns
 [2] OV_CNACGH_CGH_hg_415k_g4124a-20160128: RaggedExperiment with 245847 rows and 674 columns
 [3] OV_CNASNP-20160128: RaggedExperiment with 907765 rows and 1145 columns
 [4] OV_CNVSNP-20160128: RaggedExperiment with 261680 rows and 1141 columns
 [5] OV_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 573 columns
 [6] OV_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 70 rows and 573 columns
 [7] OV_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 573 columns
 [8] OV_miRNAArray-20160128: SummarizedExperiment with 821 rows and 573 columns
 [9] OV_mRNAArray_huex-20160128: SummarizedExperiment with 18632 rows and 575 columns
 [10] OV_mRNAArray_TX_g4502a-20160128: SummarizedExperiment with 17814 rows and 577 columns
 [11] OV_mRNAArray_TX_ht_hg_u133a-20160128: SummarizedExperiment with 12042 rows and 524 columns
 [12] OV_Mutation-20160128: RaggedExperiment with 20219 rows and 316 columns
 [13] OV_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 307 columns
 [14] OV_RNASeqGene-20160128: SummarizedExperiment with 19990 rows and 299 columns
 [15] OV_RPPAArray-20160128: SummarizedExperiment with 208 rows and 427 columns
 [16] OV_miRNASeqGene-20160128: SummarizedExperiment with 705 rows and 461 columns
 [17] OV_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18571 rows and 307 columns
 [18] OV_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 591 columns
 [19] OV_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 10 columns

> rownames( OV )
CharacterList of length 19
[["OV_CNACGH_CGH_hg_244a-20160128"]] character(0)
[["OV_CNACGH_CGH_hg_415k_g4124a-20160128"]] character(0)
[["OV_CNASNP-20160128"]] character(0)
[["OV_CNVSNP-20160128"]] character(0)
[["OV_GISTIC_AllByGene-20160128"]] character(0)
[["OV_GISTIC_Peaks-20160128"]] 34 1 2 35 3 36 4 37 ... 70 28 29 30 71 31 72
[["OV_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["OV_miRNAArray-20160128"]] DarkCorner dmr_285 ... NegativeControl SCorner3
[["OV_mRNAArray_huex-20160128"]] C9orf152 ELM02 RPS11 ... SLC39A6 CTSC AQP7
[["OV_mRNAArray_TX_g4502a-20160128"]] ELM02 CREB3L1 RPS11 ... AQP7 CTSC
...
<9 more elements>
```

```

> colnames( OV )
CharacterList of length 19
[["OV_CNACGH_CGH_hg_244a-20160128"]] TCGA-04-1331-01A-01D-0431-02 ...
[["OV_CNACGH_CGH_hg_415k_g4124a-20160128"]] TCGA-04-1353-01A-01D-1046-02 ...
[["OV_CNASNP-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_CNVSNP-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_GISTIC_AllByGene-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_GISTIC_Peaks-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_GISTIC_ThresholdedByGene-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_miRNAArray-20160128"]] TCGA-04-1331-01A-01T-0438-07 ...
[["OV_mRNAArray_huex-20160128"]] TCGA-04-1331-01A-01R-0435-03 ...
[["OV_mRNAArray_TX_g4502a-20160128"]] TCGA-09-0364-01A-02R-0363-07 ...
...
<9 more elements>

```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|----|---------------------------------------|----------|
| 1 | OV_CNACGH_CGH_hg_244a-20160128 | 3.6 Mb |
| 2 | OV_CNACGH_CGH_hg_415k_g4124a-20160128 | 6.8 Mb |
| 3 | OV_CNASNP-20160128 | 24.6 Mb |
| 4 | OV_CNVSNP-20160128 | 7.3 Mb |
| 5 | OV_GISTIC_AllByGene-20160128 | 112 Mb |
| 6 | OV_GISTIC_Peaks-20160128 | 0.5 Mb |
| 7 | OV_GISTIC_ThresholdedByGene-20160128 | 111.7 Mb |
| 8 | OV_miRNAArray-20160128 | 3.8 Mb |
| 9 | OV_mRNAArray_huex-20160128 | 84.2 Mb |
| 10 | OV_mRNAArray_TX_g4502a-20160128 | 80.7 Mb |
| 11 | OV_mRNAArray_TX_ht_hg_u133a-20160128 | 49.7 Mb |
| 12 | OV_Mutation-20160128 | 10.3 Mb |
| 13 | OV_RNASeq2Gene-20160128 | 50.6 Mb |
| 14 | OV_RNASeqGene-20160128 | 48.1 Mb |
| 15 | OV_RPPAArray-20160128 | 0.8 Mb |
| 16 | OV_miRNASeqGene-20160128 | 2.7 Mb |
| 17 | OV_RNASeq2GeneNorm-20160128 | 45.8 Mb |
| 18 | OV_Methylation_methyl27-20160128 | 4.9 Mb |
| 19 | OV_Methylation_methyl450-20160128 | 75 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

[1,] 343 343 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

OV-v2.1.1

Ovarian serous cystadenocarcinoma

Description

A document describing the TCGA cancer code Note. Only the colData has changed.

Details

```

> experiments( OV )
ExperimentList class object of length 0:

```

```

> rownames( OV )
CharacterList of length 0

```

```

> colnames( OV )
CharacterList of length 0

```

Sizes of each ExperimentList element:

```

[1] assay   size.Mb
<0 rows> (or 0-length row.names)

```

```

-----
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
[1,] 343    343  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  68.75   89.00   22

vital_status:
  0    1 NA's
  247 344   1

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  249

days_to_last_followup:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
  16    268    837    1214   1919   5481   359

tumor_tissue_site:
      omentum          ovary peritoneum ovary      NA's
      3             576             2             11

gender:
female  NA's
  581    11

date_of_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
  1992   2001   2004   2004   2007   2013   11

radiation_therapy:
  no  yes NA's
  557 5  30

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  508

histological_type:
serous cystadenocarcinoma      NA's
      581             11

residual_tumor:
  r0  r1  r2  rx NA's
  16  31  5   3  537

ethnicity:
  hispanic or latino not hispanic or latino      NA's
      11             338             243

```

Including an additional 2850 columns

PAAD

Pancreatic adenocarcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( PAAD )
ExperimentList class object of length 10:
 [1] PAAD_CNASNP-20160128: RaggedExperiment with 203871 rows and 368 columns
 [2] PAAD_CNVSNP-20160128: RaggedExperiment with 34808 rows and 365 columns
 [3] PAAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [4] PAAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 52 rows and 184 columns
 [5] PAAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [6] PAAD_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 183 columns
 [7] PAAD_Mutation-20160128: RaggedExperiment with 30357 rows and 150 columns
 [8] PAAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 183 columns
 [9] PAAD_RPPAArray-20160128: SummarizedExperiment with 195 rows and 123 columns
 [10] PAAD_Methylation-20160128: SummarizedExperiment with 485577 rows and 195 columns

> rownames( PAAD )
CharacterList of length 10
[["PAAD_CNASNP-20160128"]] character(0)
[["PAAD_CNVSNP-20160128"]] character(0)
[["PAAD_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["PAAD_GISTIC_Peaks-20160128"]] chr1:26795113-27650365 ...
[["PAAD_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["PAAD_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["PAAD_Mutation-20160128"]] character(0)
[["PAAD_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["PAAD_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["PAAD_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873

> colnames( PAAD )
CharacterList of length 10
[["PAAD_CNASNP-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_CNVSNP-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_GISTIC_AllByGene-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_GISTIC_Peaks-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_miRNASeqGene-20160128"]] TCGA-2J-AAB1-01A-11R-A41G-13 ...
[["PAAD_Mutation-20160128"]] TCGA-2J-AAB1-01A-11D-A40W-08 ...
```

```

[["PAAD_RNASeq2GeneNorm-20160128"]] TCGA-2J-AAB1-01A-11R-A41B-07 ...
[["PAAD_RPPAArray-20160128"]] TCGA-2J-AAB4-01A-21-A43K-20 ...
[["PAAD_Methylation-20160128"]] TCGA-2J-AAB1-01A-11D-A40Y-05 ...

```

Sizes of each ExperimentList element:

| | | assay | size.Mb |
|----|--|--|---------|
| 1 | | PAAD_CNASNP-20160128 | 5.6 Mb |
| 2 | | PAAD_CNVSNP-20160128 | 1 Mb |
| 3 | | PAAD_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | | PAAD_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | | PAAD_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | | PAAD_miRNASeqGene-20160128 | 0.1 Mb |
| 7 | | PAAD_Mutation-20160128 | 111 Mb |
| 8 | | PAAD_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 9 | | PAAD_RPPAArray-20160128 | 0 Mb |
| 10 | | PAAD_Methylation-20160128 | 75 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

See Also

[PAAD-v2.0.1](#)

PAAD-v2.0.1

Pancreatic adenocarcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( PAAD )
```

ExperimentList class object of length 11:

- [1] PAAD_CNASNP-20160128: RaggedExperiment with 203871 rows and 368 columns
- [2] PAAD_CNVSNP-20160128: RaggedExperiment with 34808 rows and 365 columns
- [3] PAAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
- [4] PAAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 52 rows and 184 columns
- [5] PAAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
- [6] PAAD_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 183 columns
- [7] PAAD_Mutation-20160128: RaggedExperiment with 30357 rows and 150 columns
- [8] PAAD_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 183 columns
- [9] PAAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 183 columns
- [10] PAAD_RPPAArray-20160128: SummarizedExperiment with 195 rows and 123 columns
- [11] PAAD_Methylation-20160128: SummarizedExperiment with 485577 rows and 195 columns

```

> rownames( PAAD )
CharacterList of length 11
[["PAAD_CNASNP-20160128"]] character(0)
[["PAAD_CNVSNP-20160128"]] character(0)
[["PAAD_GISTIC_AllByGene-20160128"]] character(0)
[["PAAD_GISTIC_Peaks-20160128"]] 24 1 2 3 25 4 26 5 ... 49 50 21 51 22 52 53
[["PAAD_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["PAAD_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["PAAD_Mutation-20160128"]] character(0)
[["PAAD_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["PAAD_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["PAAD_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<1 more element>

```

```

> colnames( PAAD )
CharacterList of length 11
[["PAAD_CNASNP-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_CNVSNP-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_GISTIC_AllByGene-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_GISTIC_Peaks-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_miRNASeqGene-20160128"]] TCGA-2J-AAB1-01A-11R-A41G-13 ...
[["PAAD_Mutation-20160128"]] TCGA-2J-AAB1-01A-11D-A40W-08 ...
[["PAAD_RNASeq2Gene-20160128"]] TCGA-2J-AAB1-01A-11R-A41B-07 ...
[["PAAD_RNASeq2GeneNorm-20160128"]] TCGA-2J-AAB1-01A-11R-A41B-07 ...
[["PAAD_RPPAArray-20160128"]] TCGA-2J-AAB4-01A-21-A43K-20 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | PAAD_CNASNP-20160128 | 5.6 Mb |
| 2 | PAAD_CNVSNP-20160128 | 1 Mb |
| 3 | PAAD_GISTIC_AllByGene-20160128 | 38.3 Mb |
| 4 | PAAD_GISTIC_Peaks-20160128 | 0.2 Mb |
| 5 | PAAD_GISTIC_ThresholdedByGene-20160128 | 38.1 Mb |
| 6 | PAAD_miRNASeqGene-20160128 | 1.6 Mb |
| 7 | PAAD_Mutation-20160128 | 111 Mb |
| 8 | PAAD_RNASeq2Gene-20160128 | 31.2 Mb |
| 9 | PAAD_RNASeq2GeneNorm-20160128 | 31.2 Mb |
| 10 | PAAD_RPPAArray-20160128 | 0.2 Mb |
| 11 | PAAD_Methylation-20160128 | 75 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 | 11 | 7 | white |
| NA's | 5 | | 162 |

ethnicity:

| | | | |
|---|---|-----|------|
| hispanic or latino not hispanic or latino | 5 | 137 | NA's |
| | | | 43 |

Including an additional 960 columns

Description

A document describing the TCGA cancer code

Details

```
> experiments( PAAD )
ExperimentList class object of length 11:
 [1] PAAD_CNASNP-20160128: RaggedExperiment with 203871 rows and 368 columns
 [2] PAAD_CNVSNP-20160128: RaggedExperiment with 34808 rows and 365 columns
 [3] PAAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [4] PAAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 52 rows and 184 columns
 [5] PAAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [6] PAAD_Mutation-20160128: RaggedExperiment with 30357 rows and 150 columns
 [7] PAAD_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 183 columns
 [8] PAAD_RPPAArray-20160128: SummarizedExperiment with 195 rows and 123 columns
 [9] PAAD_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 183 columns
 [10] PAAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18465 rows and 183 columns
 [11] PAAD_Methylation-20160128: SummarizedExperiment with 485577 rows and 195 columns

> rownames( PAAD )
CharacterList of length 11
[["PAAD_CNASNP-20160128"]] character(0)
[["PAAD_CNVSNP-20160128"]] character(0)
[["PAAD_GISTIC_AllByGene-20160128"]] character(0)
[["PAAD_GISTIC_Peaks-20160128"]] 24 1 2 3 25 4 26 5 ... 49 50 21 51 22 52 53
[["PAAD_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["PAAD_Mutation-20160128"]] character(0)
[["PAAD_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["PAAD_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["PAAD_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["PAAD_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZEF1 ZZZ3 psiTPTE22
...
<1 more element>

> colnames( PAAD )
CharacterList of length 11
[["PAAD_CNASNP-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_CNVSNP-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_GISTIC_AllByGene-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_GISTIC_Peaks-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_Mutation-20160128"]] TCGA-2J-AAB1-01A-11D-A40W-08 ...
[["PAAD_RNASeq2Gene-20160128"]] TCGA-2J-AAB1-01A-11R-A41B-07 ...
```

```

[["PAAD_RPPAArray-20160128"]] TCGA-2J-AAB4-01A-21-A43K-20 ...
[["PAAD_miRNASeqGene-20160128"]] TCGA-2J-AAB1-01A-11R-A41G-13 ...
[["PAAD_RNASeq2GeneNorm-20160128"]] TCGA-2J-AAB1-01 ... TCGA-Z5-AAPL-01
...
<1 more element>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | PAAD_CNASNP-20160128 | 5.6 Mb |
| 2 | PAAD_CNVSNP-20160128 | 1 Mb |
| 3 | PAAD_GISTIC_AllByGene-20160128 | 38.3 Mb |
| 4 | PAAD_GISTIC_Peaks-20160128 | 0.2 Mb |
| 5 | PAAD_GISTIC_ThresholdedByGene-20160128 | 38.1 Mb |
| 6 | PAAD_Mutation-20160128 | 111 Mb |
| 7 | PAAD_RNASeq2Gene-20160128 | 31.2 Mb |
| 8 | PAAD_RPPAArray-20160128 | 0.2 Mb |
| 9 | PAAD_miRNASeqGene-20160128 | 1.6 Mb |
| 10 | PAAD_RNASeq2GeneNorm-20160128 | 28.1 Mb |
| 11 | PAAD_Methylation-20160128 | 75 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
[1,] 100    100    1.08    0.967    1.32

```

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 10:
 [1] PCPG_CNASNP-20160128: RaggedExperiment with 297329 rows and 360 columns
 [2] PCPG_CNVSNP-20160128: RaggedExperiment with 31256 rows and 346 columns
 [3] PCPG_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 162 columns
 [4] PCPG_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 27 rows and 162 columns
 [5] PCPG_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 162 columns
 [6] PCPG_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 187 columns
 [7] PCPG_Mutation-20160128: RaggedExperiment with 4662 rows and 184 columns
 [8] PCPG_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 187 columns
 [9] PCPG_RPPAArray-20160128: SummarizedExperiment with 192 rows and 82 columns
[10] PCPG_Methylation-20160128: SummarizedExperiment with 485577 rows and 187 columns

> rownames( PCPG )
CharacterList of length 10

```

```

[["PCPG_CNASNP-20160128"]] character(0)
[["PCPG_CNVSNP-20160128"]] character(0)
[["PCPG_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["PCPG_GISTIC_Peaks-20160128"]] chr1:117751737-118152240 ...
[["PCPG_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["PCPG_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["PCPG_Mutation-20160128"]] character(0)
[["PCPG_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["PCPG_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["PCPG_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873

```

```

> colnames( PCPG )
CharacterList of length 10
[["PCPG_CNASNP-20160128"]] TCGA-P7-A5NX-10A-01D-A35A-01 ...
[["PCPG_CNVSNP-20160128"]] TCGA-P7-A5NX-10A-01D-A35A-01 ...
[["PCPG_GISTIC_AllByGene-20160128"]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[["PCPG_GISTIC_Peaks-20160128"]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[["PCPG_GISTIC_ThresholdedByGene-20160128"]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[["PCPG_miRNASeqGene-20160128"]] TCGA-P7-A5NX-01A-11R-A35M-13 ...
[["PCPG_Mutation-20160128"]] TCGA-P7-A5NX-01A-11D-A35D-08 ...
[["PCPG_RNASeq2GeneNorm-20160128"]] TCGA-P7-A5NX-01A-11R-A35K-07 ...
[["PCPG_RPPAArray-20160128"]] TCGA-P7-A5NX-01A-21-A43B-20 ...
[["PCPG_Methylation-20160128"]] TCGA-P7-A5NX-01A-11D-A35E-05 ...

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | PCPG_CNASNP-20160128 | 8.1 Mb |
| 2 | PCPG_CNVSNP-20160128 | 0.9 Mb |
| 3 | PCPG_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | PCPG_GISTIC_Peaks-20160128 | 0 Mb |
| 5 | PCPG_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | PCPG_miRNASeqGene-20160128 | 0.1 Mb |
| 7 | PCPG_Mutation-20160128 | 8.4 Mb |
| 8 | PCPG_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 9 | PCPG_RPPAArray-20160128 | 0 Mb |
| 10 | PCPG_Methylation-20160128 | 75 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

See Also

[PCPG-v2.0.1](#)

PCPG-v2.0.1

Pheochromocytoma and Paraganglioma

Description

A document describing the TCGA cancer code

Details

```

> experiments( PCPG )
ExperimentList class object of length 11:
 [1] PCPG_CNASNP-20160128: RaggedExperiment with 297329 rows and 360 columns
 [2] PCPG_CNVSNP-20160128: RaggedExperiment with 31256 rows and 346 columns
 [3] PCPG_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 162 columns
 [4] PCPG_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 27 rows and 162 columns
 [5] PCPG_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 162 columns
 [6] PCPG_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 187 columns
 [7] PCPG_Mutation-20160128: RaggedExperiment with 4662 rows and 184 columns
 [8] PCPG_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 187 columns
 [9] PCPG_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 187 columns
[10] PCPG_RPPAArray-20160128: SummarizedExperiment with 192 rows and 82 columns
[11] PCPG_Methylation-20160128: SummarizedExperiment with 485577 rows and 187 columns

```

```

> rownames( PCPG )
CharacterList of length 11
[["PCPG_CNASNP-20160128"]] character(0)
[["PCPG_CNVSNP-20160128"]] character(0)
[["PCPG_GISTIC_AllByGene-20160128"]] character(0)
[["PCPG_GISTIC_Peaks-20160128"]] 7 1 8 9 10 11 2 12 ... 22 23 5 24 25 26 6 27
[["PCPG_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["PCPG_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["PCPG_Mutation-20160128"]] character(0)
[["PCPG_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["PCPG_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["PCPG_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<1 more element>

```

```

> colnames( PCPG )
CharacterList of length 11
[["PCPG_CNASNP-20160128"]] TCGA-P7-A5NX-10A-01D-A35A-01 ...
[["PCPG_CNVSNP-20160128"]] TCGA-P7-A5NX-10A-01D-A35A-01 ...
[["PCPG_GISTIC_AllByGene-20160128"]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[["PCPG_GISTIC_Peaks-20160128"]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[["PCPG_GISTIC_ThresholdedByGene-20160128"]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[["PCPG_miRNASeqGene-20160128"]] TCGA-P7-A5NX-01A-11R-A35M-13 ...
[["PCPG_Mutation-20160128"]] TCGA-P7-A5NX-01A-11D-A35D-08 ...
[["PCPG_RNASeq2Gene-20160128"]] TCGA-P7-A5NX-01A-11R-A35K-07 ...
[["PCPG_RNASeq2GeneNorm-20160128"]] TCGA-P7-A5NX-01A-11R-A35K-07 ...
[["PCPG_RPPAArray-20160128"]] TCGA-P7-A5NX-01A-21-A43B-20 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | PCPG_CNASNP-20160128 | 8.1 Mb |
| 2 | PCPG_CNVSNP-20160128 | 0.9 Mb |
| 3 | PCPG_GISTIC_AllByGene-20160128 | 34.1 Mb |
| 4 | PCPG_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | PCPG_GISTIC_ThresholdedByGene-20160128 | 34 Mb |
| 6 | PCPG_miRNASeqGene-20160128 | 1.7 Mb |
| 7 | PCPG_Mutation-20160128 | 8.4 Mb |
| 8 | PCPG_RNASeq2Gene-20160128 | 31.8 Mb |
| 9 | PCPG_RNASeq2GeneNorm-20160128 | 31.8 Mb |
| 10 | PCPG_RPPAArray-20160128 | 0.2 Mb |
| 11 | PCPG_Methylation-20160128 | 75 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
    1
    black or african american
    20
    NA's
    4
asian
    6
white
    148

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

```

Including an additional 894 columns

PCPG-v2.1.0

Pheochromocytoma and Paraganglioma

Description

A document describing the TCGA cancer code

Details

```

> experiments( PCPG )
ExperimentList class object of length 11:
 [1] PCPG_CNASNP-20160128: RaggedExperiment with 297329 rows and 360 columns
 [2] PCPG_CNVSNP-20160128: RaggedExperiment with 31256 rows and 346 columns
 [3] PCPG_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 162 columns
 [4] PCPG_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 27 rows and 162 columns
 [5] PCPG_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 162 columns
 [6] PCPG_Mutation-20160128: RaggedExperiment with 4662 rows and 184 columns
 [7] PCPG_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 187 columns
 [8] PCPG_RPPAArray-20160128: SummarizedExperiment with 192 rows and 82 columns
 [9] PCPG_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 187 columns

```

```
[10] PCPG_RNASeq2GeneNorm-20160128: SummarizedExperiment with 17988 rows and 187 columns
[11] PCPG_Methylation-20160128: SummarizedExperiment with 485577 rows and 187 columns
```

```
> rownames( PCPG )
CharacterList of length 11
[["PCPG_CNASNP-20160128"]] character(0)
[["PCPG_CNVSNP-20160128"]] character(0)
[["PCPG_GISTIC_AllByGene-20160128"]] character(0)
[["PCPG_GISTIC_Peaks-20160128"]] 7 1 8 9 10 11 2 12 ... 22 23 5 24 25 26 6 27
[["PCPG_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["PCPG_Mutation-20160128"]] character(0)
[["PCPG_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["PCPG_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["PCPG_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["PCPG_RNASeq2GeneNorm-20160128"]] A1BG A2BP1 A2LD1 ... ZZEF1 ZZZ3 psiTPTE22
...
<1 more element>
```

```
> colnames( PCPG )
CharacterList of length 11
[["PCPG_CNASNP-20160128"]] TCGA-P7-A5NX-10A-01D-A35A-01 ...
[["PCPG_CNVSNP-20160128"]] TCGA-P7-A5NX-10A-01D-A35A-01 ...
[["PCPG_GISTIC_AllByGene-20160128"]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[["PCPG_GISTIC_Peaks-20160128"]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[["PCPG_GISTIC_ThresholdedByGene-20160128"]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[["PCPG_Mutation-20160128"]] TCGA-P7-A5NX-01A-11D-A35D-08 ...
[["PCPG_RNASeq2Gene-20160128"]] TCGA-P7-A5NX-01A-11R-A35K-07 ...
[["PCPG_RPPAArray-20160128"]] TCGA-P7-A5NX-01A-21-A43B-20 ...
[["PCPG_miRNASeqGene-20160128"]] TCGA-P7-A5NX-01A-11R-A35M-13 ...
[["PCPG_RNASeq2GeneNorm-20160128"]] TCGA-P7-A5NX-01 ... TCGA-XG-A823-01
...
<1 more element>
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | PCPG_CNASNP-20160128 | 8.1 Mb |
| 2 | PCPG_CNVSNP-20160128 | 0.9 Mb |
| 3 | PCPG_GISTIC_AllByGene-20160128 | 34.1 Mb |
| 4 | PCPG_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | PCPG_GISTIC_ThresholdedByGene-20160128 | 34 Mb |
| 6 | PCPG_Mutation-20160128 | 8.4 Mb |
| 7 | PCPG_RNASeq2Gene-20160128 | 31.8 Mb |
| 8 | PCPG_RPPAArray-20160128 | 0.2 Mb |
| 9 | PCPG_miRNASeqGene-20160128 | 1.7 Mb |
| 10 | PCPG_RNASeq2GeneNorm-20160128 | 27.9 Mb |
| 11 | PCPG_Methylation-20160128 | 75 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
[1,] 6      6  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:

| | | |
|---|------------------|-----|
| | paranglioma | 18 |
| paranglioma; 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 | 1 | asian | 6 |
| black or african american | 20 | white | 148 |
| NA's | 4 | | |

ethnicity:

| | | | | | |
|--------------------|---|------------------------|-----|------|----|
| hispanic or latino | 5 | not hispanic or latino | 138 | NA's | 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 11:

- [1] PRAD_CNASeq-20160128: RaggedExperiment with 23398 rows and 230 columns
- [2] PRAD_CNASNP-20160128: RaggedExperiment with 573776 rows and 1029 columns
- [3] PRAD_CNVSNP-20160128: RaggedExperiment with 117345 rows and 1023 columns
- [4] PRAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 492 columns
- [5] PRAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 58 rows and 492 columns
- [6] PRAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 492 columns

```
[7] PRAD_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 547 columns
[8] PRAD_Mutation-20160128: RaggedExperiment with 12348 rows and 332 columns
[9] PRAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 550 columns
[10] PRAD_RPPAArray-20160128: SummarizedExperiment with 195 rows and 352 columns
[11] PRAD_Methylation-20160128: SummarizedExperiment with 485577 rows and 549 columns
```

```
> rownames( PRAD )
CharacterList of length 11
[["PRAD_CNASeq-20160128"]] character(0)
[["PRAD_CNASNP-20160128"]] character(0)
[["PRAD_CNVSNP-20160128"]] character(0)
[["PRAD_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["PRAD_GISTIC_Peaks-20160128"]] chr1:63901623-66226788 ...
[["PRAD_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["PRAD_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["PRAD_Mutation-20160128"]] character(0)
[["PRAD_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["PRAD_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<1 more element>
```

```
> colnames( PRAD )
CharacterList of length 11
[["PRAD_CNASeq-20160128"]] TCGA-CH-5741-01A-11D-1572-02 ...
[["PRAD_CNASNP-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_CNVSNP-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_GISTIC_AllByGene-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_GISTIC_Peaks-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_miRNASeqGene-20160128"]] TCGA-2A-A8VL-01A-21R-A37H-13 ...
[["PRAD_Mutation-20160128"]] TCGA-2A-A8VL-01A-21D-A377-08 ...
[["PRAD_RNASeq2GeneNorm-20160128"]] TCGA-2A-A8VL-01A-21R-A37L-07 ...
[["PRAD_RPPAArray-20160128"]] TCGA-2A-A8VL-01A-11-A43M-20 ...
...
<1 more element>
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|---|--|---------------|
| 1 | PRAD_CNASeq-20160128 | 0.7 Mb |
| 2 | PRAD_CNASNP-20160128 | 15.6 Mb |
| 3 | PRAD_CNVSNP-20160128 | 3.4 Mb |
| 4 | PRAD_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | PRAD_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | PRAD_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | PRAD_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | PRAD_Mutation-20160128 | 21.5 Mb |
| 9 | PRAD_RNASeq2GeneNorm-20160128 | 1.3 Mb |

```

10          PRAD_RPPAArray-20160128    0 Mb
11          PRAD_Methylation-20160128 75.1 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

See Also

[PRAD-v2.0.1](#)

PRAD-v2.0.1

*Prostate adenocarcinoma***Description**

A document describing the TCGA cancer code

Details

```

> experiments( PRAD )
ExperimentList class object of length 12:
 [1] PRAD_CNASeq-20160128: RaggedExperiment with 23398 rows and 230 columns
 [2] PRAD_CNASNP-20160128: RaggedExperiment with 573776 rows and 1029 columns
 [3] PRAD_CNVSNP-20160128: RaggedExperiment with 117345 rows and 1023 columns
 [4] PRAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 492 columns
 [5] PRAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 58 rows and 492 columns
 [6] PRAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 492 columns
 [7] PRAD_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 547 columns
 [8] PRAD_Mutation-20160128: RaggedExperiment with 12348 rows and 332 columns
 [9] PRAD_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 550 columns
 [10] PRAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 550 columns
 [11] PRAD_RPPAArray-20160128: SummarizedExperiment with 195 rows and 352 columns
 [12] PRAD_Methylation-20160128: SummarizedExperiment with 485577 rows and 549 columns

> rownames( PRAD )
CharacterList of length 12
[["PRAD_CNASeq-20160128"]] character(0)
[["PRAD_CNASNP-20160128"]] character(0)
[["PRAD_CNVSNP-20160128"]] character(0)
[["PRAD_GISTIC_AllByGene-20160128"]] character(0)
[["PRAD_GISTIC_Peaks-20160128"]] 29 30 1 31 32 33 34 ... 21 60 61 22 23 62 63
[["PRAD_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["PRAD_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["PRAD_Mutation-20160128"]] character(0)
[["PRAD_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["PRAD_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
...
<2 more elements>

> colnames( PRAD )
CharacterList of length 12
[["PRAD_CNASeq-20160128"]] TCGA-CH-5741-01A-11D-1572-02 ...
[["PRAD_CNASNP-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_CNVSNP-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_GISTIC_AllByGene-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_GISTIC_Peaks-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...

```

```

[["PRAD_miRNASeqGene-20160128"]] TCGA-2A-A8VL-01A-21R-A37H-13 ...
[["PRAD_Mutation-20160128"]] TCGA-2A-A8VL-01A-21D-A377-08 ...
[["PRAD_RNASeq2Gene-20160128"]] TCGA-2A-A8VL-01A-21R-A37L-07 ...
[["PRAD_RNASeq2GeneNorm-20160128"]] TCGA-2A-A8VL-01A-21R-A37L-07 ...
...
<2 more elements>

```

Sizes of each ExperimentList element:

| | | assay | size.Mb |
|----|--|-------------------------------|---------|
| 1 | | PRAD_CNASeq-20160128 | 0.7 Mb |
| 2 | | PRAD_CNASNP-20160128 | 15.6 Mb |
| 3 | | PRAD_CNVSNP-20160128 | 3.4 Mb |
| 4 | PRAD_GISTIC_AllByGene-20160128 | | 96.6 Mb |
| 5 | | PRAD_GISTIC_Peaks-20160128 | 0.4 Mb |
| 6 | PRAD_GISTIC_ThresholdedByGene-20160128 | | 96.4 Mb |
| 7 | | PRAD_miRNASeqGene-20160128 | 4.6 Mb |
| 8 | | PRAD_Mutation-20160128 | 21.5 Mb |
| 9 | | PRAD_RNASeq2Gene-20160128 | 88.7 Mb |
| 10 | | PRAD_RNASeq2GeneNorm-20160128 | 88.7 Mb |
| 11 | | PRAD_RPPAArray-20160128 | 0.6 Mb |
| 12 | | PRAD_Methylation-20160128 | 75.1 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
NA's
342
```

```
ethnicity:
not hispanic or latino      NA's
      152          346
```

Including an additional 1126 columns

PRAD-v2.1.0

Prostate adenocarcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( PRAD )
ExperimentList class object of length 12:
 [1] PRAD_CNASeq-20160128: RaggedExperiment with 23398 rows and 230 columns
 [2] PRAD_CNASNP-20160128: RaggedExperiment with 573776 rows and 1029 columns
 [3] PRAD_CNVSNP-20160128: RaggedExperiment with 117345 rows and 1023 columns
 [4] PRAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 492 columns
 [5] PRAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 58 rows and 492 columns
 [6] PRAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 492 columns
 [7] PRAD_Mutation-20160128: RaggedExperiment with 12348 rows and 332 columns
 [8] PRAD_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 550 columns
 [9] PRAD_RPPAArray-20160128: SummarizedExperiment with 195 rows and 352 columns
[10] PRAD_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 547 columns
[11] PRAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18265 rows and 550 columns
[12] PRAD_Methylation-20160128: SummarizedExperiment with 485577 rows and 549 columns

> rownames( PRAD )
CharacterList of length 12
[["PRAD_CNASeq-20160128"]] character(0)
[["PRAD_CNASNP-20160128"]] character(0)
[["PRAD_CNVSNP-20160128"]] character(0)
[["PRAD_GISTIC_AllByGene-20160128"]] character(0)
[["PRAD_GISTIC_Peaks-20160128"]] 29 30 1 31 32 33 34 ... 21 60 61 22 23 62 63
```

```

[["PRAD_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["PRAD_Mutation-20160128"]] character(0)
[["PRAD_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
[["PRAD_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["PRAD_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
...
<2 more elements>

```

```

> colnames( PRAD )
CharacterList of length 12
[["PRAD_CNASeq-20160128"]] TCGA-CH-5741-01A-11D-1572-02 ...
[["PRAD_CNASNP-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_CNVSNP-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_GISTIC_AllByGene-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_GISTIC_Peaks-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_Mutation-20160128"]] TCGA-2A-A8VL-01A-21D-A377-08 ...
[["PRAD_RNASeq2Gene-20160128"]] TCGA-2A-A8VL-01A-21R-A37L-07 ...
[["PRAD_RPPAArray-20160128"]] TCGA-2A-A8VL-01A-11-A43M-20 ...
[["PRAD_miRNASeqGene-20160128"]] TCGA-2A-A8VL-01A-21R-A37H-13 ...
...
<2 more elements>

```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|----|--|---------|
| 1 | PRAD_CNASeq-20160128 | 0.7 Mb |
| 2 | PRAD_CNASNP-20160128 | 15.6 Mb |
| 3 | PRAD_CNVSNP-20160128 | 3.4 Mb |
| 4 | PRAD_GISTIC_AllByGene-20160128 | 96.6 Mb |
| 5 | PRAD_GISTIC_Peaks-20160128 | 0.4 Mb |
| 6 | PRAD_GISTIC_ThresholdedByGene-20160128 | 96.4 Mb |
| 7 | PRAD_Mutation-20160128 | 21.5 Mb |
| 8 | PRAD_RNASeq2Gene-20160128 | 88.7 Mb |
| 9 | PRAD_RPPAArray-20160128 | 0.6 Mb |
| 10 | PRAD_miRNASeqGene-20160128 | 4.6 Mb |
| 11 | PRAD_RNASeq2GeneNorm-20160128 | 79 Mb |
| 12 | PRAD_Methylation-20160128 | 75.1 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

```

[1,] 10 10 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 14:
 [1] READ_CNASeq-20160128: RaggedExperiment with 56380 rows and 70 columns
 [2] READ_CNASNP-20160128: RaggedExperiment with 156806 rows and 316 columns
 [3] READ_CNVSNP-20160128: RaggedExperiment with 35765 rows and 316 columns
 [4] READ_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 165 columns

```

```

[5] READ_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 55 rows and 165 columns
[6] READ_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 165 columns
[7] READ_miRNASeqGene-20160128: SummarizedExperiment with 705 rows and 76 columns
[8] READ_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 72 columns
[9] READ_Mutation-20160128: RaggedExperiment with 22075 rows and 69 columns
[10] READ_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 72 columns
[11] READ_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 72 columns
[12] READ_RPPAArray-20160128: SummarizedExperiment with 208 rows and 131 columns
[13] READ_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 73 columns
[14] READ_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 106 columns

```

```

> rownames( READ )
CharacterList of length 14
[["READ_CNASeq-20160128"]] character(0)
[["READ_CNASNP-20160128"]] character(0)
[["READ_CNVSNP-20160128"]] character(0)
[["READ_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["READ_GISTIC_Peaks-20160128"]] chr1:3814904-31841618 ...
[["READ_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["READ_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["READ_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["READ_Mutation-20160128"]] character(0)
[["READ_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
...
<4 more elements>

```

```

> colnames( READ )
CharacterList of length 14
[["READ_CNASeq-20160128"]] TCGA-AF-2691-01A-01D-1167-02 ...
[["READ_CNASNP-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_CNVSNP-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_GISTIC_AllByGene-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_GISTIC_Peaks-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_GISTIC_ThresholdedByGene-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_miRNASeqGene-20160128"]] TCGA-AF-2687-01A-02T-1735-13 ...
[["READ_mRNAArray-20160128"]] TCGA-AF-2689-11A-01R-1758-07 ...
[["READ_Mutation-20160128"]] TCGA-AF-2689-01A-01W-0831-10 ... TCGA-AG-A036-01
[["READ_RNASeq2GeneNorm-20160128"]] TCGA-AF-2691-01A-01R-0821-07 ...
...
<4 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|---|--------------------------------|---------------|
| 1 | READ_CNASeq-20160128 | 1.5 Mb |
| 2 | READ_CNASNP-20160128 | 4.3 Mb |
| 3 | READ_CNVSNP-20160128 | 1.1 Mb |
| 4 | READ_GISTIC_AllByGene-20160128 | 4.9 Mb |

| | | |
|----|--|--------|
| 5 | READ_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | READ_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | READ_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | READ_mRNAArray-20160128 | 1.1 Mb |
| 9 | READ_Mutation-20160128 | 9.6 Mb |
| 10 | READ_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 11 | READ_RNASeqGene-20160128 | 1.3 Mb |
| 12 | READ_RPPAArray-20160128 | 0 Mb |
| 13 | READ_Methylation_methyl27-20160128 | 4.9 Mb |
| 14 | READ_Methylation_methyl450-20160128 | 75 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

See Also

[READ-v2.0.1](#)

READ-v2.0.1

*Rectum adenocarcinoma***Description**

A document describing the TCGA cancer code

Details

```

> experiments( READ )
ExperimentList class object of length 16:
 [1] READ_CNASeq-20160128: RaggedExperiment with 56380 rows and 70 columns
 [2] READ_CNASNP-20160128: RaggedExperiment with 156806 rows and 316 columns
 [3] READ_CNVSNP-20160128: RaggedExperiment with 35765 rows and 316 columns
 [4] READ_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 165 columns
 [5] READ_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 55 rows and 165 columns
 [6] READ_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 165 columns
 [7] READ_miRNASeqGene-20160128: SummarizedExperiment with 705 rows and 76 columns
 [8] READ_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 72 columns
 [9] READ_Mutation-20160128: RaggedExperiment with 22075 rows and 69 columns
[10] READ_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 105 columns
[11] READ_RNASeq2GeneNorm_illuminaga-20160128: SummarizedExperiment with 20501 rows and 72 columns
[12] READ_RNASeq2GeneNorm_illuminahiseq-20160128: SummarizedExperiment with 20501 rows and 105 columns
[13] READ_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 72 columns
[14] READ_RPPAArray-20160128: SummarizedExperiment with 208 rows and 131 columns
[15] READ_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 73 columns
[16] READ_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 106 columns

> rownames( READ )
CharacterList of length 16
[["READ_CNASeq-20160128"]] character(0)
[["READ_CNASNP-20160128"]] character(0)
[["READ_CNVSNP-20160128"]] character(0)
[["READ_GISTIC_AllByGene-20160128"]] character(0)
[["READ_GISTIC_Peaks-20160128"]] 23 24 25 1 2 26 27 ... 54 55 18 19 20 56 57
[["READ_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["READ_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["READ_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["READ_Mutation-20160128"]] character(0)
[["READ_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
...
<6 more elements>

> colnames( READ )
CharacterList of length 16
[["READ_CNASeq-20160128"]] TCGA-AF-2691-01A-01D-1167-02 ...
[["READ_CNASNP-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...

```

```

[["READ_CNVSNP-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_GISTIC_AllByGene-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_GISTIC_Peaks-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_GISTIC_ThresholdedByGene-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_miRNASeqGene-20160128"]] TCGA-AF-2687-01A-02T-1735-13 ...
[["READ_mRNAArray-20160128"]] TCGA-AF-2689-11A-01R-1758-07 ...
[["READ_Mutation-20160128"]] TCGA-AF-2689-01A-01W-0831-10 ... TCGA-AG-A036-01
[["READ_RNASeq2Gene-20160128"]] TCGA-AF-2687-01A-02R-1736-07 ...
...
<6 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|---|---------------|
| 1 | READ_CNASeq-20160128 | 1.5 Mb |
| 2 | READ_CNASNP-20160128 | 4.3 Mb |
| 3 | READ_CNVSNP-20160128 | 1.1 Mb |
| 4 | READ_GISTIC_AllByGene-20160128 | 34.7 Mb |
| 5 | READ_GISTIC_Peaks-20160128 | 0.2 Mb |
| 6 | READ_GISTIC_ThresholdedByGene-20160128 | 34.5 Mb |
| 7 | READ_miRNASeqGene-20160128 | 0.5 Mb |
| 8 | READ_mRNAArray-20160128 | 12 Mb |
| 9 | READ_Mutation-20160128 | 9.6 Mb |
| 10 | READ_RNASeq2Gene-20160128 | 19 Mb |
| 11 | READ_RNASeq2GeneNorm_illumina-20160128 | 13.8 Mb |
| 12 | READ_RNASeq2GeneNorm_illuminahisec-20160128 | 19 Mb |
| 13 | READ_RNASeqGene-20160128 | 13.8 Mb |
| 14 | READ_RPPAArray-20160128 | 0.3 Mb |
| 15 | READ_Methylation_methyl27-20160128 | 4.9 Mb |
| 16 | READ_Methylation_methyl450-20160128 | 75 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

READ-v2.1.0

Rectum adenocarcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( READ )
ExperimentList class object of length 17:
 [1] READ_CNASeq-20160128: RaggedExperiment with 56380 rows and 70 columns
 [2] READ_CNASNP-20160128: RaggedExperiment with 156806 rows and 316 columns
 [3] READ_CNVSNP-20160128: RaggedExperiment with 35765 rows and 316 columns
 [4] READ_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 165 columns
 [5] READ_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 55 rows and 165 columns
 [6] READ_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 165 columns
 [7] READ_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 72 columns
 [8] READ_Mutation-20160128: RaggedExperiment with 22075 rows and 69 columns
 [9] READ_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 105 columns
[10] READ_RNASeq2GeneNorm_illumina-20160128: SummarizedExperiment with 20501 rows and 72 columns
[11] READ_RNASeq2GeneNorm_illumina-hiseq-20160128: SummarizedExperiment with 20501 rows and 105 columns
[12] READ_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 72 columns
[13] READ_RPPAArray-20160128: SummarizedExperiment with 208 rows and 131 columns
[14] READ_miRNASeqGene-20160128: SummarizedExperiment with 705 rows and 76 columns
[15] READ_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18115 rows and 177 columns
[16] READ_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 73 columns
[17] READ_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 106 columns
```

```
> rownames( READ )
CharacterList of length 17
[["READ_CNASeq-20160128"]] character(0)
[["READ_CNASNP-20160128"]] character(0)
[["READ_CNVSNP-20160128"]] character(0)
[["READ_GISTIC_AllByGene-20160128"]] character(0)
[["READ_GISTIC_Peaks-20160128"]] 23 24 25 1 2 26 27 ... 54 55 18 19 20 56 57
[["READ_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["READ_mRNAArray-20160128"]] ELMO2 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["READ_Mutation-20160128"]] character(0)
[["READ_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["READ_RNASeq2GeneNorm_illumina-20160128"]] A1BG A1CF ... psiTPTE22 tAKR
...
<7 more elements>
```

```
> colnames( READ )
CharacterList of length 17
[["READ_CNASeq-20160128"]] TCGA-AF-2691-01A-01D-1167-02 ...
[["READ_CNASNP-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_CNVSNP-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_GISTIC_AllByGene-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_GISTIC_Peaks-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_GISTIC_ThresholdedByGene-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_mRNAArray-20160128"]] TCGA-AF-2689-11A-01R-1758-07 ...
[["READ_Mutation-20160128"]] TCGA-AF-2689-01A-01W-0831-10 ... TCGA-AG-A036-01
[["READ_RNASeq2Gene-20160128"]] TCGA-AF-2687-01A-02R-1736-07 ...
[["READ_RNASeq2GeneNorm_illumina-20160128"]] TCGA-AF-2691-01A-01R-0821-07...
...
<7 more elements>
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|---|---------------|
| 1 | READ_CNASeq-20160128 | 1.5 Mb |
| 2 | READ_CNASNP-20160128 | 4.3 Mb |
| 3 | READ_CNVSNP-20160128 | 1.1 Mb |
| 4 | READ_GISTIC_AllByGene-20160128 | 34.7 Mb |
| 5 | READ_GISTIC_Peaks-20160128 | 0.2 Mb |
| 6 | READ_GISTIC_ThresholdedByGene-20160128 | 34.5 Mb |
| 7 | READ_mRNAArray-20160128 | 12 Mb |
| 8 | READ_Mutation-20160128 | 9.6 Mb |
| 9 | READ_RNASeq2Gene-20160128 | 19 Mb |
| 10 | READ_RNASeq2GeneNorm_illumina-20160128 | 13.8 Mb |
| 11 | READ_RNASeq2GeneNorm_illuminahisec-20160128 | 19 Mb |
| 12 | READ_RNASeqGene-20160128 | 13.8 Mb |
| 13 | READ_RPPAArray-20160128 | 0.3 Mb |
| 14 | READ_miRNASeqGene-20160128 | 0.5 Mb |
| 15 | READ_RNASeq2GeneNorm-20160128 | 26.7 Mb |

```

16      READ_Methylation_methyl27-20160128  4.9 Mb
17      READ_Methylation_methyl450-20160128  75 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
[1,] 27      27      2      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 10:
 [1] SARC_CNASNP-20160128: RaggedExperiment with 337377 rows and 516 columns
 [2] SARC_CNVSNP-20160128: RaggedExperiment with 106739 rows and 513 columns
 [3] SARC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 257 columns
 [4] SARC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 64 rows and 257 columns
 [5] SARC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 257 columns
 [6] SARC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 263 columns
 [7] SARC_Mutation-20160128: RaggedExperiment with 20376 rows and 247 columns
 [8] SARC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 265 columns
 [9] SARC_RPPAArray-20160128: SummarizedExperiment with 192 rows and 226 columns
[10] SARC_Methylation-20160128: SummarizedExperiment with 485577 rows and 269 columns

> rownames( SARC )
CharacterList of length 10
[["SARC_CNASNP-20160128"]] character(0)
[["SARC_CNVSNP-20160128"]] character(0)
[["SARC_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["SARC_GISTIC_Peaks-20160128"]] chr1:1-5923787 ... chr22:45095899-51304566
[["SARC_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["SARC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["SARC_Mutation-20160128"]] character(0)
[["SARC_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["SARC_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["SARC_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873

> colnames( SARC )
CharacterList of length 10
[["SARC_CNASNP-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_CNVSNP-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_GISTIC_AllByGene-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_GISTIC_Peaks-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_GISTIC_ThresholdedByGene-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_miRNASeqGene-20160128"]] TCGA-3B-A9HI-01A-11R-A38N-13 ...
[["SARC_Mutation-20160128"]] TCGA-3B-A9HI-01A-11D-A387-09 ...
[["SARC_RNASeq2GeneNorm-20160128"]] TCGA-3B-A9HI-01A-11R-A38C-07 ...
[["SARC_RPPAArray-20160128"]] TCGA-3B-A9HI-01A-21-A456-20 ...
[["SARC_Methylation-20160128"]] TCGA-3B-A9HI-01A-11D-A388-05 ...

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|---|--|---------------|
| 1 | SARC_CNASNP-20160128 | 9.2 Mb |
| 2 | SARC_CNVSNP-20160128 | 3 Mb |
| 3 | SARC_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | SARC_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | SARC_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |

```

6          SARC_miRNASeqGene-20160128  0.1 Mb
7          SARC_Mutation-20160128    19.5 Mb
8          SARC_RNASeq2GeneNorm-20160128  1.3 Mb
9          SARC_RPPAArray-20160128      0 Mb
10         SARC_Methylation-20160128    75 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

See Also

[SARC-v2.0.1](#)

SARC-v2.0.1

Sarcoma

Description

A document describing the TCGA cancer code

Details

```

> experiments( SARC )
ExperimentList class object of length 11:
 [1] SARC_CNASNP-20160128: RaggedExperiment with 337377 rows and 516 columns
 [2] SARC_CNVSNP-20160128: RaggedExperiment with 106739 rows and 513 columns
 [3] SARC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 257 columns
 [4] SARC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 64 rows and 257 columns
 [5] SARC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 257 columns
 [6] SARC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 263 columns
 [7] SARC_Mutation-20160128: RaggedExperiment with 20376 rows and 247 columns
 [8] SARC_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 265 columns
 [9] SARC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 265 columns
[10] SARC_RPPAArray-20160128: SummarizedExperiment with 192 rows and 226 columns
[11] SARC_Methylation-20160128: SummarizedExperiment with 485577 rows and 269 columns

```

```

> rownames( SARC )
CharacterList of length 11
[["SARC_CNASNP-20160128"]] character(0)
[["SARC_CNVSNP-20160128"]] character(0)
[["SARC_GISTIC_AllByGene-20160128"]] character(0)
[["SARC_GISTIC_Peaks-20160128"]] 26 1 2 3 27 28 4 29 ... 21 63 22 64 23 65 66
[["SARC_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["SARC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["SARC_Mutation-20160128"]] character(0)
[["SARC_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["SARC_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["SARC_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<1 more element>

```

```

> colnames( SARC )
CharacterList of length 11
[["SARC_CNASNP-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_CNVSNP-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_GISTIC_AllByGene-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_GISTIC_Peaks-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_GISTIC_ThresholdedByGene-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_miRNASeqGene-20160128"]] TCGA-3B-A9HI-01A-11R-A38N-13 ...
[["SARC_Mutation-20160128"]] TCGA-3B-A9HI-01A-11D-A387-09 ...
[["SARC_RNASeq2Gene-20160128"]] TCGA-3B-A9HI-01A-11R-A38C-07 ...
[["SARC_RNASeq2GeneNorm-20160128"]] TCGA-3B-A9HI-01A-11R-A38C-07 ...
[["SARC_RPPAArray-20160128"]] TCGA-3B-A9HI-01A-21-A456-20 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | SARC_CNASNP-20160128 | 9.2 Mb |
| 2 | SARC_CNVSNP-20160128 | 3 Mb |
| 3 | SARC_GISTIC_AllByGene-20160128 | 52.2 Mb |
| 4 | SARC_GISTIC_Peaks-20160128 | 0.2 Mb |
| 5 | SARC_GISTIC_ThresholdedByGene-20160128 | 51.9 Mb |
| 6 | SARC_miRNASeqGene-20160128 | 2.3 Mb |
| 7 | SARC_Mutation-20160128 | 19.5 Mb |
| 8 | SARC_RNASeq2Gene-20160128 | 44 Mb |
| 9 | SARC_RNASeq2GeneNorm-20160128 | 44 Mb |
| 10 | SARC_RPPAArray-20160128 | 0.4 Mb |
| 11 | SARC_Methylation-20160128 | 75 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 | 228 |
| 18 | |
| NA's | |
| 9 | |
| ethnicity: | |
| hispanic or latino not hispanic or latino | NA's |
| 5 | 33 |
| 223 | |

Including an additional 1413 columns

SARC-v2.1.0

Sarcoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( SARC )
ExperimentList class object of length 11:
 [1] SARC_CNASNP-20160128: RaggedExperiment with 337377 rows and 516 columns
 [2] SARC_CNVSNP-20160128: RaggedExperiment with 106739 rows and 513 columns
 [3] SARC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 257 columns
 [4] SARC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 64 rows and 257 columns
 [5] SARC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 257 columns
 [6] SARC_Mutation-20160128: RaggedExperiment with 20376 rows and 247 columns
 [7] SARC_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 265 columns
 [8] SARC_RPPAArray-20160128: SummarizedExperiment with 192 rows and 226 columns
 [9] SARC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 263 columns
[10] SARC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18165 rows and 265 columns
[11] SARC_Methylation-20160128: SummarizedExperiment with 485577 rows and 269 columns

> rownames( SARC )
CharacterList of length 11
[["SARC_CNASNP-20160128"]] character(0)
[["SARC_CNVSNP-20160128"]] character(0)
[["SARC_GISTIC_AllByGene-20160128"]] character(0)
[["SARC_GISTIC_Peaks-20160128"]] 26 1 2 3 27 28 4 29 ... 21 63 22 64 23 65 66
[["SARC_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["SARC_Mutation-20160128"]] character(0)
[["SARC_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["SARC_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["SARC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["SARC_RNASeq2GeneNorm-20160128"]] A1BG A2BP1 A2LD1 ... ZZEF1 ZZZ3 psiTPTE22
...
```

```

<1 more element>

> colnames( SARC )
CharacterList of length 11
[["SARC_CNASNP-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_CNVSNP-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_GISTIC_AllByGene-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_GISTIC_Peaks-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_GISTIC_ThresholdedByGene-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_Mutation-20160128"]] TCGA-3B-A9HI-01A-11D-A387-09 ...
[["SARC_RNASeq2Gene-20160128"]] TCGA-3B-A9HI-01A-11R-A38C-07 ...
[["SARC_RPPAArray-20160128"]] TCGA-3B-A9HI-01A-21-A456-20 ...
[["SARC_miRNASeqGene-20160128"]] TCGA-3B-A9HI-01A-11R-A38N-13 ...
[["SARC_RNASeq2GeneNorm-20160128"]] TCGA-3B-A9HI-01 ... TCGA-Z4-AAPG-01
...
<1 more element>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | SARC_CNASNP-20160128 | 9.2 Mb |
| 2 | SARC_CNVSNP-20160128 | 3 Mb |
| 3 | SARC_GISTIC_AllByGene-20160128 | 52.2 Mb |
| 4 | SARC_GISTIC_Peaks-20160128 | 0.2 Mb |
| 5 | SARC_GISTIC_ThresholdedByGene-20160128 | 51.9 Mb |
| 6 | SARC_Mutation-20160128 | 19.5 Mb |
| 7 | SARC_RNASeq2Gene-20160128 | 44 Mb |
| 8 | SARC_RPPAArray-20160128 | 0.4 Mb |
| 9 | SARC_miRNASeqGene-20160128 | 2.3 Mb |
| 10 | SARC_RNASeq2GeneNorm-20160128 | 39 Mb |
| 11 | SARC_Methylation-20160128 | 75 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
[1,] 99 99 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

Description

A document describing the TCGA cancer code

Details

```

> experiments( SKCM )
ExperimentList class object of length 11:
 [1] SKCM_CNASeq-20160128: RaggedExperiment with 31416 rows and 238 columns
 [2] SKCM_CNASNP-20160128: RaggedExperiment with 452114 rows and 938 columns
 [3] SKCM_CNVSNP-20160128: RaggedExperiment with 108084 rows and 937 columns
 [4] SKCM_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 367 columns
 [5] SKCM_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 53 rows and 367 columns
 [6] SKCM_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 367 columns
 [7] SKCM_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 452 columns
 [8] SKCM_Mutation-20160128: RaggedExperiment with 290322 rows and 345 columns
 [9] SKCM_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 473 columns
 [10] SKCM_RPPAArray-20160128: SummarizedExperiment with 208 rows and 355 columns
 [11] SKCM_Methylation-20160128: SummarizedExperiment with 485577 rows and 475 columns

> rownames( SKCM )
CharacterList of length 11
[["SKCM_CNASeq-20160128"]] character(0)
[["SKCM_CNASNP-20160128"]] character(0)
[["SKCM_CNVSNP-20160128"]] character(0)
[["SKCM_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["SKCM_GISTIC_Peaks-20160128"]] chr1:1-6847369 ... chr22:41468899-41849552
[["SKCM_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["SKCM_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["SKCM_Mutation-20160128"]] character(0)
[["SKCM_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPT22 tAKR
[["SKCM_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<1 more element>

> colnames( SKCM )
CharacterList of length 11
[["SKCM_CNASeq-20160128"]] TCGA-BF-A1PU-01A-11D-A18Z-02 ...
[["SKCM_CNASNP-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_CNVSNP-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_GISTIC_AllByGene-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_GISTIC_Peaks-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_GISTIC_ThresholdedByGene-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_miRNASeqGene-20160128"]] TCGA-3N-A9WC-06A-11R-A38N-13 ...
[["SKCM_Mutation-20160128"]] TCGA-BF-A1PU-01A-11D-A19A-08 ...
[["SKCM_RNASeq2GeneNorm-20160128"]] TCGA-3N-A9WB-06A-11R-A38C-07 ...
[["SKCM_RPPAArray-20160128"]] TCGA-3N-A9WC-06A-21-A444-20 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|----|--|----------|
| 1 | SKCM_CNASeq-20160128 | 0.9 Mb |
| 2 | SKCM_CNASNP-20160128 | 12.3 Mb |
| 3 | SKCM_CNVSNP-20160128 | 3.2 Mb |
| 4 | SKCM_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | SKCM_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | SKCM_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | SKCM_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | SKCM_Mutation-20160128 | 299.6 Mb |
| 9 | SKCM_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 10 | SKCM_RPPAArray-20160128 | 0 Mb |
| 11 | SKCM_Methylation-20160128 | 75.1 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

See Also

[SKCM-v2.0.1](#)

Description

A document describing the TCGA cancer code

Details

```
> experiments( SKCM )
ExperimentList class object of length 12:
 [1] SKCM_CNASeq-20160128: RaggedExperiment with 31416 rows and 238 columns
 [2] SKCM_CNASNP-20160128: RaggedExperiment with 452114 rows and 938 columns
 [3] SKCM_CNVSNP-20160128: RaggedExperiment with 108084 rows and 937 columns
 [4] SKCM_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 367 columns
 [5] SKCM_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 53 rows and 367 columns
 [6] SKCM_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 367 columns
 [7] SKCM_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 452 columns
 [8] SKCM_Mutation-20160128: RaggedExperiment with 290322 rows and 345 columns
 [9] SKCM_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 473 columns
 [10] SKCM_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 473 columns
 [11] SKCM_RPPAArray-20160128: SummarizedExperiment with 208 rows and 355 columns
 [12] SKCM_Methylation-20160128: SummarizedExperiment with 485577 rows and 475 columns

> rownames( SKCM )
CharacterList of length 12
[["SKCM_CNASeq-20160128"]] character(0)
[["SKCM_CNASNP-20160128"]] character(0)
[["SKCM_CNVSNP-20160128"]] character(0)
[["SKCM_GISTIC_AllByGene-20160128"]] character(0)
[["SKCM_GISTIC_Peaks-20160128"]] 21 22 1 2 3 23 24 4 ... 50 51 52 18 53 19 20
[["SKCM_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["SKCM_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["SKCM_Mutation-20160128"]] character(0)
[["SKCM_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["SKCM_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
...
<2 more elements>

> colnames( SKCM )
CharacterList of length 12
[["SKCM_CNASeq-20160128"]] TCGA-BF-A1PU-01A-11D-A18Z-02 ...
[["SKCM_CNASNP-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_CNVSNP-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_GISTIC_AllByGene-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_GISTIC_Peaks-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_GISTIC_ThresholdedByGene-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
```

```

[["SKCM_miRNASeqGene-20160128"]] TCGA-3N-A9WC-06A-11R-A38N-13 ...
[["SKCM_Mutation-20160128"]] TCGA-BF-A1PU-01A-11D-A19A-08 ...
[["SKCM_RNASeq2Gene-20160128"]] TCGA-3N-A9WB-06A-11R-A38C-07 ...
[["SKCM_RNASeq2GeneNorm-20160128"]] TCGA-3N-A9WB-06A-11R-A38C-07 ...
...
<2 more elements>

```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|----|--|----------|
| 1 | SKCM_CNASeq-20160128 | 0.9 Mb |
| 2 | SKCM_CNASNP-20160128 | 12.3 Mb |
| 3 | SKCM_CNVSNP-20160128 | 3.2 Mb |
| 4 | SKCM_GISTIC_AllByGene-20160128 | 73 Mb |
| 5 | SKCM_GISTIC_Peaks-20160128 | 0.3 Mb |
| 6 | SKCM_GISTIC_ThresholdedByGene-20160128 | 72.8 Mb |
| 7 | SKCM_miRNASeqGene-20160128 | 3.8 Mb |
| 8 | SKCM_Mutation-20160128 | 299.6 Mb |
| 9 | SKCM_RNASeq2Gene-20160128 | 76.6 Mb |
| 10 | SKCM_RNASeq2GeneNorm-20160128 | 76.6 Mb |
| 11 | SKCM_RPPAArray-20160128 | 0.7 Mb |
| 12 | SKCM_Methylation-20160128 | 75.1 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: | | | | | | | |
| | -2.0 | 477.5 | 1146.0 | 1885.3 | 2658.8 | 11252.0 | 230 |
| days_to_submitted_specimen_dx: | | | | | | | |
| | -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: | | | | | | | |
| | 0.000 | 1.300 | 3.000 | 5.585 | 6.950 | 75.000 | 111 |
| gender: | | | | | | | |
| female male | 180 | 290 | | | | | |
| date_of_initial_pathologic_diagnosis: | | | | | | | |
| | 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

SKCM-v2.1.0

Skin Cutaneous Melanoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( SKCM )
ExperimentList class object of length 12:
 [1] SKCM_CNASeq-20160128: RaggedExperiment with 31416 rows and 238 columns
 [2] SKCM_CNASNP-20160128: RaggedExperiment with 452114 rows and 938 columns
 [3] SKCM_CNVSNP-20160128: RaggedExperiment with 108084 rows and 937 columns
 [4] SKCM_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 367 columns
 [5] SKCM_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 53 rows and 367 columns
 [6] SKCM_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 367 columns
 [7] SKCM_Mutation-20160128: RaggedExperiment with 290322 rows and 345 columns
 [8] SKCM_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 473 columns
 [9] SKCM_RPPAArray-20160128: SummarizedExperiment with 208 rows and 355 columns
 [10] SKCM_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 452 columns
 [11] SKCM_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18071 rows and 473 columns
 [12] SKCM_Methylation-20160128: SummarizedExperiment with 485577 rows and 475 columns

> rownames( SKCM )
CharacterList of length 12
[["SKCM_CNASeq-20160128"]] character(0)
[["SKCM_CNASNP-20160128"]] character(0)
[["SKCM_CNVSNP-20160128"]] character(0)
[["SKCM_GISTIC_AllByGene-20160128"]] character(0)
[["SKCM_GISTIC_Peaks-20160128"]] 21 22 1 2 3 23 24 4 ... 50 51 52 18 53 19 20
[["SKCM_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["SKCM_Mutation-20160128"]] character(0)
[["SKCM_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
[["SKCM_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["SKCM_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
...
<2 more elements>

> colnames( SKCM )
CharacterList of length 12
[["SKCM_CNASeq-20160128"]] TCGA-BF-A1PU-01A-11D-A18Z-02 ...
[["SKCM_CNASNP-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_CNVSNP-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
```



```

[["SKCM_GISTIC_AllByGene-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_GISTIC_Peaks-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_GISTIC_ThresholdedByGene-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_Mutation-20160128"]] TCGA-BF-A1PU-01A-11D-A19A-08 ...
[["SKCM_RNASeq2Gene-20160128"]] TCGA-3N-A9WB-06A-11R-A38C-07 ...
[["SKCM_RPPAArray-20160128"]] TCGA-3N-A9WC-06A-21-A444-20 ...
[["SKCM_miRNASeqGene-20160128"]] TCGA-3N-A9WC-06A-11R-A38N-13 ...
...
<2 more elements>

```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|----|--|----------|
| 1 | SKCM_CNASeq-20160128 | 0.9 Mb |
| 2 | SKCM_CNASNP-20160128 | 12.3 Mb |
| 3 | SKCM_CNVSNP-20160128 | 3.2 Mb |
| 4 | SKCM_GISTIC_AllByGene-20160128 | 73 Mb |
| 5 | SKCM_GISTIC_Peaks-20160128 | 0.3 Mb |
| 6 | SKCM_GISTIC_ThresholdedByGene-20160128 | 72.8 Mb |
| 7 | SKCM_Mutation-20160128 | 299.6 Mb |
| 8 | SKCM_RNASeq2Gene-20160128 | 76.6 Mb |
| 9 | SKCM_RPPAArray-20160128 | 0.7 Mb |
| 10 | SKCM_miRNASeqGene-20160128 | 3.8 Mb |
| 11 | SKCM_RNASeq2GeneNorm-20160128 | 67.5 Mb |
| 12 | SKCM_Methylation-20160128 | 75.1 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
[1,] 221    221   2.99    2.4    3.9

```

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

SKCM-v2.1.1

Skin Cutaneous Melanoma

Description

A document describing the TCGA cancer code Note. Only the colData has changed.

Details

```

> experiments( SKCM )
ExperimentList class object of length 0:

```

```

> rownames( SKCM )
CharacterList of length 0

```

```

> colnames( SKCM )
CharacterList of length 0

```

Sizes of each ExperimentList element:

```

[1] assay   size.Mb
<0 rows> (or 0-length row.names)

```

```

-----
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
[1,] 221    221    2.99    2.4    3.9

```

```

-----
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 13:
 [1] STAD_CNASeq-20160128: RaggedExperiment with 31824 rows and 214 columns
 [2] STAD_CNASNP-20160128: RaggedExperiment with 443042 rows and 906 columns
 [3] STAD_CNVSNP-20160128: RaggedExperiment with 118389 rows and 904 columns
 [4] STAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 441 columns
 [5] STAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 84 rows and 441 columns
 [6] STAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 441 columns
 [7] STAD_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 430 columns
 [8] STAD_Mutation-20160128: RaggedExperiment with 148520 rows and 289 columns
 [9] STAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 450 columns
 [10] STAD_RNASeqGene-20160128: SummarizedExperiment with 26120 rows and 36 columns
 [11] STAD_RPPAArray-20160128: SummarizedExperiment with 195 rows and 357 columns
 [12] STAD_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 73 columns
 [13] STAD_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 397 columns

> rownames( STAD )
CharacterList of length 13
[["STAD_CNASeq-20160128"]] character(0)
[["STAD_CNASNP-20160128"]] character(0)
[["STAD_CNVSNP-20160128"]] character(0)
[["STAD_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["STAD_GISTIC_Peaks-20160128"]] chr1:10686864-11068052 ...
[["STAD_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["STAD_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["STAD_Mutation-20160128"]] character(0)
[["STAD_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["STAD_RNASeqGene-20160128"]] AADACL3 AADACL4 AB007962 ... VCY XKRY ZFY
```

```

...
<3 more elements>

> colnames( STAD )
CharacterList of length 13
[["STAD_CNASeq-20160128"]] TCGA-B7-5816-01A-21D-1598-02 ...
[["STAD_CNASNP-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_CNVSNP-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_GISTIC_AllByGene-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_GISTIC_Peaks-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_miRNASeqGene-20160128"]] TCGA-3M-AB46-01A-11R-A415-13 ...
[["STAD_Mutation-20160128"]] TCGA-B7-5816-01A-21D-1600-08 ...
[["STAD_RNASeq2GeneNorm-20160128"]] TCGA-3M-AB46-01A-11R-A414-31 ...
[["STAD_RNASeqGene-20160128"]] TCGA-BR-4191-01A-02R-1131-13 ...
...
<3 more elements>

```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|----|--|----------|
| 1 | STAD_CNASeq-20160128 | 0.9 Mb |
| 2 | STAD_CNASNP-20160128 | 12.1 Mb |
| 3 | STAD_CNVSNP-20160128 | 3.4 Mb |
| 4 | STAD_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | STAD_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | STAD_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | STAD_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | STAD_Mutation-20160128 | 161.5 Mb |
| 9 | STAD_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 10 | STAD_RNASeqGene-20160128 | 1.7 Mb |
| 11 | STAD_RPPAArray-20160128 | 0 Mb |
| 12 | STAD_Methylation_methyl27-20160128 | 4.9 Mb |
| 13 | STAD_Methylation_methyl450-20160128 | 75 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 | 5 | 318 | NA's |
| not hispanic or latino | | | 120 |

Including an additional 1390 columns

See Also

[STAD-v2.0.1](#)

STAD-v2.0.1

Stomach adenocarcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( STAD )
ExperimentList class object of length 14:
 [1] STAD_CNASeq-20160128: RaggedExperiment with 31824 rows and 214 columns
 [2] STAD_CNASNP-20160128: RaggedExperiment with 443042 rows and 906 columns
 [3] STAD_CNVSNP-20160128: RaggedExperiment with 118389 rows and 904 columns
 [4] STAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 441 columns
 [5] STAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 84 rows and 441 columns
 [6] STAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 441 columns
 [7] STAD_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 430 columns
 [8] STAD_Mutation-20160128: RaggedExperiment with 148520 rows and 289 columns
 [9] STAD_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 450 columns
 [10] STAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 450 columns
 [11] STAD_RNASeqGene-20160128: SummarizedExperiment with 26120 rows and 271 columns
```



```
[12] STAD_RPPAArray-20160128: SummarizedExperiment with 195 rows and 357 columns
[13] STAD_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 73 columns
[14] STAD_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 397 columns
```

```
> rownames( STAD )
CharacterList of length 14
[["STAD_CNASeq-20160128"]] character(0)
[["STAD_CNASNP-20160128"]] character(0)
[["STAD_CNVSNP-20160128"]] character(0)
[["STAD_GISTIC_AllByGene-20160128"]] character(0)
[["STAD_GISTIC_Peaks-20160128"]] 1 37 38 2 3 39 40 ... 81 34 82 35 83 84 85
[["STAD_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["STAD_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["STAD_Mutation-20160128"]] character(0)
[["STAD_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["STAD_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
...
<4 more elements>
```

```
> colnames( STAD )
CharacterList of length 14
[["STAD_CNASeq-20160128"]] TCGA-B7-5816-01A-21D-1598-02 ...
[["STAD_CNASNP-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_CNVSNP-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_GISTIC_AllByGene-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_GISTIC_Peaks-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_miRNASeqGene-20160128"]] TCGA-3M-AB46-01A-11R-A415-13 ...
[["STAD_Mutation-20160128"]] TCGA-B7-5816-01A-21D-1600-08 ...
[["STAD_RNASeq2Gene-20160128"]] TCGA-3M-AB46-01A-11R-A414-31 ...
[["STAD_RNASeq2GeneNorm-20160128"]] TCGA-3M-AB46-01A-11R-A414-31 ...
...
<4 more elements>
```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|----|--|----------|
| 1 | STAD_CNASeq-20160128 | 0.9 Mb |
| 2 | STAD_CNASNP-20160128 | 12.1 Mb |
| 3 | STAD_CNVSNP-20160128 | 3.4 Mb |
| 4 | STAD_GISTIC_AllByGene-20160128 | 87 Mb |
| 5 | STAD_GISTIC_Peaks-20160128 | 0.4 Mb |
| 6 | STAD_GISTIC_ThresholdedByGene-20160128 | 86.8 Mb |
| 7 | STAD_miRNASeqGene-20160128 | 3.7 Mb |
| 8 | STAD_Mutation-20160128 | 161.5 Mb |
| 9 | STAD_RNASeq2Gene-20160128 | 73 Mb |
| 10 | STAD_RNASeq2GeneNorm-20160128 | 73 Mb |
| 11 | STAD_RNASeqGene-20160128 | 57.4 Mb |

```

12          STAD_RPPAArray-20160128    0.6 Mb
13  STAD_Methylation_methyl27-20160128  4.9 Mb
14  STAD_Methylation_methyl450-20160128 75.1 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

STAD-v2.1.0

Stomach adenocarcinoma

Description

A document describing the TCGA cancer code

Details

```

> experiments( STAD )
ExperimentList class object of length 14:
 [1] STAD_CNASeq-20160128: RaggedExperiment with 31824 rows and 214 columns
 [2] STAD_CNASNP-20160128: RaggedExperiment with 443042 rows and 906 columns
 [3] STAD_CNVSNP-20160128: RaggedExperiment with 118389 rows and 904 columns
 [4] STAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 441 columns
 [5] STAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 84 rows and 441 columns
 [6] STAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 441 columns
 [7] STAD_Mutation-20160128: RaggedExperiment with 148520 rows and 289 columns
 [8] STAD_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 450 columns
 [9] STAD_RNASeqGene-20160128: SummarizedExperiment with 26120 rows and 271 columns
[10] STAD_RPPAArray-20160128: SummarizedExperiment with 195 rows and 357 columns
[11] STAD_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 430 columns
[12] STAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18664 rows and 450 columns
[13] STAD_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 73 columns
[14] STAD_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 397 columns

> rownames( STAD )
CharacterList of length 14
[["STAD_CNASeq-20160128"]] character(0)
[["STAD_CNASNP-20160128"]] character(0)
[["STAD_CNVSNP-20160128"]] character(0)
[["STAD_GISTIC_AllByGene-20160128"]] character(0)
[["STAD_GISTIC_Peaks-20160128"]] 1 37 38 2 3 39 40 ... 81 34 82 35 83 84 85
[["STAD_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["STAD_Mutation-20160128"]] character(0)
[["STAD_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["STAD_RNASeqGene-20160128"]] AADACL3 AADACL4 AB007962 ... VCY XKRY ZFY
[["STAD_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<4 more elements>

> colnames( STAD )
CharacterList of length 14
[["STAD_CNASeq-20160128"]] TCGA-B7-5816-01A-21D-1598-02 ...
[["STAD_CNASNP-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_CNVSNP-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_GISTIC_AllByGene-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_GISTIC_Peaks-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_Mutation-20160128"]] TCGA-B7-5816-01A-21D-1600-08 ...
[["STAD_RNASeq2Gene-20160128"]] TCGA-3M-AB46-01A-11R-A414-31 ...
[["STAD_RNASeqGene-20160128"]] TCGA-B7-5816-01A-21R-1602-13 ...
[["STAD_RPPAArray-20160128"]] TCGA-3M-AB47-01A-11-A43D-20 ...
...
<4 more elements>

```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|----|--|----------|
| 1 | STAD_CNASeq-20160128 | 0.9 Mb |
| 2 | STAD_CNASNP-20160128 | 12.1 Mb |
| 3 | STAD_CNVSNP-20160128 | 3.4 Mb |
| 4 | STAD_GISTIC_AllByGene-20160128 | 87 Mb |
| 5 | STAD_GISTIC_Peaks-20160128 | 0.4 Mb |
| 6 | STAD_GISTIC_ThresholdedByGene-20160128 | 86.8 Mb |
| 7 | STAD_Mutation-20160128 | 161.5 Mb |
| 8 | STAD_RNASeq2Gene-20160128 | 73 Mb |
| 9 | STAD_RNASeqGene-20160128 | 57.4 Mb |
| 10 | STAD_RPPAArray-20160128 | 0.6 Mb |
| 11 | STAD_miRNASeqGene-20160128 | 3.7 Mb |
| 12 | STAD_RNASeq2GeneNorm-20160128 | 66.5 Mb |
| 13 | STAD_Methylation_methyl27-20160128 | 4.9 Mb |
| 14 | STAD_Methylation_methyl450-20160128 | 75.1 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
[1,] 170 170 0.948 0.792 1.08

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 10:
 [1] TGCT_CNASNP-20160128: RaggedExperiment with 137968 rows and 271 columns
 [2] TGCT_CNVSNP-20160128: RaggedExperiment with 25479 rows and 271 columns
 [3] TGCT_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 134 columns
 [4] TGCT_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 48 rows and 134 columns
 [5] TGCT_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 134 columns
 [6] TGCT_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 139 columns
 [7] TGCT_Mutation-20160128: RaggedExperiment with 14672 rows and 138 columns
 [8] TGCT_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 139 columns
 [9] TGCT_RPPAArray-20160128: SummarizedExperiment with 192 rows and 107 columns
 [10] TGCT_Methylation-20160128: SummarizedExperiment with 485577 rows and 139 columns

> rownames( TGCT )
CharacterList of length 10
[["TGCT_CNASNP-20160128"]] character(0)
[["TGCT_CNVSNP-20160128"]] character(0)
[["TGCT_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["TGCT_GISTIC_Peaks-20160128"]] chr1:1-48649489 ... chr22:18613558-22141824
[["TGCT_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["TGCT_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["TGCT_Mutation-20160128"]] character(0)
[["TGCT_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["TGCT_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["TGCT_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873

> colnames( TGCT )
CharacterList of length 10
[["TGCT_CNASNP-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_CNVSNP-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_GISTIC_AllByGene-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_GISTIC_Peaks-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_GISTIC_ThresholdedByGene-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_miRNASeqGene-20160128"]] TCGA-2G-AAEW-01A-11R-A439-13 ...
```

```

[["TGCT_Mutation-20160128"]] TCGA-2G-AAEW-01A-11D-A42Y-10 ...
[["TGCT_RNASeq2GeneNorm-20160128"]] TCGA-2G-AAEW-01A-11R-A430-07 ...
[["TGCT_RPPAArray-20160128"]] TCGA-2G-AAEW-01A-21-A45P-20 ...
[["TGCT_Methylation-20160128"]] TCGA-2G-AAEW-01A-11D-A42Z-05 ...

```

Sizes of each ExperimentList element:

| | | assay | size.Mb |
|----|--|--|---------|
| 1 | | TGCT_CNASNP-20160128 | 3.8 Mb |
| 2 | | TGCT_CNVSNP-20160128 | 0.8 Mb |
| 3 | | TGCT_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | | TGCT_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | | TGCT_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | | TGCT_miRNASeqGene-20160128 | 0.1 Mb |
| 7 | | TGCT_Mutation-20160128 | 10 Mb |
| 8 | | TGCT_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 9 | | TGCT_RPPAArray-20160128 | 0 Mb |
| 10 | | TGCT_Methylation-20160128 | 75 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

See Also[TGCT-v2.0.1](#)

TGCT-v2.0.1

*Testicular Germ Cell Tumors***Description**

A document describing the TCGA cancer code

Details

```

> experiments( TGCT )
ExperimentList class object of length 11:
 [1] TGCT_CNASNP-20160128: RaggedExperiment with 137968 rows and 271 columns
 [2] TGCT_CNVSNP-20160128: RaggedExperiment with 25479 rows and 271 columns
 [3] TGCT_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 134 columns
 [4] TGCT_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 48 rows and 134 columns
 [5] TGCT_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 134 columns
 [6] TGCT_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 139 columns
 [7] TGCT_Mutation-20160128: RaggedExperiment with 14672 rows and 138 columns
 [8] TGCT_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 139 columns
 [9] TGCT_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 139 columns
 [10] TGCT_RPPAArray-20160128: SummarizedExperiment with 192 rows and 107 columns
 [11] TGCT_Methylation-20160128: SummarizedExperiment with 485577 rows and 139 columns

> rownames( TGCT )
CharacterList of length 11
[["TGCT_CNASNP-20160128"]] character(0)
[["TGCT_CNVSNP-20160128"]] character(0)
[["TGCT_GISTIC_AllByGene-20160128"]] character(0)
[["TGCT_GISTIC_Peaks-20160128"]] 17 18 1 19 2 20 21 ... 44 45 47 46 48 15 16
[["TGCT_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["TGCT_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["TGCT_Mutation-20160128"]] character(0)
[["TGCT_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["TGCT_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["TGCT_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<1 more element>

> colnames( TGCT )
CharacterList of length 11
[["TGCT_CNASNP-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_CNVSNP-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_GISTIC_AllByGene-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_GISTIC_Peaks-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...

```

```

[["TGCT_GISTIC_ThresholdedByGene-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_miRNASeqGene-20160128"]] TCGA-2G-AAEW-01A-11R-A439-13 ...
[["TGCT_Mutation-20160128"]] TCGA-2G-AAEW-01A-11D-A42Y-10 ...
[["TGCT_RNASeq2Gene-20160128"]] TCGA-2G-AAEW-01A-11R-A430-07 ...
[["TGCT_RNASeq2GeneNorm-20160128"]] TCGA-2G-AAEW-01A-11R-A430-07 ...
[["TGCT_RPPAArray-20160128"]] TCGA-2G-AAEW-01A-21-A45P-20 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

| | | assay | size.Mb |
|----|--|-------|---------|
| 1 | TGCT_CNASNP-20160128 | | 3.8 Mb |
| 2 | TGCT_CNVSNP-20160128 | | 0.8 Mb |
| 3 | TGCT_GISTIC_AllByGene-20160128 | | 28.8 Mb |
| 4 | TGCT_GISTIC_Peaks-20160128 | | 0.1 Mb |
| 5 | TGCT_GISTIC_ThresholdedByGene-20160128 | | 28.7 Mb |
| 6 | TGCT_miRNASeqGene-20160128 | | 1.3 Mb |
| 7 | TGCT_Mutation-20160128 | | 10 Mb |
| 8 | TGCT_RNASeq2Gene-20160128 | | 24.3 Mb |
| 9 | TGCT_RNASeq2GeneNorm-20160128 | | 24.3 Mb |
| 10 | TGCT_RPPAArray-20160128 | | 0.2 Mb |
| 11 | TGCT_Methylation-20160128 | | 75 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

TGCT-v2.1.0

Testicular Germ Cell Tumors

Description

A document describing the TCGA cancer code

Details

```
> experiments( TGCT )
ExperimentList class object of length 11:
 [1] TGCT_CNASNP-20160128: RaggedExperiment with 137968 rows and 271 columns
 [2] TGCT_CNVSNP-20160128: RaggedExperiment with 25479 rows and 271 columns
 [3] TGCT_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 134 columns
 [4] TGCT_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 48 rows and 134 columns
 [5] TGCT_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 134 columns
 [6] TGCT_Mutation-20160128: RaggedExperiment with 14672 rows and 138 columns
 [7] TGCT_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 139 columns
 [8] TGCT_RPPAArray-20160128: SummarizedExperiment with 192 rows and 107 columns
 [9] TGCT_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 139 columns
 [10] TGCT_RNASeq2GeneNorm-20160128: SummarizedExperiment with 19036 rows and 139 columns
 [11] TGCT_Methylation-20160128: SummarizedExperiment with 485577 rows and 139 columns

> rownames( TGCT )
CharacterList of length 11
[["TGCT_CNASNP-20160128"]] character(0)
[["TGCT_CNVSNP-20160128"]] character(0)
[["TGCT_GISTIC_AllByGene-20160128"]] character(0)
[["TGCT_GISTIC_Peaks-20160128"]] 17 18 1 19 2 20 21 ... 44 45 47 46 48 15 16
[["TGCT_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["TGCT_Mutation-20160128"]] character(0)
[["TGCT_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["TGCT_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["TGCT_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["TGCT_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZEF1 ZZZ3 psiTPTE22
...
<1 more element>

> colnames( TGCT )
CharacterList of length 11
[["TGCT_CNASNP-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_CNVSNP-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
```

```

[["TGCT_GISTIC_AllByGene-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_GISTIC_Peaks-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_GISTIC_ThresholdedByGene-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_Mutation-20160128"]] TCGA-2G-AAEW-01A-11D-A42Y-10 ...
[["TGCT_RNASeq2Gene-20160128"]] TCGA-2G-AAEW-01A-11R-A430-07 ...
[["TGCT_RPPAArray-20160128"]] TCGA-2G-AAEW-01A-21-A45P-20 ...
[["TGCT_miRNASeqGene-20160128"]] TCGA-2G-AAEW-01A-11R-A439-13 ...
[["TGCT_RNASeq2GeneNorm-20160128"]] TCGA-2G-AAEW-01 ... TCGA-ZM-AA0N-01
...
<1 more element>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | TGCT_CNASNP-20160128 | 3.8 Mb |
| 2 | TGCT_CNVSNP-20160128 | 0.8 Mb |
| 3 | TGCT_GISTIC_AllByGene-20160128 | 28.8 Mb |
| 4 | TGCT_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | TGCT_GISTIC_ThresholdedByGene-20160128 | 28.7 Mb |
| 6 | TGCT_Mutation-20160128 | 10 Mb |
| 7 | TGCT_RNASeq2Gene-20160128 | 24.3 Mb |
| 8 | TGCT_RPPAArray-20160128 | 0.2 Mb |
| 9 | TGCT_miRNASeqGene-20160128 | 1.3 Mb |
| 10 | TGCT_RNASeq2GeneNorm-20160128 | 22.6 Mb |
| 11 | TGCT_Methylation-20160128 | 75 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
[1,] 4      4  1.55  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 |
| NA's | 119 |
| 5 | |

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

Including an additional 762 columns

| | |
|------|--------------------------|
| THCA | <i>Thyroid carcinoma</i> |
|------|--------------------------|

Description

A document describing the TCGA cancer code

Details

```
> experiments( THCA )
ExperimentList class object of length 12:
 [1] THCA_CNASeq-20160128: RaggedExperiment with 5953 rows and 203 columns
 [2] THCA_CNASNP-20160128: RaggedExperiment with 389998 rows and 1013 columns
 [3] THCA_CNVSNP-20160128: RaggedExperiment with 55117 rows and 1013 columns
 [4] THCA_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 499 columns
 [5] THCA_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 38 rows and 499 columns
 [6] THCA_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 499 columns
 [7] THCA_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 569 columns
 [8] THCA_Mutation-20160128: RaggedExperiment with 7458 rows and 405 columns
 [9] THCA_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 568 columns
 [10] THCA_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 4 columns
 [11] THCA_RPPAArray-20160128: SummarizedExperiment with 175 rows and 224 columns
 [12] THCA_Methylation-20160128: SummarizedExperiment with 485577 rows and 567 columns

> rownames( THCA )
CharacterList of length 12
[["THCA_CNASeq-20160128"]] character(0)
[["THCA_CNASNP-20160128"]] character(0)
[["THCA_CNVSNP-20160128"]] character(0)
[["THCA_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["THCA_GISTIC_Peaks-20160128"]] chr1:158681167-215338621 ...
[["THCA_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["THCA_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["THCA_Mutation-20160128"]] character(0)
[["THCA_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["THCA_RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
...
<2 more elements>

> colnames( THCA )
```



```

CharacterList of length 12
[["THCA_CNASeq-20160128"]] TCGA-BJ-A0Z2-01A-11D-A10R-02 ...
[["THCA_CNASNP-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_CNVSNP-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_GISTIC_AllByGene-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_GISTIC_Peaks-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_GISTIC_ThresholdedByGene-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_miRNASeqGene-20160128"]] TCGA-4C-A93U-01A-11R-A39B-13 ...
[["THCA_Mutation-20160128"]] TCGA-BJ-A0YZ-01A-11D-A10S-08 ...
[["THCA_RNASeq2GeneNorm-20160128"]] TCGA-4C-A93U-01A-11R-A39I-07 ...
[["THCA_RNASeqGene-20160128"]] TCGA-DJ-A1QE-01A-21R-A14Y-07 ...
...
<2 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | THCA_CNASeq-20160128 | 0.2 Mb |
| 2 | THCA_CNASNP-20160128 | 10.7 Mb |
| 3 | THCA_CNVSNP-20160128 | 1.8 Mb |
| 4 | THCA_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | THCA_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | THCA_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | THCA_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | THCA_Mutation-20160128 | 14 Mb |
| 9 | THCA_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 10 | THCA_RNASeqGene-20160128 | 1.3 Mb |
| 11 | THCA_RPPAArray-20160128 | 0 Mb |
| 12 | THCA_Methylation-20160128 | 75.1 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) | very advanced (t4b) | none |
|--------------|-------------------------|---------------------|------|
| 133 | 18 | | 333 |
| | | 1 | 18 |
| | | | NA's |

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

See Also

[THCA-v2.0.1](#)

THCA-v2.0.1

Thyroid carcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( THCA )
```

```
ExperimentList class object of length 13:
```

```
[1] THCA_CNASeq-20160128: RaggedExperiment with 5953 rows and 203 columns
[2] THCA_CNASNP-20160128: RaggedExperiment with 389998 rows and 1013 columns
[3] THCA_CNVSNP-20160128: RaggedExperiment with 55117 rows and 1013 columns
[4] THCA_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 499 columns
[5] THCA_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 38 rows and 499 columns
[6] THCA_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 499 columns
[7] THCA_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 569 columns
[8] THCA_Mutation-20160128: RaggedExperiment with 7458 rows and 405 columns
[9] THCA_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 568 columns
[10] THCA_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 568 columns
[11] THCA_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 4 columns
[12] THCA_RPPAArray-20160128: SummarizedExperiment with 175 rows and 224 columns
[13] THCA_Methylation-20160128: SummarizedExperiment with 485577 rows and 567 columns
```

```
> rownames( THCA )
```

```
CharacterList of length 13
```

```

[[ "THCA_CNASeq-20160128" ]] character(0)
[[ "THCA_CNASNP-20160128" ]] character(0)
[[ "THCA_CNVSNP-20160128" ]] character(0)
[[ "THCA_GISTIC_AllByGene-20160128" ]] character(0)
[[ "THCA_GISTIC_Peaks-20160128" ]] 1 10 11 12 2 13 3 14 ... 36 37 38 39 7 40 41
[[ "THCA_GISTIC_ThresholdedByGene-20160128" ]] character(0)
[[ "THCA_miRNASeqGene-20160128" ]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[[ "THCA_Mutation-20160128" ]] character(0)
[[ "THCA_RNASeq2Gene-20160128" ]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[[ "THCA_RNASeq2GeneNorm-20160128" ]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
...
<3 more elements>

```

```

> colnames( THCA )
CharacterList of length 13
[[ "THCA_CNASeq-20160128" ]] TCGA-BJ-A0Z2-01A-11D-A10R-02 ...
[[ "THCA_CNASNP-20160128" ]] TCGA-4C-A93U-01A-11D-A396-01 ...
[[ "THCA_CNVSNP-20160128" ]] TCGA-4C-A93U-01A-11D-A396-01 ...
[[ "THCA_GISTIC_AllByGene-20160128" ]] TCGA-4C-A93U-01A-11D-A396-01 ...
[[ "THCA_GISTIC_Peaks-20160128" ]] TCGA-4C-A93U-01A-11D-A396-01 ...
[[ "THCA_GISTIC_ThresholdedByGene-20160128" ]] TCGA-4C-A93U-01A-11D-A396-01 ...
[[ "THCA_miRNASeqGene-20160128" ]] TCGA-4C-A93U-01A-11R-A39B-13 ...
[[ "THCA_Mutation-20160128" ]] TCGA-BJ-A0YZ-01A-11D-A10S-08 ...
[[ "THCA_RNASeq2Gene-20160128" ]] TCGA-4C-A93U-01A-11R-A39I-07 ...
[[ "THCA_RNASeq2GeneNorm-20160128" ]] TCGA-4C-A93U-01A-11R-A39I-07 ...
...
<3 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | THCA_CNASeq-20160128 | 0.2 Mb |
| 2 | THCA_CNASNP-20160128 | 10.7 Mb |
| 3 | THCA_CNVSNP-20160128 | 1.8 Mb |
| 4 | THCA_GISTIC_AllByGene-20160128 | 97.8 Mb |
| 5 | THCA_GISTIC_Peaks-20160128 | 0.3 Mb |
| 6 | THCA_GISTIC_ThresholdedByGene-20160128 | 97.7 Mb |
| 7 | THCA_miRNASeqGene-20160128 | 4.8 Mb |
| 8 | THCA_Mutation-20160128 | 14 Mb |
| 9 | THCA_RNASeq2Gene-20160128 | 91.5 Mb |
| 10 | THCA_RNASeq2GeneNorm-20160128 | 91.5 Mb |
| 11 | THCA_RNASeqGene-20160128 | 3.2 Mb |
| 12 | THCA_RPPAArray-20160128 | 0.4 Mb |
| 13 | THCA_Methylation-20160128 | 75.1 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

THCA-v2.1.0

Thyroid carcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( THCA )
```

```
ExperimentList class object of length 13:
```

- [1] THCA_CNASeq-20160128: RaggedExperiment with 5953 rows and 203 columns
- [2] THCA_CNASNP-20160128: RaggedExperiment with 389998 rows and 1013 columns
- [3] THCA_CNVSNP-20160128: RaggedExperiment with 55117 rows and 1013 columns
- [4] THCA_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 499 columns
- [5] THCA_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 38 rows and 499 columns

```

[6] THCA_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 499 columns
[7] THCA_Mutation-20160128: RaggedExperiment with 7458 rows and 405 columns
[8] THCA_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 568 columns
[9] THCA_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 4 columns
[10] THCA_RPPAArray-20160128: SummarizedExperiment with 175 rows and 224 columns
[11] THCA_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 569 columns
[12] THCA_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18003 rows and 568 columns
[13] THCA_Methylation-20160128: SummarizedExperiment with 485577 rows and 567 columns

```

```

> rownames( THCA )
CharacterList of length 13
[["THCA_CNASeq-20160128"]] character(0)
[["THCA_CNASNP-20160128"]] character(0)
[["THCA_CNVSNP-20160128"]] character(0)
[["THCA_GISTIC_AllByGene-20160128"]] character(0)
[["THCA_GISTIC_Peaks-20160128"]] 1 10 11 12 2 13 3 14 ... 36 37 38 39 7 40 41
[["THCA_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["THCA_Mutation-20160128"]] character(0)
[["THCA_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["THCA_RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["THCA_RPPAArray-20160128"]] 14-3-3_epsilon 4E-BP1 ... p90RSK_pT359_S363
...
<3 more elements>

```

```

> colnames( THCA )
CharacterList of length 13
[["THCA_CNASeq-20160128"]] TCGA-BJ-A0Z2-01A-11D-A10R-02 ...
[["THCA_CNASNP-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_CNVSNP-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_GISTIC_AllByGene-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_GISTIC_Peaks-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_GISTIC_ThresholdedByGene-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_Mutation-20160128"]] TCGA-BJ-A0YZ-01A-11D-A10S-08 ...
[["THCA_RNASeq2Gene-20160128"]] TCGA-4C-A93U-01A-11R-A39I-07 ...
[["THCA_RNASeqGene-20160128"]] TCGA-DJ-A1QE-01A-21R-A14Y-07 ...
[["THCA_RPPAArray-20160128"]] TCGA-BJ-A0YZ-01A-21-A21L-20 ...
...
<3 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|---|--|---------------|
| 1 | THCA_CNASeq-20160128 | 0.2 Mb |
| 2 | THCA_CNASNP-20160128 | 10.7 Mb |
| 3 | THCA_CNVSNP-20160128 | 1.8 Mb |
| 4 | THCA_GISTIC_AllByGene-20160128 | 97.8 Mb |
| 5 | THCA_GISTIC_Peaks-20160128 | 0.3 Mb |
| 6 | THCA_GISTIC_ThresholdedByGene-20160128 | 97.7 Mb |

| | | |
|----|-------------------------------|---------|
| 7 | THCA_Mutation-20160128 | 14 Mb |
| 8 | THCA_RNASeq2Gene-20160128 | 91.5 Mb |
| 9 | THCA_RNASeqGene-20160128 | 3.2 Mb |
| 10 | THCA_RPPAArray-20160128 | 0.4 Mb |
| 11 | THCA_miRNASeqGene-20160128 | 4.8 Mb |
| 12 | THCA_RNASeq2GeneNorm-20160128 | 80.3 Mb |
| 13 | THCA_Methylation-20160128 | 75.1 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
[1,] 16 16 2.8 2.23 4.8

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) | very advanced (t4b) | none |
|--------------|-------------------------|---------------------|------|
| 133 | 18 | NA's | 333 |
| | | 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 10:
 [1] THYM_CNASNP-20160128: RaggedExperiment with 105646 rows and 248 columns
 [2] THYM_CNVSNP-20160128: RaggedExperiment with 15571 rows and 248 columns
 [3] THYM_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 123 columns
 [4] THYM_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 16 rows and 123 columns
 [5] THYM_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 123 columns
 [6] THYM_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 126 columns
 [7] THYM_Mutation-20160128: RaggedExperiment with 3064 rows and 123 columns
 [8] THYM_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 122 columns
 [9] THYM_RPPAArray-20160128: SummarizedExperiment with 192 rows and 90 columns
 [10] THYM_Methylation-20160128: SummarizedExperiment with 485577 rows and 126 columns

> rownames( THYM )
CharacterList of length 10
[["THYM_CNASNP-20160128"]] character(0)
[["THYM_CNVSNP-20160128"]] character(0)
[["THYM_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["THYM_GISTIC_Peaks-20160128"]] chr1:208606110-249250621 ...
[["THYM_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["THYM_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["THYM_Mutation-20160128"]] character(0)
[["THYM_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["THYM_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["THYM_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873

> colnames( THYM )
CharacterList of length 10
[["THYM_CNASNP-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_CNVSNP-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_GISTIC_AllByGene-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_GISTIC_Peaks-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_GISTIC_ThresholdedByGene-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_miRNASeqGene-20160128"]] TCGA-3G-AB00-01A-22R-A42W-13 ...
[["THYM_Mutation-20160128"]] TCGA-3G-AB00-01A-22D-A423-09 ...
[["THYM_RNASeq2GeneNorm-20160128"]] TCGA-3G-AB00-01A-22R-A42C-07 ...
[["THYM_RPPAArray-20160128"]] TCGA-3G-AB00-01A-11-A45R-20 ...
[["THYM_Methylation-20160128"]] TCGA-3G-AB00-01A-22D-A424-05 ...

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|---|--|---------------|
| 1 | THYM_CNASNP-20160128 | 2.9 Mb |
| 2 | THYM_CNVSNP-20160128 | 0.5 Mb |
| 3 | THYM_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | THYM_GISTIC_Peaks-20160128 | 0 Mb |
| 5 | THYM_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |

| | | |
|----|-------------------------------|--------|
| 6 | THYM_miRNASeqGene-20160128 | 0.1 Mb |
| 7 | THYM_Mutation-20160128 | 3.3 Mb |
| 8 | THYM_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 9 | THYM_RPPAArray-20160128 | 0 Mb |
| 10 | THYM_Methylation-20160128 | 75 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

See Also

[THYM-v2.0.1](#)

THYM-v2.0.1

Thymoma

Description

A document describing the TCGA cancer code

Details

```

> experiments( THYM )
ExperimentList class object of length 11:
 [1] THYM_CNASNP-20160128: RaggedExperiment with 105646 rows and 248 columns
 [2] THYM_CNVSNP-20160128: RaggedExperiment with 15571 rows and 248 columns
 [3] THYM_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 123 columns
 [4] THYM_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 16 rows and 123 columns
 [5] THYM_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 123 columns
 [6] THYM_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 126 columns
 [7] THYM_Mutation-20160128: RaggedExperiment with 3064 rows and 123 columns
 [8] THYM_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 122 columns
 [9] THYM_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 122 columns
[10] THYM_RPPAArray-20160128: SummarizedExperiment with 192 rows and 90 columns
[11] THYM_Methylation-20160128: SummarizedExperiment with 485577 rows and 126 columns

> rownames( THYM )

```

```

CharacterList of length 11
[["THYM_CNASNP-20160128"]] character(0)
[["THYM_CNVSNP-20160128"]] character(0)
[["THYM_GISTIC_AllByGene-20160128"]] character(0)
[["THYM_GISTIC_Peaks-20160128"]] 1 8 9 10 11 12 13 14 2 15 3 4 16 5 17 18
[["THYM_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["THYM_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["THYM_Mutation-20160128"]] character(0)
[["THYM_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["THYM_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["THYM_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<1 more element>

```

```

> colnames( THYM )
CharacterList of length 11
[["THYM_CNASNP-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_CNVSNP-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_GISTIC_AllByGene-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_GISTIC_Peaks-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_GISTIC_ThresholdedByGene-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_miRNASeqGene-20160128"]] TCGA-3G-AB00-01A-22R-A42W-13 ...
[["THYM_Mutation-20160128"]] TCGA-3G-AB00-01A-22D-A423-09 ...
[["THYM_RNASeq2Gene-20160128"]] TCGA-3G-AB00-01A-22R-A42C-07 ...
[["THYM_RNASeq2GeneNorm-20160128"]] TCGA-3G-AB00-01A-22R-A42C-07 ...
[["THYM_RPPAArray-20160128"]] TCGA-3G-AB00-01A-11-A45R-20 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | THYM_CNASNP-20160128 | 2.9 Mb |
| 2 | THYM_CNVSNP-20160128 | 0.5 Mb |
| 3 | THYM_GISTIC_AllByGene-20160128 | 26.7 Mb |
| 4 | THYM_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | THYM_GISTIC_ThresholdedByGene-20160128 | 26.6 Mb |
| 6 | THYM_miRNASeqGene-20160128 | 1.2 Mb |
| 7 | THYM_Mutation-20160128 | 3.3 Mb |
| 8 | THYM_RNASeq2Gene-20160128 | 21.7 Mb |
| 9 | THYM_RNASeq2GeneNorm-20160128 | 21.7 Mb |
| 10 | THYM_RPPAArray-20160128 | 0.2 Mb |
| 11 | THYM_Methylation-20160128 | 75 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

THYM-v2.1.0

Thymoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( THYM )
ExperimentList class object of length 11:
 [1] THYM_CNASNP-20160128: RaggedExperiment with 105646 rows and 248 columns
 [2] THYM_CNVSNP-20160128: RaggedExperiment with 15571 rows and 248 columns
 [3] THYM_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 123 columns
 [4] THYM_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 16 rows and 123 columns
 [5] THYM_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 123 columns
 [6] THYM_Mutation-20160128: RaggedExperiment with 3064 rows and 123 columns
 [7] THYM_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 122 columns
 [8] THYM_RPPAArray-20160128: SummarizedExperiment with 192 rows and 90 columns
 [9] THYM_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 126 columns
 [10] THYM_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18286 rows and 122 columns
 [11] THYM_Methylation-20160128: SummarizedExperiment with 485577 rows and 126 columns

> rownames( THYM )
CharacterList of length 11
[["THYM_CNASNP-20160128"]] character(0)
[["THYM_CNVSNP-20160128"]] character(0)
[["THYM_GISTIC_AllByGene-20160128"]] character(0)
[["THYM_GISTIC_Peaks-20160128"]] 1 8 9 10 11 12 13 14 2 15 3 4 16 5 17 18
[["THYM_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["THYM_Mutation-20160128"]] character(0)
[["THYM_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["THYM_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["THYM_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["THYM_RNASeq2GeneNorm-20160128"]] A1BG A2BP1 A2LD1 ... ZZEF1 ZZZ3 psiTPTE22
...
<1 more element>
```

```
> colnames( THYM )
CharacterList of length 11
[["THYM_CNASNP-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_CNVSNP-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_GISTIC_AllByGene-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_GISTIC_Peaks-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_GISTIC_ThresholdedByGene-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_Mutation-20160128"]] TCGA-3G-AB00-01A-22D-A423-09 ...
[["THYM_RNASeq2Gene-20160128"]] TCGA-3G-AB00-01A-22R-A42C-07 ...
[["THYM_RPPAArray-20160128"]] TCGA-3G-AB00-01A-11-A45R-20 ...
[["THYM_miRNASeqGene-20160128"]] TCGA-3G-AB00-01A-22R-A42W-13 ...
[["THYM_RNASeq2GeneNorm-20160128"]] TCGA-3G-AB00-01 ... TCGA-ZT-A80M-01
...
<1 more element>
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|--|---------------|
| 1 | THYM_CNASNP-20160128 | 2.9 Mb |
| 2 | THYM_CNVSNP-20160128 | 0.5 Mb |
| 3 | THYM_GISTIC_AllByGene-20160128 | 26.7 Mb |
| 4 | THYM_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | THYM_GISTIC_ThresholdedByGene-20160128 | 26.6 Mb |
| 6 | THYM_Mutation-20160128 | 3.3 Mb |
| 7 | THYM_RNASeq2Gene-20160128 | 21.7 Mb |
| 8 | THYM_RPPAArray-20160128 | 0.2 Mb |
| 9 | THYM_miRNASeqGene-20160128 | 1.2 Mb |
| 10 | THYM_RNASeq2GeneNorm-20160128 | 19.3 Mb |
| 11 | THYM_Methylation-20160128 | 75 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
[1,] 9      9  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

Description

A document describing the TCGA cancer code

Details

```
> experiments( UCEC )
ExperimentList class object of length 14:
 [1] UCEC_CNASeq-20160128: RaggedExperiment with 36400 rows and 213 columns
 [2] UCEC_CNASNP-20160128: RaggedExperiment with 619412 rows and 1083 columns
 [3] UCEC_CNVSNP-20160128: RaggedExperiment with 127094 rows and 1078 columns
 [4] UCEC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 539 columns
 [5] UCEC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 98 rows and 539 columns
 [6] UCEC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 539 columns
 [7] UCEC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 433 columns
 [8] UCEC_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 54 columns
 [9] UCEC_Mutation-20160128: RaggedExperiment with 184861 rows and 248 columns
[10] UCEC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 380 columns
[11] UCEC_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 269 columns
[12] UCEC_RPPAArray-20160128: SummarizedExperiment with 208 rows and 440 columns
[13] UCEC_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 118 columns
[14] UCEC_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 466 columns

> rownames( UCEC )
CharacterList of length 14
[["UCEC_CNASeq-20160128"]] character(0)
[["UCEC_CNASNP-20160128"]] character(0)
[["UCEC_CNVSNP-20160128"]] character(0)
[["UCEC_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["UCEC_GISTIC_Peaks-20160128"]] chr1:13949775-15575840 ...
[["UCEC_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["UCEC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["UCEC_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["UCEC_Mutation-20160128"]] character(0)
[["UCEC_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
...
<4 more elements>

> colnames( UCEC )
CharacterList of length 14
[["UCEC_CNASeq-20160128"]] TCGA-A5-A0G5-01A-11D-A043-02 ...
[["UCEC_CNASNP-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_CNVSNP-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_GISTIC_AllByGene-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_GISTIC_Peaks-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_GISTIC_ThresholdedByGene-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_miRNASeqGene-20160128"]] TCGA-2E-A9G8-01A-11R-A404-13 ...
[["UCEC_mRNAArray-20160128"]] TCGA-A5-A0G2-01A-11R-A040-07 ...
[["UCEC_Mutation-20160128"]] TCGA-A5-A0G3-01A-11W-A062-09 ...
```

```
[[ "UCEC_RNASeq2GeneNorm-20160128" ]] TCGA-A5-A0G1-01A-11R-A118-07 ...
...
<4 more elements>
```

Sizes of each ExperimentList element:

| | | assay | size.Mb |
|----|--|--|---------|
| 1 | | UCEC_CNASeq-20160128 | 1 Mb |
| 2 | | UCEC_CNASNP-20160128 | 16.9 Mb |
| 3 | | UCEC_CNVSNP-20160128 | 3.7 Mb |
| 4 | | UCEC_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 5 | | UCEC_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | | UCEC_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 7 | | UCEC_miRNASeqGene-20160128 | 0.1 Mb |
| 8 | | UCEC_mRNAArray-20160128 | 1.1 Mb |
| 9 | | UCEC_Mutation-20160128 | 73.1 Mb |
| 10 | | UCEC_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 11 | | UCEC_RNASeqGene-20160128 | 1.3 Mb |
| 12 | | UCEC_RPPAArray-20160128 | 0.1 Mb |
| 13 | | UCEC_Methylation_methyl27-20160128 | 4.9 Mb |
| 14 | | UCEC_Methylation_methyl450-20160128 | 75.1 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
                411
      mixed serous and endometrioid
                22
      serous endometrial adenocarcinoma
                115
```

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

Including an additional 1779 columns

See Also

[UCEC-v2.0.1](#)

UCEC-v2.0.1

Uterine Corpus Endometrial Carcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( UCEC )
ExperimentList class object of length 16:
 [1] UCEC_CNASeq-20160128: RaggedExperiment with 36400 rows and 213 columns
 [2] UCEC_CNASNP-20160128: RaggedExperiment with 619412 rows and 1083 columns
 [3] UCEC_CNVSNP-20160128: RaggedExperiment with 127094 rows and 1078 columns
 [4] UCEC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 539 columns
 [5] UCEC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 98 rows and 539 columns
 [6] UCEC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 539 columns
 [7] UCEC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 433 columns
 [8] UCEC_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 54 columns
 [9] UCEC_Mutation-20160128: RaggedExperiment with 184861 rows and 248 columns
[10] UCEC_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 190 columns
[11] UCEC_RNASeq2GeneNorm_illumina-20160128: SummarizedExperiment with 20501 rows and 380 columns
[12] UCEC_RNASeq2GeneNorm_illumina-hiseq-20160128: SummarizedExperiment with 20501 rows and 190 columns
[13] UCEC_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 269 columns
[14] UCEC_RPPAArray-20160128: SummarizedExperiment with 208 rows and 440 columns
[15] UCEC_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 118 columns
```

[16] UCEC_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 466 columns

```
> rownames( UCEC )
CharacterList of length 16
[["UCEC_CNASeq-20160128"]] character(0)
[["UCEC_CNASNP-20160128"]] character(0)
[["UCEC_CNVSNP-20160128"]] character(0)
[["UCEC_GISTIC_AllByGene-20160128"]] character(0)
[["UCEC_GISTIC_Peaks-20160128"]] 51 52 1 2 3 4 5 53 ... 98 45 46 47 99 48 100
[["UCEC_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["UCEC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["UCEC_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["UCEC_Mutation-20160128"]] character(0)
[["UCEC_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
...
<6 more elements>
```

```
> colnames( UCEC )
CharacterList of length 16
[["UCEC_CNASeq-20160128"]] TCGA-A5-A0G5-01A-11D-A043-02 ...
[["UCEC_CNASNP-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_CNVSNP-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_GISTIC_AllByGene-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_GISTIC_Peaks-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_GISTIC_ThresholdedByGene-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_miRNASeqGene-20160128"]] TCGA-2E-A9G8-01A-11R-A404-13 ...
[["UCEC_mRNAArray-20160128"]] TCGA-A5-A0G2-01A-11R-A040-07 ...
[["UCEC_Mutation-20160128"]] TCGA-A5-A0G3-01A-11W-A062-09 ...
[["UCEC_RNASeq2Gene-20160128"]] TCGA-2E-A9G8-01A-11R-A40A-07 ...
...
<6 more elements>
```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|----|---|----------|
| 1 | UCEC_CNASeq-20160128 | 1 Mb |
| 2 | UCEC_CNASNP-20160128 | 16.9 Mb |
| 3 | UCEC_CNVSNP-20160128 | 3.7 Mb |
| 4 | UCEC_GISTIC_AllByGene-20160128 | 105.5 Mb |
| 5 | UCEC_GISTIC_Peaks-20160128 | 0.6 Mb |
| 6 | UCEC_GISTIC_ThresholdedByGene-20160128 | 105.3 Mb |
| 7 | UCEC_miRNASeqGene-20160128 | 3.7 Mb |
| 8 | UCEC_mRNAArray-20160128 | 9.6 Mb |
| 9 | UCEC_Mutation-20160128 | 73.1 Mb |
| 10 | UCEC_RNASeq2Gene-20160128 | 32.3 Mb |
| 11 | UCEC_RNASeq2GeneNorm_illumina-20160128 | 62 Mb |
| 12 | UCEC_RNASeq2GeneNorm_illuminahisec-20160128 | 32.3 Mb |
| 13 | UCEC_RNASeqGene-20160128 | 44.7 Mb |

| | | |
|----|-------------------------------------|---------|
| 14 | UCEC_RPPAArray-20160128 | 0.8 Mb |
| 15 | UCEC_Methylation_methyl27-20160128 | 4.9 Mb |
| 16 | UCEC_Methylation_methyl450-20160128 | 75.1 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 |
|-----------------------------------|----------------------------|
| | 411 |
| mixed serous and endometrioid | |
| | 22 |
| serous endometrial adenocarcinoma | |
| | 115 |

residual_tumor:

| r0 | r1 | r2 | rx | NA's |
|-----|----|----|----|------|
| 376 | 22 | 16 | 41 | 93 |

Including an additional 1779 columns

UCEC-v2.1.0

*Uterine Corpus Endometrial Carcinoma***Description**

A document describing the TCGA cancer code

Details

```

> experiments( UCEC )
ExperimentList class object of length 17:
 [1] UCEC_CNASeq-20160128: RaggedExperiment with 36400 rows and 213 columns
 [2] UCEC_CNASNP-20160128: RaggedExperiment with 619412 rows and 1083 columns
 [3] UCEC_CNVSNP-20160128: RaggedExperiment with 127094 rows and 1078 columns
 [4] UCEC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 539 columns
 [5] UCEC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 98 rows and 539 columns
 [6] UCEC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 539 columns
 [7] UCEC_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 54 columns
 [8] UCEC_Mutation-20160128: RaggedExperiment with 184861 rows and 248 columns
 [9] UCEC_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 190 columns
 [10] UCEC_RNASeq2GeneNorm_illumina-20160128: SummarizedExperiment with 20501 rows and 380 columns
 [11] UCEC_RNASeq2GeneNorm_illumina-hiseq-20160128: SummarizedExperiment with 20501 rows and 190 columns
 [12] UCEC_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 269 columns
 [13] UCEC_RPPAArray-20160128: SummarizedExperiment with 208 rows and 440 columns
 [14] UCEC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 433 columns
 [15] UCEC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18515 rows and 569 columns
 [16] UCEC_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 118 columns
 [17] UCEC_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 466 columns

> rownames( UCEC )
CharacterList of length 17
[["UCEC_CNASeq-20160128"]] character(0)
[["UCEC_CNASNP-20160128"]] character(0)
[["UCEC_CNVSNP-20160128"]] character(0)
[["UCEC_GISTIC_AllByGene-20160128"]] character(0)
[["UCEC_GISTIC_Peaks-20160128"]] 51 52 1 2 3 4 5 53 ... 98 45 46 47 99 48 100
[["UCEC_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["UCEC_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["UCEC_Mutation-20160128"]] character(0)
[["UCEC_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["UCEC_RNASeq2GeneNorm_illumina-20160128"]] A1BG A1CF ... psiTPTE22 tAKR
...
<7 more elements>

> colnames( UCEC )
CharacterList of length 17
[["UCEC_CNASeq-20160128"]] TCGA-A5-A0G5-01A-11D-A043-02 ...

```

```

[["UCEC_CNASNP-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_CNVSNP-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_GISTIC_AllByGene-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_GISTIC_Peaks-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_GISTIC_ThresholdedByGene-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_mRNAArray-20160128"]] TCGA-A5-A0G2-01A-11R-A040-07 ...
[["UCEC_Mutation-20160128"]] TCGA-A5-A0G3-01A-11W-A062-09 ...
[["UCEC_RNASeq2Gene-20160128"]] TCGA-2E-A9G8-01A-11R-A40A-07 ...
[["UCEC_RNASeq2GeneNorm_illumina-20160128"]] TCGA-A5-A0G1-01A-11R-A118-07...
...
<7 more elements>

```

Sizes of each ExperimentList element:

| | assay | size.Mb |
|----|---|----------|
| 1 | UCEC_CNASeq-20160128 | 1 Mb |
| 2 | UCEC_CNASNP-20160128 | 16.9 Mb |
| 3 | UCEC_CNVSNP-20160128 | 3.7 Mb |
| 4 | UCEC_GISTIC_AllByGene-20160128 | 105.5 Mb |
| 5 | UCEC_GISTIC_Peaks-20160128 | 0.6 Mb |
| 6 | UCEC_GISTIC_ThresholdedByGene-20160128 | 105.3 Mb |
| 7 | UCEC_mRNAArray-20160128 | 9.6 Mb |
| 8 | UCEC_Mutation-20160128 | 73.1 Mb |
| 9 | UCEC_RNASeq2Gene-20160128 | 32.3 Mb |
| 10 | UCEC_RNASeq2GeneNorm_illumina-20160128 | 62 Mb |
| 11 | UCEC_RNASeq2GeneNorm_illuminahisec-20160128 | 32.3 Mb |
| 12 | UCEC_RNASeqGene-20160128 | 44.7 Mb |
| 13 | UCEC_RPPAArray-20160128 | 0.8 Mb |
| 14 | UCEC_miRNASeqGene-20160128 | 3.7 Mb |
| 15 | UCEC_RNASeq2GeneNorm-20160128 | 82.8 Mb |
| 16 | UCEC_Methylation_methyl27-20160128 | 4.9 Mb |
| 17 | UCEC_Methylation_methyl450-20160128 | 75.1 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
                                     411
      mixed serous and endometrioid
                                     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 10:
 [1] UCS_CNASNP-20160128: RaggedExperiment with 54944 rows and 111 columns
 [2] UCS_CNVSNP-20160128: RaggedExperiment with 19298 rows and 111 columns
 [3] UCS_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 56 columns
 [4] UCS_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 56 rows and 56 columns
 [5] UCS_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 56 columns
 [6] UCS_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 56 columns
 [7] UCS_Mutation-20160128: RaggedExperiment with 11339 rows and 57 columns
 [8] UCS_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 57 columns

```

```
[9] UCS_RPPAArray-20160128: SummarizedExperiment with 192 rows and 48 columns
[10] UCS_Methylation-20160128: SummarizedExperiment with 485577 rows and 57 columns
```

```
> rownames( UCS )
CharacterList of length 10
[["UCS_CNASNP-20160128"]] character(0)
[["UCS_CNVSNP-20160128"]] character(0)
[["UCS_GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["UCS_GISTIC_Peaks-20160128"]] chr1:1-19401404 ... chr22:41958863-51304566
[["UCS_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["UCS_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["UCS_Mutation-20160128"]] character(0)
[["UCS_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["UCS_RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363
[["UCS_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
```

```
> colnames( UCS )
CharacterList of length 10
[["UCS_CNASNP-20160128"]] TCGA-N5-A4R8-10A-01D-A28T-01 ...
[["UCS_CNVSNP-20160128"]] TCGA-N5-A4R8-10A-01D-A28T-01 ...
[["UCS_GISTIC_AllByGene-20160128"]] TCGA-N5-A4RA-01A-11D-A28Q-01 ...
[["UCS_GISTIC_Peaks-20160128"]] TCGA-N5-A4RA-01A-11D-A28Q-01 ...
[["UCS_GISTIC_ThresholdedByGene-20160128"]] TCGA-N5-A4RA-01A-11D-A28Q-01 ...
[["UCS_miRNASeqGene-20160128"]] TCGA-N5-A4R8-01A-11R-A28Z-13 ...
[["UCS_Mutation-20160128"]] TCGA-N5-A4R8-01A-11D-A28R-08 ...
[["UCS_RNASeq2GeneNorm-20160128"]] TCGA-N5-A4R8-01A-11R-A28V-07 ...
[["UCS_RPPAArray-20160128"]] TCGA-N5-A4R8-01A-21-A41P-20 ...
[["UCS_Methylation-20160128"]] TCGA-N5-A4R8-01A-11D-A28S-05 ...
```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|---------------------------------------|---------------|
| 1 | UCS_CNASNP-20160128 | 1.5 Mb |
| 2 | UCS_CNVSNP-20160128 | 0.6 Mb |
| 3 | UCS_GISTIC_AllByGene-20160128 | 4.9 Mb |
| 4 | UCS_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | UCS_GISTIC_ThresholdedByGene-20160128 | 4.9 Mb |
| 6 | UCS_miRNASeqGene-20160128 | 0.1 Mb |
| 7 | UCS_Mutation-20160128 | 19.7 Mb |
| 8 | UCS_RNASeq2GeneNorm-20160128 | 1.3 Mb |
| 9 | UCS_RPPAArray-20160128 | 0 Mb |
| 10 | UCS_Methylation-20160128 | 75 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 (mmt): nos | 24 |
| uterine carcinosarcoma/ mmt: heterologous type | 20 |

uterine carcinosarcoma/mmt: 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

See Also

[UCS-v2.0.1](#)

UCS-v2.0.1

Uterine Carcinosarcoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( UCS )
ExperimentList class object of length 11:
 [1] UCS_CNASNP-20160128: RaggedExperiment with 54944 rows and 111 columns
 [2] UCS_CNVSNP-20160128: RaggedExperiment with 19298 rows and 111 columns
 [3] UCS_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 56 columns
 [4] UCS_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 56 rows and 56 columns
 [5] UCS_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 56 columns
 [6] UCS_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 56 columns
 [7] UCS_Mutation-20160128: RaggedExperiment with 11339 rows and 57 columns
 [8] UCS_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 57 columns
 [9] UCS_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 57 columns
 [10] UCS_RPPAArray-20160128: SummarizedExperiment with 192 rows and 48 columns
 [11] UCS_Methylation-20160128: SummarizedExperiment with 485577 rows and 57 columns

> rownames( UCS )
CharacterList of length 11
[["UCS_CNASNP-20160128"]] character(0)
[["UCS_CNVSNP-20160128"]] character(0)
[["UCS_GISTIC_AllByGene-20160128"]] character(0)
```

```

[["UCS_GISTIC_Peaks-20160128"]] 26 1 2 3 27 4 28 29 ... 21 22 56 57 23 24 58
[["UCS_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["UCS_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["UCS_Mutation-20160128"]] character(0)
[["UCS_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["UCS_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["UCS_RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363
...
<1 more element>

```

```

> colnames( UCS )
CharacterList of length 11
[["UCS_CNASNP-20160128"]] TCGA-N5-A4R8-10A-01D-A28T-01 ...
[["UCS_CNVSNP-20160128"]] TCGA-N5-A4R8-10A-01D-A28T-01 ...
[["UCS_GISTIC_AllByGene-20160128"]] TCGA-N5-A4RA-01A-11D-A28Q-01 ...
[["UCS_GISTIC_Peaks-20160128"]] TCGA-N5-A4RA-01A-11D-A28Q-01 ...
[["UCS_GISTIC_ThresholdedByGene-20160128"]] TCGA-N5-A4RA-01A-11D-A28Q-01 ...
[["UCS_miRNASeqGene-20160128"]] TCGA-N5-A4R8-01A-11R-A28Z-13 ...
[["UCS_Mutation-20160128"]] TCGA-N5-A4R8-01A-11D-A28R-08 ...
[["UCS_RNASeq2Gene-20160128"]] TCGA-N5-A4R8-01A-11R-A28V-07 ...
[["UCS_RNASeq2GeneNorm-20160128"]] TCGA-N5-A4R8-01A-11R-A28V-07 ...
[["UCS_RPPAArray-20160128"]] TCGA-N5-A4R8-01A-21-A41P-20 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|---------------------------------------|---------------|
| 1 | UCS_CNASNP-20160128 | 1.5 Mb |
| 2 | UCS_CNVSNP-20160128 | 0.6 Mb |
| 3 | UCS_GISTIC_AllByGene-20160128 | 14.1 Mb |
| 4 | UCS_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | UCS_GISTIC_ThresholdedByGene-20160128 | 13.9 Mb |
| 6 | UCS_miRNASeqGene-20160128 | 0.6 Mb |
| 7 | UCS_Mutation-20160128 | 19.7 Mb |
| 8 | UCS_RNASeq2Gene-20160128 | 11.5 Mb |
| 9 | UCS_RNASeq2GeneNorm-20160128 | 11.5 Mb |
| 10 | UCS_RPPAArray-20160128 | 0.1 Mb |
| 11 | UCS_Methylation-20160128 | 75 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 (mmt): nos | 24 |
| uterine carcinosarcoma/ mmt: heterologous type | 20 |
| uterine carcinosarcoma/mmt: 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

UCS-v2.1.0

Uterine Carcinosarcoma

Description

A document describing the TCGA cancer code

Details

```

> experiments( UCS )
ExperimentList class object of length 11:
 [1] UCS_CNASNP-20160128: RaggedExperiment with 54944 rows and 111 columns
 [2] UCS_CNVSNP-20160128: RaggedExperiment with 19298 rows and 111 columns
 [3] UCS_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 56 columns
 [4] UCS_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 56 rows and 56 columns
 [5] UCS_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 56 columns
 [6] UCS_Mutation-20160128: RaggedExperiment with 11339 rows and 57 columns
 [7] UCS_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 57 columns
 [8] UCS_RPPAArray-20160128: SummarizedExperiment with 192 rows and 48 columns
 [9] UCS_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 56 columns
[10] UCS_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18645 rows and 57 columns
[11] UCS_Methylation-20160128: SummarizedExperiment with 485577 rows and 57 columns

> rownames( UCS )
CharacterList of length 11
[["UCS_CNASNP-20160128"]] character(0)
[["UCS_CNVSNP-20160128"]] character(0)
[["UCS_GISTIC_AllByGene-20160128"]] character(0)
[["UCS_GISTIC_Peaks-20160128"]] 26 1 2 3 27 4 28 29 ... 21 22 56 57 23 24 58
[["UCS_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["UCS_Mutation-20160128"]] character(0)
[["UCS_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["UCS_RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363
[["UCS_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["UCS_RNASeq2GeneNorm-20160128"]] A1BG A2BP1 A2LD1 ... ZZEF1 ZZZ3 psiTPTE22

```

```

...
<1 more element>

> colnames( UCS )
CharacterList of length 11
[["UCS_CNASNP-20160128"]] TCGA-N5-A4R8-10A-01D-A28T-01 ...
[["UCS_CNVSNP-20160128"]] TCGA-N5-A4R8-10A-01D-A28T-01 ...
[["UCS_GISTIC_AllByGene-20160128"]] TCGA-N5-A4RA-01A-11D-A28Q-01 ...
[["UCS_GISTIC_Peaks-20160128"]] TCGA-N5-A4RA-01A-11D-A28Q-01 ...
[["UCS_GISTIC_ThresholdedByGene-20160128"]] TCGA-N5-A4RA-01A-11D-A28Q-01 ...
[["UCS_Mutation-20160128"]] TCGA-N5-A4R8-01A-11D-A28R-08 ...
[["UCS_RNASeq2Gene-20160128"]] TCGA-N5-A4R8-01A-11R-A28V-07 ...
[["UCS_RPPAArray-20160128"]] TCGA-N5-A4R8-01A-21-A41P-20 ...
[["UCS_miRNASeqGene-20160128"]] TCGA-N5-A4R8-01A-11R-A28Z-13 ...
[["UCS_RNASeq2GeneNorm-20160128"]] TCGA-N5-A4R8-01 ... TCGA-QN-A5NN-01
...
<1 more element>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|---------------------------------------|---------------|
| 1 | UCS_CNASNP-20160128 | 1.5 Mb |
| 2 | UCS_CNVSNP-20160128 | 0.6 Mb |
| 3 | UCS_GISTIC_AllByGene-20160128 | 14.1 Mb |
| 4 | UCS_GISTIC_Peaks-20160128 | 0.1 Mb |
| 5 | UCS_GISTIC_ThresholdedByGene-20160128 | 13.9 Mb |
| 6 | UCS_Mutation-20160128 | 19.7 Mb |
| 7 | UCS_RNASeq2Gene-20160128 | 11.5 Mb |
| 8 | UCS_RPPAArray-20160128 | 0.1 Mb |
| 9 | UCS_miRNASeqGene-20160128 | 0.6 Mb |
| 10 | UCS_RNASeq2GeneNorm-20160128 | 10.4 Mb |
| 11 | UCS_Methylation-20160128 | 75 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
[1,] 35 35 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 (mmt): nos
  24
  uterine carcinosarcoma/ mmt: heterologous type
  20
  uterine carcinosarcoma/mmt: 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 | <i>Uveal Melanoma</i> |
|-----|-----------------------|

Description

A document describing the TCGA cancer code

Details

```
> experiments( UVM )
ExperimentList class object of length 11:
 [1] UVM_CNASeq-20160128: RaggedExperiment with 6496 rows and 102 columns
 [2] UVM_CNASNP-20160128: RaggedExperiment with 69487 rows and 160 columns
 [3] UVM_CNVSNP-20160128: RaggedExperiment with 12973 rows and 160 columns
 [4] UVM_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 80 columns
 [5] UVM_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 21 rows and 80 columns
 [6] UVM_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 80 columns
 [7] UVM_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 80 columns
 [8] UVM_Mutation-20160128: RaggedExperiment with 2174 rows and 80 columns
 [9] UVM_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 80 columns
 [10] UVM_RPPAArray-20160128: SummarizedExperiment with 192 rows and 12 columns
 [11] UVM_Methylation-20160128: SummarizedExperiment with 485577 rows and 80 columns

> rownames( UVM )
CharacterList of length 11
[["UVM_CNASeq-20160128"]] character(0)
[["UVM_CNASNP-20160128"]] character(0)
[["UVM_CNVSNP-20160128"]] character(0)
[["UVM_GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["UVM_GISTIC_Peaks-20160128"]] chr1:19073360-24108626 ...
[["UVM_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["UVM_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["UVM_Mutation-20160128"]] character(0)
[["UVM_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["UVM_RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363
...
<1 more element>

> colnames( UVM )
CharacterList of length 11
[["UVM_CNASeq-20160128"]] TCGA-RZ-AB0B-01A-11D-A40D-26 ...
[["UVM_CNASNP-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
```

```

[["UVM_CNVSNP-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["UVM_GISTIC_AllByGene-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["UVM_GISTIC_Peaks-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["UVM_GISTIC_ThresholdedByGene-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["UVM_miRNASeqGene-20160128"]] TCGA-RZ-AB0B-01A-11R-A40B-13 ...
[["UVM_Mutation-20160128"]] TCGA-RZ-AB0B-01A-11D-A39W-08 ...
[["UVM_RNASeq2GeneNorm-20160128"]] TCGA-RZ-AB0B-01A-11R-A405-07 ...
[["UVM_RPPAArray-20160128"]] TCGA-V3-A9ZX-01A-21-A41Z-20 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

| | | assay | size.Mb |
|----|---------------------------------------|---------------------|---------|
| 1 | | UVM_CNASeq-20160128 | 0.2 Mb |
| 2 | | UVM_CNASNP-20160128 | 1.9 Mb |
| 3 | | UVM_CNVSNP-20160128 | 0.4 Mb |
| 4 | UVM_GISTIC_AllByGene-20160128 | | 4.9 Mb |
| 5 | UVM_GISTIC_Peaks-20160128 | | 0 Mb |
| 6 | UVM_GISTIC_ThresholdedByGene-20160128 | | 4.9 Mb |
| 7 | UVM_miRNASeqGene-20160128 | | 0.1 Mb |
| 8 | UVM_Mutation-20160128 | | 12.3 Mb |
| 9 | UVM_RNASeq2GeneNorm-20160128 | | 1.3 Mb |
| 10 | UVM_RPPAArray-20160128 | | 0 Mb |
| 11 | UVM_Methylation-20160128 | | 75 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

See Also[UVM-v2.0.1](#)

Description

A document describing the TCGA cancer code

Details

```
> experiments( UVM )
ExperimentList class object of length 12:
 [1] UVM_CNASeq-20160128: RaggedExperiment with 6496 rows and 102 columns
 [2] UVM_CNASNP-20160128: RaggedExperiment with 69487 rows and 160 columns
 [3] UVM_CNVSNP-20160128: RaggedExperiment with 12973 rows and 160 columns
 [4] UVM_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 80 columns
 [5] UVM_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 21 rows and 80 columns
 [6] UVM_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 80 columns
 [7] UVM_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 80 columns
 [8] UVM_Mutation-20160128: RaggedExperiment with 2174 rows and 80 columns
 [9] UVM_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 80 columns
 [10] UVM_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 80 columns
 [11] UVM_RPPAArray-20160128: SummarizedExperiment with 192 rows and 12 columns
 [12] UVM_Methylation-20160128: SummarizedExperiment with 485577 rows and 80 columns

> rownames( UVM )
CharacterList of length 12
[["UVM_CNASeq-20160128"]] character(0)
[["UVM_CNASNP-20160128"]] character(0)
[["UVM_CNVSNP-20160128"]] character(0)
[["UVM_GISTIC_AllByGene-20160128"]] character(0)
[["UVM_GISTIC_Peaks-20160128"]] 4 5 6 7 8 9 10 11 ... 2 16 17 18 19 20 21 3
[["UVM_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["UVM_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["UVM_Mutation-20160128"]] character(0)
[["UVM_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["UVM_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
...
<2 more elements>

> colnames( UVM )
CharacterList of length 12
[["UVM_CNASeq-20160128"]] TCGA-RZ-AB0B-01A-11D-A40D-26 ...
[["UVM_CNASNP-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["UVM_CNVSNP-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["UVM_GISTIC_AllByGene-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["UVM_GISTIC_Peaks-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["UVM_GISTIC_ThresholdedByGene-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
```

```

[["UVM_miRNASeqGene-20160128"]] TCGA-RZ-AB0B-01A-11R-A40B-13 ...
[["UVM_Mutation-20160128"]] TCGA-RZ-AB0B-01A-11D-A39W-08 ...
[["UVM_RNASeq2Gene-20160128"]] TCGA-RZ-AB0B-01A-11R-A405-07 ...
[["UVM_RNASeq2GeneNorm-20160128"]] TCGA-RZ-AB0B-01A-11R-A405-07 ...
...
<2 more elements>

```

Sizes of each ExperimentList element:

| | | assay size.Mb |
|----|---------------------------------------|---------------|
| 1 | UVM_CNASeq-20160128 | 0.2 Mb |
| 2 | UVM_CNASNP-20160128 | 1.9 Mb |
| 3 | UVM_CNVSNP-20160128 | 0.4 Mb |
| 4 | UVM_GISTIC_AllByGene-20160128 | 18.5 Mb |
| 5 | UVM_GISTIC_Peaks-20160128 | 0.1 Mb |
| 6 | UVM_GISTIC_ThresholdedByGene-20160128 | 18.5 Mb |
| 7 | UVM_miRNASeqGene-20160128 | 0.8 Mb |
| 8 | UVM_Mutation-20160128 | 12.3 Mb |
| 9 | UVM_RNASeq2Gene-20160128 | 15.1 Mb |
| 10 | UVM_RNASeq2GeneNorm-20160128 | 15.1 Mb |
| 11 | UVM_RPPAArray-20160128 | 0.1 Mb |
| 12 | UVM_Methylation-20160128 | 75 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

Description

A document describing the TCGA cancer code

Details

```
> experiments( UVM )
ExperimentList class object of length 12:
 [1] UVM_CNASeq-20160128: RaggedExperiment with 6496 rows and 102 columns
 [2] UVM_CNASNP-20160128: RaggedExperiment with 69487 rows and 160 columns
 [3] UVM_CNVSNP-20160128: RaggedExperiment with 12973 rows and 160 columns
 [4] UVM_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 80 columns
 [5] UVM_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 21 rows and 80 columns
 [6] UVM_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 80 columns
 [7] UVM_Mutation-20160128: RaggedExperiment with 2174 rows and 80 columns
 [8] UVM_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 80 columns
 [9] UVM_RPPAArray-20160128: SummarizedExperiment with 192 rows and 12 columns
 [10] UVM_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 80 columns
 [11] UVM_RNASeq2GeneNorm-20160128: SummarizedExperiment with 17345 rows and 80 columns
 [12] UVM_Methylation-20160128: SummarizedExperiment with 485577 rows and 80 columns

> rownames( UVM )
CharacterList of length 12
[["UVM_CNASeq-20160128"]] character(0)
[["UVM_CNASNP-20160128"]] character(0)
[["UVM_CNVSNP-20160128"]] character(0)
[["UVM_GISTIC_AllByGene-20160128"]] character(0)
[["UVM_GISTIC_Peaks-20160128"]] 4 5 6 7 8 9 10 11 ... 2 16 17 18 19 20 21 3
[["UVM_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["UVM_Mutation-20160128"]] character(0)
[["UVM_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["UVM_RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363
[["UVM_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
...
<2 more elements>

> colnames( UVM )
CharacterList of length 12
[["UVM_CNASeq-20160128"]] TCGA-RZ-AB0B-01A-11D-A40D-26 ...
[["UVM_CNASNP-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["UVM_CNVSNP-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["UVM_GISTIC_AllByGene-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["UVM_GISTIC_Peaks-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["UVM_GISTIC_ThresholdedByGene-20160128"]] TCGA-RZ-AB0B-01A-11D-A39V-01 ...
[["UVM_Mutation-20160128"]] TCGA-RZ-AB0B-01A-11D-A39W-08 ...
[["UVM_RNASeq2Gene-20160128"]] TCGA-RZ-AB0B-01A-11R-A405-07 ...
[["UVM_RPPAArray-20160128"]] TCGA-V3-A9ZX-01A-21-A41Z-20 ...
[["UVM_miRNASeqGene-20160128"]] TCGA-RZ-AB0B-01A-11R-A40B-13 ...
...
```


<2 more elements>

Sizes of each ExperimentList element:

| | | assay | size.Mb |
|----|---------------------------------------|---------------------|---------|
| 1 | | UVM_CNASeq-20160128 | 0.2 Mb |
| 2 | | UVM_CNASNP-20160128 | 1.9 Mb |
| 3 | | UVM_CNVSNP-20160128 | 0.4 Mb |
| 4 | UVM_GISTIC_AllByGene-20160128 | | 18.5 Mb |
| 5 | UVM_GISTIC_Peaks-20160128 | | 0.1 Mb |
| 6 | UVM_GISTIC_ThresholdedByGene-20160128 | | 18.5 Mb |
| 7 | UVM_Mutation-20160128 | | 12.3 Mb |
| 8 | UVM_RNASeq2Gene-20160128 | | 15.1 Mb |
| 9 | UVM_RPPAArray-20160128 | | 0.1 Mb |
| 10 | UVM_miRNASeqGene-20160128 | | 0.8 Mb |
| 11 | UVM_RNASeq2GeneNorm-20160128 | | 12.8 Mb |
| 12 | UVM_Methylation-20160128 | | 75 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
[1,] 23 23 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

1

52

NA's

27

Including an additional 448 columns

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