

# Package ‘curatedTCGAData’

October 17, 2019

**Type** Package

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

**Version** 1.6.0

**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

**Depends** R (>= 3.5.0), MultiAssayExperiment

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

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

**VignetteBuilder** knitr

**biocViews** Homo\_sapiens\_Data, ReproducibleResearch, CancerData,  
ExperimentHub

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

**RoxygenNote** 6.1.1

**git\_url** <https://git.bioconductor.org/packages/curatedTCGAData>

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**Author** Marcel Ramos [aut, cre],  
Levi Waldron [ctb],  
Lucas Schiffer [ctb],  
Ludwig Geistlinger [ctb],  
Valerie Obenchain [ctb],  
Martin Morgan [ctb]

**Maintainer** Marcel Ramos <marcel.ramos@roswellpark.org>

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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)

**Maintainer:** Marcel Ramos <marcel.ramos@roswellpark.org>

Other contributors:

- Levi Waldron <lwaldron.research@gmail.com> [contributor]

- Lucas Schiffer <schiffer.lucas@gmail.com> [contributor]
- Ludwig Geistlinger <ludwig.geistlinger@sph.cuny.edu> [contributor]
- Valerie Obenchain <valerie.obenchain@roswellpark.org> [contributor]
- 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	1
NA's	78
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
	NA's	327
	18	

ethnicity:

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

Including an additional 1695 columns

---

BRCA

*Breast invasive carcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

```
> experiments( BRCA )
ExperimentList class object of length 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"]] ELMO2 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 1  
 asian 61

black or african american	white
183	757
NA's	
96	
ethnicity:	
hispanic or latino not hispanic or latino	NA's
39	884
	175

Including an additional 2667 columns

---

CESC *Cervical squamous cell carcinoma and endocervical adenocarcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

```
> experiments( CESC )
ExperimentList class object of length 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-A37O-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 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



menopause\_status:

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

lymphovascular\_involvement:

absent	present	NA's
72	80	155

lymph\_nodes\_examined\_he\_count:

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

lymph\_nodes\_examined:

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

keratinization\_squamous\_cell:

keratinizing squamous cell carcinoma	55
non-keratinizing squamous cell carcinoma	120
NA's	132

initial\_pathologic\_dx\_year:

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

hysterectomy\_type:

hysterectomy_performed_type hysterectomy_performed_text	307
---	-----

history\_hormonal\_contraceptives\_use:

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

height\_cm\_at\_diagnosis:

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

corpus\_involvement:

absent	present	NA's
--------	---------	------

```

          99      19      189

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

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

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

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

```

Including an additional 1330 columns

---

CHOL

*Cholangiocarcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

```

> experiments( CHOL )
ExperimentList class object of length 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
cholangiocarcinoma; intrahepatic	4
	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"]] ELMO2 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

---

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 = "*", dry.run = TRUE, ...)
```

## Arguments

diseaseCode	a character vector containing the name(s) of TCGA cohorts
assays	a character vector of TCGA assays, glob matches allowed; see below for more details
dry.run	logical (default TRUE) whether to return the dataset names before actual download
...	Additional arguments passed on to the <a href="#">ExperimentHub</a> 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

**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	RSEM TPM gene expression values
RNASeq2GeneNorm	Upper quartile 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

```

## See Also

curatedTCGAData-package

## Examples

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

---

DLBC

*Lymphoid Neoplasm Diffuse Large B-cell Lymphoma*

---

## Description

A document describing the TCGA cancer code

## Details

```

> experiments( DLBC )
ExperimentList class object of length 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
                                                                 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	white
46	5	114
NA's		
20		

ethnicity:

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

Including an additional 940 columns

GBM

*Glioblastoma multiforme***Description**

A document describing the TCGA cancer code

**Details**

```

> experiments( GBM )
ExperimentList class object of length 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

---

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	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

**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

```

---

KIRC

*Kidney renal clear cell carcinoma*


---

### Description

A document describing the TCGA cancer code





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	466
NA's	
7	

ethnicity:

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

Including an additional 2250 columns

KIRP

*Kidney renal papillary cell carcinoma***Description**

A document describing the TCGA cancer code

**Details**

```
> experiments( KIRP )
ExperimentList class object of length 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"]] ELMO2 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:

NA's
34
1 290

radiation\_therapy:

no	yes	NA's
209	1	81

karnofsky\_performance\_score:

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

histological\_type:

kidney papillary renal cell carcinoma  
291

number\_pack\_years\_smoked:

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

year\_of\_tobacco\_smoking\_onset:

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

race:

american indian or alaska native

asian

	2	6
black or african american		white
	61	207
NA's		
	15	
ethnicity:		
hispanic or latino not hispanic or latino		NA's
	12	243
		36

Including an additional 1686 columns

---

LAML

*Acute Myeloid Leukemia*

---

## Description

A document describing the TCGA cancer code

## Details

```
> experiments( LAML )
ExperimentList class object of length 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

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"]] ELMO2 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	asian

	1	8
black or african american		white
	21	475
	NA's	
	11	
ethnicity:		
hispanic or latino not hispanic or latino		NA's
	32	449
		35

Including an additional 1764 columns

---

LIHC *Liver hepatocellular carcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

```
> experiments( LIHC )
ExperimentList class object of length 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	3	hepatocellular carcinoma	367
hepatocholangiocarcinoma (mixed)	7		

residual\_tumor:

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

race:

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



```

[["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	1	asian	8
black or african american	53	white	392
NA's	66		
ethnicity:			
hispanic or latino not hispanic or latino	7	388	NA's 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 ELM02 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          351
      NA's
      113

```

```

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

```

Including an additional 2238 columns

---

MESO

*Mesothelioma*

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## 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_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 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_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	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_RNASeq2GeneNorm-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

---

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 ELMO2 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

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

-----

Call: survfit(formula = survival::Surv(colDat\$days\_to\_death/365, colDat\$vital\_status) ~  
-1)

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

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PAAD	<i>Pancreatic adenocarcinoma</i>
------	----------------------------------

---

## 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
```

---

```
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

---

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

---

READ	<i>Rectum adenocarcinoma</i>
------	------------------------------

---

## 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"]] ELMO2 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

---

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

---

SKCM

*Skin Cutaneous Melanoma*

---

## 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 psiTPTE22 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

---

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

```



```
> 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



THCA

*Thyroid carcinoma***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) 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

## 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	103
NA's	
2	

ethnicity:

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

Including an additional 685 columns

UCEC

*Uterine Corpus Endometrial Carcinoma***Description**

A document describing the TCGA cancer code

**Details**

```

> experiments( UCEC )
ExperimentList class object of length 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"]] ELMO2 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

---

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
NA's	44
1	

## ethnicity:

hispanic or latino not hispanic or latino	NA's
---	------

1

43

13

Including an additional 632 columns

---

UVM

*Uveal Melanoma*


---

## Description

A document describing the TCGA cancer code

## Details

```
> experiments( UVM )
ExperimentList class object of length 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

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