

# Package ‘curatedTCGAData’

December 19, 2024

**Type** Package

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

**Version** 1.29.2

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

**License** Artistic-2.0

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

**Depends** R (>= 4.5.0), MultiAssayExperiment

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

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

**VignetteBuilder** knitr

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

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**RoxygenNote** 7.3.2

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## Contents

curatedTCGAData-package . . . . .	4
ACC . . . . .	6
ACC-v2.0.1 . . . . .	9
ACC-v2.1.0 . . . . .	12
BLCA . . . . .	15
BLCA-v2.0.1 . . . . .	19
BLCA-v2.1.0 . . . . .	22
BRCA . . . . .	25
BRCA-v2.0.1 . . . . .	29
BRCA-v2.1.0 . . . . .	32
CESC . . . . .	35
CESC-v2.0.1 . . . . .	41
CESC-v2.1.0 . . . . .	47
CHOL . . . . .	52
CHOL-v2.0.1 . . . . .	55
CHOL-v2.1.0 . . . . .	59
COAD . . . . .	62
COAD-v2.0.1 . . . . .	64
COAD-v2.1.0 . . . . .	67
curatedTCGAData . . . . .	69
DLBC . . . . .	72
DLBC-v2.0.1 . . . . .	75
DLBC-v2.1.0 . . . . .	77
ESCA . . . . .	80
ESCA-v2.0.1 . . . . .	84
ESCA-v2.1.0 . . . . .	87
GBM . . . . .	90
GBM-v2.0.1 . . . . .	93
GBM-v2.1.0 . . . . .	97
HNSC . . . . .	100
HNSC-v2.0.1 . . . . .	103
HNSC-v2.1.0 . . . . .	107
KICH . . . . .	110
KICH-v2.0.1 . . . . .	114
KICH-v2.1.0 . . . . .	117

KIRC . . . . .	120
KIRC-v2.0.1 . . . . .	124
KIRC-v2.1.0 . . . . .	127
KIRP . . . . .	131
KIRP-v2.0.1 . . . . .	134
KIRP-v2.1.0 . . . . .	138
LAML . . . . .	141
LAML-v2.0.1 . . . . .	144
LAML-v2.1.0 . . . . .	147
LGG . . . . .	149
LGG-v2.0.1 . . . . .	152
LGG-v2.1.0 . . . . .	155
LIHC . . . . .	158
LIHC-v2.0.1 . . . . .	161
LIHC-v2.1.0 . . . . .	165
LUAD . . . . .	168
LUAD-v2.0.1 . . . . .	171
LUAD-v2.1.0 . . . . .	175
LUSC . . . . .	178
LUSC-v2.0.1 . . . . .	182
LUSC-v2.1.0 . . . . .	185
MESO . . . . .	189
MESO-v2.0.1 . . . . .	192
MESO-v2.1.0 . . . . .	195
OV . . . . .	198
OV-v2.0.1 . . . . .	201
OV-v2.1.0 . . . . .	205
OV-v2.1.1 . . . . .	208
PAAD . . . . .	210
PAAD-v2.0.1 . . . . .	213
PAAD-v2.1.0 . . . . .	217
PCPG . . . . .	220
PCPG-v2.0.1 . . . . .	223
PCPG-v2.1.0 . . . . .	226
PRAD . . . . .	229
PRAD-v2.0.1 . . . . .	233
PRAD-v2.1.0 . . . . .	236
READ . . . . .	239
READ-v2.0.1 . . . . .	243
READ-v2.1.0 . . . . .	246
SARC . . . . .	249
SARC-v2.0.1 . . . . .	252
SARC-v2.1.0 . . . . .	255
SKCM . . . . .	257
SKCM-v2.0.1 . . . . .	261
SKCM-v2.1.0 . . . . .	264
SKCM-v2.1.1 . . . . .	267
STAD . . . . .	269

STAD-v2.0.1	272
STAD-v2.1.0	275
TGCT	279
TGCT-v2.0.1	282
TGCT-v2.1.0	285
THCA	288
THCA-v2.0.1	291
THCA-v2.1.0	294
THYM	297
THYM-v2.0.1	300
THYM-v2.1.0	303
UCEC	305
UCEC-v2.0.1	308
UCEC-v2.1.0	311
UCS	313
UCS-v2.0.1	316
UCS-v2.1.0	319
UVM	322
UVM-v2.0.1	325
UVM-v2.1.0	327

**Index****331**


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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

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

**See Also**

Useful links:

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

**Examples**

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

---

 ACC

*Adrenocortical carcinoma*


---

**Description**

A document describing the TCGA cancer code

**Details**

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

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

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

```

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

```

Sizes of each ExperimentList element:

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

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

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

```

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

```

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

years\_to\_birth:

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

vital\_status:

```

0 1
58 34

```

days\_to\_death:

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

days\_to\_last\_followup:

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

tumor\_tissue\_site:

adrenal	92
---------	----

pathologic\_stage:

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

pathology\_T\_stage:

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

pathology\_N\_stage:

n0	n1	NA's
80	10	2

gender:

female	male
60	32

date\_of\_initial\_pathologic\_diagnosis:

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

radiation\_therapy:

no	yes	NA's
71	18	3

histological\_type:

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

residual\_tumor:

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

number\_of\_lymph\_nodes:

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

race:



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

ethnicity:

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

Including an additional 806 columns

### See Also

[ACC-v2.0.1](#)

---

ACC-v2.0.1

*Adrenocortical carcinoma*

---

### Description

A document describing the TCGA cancer code

### Details

```
> experiments( ACC )
ExperimentList class object of length 11:
 [1] ACC_CNASNP-20160128: RaggedExperiment with 79861 rows and 180 columns
 [2] ACC_CNVSNP-20160128: RaggedExperiment with 21052 rows and 180 columns
 [3] ACC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 90 columns
 [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_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 79 columns
 [9] ACC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 79 columns
 [10] ACC_RPPAArray-20160128: SummarizedExperiment with 192 rows and 46 columns
 [11] ACC_Methylation-20160128: SummarizedExperiment with 485577 rows and 80 columns

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

```

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

```

```

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

```

Sizes of each ExperimentList element:

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

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

```

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

```

```

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

```

```

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

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

vital_status:
  0 1
58 34

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

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

tumor_tissue_site:
adrenal
  92

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

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

pathology_N_stage:
  n0  n1  NA's
  80  10  2

gender:
female  male
  60    32

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

radiation_therapy:
  no  yes  NA's
  71  18   3

```

## histological\_type:

```

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

```

## residual\_tumor:

```

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

```

## number\_of\_lymph\_nodes:

```

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

```

## race:

```

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

```

## ethnicity:

```

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

```

Including an additional 806 columns

---

ACC-v2.1.0

*Adrenocortical carcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

```

> experiments( ACC )
ExperimentList class object of length 11:
 [1] ACC_CNASNP-20160128: RaggedExperiment with 79861 rows and 180 columns
 [2] ACC_CNVSNP-20160128: RaggedExperiment with 21052 rows and 180 columns
 [3] ACC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 90 columns
 [4] ACC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 42 rows and 90 columns
 [5] ACC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 90 columns
 [6] ACC_Mutation-20160128: RaggedExperiment with 20166 rows and 90 columns
 [7] ACC_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 79 columns
 [8] ACC_RPPAArray-20160128: SummarizedExperiment with 192 rows and 46 columns

```

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

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

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

Sizes of each ExperimentList element:

		assay size.Mb
1	ACC_CNASNP-20160128	2.2 Mb
2	ACC_CNVSNP-20160128	0.6 Mb
3	ACC_GISTIC_AllByGene-20160128	20.5 Mb
4	ACC_GISTIC_Peaks-20160128	0.1 Mb
5	ACC_GISTIC_ThresholdedByGene-20160128	20.4 Mb
6	ACC_Mutation-20160128	12.6 Mb
7	ACC_RNASeq2Gene-20160128	14.9 Mb
8	ACC_RPPAArray-20160128	0.1 Mb
9	ACC_miRNASeqGene-20160128	0.8 Mb
10	ACC_RNASeq2GeneNorm-20160128	12.9 Mb
11	ACC_Methylation-20160128	75 Mb

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

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

```
58 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
[1,] 34 34 1.51 1.34 3.03
```

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

```
years_to_birth:
```

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

```
vital_status:
```

```
0 1
58 34
```

```
days_to_death:
```

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

```
days_to_last_followup:
```

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

```
tumor_tissue_site:
```

```
adrenal
92
```

```
pathologic_stage:
```

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

```
pathology_T_stage:
```

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

```
pathology_N_stage:
```

n0	n1	NA's
80	10	2

```

gender:
female  male
   60    32

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

radiation_therapy:
no  yes  NA's
 71  18   3

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

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

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

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

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

Including an additional 806 columns

```

---

BLCA

*Bladder Urothelial Carcinoma*


---

### Description

A document describing the TCGA cancer code

**Details**

```

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

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

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

```

Sizes of each ExperimentList element:



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

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

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

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

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

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

vital\_status:  
0 1  
230 182

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

days\_to\_last\_followup:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
-64.0 398.2 639.0 1016.7 1458.8 5050.0 182

tumor\_tissue\_site:  
bladder

412

pathologic\_stage:

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

pathology\_M\_stage:

m0	m1	mx	NA's
196	11	202	3

gender:

female	male
108	304

date\_of\_initial\_pathologic\_diagnosis:

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

radiation\_therapy:

no	yes	NA's
366	20	26

karnofsky\_performance\_score:

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

histological\_type:

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

number\_pack\_years\_smoked:

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

number\_of\_lymph\_nodes:

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

race:

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

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

Including an additional 1695 columns

### See Also

[BLCA-v2.0.1](#)

---

BLCA-v2.0.1

*Bladder Urothelial Carcinoma*

---

### Description

A document describing the TCGA cancer code

### Details

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

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

```

...
<3 more elements>

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

```

Sizes of each ExperimentList element:

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

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

```

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

```

```

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

```

-----

Available sample meta-data:

-----

years\_to\_birth:

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

vital\_status:

0	1
230	182

days\_to\_death:

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

days\_to\_last\_followup:

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

tumor\_tissue\_site:

bladder
412

pathologic\_stage:

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

pathology\_M\_stage:

m0	m1	mx	NA's
196	11	202	3

gender:

female	male
108	304

date\_of\_initial\_pathologic\_diagnosis:

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

radiation\_therapy:

no	yes	NA's
366	20	26

karnofsky\_performance\_score:

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

histological\_type:

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

number\_pack\_years\_smoked:

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

number\_of\_lymph\_nodes:

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

race:

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

ethnicity:

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

Including an additional 1695 columns

---

BLCA-v2.1.0

*Bladder Urothelial Carcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

```
> experiments( BLCA )
```

ExperimentList class object of length 13:

- [1] BLCA\_CNASeq-20160128: RaggedExperiment with 35692 rows and 232 columns
- [2] BLCA\_CNASNP-20160128: RaggedExperiment with 479978 rows and 806 columns
- [3] BLCA\_CNVSNP-20160128: RaggedExperiment with 104349 rows and 797 columns
- [4] BLCA\_GISTIC\_AllByGene-20160128: SummarizedExperiment with 24776 rows and 408 columns
- [5] BLCA\_GISTIC\_Peaks-20160128: RangedSummarizedExperiment with 71 rows and 408 columns
- [6] BLCA\_GISTIC\_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 408 columns
- [7] BLCA\_Mutation-20160128: RaggedExperiment with 39312 rows and 130 columns
- [8] BLCA\_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 427 columns
- [9] BLCA\_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 67 columns

```

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

```

```

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

```

```

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

```

Sizes of each ExperimentList element:

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

```

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

```

```

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

```

```

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

```

```

      232 observations deleted due to missingness
      n events median 0.95LCL 0.95UCL
[1,] 180    180    1.12    0.992    1.33

```

```

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

```

```

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

```

```

vital_status:
  0  1
230 182

```

```

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

```

```

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

```

```

tumor_tissue_site:
bladder
  412

```

```

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

```

```

pathology_M_stage:
  m0  m1  mx NA's

```



196 11 202 3

gender:

female male

108 304

date\_of\_initial\_pathologic\_diagnosis:

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

radiation\_therapy:

no yes NA's

366 20 26

karnofsky\_performance\_score:

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

histological\_type:

muscle invasive urothelial carcinoma (pt2 or above)

409

NA's

3

number\_pack\_years\_smoked:

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

number\_of\_lymph\_nodes:

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

race:

asian black or african american

44

23

white

327

NA's

18

ethnicity:

hispanic or latino not hispanic or latino

9

371

NA's

32

Including an additional 1695 columns

**Description**

A document describing the TCGA cancer code

**Details**

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

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

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

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

Sizes of each ExperimentList element:

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

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

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

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

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

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

```
vital_status:
  0    1 NA's
945 152   1
```

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

116.0	700.5	1272.0	1644.7	2367.0	7455.0	947
days_to_last_followup:						
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
-7	440	761	1183	1572	8605	153
tumor_tissue_site:						
breast	NA's					
1097	1					
pathology_M_stage:						
cm0 (i+)	m0	m1	mx	NA's		
6	906	22	163	1		
gender:						
female	male	NA's				
1085	12	1				
date_of_initial_pathologic_diagnosis:						
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1988	2007	2009	2008	2010	2013	3
days_to_last_known_alive:						
735	2576	NA's				
1	1	1096				
radiation_therapy:						
no	yes	NA's				
446	556	96				
number_of_lymph_nodes:						
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.000	0.000	1.000	2.363	2.000	35.000	169
race:						
american indian or alaska native						asian
	1					61
black or african american						white
	183					757
	NA's					
	96					
ethnicity:						
hispanic or latino	not hispanic or latino	NA's				

39

884

175

Including an additional 2667 columns

### See Also

[BRCA-v2.0.1](#)

---

BRCA-v2.0.1

*Breast invasive carcinoma*

---

### Description

A document describing the TCGA cancer code

### Details

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

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

```

...
<5 more elements>

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

```

Sizes of each ExperimentList element:

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

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

```

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

```

```

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

```

```

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

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

vital_status:
  0     1 NA's
 945 152   1

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

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

tumor_tissue_site:
breast  NA's
 1097    1

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

gender:
female  male  NA's
 1085    12    1

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

days_to_last_known_alive:
 735 2576 NA's
  1   1 1096

radiation_therapy:
  no  yes NA's
 446 556  96

```

```

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

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

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

```

Including an additional 2667 columns

---

BRCA-v2.1.0

*Breast invasive carcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

```

> experiments( BRCA )
ExperimentList class object of length 15:
 [1] BRCA_CNASeq-20160128: RaggedExperiment with 5298 rows and 38 columns
 [2] BRCA_CNASNP-20160128: RaggedExperiment with 1132786 rows and 2209 columns
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 [7] BRCA_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 590 columns
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 [9] BRCA_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 1212 columns
 [10] BRCA_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 878 columns
 [11] BRCA_RPPAArray-20160128: SummarizedExperiment with 226 rows and 937 columns
 [12] BRCA_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 849 columns
 [13] BRCA_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18300 rows and 1212 columns
 [14] BRCA_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 343 columns
 [15] BRCA_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 885 columns

> rownames( BRCA )

```



```

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

```

```

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

```

Sizes of each ExperimentList element:

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

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

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

```
947 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
[1,] 151 151 3.48 2.83 4.5
```

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

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

```
vital_status:
  0    1 NA's
945 152   1
```

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

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

```
tumor_tissue_site:
breast  NA's
 1097    1
```

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

```
gender:
female  male  NA's
 1085    12    1
```

```
date_of_initial_pathologic_diagnosis:
```

```

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

days_to_last_known_alive:
      735 2576 NA's
      1   1 1096

radiation_therapy:
      no  yes NA's
      446 556  96

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

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

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

Including an additional 2667 columns

```

---

CESC

*Cervical squamous cell carcinoma and endocervical adenocarcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

```

> experiments( CESC )
ExperimentList class object of length 11:
 [1] CESC_CNASeq-20160128: RaggedExperiment with 7834 rows and 100 columns
 [2] CESC_CNASNP-20160128: RaggedExperiment with 267855 rows and 586 columns
 [3] CESC_CNVSNP-20160128: RaggedExperiment with 59450 rows and 586 columns
 [4] CESC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 295 columns
 [5] CESC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 60 rows and 295 columns
 [6] CESC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 295 columns

```

```

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

```

```

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

```

```

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

```

Sizes of each ExperimentList element:

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

```

10          CESC_RPPAArray-20160128    0 Mb
11          CESC_Methylation-20160128  75 Mb

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

vital_status:
  0  1
235 72

```

```

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

```

```

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

```

```

tumor_tissue_site:
cervical
  307

```

```

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

```

```

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

```

gender:

female

307

date\_of\_initial\_pathologic\_diagnosis:

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

radiation\_therapy:

no yes NA's

55 129 123

number\_pack\_years\_smoked:

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

number\_of\_lymph\_nodes:

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

ethnicity:

hispanic or latino not hispanic or latino

24

171

NA's

112

weight\_kg\_at\_diagnosis:

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

tumor\_status:

tumor free with tumor NA's

201

80

26

tobacco\_smoking\_year\_stopped:

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

tobacco\_smoking\_pack\_years\_smoked:

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

tobacco\_smoking\_history:

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

agebegansmokinginyears:

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

radiation\_therapy\_status:

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

pregnancies\_count\_total:

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

pregnancies\_count\_stillbirth:

0	1	3	NA's
106	5	1	195

pregnancy\_spontaneous\_abortion\_count:

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

pregnancies\_count\_live\_birth:

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

pregnancy\_therapeutic\_abortion\_count:

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

pregnancies\_count\_ectopic:

0	1	2	NA's
104	11	1	191

lymph\_node\_location:

lymph_node_location_positive_pathology_name	lymph_node_location_positive_pathology_text
	307

menopause\_status:

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

## lymphovascular\_involvement:

absent	present	NA's
72	80	155

## lymph\_nodes\_examined\_he\_count:

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

## lymph\_nodes\_examined:

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

## keratinization\_squamous\_cell:

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

## initial\_pathologic\_dx\_year:

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

## hysterectomy\_type:

hysterectomy_performed_type hysterectomy_performed_text	307
---	-----

## history\_hormonal\_contraceptives\_use:

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

## height\_cm\_at\_diagnosis:

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

## corpus\_involvement:

absent	present	NA's
99	19	189

## chemo\_concurrent\_type:

carboplatin	cisplatin	other	NA's
7	104	2	194

## cervix\_suv\_results:

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



```

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

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

```

Including an additional 1330 columns

### See Also

[CESC-v2.0.1](#)

---

CESC-v2.0.1

*Cervical squamous cell carcinoma and endocervical adenocarcinoma*

---

### Description

A document describing the TCGA cancer code

### Details

```

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

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

```

```

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

```

```

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

```

Sizes of each ExperimentList element:

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

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

```

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

```

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

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

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

vital\_status:  
 0 1  
 235 72

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

days\_to\_last\_followup:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 0 374 688 1071 1362 6408 72

tumor\_tissue\_site:  
 cervical  
 307

pathology\_N\_stage:  
 n0 n1 nx NA's  
 135 60 67 45

pathology\_M\_stage:  
 m0 m1 mx NA's  
 116 10 131 50

gender:  
 female  
 307

date\_of\_initial\_pathologic\_diagnosis:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 1994 2006 2010 2008 2012 2013 2

radiation\_therapy:  
 no yes NA's

55 129 123

number\_pack\_years\_smoked:

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

number\_of\_lymph\_nodes:

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

ethnicity:

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

weight\_kg\_at\_diagnosis:

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

tumor\_status:

tumor free	with tumor	NA's
201	80	26

tobacco\_smoking\_year\_stopped:

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

tobacco\_smoking\_pack\_years\_smoked:

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

tobacco\_smoking\_history:

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

agebeganmokinginyears:

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

radiation\_therapy\_status:

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

pregnancies\_count\_total:

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

pregnancies\_count\_stillbirth:

0	1	3	NA's
106	5	1	195

pregnancy\_spontaneous\_abortion\_count:

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

pregnancies\_count\_live\_birth:

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

pregnancy\_therapeutic\_abortion\_count:

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

pregnancies\_count\_ectopic:

0	1	2	NA's
104	11	1	191

lymph\_node\_location:

lymph\_node\_location\_positive\_pathology\_name|lymph\_node\_location\_positive\_pathology\_text  
307

menopause\_status:

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

lymphovascular\_involvement:

absent	present	NA's
72	80	155

lymph\_nodes\_examined\_he\_count:

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

lymph\_nodes\_examined:

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

keratinization\_squamous\_cell:  
keratinizing squamous cell carcinoma  
55  
non-keratinizing squamous cell carcinoma  
120  
NA's  
132

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

hysterectomy\_type:  
hysterectomy\_performed\_type|hysterectomy\_performed\_text  
307

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

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

absent	present	NA's
99	19	189

carboplatin	cisplatin	other	NA's
7	104	2	194

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

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

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

Including an additional 1330 columns

---

CESC-v2.1.0

*Cervical squamous cell carcinoma and endocervical adenocarcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

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

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

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

```

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

```

Sizes of each ExperimentList element:

		assay	size.Mb
1		CESC_CNASeq-20160128	0.3 Mb
2		CESC_CNASNP-20160128	7.3 Mb
3		CESC_CNVSNP-20160128	1.8 Mb
4	CESC_GISTIC_AllByGene-20160128		59.3 Mb
5		CESC_GISTIC_Peaks-20160128	0.3 Mb
6	CESC_GISTIC_ThresholdedByGene-20160128		59.1 Mb
7		CESC_Mutation-20160128	32.9 Mb
8		CESC_RNASeq2Gene-20160128	50.9 Mb
9		CESC_RPPAArray-20160128	0.3 Mb
10		CESC_miRNASeqGene-20160128	2.7 Mb
11	CESC_RNASeq2GeneNorm-20160128		45.1 Mb
12		CESC_Methylation-20160128	75 Mb

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

```

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

```

```

235 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
[1,] 72      72      1.7      1.39      2.29

```

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

```

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

```

vital\_status:



0 1  
235 72

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

days\_to\_last\_followup:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 0 374 688 1071 1362 6408 72

tumor\_tissue\_site:  
 cervical  
 307

pathology\_N\_stage:  
 n0 n1 nx NA's  
 135 60 67 45

pathology\_M\_stage:  
 m0 m1 mx NA's  
 116 10 131 50

gender:  
 female  
 307

date\_of\_initial\_pathologic\_diagnosis:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 1994 2006 2010 2008 2012 2013 2

radiation\_therapy:  
 no yes NA's  
 55 129 123

number\_pack\_years\_smoked:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 0.20 6.50 15.00 17.38 25.00 57.00 214

number\_of\_lymph\_nodes:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 0.000 0.000 0.000 1.044 1.000 16.000 148

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

	24		171		112	
weight_kg_at_diagnosis:						
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
31.00	58.25	70.50	73.04	83.75	210.00	29
tumor_status:						
tumor free with tumor			NA's			
201	80		26			
tobacco_smoking_year_stopped:						
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1949	1995	2003	2000	2010	2013	264
tobacco_smoking_pack_years_smoked:						
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.20	6.50	15.00	17.38	25.00	57.00	214
tobacco_smoking_history:						
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1.000	1.000	1.000	1.829	2.000	5.000	44
agebeganmokinginyears:						
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
11.00	16.00	18.00	21.14	24.00	44.00	222
radiation_therapy_status:						
completed as planned			treatment not completed			NA's
		29		3		275
pregnancies_count_total:						
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.00	2.00	3.00	3.61	5.00	15.00	40
pregnancies_count_stillbirth:						
0	1	3	NA's			
106	5	1	195			
pregnancy_spontaneous_abortion_count:						
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.0000	0.0000	0.0000	0.5442	1.0000	6.0000	160
pregnancies_count_live_birth:						
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.000	1.250	2.000	2.844	4.000	11.000	45
pregnancy_therapeutic_abortion_count:						

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

pregnancies\_count\_ectopic:

0	1	2	NA's
104	11	1	191

lymph\_node\_location:

lymph_node_location_positive_pathology_name	lymph_node_location_positive_pathology_text
	307

menopause\_status:

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

lymphovascular\_involvement:

absent	present	NA's
72	80	155

lymph\_nodes\_examined\_he\_count:

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

lymph\_nodes\_examined:

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

keratinization\_squamous\_cell:

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

initial\_pathologic\_dx\_year:

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

```

hysterectomy_type:
hysterectomy_performed_type|hysterectomy_performed_text
                                307

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

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

corpus_involvement:
absent present  NA's
  99    19    189

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

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

cause_of_death:
cardiopulmonary arrest          lung cancer          renal failure
              1                   1                   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 4  
2  
cholangiocarcinoma; intrahepatic 30

residual\_tumor:  
r0 r1 rx  
28 5 3

race:  
asian black or african american white  
3 2 31

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

Including an additional 622 columns

**See Also**

[CHOL-v2.0.1](#)

**Description**

A document describing the TCGA cancer code

**Details**

```

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

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

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

```



Sizes of each ExperimentList element:

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

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

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

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

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

years\_to\_birth:

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

vital\_status:

0 1  
18 18

days\_to\_death:

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

days\_to\_last\_followup:

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

tumor\_tissue\_site:  
 bile duct  
     36

pathology\_T\_stage:  
 t1 t2 t2a t2b t3  
 19 6 2 4 5

pathology\_N\_stage:  
 n0 n1 nx  
 26 5 5

pathology\_M\_stage:  
 m0 m1 mx  
 28 5 3

gender:  
 female male  
     20 16

date\_of\_initial\_pathologic\_diagnosis:  
     Min. 1st Qu. Median Mean 3rd Qu. Max.  
     2005 2010 2011 2010 2012 2013

radiation\_therapy:  
 no NA's  
 35 1

histological\_type:  
     cholangiocarcinoma; distal cholangiocarcinoma; hilar/perihilar  
   2  4  
     cholangiocarcinoma; intrahepatic  
   30

residual\_tumor:  
 r0 r1 rx  
 28 5 3

race:  
                                   asian black or african american  white  
   3  2  31

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

Including an additional 622 columns

CHOL-v2.1.0

*Cholangiocarcinoma***Description**

A document describing the TCGA cancer code

**Details**

```

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

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

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

```

```

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

```

Sizes of each ExperimentList element:

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

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

```

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

```

```

18 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
[1,] 18 18 1.37 0.742 2.53

```

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

```

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

```

```

vital_status:
 0 1
18 18

```

```

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

```

days\_to\_last\_followup:

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

tumor\_tissue\_site:

bile duct	36
-----------	----

pathology\_T\_stage:

t1	t2	t2a	t2b	t3
19	6	2	4	5

pathology\_N\_stage:

n0	n1	nx
26	5	5

pathology\_M\_stage:

m0	m1	mx
28	5	3

gender:

female	male
20	16

date\_of\_initial\_pathologic\_diagnosis:

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

radiation\_therapy:

no NA's
35

histological\_type:

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

residual\_tumor:

r0	r1	rx
28	5	3

race:

asian	black or african american	white
3	2	31

ethnicity:

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

Including an additional 622 columns

---

COAD

*Colon adenocarcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

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

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

```

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

```

Sizes of each ExperimentList element:

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

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

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

tumor\_tissue\_site:

colon	NA's
456	1

```

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

radiation_therapy:
  no  yes NA's
  378  9  70

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

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

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

```

Including an additional 2604 columns

### See Also

[COAD-v2.0.1](#)

---

COAD-v2.0.1

*Colon adenocarcinoma*

---

### Description

A document describing the TCGA cancer code

### Details

```

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

```



```

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

```

```

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

```

```

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

```

Sizes of each ExperimentList element:

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

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

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

years\_to\_birth:

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

tumor\_tissue\_site:

colon	NA's
456	1

date\_of\_initial\_pathologic\_diagnosis:

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

radiation\_therapy:

no	yes	NA's
378	9	70

number\_of\_lymph\_nodes:

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

race:

american indian or alaska native	1	asian	11
black or african american		white	

59  
NA's  
173

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

Including an additional 2604 columns

---

COAD-v2.1.0 *Colon adenocarcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

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

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

```

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

```

```

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

```

Sizes of each ExperimentList element:

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

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

```

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

tumor_tissue_site:
colon NA's
  456    1

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

radiation_therapy:
  no  yes NA's
  378  9  70

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

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

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

```

Including an additional 2604 columns

---

curatedTCGAData

*Create a MultiAssayExperiment from specific assays and cohorts*

---

## Description

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

**Usage**

```

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

```

**Arguments**

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

**Available Assays**

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

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

-----

SummarizedExperiment*	
-----------------------	--

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

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

## version

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

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

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

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

### See Also

curatedTCGAData-package

### Examples

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

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

---

DLBC

*Lymphoid Neoplasm Diffuse Large B-cell Lymphoma*

---

### Description

A document describing the TCGA cancer code

### Details

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

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



```

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

```

```

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

```

Sizes of each ExperimentList element:

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

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

```

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

```

```

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

```

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

years\_to\_birth:

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

vital\_status:

0	1
39	9

days\_to\_death:

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

days\_to\_last\_followup:

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

gender:

female	male
26	22

date\_of\_initial\_pathologic\_diagnosis:

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

radiation\_therapy:

no	yes	NA's
40	7	1

histological\_type:

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

race:

asian black or african american	white
18	29

ethnicity:

hispanic or latino not hispanic or latino  
 12 36

Including an additional 607 columns

### See Also

[DLBC-v2.0.1](#)

---

DLBC-v2.0.1

*Lymphoid Neoplasm Diffuse Large B-cell Lymphoma*

---

### Description

A document describing the TCGA cancer code

### Details

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

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

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

Sizes of each ExperimentList element:

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

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

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

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

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

```
years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
```

23.00 46.00 57.50 56.27 67.00 82.00

## vital\_status:

0 1

39 9

## days\_to\_death:

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

## days\_to\_last\_followup:

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

## gender:

female male

26 22

## date\_of\_initial\_pathologic\_diagnosis:

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

## radiation\_therapy:

no yes NA's

40 7 1

## histological\_type:

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

## race:

asian black or african american

18 1

white

29

## ethnicity:

hispanic or latino not hispanic or latino

12 36

Including an additional 607 columns

## Description

A document describing the TCGA cancer code

## Details

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

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

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

Sizes of each ExperimentList element:

		assay	size.Mb
1	DLBC_CNASNP-20160128		1.2 Mb
2	DLBC_CNVSNP-20160128		0.3 Mb
3	DLBC_GISTIC_AllByGene-20160128		12.5 Mb
4	DLBC_GISTIC_Peaks-20160128		0.1 Mb
5	DLBC_GISTIC_ThresholdedByGene-20160128		12.4 Mb
6	DLBC_Mutation-20160128		12.6 Mb
7	DLBC_RNASeq2Gene-20160128		10.1 Mb
8	DLBC_RPPAArray-20160128		0.1 Mb
9	DLBC_miRNASeqGene-20160128		0.5 Mb
10	DLBC_RNASeq2GeneNorm-20160128		8.7 Mb
11	DLBC_Methylation-20160128		75 Mb

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

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

39 observations deleted due to missingness  
n events median 0.95LCL 0.95UCL  
[1,] 9 9 1.63 0.858 NA

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

years\_to\_birth:  
Min. 1st Qu. Median Mean 3rd Qu. Max.  
23.00 46.00 57.50 56.27 67.00 82.00

vital\_status:  
0 1  
39 9

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

days\_to\_last\_followup:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
0 616 946 1328 1581 5980 9

```

gender:
female   male
   26    22

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

radiation_therapy:
no  yes NA's
40  7    1

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

race:
                                     asian black or african american
                                     18
                                                                                   white
                                                                                   29

ethnicity:
  hispanic or latino not hispanic or latino
                                     12
                                                                                   36

Including an additional 607 columns

```

---

ESCA

*Esophageal carcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

```

> experiments( ESCA )
ExperimentList class object of length 12:
 [1] ESCA_CNASeq-20160128: RaggedExperiment with 17059 rows and 104 columns
 [2] ESCA_CNASNP-20160128: RaggedExperiment with 203186 rows and 373 columns
 [3] ESCA_CNVSNP-20160128: RaggedExperiment with 60803 rows and 373 columns
 [4] ESCA_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [5] ESCA_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 77 rows and 184 columns

```



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

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

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

Sizes of each ExperimentList element:

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

8	ESCA_Mutation-20160128	45 Mb
9	ESCA_RNASeq2GeneNorm-20160128	1.3 Mb
10	ESCA_RNASeqGene-20160128	1.7 Mb
11	ESCA_RPPAArray-20160128	0 Mb
12	ESCA_Methylation-20160128	75 Mb

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

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

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

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

years\_to\_birth:

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

vital\_status:

0	1
108	77

days\_to\_death:

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

days\_to\_last\_followup:

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

tumor\_tissue\_site:

esophagus
185

pathology\_M\_stage:

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

```

gender:
female  male
   27   158

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

radiation_therapy:
  no  yes  NA's
 124  43   18

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

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

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

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

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

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

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

```

Including an additional 940 columns

### See Also

[ESCA-v2.0.1](#)

---

 ESCA-v2.0.1

*Esophageal carcinoma*


---

## Description

A document describing the TCGA cancer code

## Details

```

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

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

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

```

```

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

```

Sizes of each ExperimentList element:

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

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

```

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

```

```

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

```

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

```

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

```

```

vital_status:
  0  1
108 77

```

## days\_to\_death:

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

## days\_to\_last\_followup:

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

## tumor\_tissue\_site:

esophagus	185
-----------	-----

## pathology\_M\_stage:

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

## gender:

female	male
27	158

## date\_of\_initial\_pathologic\_diagnosis:

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

## radiation\_therapy:

no	yes	NA's
124	43	18

## karnofsky\_performance\_score:

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

## histological\_type:

esophagus adenocarcinoma, nos	89	esophagus squamous cell carcinoma	96
-------------------------------	----	-----------------------------------	----

## number\_pack\_years\_smoked:

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

## residual\_tumor:

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

```

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

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

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

```

Including an additional 940 columns

---

ESCA-v2.1.0

*Esophageal carcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

```

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

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

```

```

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

```

```

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

```

Sizes of each ExperimentList element:

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

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

```

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

```



108 observations deleted due to missingness  
 n events median 0.95LCL 0.95UCL  
 [1,] 77 77 0.962 0.677 1.35

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

years\_to\_birth:

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

vital\_status:

0	1
108	77

days\_to\_death:

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

days\_to\_last\_followup:

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

tumor\_tissue\_site:

esophagus	185
-----------	-----

pathology\_M\_stage:

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

gender:

female	male
27	158

date\_of\_initial\_pathologic\_diagnosis:

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

radiation\_therapy:

no	yes	NA's
124	43	18

karnofsky\_performance\_score:

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

histological\_type:

esophagus adenocarcinoma, nos	89	esophagus squamous cell carcinoma	96
-------------------------------	----	-----------------------------------	----

number\_pack\_years\_smoked:

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

residual\_tumor:

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

number\_of\_lymph\_nodes:

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

race:

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

ethnicity:

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

Including an additional 940 columns

---

GBM

*Glioblastoma multiforme*

---

## Description

A document describing the TCGA cancer code

## Details

```
> experiments( GBM )
ExperimentList class object of length 18:
[1] GBM_CNACGH_CGH_hg_244a-20160128: RaggedExperiment with 81512 rows and 438 columns
[2] GBM_CNACGH_CGH_hg_415k_g4124a-20160128: RaggedExperiment with 57975 rows and 338 columns
[3] GBM_CNASNP-20160128: RaggedExperiment with 602338 rows and 1104 columns
[4] GBM_CNVSNP-20160128: RaggedExperiment with 146852 rows and 1104 columns
```

```

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

```

```

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

```

```

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

```

Sizes of each ExperimentList element:

assay size.Mb

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

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

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

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

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

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

vital\_status:  
0 1 NA's  
104 491 4

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

days\_to\_last\_followup:

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

tumor\_tissue\_site:

brain	NA's
595	4

gender:

female	male	NA's
230	365	4

date\_of\_initial\_pathologic\_diagnosis:

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

radiation\_therapy:

no	yes	NA's
78	489	32

karnofsky\_performance\_score:

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

histological\_type:

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

race:

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

ethnicity:

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

Including an additional 4368 columns

### See Also

[GBM-v2.0.1](#)

**Description**

A document describing the TCGA cancer code

**Details**

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

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

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

```

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

```

Sizes of each ExperimentList element:

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

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

```

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

```

```

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

```

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

years\_to\_birth:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
------	---------	--------	------	---------	------	------

10.00	50.00	59.00	57.82	68.00	89.00	4
-------	-------	-------	-------	-------	-------	---

## vital\_status:

0	1	NA's
104	491	4

## days\_to\_death:

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

## days\_to\_last\_followup:

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

## tumor\_tissue\_site:

brain	NA's
595	4

## gender:

female	male	NA's
230	365	4

## date\_of\_initial\_pathologic\_diagnosis:

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

## radiation\_therapy:

no	yes	NA's
78	489	32

## karnofsky\_performance\_score:

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

## histological\_type:

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

## race:

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

## ethnicity:

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



13

489

97

Including an additional 4368 columns

---

 GBM-v2.1.0

*Glioblastoma multiforme*


---

## Description

A document describing the TCGA cancer code

## Details

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

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

<8 more elements>

```
> colnames( GBM )
```

CharacterList of length 18

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

...

<8 more elements>

Sizes of each ExperimentList element:

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

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

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

```
109 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
```

[1,] 490 490 1.05 0.981 1.16

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

years\_to\_birth:

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

vital\_status:

0	1	NA's
104	491	4

days\_to\_death:

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

days\_to\_last\_followup:

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

tumor\_tissue\_site:

brain	NA's
595	4

gender:

female	male	NA's
230	365	4

date\_of\_initial\_pathologic\_diagnosis:

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

radiation\_therapy:

no	yes	NA's
78	489	32

karnofsky\_performance\_score:

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

histological\_type:

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

```

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

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

```

Including an additional 4368 columns

---

HNSC

*Head and Neck squamous cell carcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

```

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

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

```

```

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

```

```

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

```

Sizes of each ExperimentList element:

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

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

```

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

```

```

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

```

```

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

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

vital_status:
  0  1
304 224

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

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

tumor_tissue_site:
head and neck
      528

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

gender:
female  male
  142   386

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

days_to_last_known_alive:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
  98.0  483.0   848.5  1226.9  1647.5  3930.0   506

radiation_therapy:
  no  yes NA's
  163 303  62

histological_type:

```

```

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

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

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

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

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

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

```

Including an additional 1426 columns

**See Also**

[HNSC-v2.0.1](#)

---

HNSC-v2.0.1

*Head and Neck squamous cell carcinoma*

---

**Description**

A document describing the TCGA cancer code

**Details**

```

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

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

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

Sizes of each ExperimentList element:

```



	assay	size.Mb
1	HNSC_CNASeq-20160128	1 Mb
2	HNSC_CNASNP-20160128	13.6 Mb
3	HNSC_CNVSNP-20160128	3.3 Mb
4	HNSC_GISTIC_AllByGene-20160128	102.3 Mb
5	HNSC_GISTIC_Peaks-20160128	0.5 Mb
6	HNSC_GISTIC_ThresholdedByGene-20160128	102.1 Mb
7	HNSC_miRNASeqGene-20160128	4.5 Mb
8	HNSC_Mutation-20160128	68.9 Mb
9	HNSC_RNASeq2Gene-20160128	91.2 Mb
10	HNSC_RNASeq2GeneNorm-20160128	91.2 Mb
11	HNSC_RNASeqGene-20160128	48.6 Mb
12	HNSC_RPPAArray-20160128	0.3 Mb
13	HNSC_Methylation-20160128	75.1 Mb

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

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

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

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

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

vital\_status:  
0 1  
304 224

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

days\_to\_last\_followup:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
11.0 529.5 851.0 1042.9 1404.0 5480.0 225

tumor\_tissue\_site:  
 head and neck  
 528

pathology\_M\_stage:  
 m0 m1 mx NA's  
 191 1 65 271

gender:  
 female male  
 142 386

date\_of\_initial\_pathologic\_diagnosis:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 1992 2007 2010 2008 2011 2013 1

days\_to\_last\_known\_alive:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 98.0 483.0 848.5 1226.9 1647.5 3930.0 506

radiation\_therapy:  
 no yes NA's  
 163 303 62

histological\_type:  
 head & neck squamous cell carcinoma  
 517  
 head & neck squamous cell carcinoma basaloid type  
 10  
 head & neck squamous cell carcinoma, spindle cell variant  
 1

number\_pack\_years\_smoked:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 0.01685 25.00000 40.00000 45.75496 60.00000 300.00000 230

year\_of\_tobacco\_smoking\_onset:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 1936 1959 1968 1967 1975 2001 246

number\_of\_lymph\_nodes:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 0.000 0.000 1.000 2.186 3.000 44.000 115

race:

american indian or alaska native	2	asian	11
black or african american	48	white	452
NA's	15		
ethnicity:			
hispanic or latino	26	not hispanic or latino	465
		NA's	37

Including an additional 1426 columns

---

HNSC-v2.1.0

*Head and Neck squamous cell carcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

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

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

```

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

```

<3 more elements>

```
> colnames( HNSC )
```

CharacterList of length 13

```

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

```

<3 more elements>

Sizes of each ExperimentList element:

	assay	size.Mb
1	HNSC_CNASeq-20160128	1 Mb
2	HNSC_CNASNP-20160128	13.6 Mb
3	HNSC_CNVSNP-20160128	3.3 Mb
4	HNSC_GISTIC_AllByGene-20160128	102.3 Mb
5	HNSC_GISTIC_Peaks-20160128	0.5 Mb
6	HNSC_GISTIC_ThresholdedByGene-20160128	102.1 Mb
7	HNSC_Mutation-20160128	68.9 Mb
8	HNSC_RNASeq2Gene-20160128	91.2 Mb
9	HNSC_RNASeqGene-20160128	48.6 Mb
10	HNSC_RPPAArray-20160128	0.3 Mb
11	HNSC_miRNASeqGene-20160128	4.5 Mb
12	HNSC_RNASeq2GeneNorm-20160128	81.6 Mb
13	HNSC_Methylation-20160128	75.1 Mb

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

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

```

305 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
[1,] 223 223 1.18 1.06 1.35

```

```

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

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

vital_status:
  0  1
304 224

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

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

tumor_tissue_site:
head and neck
      528

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

gender:
female  male
   142   386

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

days_to_last_known_alive:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
  98.0  483.0   848.5  1226.9  1647.5  3930.0   506

radiation_therapy:
  no  yes NA's
  163 303  62

```

```

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

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

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

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

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

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

Including an additional 1426 columns

```

---

KICH

*Kidney Chromophobe*


---

## Description

A document describing the TCGA cancer code

## Details

```

> experiments( KICH )
ExperimentList class object of length 10:
 [1] KICH_CNASNP-20160128: RaggedExperiment with 57729 rows and 132 columns

```

```

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

```

```
> rownames( KICH )
```

```
CharacterList of length 10
```

```

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

```

```
> colnames( KICH )
```

```
CharacterList of length 10
```

```

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

```

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

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

10 KICH\_Methylation-20160128 75 Mb

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

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

57 observations deleted due to missingness

n	events	median	0.95LCL	0.95UCL
9.00	9.00	2.34	1.99	NA

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

years\_to\_birth:

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

vital\_status:

0	1
56	10

days\_to\_death:

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

days\_to\_last\_followup:

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

tumor\_tissue\_site:

kidney
66

pathologic\_stage:

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

pathology\_N\_stage:

n0	n1	n2	nx
40	3	2	21

pathology\_M\_stage:



m0	m1	mx	NA's
34	2	9	21

gender:	
female	male
27	39

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

radiation_therapy:	
no	
66	

karnofsky_performance_score:		
90	100	NA's
3	10	53

histological_type:	
kidney chromophobe	
	66

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

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

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

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

Including an additional 718 columns

### See Also

[KICH-v2.0.1](#)

KICH-v2.0.1

*Kidney Chromophobe***Description**

A document describing the TCGA cancer code

**Details**

```

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

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

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

```

```

[["KICH_RNASeq2Gene-20160128"]] TCGA-KL-8323-01A-21R-2315-07 ...
[["KICH_RNASeq2GeneNorm-20160128"]] TCGA-KL-8323-01A-21R-2315-07 ...
[["KICH_RPPAArray-20160128"]] TCGA-KL-8324-01A-21-A421-20 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

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

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

```

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

```

```

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

```

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

```

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

```

```

vital_status:
 0  1
56 10

```

```

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

```

days\_to\_last\_followup:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 30 1366 2713 2320 3138 4676 10

tumor\_tissue\_site:  
 kidney  
 66

pathologic\_stage:  
 stage i stage ii stage iii stage iv  
 21 25 14 6

pathology\_N\_stage:  
 n0 n1 n2 nx  
 40 3 2 21

pathology\_M\_stage:  
 m0 m1 mx NA's  
 34 2 9 21

gender:  
 female male  
 27 39

date\_of\_initial\_pathologic\_diagnosis:  
 Min. 1st Qu. Median Mean 3rd Qu. Max.  
 2000 2004 2005 2005 2007 2011

radiation\_therapy:  
 no  
 66

karnofsky\_performance\_score:  
 90 100 NA's  
 3 10 53

histological\_type:  
 kidney chromophobe  
 66

number\_pack\_years\_smoked:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 1.00 8.00 24.00 25.09 31.00 75.00 55

year\_of\_tobacco\_smoking\_onset:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's

	1949	1964	1974	1974	1984	1997	58
race:							
			asian	black or african	american		white
			2			4	58
			NA's				
			2				
ethnicity:							
			hispanic or latino	not hispanic or latino			NA's
			4		32		30

Including an additional 718 columns

KICH-v2.1.0

*Kidney Chromophobe***Description**

A document describing the TCGA cancer code

**Details**

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

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

```

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

```

```

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

```

Sizes of each ExperimentList element:

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

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

```

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

```

```

57 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
[1,] 9 9 2.34 1.99 NA

```

-----

Available sample meta-data:

-----

years\_to\_birth:

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

vital\_status:

0	1
56	10

days\_to\_death:

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

days\_to\_last\_followup:

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

tumor\_tissue\_site:

kidney
66

pathologic\_stage:

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

pathology\_N\_stage:

n0	n1	n2	nx
40	3	2	21

pathology\_M\_stage:

m0	m1	mx	NA's
34	2	9	21

gender:

female	male
27	39

date\_of\_initial\_pathologic\_diagnosis:

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

radiation\_therapy:

no
66

karnofsky\_performance\_score:

90 100 NA's  
3 10 53

histological\_type:

kidney chromophobe  
66

number\_pack\_years\_smoked:

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

year\_of\_tobacco\_smoking\_onset:

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

race:

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

ethnicity:

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

Including an additional 718 columns

---

KIRC

*Kidney renal clear cell carcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

```
> experiments( KIRC )
```

ExperimentList class object of length 13:

- [1] KIRC\_CNASNP-20160128: RaggedExperiment with 488691 rows and 1059 columns
- [2] KIRC\_CNVSNP-20160128: RaggedExperiment with 85036 rows and 1059 columns
- [3] KIRC\_GISTIC\_AllByGene-20160128: SummarizedExperiment with 24776 rows and 528 columns
- [4] KIRC\_GISTIC\_Peaks-20160128: RangedSummarizedExperiment with 26 rows and 528 columns
- [5] KIRC\_GISTIC\_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 528 columns
- [6] KIRC\_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 326 columns
- [7] KIRC\_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 72 columns
- [8] KIRC\_Mutation-20160128: RaggedExperiment with 26369 rows and 437 columns



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

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

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

Sizes of each ExperimentList element:

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

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

vital_status:
  0  1
360 177

```

```

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

```

```

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

```

```

tumor_tissue_site:
kidney
 537

```

```

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

```

```

pathology_N_stage:
n0 n1 nx

```

240 17 280

pathology\_M\_stage:

m0	m1	mx	NA's
426	79	30	2

gender:

female	male
191	346

date\_of\_initial\_pathologic\_diagnosis:

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

days\_to\_last\_known\_alive:

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

radiation\_therapy:

no	yes	NA's
142	2	393

karnofsky\_performance\_score:

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

histological\_type:

kidney clear cell renal carcinoma  
537

number\_pack\_years\_smoked:

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

year\_of\_tobacco\_smoking\_onset:

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

race:

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

ethnicity:

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

Including an additional 2250 columns

### See Also

[KIRC-v2.0.1](#)

---

KIRC-v2.0.1

*Kidney renal clear cell carcinoma*

---

### Description

A document describing the TCGA cancer code

### Details

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

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

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

Sizes of each ExperimentList element:

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

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

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

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

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

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

vital\_status:  
 0 1  
 360 177

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

days\_to\_last\_followup:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 0.0 710.5 1454.5 1536.9 2172.0 4537.0 177

tumor\_tissue\_site:  
 kidney  
 537

pathologic\_stage:  
 stage i stage ii stage iii stage iv NA's  
 269 57 125 84 2

pathology\_N\_stage:  
 n0 n1 nx  
 240 17 280

pathology\_M\_stage:  
 m0 m1 mx NA's  
 426 79 30 2

gender:  
 female male  
 191 346

date\_of\_initial\_pathologic\_diagnosis:  
 Min. 1st Qu. Median Mean 3rd Qu. Max.  
 1998 2004 2006 2006 2007 2013

days\_to\_last\_known\_alive:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 0 191 1172 1117 1887 2799 510

radiation\_therapy:  
 no yes NA's

142 2 393

karnofsky\_performance\_score:

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

histological\_type:

kidney clear cell renal carcinoma  
537

number\_pack\_years\_smoked:

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

year\_of\_tobacco\_smoking\_onset:

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

race:

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

ethnicity:

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

Including an additional 2250 columns

---

KIRC-v2.1.0

*Kidney renal clear cell carcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

```
> experiments( KIRC )
```

ExperimentList class object of length 14:

- [1] KIRC\_CNASNP-20160128: RaggedExperiment with 488691 rows and 1059 columns
- [2] KIRC\_CNVSNP-20160128: RaggedExperiment with 85036 rows and 1059 columns
- [3] KIRC\_GISTIC\_AllByGene-20160128: SummarizedExperiment with 24776 rows and 528 columns
- [4] KIRC\_GISTIC\_Peaks-20160128: RangedSummarizedExperiment with 26 rows and 528 columns
- [5] KIRC\_GISTIC\_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 528 columns
- [6] KIRC\_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 72 columns

```

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

```

```

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

```

```

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

```

Sizes of each ExperimentList element:

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



7	KIRC_Mutation-20160128	8.2 Mb
8	KIRC_RNASeq2Gene-20160128	97.4 Mb
9	KIRC_RNASeqGene-20160128	86.6 Mb
10	KIRC_RPPAArray-20160128	0.9 Mb
11	KIRC_miRNASeqGene-20160128	2.8 Mb
12	KIRC_RNASeq2GeneNorm-20160128	86.9 Mb
13	KIRC_Methylation_methyl27-20160128	4.9 Mb
14	KIRC_Methylation_methyl450-20160128	75.1 Mb

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

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

360 observations deleted due to missingness  
n events median 0.95LCL 0.95UCL  
[1,] 177 177 2.24 1.77 2.61

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

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

vital\_status:  
0 1  
360 177

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

days\_to\_last\_followup:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
0.0 710.5 1454.5 1536.9 2172.0 4537.0 177

tumor\_tissue\_site:  
kidney  
537

pathologic\_stage:  
stage i stage ii stage iii stage iv NA's  
269 57 125 84 2

pathology\_N\_stage:

n0 n1 nx

240 17 280

pathology\_M\_stage:

m0 m1 mx NA's

426 79 30 2

gender:

female male

191 346

date\_of\_initial\_pathologic\_diagnosis:

Min. 1st Qu. Median Mean 3rd Qu. Max.

1998 2004 2006 2006 2007 2013

days\_to\_last\_known\_alive:

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

0 191 1172 1117 1887 2799 510

radiation\_therapy:

no yes NA's

142 2 393

karnofsky\_performance\_score:

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

0.00 90.00 90.00 85.56 100.00 100.00 483

histological\_type:

kidney clear cell renal carcinoma

537

number\_pack\_years\_smoked:

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

7.00 14.00 30.00 28.33 40.00 65.00 516

year\_of\_tobacco\_smoking\_onset:

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

1946 1966 1978 1979 1996 2001 525

race:

asian black or african american

8 56

NA's

7

white

466

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

Including an additional 2250 columns

---

KIRP	<i>Kidney renal papillary cell carcinoma</i>
------	--

---

## Description

A document describing the TCGA cancer code

## Details

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

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

> colnames( KIRP )
```

```

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

```

Sizes of each ExperimentList element:

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

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

```

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

```

```

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

```

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

years\_to\_birth:

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

vital\_status:

0	1
247	44

days\_to\_death:

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

days\_to\_last\_followup:

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

tumor\_tissue\_site:

kidney
291

pathologic\_stage:

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

pathology\_N\_stage:

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

pathology\_M\_stage:

m0	m1	mx	NA's
95	9	172	15

gender:

female	male
77	214

date\_of\_initial\_pathologic\_diagnosis:

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

days\_to\_last\_known\_alive:

34	NA's
1	290

radiation\_therapy:

no	yes	NA's
209	1	81

```

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

histological_type:
kidney papillary renal cell carcinoma
                                291

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

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

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

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

```

Including an additional 1686 columns

### See Also

[KIRP-v2.0.1](#)

---

KIRP-v2.0.1

*Kidney renal papillary cell carcinoma*

---

### Description

A document describing the TCGA cancer code

### Details

```

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

```

```

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

```

```
> rownames( KIRP )
```

```
CharacterList of length 14
```

```

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

```

```
...
```

```
<4 more elements>
```

```
> colnames( KIRP )
```

```
CharacterList of length 14
```

```

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

```

```
...
```

```
<4 more elements>
```

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

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

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

vital_status:
  0  1
247 44

```

```

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

```

```

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

```

```

tumor_tissue_site:
kidney
291

```



```

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

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

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

gender:
  female  male
    77    214

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

days_to_last_known_alive:
  34 NA's
  1 290

radiation_therapy:
  no  yes  NA's
  209  1   81

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

histological_type:
  kidney papillary renal cell carcinoma
                                291

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

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

race:
  american indian or alaska native  asian

```

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

Including an additional 1686 columns

---

KIRP-v2.1.0

*Kidney renal papillary cell carcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

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

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

```

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

```

```

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

```

Sizes of each ExperimentList element:

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

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

```

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

```

```

247 observations deleted due to missingness
n events median 0.95LCL 0.95UCL

```

[1,] 44 44 1.76 1.35 3.6

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

years\_to\_birth:

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

vital\_status:

0	1
247	44

days\_to\_death:

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

days\_to\_last\_followup:

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

tumor\_tissue\_site:

kidney
291

pathologic\_stage:

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

pathology\_N\_stage:

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

pathology\_M\_stage:

m0	m1	mx	NA's
95	9	172	15

gender:

female	male
77	214

date\_of\_initial\_pathologic\_diagnosis:

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

days\_to\_last\_known\_alive:

34 NA's

1 290

radiation\_therapy:

no yes NA's

209 1 81

karnofsky\_performance\_score:

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

histological\_type:

kidney papillary renal cell carcinoma  
291

number\_pack\_years\_smoked:

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

year\_of\_tobacco\_smoking\_onset:

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

race:

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

ethnicity:

hispanic or latino	12	not hispanic or latino	243	NA's	36
--------------------	----	------------------------	-----	------	----

Including an additional 1686 columns

---

LAML

*Acute Myeloid Leukemia*

---

## Description

A document describing the TCGA cancer code

**Details**

```

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

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

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

```

Sizes of each ExperimentList element:

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

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

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

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

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

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

years\_to\_birth:

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

vital\_status:

0	1
67	133

days\_to\_death:

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

days\_to\_last\_followup:

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

tumor\_tissue\_site:

bone marrow	NA's
199	1

gender:

female	male
91	109

date\_of\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
------	---------	--------	------	---------	------

	2001	2004	2006	2006	2008	2010	
race:							
			asian	black or african	american		white
			2		15		181
			NA's				
			2				
ethnicity:							
			hispanic or latino	not hispanic or latino			NA's
			3		194		3

Including an additional 478 columns

### See Also

[LAML-v2.0.1](#)

---

LAML-v2.0.1

*Acute Myeloid Leukemia*

---

### Description

A document describing the TCGA cancer code

### Details

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

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



```

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

```

```

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

```

Sizes of each ExperimentList element:

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

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

```

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

```

```

80 observations deleted due to missingness
n events median 0.95LCL 0.95UCL

```

120.000 120.000 0.748 0.586 0.918

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

years\_to\_birth:

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

vital\_status:

0	1
67	133

days\_to\_death:

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

days\_to\_last\_followup:

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

tumor\_tissue\_site:

bone marrow	NA's
199	1

gender:

female	male
91	109

date\_of\_initial\_pathologic\_diagnosis:

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

race:

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

ethnicity:

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

Including an additional 478 columns

**Description**

A document describing the TCGA cancer code

**Details**

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

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

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

```

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

```

<1 more element>

Sizes of each ExperimentList element:

		assay size.Mb
1	LAML_CNASNP-20160128	23.5 Mb
2	LAML_CNVSNP-20160128	0.9 Mb
3	LAML_GISTIC_AllByGene-20160128	39.5 Mb
4	LAML_GISTIC_Peaks-20160128	0.1 Mb
5	LAML_GISTIC_ThresholdedByGene-20160128	39.5 Mb
6	LAML_Mutation-20160128	2.8 Mb
7	LAML_RNASeq2Gene-20160128	29.6 Mb
8	LAML_RNASeqGene-20160128	29.8 Mb
9	LAML_RNASeq2GeneNorm-20160128	24.9 Mb
10	LAML_Methylation_methyl27-20160128	4.9 Mb
11	LAML_Methylation_methyl450-20160128	75 Mb

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

```

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

```

```

      80 observations deleted due to missingness
      n events median 0.95LCL 0.95UCL
[1,] 120    120  0.748   0.586   0.918

```

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

```

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

```

```

vital_status:
  0    1
67 133

```

```

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

```

```

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

tumor_tissue_site:
bone marrow      NA's
      199          1

gender:
female  male
   91   109

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

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

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

Including an additional 478 columns

```

---

LGG

*Brain Lower Grade Glioma*


---

## Description

A document describing the TCGA cancer code

## Details

```

> experiments( LGG )
ExperimentList class object of length 12:
 [1] LGG_CNASeq-20160128: RaggedExperiment with 6360 rows and 104 columns
 [2] LGG_CNASNP-20160128: RaggedExperiment with 411918 rows and 1015 columns
 [3] LGG_CNVSNP-20160128: RaggedExperiment with 79791 rows and 1015 columns
 [4] LGG_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 513 columns
 [5] LGG_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 46 rows and 513 columns
 [6] LGG_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 513 columns
 [7] LGG_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 526 columns

```

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

```
> rownames( LGG )
CharacterList of length 12
[["LGG_CNASeq-20160128"]] character(0)
[["LGG_CNASNP-20160128"]] character(0)
[["LGG_CNVSNP-20160128"]] character(0)
[["LGG_GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["LGG_GISTIC_Peaks-20160128"]] chr1:3814904-5625565 ...
[["LGG_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["LGG_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["LGG_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["LGG_Mutation-20160128"]] character(0)
[["LGG_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
...
<2 more elements>
```

```
> colnames( LGG )
CharacterList of length 12
[["LGG_CNASeq-20160128"]] TCGA-CS-4938-01B-11D-1891-02 ...
[["LGG_CNASNP-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["LGG_CNVSNP-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["LGG_GISTIC_AllByGene-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["LGG_GISTIC_Peaks-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["LGG_GISTIC_ThresholdedByGene-20160128"]] TCGA-CS-4938-01B-11D-1892-01 ...
[["LGG_miRNASeqGene-20160128"]] TCGA-CS-4938-01B-11R-1895-13 ...
[["LGG_mRNAArray-20160128"]] TCGA-CS-4942-01A-01R-1470-07 ...
[["LGG_Mutation-20160128"]] TCGA-CS-4938-01B-11D-1893-08 ...
[["LGG_RNASeq2GeneNorm-20160128"]] TCGA-CS-4938-01B-11R-1896-07 ...
...
<2 more elements>
```

Sizes of each ExperimentList element:

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

```

10      LGG_RNASeq2GeneNorm-20160128  1.3 Mb
11      LGG_RPPAArray-20160128      0.1 Mb
12      LGG_Methylation-20160128    75.1 Mb

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

vital_status:
  0    1 NA's
389 126   1

```

```

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

```

```

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

```

```

tumor_tissue_site:
central nervous system      NA's
                        515          1

```

```

gender:
female  male  NA's
  230   285    1

```

```

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

```

radiation\_therapy:

no	yes	NA's
186	296	34

karnofsky\_performance\_score:

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

histological\_type:

astrocytoma	oligoastrocytoma	oligodendroglioma	NA's
194		130	191
			1

race:

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

ethnicity:

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

Including an additional 1764 columns

### See Also

[LGG-v2.0.1](#)

---

LGG-v2.0.1

*Brain Lower Grade Glioma*

---

### Description

A document describing the TCGA cancer code

### Details

```
> experiments( LGG )
```

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

- [1] LGG\_CNASeq-20160128: RaggedExperiment with 6360 rows and 104 columns
- [2] LGG\_CNASNP-20160128: RaggedExperiment with 411918 rows and 1015 columns
- [3] LGG\_CNVSNP-20160128: RaggedExperiment with 79791 rows and 1015 columns
- [4] LGG\_GISTIC\_AllByGene-20160128: SummarizedExperiment with 24776 rows and 513 columns
- [5] LGG\_GISTIC\_Peaks-20160128: RangedSummarizedExperiment with 46 rows and 513 columns
- [6] LGG\_GISTIC\_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 513 columns



```

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

```

```

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

```

```

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

```

Sizes of each ExperimentList element:

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

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

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

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

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

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

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

vital\_status:  
0 1 NA's  
389 126 1

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

days\_to\_last\_followup:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
-1.0 384.0 629.0 880.1 1147.0 6423.0 127

tumor\_tissue\_site:  
central nervous system NA's  
515 1

gender:  
female male NA's  
230 285 1

date\_of\_initial\_pathologic\_diagnosis:

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

radiation\_therapy:

no	yes	NA's
186	296	34

karnofsky\_performance\_score:

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

histological\_type:

astrocytoma	oligoastrocytoma	oligodendroglioma	NA's
194	130	191	1

race:

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

ethnicity:

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

Including an additional 1764 columns

---

LGG-v2.1.0

*Brain Lower Grade Glioma*

---

## Description

A document describing the TCGA cancer code

## Details

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

```

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

```

```

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

```

```

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

```

Sizes of each ExperimentList element:

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

9	LGG_RNASeq2Gene-20160128	85.5 Mb
10	LGG_RPPAArray-20160128	0.8 Mb
11	LGG_miRNASeqGene-20160128	4.4 Mb
12	LGG_RNASeq2GeneNorm-20160128	76.4 Mb
13	LGG_Methylation-20160128	75.1 Mb

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

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

391 observations deleted due to missingness  
n events median 0.95LCL 0.95UCL  
[1,] 125 125 2.23 1.87 2.83

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

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

vital\_status:  
0 1 NA's  
389 126 1

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

days\_to\_last\_followup:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
-1.0 384.0 629.0 880.1 1147.0 6423.0 127

tumor\_tissue\_site:  
central nervous system NA's  
515 1

gender:  
female male NA's  
230 285 1

date\_of\_initial\_pathologic\_diagnosis:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's

	1992	2008	2011	2009	2012	2013	1
radiation_therapy:							
no	186	296	34				
yes							
NA's							
karnofsky_performance_score:							
Min.	40.00	80.00	90.00	86.64	100.00	100.00	209
1st Qu.							
Median							
Mean							
3rd Qu.							
Max.							
NA's							
histological_type:							
astrocytoma	194						
oligoastrocytoma				130			
oligodendroglioma					191		
NA's							1
race:							
american indian or alaska native				1			asian
black or african american				21			white
NA's				11			475
ethnicity:							
hispanic or latino		32					NA's
not hispanic or latino					449		35

Including an additional 1764 columns

---

 LIHC

*Liver hepatocellular carcinoma*


---

## Description

A document describing the TCGA cancer code

## Details

```
> experiments( LIHC )
ExperimentList class object of length 11:
 [1] LIHC_CNASNP-20160128: RaggedExperiment with 363628 rows and 760 columns
 [2] LIHC_CNVSNP-20160128: RaggedExperiment with 93328 rows and 760 columns
 [3] LIHC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 370 columns
 [4] LIHC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 59 rows and 370 columns
 [5] LIHC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 370 columns
 [6] LIHC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 424 columns
 [7] LIHC_Mutation-20160128: RaggedExperiment with 27892 rows and 198 columns
 [8] LIHC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 423 columns
```

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

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

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

Sizes of each ExperimentList element:

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

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

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

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

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

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

```
vital_status:
 0  1
245 132
```

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

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

```
tumor_tissue_site:
liver
 377
```

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

```
pathology_M_stage:
  m0  m1  mx
272   4 101
```

```
gender:
```



female male  
122 255

date\_of\_initial\_pathologic\_diagnosis:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
1995 2008 2011 2010 2012 2013 3

radiation\_therapy:  
no yes NA's  
345 9 23

histological\_type:  
fibrolamellar carcinoma hepatocellular carcinoma  
3 367  
hepatocholangiocarcinoma (mixed)  
7

residual\_tumor:  
r0 r1 r2 rx NA's  
330 17 1 22 7

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

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

Including an additional 1218 columns

**See Also**

[LIHC-v2.0.1](#)

---

LIHC-v2.0.1 *Liver hepatocellular carcinoma*

---

**Description**

A document describing the TCGA cancer code

**Details**

```

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

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

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

```

Sizes of each ExperimentList element:

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

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

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

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

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

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

vital\_status:  
0 1  
245 132

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

days\_to\_last\_followup:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
0.0 395.8 649.5 885.8 1222.0 3675.0 133

tumor\_tissue\_site:  
liver

377

pathology\_N\_stage:  
 n0 n1 nx NA's  
 257 4 115 1

pathology\_M\_stage:  
 m0 m1 mx  
 272 4 101

gender:  
 female male  
 122 255

date\_of\_initial\_pathologic\_diagnosis:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 1995 2008 2011 2010 2012 2013 3

radiation\_therapy:  
 no yes NA's  
 345 9 23

histological\_type:  
 fibrolamellar carcinoma hepatocellular carcinoma  
 3 367  
 hepatocholangiocarcinoma (mixed)  
 7

residual\_tumor:  
 r0 r1 r2 rx NA's  
 330 17 1 22 7

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

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

Including an additional 1218 columns

LIHC-v2.1.0

*Liver hepatocellular carcinoma***Description**

A document describing the TCGA cancer code

**Details**

```

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

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

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

```

```

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

```

Sizes of each ExperimentList element:

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

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

```

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

```

```

245 observations deleted due to missingness
      n events median 0.95LCL 0.95UCL
[1,] 132   132   1.14   0.956   1.63

```

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

```

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

```

```

vital_status:
  0  1
245 132

```

```

days_to_death:

```

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

days\_to\_last\_followup:

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

tumor\_tissue\_site:

liver  
377

pathology\_N\_stage:

n0	n1	nx	NA's
257	4	115	1

pathology\_M\_stage:

m0	m1	mx
272	4	101

gender:

female	male
122	255

date\_of\_initial\_pathologic\_diagnosis:

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

radiation\_therapy:

no	yes	NA's
345	9	23

histological\_type:

fibrolamellar carcinoma	hepatocellular carcinoma
3	367
hepatocholangiocarcinoma (mixed)	
7	

residual\_tumor:

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

race:

american indian or alaska native	asian
2	161
black or african american	white
17	187

NA's  
10

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

Including an additional 1218 columns

---

LUAD *Lung adenocarcinoma*

---

### Description

A document describing the TCGA cancer code

### Details

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

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



```

...
<4 more elements>

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

```

Sizes of each ExperimentList element:

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

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

```

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

```

```

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

```

```

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

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

vital_status:
  0  1
332 188

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

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

tumor_tissue_site:
lung
520

gender:
female  male
  279   241

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

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

radiation_therapy:
  no  yes  NA's
  413  61   46

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

```

```

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

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

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

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

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

```

Including an additional 2607 columns

### See Also

[LUAD-v2.0.1](#)

---

LUAD-v2.0.1

*Lung adenocarcinoma*

---

### Description

A document describing the TCGA cancer code

### Details

```

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

```

```

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

```

```

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

```

```

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

```

Sizes of each ExperimentList element:

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

5	LUAD_GISTIC_Peaks-20160128	0.5 Mb
6	LUAD_GISTIC_ThresholdedByGene-20160128	101 Mb
7	LUAD_miRNASeqGene-20160128	4.2 Mb
8	LUAD_mRNAArray-20160128	6.6 Mb
9	LUAD_Mutation-20160128	92.9 Mb
10	LUAD_RNASeq2Gene-20160128	92.7 Mb
11	LUAD_RNASeq2GeneNorm-20160128	92.7 Mb
12	LUAD_RNASeqGene-20160128	27.9 Mb
13	LUAD_RPPAArray-20160128	0.7 Mb
14	LUAD_Methylation_methyl27-20160128	4.9 Mb
15	LUAD_Methylation_methyl450-20160128	75.1 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

Call: survfit(formula = survival::Surv(colDat\$days\_to\_death/365, colDat\$vital\_status) ~  
-1)

336 observations deleted due to missingness  
n events median 0.95LCL 0.95UCL  
184.00 184.00 1.70 1.37 2.00

-----  
Available sample meta-data:  
-----

years\_to\_birth:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
33.00 59.00 66.00 65.22 72.00 88.00 31

vital\_status:  
0 1  
332 188

days\_to\_death:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
0.0 297.8 619.0 791.4 1120.0 4961.0 336

days\_to\_last\_followup:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
0.0 459.5 670.0 968.7 1139.0 7248.0 193

tumor\_tissue\_site:  
lung  
520

## gender:

female	male
279	241

## date\_of\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1991	2007	2010	2008	2011	2013	19

## days\_to\_last\_known\_alive:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
9.0	96.5	141.0	327.6	386.0	1178.0	513

## radiation\_therapy:

no	yes	NA's
413	61	46

## karnofsky\_performance\_score:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.00	80.00	90.00	78.55	100.00	100.00	382

## number\_pack\_years\_smoked:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.15	20.50	40.00	41.79	50.00	154.00	165

## year\_of\_tobacco\_smoking\_onset:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1930	1956	1965	1965	1972	1999	241

## residual\_tumor:

r0	r1	r2	rx	NA's
347	13	4	26	130

## race:

american indian or alaska native	1	asian	8
black or african american	53	white	392
NA's	66		

## ethnicity:

hispanic or latino	not hispanic or latino	NA's
7	388	125

Including an additional 2607 columns

---

LUAD-v2.1.0

*Lung adenocarcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

```
> experiments( LUAD )
ExperimentList class object of length 15:
 [1] LUAD_CNASeq-20160128: RaggedExperiment with 399592 rows and 249 columns
 [2] LUAD_CNASNP-20160128: RaggedExperiment with 501475 rows and 1095 columns
 [3] LUAD_CNVSNP-20160128: RaggedExperiment with 115836 rows and 1095 columns
 [4] LUAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 516 columns
 [5] LUAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 73 rows and 516 columns
 [6] LUAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 516 columns
 [7] LUAD_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 32 columns
 [8] LUAD_Mutation-20160128: RaggedExperiment with 72541 rows and 230 columns
 [9] LUAD_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 576 columns
 [10] LUAD_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 162 columns
 [11] LUAD_RPPAArray-20160128: SummarizedExperiment with 223 rows and 365 columns
 [12] LUAD_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 498 columns
 [13] LUAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18289 rows and 576 columns
 [14] LUAD_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 89 columns
 [15] LUAD_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 492 columns

> rownames( LUAD )
CharacterList of length 15
[["LUAD_CNASeq-20160128"]] character(0)
[["LUAD_CNASNP-20160128"]] character(0)
[["LUAD_CNVSNP-20160128"]] character(0)
[["LUAD_GISTIC_AllByGene-20160128"]] character(0)
[["LUAD_GISTIC_Peaks-20160128"]] 30 1 31 2 32 33 34 ... 71 26 72 27 73 28 74
[["LUAD_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["LUAD_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["LUAD_Mutation-20160128"]] character(0)
[["LUAD_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["LUAD_RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
...
<5 more elements>

> colnames( LUAD )
CharacterList of length 15
```

```

[["LUAD_CNASeq-20160128"]] TCGA-05-4249-01A-01D-1103-02 ...
[["LUAD_CNASNP-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["LUAD_CNVSNP-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["LUAD_GISTIC_AllByGene-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["LUAD_GISTIC_Peaks-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["LUAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-05-4244-01A-01D-1877-01 ...
[["LUAD_mRNAArray-20160128"]] TCGA-05-4244-01A-01R-1107-07 ...
[["LUAD_Mutation-20160128"]] TCGA-05-4249-01A-01D-1105-08 ...
[["LUAD_RNASeq2Gene-20160128"]] TCGA-05-4244-01A-01R-1107-07 ...
[["LUAD_RNASeqGene-20160128"]] TCGA-05-4244-01A-01R-1107-07 ...

```

...  
<5 more elements>

Sizes of each ExperimentList element:

	assay	size.Mb
1	LUAD_CNASeq-20160128	10.8 Mb
2	LUAD_CNASNP-20160128	13.7 Mb
3	LUAD_CNVSNP-20160128	3.4 Mb
4	LUAD_GISTIC_AllByGene-20160128	101.2 Mb
5	LUAD_GISTIC_Peaks-20160128	0.5 Mb
6	LUAD_GISTIC_ThresholdedByGene-20160128	101 Mb
7	LUAD_mRNAArray-20160128	6.6 Mb
8	LUAD_Mutation-20160128	92.9 Mb
9	LUAD_RNASeq2Gene-20160128	92.7 Mb
10	LUAD_RNASeqGene-20160128	27.9 Mb
11	LUAD_RPPAArray-20160128	0.7 Mb
12	LUAD_miRNASeqGene-20160128	4.2 Mb
13	LUAD_RNASeq2GeneNorm-20160128	82.7 Mb
14	LUAD_Methylation_methyl27-20160128	4.9 Mb
15	LUAD_Methylation_methyl450-20160128	75.1 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

336 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
[1,] 184 184 1.7 1.37 2

```

-----  
Available sample meta-data:  
-----



years\_to\_birth:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 33.00 59.00 66.00 65.22 72.00 88.00 31

vital\_status:  
 0 1  
 332 188

days\_to\_death:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 0.0 297.8 619.0 791.4 1120.0 4961.0 336

days\_to\_last\_followup:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 0.0 459.5 670.0 968.7 1139.0 7248.0 193

tumor\_tissue\_site:  
 lung  
 520

gender:  
 female male  
 279 241

date\_of\_initial\_pathologic\_diagnosis:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 1991 2007 2010 2008 2011 2013 19

days\_to\_last\_known\_alive:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 9.0 96.5 141.0 327.6 386.0 1178.0 513

radiation\_therapy:  
 no yes NA's  
 413 61 46

karnofsky\_performance\_score:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 0.00 80.00 90.00 78.55 100.00 100.00 382

number\_pack\_years\_smoked:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 0.15 20.50 40.00 41.79 50.00 154.00 165

```

year_of_tobacco_smoking_onset:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
  1930   1956   1965   1965   1972   1999   241

residual_tumor:
  r0  r1  r2  rx NA's
  347  13  4  26 130

race:
american indian or alaska native          asian
                                1              8
      black or african american          white
                                53             392
                                NA's
                                66

ethnicity:
  hispanic or latino not hispanic or latino    NA's
                                7              388
                                125

Including an additional 2607 columns

```

---

LUSC

*Lung squamous cell carcinoma*


---

## Description

A document describing the TCGA cancer code

## Details

```

> experiments( LUSC )
ExperimentList class object of length 16:
 [1] LUSC_CNACGH-20160128: RaggedExperiment with 87417 rows and 407 columns
 [2] LUSC_CNASNP-20160128: RaggedExperiment with 543091 rows and 1035 columns
 [3] LUSC_CNVSNP-20160128: RaggedExperiment with 134864 rows and 1032 columns
 [4] LUSC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 501 columns
 [5] LUSC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 78 rows and 501 columns
 [6] LUSC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 501 columns
 [7] LUSC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 387 columns
 [8] LUSC_mRNAArray_huex-20160128: SummarizedExperiment with 18632 rows and 112 columns
 [9] LUSC_mRNAArray_TX_g4502a-20160128: SummarizedExperiment with 17814 rows and 154 columns
[10] LUSC_mRNAArray_TX_ht_hg_u133a-20160128: SummarizedExperiment with 12042 rows and 133 columns
[11] LUSC_Mutation-20160128: RaggedExperiment with 65305 rows and 178 columns
[12] LUSC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 552 columns
[13] LUSC_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 240 columns

```

```
[14] LUSC_RPPAArray-20160128: SummarizedExperiment with 223 rows and 328 columns
[15] LUSC_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 160 columns
[16] LUSC_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 412 columns
```

```
> rownames( LUSC )
CharacterList of length 16
[["LUSC_CNACGH-20160128"]] character(0)
[["LUSC_CNASNP-20160128"]] character(0)
[["LUSC_CNVSNP-20160128"]] character(0)
[["LUSC_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["LUSC_GISTIC_Peaks-20160128"]] chr1:1-31262836 ... chr22:45736500-51304566
[["LUSC_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["LUSC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["LUSC_mRNAArray_huex-20160128"]] C9orf152 ELMO2 RPS11 ... SLC39A6 CTSC AQP7
[["LUSC_mRNAArray_TX_g4502a-20160128"]] ELMO2 CREB3L1 RPS11 ... AQP7 CTSC
[["LUSC_mRNAArray_TX_ht_hg_u133a-20160128"]] AACS FSTL1 ELMO2 ... CTSC AQP7
...
<6 more elements>
```

```
> colnames( LUSC )
CharacterList of length 16
[["LUSC_CNACGH-20160128"]] TCGA-18-3406-01A-01D-1519-02 ...
[["LUSC_CNASNP-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_CNVSNP-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_GISTIC_AllByGene-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_GISTIC_Peaks-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_GISTIC_ThresholdedByGene-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_miRNASeqGene-20160128"]] TCGA-18-5592-01A-01T-1634-13 ...
[["LUSC_mRNAArray_huex-20160128"]] TCGA-18-3406-01A-01R-1030-03 ...
[["LUSC_mRNAArray_TX_g4502a-20160128"]] TCGA-18-3406-01A-01R-0980-07 ...
[["LUSC_mRNAArray_TX_ht_hg_u133a-20160128"]] TCGA-18-3406-01A-01R-1031-01 ...
...
<6 more elements>
```

Sizes of each ExperimentList element:

		assay size.Mb
1	LUSC_CNACGH-20160128	2.5 Mb
2	LUSC_CNASNP-20160128	14.8 Mb
3	LUSC_CNVSNP-20160128	3.9 Mb
4	LUSC_GISTIC_AllByGene-20160128	4.9 Mb
5	LUSC_GISTIC_Peaks-20160128	0.1 Mb
6	LUSC_GISTIC_ThresholdedByGene-20160128	4.9 Mb
7	LUSC_miRNASeqGene-20160128	0.1 Mb
8	LUSC_mRNAArray_huex-20160128	1.2 Mb
9	LUSC_mRNAArray_TX_g4502a-20160128	1.1 Mb
10	LUSC_mRNAArray_TX_ht_hg_u133a-20160128	0.8 Mb
11	LUSC_Mutation-20160128	81 Mb

```

12      LUSC_RNASeq2GeneNorm-20160128  1.3 Mb
13      LUSC_RNASeqGene-20160128     1.3 Mb
14      LUSC_RPPAArray-20160128      0 Mb
15      LUSC_Methylation_methyl27-20160128  4.9 Mb
16      LUSC_Methylation_methyl450-20160128  75 Mb

```

```

-----
Overall survival time-to-event summary (in years):
-----

```

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

289 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
215.00 215.00   1.51   1.25   1.88

```

```

-----
Available sample meta-data:
-----

```

```

years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
 39.00  62.00   68.00   67.26  73.00   90.00    10

```

```

vital_status:
 0  1
284 220

```

```

days_to_death:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
  1.0  280.0   550.0   872.3 1110.5  5287.0   289

```

```

days_to_last_followup:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
  0     394     757   1049  1374   4765   221

```

```

tumor_tissue_site:
lung
504

```

```

pathology_N_stage:
  n0  n1  n2  n3  nx
320 133  40  5  6

```

gender:

female	male
131	373

date\_of\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1992	2005	2009	2008	2011	2013	25

days\_to\_last\_known\_alive:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
4.0	298.8	706.0	904.8	1051.8	3724.0	436

radiation\_therapy:

no	yes	NA's
387	53	64

karnofsky\_performance\_score:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.0	0.0	80.0	60.3	90.0	100.0	338

histological\_type:

lung basaloid squamous cell carcinoma	15
lung papillary squamous cell carcinoma	6
lung small cell squamous cell carcinoma	1
lung squamous cell carcinoma- not otherwise specified (nos)	482

number\_pack\_years\_smoked:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1.00	31.12	50.00	52.91	64.50	240.00	77

year\_of\_tobacco\_smoking\_onset:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1933	1952	1960	1960	1968	1997	183

residual\_tumor:

r0	r1	r2	rx	NA's
401	12	4	23	64

race:

asian black or african american	white
9	31
NA's	351
113	

```
ethnicity:
  hispanic or latino not hispanic or latino      NA's
                8                319                177
```

Including an additional 2238 columns

### See Also

[LUSC-v2.0.1](#)

---

LUSC-v2.0.1

*Lung squamous cell carcinoma*

---

### Description

A document describing the TCGA cancer code

### Details

```
> experiments( LUSC )
ExperimentList class object of length 17:
 [1] LUSC_CNACGH-20160128: RaggedExperiment with 87417 rows and 407 columns
 [2] LUSC_CNASNP-20160128: RaggedExperiment with 543091 rows and 1035 columns
 [3] LUSC_CNVSNP-20160128: RaggedExperiment with 134864 rows and 1032 columns
 [4] LUSC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 501 columns
 [5] LUSC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 78 rows and 501 columns
 [6] LUSC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 501 columns
 [7] LUSC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 387 columns
 [8] LUSC_mRNAArray_huex-20160128: SummarizedExperiment with 18632 rows and 112 columns
 [9] LUSC_mRNAArray_TX_g4502a-20160128: SummarizedExperiment with 17814 rows and 154 columns
 [10] LUSC_mRNAArray_TX_ht_hg_u133a-20160128: SummarizedExperiment with 12042 rows and 133 columns
 [11] LUSC_Mutation-20160128: RaggedExperiment with 65305 rows and 178 columns
 [12] LUSC_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 552 columns
 [13] LUSC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 552 columns
 [14] LUSC_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 240 columns
 [15] LUSC_RPPAArray-20160128: SummarizedExperiment with 223 rows and 328 columns
 [16] LUSC_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 160 columns
 [17] LUSC_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 412 columns

> rownames( LUSC )
CharacterList of length 17
[["LUSC_CNACGH-20160128"]] character(0)
[["LUSC_CNASNP-20160128"]] character(0)
[["LUSC_CNVSNP-20160128"]] character(0)
[["LUSC_GISTIC_AllByGene-20160128"]] character(0)
[["LUSC_GISTIC_Peaks-20160128"]] 31 32 1 33 2 34 3 ... 27 28 76 77 78 29 79
```

```

[["LUSC_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["LUSC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["LUSC_mRNAArray_huex-20160128"]] C9orf152 ELMO2 RPS11 ... SLC39A6 CTSC AQP7
[["LUSC_mRNAArray_TX_g4502a-20160128"]] ELMO2 CREB3L1 RPS11 ... AQP7 CTSC
[["LUSC_mRNAArray_TX_ht_hg_u133a-20160128"]] AACS FSTL1 ELMO2 ... CTSC AQP7
...
<7 more elements>

```

```

> colnames( LUSC )
CharacterList of length 17
[["LUSC_CNACGH-20160128"]] TCGA-18-3406-01A-01D-1519-02 ...
[["LUSC_CNASNP-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_CNVSNP-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_GISTIC_AllByGene-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_GISTIC_Peaks-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_GISTIC_ThresholdedByGene-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_miRNASeqGene-20160128"]] TCGA-18-5592-01A-01T-1634-13 ...
[["LUSC_mRNAArray_huex-20160128"]] TCGA-18-3406-01A-01R-1030-03 ...
[["LUSC_mRNAArray_TX_g4502a-20160128"]] TCGA-18-3406-01A-01R-0980-07 ...
[["LUSC_mRNAArray_TX_ht_hg_u133a-20160128"]] TCGA-18-3406-01A-01R-1031-01 ...
...
<7 more elements>

```

Sizes of each ExperimentList element:

		assay size.Mb
1	LUSC_CNACGH-20160128	2.5 Mb
2	LUSC_CNASNP-20160128	14.8 Mb
3	LUSC_CNVSNP-20160128	3.9 Mb
4	LUSC_GISTIC_AllByGene-20160128	98.3 Mb
5	LUSC_GISTIC_Peaks-20160128	0.5 Mb
6	LUSC_GISTIC_ThresholdedByGene-20160128	98.1 Mb
7	LUSC_miRNASeqGene-20160128	3.3 Mb
8	LUSC_mRNAArray_huex-20160128	18.3 Mb
9	LUSC_mRNAArray_TX_g4502a-20160128	23.2 Mb
10	LUSC_mRNAArray_TX_ht_hg_u133a-20160128	13.7 Mb
11	LUSC_Mutation-20160128	81 Mb
12	LUSC_RNASeq2Gene-20160128	89 Mb
13	LUSC_RNASeq2GeneNorm-20160128	89 Mb
14	LUSC_RNASeqGene-20160128	40.1 Mb
15	LUSC_RPPAArray-20160128	0.6 Mb
16	LUSC_Methylation_methyl27-20160128	4.9 Mb
17	LUSC_Methylation_methyl450-20160128	75.1 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```
Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)
```

```
289 observations deleted due to missingness
  n events median 0.95LCL 0.95UCL
215.00 215.00  1.51  1.25  1.88
```

```
-----
Available sample meta-data:
-----
```

```
years_to_birth:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
39.00	62.00	68.00	67.26	73.00	90.00	10

```
vital_status:
```

```
  0  1
284 220
```

```
days_to_death:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1.0	280.0	550.0	872.3	1110.5	5287.0	289

```
days_to_last_followup:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0	394	757	1049	1374	4765	221

```
tumor_tissue_site:
```

```
lung
504
```

```
pathology_N_stage:
```

n0	n1	n2	n3	nx
320	133	40	5	6

```
gender:
```

female	male
131	373

```
date_of_initial_pathologic_diagnosis:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1992	2005	2009	2008	2011	2013	25

```
days_to_last_known_alive:
```



Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
4.0	298.8	706.0	904.8	1051.8	3724.0	436

radiation\_therapy:

no	yes	NA's
387	53	64

karnofsky\_performance\_score:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.0	0.0	80.0	60.3	90.0	100.0	338

histological\_type:

lung basaloid squamous cell carcinoma	15
lung papillary squamous cell carcinoma	6
lung small cell squamous cell carcinoma	1
lung squamous cell carcinoma- not otherwise specified (nos)	482

number\_pack\_years\_smoked:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1.00	31.12	50.00	52.91	64.50	240.00	77

year\_of\_tobacco\_smoking\_onset:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1933	1952	1960	1960	1968	1997	183

residual\_tumor:

r0	r1	r2	rx	NA's
401	12	4	23	64

race:

asian black or african american	white
9	31
NA's	351
113	

ethnicity:

hispanic or latino	not hispanic or latino	NA's
8	319	177

Including an additional 2238 columns

**Description**

A document describing the TCGA cancer code

**Details**

```

> experiments( LUSC )
ExperimentList class object of length 17:
 [1] LUSC_CNACGH-20160128: RaggedExperiment with 87417 rows and 407 columns
 [2] LUSC_CNASNP-20160128: RaggedExperiment with 543091 rows and 1035 columns
 [3] LUSC_CNVSNP-20160128: RaggedExperiment with 134864 rows and 1032 columns
 [4] LUSC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 501 columns
 [5] LUSC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 78 rows and 501 columns
 [6] LUSC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 501 columns
 [7] LUSC_mRNAArray_huex-20160128: SummarizedExperiment with 18632 rows and 112 columns
 [8] LUSC_mRNAArray_TX_g4502a-20160128: SummarizedExperiment with 17814 rows and 154 columns
 [9] LUSC_mRNAArray_TX_ht_hg_u133a-20160128: SummarizedExperiment with 12042 rows and 133 columns
 [10] LUSC_Mutation-20160128: RaggedExperiment with 65305 rows and 178 columns
 [11] LUSC_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 552 columns
 [12] LUSC_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 240 columns
 [13] LUSC_RPPAArray-20160128: SummarizedExperiment with 223 rows and 328 columns
 [14] LUSC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 387 columns
 [15] LUSC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18520 rows and 552 columns
 [16] LUSC_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 160 columns
 [17] LUSC_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 412 columns

> rownames( LUSC )
CharacterList of length 17
[["LUSC_CNACGH-20160128"]] character(0)
[["LUSC_CNASNP-20160128"]] character(0)
[["LUSC_CNVSNP-20160128"]] character(0)
[["LUSC_GISTIC_AllByGene-20160128"]] character(0)
[["LUSC_GISTIC_Peaks-20160128"]] 31 32 1 33 2 34 3 ... 27 28 76 77 78 29 79
[["LUSC_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["LUSC_mRNAArray_huex-20160128"]] C9orf152 ELMO2 RPS11 ... SLC39A6 CTSC AQP7
[["LUSC_mRNAArray_TX_g4502a-20160128"]] ELMO2 CREB3L1 RPS11 ... AQP7 CTSC
[["LUSC_mRNAArray_TX_ht_hg_u133a-20160128"]] AACS FSTL1 ELMO2 ... CTSC AQP7
[["LUSC_Mutation-20160128"]] character(0)
...
<7 more elements>

> colnames( LUSC )
CharacterList of length 17
[["LUSC_CNACGH-20160128"]] TCGA-18-3406-01A-01D-1519-02 ...
[["LUSC_CNASNP-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_CNVSNP-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_GISTIC_AllByGene-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_GISTIC_Peaks-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...
[["LUSC_GISTIC_ThresholdedByGene-20160128"]] TCGA-18-3406-01A-01D-0978-01 ...

```

```

[["LUSC_mRNAArray_huex-20160128"]] TCGA-18-3406-01A-01R-1030-03 ...
[["LUSC_mRNAArray_TX_g4502a-20160128"]] TCGA-18-3406-01A-01R-0980-07 ...
[["LUSC_mRNAArray_TX_ht_hg_u133a-20160128"]] TCGA-18-3406-01A-01R-1031-01 ...
[["LUSC_Mutation-20160128"]] TCGA-18-3406-01A-01D-0983-08 ...
...
<7 more elements>

```

Sizes of each ExperimentList element:

		assay size.Mb
1	LUSC_CNACGH-20160128	2.5 Mb
2	LUSC_CNASNP-20160128	14.8 Mb
3	LUSC_CNVSNP-20160128	3.9 Mb
4	LUSC_GISTIC_AllByGene-20160128	98.3 Mb
5	LUSC_GISTIC_Peaks-20160128	0.5 Mb
6	LUSC_GISTIC_ThresholdedByGene-20160128	98.1 Mb
7	LUSC_mRNAArray_huex-20160128	18.3 Mb
8	LUSC_mRNAArray_TX_g4502a-20160128	23.2 Mb
9	LUSC_mRNAArray_TX_ht_hg_u133a-20160128	13.7 Mb
10	LUSC_Mutation-20160128	81 Mb
11	LUSC_RNASeq2Gene-20160128	89 Mb
12	LUSC_RNASeqGene-20160128	40.1 Mb
13	LUSC_RPPAArray-20160128	0.6 Mb
14	LUSC_miRNASeqGene-20160128	3.3 Mb
15	LUSC_RNASeq2GeneNorm-20160128	80.4 Mb
16	LUSC_Methylation_methyl27-20160128	4.9 Mb
17	LUSC_Methylation_methyl450-20160128	75.1 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

289 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
[1,] 215 215 1.51 1.25 1.88

```

-----  
Available sample meta-data:  
-----

```

years_to_birth:
  Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
39.00 62.00 68.00 67.26 73.00 90.00 10

```

## vital\_status:

0	1
284	220

## days\_to\_death:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1.0	280.0	550.0	872.3	1110.5	5287.0	289

## days\_to\_last\_followup:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0	394	757	1049	1374	4765	221

## tumor\_tissue\_site:

lung
504

## pathology\_N\_stage:

n0	n1	n2	n3	nx
320	133	40	5	6

## gender:

female	male
131	373

## date\_of\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1992	2005	2009	2008	2011	2013	25

## days\_to\_last\_known\_alive:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
4.0	298.8	706.0	904.8	1051.8	3724.0	436

## radiation\_therapy:

no	yes	NA's
387	53	64

## karnofsky\_performance\_score:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.0	0.0	80.0	60.3	90.0	100.0	338

## histological\_type:

lung basaloid squamous cell carcinoma	15
lung papillary squamous cell carcinoma	6

```

lung small cell squamous cell carcinoma
1
lung squamous cell carcinoma- not otherwise specified (nos)
482

number_pack_years_smoked:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.    NA's
  1.00  31.12  50.00  52.91  64.50 240.00   77

year_of_tobacco_smoking_onset:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.    NA's
 1933  1952  1960  1960  1968  1997   183

residual_tumor:
  r0  r1  r2  rx NA's
 401  12  4  23  64

race:
              asian black or african american              white
              9              31              351
              NA's
              113

ethnicity:
  hispanic or latino not hispanic or latino              NA's
              8              319              177

Including an additional 2238 columns

```

---

MESO

*Mesothelioma*

---

## Description

A document describing the TCGA cancer code

## Details

```

> experiments( MESO )
ExperimentList class object of length 9:
 [1] MESO_CNASNP-20160128: RaggedExperiment with 90003 rows and 173 columns
 [2] MESO_CNVSNP-20160128: RaggedExperiment with 18335 rows and 172 columns
 [3] MESO_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 87 columns
 [4] MESO_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 21 rows and 87 columns
 [5] MESO_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 87 columns
 [6] MESO_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 87 columns
 [7] MESO_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 87 columns

```

```
[8] MESO_RPPAArray-20160128: SummarizedExperiment with 193 rows and 63 columns
[9] MESO_Methylation-20160128: SummarizedExperiment with 485577 rows and 87 columns
```

```
> rownames( MESO )
CharacterList of length 9
[["MESO_CNASNP-20160128"]] character(0)
[["MESO_CNVSNP-20160128"]] character(0)
[["MESO_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["MESO_GISTIC_Peaks-20160128"]] chr1:1-31262836 ... chr22:29969457-30128393
[["MESO_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["MESO_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["MESO_RNASeqGeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["MESO_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["MESO_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
```

```
> colnames( MESO )
CharacterList of length 9
[["MESO_CNASNP-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_CNVSNP-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_GISTIC_AllByGene-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_GISTIC_Peaks-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_GISTIC_ThresholdedByGene-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_miRNASeqGene-20160128"]] TCGA-3H-AB3K-01A-11R-A404-13 ...
[["MESO_RNASeqGeneNorm-20160128"]] TCGA-3H-AB3K-01A-11R-A40A-07 ...
[["MESO_RPPAArray-20160128"]] TCGA-3H-AB3K-01A-21-A450-20 ...
[["MESO_Methylation-20160128"]] TCGA-3H-AB3K-01A-11D-A39S-05 ...
```

Sizes of each ExperimentList element:

		assay size.Mb
1	MESO_CNASNP-20160128	2.5 Mb
2	MESO_CNVSNP-20160128	0.6 Mb
3	MESO_GISTIC_AllByGene-20160128	4.9 Mb
4	MESO_GISTIC_Peaks-20160128	0 Mb
5	MESO_GISTIC_ThresholdedByGene-20160128	4.9 Mb
6	MESO_miRNASeqGene-20160128	0.1 Mb
7	MESO_RNASeqGeneNorm-20160128	1.3 Mb
8	MESO_RPPAArray-20160128	0 Mb
9	MESO_Methylation-20160128	75 Mb

```
-----
Overall survival time-to-event summary (in years):
-----
```

```
Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)
```

14 observations deleted due to missingness

n	events	median	0.95LCL	0.95UCL
73.00	73.00	1.25	1.11	1.67

-----  
 Available sample meta-data:  
 -----

years\_to\_birth:  
 Min. 1st Qu. Median Mean 3rd Qu. Max.  
 28.00 57.00 64.00 62.99 69.00 81.00

vital\_status:  
 0 1  
 13 74

days\_to\_death:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 20.0 253.0 457.0 584.1 789.0 2790.0 14

days\_to\_last\_followup:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 -8 499 1168 1091 1490 2359 74

tumor\_tissue\_site:  
 pleura  
 87

pathology\_N\_stage:  
 n0 n1 n2 n3 nx  
 44 10 26 3 4

pathology\_M\_stage:  
 m0 m1 mx  
 57 3 27

gender:  
 female male  
 16 71

date\_of\_initial\_pathologic\_diagnosis:  
 Min. 1st Qu. Median Mean 3rd Qu. Max.  
 1999 2008 2010 2009 2012 2013

radiation\_therapy:  
 no yes NA's

62 24 1

karnofsky\_performance\_score:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.00	80.00	90.00	77.65	90.00	100.00	70

histological\_type:

biphasic mesothelioma	diffuse malignant mesothelioma - nos	23	5
epithelioid mesothelioma	sarcomatoid mesothelioma	57	2

residual\_tumor:

r0	r1	r2	rx	NA's
17	3	15	11	41

race:

asian	black or african american	white
1	1	85

ethnicity:

not hispanic or latino	NA's
73	14

Including an additional 636 columns

## See Also

[MESO-v2.0.1](#)

---

MESO-v2.0.1

*Mesothelioma*

---

## Description

A document describing the TCGA cancer code

## Details

```
> experiments( MESO )
```

ExperimentList class object of length 10:

- [1] MESO\_CNASNP-20160128: RaggedExperiment with 90003 rows and 173 columns
- [2] MESO\_CNVSNP-20160128: RaggedExperiment with 18335 rows and 172 columns
- [3] MESO\_GISTIC\_AllByGene-20160128: SummarizedExperiment with 24776 rows and 87 columns
- [4] MESO\_GISTIC\_Peaks-20160128: RangedSummarizedExperiment with 21 rows and 87 columns
- [5] MESO\_GISTIC\_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 87 columns
- [6] MESO\_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 87 columns



```

[7] MESO_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 87 columns
[8] MESO_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 87 columns
[9] MESO_RPPAArray-20160128: SummarizedExperiment with 193 rows and 63 columns
[10] MESO_Methylation-20160128: SummarizedExperiment with 485577 rows and 87 columns

```

```

> rownames( MESO )
CharacterList of length 10
[["MESO_CNASNP-20160128"]] character(0)
[["MESO_CNVSNP-20160128"]] character(0)
[["MESO_GISTIC_AllByGene-20160128"]] character(0)
[["MESO_GISTIC_Peaks-20160128"]] 1 2 3 4 5 6 7 8 ... 14 15 16 17 18 19 20 21
[["MESO_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["MESO_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["MESO_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["MESO_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["MESO_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["MESO_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873

> colnames( MESO )
CharacterList of length 10
[["MESO_CNASNP-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_CNVSNP-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_GISTIC_AllByGene-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_GISTIC_Peaks-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_GISTIC_ThresholdedByGene-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_miRNASeqGene-20160128"]] TCGA-3H-AB3K-01A-11R-A404-13 ...
[["MESO_RNASeq2Gene-20160128"]] TCGA-3H-AB3K-01A-11R-A40A-07 ...
[["MESO_RNASeq2GeneNorm-20160128"]] TCGA-3H-AB3K-01A-11R-A40A-07 ...
[["MESO_RPPAArray-20160128"]] TCGA-3H-AB3K-01A-21-A450-20 ...
[["MESO_Methylation-20160128"]] TCGA-3H-AB3K-01A-11D-A39S-05 ...

```

Sizes of each ExperimentList element:

		assay size.Mb
1	MESO_CNASNP-20160128	2.5 Mb
2	MESO_CNVSNP-20160128	0.6 Mb
3	MESO_GISTIC_AllByGene-20160128	19.9 Mb
4	MESO_GISTIC_Peaks-20160128	0.1 Mb
5	MESO_GISTIC_ThresholdedByGene-20160128	19.8 Mb
6	MESO_miRNASeqGene-20160128	0.9 Mb
7	MESO_RNASeq2Gene-20160128	16.2 Mb
8	MESO_RNASeq2GeneNorm-20160128	16.2 Mb
9	MESO_RPPAArray-20160128	0.1 Mb
10	MESO_Methylation-20160128	75 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```
Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)
```

```
14 observations deleted due to missingness
  n events median 0.95LCL 0.95UCL
73.00  73.00   1.25   1.11   1.67
```

```
-----
Available sample meta-data:
-----
```

```
years_to_birth:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
28.00	57.00	64.00	62.99	69.00	81.00

```
vital_status:
```

```
0 1
13 74
```

```
days_to_death:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
20.0	253.0	457.0	584.1	789.0	2790.0	14

```
days_to_last_followup:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
-8	499	1168	1091	1490	2359	74

```
tumor_tissue_site:
```

```
pleura
87
```

```
pathology_N_stage:
```

```
n0 n1 n2 n3 nx
44 10 26 3 4
```

```
pathology_M_stage:
```

```
m0 m1 mx
57 3 27
```

```
gender:
```

```
female male
16 71
```

```
date_of_initial_pathologic_diagnosis:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
1999	2008	2010	2009	2012	2013

radiation\_therapy:

no	yes	NA's
62	24	1

karnofsky\_performance\_score:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.00	80.00	90.00	77.65	90.00	100.00	70

histological\_type:

biphasic mesothelioma	diffuse malignant mesothelioma - nos	23	5
epithelioid mesothelioma	sarcomatoid mesothelioma	57	2

residual\_tumor:

r0	r1	r2	rx	NA's
17	3	15	11	41

race:

asian	black or african american	white
1	1	85

ethnicity:

not hispanic or latino	NA's
73	14

Including an additional 636 columns

MESO-v2.1.0

*Mesothelioma***Description**

A document describing the TCGA cancer code

**Details**

&gt; experiments( MESO )

ExperimentList class object of length 10:

- [1] MESO\_CNASNP-20160128: RaggedExperiment with 90003 rows and 173 columns
- [2] MESO\_CNVSNP-20160128: RaggedExperiment with 18335 rows and 172 columns
- [3] MESO\_GISTIC\_AllByGene-20160128: SummarizedExperiment with 24776 rows and 87 columns
- [4] MESO\_GISTIC\_Peaks-20160128: RangedSummarizedExperiment with 21 rows and 87 columns
- [5] MESO\_GISTIC\_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 87 columns

```
[6] MESO_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 87 columns
[7] MESO_RPPAArray-20160128: SummarizedExperiment with 193 rows and 63 columns
[8] MESO_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 87 columns
[9] MESO_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18192 rows and 87 columns
[10] MESO_Methylation-20160128: SummarizedExperiment with 485577 rows and 87 columns
```

```
> rownames( MESO )
CharacterList of length 10
[["MESO_CNASNP-20160128"]] character(0)
[["MESO_CNVSNP-20160128"]] character(0)
[["MESO_GISTIC_AllByGene-20160128"]] character(0)
[["MESO_GISTIC_Peaks-20160128"]] 1 2 3 4 5 6 7 8 ... 14 15 16 17 18 19 20 21
[["MESO_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["MESO_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
[["MESO_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["MESO_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["MESO_RNASeq2GeneNorm-20160128"]] A1BG A2BP1 A2LD1 ... ZZEF1 ZZZ3 psiTPTE22
[["MESO_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
```

```
> colnames( MESO )
CharacterList of length 10
[["MESO_CNASNP-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_CNVSNP-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_GISTIC_AllByGene-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_GISTIC_Peaks-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_GISTIC_ThresholdedByGene-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["MESO_RNASeq2Gene-20160128"]] TCGA-3H-AB3K-01A-11R-A40A-07 ...
[["MESO_RPPAArray-20160128"]] TCGA-3H-AB3K-01A-21-A450-20 ...
[["MESO_miRNASeqGene-20160128"]] TCGA-3H-AB3K-01A-11R-A404-13 ...
[["MESO_RNASeq2GeneNorm-20160128"]] TCGA-3H-AB3K-01 ... TCGA-ZN-A9VW-01
[["MESO_Methylation-20160128"]] TCGA-3H-AB3K-01A-11D-A39S-05 ...
```

Sizes of each ExperimentList element:

		assay size.Mb
1	MESO_CNASNP-20160128	2.5 Mb
2	MESO_CNVSNP-20160128	0.6 Mb
3	MESO_GISTIC_AllByGene-20160128	19.9 Mb
4	MESO_GISTIC_Peaks-20160128	0.1 Mb
5	MESO_GISTIC_ThresholdedByGene-20160128	19.8 Mb
6	MESO_RNASeq2Gene-20160128	16.2 Mb
7	MESO_RPPAArray-20160128	0.1 Mb
8	MESO_miRNASeqGene-20160128	0.9 Mb
9	MESO_RNASeq2GeneNorm-20160128	14.3 Mb
10	MESO_Methylation-20160128	75 Mb

-----  
Overall survival time-to-event summary (in years):

```
-----
Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)
```

```
14 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
[1,] 73      73   1.25   1.11   1.67
```

```
-----
Available sample meta-data:
-----
```

years\_to\_birth:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
28.00	57.00	64.00	62.99	69.00	81.00

vital\_status:

0	1
13	74

days\_to\_death:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
20.0	253.0	457.0	584.1	789.0	2790.0	14

days\_to\_last\_followup:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
-8	499	1168	1091	1490	2359	74

tumor\_tissue\_site:

pleura
87

pathology\_N\_stage:

n0	n1	n2	n3	nx
44	10	26	3	4

pathology\_M\_stage:

m0	m1	mx
57	3	27

gender:

female	male
16	71

```

date_of_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
  1999   2008   2010   2009   2012   2013

radiation_therapy:
  no  yes NA's
  62  24   1

karnofsky_performance_score:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.  NA's
  0.00  80.00  90.00  77.65  90.00  100.00  70

histological_type:
      biphasic mesothelioma diffuse malignant mesothelioma - nos
                                23                                5
      epithelioid mesothelioma                sarcomatoid mesothelioma
                                57                                2

residual_tumor:
  r0  r1  r2  rx NA's
  17   3  15  11  41

race:
                asian black or african american                white
                1                                1                85

ethnicity:
not hispanic or latino                NA's
                73                                14

Including an additional 636 columns

```

---

OV

*Ovarian serous cystadenocarcinoma*


---

## Description

A document describing the TCGA cancer code

## Details

```

> experiments( OV )
ExperimentList class object of length 19:
[1] OV_CNACGH_CGH_hg_244a-20160128: RaggedExperiment with 128946 rows and 472 columns
[2] OV_CNACGH_CGH_hg_415k_g4124a-20160128: RaggedExperiment with 245847 rows and 674 columns
[3] OV_CNASNP-20160128: RaggedExperiment with 907765 rows and 1145 columns
[4] OV_CNVSNP-20160128: RaggedExperiment with 261680 rows and 1141 columns

```

```

[5] OV_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 573 columns
[6] OV_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 70 rows and 573 columns
[7] OV_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 573 columns
[8] OV_miRNAArray-20160128: SummarizedExperiment with 821 rows and 573 columns
[9] OV_miRNASeqGene-20160128: SummarizedExperiment with 705 rows and 461 columns
[10] OV_mRNAArray_huex-20160128: SummarizedExperiment with 18632 rows and 575 columns
[11] OV_mRNAArray_TX_g4502a_1-20160128: SummarizedExperiment with 17814 rows and 546 columns
[12] OV_mRNAArray_TX_g4502a-20160128: SummarizedExperiment with 17814 rows and 31 columns
[13] OV_mRNAArray_TX_ht_hg_u133a-20160128: SummarizedExperiment with 12042 rows and 524 columns
[14] OV_Mutation-20160128: RaggedExperiment with 20219 rows and 316 columns
[15] OV_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 307 columns
[16] OV_RNASeqGene-20160128: SummarizedExperiment with 19990 rows and 299 columns
[17] OV_RPPAArray-20160128: SummarizedExperiment with 208 rows and 427 columns
[18] OV_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 591 columns
[19] OV_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 10 columns

```

```
> rownames( OV )
```

```
CharacterList of length 19
```

```

[["OV_CNACGH_CGH_hg_244a-20160128"]] character(0)
[["OV_CNACGH_CGH_hg_415k_g4124a-20160128"]] character(0)
[["OV_CNASNP-20160128"]] character(0)
[["OV_CNVSNP-20160128"]] character(0)
[["OV_GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["OV_GISTIC_Peaks-20160128"]] chr1:26963410-27570286 ...
[["OV_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["OV_miRNAArray-20160128"]] DarkCorner dmr_285 ... NegativeControl SCorner3
[["OV_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["OV_mRNAArray_huex-20160128"]] C9orf152 ELM02 RPS11 ... SLC39A6 CTSC AQP7
...
<9 more elements>

```

```
> colnames( OV )
```

```
CharacterList of length 19
```

```

[["OV_CNACGH_CGH_hg_244a-20160128"]] TCGA-04-1331-01A-01D-0431-02 ...
[["OV_CNACGH_CGH_hg_415k_g4124a-20160128"]] TCGA-04-1353-01A-01D-1046-02 ...
[["OV_CNASNP-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_CNVSNP-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_GISTIC_AllByGene-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_GISTIC_Peaks-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_GISTIC_ThresholdedByGene-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_miRNAArray-20160128"]] TCGA-04-1331-01A-01T-0438-07 ...
[["OV_miRNASeqGene-20160128"]] TCGA-04-1331-01A-01R-1569-13 ...
[["OV_mRNAArray_huex-20160128"]] TCGA-04-1331-01A-01R-0435-03 ...
...
<9 more elements>

```

```
Sizes of each ExperimentList element:
```

		assay	size.Mb
1		OV_CNACGH_CGH_hg_244a-20160128	3.6 Mb
2	OV_CNACGH_CGH_hg_415k_g4124a-20160128		6.8 Mb
3		OV_CNASNP-20160128	24.6 Mb
4		OV_CNVSNP-20160128	7.3 Mb
5		OV_GISTIC_AllByGene-20160128	4.9 Mb
6		OV_GISTIC_Peaks-20160128	0.1 Mb
7	OV_GISTIC_ThresholdedByGene-20160128		4.9 Mb
8		OV_miRNAArray-20160128	0.1 Mb
9		OV_miRNASeqGene-20160128	0.1 Mb
10		OV_mRNAArray_huex-20160128	1.2 Mb
11	OV_mRNAArray_TX_g4502a_1-20160128		1.2 Mb
12	OV_mRNAArray_TX_g4502a-20160128		1.1 Mb
13	OV_mRNAArray_TX_ht_hg_u133a-20160128		0.8 Mb
14		OV_Mutation-20160128	10.3 Mb
15		OV_RNASeq2GeneNorm-20160128	1.3 Mb
16		OV_RNASeqGene-20160128	1.3 Mb
17		OV_RPPAArray-20160128	0.1 Mb
18	OV_Methylation_methyl27-20160128		4.9 Mb
19	OV_Methylation_methyl450-20160128		75 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

Call: survfit(formula = survival::Surv(colDat\$days\_to\_death/365, colDat\$vital\_status) ~  
-1)

247 observations deleted due to missingness  
n events median 0.95LCL 0.95UCL  
343.00 343.00 2.94 2.76 3.17

-----  
Available sample meta-data:  
-----

years\_to\_birth:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
26.00 51.00 59.00 59.78 69.00 89.00 21

vital\_status:  
0 1  
246 344

days\_to\_death:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
8.0 567.5 1073.0 1147.4 1557.0 4624.0 247



```

days_to_last_followup:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
    16   266   842   1216   1931   5481   358

tumor_tissue_site:
      omentum          ovary peritoneum ovary          NA's
           3             575             2             10

gender:
female  NA's
  580    10

date_of_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
 1992   2001   2004   2004   2007   2013   10

radiation_therapy:
  no  yes  NA's
 556   5   29

karnofsky_performance_score:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
 40.00  60.00  80.00  75.83  80.00  100.00  506

histological_type:
serous cystadenocarcinoma          NA's
                          580             10

residual_tumor:
  r0  r1  r2  rx  NA's
  15  31  5   3  536

ethnicity:
  hispanic or latino not hispanic or latino          NA's
                          11             338             241

```

Including an additional 2869 columns

**See Also**

[OV-v2.0.1](#)

**Description**

A document describing the TCGA cancer code

**Details**

```
> experiments( OV )
ExperimentList class object of length 19:
 [1] OV_CNACGH_CGH_hg_244a-20160128: RaggedExperiment with 128946 rows and 472 columns
 [2] OV_CNACGH_CGH_hg_415k_g4124a-20160128: RaggedExperiment with 245847 rows and 674 columns
 [3] OV_CNASNP-20160128: RaggedExperiment with 907765 rows and 1145 columns
 [4] OV_CNVSNP-20160128: RaggedExperiment with 261680 rows and 1141 columns
 [5] OV_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 573 columns
 [6] OV_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 70 rows and 573 columns
 [7] OV_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 573 columns
 [8] OV_miRNAArray-20160128: SummarizedExperiment with 821 rows and 573 columns
 [9] OV_miRNASeqGene-20160128: SummarizedExperiment with 705 rows and 461 columns
 [10] OV_mRNAArray_huex-20160128: SummarizedExperiment with 18632 rows and 575 columns
 [11] OV_mRNAArray_TX_g4502a-20160128: SummarizedExperiment with 17814 rows and 577 columns
 [12] OV_mRNAArray_TX_ht_hg_u133a-20160128: SummarizedExperiment with 12042 rows and 524 columns
 [13] OV_Mutation-20160128: RaggedExperiment with 20219 rows and 316 columns
 [14] OV_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 307 columns
 [15] OV_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 307 columns
 [16] OV_RNASeqGene-20160128: SummarizedExperiment with 19990 rows and 299 columns
 [17] OV_RPPAArray-20160128: SummarizedExperiment with 208 rows and 427 columns
 [18] OV_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 591 columns
 [19] OV_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 10 columns

> rownames( OV )
CharacterList of length 19
[["OV_CNACGH_CGH_hg_244a-20160128"]] character(0)
[["OV_CNACGH_CGH_hg_415k_g4124a-20160128"]] character(0)
[["OV_CNASNP-20160128"]] character(0)
[["OV_CNVSNP-20160128"]] character(0)
[["OV_GISTIC_AllByGene-20160128"]] character(0)
[["OV_GISTIC_Peaks-20160128"]] 34 1 2 35 3 36 4 37 ... 70 28 29 30 71 31 72
[["OV_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["OV_miRNAArray-20160128"]] DarkCorner dmr_285 ... NegativeControl SCorner3
[["OV_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["OV_mRNAArray_huex-20160128"]] C9orf152 ELM02 RPS11 ... SLC39A6 CTSC AQP7
...
<9 more elements>

> colnames( OV )
CharacterList of length 19
[["OV_CNACGH_CGH_hg_244a-20160128"]] TCGA-04-1331-01A-01D-0431-02 ...
[["OV_CNACGH_CGH_hg_415k_g4124a-20160128"]] TCGA-04-1353-01A-01D-1046-02 ...
[["OV_CNASNP-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_CNVSNP-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
```

```

[["OV_GISTIC_AllByGene-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_GISTIC_Peaks-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_GISTIC_ThresholdedByGene-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_miRNAArray-20160128"]] TCGA-04-1331-01A-01T-0438-07 ...
[["OV_miRNASeqGene-20160128"]] TCGA-04-1331-01A-01R-1569-13 ...
[["OV_mRNAArray_huex-20160128"]] TCGA-04-1331-01A-01R-0435-03 ...
...
<9 more elements>

```

Sizes of each ExperimentList element:

	assay	size.Mb
1	OV_CNACGH_CGH_hg_244a-20160128	3.6 Mb
2	OV_CNACGH_CGH_hg_415k_g4124a-20160128	6.8 Mb
3	OV_CNASNP-20160128	24.6 Mb
4	OV_CNVSNP-20160128	7.3 Mb
5	OV_GISTIC_AllByGene-20160128	112 Mb
6	OV_GISTIC_Peaks-20160128	0.5 Mb
7	OV_GISTIC_ThresholdedByGene-20160128	111.7 Mb
8	OV_miRNAArray-20160128	3.8 Mb
9	OV_miRNASeqGene-20160128	2.7 Mb
10	OV_mRNAArray_huex-20160128	84.2 Mb
11	OV_mRNAArray_TX_g4502a-20160128	80.7 Mb
12	OV_mRNAArray_TX_ht_hg_u133a-20160128	49.7 Mb
13	OV_Mutation-20160128	10.3 Mb
14	OV_RNASeq2Gene-20160128	50.6 Mb
15	OV_RNASeq2GeneNorm-20160128	50.6 Mb
16	OV_RNASeqGene-20160128	48.1 Mb
17	OV_RPPAArray-20160128	0.8 Mb
18	OV_Methylation_methyl27-20160128	4.9 Mb
19	OV_Methylation_methyl450-20160128	75 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

247 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
343.00 343.00   2.94   2.76   3.17

```

-----  
Available sample meta-data:  
-----

years\_to\_birth:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
26.00	51.00	59.00	59.78	69.00	89.00	21

vital\_status:

0	1
246	344

days\_to\_death:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
8.0	567.5	1073.0	1147.4	1557.0	4624.0	247

days\_to\_last\_followup:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
16	266	842	1216	1931	5481	358

tumor\_tissue\_site:

omentum	ovary	peritoneum	ovary	NA's
3	575		2	10

gender:

female	NA's
580	10

date\_of\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1992	2001	2004	2004	2007	2013	10

radiation\_therapy:

no	yes	NA's
556	5	29

karnofsky\_performance\_score:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
40.00	60.00	80.00	75.83	80.00	100.00	506

histological\_type:

serous cystadenocarcinoma	NA's
580	10

residual\_tumor:

r0	r1	r2	rx	NA's
15	31	5	3	536

ethnicity:

hispanic or latino	not hispanic or latino	NA's
11	338	241

Including an additional 2869 columns

---

OV-v2.1.0

*Ovarian serous cystadenocarcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

```
> experiments( OV )
ExperimentList class object of length 19:
 [1] OV_CNACGH_CGH_hg_244a-20160128: RaggedExperiment with 128946 rows and 472 columns
 [2] OV_CNACGH_CGH_hg_415k_g4124a-20160128: RaggedExperiment with 245847 rows and 674 columns
 [3] OV_CNASNP-20160128: RaggedExperiment with 907765 rows and 1145 columns
 [4] OV_CNVSNP-20160128: RaggedExperiment with 261680 rows and 1141 columns
 [5] OV_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 573 columns
 [6] OV_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 70 rows and 573 columns
 [7] OV_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 573 columns
 [8] OV_miRNAArray-20160128: SummarizedExperiment with 821 rows and 573 columns
 [9] OV_mRNAArray_huex-20160128: SummarizedExperiment with 18632 rows and 575 columns
 [10] OV_mRNAArray_TX_g4502a-20160128: SummarizedExperiment with 17814 rows and 577 columns
 [11] OV_mRNAArray_TX_ht_hg_u133a-20160128: SummarizedExperiment with 12042 rows and 524 columns
 [12] OV_Mutation-20160128: RaggedExperiment with 20219 rows and 316 columns
 [13] OV_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 307 columns
 [14] OV_RNASeqGene-20160128: SummarizedExperiment with 19990 rows and 299 columns
 [15] OV_RPPAArray-20160128: SummarizedExperiment with 208 rows and 427 columns
 [16] OV_miRNASeqGene-20160128: SummarizedExperiment with 705 rows and 461 columns
 [17] OV_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18571 rows and 307 columns
 [18] OV_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 591 columns
 [19] OV_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 10 columns

> rownames( OV )
CharacterList of length 19
[["OV_CNACGH_CGH_hg_244a-20160128"]] character(0)
[["OV_CNACGH_CGH_hg_415k_g4124a-20160128"]] character(0)
[["OV_CNASNP-20160128"]] character(0)
[["OV_CNVSNP-20160128"]] character(0)
[["OV_GISTIC_AllByGene-20160128"]] character(0)
[["OV_GISTIC_Peaks-20160128"]] 34 1 2 35 3 36 4 37 ... 70 28 29 30 71 31 72
[["OV_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["OV_miRNAArray-20160128"]] DarkCorner dmr_285 ... NegativeControl SCorner3
[["OV_mRNAArray_huex-20160128"]] C9orf152 ELM02 RPS11 ... SLC39A6 CTSC AQP7
[["OV_mRNAArray_TX_g4502a-20160128"]] ELM02 CREB3L1 RPS11 ... AQP7 CTSC
...
<9 more elements>
```

```
> colnames( OV )
CharacterList of length 19
[["OV_CNACGH_CGH_hg_244a-20160128"]] TCGA-04-1331-01A-01D-0431-02 ...
[["OV_CNACGH_CGH_hg_415k_g4124a-20160128"]] TCGA-04-1353-01A-01D-1046-02 ...
[["OV_CNASNP-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_CNVSNP-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_GISTIC_AllByGene-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_GISTIC_Peaks-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_GISTIC_ThresholdedByGene-20160128"]] TCGA-04-1331-01A-01D-0428-01 ...
[["OV_miRNAArray-20160128"]] TCGA-04-1331-01A-01T-0438-07 ...
[["OV_mRNAArray_huex-20160128"]] TCGA-04-1331-01A-01R-0435-03 ...
[["OV_mRNAArray_TX_g4502a-20160128"]] TCGA-09-0364-01A-02R-0363-07 ...
...
<9 more elements>
```

Sizes of each ExperimentList element:

	assay	size.Mb
1	OV_CNACGH_CGH_hg_244a-20160128	3.6 Mb
2	OV_CNACGH_CGH_hg_415k_g4124a-20160128	6.8 Mb
3	OV_CNASNP-20160128	24.6 Mb
4	OV_CNVSNP-20160128	7.3 Mb
5	OV_GISTIC_AllByGene-20160128	112 Mb
6	OV_GISTIC_Peaks-20160128	0.5 Mb
7	OV_GISTIC_ThresholdedByGene-20160128	111.7 Mb
8	OV_miRNAArray-20160128	3.8 Mb
9	OV_mRNAArray_huex-20160128	84.2 Mb
10	OV_mRNAArray_TX_g4502a-20160128	80.7 Mb
11	OV_mRNAArray_TX_ht_hg_u133a-20160128	49.7 Mb
12	OV_Mutation-20160128	10.3 Mb
13	OV_RNASeq2Gene-20160128	50.6 Mb
14	OV_RNASeqGene-20160128	48.1 Mb
15	OV_RPPAArray-20160128	0.8 Mb
16	OV_miRNASeqGene-20160128	2.7 Mb
17	OV_RNASeq2GeneNorm-20160128	45.8 Mb
18	OV_Methylation_methyl27-20160128	4.9 Mb
19	OV_Methylation_methyl450-20160128	75 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```
Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)
```

```
247 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
```

[1,] 343 343 2.94 2.76 3.17

-----  
 Available sample meta-data:  
 -----

years\_to\_birth:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
26.00	51.00	59.00	59.78	69.00	89.00	21

vital\_status:

0	1
246	344

days\_to\_death:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
8.0	567.5	1073.0	1147.4	1557.0	4624.0	247

days\_to\_last\_followup:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
16	266	842	1216	1931	5481	358

tumor\_tissue\_site:

omentum	ovary	peritoneum	ovary	NA's
3	575		2	10

gender:

female	NA's
580	10

date\_of\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1992	2001	2004	2004	2007	2013	10

radiation\_therapy:

no	yes	NA's
556	5	29

karnofsky\_performance\_score:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
40.00	60.00	80.00	75.83	80.00	100.00	506

histological\_type:

serous cystadenocarcinoma	NA's
580	10

residual\_tumor:

```
r0  r1  r2  rx NA's
15  31  5   3  536
```

```
ethnicity:
  hispanic or latino not hispanic or latino      NA's
                11                338                241
```

Including an additional 2869 columns

---

OV-v2.1.1

*Ovarian serous cystadenocarcinoma*

---

### Description

A document describing the TCGA cancer code Note. Only the colData has changed.

### Details

```
> experiments( OV )
ExperimentList class object of length 0:
```

```
> rownames( OV )
CharacterList of length 0
```

```
> colnames( OV )
CharacterList of length 0
```

Sizes of each ExperimentList element:

```
[1] assay  size.Mb
<0 rows> (or 0-length row.names)
```

```
-----
Overall survival time-to-event summary (in years):
-----
```

```
Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)
```

```
249 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
[1,] 343 343 2.94 2.76 3.17
```

```
-----
Available sample meta-data:
-----
```



```

years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
  26.00  51.00   59.00   59.78  68.75   89.00   22

vital_status:
  0    1 NA's
  247 344   1

days_to_death:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
  8.0   567.5  1073.0  1147.4  1557.0  4624.0  249

days_to_last_followup:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
  16    268    837    1214   1919   5481   359

tumor_tissue_site:
      omentum          ovary peritoneum ovary      NA's
      3             576             2             11

gender:
female  NA's
  581    11

date_of_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
  1992   2001   2004   2004   2007   2013   11

radiation_therapy:
  no  yes NA's
  557  5  30

karnofsky_performance_score:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.   NA's
  40.00  60.00   80.00   75.83  80.00  100.00  508

histological_type:
serous cystadenocarcinoma      NA's
      581             11

residual_tumor:
  r0  r1  r2  rx NA's
  16  31  5   3  537

ethnicity:
  hispanic or latino not hispanic or latino      NA's
      11             338             243

```

Including an additional 2850 columns

---

PAAD

*Pancreatic adenocarcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

```
> experiments( PAAD )
ExperimentList class object of length 10:
 [1] PAAD_CNASNP-20160128: RaggedExperiment with 203871 rows and 368 columns
 [2] PAAD_CNVSNP-20160128: RaggedExperiment with 34808 rows and 365 columns
 [3] PAAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [4] PAAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 52 rows and 184 columns
 [5] PAAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [6] PAAD_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 183 columns
 [7] PAAD_Mutation-20160128: RaggedExperiment with 30357 rows and 150 columns
 [8] PAAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 183 columns
 [9] PAAD_RPPAArray-20160128: SummarizedExperiment with 195 rows and 123 columns
 [10] PAAD_Methylation-20160128: SummarizedExperiment with 485577 rows and 195 columns

> rownames( PAAD )
CharacterList of length 10
[["PAAD_CNASNP-20160128"]] character(0)
[["PAAD_CNVSNP-20160128"]] character(0)
[["PAAD_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["PAAD_GISTIC_Peaks-20160128"]] chr1:26795113-27650365 ...
[["PAAD_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["PAAD_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["PAAD_Mutation-20160128"]] character(0)
[["PAAD_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["PAAD_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["PAAD_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873

> colnames( PAAD )
CharacterList of length 10
[["PAAD_CNASNP-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_CNVSNP-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_GISTIC_AllByGene-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_GISTIC_Peaks-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_miRNASeqGene-20160128"]] TCGA-2J-AAB1-01A-11R-A41G-13 ...
[["PAAD_Mutation-20160128"]] TCGA-2J-AAB1-01A-11D-A40W-08 ...
```

```

[["PAAD_RNASeq2GeneNorm-20160128"]] TCGA-2J-AAB1-01A-11R-A41B-07 ...
[["PAAD_RPPAArray-20160128"]] TCGA-2J-AAB4-01A-21-A43K-20 ...
[["PAAD_Methylation-20160128"]] TCGA-2J-AAB1-01A-11D-A40Y-05 ...

```

Sizes of each ExperimentList element:

		assay	size.Mb
1		PAAD_CNASNP-20160128	5.6 Mb
2		PAAD_CNVSNP-20160128	1 Mb
3		PAAD_GISTIC_AllByGene-20160128	4.9 Mb
4		PAAD_GISTIC_Peaks-20160128	0.1 Mb
5		PAAD_GISTIC_ThresholdedByGene-20160128	4.9 Mb
6		PAAD_miRNASeqGene-20160128	0.1 Mb
7		PAAD_Mutation-20160128	111 Mb
8		PAAD_RNASeq2GeneNorm-20160128	1.3 Mb
9		PAAD_RPPAArray-20160128	0 Mb
10		PAAD_Methylation-20160128	75 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

85 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
100.000 100.000 1.079 0.967 1.315

```

-----  
Available sample meta-data:  
-----

years\_to\_birth:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
35.00	57.00	65.00	64.86	73.00	88.00

vital\_status:

```

0 1
85 100

```

days\_to\_death:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
12.0	228.5	394.0	459.5	596.5	2182.0	85

days\_to\_last\_followup:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
------	---------	--------	------	---------	------	------

0.0 338.0 517.0 692.4 951.0 2741.0 100

tumor\_tissue\_site:

pancreas

185

pathology\_N\_stage:

n0 n1 n1b nx NA's

50 126 4 4 1

pathology\_M\_stage:

m0 m1 mx

85 5 95

gender:

female male

83 102

date\_of\_initial\_pathologic\_diagnosis:

Min. 1st Qu. Median Mean 3rd Qu. Max. NA's

2001 2010 2012 2011 2012 2013 1

radiation\_therapy:

no yes NA's

125 45 15

histological\_type:

pancreas-adenocarcinoma ductal type

154

pancreas-adenocarcinoma-other subtype

25

pancreas-colloid (mucinous non-cystic) carcinoma

4

pancreas-undifferentiated carcinoma

1

NA's

1

number\_pack\_years\_smoked:

Min. 1st Qu. Median Mean 3rd Qu. Max. NA's

0.30 15.00 25.00 26.84 40.00 75.00 128

year\_of\_tobacco\_smoking\_onset:

Min. 1st Qu. Median Mean 3rd Qu. Max. NA's

1948 1960 1971 1971 1982 1993 138

residual\_tumor:

r0	r1	r2	rx	NA's
111	53	5	4	12

number\_of\_lymph\_nodes:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.000	0.000	2.000	2.989	4.000	16.000	4

race:

asian	black or african american	white
11	7	162
NA's		
5		

ethnicity:

hispanic or latino	not hispanic or latino	NA's
5	137	43

Including an additional 960 columns

### See Also

[PAAD-v2.0.1](#)

---

PAAD-v2.0.1

*Pancreatic adenocarcinoma*

---

### Description

A document describing the TCGA cancer code

### Details

```
> experiments( PAAD )
ExperimentList class object of length 11:
 [1] PAAD_CNASNP-20160128: RaggedExperiment with 203871 rows and 368 columns
 [2] PAAD_CNVSNP-20160128: RaggedExperiment with 34808 rows and 365 columns
 [3] PAAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [4] PAAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 52 rows and 184 columns
 [5] PAAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [6] PAAD_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 183 columns
 [7] PAAD_Mutation-20160128: RaggedExperiment with 30357 rows and 150 columns
 [8] PAAD_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 183 columns
 [9] PAAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 183 columns
 [10] PAAD_RPPAArray-20160128: SummarizedExperiment with 195 rows and 123 columns
 [11] PAAD_Methylation-20160128: SummarizedExperiment with 485577 rows and 195 columns
```

```

> rownames( PAAD )
CharacterList of length 11
[["PAAD_CNASNP-20160128"]] character(0)
[["PAAD_CNVSNP-20160128"]] character(0)
[["PAAD_GISTIC_AllByGene-20160128"]] character(0)
[["PAAD_GISTIC_Peaks-20160128"]] 24 1 2 3 25 4 26 5 ... 49 50 21 51 22 52 53
[["PAAD_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["PAAD_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["PAAD_Mutation-20160128"]] character(0)
[["PAAD_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["PAAD_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["PAAD_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<1 more element>

```

```

> colnames( PAAD )
CharacterList of length 11
[["PAAD_CNASNP-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_CNVSNP-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_GISTIC_AllByGene-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_GISTIC_Peaks-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_miRNASeqGene-20160128"]] TCGA-2J-AAB1-01A-11R-A41G-13 ...
[["PAAD_Mutation-20160128"]] TCGA-2J-AAB1-01A-11D-A40W-08 ...
[["PAAD_RNASeq2Gene-20160128"]] TCGA-2J-AAB1-01A-11R-A41B-07 ...
[["PAAD_RNASeq2GeneNorm-20160128"]] TCGA-2J-AAB1-01A-11R-A41B-07 ...
[["PAAD_RPPAArray-20160128"]] TCGA-2J-AAB4-01A-21-A43K-20 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

		assay size.Mb
1	PAAD_CNASNP-20160128	5.6 Mb
2	PAAD_CNVSNP-20160128	1 Mb
3	PAAD_GISTIC_AllByGene-20160128	38.3 Mb
4	PAAD_GISTIC_Peaks-20160128	0.2 Mb
5	PAAD_GISTIC_ThresholdedByGene-20160128	38.1 Mb
6	PAAD_miRNASeqGene-20160128	1.6 Mb
7	PAAD_Mutation-20160128	111 Mb
8	PAAD_RNASeq2Gene-20160128	31.2 Mb
9	PAAD_RNASeq2GeneNorm-20160128	31.2 Mb
10	PAAD_RPPAArray-20160128	0.2 Mb
11	PAAD_Methylation-20160128	75 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

Call: survfit(formula = survival::Surv(colDat\$days\_to\_death/365, colDat\$vital\_status) ~  
-1)

85 observations deleted due to missingness  
n events median 0.95LCL 0.95UCL  
100.000 100.000 1.079 0.967 1.315

-----  
Available sample meta-data:  
-----

years\_to\_birth:  
Min. 1st Qu. Median Mean 3rd Qu. Max.  
35.00 57.00 65.00 64.86 73.00 88.00

vital\_status:  
0 1  
85 100

days\_to\_death:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
12.0 228.5 394.0 459.5 596.5 2182.0 85

days\_to\_last\_followup:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
0.0 338.0 517.0 692.4 951.0 2741.0 100

tumor\_tissue\_site:  
pancreas  
185

pathology\_N\_stage:  
n0 n1 n1b nx NA's  
50 126 4 4 1

pathology\_M\_stage:  
m0 m1 mx  
85 5 95

gender:  
female male  
83 102

date\_of\_initial\_pathologic\_diagnosis:

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
	2001	2010	2012	2011	2012	2013	
							1
radiation_therapy:							
no	yes	NA's					
125	45	15					
histological_type:							
pancreas-adenocarcinoma ductal type							154
pancreas-adenocarcinoma-other subtype							25
pancreas-colloid (mucinous non-cystic) carcinoma							4
pancreas-undifferentiated carcinoma							1
							NA's
							1
number_pack_years_smoked:							
	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
	0.30	15.00	25.00	26.84	40.00	75.00	128
year_of_tobacco_smoking_onset:							
	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
	1948	1960	1971	1971	1982	1993	138
residual_tumor:							
r0	r1	r2	rx	NA's			
111	53	5	4	12			
number_of_lymph_nodes:							
	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
	0.000	0.000	2.000	2.989	4.000	16.000	4
race:							
asian black or african american							white
11							7
NA's							162
5							
ethnicity:							
hispanic or latino not hispanic or latino							NA's
5							137
							43

Including an additional 960 columns



PAAD-v2.1.0

*Pancreatic adenocarcinoma***Description**

A document describing the TCGA cancer code

**Details**

```

> experiments( PAAD )
ExperimentList class object of length 11:
 [1] PAAD_CNASNP-20160128: RaggedExperiment with 203871 rows and 368 columns
 [2] PAAD_CNVSNP-20160128: RaggedExperiment with 34808 rows and 365 columns
 [3] PAAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [4] PAAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 52 rows and 184 columns
 [5] PAAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 184 columns
 [6] PAAD_Mutation-20160128: RaggedExperiment with 30357 rows and 150 columns
 [7] PAAD_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 183 columns
 [8] PAAD_RPPAArray-20160128: SummarizedExperiment with 195 rows and 123 columns
 [9] PAAD_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 183 columns
[10] PAAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18465 rows and 183 columns
[11] PAAD_Methylation-20160128: SummarizedExperiment with 485577 rows and 195 columns

> rownames( PAAD )
CharacterList of length 11
[["PAAD_CNASNP-20160128"]] character(0)
[["PAAD_CNVSNP-20160128"]] character(0)
[["PAAD_GISTIC_AllByGene-20160128"]] character(0)
[["PAAD_GISTIC_Peaks-20160128"]] 24 1 2 3 25 4 26 5 ... 49 50 21 51 22 52 53
[["PAAD_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["PAAD_Mutation-20160128"]] character(0)
[["PAAD_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["PAAD_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["PAAD_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["PAAD_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZEF1 ZZZ3 psiTPTE22
...
<1 more element>

> colnames( PAAD )
CharacterList of length 11
[["PAAD_CNASNP-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_CNVSNP-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_GISTIC_AllByGene-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_GISTIC_Peaks-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["PAAD_Mutation-20160128"]] TCGA-2J-AAB1-01A-11D-A40W-08 ...
[["PAAD_RNASeq2Gene-20160128"]] TCGA-2J-AAB1-01A-11R-A41B-07 ...

```

```

[["PAAD_RPPAArray-20160128"]] TCGA-2J-AAB4-01A-21-A43K-20 ...
[["PAAD_miRNASeqGene-20160128"]] TCGA-2J-AAB1-01A-11R-A41G-13 ...
[["PAAD_RNASeq2GeneNorm-20160128"]] TCGA-2J-AAB1-01 ... TCGA-Z5-AAPL-01
...
<1 more element>

```

Sizes of each ExperimentList element:

		assay	size.Mb
1	PAAD_CNASNP-20160128	5.6	Mb
2	PAAD_CNVSNP-20160128	1	Mb
3	PAAD_GISTIC_AllByGene-20160128	38.3	Mb
4	PAAD_GISTIC_Peaks-20160128	0.2	Mb
5	PAAD_GISTIC_ThresholdedByGene-20160128	38.1	Mb
6	PAAD_Mutation-20160128	111	Mb
7	PAAD_RNASeq2Gene-20160128	31.2	Mb
8	PAAD_RPPAArray-20160128	0.2	Mb
9	PAAD_miRNASeqGene-20160128	1.6	Mb
10	PAAD_RNASeq2GeneNorm-20160128	28.1	Mb
11	PAAD_Methylation-20160128	75	Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

      85 observations deleted due to missingness
      n events median 0.95LCL 0.95UCL
[1,] 100    100    1.08    0.967    1.32

```

-----  
Available sample meta-data:  
-----

```

years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 35.00  57.00   65.00   64.86  73.00   88.00

```

```

vital_status:
 0    1
85 100

```

```

days_to_death:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
 12.0   228.5   394.0   459.5  596.5  2182.0    85

```

days\_to\_last\_followup:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 0.0 338.0 517.0 692.4 951.0 2741.0 100

tumor\_tissue\_site:  
 pancreas  
 185

pathology\_N\_stage:  
 n0 n1 n1b nx NA's  
 50 126 4 4 1

pathology\_M\_stage:  
 m0 m1 mx  
 85 5 95

gender:  
 female male  
 83 102

date\_of\_initial\_pathologic\_diagnosis:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 2001 2010 2012 2011 2012 2013 1

radiation\_therapy:  
 no yes NA's  
 125 45 15

histological\_type:  
 pancreas-adenocarcinoma ductal type  
 154  
 pancreas-adenocarcinoma-other subtype  
 25  
 pancreas-colloid (mucinous non-cystic) carcinoma  
 4  
 pancreas-undifferentiated carcinoma  
 1  
 NA's  
 1

number\_pack\_years\_smoked:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 0.30 15.00 25.00 26.84 40.00 75.00 128

year\_of\_tobacco\_smoking\_onset:

```

      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
      1948   1960   1971   1971   1982   1993   138

residual_tumor:
  r0  r1  r2  rx NA's
 111  53   5   4  12

number_of_lymph_nodes:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
 0.000  0.000  2.000  2.989  4.000 16.000    4

race:
              asian black or african american              white
              11              7              162
              NA's
              5

ethnicity:
  hispanic or latino not hispanic or latino              NA's
              5              137              43

Including an additional 960 columns

```

---

PCPG

*Pheochromocytoma and Paraganglioma*


---

## Description

A document describing the TCGA cancer code

## Details

```

> experiments( PCPG )
ExperimentList class object of length 10:
 [1] PCPG_CNASNP-20160128: RaggedExperiment with 297329 rows and 360 columns
 [2] PCPG_CNVSNP-20160128: RaggedExperiment with 31256 rows and 346 columns
 [3] PCPG_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 162 columns
 [4] PCPG_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 27 rows and 162 columns
 [5] PCPG_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 162 columns
 [6] PCPG_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 187 columns
 [7] PCPG_Mutation-20160128: RaggedExperiment with 4662 rows and 184 columns
 [8] PCPG_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 187 columns
 [9] PCPG_RPPAArray-20160128: SummarizedExperiment with 192 rows and 82 columns
[10] PCPG_Methylation-20160128: SummarizedExperiment with 485577 rows and 187 columns

> rownames( PCPG )
CharacterList of length 10

```

```

[["PCPG_CNASNP-20160128"]] character(0)
[["PCPG_CNVSNP-20160128"]] character(0)
[["PCPG_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["PCPG_GISTIC_Peaks-20160128"]] chr1:117751737-118152240 ...
[["PCPG_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["PCPG_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["PCPG_Mutation-20160128"]] character(0)
[["PCPG_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["PCPG_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["PCPG_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873

```

```

> colnames( PCPG )
CharacterList of length 10
[["PCPG_CNASNP-20160128"]] TCGA-P7-A5NX-10A-01D-A35A-01 ...
[["PCPG_CNVSNP-20160128"]] TCGA-P7-A5NX-10A-01D-A35A-01 ...
[["PCPG_GISTIC_AllByGene-20160128"]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[["PCPG_GISTIC_Peaks-20160128"]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[["PCPG_GISTIC_ThresholdedByGene-20160128"]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[["PCPG_miRNASeqGene-20160128"]] TCGA-P7-A5NX-01A-11R-A35M-13 ...
[["PCPG_Mutation-20160128"]] TCGA-P7-A5NX-01A-11D-A35D-08 ...
[["PCPG_RNASeq2GeneNorm-20160128"]] TCGA-P7-A5NX-01A-11R-A35K-07 ...
[["PCPG_RPPAArray-20160128"]] TCGA-P7-A5NX-01A-21-A43B-20 ...
[["PCPG_Methylation-20160128"]] TCGA-P7-A5NX-01A-11D-A35E-05 ...

```

Sizes of each ExperimentList element:

		assay size.Mb
1	PCPG_CNASNP-20160128	8.1 Mb
2	PCPG_CNVSNP-20160128	0.9 Mb
3	PCPG_GISTIC_AllByGene-20160128	4.9 Mb
4	PCPG_GISTIC_Peaks-20160128	0 Mb
5	PCPG_GISTIC_ThresholdedByGene-20160128	4.9 Mb
6	PCPG_miRNASeqGene-20160128	0.1 Mb
7	PCPG_Mutation-20160128	8.4 Mb
8	PCPG_RNASeq2GeneNorm-20160128	1.3 Mb
9	PCPG_RPPAArray-20160128	0 Mb
10	PCPG_Methylation-20160128	75 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

173 observations deleted due to missingness
  n  events  median 0.95LCL 0.95UCL
6.00  6.00  1.24  0.26  NA

```

```

-----
Available sample meta-data:
-----

years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
  19.00  35.00  46.00  47.33  58.50  83.00

vital_status:
  0  1
173 6

days_to_death:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.  NA's
  88.0  148.5  452.5  901.0  715.2  3563.0  173

days_to_last_followup:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.  NA's
  2  352  766  1071  1301  9634  6

tumor_tissue_site:
      adrenal gland extra-adrenal site
              147              32

gender:
female  male
  101    78

date_of_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
  1988  2009  2011  2010  2012  2013

radiation_therapy:
  no  yes  NA's
  172  5  2

karnofsky_performance_score:
  70  80  90  100  NA's
  1  2  13  46  117

histological_type:
                                paraganglioma
                                18
paraganglioma; extra-adrenal pheochromocytoma
                                13
                                pheochromocytoma

```

148

```

number_of_lymph_nodes:
  0   1   2  13 NA's
 16  3   1   1 158

race:
american indian or alaska native          asian
                                   1           6
      black or african american          white
                                   20          148
                                   NA's
                                   4

ethnicity:
  hispanic or latino not hispanic or latino  NA's
                                   5           138          36

```

Including an additional 894 columns

### See Also

[PCPG-v2.0.1](#)

---

PCPG-v2.0.1

*Pheochromocytoma and Paraganglioma*

---

### Description

A document describing the TCGA cancer code

### Details

```

> experiments( PCPG )
ExperimentList class object of length 11:
 [1] PCPG_CNASNP-20160128: RaggedExperiment with 297329 rows and 360 columns
 [2] PCPG_CNVSNP-20160128: RaggedExperiment with 31256 rows and 346 columns
 [3] PCPG_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 162 columns
 [4] PCPG_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 27 rows and 162 columns
 [5] PCPG_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 162 columns
 [6] PCPG_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 187 columns
 [7] PCPG_Mutation-20160128: RaggedExperiment with 4662 rows and 184 columns
 [8] PCPG_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 187 columns
 [9] PCPG_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 187 columns
[10] PCPG_RPPAArray-20160128: SummarizedExperiment with 192 rows and 82 columns
[11] PCPG_Methylation-20160128: SummarizedExperiment with 485577 rows and 187 columns

```

```

> rownames( PCPG )
CharacterList of length 11
[["PCPG_CNASNP-20160128"]] character(0)
[["PCPG_CNVSNP-20160128"]] character(0)
[["PCPG_GISTIC_AllByGene-20160128"]] character(0)
[["PCPG_GISTIC_Peaks-20160128"]] 7 1 8 9 10 11 2 12 ... 22 23 5 24 25 26 6 27
[["PCPG_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["PCPG_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["PCPG_Mutation-20160128"]] character(0)
[["PCPG_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["PCPG_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["PCPG_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<1 more element>

```

```

> colnames( PCPG )
CharacterList of length 11
[["PCPG_CNASNP-20160128"]] TCGA-P7-A5NX-10A-01D-A35A-01 ...
[["PCPG_CNVSNP-20160128"]] TCGA-P7-A5NX-10A-01D-A35A-01 ...
[["PCPG_GISTIC_AllByGene-20160128"]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[["PCPG_GISTIC_Peaks-20160128"]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[["PCPG_GISTIC_ThresholdedByGene-20160128"]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[["PCPG_miRNASeqGene-20160128"]] TCGA-P7-A5NX-01A-11R-A35M-13 ...
[["PCPG_Mutation-20160128"]] TCGA-P7-A5NX-01A-11D-A35D-08 ...
[["PCPG_RNASeq2Gene-20160128"]] TCGA-P7-A5NX-01A-11R-A35K-07 ...
[["PCPG_RNASeq2GeneNorm-20160128"]] TCGA-P7-A5NX-01A-11R-A35K-07 ...
[["PCPG_RPPAArray-20160128"]] TCGA-P7-A5NX-01A-21-A43B-20 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

		assay size.Mb
1	PCPG_CNASNP-20160128	8.1 Mb
2	PCPG_CNVSNP-20160128	0.9 Mb
3	PCPG_GISTIC_AllByGene-20160128	34.1 Mb
4	PCPG_GISTIC_Peaks-20160128	0.1 Mb
5	PCPG_GISTIC_ThresholdedByGene-20160128	34 Mb
6	PCPG_miRNASeqGene-20160128	1.7 Mb
7	PCPG_Mutation-20160128	8.4 Mb
8	PCPG_RNASeq2Gene-20160128	31.8 Mb
9	PCPG_RNASeq2GeneNorm-20160128	31.8 Mb
10	PCPG_RPPAArray-20160128	0.2 Mb
11	PCPG_Methylation-20160128	75 Mb

-----  
Overall survival time-to-event summary (in years):  
-----



```
Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)
```

```
173 observations deleted due to missingness
  n events median 0.95LCL 0.95UCL
6.00  6.00  1.24  0.26    NA
```

```
-----
Available sample meta-data:
-----
```

```
years_to_birth:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
19.00	35.00	46.00	47.33	58.50	83.00

```
vital_status:
```

0	1
173	6

```
days_to_death:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
88.0	148.5	452.5	901.0	715.2	3563.0	173

```
days_to_last_followup:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
2	352	766	1071	1301	9634	6

```
tumor_tissue_site:
```

adrenal gland	extra-adrenal site
147	32

```
gender:
```

female	male
101	78

```
date_of_initial_pathologic_diagnosis:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
1988	2009	2011	2010	2012	2013

```
radiation_therapy:
```

no	yes	NA's
172	5	2

```
karnofsky_performance_score:
```

70	80	90	100	NA's
1	2	13	46	117

```

histological_type:
    paraganglioma
    18
paraganglioma; extra-adrenal pheochromocytoma
    13
pheochromocytoma
    148

number_of_lymph_nodes:
    0  1  2  13 NA's
    16  3  1  1  158

race:
american indian or alaska native
    1
    black or african american
    20
    NA's
    4
asian
    6
white
    148

ethnicity:
hispanic or latino not hispanic or latino
    5
    138
    NA's
    36

```

Including an additional 894 columns

---

PCPG-v2.1.0

*Pheochromocytoma and Paraganglioma*

---

## Description

A document describing the TCGA cancer code

## Details

```

> experiments( PCPG )
ExperimentList class object of length 11:
 [1] PCPG_CNASNP-20160128: RaggedExperiment with 297329 rows and 360 columns
 [2] PCPG_CNVSNP-20160128: RaggedExperiment with 31256 rows and 346 columns
 [3] PCPG_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 162 columns
 [4] PCPG_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 27 rows and 162 columns
 [5] PCPG_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 162 columns
 [6] PCPG_Mutation-20160128: RaggedExperiment with 4662 rows and 184 columns
 [7] PCPG_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 187 columns
 [8] PCPG_RPPAArray-20160128: SummarizedExperiment with 192 rows and 82 columns
 [9] PCPG_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 187 columns

```

```
[10] PCPG_RNASeq2GeneNorm-20160128: SummarizedExperiment with 17988 rows and 187 columns
[11] PCPG_Methylation-20160128: SummarizedExperiment with 485577 rows and 187 columns
```

```
> rownames( PCPG )
CharacterList of length 11
[["PCPG_CNASNP-20160128"]] character(0)
[["PCPG_CNVSNP-20160128"]] character(0)
[["PCPG_GISTIC_AllByGene-20160128"]] character(0)
[["PCPG_GISTIC_Peaks-20160128"]] 7 1 8 9 10 11 2 12 ... 22 23 5 24 25 26 6 27
[["PCPG_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["PCPG_Mutation-20160128"]] character(0)
[["PCPG_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["PCPG_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["PCPG_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["PCPG_RNASeq2GeneNorm-20160128"]] A1BG A2BP1 A2LD1 ... ZZEF1 ZZZ3 psiTPTE22
...
<1 more element>
```

```
> colnames( PCPG )
CharacterList of length 11
[["PCPG_CNASNP-20160128"]] TCGA-P7-A5NX-10A-01D-A35A-01 ...
[["PCPG_CNVSNP-20160128"]] TCGA-P7-A5NX-10A-01D-A35A-01 ...
[["PCPG_GISTIC_AllByGene-20160128"]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[["PCPG_GISTIC_Peaks-20160128"]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[["PCPG_GISTIC_ThresholdedByGene-20160128"]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[["PCPG_Mutation-20160128"]] TCGA-P7-A5NX-01A-11D-A35D-08 ...
[["PCPG_RNASeq2Gene-20160128"]] TCGA-P7-A5NX-01A-11R-A35K-07 ...
[["PCPG_RPPAArray-20160128"]] TCGA-P7-A5NX-01A-21-A43B-20 ...
[["PCPG_miRNASeqGene-20160128"]] TCGA-P7-A5NX-01A-11R-A35M-13 ...
[["PCPG_RNASeq2GeneNorm-20160128"]] TCGA-P7-A5NX-01 ... TCGA-XG-A823-01
...
<1 more element>
```

Sizes of each ExperimentList element:

		assay size.Mb
1	PCPG_CNASNP-20160128	8.1 Mb
2	PCPG_CNVSNP-20160128	0.9 Mb
3	PCPG_GISTIC_AllByGene-20160128	34.1 Mb
4	PCPG_GISTIC_Peaks-20160128	0.1 Mb
5	PCPG_GISTIC_ThresholdedByGene-20160128	34 Mb
6	PCPG_Mutation-20160128	8.4 Mb
7	PCPG_RNASeq2Gene-20160128	31.8 Mb
8	PCPG_RPPAArray-20160128	0.2 Mb
9	PCPG_miRNASeqGene-20160128	1.7 Mb
10	PCPG_RNASeq2GeneNorm-20160128	27.9 Mb
11	PCPG_Methylation-20160128	75 Mb

```
-----
Overall survival time-to-event summary (in years):
-----
```

```
Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)
```

```
173 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
[1,] 6      6  1.24  0.26  NA
```

```
-----
Available sample meta-data:
-----
```

```
years_to_birth:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
19.00	35.00	46.00	47.33	58.50	83.00

```
vital_status:
```

0	1
173	6

```
days_to_death:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
88.0	148.5	452.5	901.0	715.2	3563.0	173

```
days_to_last_followup:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
2	352	766	1071	1301	9634	6

```
tumor_tissue_site:
```

adrenal gland	extra-adrenal site
147	32

```
gender:
```

female	male
101	78

```
date_of_initial_pathologic_diagnosis:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
1988	2009	2011	2010	2012	2013

```
radiation_therapy:
```

no	yes	NA's
172	5	2

karnofsky\_performance\_score:

70	80	90	100	NA's
1	2	13	46	117

histological\_type:

	paranglioma	18
paranglioma; extra-adrenal pheochromocytoma		13
	pheochromocytoma	148

number\_of\_lymph\_nodes:

0	1	2	13	NA's
16	3	1	1	158

race:

american indian or alaska native	1	asian	6
black or african american	20	white	148
NA's	4		

ethnicity:

hispanic or latino	5	not hispanic or latino	138	NA's	36
--------------------	---	------------------------	-----	------	----

Including an additional 894 columns

---

PRAD

*Prostate adenocarcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

```
> experiments( PRAD )
```

ExperimentList class object of length 11:

- [1] PRAD\_CNASeq-20160128: RaggedExperiment with 23398 rows and 230 columns
- [2] PRAD\_CNASNP-20160128: RaggedExperiment with 573776 rows and 1029 columns
- [3] PRAD\_CNVSNP-20160128: RaggedExperiment with 117345 rows and 1023 columns
- [4] PRAD\_GISTIC\_AllByGene-20160128: SummarizedExperiment with 24776 rows and 492 columns
- [5] PRAD\_GISTIC\_Peaks-20160128: RangedSummarizedExperiment with 58 rows and 492 columns
- [6] PRAD\_GISTIC\_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 492 columns

```
[7] PRAD_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 547 columns
[8] PRAD_Mutation-20160128: RaggedExperiment with 12348 rows and 332 columns
[9] PRAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 550 columns
[10] PRAD_RPPAArray-20160128: SummarizedExperiment with 195 rows and 352 columns
[11] PRAD_Methylation-20160128: SummarizedExperiment with 485577 rows and 549 columns
```

```
> rownames( PRAD )
CharacterList of length 11
[["PRAD_CNASeq-20160128"]] character(0)
[["PRAD_CNASNP-20160128"]] character(0)
[["PRAD_CNVSNP-20160128"]] character(0)
[["PRAD_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["PRAD_GISTIC_Peaks-20160128"]] chr1:63901623-66226788 ...
[["PRAD_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["PRAD_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["PRAD_Mutation-20160128"]] character(0)
[["PRAD_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["PRAD_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<1 more element>
```

```
> colnames( PRAD )
CharacterList of length 11
[["PRAD_CNASeq-20160128"]] TCGA-CH-5741-01A-11D-1572-02 ...
[["PRAD_CNASNP-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_CNVSNP-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_GISTIC_AllByGene-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_GISTIC_Peaks-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_miRNASeqGene-20160128"]] TCGA-2A-A8VL-01A-21R-A37H-13 ...
[["PRAD_Mutation-20160128"]] TCGA-2A-A8VL-01A-21D-A377-08 ...
[["PRAD_RNASeq2GeneNorm-20160128"]] TCGA-2A-A8VL-01A-21R-A37L-07 ...
[["PRAD_RPPAArray-20160128"]] TCGA-2A-A8VL-01A-11-A43M-20 ...
...
<1 more element>
```

Sizes of each ExperimentList element:

		assay size.Mb
1	PRAD_CNASeq-20160128	0.7 Mb
2	PRAD_CNASNP-20160128	15.6 Mb
3	PRAD_CNVSNP-20160128	3.4 Mb
4	PRAD_GISTIC_AllByGene-20160128	4.9 Mb
5	PRAD_GISTIC_Peaks-20160128	0.1 Mb
6	PRAD_GISTIC_ThresholdedByGene-20160128	4.9 Mb
7	PRAD_miRNASeqGene-20160128	0.1 Mb
8	PRAD_Mutation-20160128	21.5 Mb
9	PRAD_RNASeq2GeneNorm-20160128	1.3 Mb

```

10          PRAD_RPPAArray-20160128    0 Mb
11          PRAD_Methylation-20160128 75.1 Mb

```

```

-----
Overall survival time-to-event summary (in years):
-----

```

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

488 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
10.00  10.00   3.02   1.99     NA

```

```

-----
Available sample meta-data:
-----

```

```

years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
41.00  56.00   61.00   61.02  66.00   78.00    11

```

```

vital_status:
  0  1
488 10

```

```

days_to_death:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
146.0  743.8 1102.0 1579.0 2315.5 3502.0   488

```

```

days_to_last_followup:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
 23.0  523.5  926.0 1076.5 1458.0 5024.0    10

```

```

tumor_tissue_site:
prostate
  498

```

```

pathology_N_stage:
  n0  n1 NA's
346  79  73

```

```

gender:
male
  498

```

```

date_of_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.    NA's
  2000   2009   2011   2010   2012   2013     31

radiation_therapy:
  no  yes NA's
  395 59  44

histological_type:
  prostate adenocarcinoma acinar type prostate adenocarcinoma, other subtype
                                483                                15

residual_tumor:
  r0  r1  r2  rx NA's
  316 147  5  15  15

number_of_lymph_nodes:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.    NA's
  0.0000 0.0000 0.0000 0.4447 0.0000 15.0000     91

gleason_score:
  6  7  8  9  10
  45 248 64 137  4

psa_value:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.    NA's
  0.000 0.030 0.100 1.742 0.110 323.000     57

days_to_psa:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.    NA's
  -164.0 191.0 512.0 685.6 926.0 3447.0     53

race:
                                asian black or african american                                white
                                2                                7                                147
                                NA's
                                342

ethnicity:
not hispanic or latino                                NA's
                                152                                346

```

Including an additional 1126 columns

### See Also

[PRAD-v2.0.1](#)



PRAD-v2.0.1

*Prostate adenocarcinoma***Description**

A document describing the TCGA cancer code

**Details**

```

> experiments( PRAD )
ExperimentList class object of length 12:
 [1] PRAD_CNASeq-20160128: RaggedExperiment with 23398 rows and 230 columns
 [2] PRAD_CNASNP-20160128: RaggedExperiment with 573776 rows and 1029 columns
 [3] PRAD_CNVSNP-20160128: RaggedExperiment with 117345 rows and 1023 columns
 [4] PRAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 492 columns
 [5] PRAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 58 rows and 492 columns
 [6] PRAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 492 columns
 [7] PRAD_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 547 columns
 [8] PRAD_Mutation-20160128: RaggedExperiment with 12348 rows and 332 columns
 [9] PRAD_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 550 columns
 [10] PRAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 550 columns
 [11] PRAD_RPPAArray-20160128: SummarizedExperiment with 195 rows and 352 columns
 [12] PRAD_Methylation-20160128: SummarizedExperiment with 485577 rows and 549 columns

> rownames( PRAD )
CharacterList of length 12
[["PRAD_CNASeq-20160128"]] character(0)
[["PRAD_CNASNP-20160128"]] character(0)
[["PRAD_CNVSNP-20160128"]] character(0)
[["PRAD_GISTIC_AllByGene-20160128"]] character(0)
[["PRAD_GISTIC_Peaks-20160128"]] 29 30 1 31 32 33 34 ... 21 60 61 22 23 62 63
[["PRAD_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["PRAD_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["PRAD_Mutation-20160128"]] character(0)
[["PRAD_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["PRAD_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
...
<2 more elements>

> colnames( PRAD )
CharacterList of length 12
[["PRAD_CNASeq-20160128"]] TCGA-CH-5741-01A-11D-1572-02 ...
[["PRAD_CNASNP-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_CNVSNP-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_GISTIC_AllByGene-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_GISTIC_Peaks-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...

```

```

[["PRAD_miRNASeqGene-20160128"]] TCGA-2A-A8VL-01A-21R-A37H-13 ...
[["PRAD_Mutation-20160128"]] TCGA-2A-A8VL-01A-21D-A377-08 ...
[["PRAD_RNASeq2Gene-20160128"]] TCGA-2A-A8VL-01A-21R-A37L-07 ...
[["PRAD_RNASeq2GeneNorm-20160128"]] TCGA-2A-A8VL-01A-21R-A37L-07 ...
...
<2 more elements>

```

Sizes of each ExperimentList element:

		assay	size.Mb
1		PRAD_CNASeq-20160128	0.7 Mb
2		PRAD_CNASNP-20160128	15.6 Mb
3		PRAD_CNVSNP-20160128	3.4 Mb
4	PRAD_GISTIC_AllByGene-20160128		96.6 Mb
5		PRAD_GISTIC_Peaks-20160128	0.4 Mb
6	PRAD_GISTIC_ThresholdedByGene-20160128		96.4 Mb
7		PRAD_miRNASeqGene-20160128	4.6 Mb
8		PRAD_Mutation-20160128	21.5 Mb
9		PRAD_RNASeq2Gene-20160128	88.7 Mb
10		PRAD_RNASeq2GeneNorm-20160128	88.7 Mb
11		PRAD_RPPAArray-20160128	0.6 Mb
12		PRAD_Methylation-20160128	75.1 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

488 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
10.00  10.00   3.02   1.99     NA

```

-----  
Available sample meta-data:  
-----

```

years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
 41.00  56.00   61.00   61.02  66.00   78.00    11

```

```

vital_status:
  0  1
488 10

```

```

days_to_death:

```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
146.0	743.8	1102.0	1579.0	2315.5	3502.0	488

days\_to\_last\_followup:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
23.0	523.5	926.0	1076.5	1458.0	5024.0	10

tumor\_tissue\_site:

prostate  
498

pathology\_N\_stage:

n0	n1	NA's
346	79	73

gender:

male  
498

date\_of\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
2000	2009	2011	2010	2012	2013	31

radiation\_therapy:

no	yes	NA's
395	59	44

histological\_type:

prostate adenocarcinoma acinar type	prostate adenocarcinoma, other subtype
483	15

residual\_tumor:

r0	r1	r2	rx	NA's
316	147	5	15	15

number\_of\_lymph\_nodes:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.0000	0.0000	0.0000	0.4447	0.0000	15.0000	91

gleason\_score:

6	7	8	9	10
45	248	64	137	4

psa\_value:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.000	0.030	0.100	1.742	0.110	323.000	57

```
days_to_psa:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
-164.0  191.0   512.0   685.6  926.0  3447.0   53
```

```
race:
      asian black or african american      white
      2              7              147
NA's
342
```

```
ethnicity:
not hispanic or latino      NA's
      152              346
```

Including an additional 1126 columns

---

PRAD-v2.1.0

*Prostate adenocarcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

```
> experiments( PRAD )
ExperimentList class object of length 12:
 [1] PRAD_CNASeq-20160128: RaggedExperiment with 23398 rows and 230 columns
 [2] PRAD_CNASNP-20160128: RaggedExperiment with 573776 rows and 1029 columns
 [3] PRAD_CNVSNP-20160128: RaggedExperiment with 117345 rows and 1023 columns
 [4] PRAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 492 columns
 [5] PRAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 58 rows and 492 columns
 [6] PRAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 492 columns
 [7] PRAD_Mutation-20160128: RaggedExperiment with 12348 rows and 332 columns
 [8] PRAD_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 550 columns
 [9] PRAD_RPPAArray-20160128: SummarizedExperiment with 195 rows and 352 columns
[10] PRAD_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 547 columns
[11] PRAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18265 rows and 550 columns
[12] PRAD_Methylation-20160128: SummarizedExperiment with 485577 rows and 549 columns

> rownames( PRAD )
CharacterList of length 12
[["PRAD_CNASeq-20160128"]] character(0)
[["PRAD_CNASNP-20160128"]] character(0)
[["PRAD_CNVSNP-20160128"]] character(0)
[["PRAD_GISTIC_AllByGene-20160128"]] character(0)
[["PRAD_GISTIC_Peaks-20160128"]] 29 30 1 31 32 33 34 ... 21 60 61 22 23 62 63
```

```

[["PRAD_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["PRAD_Mutation-20160128"]] character(0)
[["PRAD_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
[["PRAD_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["PRAD_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
...
<2 more elements>

```

```

> colnames( PRAD )
CharacterList of length 12
[["PRAD_CNASeq-20160128"]] TCGA-CH-5741-01A-11D-1572-02 ...
[["PRAD_CNASNP-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_CNVSNP-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_GISTIC_AllByGene-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_GISTIC_Peaks-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-2A-A8VL-01A-21D-A376-01 ...
[["PRAD_Mutation-20160128"]] TCGA-2A-A8VL-01A-21D-A377-08 ...
[["PRAD_RNASeq2Gene-20160128"]] TCGA-2A-A8VL-01A-21R-A37L-07 ...
[["PRAD_RPPAArray-20160128"]] TCGA-2A-A8VL-01A-11-A43M-20 ...
[["PRAD_miRNASeqGene-20160128"]] TCGA-2A-A8VL-01A-21R-A37H-13 ...
...
<2 more elements>

```

Sizes of each ExperimentList element:

	assay	size.Mb
1	PRAD_CNASeq-20160128	0.7 Mb
2	PRAD_CNASNP-20160128	15.6 Mb
3	PRAD_CNVSNP-20160128	3.4 Mb
4	PRAD_GISTIC_AllByGene-20160128	96.6 Mb
5	PRAD_GISTIC_Peaks-20160128	0.4 Mb
6	PRAD_GISTIC_ThresholdedByGene-20160128	96.4 Mb
7	PRAD_Mutation-20160128	21.5 Mb
8	PRAD_RNASeq2Gene-20160128	88.7 Mb
9	PRAD_RPPAArray-20160128	0.6 Mb
10	PRAD_miRNASeqGene-20160128	4.6 Mb
11	PRAD_RNASeq2GeneNorm-20160128	79 Mb
12	PRAD_Methylation-20160128	75.1 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

488 observations deleted due to missingness
n events median 0.95LCL 0.95UCL

```

[1,] 10 10 3.02 1.99 NA

-----  
 Available sample meta-data:  
 -----

years\_to\_birth:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
41.00	56.00	61.00	61.02	66.00	78.00	11

vital\_status:

0	1
488	10

days\_to\_death:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
146.0	743.8	1102.0	1579.0	2315.5	3502.0	488

days\_to\_last\_followup:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
23.0	523.5	926.0	1076.5	1458.0	5024.0	10

tumor\_tissue\_site:

prostate
498

pathology\_N\_stage:

n0	n1	NA's
346	79	73

gender:

male
498

date\_of\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
2000	2009	2011	2010	2012	2013	31

radiation\_therapy:

no	yes	NA's
395	59	44

histological\_type:

prostate adenocarcinoma acinar type prostate adenocarcinoma, other subtype
483 15

residual\_tumor:

r0	r1	r2	rx	NA's
316	147	5	15	15

number\_of\_lymph\_nodes:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.0000	0.0000	0.0000	0.4447	0.0000	15.0000	91

gleason\_score:

6	7	8	9	10
45	248	64	137	4

psa\_value:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.000	0.030	0.100	1.742	0.110	323.000	57

days\_to\_psa:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
-164.0	191.0	512.0	685.6	926.0	3447.0	53

race:

asian	black or african american	white
2	7	147
NA's		
342		

ethnicity:

not hispanic or latino	NA's
152	346

Including an additional 1126 columns

---

READ

*Rectum adenocarcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

```
> experiments( READ )
```

ExperimentList class object of length 14:

- [1] READ\_CNASeq-20160128: RaggedExperiment with 56380 rows and 70 columns
- [2] READ\_CNASNP-20160128: RaggedExperiment with 156806 rows and 316 columns
- [3] READ\_CNVSNP-20160128: RaggedExperiment with 35765 rows and 316 columns
- [4] READ\_GISTIC\_AllByGene-20160128: SummarizedExperiment with 24776 rows and 165 columns

```

[5] READ_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 55 rows and 165 columns
[6] READ_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 165 columns
[7] READ_miRNASeqGene-20160128: SummarizedExperiment with 705 rows and 76 columns
[8] READ_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 72 columns
[9] READ_Mutation-20160128: RaggedExperiment with 22075 rows and 69 columns
[10] READ_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 72 columns
[11] READ_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 72 columns
[12] READ_RPPAArray-20160128: SummarizedExperiment with 208 rows and 131 columns
[13] READ_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 73 columns
[14] READ_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 106 columns

```

```

> rownames( READ )
CharacterList of length 14
[["READ_CNASeq-20160128"]] character(0)
[["READ_CNASNP-20160128"]] character(0)
[["READ_CNVSNP-20160128"]] character(0)
[["READ_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["READ_GISTIC_Peaks-20160128"]] chr1:3814904-31841618 ...
[["READ_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["READ_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["READ_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["READ_Mutation-20160128"]] character(0)
[["READ_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
...
<4 more elements>

```

```

> colnames( READ )
CharacterList of length 14
[["READ_CNASeq-20160128"]] TCGA-AF-2691-01A-01D-1167-02 ...
[["READ_CNASNP-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_CNVSNP-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_GISTIC_AllByGene-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_GISTIC_Peaks-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_GISTIC_ThresholdedByGene-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_miRNASeqGene-20160128"]] TCGA-AF-2687-01A-02T-1735-13 ...
[["READ_mRNAArray-20160128"]] TCGA-AF-2689-11A-01R-1758-07 ...
[["READ_Mutation-20160128"]] TCGA-AF-2689-01A-01W-0831-10 ... TCGA-AG-A036-01
[["READ_RNASeq2GeneNorm-20160128"]] TCGA-AF-2691-01A-01R-0821-07 ...
...
<4 more elements>

```

Sizes of each ExperimentList element:

		assay size.Mb
1	READ_CNASeq-20160128	1.5 Mb
2	READ_CNASNP-20160128	4.3 Mb
3	READ_CNVSNP-20160128	1.1 Mb
4	READ_GISTIC_AllByGene-20160128	4.9 Mb



5	READ_GISTIC_Peaks-20160128	0.1 Mb
6	READ_GISTIC_ThresholdedByGene-20160128	4.9 Mb
7	READ_miRNASeqGene-20160128	0.1 Mb
8	READ_mRNAArray-20160128	1.1 Mb
9	READ_Mutation-20160128	9.6 Mb
10	READ_RNASeq2GeneNorm-20160128	1.3 Mb
11	READ_RNASeqGene-20160128	1.3 Mb
12	READ_RPPAArray-20160128	0 Mb
13	READ_Methylation_methyl27-20160128	4.9 Mb
14	READ_Methylation_methyl450-20160128	75 Mb

-----  
 Overall survival time-to-event summary (in years):  
 -----

Call: survfit(formula = survival::Surv(colDat\$days\_to\_death/365, colDat\$vital\_status) ~  
 -1)

142 observations deleted due to missingness  
 n events median 0.95LCL 0.95UCL  
 27.00 27.00 2.00 1.44 3.25

-----  
 Available sample meta-data:  
 -----

years\_to\_birth:  
 Min. 1st Qu. Median Mean 3rd Qu. Max.  
 31.00 57.00 66.00 64.37 72.00 90.00

vital\_status:  
 0 1  
 141 28

days\_to\_death:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 59.0 347.5 730.0 786.1 1193.0 1741.0 142

days\_to\_last\_followup:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 0.0 366.0 625.0 779.5 1096.0 3932.0 28

tumor\_tissue\_site:  
 rectum NA's  
 166 3

pathology\_M\_stage:

m0	m1	m1a	mx	NA's
128	22	2	14	3

gender:

female	male
77	92

date\_of\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
1999	2007	2009	2008	2010	2012

days\_to\_last\_known\_alive:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
31.0	292.2	863.0	1420.1	2214.5	3667.0	161

radiation\_therapy:

no	yes	NA's
114	22	33

histological\_type:

rectal adenocarcinoma	rectal mucinous adenocarcinoma
150	13
NA's	
6	

tumor\_stage:

stage iia	NA's
1	168

residual\_tumor:

r0	r1	r2	rx	NA's
126	2	12	5	24

number\_of\_lymph\_nodes:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.000	0.000	0.000	2.692	3.000	31.000	10

ethnicity:

hispanic or latino	not hispanic or latino	NA's
1	84	84

Including an additional 2242 columns

### See Also

[READ-v2.0.1](#)

---

 READ-v2.0.1

 Rectum adenocarcinoma
 

---

## Description

A document describing the TCGA cancer code

## Details

```

> experiments( READ )
ExperimentList class object of length 16:
 [1] READ_CNASeq-20160128: RaggedExperiment with 56380 rows and 70 columns
 [2] READ_CNASNP-20160128: RaggedExperiment with 156806 rows and 316 columns
 [3] READ_CNVSNP-20160128: RaggedExperiment with 35765 rows and 316 columns
 [4] READ_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 165 columns
 [5] READ_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 55 rows and 165 columns
 [6] READ_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 165 columns
 [7] READ_miRNASeqGene-20160128: SummarizedExperiment with 705 rows and 76 columns
 [8] READ_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 72 columns
 [9] READ_Mutation-20160128: RaggedExperiment with 22075 rows and 69 columns
[10] READ_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 105 columns
[11] READ_RNASeq2GeneNorm_illumina-20160128: SummarizedExperiment with 20501 rows and 72 columns
[12] READ_RNASeq2GeneNorm_illumina-hiseq-20160128: SummarizedExperiment with 20501 rows and 105 columns
[13] READ_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 72 columns
[14] READ_RPPAArray-20160128: SummarizedExperiment with 208 rows and 131 columns
[15] READ_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 73 columns
[16] READ_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 106 columns

> rownames( READ )
CharacterList of length 16
[["READ_CNASeq-20160128"]] character(0)
[["READ_CNASNP-20160128"]] character(0)
[["READ_CNVSNP-20160128"]] character(0)
[["READ_GISTIC_AllByGene-20160128"]] character(0)
[["READ_GISTIC_Peaks-20160128"]] 23 24 25 1 2 26 27 ... 54 55 18 19 20 56 57
[["READ_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["READ_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["READ_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["READ_Mutation-20160128"]] character(0)
[["READ_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
...
<6 more elements>

> colnames( READ )
CharacterList of length 16
[["READ_CNASeq-20160128"]] TCGA-AF-2691-01A-01D-1167-02 ...
[["READ_CNASNP-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...

```

```

[["READ_CNVSNP-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_GISTIC_AllByGene-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_GISTIC_Peaks-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_GISTIC_ThresholdedByGene-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_miRNASeqGene-20160128"]] TCGA-AF-2687-01A-02T-1735-13 ...
[["READ_mRNAArray-20160128"]] TCGA-AF-2689-11A-01R-1758-07 ...
[["READ_Mutation-20160128"]] TCGA-AF-2689-01A-01W-0831-10 ... TCGA-AG-A036-01
[["READ_RNASeq2Gene-20160128"]] TCGA-AF-2687-01A-02R-1736-07 ...
...
<6 more elements>

```

Sizes of each ExperimentList element:

		assay size.Mb
1	READ_CNASeq-20160128	1.5 Mb
2	READ_CNASNP-20160128	4.3 Mb
3	READ_CNVSNP-20160128	1.1 Mb
4	READ_GISTIC_AllByGene-20160128	34.7 Mb
5	READ_GISTIC_Peaks-20160128	0.2 Mb
6	READ_GISTIC_ThresholdedByGene-20160128	34.5 Mb
7	READ_miRNASeqGene-20160128	0.5 Mb
8	READ_mRNAArray-20160128	12 Mb
9	READ_Mutation-20160128	9.6 Mb
10	READ_RNASeq2Gene-20160128	19 Mb
11	READ_RNASeq2GeneNorm_illumina-20160128	13.8 Mb
12	READ_RNASeq2GeneNorm_illuminahisec-20160128	19 Mb
13	READ_RNASeqGene-20160128	13.8 Mb
14	READ_RPPAArray-20160128	0.3 Mb
15	READ_Methylation_methyl27-20160128	4.9 Mb
16	READ_Methylation_methyl450-20160128	75 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

142 observations deleted due to missingness
  n  events  median 0.95LCL 0.95UCL
27.00  27.00   2.00   1.44   3.25

```

-----  
Available sample meta-data:  
-----

years\_to\_birth:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
31.00	57.00	66.00	64.37	72.00	90.00

vital\_status:

0	1
141	28

days\_to\_death:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
59.0	347.5	730.0	786.1	1193.0	1741.0	142

days\_to\_last\_followup:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.0	366.0	625.0	779.5	1096.0	3932.0	28

tumor\_tissue\_site:

rectum	NA's
166	3

pathology\_M\_stage:

m0	m1	m1a	mx	NA's
128	22	2	14	3

gender:

female	male
77	92

date\_of\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
1999	2007	2009	2008	2010	2012

days\_to\_last\_known\_alive:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
31.0	292.2	863.0	1420.1	2214.5	3667.0	161

radiation\_therapy:

no	yes	NA's
114	22	33

histological\_type:

rectal adenocarcinoma	rectal mucinous adenocarcinoma
150	13
NA's	
6	

```
tumor_stage:
stage iia      NA's
      1        168

residual_tumor:
  r0  r1  r2  rx NA's
126   2  12   5  24

number_of_lymph_nodes:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
 0.000  0.000  0.000  2.692  3.000  31.000    10

ethnicity:
  hispanic or latino not hispanic or latino      NA's
                1                84                84
```

Including an additional 2242 columns

---

READ-v2.1.0

*Rectum adenocarcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

```
> experiments( READ )
ExperimentList class object of length 17:
 [1] READ_CNASeq-20160128: RaggedExperiment with 56380 rows and 70 columns
 [2] READ_CNASNP-20160128: RaggedExperiment with 156806 rows and 316 columns
 [3] READ_CNVSNP-20160128: RaggedExperiment with 35765 rows and 316 columns
 [4] READ_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 165 columns
 [5] READ_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 55 rows and 165 columns
 [6] READ_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 165 columns
 [7] READ_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 72 columns
 [8] READ_Mutation-20160128: RaggedExperiment with 22075 rows and 69 columns
 [9] READ_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 105 columns
[10] READ_RNASeq2GeneNorm_illumina-20160128: SummarizedExperiment with 20501 rows and 72 columns
[11] READ_RNASeq2GeneNorm_illumina-hiseq-20160128: SummarizedExperiment with 20501 rows and 105 columns
[12] READ_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 72 columns
[13] READ_RPPAArray-20160128: SummarizedExperiment with 208 rows and 131 columns
[14] READ_miRNASeqGene-20160128: SummarizedExperiment with 705 rows and 76 columns
[15] READ_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18115 rows and 177 columns
[16] READ_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 73 columns
[17] READ_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 106 columns
```

```
> rownames( READ )
CharacterList of length 17
[["READ_CNASeq-20160128"]] character(0)
[["READ_CNASNP-20160128"]] character(0)
[["READ_CNVSNP-20160128"]] character(0)
[["READ_GISTIC_AllByGene-20160128"]] character(0)
[["READ_GISTIC_Peaks-20160128"]] 23 24 25 1 2 26 27 ... 54 55 18 19 20 56 57
[["READ_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["READ_mRNAArray-20160128"]] ELMO2 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["READ_Mutation-20160128"]] character(0)
[["READ_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["READ_RNASeq2GeneNorm_illumina-20160128"]] A1BG A1CF ... psiTPTE22 tAKR
...
<7 more elements>
```

```
> colnames( READ )
CharacterList of length 17
[["READ_CNASeq-20160128"]] TCGA-AF-2691-01A-01D-1167-02 ...
[["READ_CNASNP-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_CNVSNP-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_GISTIC_AllByGene-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_GISTIC_Peaks-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_GISTIC_ThresholdedByGene-20160128"]] TCGA-AF-2687-01A-02D-1732-01 ...
[["READ_mRNAArray-20160128"]] TCGA-AF-2689-11A-01R-1758-07 ...
[["READ_Mutation-20160128"]] TCGA-AF-2689-01A-01W-0831-10 ... TCGA-AG-A036-01
[["READ_RNASeq2Gene-20160128"]] TCGA-AF-2687-01A-02R-1736-07 ...
[["READ_RNASeq2GeneNorm_illumina-20160128"]] TCGA-AF-2691-01A-01R-0821-07...
...
<7 more elements>
```

Sizes of each ExperimentList element:

		assay size.Mb
1	READ_CNASeq-20160128	1.5 Mb
2	READ_CNASNP-20160128	4.3 Mb
3	READ_CNVSNP-20160128	1.1 Mb
4	READ_GISTIC_AllByGene-20160128	34.7 Mb
5	READ_GISTIC_Peaks-20160128	0.2 Mb
6	READ_GISTIC_ThresholdedByGene-20160128	34.5 Mb
7	READ_mRNAArray-20160128	12 Mb
8	READ_Mutation-20160128	9.6 Mb
9	READ_RNASeq2Gene-20160128	19 Mb
10	READ_RNASeq2GeneNorm_illumina-20160128	13.8 Mb
11	READ_RNASeq2GeneNorm_illuminahisec-20160128	19 Mb
12	READ_RNASeqGene-20160128	13.8 Mb
13	READ_RPPAArray-20160128	0.3 Mb
14	READ_miRNASeqGene-20160128	0.5 Mb
15	READ_RNASeq2GeneNorm-20160128	26.7 Mb

```

16      READ_Methylation_methyl27-20160128  4.9 Mb
17      READ_Methylation_methyl450-20160128  75 Mb

```

```

-----
Overall survival time-to-event summary (in years):
-----

```

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

142 observations deleted due to missingness
      n events median 0.95LCL 0.95UCL
[1,] 27      27      2      1.44   3.25

```

```

-----
Available sample meta-data:
-----

```

```

years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 31.00  57.00   66.00   64.37  72.00   90.00

```

```

vital_status:
  0  1
141 28

```

```

days_to_death:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
 59.0   347.5   730.0   786.1 1193.0 1741.0   142

```

```

days_to_last_followup:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
  0.0   366.0   625.0   779.5 1096.0 3932.0    28

```

```

tumor_tissue_site:
rectum  NA's
 166     3

```

```

pathology_M_stage:
  m0  m1  m1a  mx NA's
 128  22   2  14   3

```

```

gender:
female  male

```



77 92

date\_of\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
1999	2007	2009	2008	2010	2012

days\_to\_last\_known\_alive:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
31.0	292.2	863.0	1420.1	2214.5	3667.0	161

radiation\_therapy:

no	yes	NA's
114	22	33

histological\_type:

rectal adenocarcinoma	rectal mucinous adenocarcinoma
150	13
NA's	
6	

tumor\_stage:

stage iia	NA's
1	168

residual\_tumor:

r0	r1	r2	rx	NA's
126	2	12	5	24

number\_of\_lymph\_nodes:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.000	0.000	0.000	2.692	3.000	31.000	10

ethnicity:

hispanic or latino	not hispanic or latino	NA's
1	84	84

Including an additional 2242 columns

SARC

*Sarcoma***Description**

A document describing the TCGA cancer code

**Details**

```

> experiments( SARC )
ExperimentList class object of length 10:
 [1] SARC_CNASNP-20160128: RaggedExperiment with 337377 rows and 516 columns
 [2] SARC_CNVSNP-20160128: RaggedExperiment with 106739 rows and 513 columns
 [3] SARC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 257 columns
 [4] SARC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 64 rows and 257 columns
 [5] SARC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 257 columns
 [6] SARC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 263 columns
 [7] SARC_Mutation-20160128: RaggedExperiment with 20376 rows and 247 columns
 [8] SARC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 265 columns
 [9] SARC_RPPAArray-20160128: SummarizedExperiment with 192 rows and 226 columns
[10] SARC_Methylation-20160128: SummarizedExperiment with 485577 rows and 269 columns

> rownames( SARC )
CharacterList of length 10
[["SARC_CNASNP-20160128"]] character(0)
[["SARC_CNVSNP-20160128"]] character(0)
[["SARC_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["SARC_GISTIC_Peaks-20160128"]] chr1:1-5923787 ... chr22:45095899-51304566
[["SARC_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["SARC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["SARC_Mutation-20160128"]] character(0)
[["SARC_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["SARC_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["SARC_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873

> colnames( SARC )
CharacterList of length 10
[["SARC_CNASNP-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_CNVSNP-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_GISTIC_AllByGene-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_GISTIC_Peaks-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_GISTIC_ThresholdedByGene-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_miRNASeqGene-20160128"]] TCGA-3B-A9HI-01A-11R-A38N-13 ...
[["SARC_Mutation-20160128"]] TCGA-3B-A9HI-01A-11D-A387-09 ...
[["SARC_RNASeq2GeneNorm-20160128"]] TCGA-3B-A9HI-01A-11R-A38C-07 ...
[["SARC_RPPAArray-20160128"]] TCGA-3B-A9HI-01A-21-A456-20 ...
[["SARC_Methylation-20160128"]] TCGA-3B-A9HI-01A-11D-A388-05 ...

```

Sizes of each ExperimentList element:

		assay size.Mb
1	SARC_CNASNP-20160128	9.2 Mb
2	SARC_CNVSNP-20160128	3 Mb
3	SARC_GISTIC_AllByGene-20160128	4.9 Mb
4	SARC_GISTIC_Peaks-20160128	0.1 Mb
5	SARC_GISTIC_ThresholdedByGene-20160128	4.9 Mb

```

6          SARC_miRNASeqGene-20160128  0.1 Mb
7          SARC_Mutation-20160128    19.5 Mb
8          SARC_RNASeq2GeneNorm-20160128  1.3 Mb
9          SARC_RPPAArray-20160128      0 Mb
10         SARC_Methylation-20160128    75 Mb

```

```

-----
Overall survival time-to-event summary (in years):
-----

```

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

162 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
99.00  99.00   1.78   1.51   2.46

```

```

-----
Available sample meta-data:
-----

```

```

years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
20.00  53.00   61.00   60.88  71.00   90.00    1

```

```

vital_status:
 0  1
162 99

```

```

days_to_death:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
 17.0  322.5   648.0   863.6 1169.5  2694.0  162

```

```

days_to_last_followup:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
 15.0  585.8  1092.0  1391.1 1891.8  5723.0   99

```

```

gender:
female  male
 142    119

```

```

date_of_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
 1994   2007   2010   2009   2012   2013    4

```

```

radiation_therapy:

```

```

no  yes  NA's
181 74   6

```

```

residual_tumor:
  r0  r1  r2  rx  NA's
155  70  9  26  1

```

```

race:
      asian black or african american      white
      6          18          228
      NA's
      9

```

```

ethnicity:
  hispanic or latino not hispanic or latino  NA's
      5          223          33

```

Including an additional 1413 columns

### See Also

[SARC-v2.0.1](#)

---

SARC-v2.0.1

*Sarcoma*

---

### Description

A document describing the TCGA cancer code

### Details

```

> experiments( SARC )
ExperimentList class object of length 11:
 [1] SARC_CNASNP-20160128: RaggedExperiment with 337377 rows and 516 columns
 [2] SARC_CNVSNP-20160128: RaggedExperiment with 106739 rows and 513 columns
 [3] SARC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 257 columns
 [4] SARC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 64 rows and 257 columns
 [5] SARC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 257 columns
 [6] SARC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 263 columns
 [7] SARC_Mutation-20160128: RaggedExperiment with 20376 rows and 247 columns
 [8] SARC_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 265 columns
 [9] SARC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 265 columns
[10] SARC_RPPAArray-20160128: SummarizedExperiment with 192 rows and 226 columns
[11] SARC_Methylation-20160128: SummarizedExperiment with 485577 rows and 269 columns

```

```

> rownames( SARC )
CharacterList of length 11
[["SARC_CNASNP-20160128"]] character(0)
[["SARC_CNVSNP-20160128"]] character(0)
[["SARC_GISTIC_AllByGene-20160128"]] character(0)
[["SARC_GISTIC_Peaks-20160128"]] 26 1 2 3 27 28 4 29 ... 21 63 22 64 23 65 66
[["SARC_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["SARC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["SARC_Mutation-20160128"]] character(0)
[["SARC_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["SARC_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["SARC_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<1 more element>

```

```

> colnames( SARC )
CharacterList of length 11
[["SARC_CNASNP-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_CNVSNP-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_GISTIC_AllByGene-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_GISTIC_Peaks-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_GISTIC_ThresholdedByGene-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_miRNASeqGene-20160128"]] TCGA-3B-A9HI-01A-11R-A38N-13 ...
[["SARC_Mutation-20160128"]] TCGA-3B-A9HI-01A-11D-A387-09 ...
[["SARC_RNASeq2Gene-20160128"]] TCGA-3B-A9HI-01A-11R-A38C-07 ...
[["SARC_RNASeq2GeneNorm-20160128"]] TCGA-3B-A9HI-01A-11R-A38C-07 ...
[["SARC_RPPAArray-20160128"]] TCGA-3B-A9HI-01A-21-A456-20 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

		assay size.Mb
1	SARC_CNASNP-20160128	9.2 Mb
2	SARC_CNVSNP-20160128	3 Mb
3	SARC_GISTIC_AllByGene-20160128	52.2 Mb
4	SARC_GISTIC_Peaks-20160128	0.2 Mb
5	SARC_GISTIC_ThresholdedByGene-20160128	51.9 Mb
6	SARC_miRNASeqGene-20160128	2.3 Mb
7	SARC_Mutation-20160128	19.5 Mb
8	SARC_RNASeq2Gene-20160128	44 Mb
9	SARC_RNASeq2GeneNorm-20160128	44 Mb
10	SARC_RPPAArray-20160128	0.4 Mb
11	SARC_Methylation-20160128	75 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```
Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)
```

```
162 observations deleted due to missingness
  n events median 0.95LCL 0.95UCL
99.00  99.00   1.78   1.51   2.46
```

```
-----
Available sample meta-data:
-----
```

```
years_to_birth:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
20.00	53.00	61.00	60.88	71.00	90.00	1

```
vital_status:
```

0	1
162	99

```
days_to_death:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
17.0	322.5	648.0	863.6	1169.5	2694.0	162

```
days_to_last_followup:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
15.0	585.8	1092.0	1391.1	1891.8	5723.0	99

```
gender:
```

female	male
142	119

```
date_of_initial_pathologic_diagnosis:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1994	2007	2010	2009	2012	2013	4

```
radiation_therapy:
```

no	yes	NA's
181	74	6

```
residual_tumor:
```

r0	r1	r2	rx	NA's
155	70	9	26	1

```
race:
```

asian black or african american	white
6	228
18	
NA's	
9	
ethnicity:	
hispanic or latino not hispanic or latino	NA's
5	33
223	

Including an additional 1413 columns

---

SARC-v2.1.0

*Sarcoma*

---

## Description

A document describing the TCGA cancer code

## Details

```
> experiments( SARC )
ExperimentList class object of length 11:
 [1] SARC_CNASNP-20160128: RaggedExperiment with 337377 rows and 516 columns
 [2] SARC_CNVSNP-20160128: RaggedExperiment with 106739 rows and 513 columns
 [3] SARC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 257 columns
 [4] SARC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 64 rows and 257 columns
 [5] SARC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 257 columns
 [6] SARC_Mutation-20160128: RaggedExperiment with 20376 rows and 247 columns
 [7] SARC_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 265 columns
 [8] SARC_RPPAArray-20160128: SummarizedExperiment with 192 rows and 226 columns
 [9] SARC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 263 columns
 [10] SARC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18165 rows and 265 columns
 [11] SARC_Methylation-20160128: SummarizedExperiment with 485577 rows and 269 columns

> rownames( SARC )
CharacterList of length 11
[["SARC_CNASNP-20160128"]] character(0)
[["SARC_CNVSNP-20160128"]] character(0)
[["SARC_GISTIC_AllByGene-20160128"]] character(0)
[["SARC_GISTIC_Peaks-20160128"]] 26 1 2 3 27 28 4 29 ... 21 63 22 64 23 65 66
[["SARC_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["SARC_Mutation-20160128"]] character(0)
[["SARC_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["SARC_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["SARC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["SARC_RNASeq2GeneNorm-20160128"]] A1BG A2BP1 A2LD1 ... ZZEF1 ZZZ3 psiTPTE22
...
```

```

<1 more element>

> colnames( SARC )
CharacterList of length 11
[["SARC_CNASNP-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_CNVSNP-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_GISTIC_AllByGene-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_GISTIC_Peaks-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_GISTIC_ThresholdedByGene-20160128"]] TCGA-3B-A9HI-01A-11D-A386-01 ...
[["SARC_Mutation-20160128"]] TCGA-3B-A9HI-01A-11D-A387-09 ...
[["SARC_RNASeq2Gene-20160128"]] TCGA-3B-A9HI-01A-11R-A38C-07 ...
[["SARC_RPPAArray-20160128"]] TCGA-3B-A9HI-01A-21-A456-20 ...
[["SARC_miRNASeqGene-20160128"]] TCGA-3B-A9HI-01A-11R-A38N-13 ...
[["SARC_RNASeq2GeneNorm-20160128"]] TCGA-3B-A9HI-01 ... TCGA-Z4-AAPG-01
...
<1 more element>

```

Sizes of each ExperimentList element:

		assay size.Mb
1	SARC_CNASNP-20160128	9.2 Mb
2	SARC_CNVSNP-20160128	3 Mb
3	SARC_GISTIC_AllByGene-20160128	52.2 Mb
4	SARC_GISTIC_Peaks-20160128	0.2 Mb
5	SARC_GISTIC_ThresholdedByGene-20160128	51.9 Mb
6	SARC_Mutation-20160128	19.5 Mb
7	SARC_RNASeq2Gene-20160128	44 Mb
8	SARC_RPPAArray-20160128	0.4 Mb
9	SARC_miRNASeqGene-20160128	2.3 Mb
10	SARC_RNASeq2GeneNorm-20160128	39 Mb
11	SARC_Methylation-20160128	75 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

162 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
[1,] 99 99 1.78 1.51 2.46

```

-----  
Available sample meta-data:  
-----



years\_to\_birth:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 20.00 53.00 61.00 60.88 71.00 90.00 1

vital\_status:  
 0 1  
 162 99

days\_to\_death:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 17.0 322.5 648.0 863.6 1169.5 2694.0 162

days\_to\_last\_followup:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 15.0 585.8 1092.0 1391.1 1891.8 5723.0 99

gender:  
 female male  
 142 119

date\_of\_initial\_pathologic\_diagnosis:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 1994 2007 2010 2009 2012 2013 4

radiation\_therapy:  
 no yes NA's  
 181 74 6

residual\_tumor:  
 r0 r1 r2 rx NA's  
 155 70 9 26 1

race:  
 asian black or african american white  
 6 18 228  
 NA's  
 9

ethnicity:  
 hispanic or latino not hispanic or latino NA's  
 5 223 33

Including an additional 1413 columns

**Description**

A document describing the TCGA cancer code

**Details**

```
> experiments( SKCM )
ExperimentList class object of length 11:
 [1] SKCM_CNASeq-20160128: RaggedExperiment with 31416 rows and 238 columns
 [2] SKCM_CNASNP-20160128: RaggedExperiment with 452114 rows and 938 columns
 [3] SKCM_CNVSNP-20160128: RaggedExperiment with 108084 rows and 937 columns
 [4] SKCM_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 367 columns
 [5] SKCM_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 53 rows and 367 columns
 [6] SKCM_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 367 columns
 [7] SKCM_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 452 columns
 [8] SKCM_Mutation-20160128: RaggedExperiment with 290322 rows and 345 columns
 [9] SKCM_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 473 columns
 [10] SKCM_RPPAArray-20160128: SummarizedExperiment with 208 rows and 355 columns
 [11] SKCM_Methylation-20160128: SummarizedExperiment with 485577 rows and 475 columns

> rownames( SKCM )
CharacterList of length 11
[["SKCM_CNASeq-20160128"]] character(0)
[["SKCM_CNASNP-20160128"]] character(0)
[["SKCM_CNVSNP-20160128"]] character(0)
[["SKCM_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["SKCM_GISTIC_Peaks-20160128"]] chr1:1-6847369 ... chr22:41468899-41849552
[["SKCM_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["SKCM_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["SKCM_Mutation-20160128"]] character(0)
[["SKCM_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPT22 tAKR
[["SKCM_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<1 more element>

> colnames( SKCM )
CharacterList of length 11
[["SKCM_CNASeq-20160128"]] TCGA-BF-A1PU-01A-11D-A18Z-02 ...
[["SKCM_CNASNP-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_CNVSNP-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_GISTIC_AllByGene-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_GISTIC_Peaks-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_GISTIC_ThresholdedByGene-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_miRNASeqGene-20160128"]] TCGA-3N-A9WC-06A-11R-A38N-13 ...
[["SKCM_Mutation-20160128"]] TCGA-BF-A1PU-01A-11D-A19A-08 ...
[["SKCM_RNASeq2GeneNorm-20160128"]] TCGA-3N-A9WB-06A-11R-A38C-07 ...
[["SKCM_RPPAArray-20160128"]] TCGA-3N-A9WC-06A-21-A444-20 ...
...
<1 more element>
```

Sizes of each ExperimentList element:

	assay	size.Mb
1	SKCM_CNASeq-20160128	0.9 Mb
2	SKCM_CNASNP-20160128	12.3 Mb
3	SKCM_CNVSNP-20160128	3.2 Mb
4	SKCM_GISTIC_AllByGene-20160128	4.9 Mb
5	SKCM_GISTIC_Peaks-20160128	0.1 Mb
6	SKCM_GISTIC_ThresholdedByGene-20160128	4.9 Mb
7	SKCM_miRNASeqGene-20160128	0.1 Mb
8	SKCM_Mutation-20160128	299.6 Mb
9	SKCM_RNASeq2GeneNorm-20160128	1.3 Mb
10	SKCM_RPPAArray-20160128	0 Mb
11	SKCM_Methylation-20160128	75.1 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

Call: survfit(formula = survival::Surv(colDat\$days\_to\_death/365, colDat\$vital\_status) ~  
-1)

249 observations deleted due to missingness

n	events	median	0.95LCL	0.95UCL
221.00	221.00	2.99	2.40	3.90

-----  
Available sample meta-data:  
-----

years\_to\_birth:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
15.00	48.00	58.00	58.24	71.00	90.00	8

vital\_status:

0	1
247	223

days\_to\_death:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
79	518	1093	1789	2073	10870	249

days\_to\_last\_followup:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
-2.0	477.5	1146.0	1885.3	2658.8	11252.0	230

```

days_to_submitted_specimen_dx:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
   -2      0     344   1017  1372   10847    14

```

```

melanoma_ulceration:
  no  yes NA's
 146 167 157

```

```

melanoma_primary_known:
  no  yes
  47 423

```

```

Breslow_thickness:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
 0.000  1.300   3.000   5.585  6.950   75.000   111

```

```

gender:
  female  male
   180    290

```

```

date_of_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
 1978   2003   2008   2006   2011   2013    11

```

```

radiation_therapy:
  no  yes NA's
 420  49   1

```

```

race:
          asian black or african american          white
           12                             1          447
          NA's
           10

```

```

ethnicity:
  hispanic or latino not hispanic or latino  NA's
           11                             446          13

```

Including an additional 1517 columns

### See Also

[SKCM-v2.0.1](#)

**Description**

A document describing the TCGA cancer code

**Details**

```
> experiments( SKCM )
ExperimentList class object of length 12:
 [1] SKCM_CNASeq-20160128: RaggedExperiment with 31416 rows and 238 columns
 [2] SKCM_CNASNP-20160128: RaggedExperiment with 452114 rows and 938 columns
 [3] SKCM_CNVSNP-20160128: RaggedExperiment with 108084 rows and 937 columns
 [4] SKCM_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 367 columns
 [5] SKCM_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 53 rows and 367 columns
 [6] SKCM_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 367 columns
 [7] SKCM_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 452 columns
 [8] SKCM_Mutation-20160128: RaggedExperiment with 290322 rows and 345 columns
 [9] SKCM_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 473 columns
 [10] SKCM_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 473 columns
 [11] SKCM_RPPAArray-20160128: SummarizedExperiment with 208 rows and 355 columns
 [12] SKCM_Methylation-20160128: SummarizedExperiment with 485577 rows and 475 columns

> rownames( SKCM )
CharacterList of length 12
[["SKCM_CNASeq-20160128"]] character(0)
[["SKCM_CNASNP-20160128"]] character(0)
[["SKCM_CNVSNP-20160128"]] character(0)
[["SKCM_GISTIC_AllByGene-20160128"]] character(0)
[["SKCM_GISTIC_Peaks-20160128"]] 21 22 1 2 3 23 24 4 ... 50 51 52 18 53 19 20
[["SKCM_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["SKCM_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["SKCM_Mutation-20160128"]] character(0)
[["SKCM_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["SKCM_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
...
<2 more elements>

> colnames( SKCM )
CharacterList of length 12
[["SKCM_CNASeq-20160128"]] TCGA-BF-A1PU-01A-11D-A18Z-02 ...
[["SKCM_CNASNP-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_CNVSNP-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_GISTIC_AllByGene-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_GISTIC_Peaks-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_GISTIC_ThresholdedByGene-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
```

```

[["SKCM_miRNASeqGene-20160128"]] TCGA-3N-A9WC-06A-11R-A38N-13 ...
[["SKCM_Mutation-20160128"]] TCGA-BF-A1PU-01A-11D-A19A-08 ...
[["SKCM_RNASeq2Gene-20160128"]] TCGA-3N-A9WB-06A-11R-A38C-07 ...
[["SKCM_RNASeq2GeneNorm-20160128"]] TCGA-3N-A9WB-06A-11R-A38C-07 ...
...
<2 more elements>

```

Sizes of each ExperimentList element:

	assay	size.Mb
1	SKCM_CNASeq-20160128	0.9 Mb
2	SKCM_CNASNP-20160128	12.3 Mb
3	SKCM_CNVSNP-20160128	3.2 Mb
4	SKCM_GISTIC_AllByGene-20160128	73 Mb
5	SKCM_GISTIC_Peaks-20160128	0.3 Mb
6	SKCM_GISTIC_ThresholdedByGene-20160128	72.8 Mb
7	SKCM_miRNASeqGene-20160128	3.8 Mb
8	SKCM_Mutation-20160128	299.6 Mb
9	SKCM_RNASeq2Gene-20160128	76.6 Mb
10	SKCM_RNASeq2GeneNorm-20160128	76.6 Mb
11	SKCM_RPPAArray-20160128	0.7 Mb
12	SKCM_Methylation-20160128	75.1 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

249 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
221.00 221.00   2.99   2.40   3.90

```

-----  
Available sample meta-data:  
-----

```

years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
 15.00  48.00   58.00   58.24  71.00   90.00    8

```

```

vital_status:
  0  1
247 223

```

```

days_to_death:

```

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
	79	518	1093	1789	2073	10870	249
days_to_last_followup:							
	-2.0	477.5	1146.0	1885.3	2658.8	11252.0	230
days_to_submitted_specimen_dx:							
	-2	0	344	1017	1372	10847	14
melanoma_ulceration:							
no yes NA's	146	167	157				
melanoma_primary_known:							
no yes	47	423					
Breslow_thickness:							
	0.000	1.300	3.000	5.585	6.950	75.000	111
gender:							
female male	180	290					
date_of_initial_pathologic_diagnosis:							
	1978	2003	2008	2006	2011	2013	11
radiation_therapy:							
no yes NA's	420	49	1				
race:							
		asian	black or african american			white	
		12			1	447	
		NA's					
		10					
ethnicity:							
	hispanic or latino	not hispanic or latino				NA's	
		11		446		13	

Including an additional 1517 columns

---

SKCM-v2.1.0

*Skin Cutaneous Melanoma*

---

## Description

A document describing the TCGA cancer code

## Details

```
> experiments( SKCM )
ExperimentList class object of length 12:
 [1] SKCM_CNASeq-20160128: RaggedExperiment with 31416 rows and 238 columns
 [2] SKCM_CNASNP-20160128: RaggedExperiment with 452114 rows and 938 columns
 [3] SKCM_CNVSNP-20160128: RaggedExperiment with 108084 rows and 937 columns
 [4] SKCM_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 367 columns
 [5] SKCM_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 53 rows and 367 columns
 [6] SKCM_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 367 columns
 [7] SKCM_Mutation-20160128: RaggedExperiment with 290322 rows and 345 columns
 [8] SKCM_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 473 columns
 [9] SKCM_RPPAArray-20160128: SummarizedExperiment with 208 rows and 355 columns
 [10] SKCM_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 452 columns
 [11] SKCM_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18071 rows and 473 columns
 [12] SKCM_Methylation-20160128: SummarizedExperiment with 485577 rows and 475 columns

> rownames( SKCM )
CharacterList of length 12
[["SKCM_CNASeq-20160128"]] character(0)
[["SKCM_CNASNP-20160128"]] character(0)
[["SKCM_CNVSNP-20160128"]] character(0)
[["SKCM_GISTIC_AllByGene-20160128"]] character(0)
[["SKCM_GISTIC_Peaks-20160128"]] 21 22 1 2 3 23 24 4 ... 50 51 52 18 53 19 20
[["SKCM_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["SKCM_Mutation-20160128"]] character(0)
[["SKCM_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
[["SKCM_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["SKCM_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
...
<2 more elements>

> colnames( SKCM )
CharacterList of length 12
[["SKCM_CNASeq-20160128"]] TCGA-BF-A1PU-01A-11D-A18Z-02 ...
[["SKCM_CNASNP-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_CNVSNP-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
```



```

[["SKCM_GISTIC_AllByGene-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_GISTIC_Peaks-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_GISTIC_ThresholdedByGene-20160128"]] TCGA-3N-A9WB-06A-11D-A38F-01 ...
[["SKCM_Mutation-20160128"]] TCGA-BF-A1PU-01A-11D-A19A-08 ...
[["SKCM_RNASeq2Gene-20160128"]] TCGA-3N-A9WB-06A-11R-A38C-07 ...
[["SKCM_RPPAArray-20160128"]] TCGA-3N-A9WC-06A-21-A444-20 ...
[["SKCM_miRNASeqGene-20160128"]] TCGA-3N-A9WC-06A-11R-A38N-13 ...
...
<2 more elements>

```

Sizes of each ExperimentList element:

	assay	size.Mb
1	SKCM_CNASeq-20160128	0.9 Mb
2	SKCM_CNASNP-20160128	12.3 Mb
3	SKCM_CNVSNP-20160128	3.2 Mb
4	SKCM_GISTIC_AllByGene-20160128	73 Mb
5	SKCM_GISTIC_Peaks-20160128	0.3 Mb
6	SKCM_GISTIC_ThresholdedByGene-20160128	72.8 Mb
7	SKCM_Mutation-20160128	299.6 Mb
8	SKCM_RNASeq2Gene-20160128	76.6 Mb
9	SKCM_RPPAArray-20160128	0.7 Mb
10	SKCM_miRNASeqGene-20160128	3.8 Mb
11	SKCM_RNASeq2GeneNorm-20160128	67.5 Mb
12	SKCM_Methylation-20160128	75.1 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

249 observations deleted due to missingness
      n events median 0.95LCL 0.95UCL
[1,] 221    221   2.99    2.4    3.9

```

-----  
Available sample meta-data:  
-----

```

years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
 15.00  48.00   58.00   58.24  71.00   90.00    8

```

```

vital_status:
 0  1

```

247 223

days\_to\_death:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
79	518	1093	1789	2073	10870	249

days\_to\_last\_followup:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
-2.0	477.5	1146.0	1885.3	2658.8	11252.0	230

days\_to\_submitted\_specimen\_dx:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
-2	0	344	1017	1372	10847	14

melanoma\_ulceration:

no	yes	NA's
146	167	157

melanoma\_primary\_known:

no	yes
47	423

Breslow\_thickness:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.000	1.300	3.000	5.585	6.950	75.000	111

gender:

female	male
180	290

date\_of\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1978	2003	2008	2006	2011	2013	11

radiation\_therapy:

no	yes	NA's
420	49	1

race:

asian	black or african american	white
12	1	447
NA's		
10		

```
ethnicity:
  hispanic or latino not hispanic or latino      NA's
                11                446                13
```

Including an additional 1517 columns

---

SKCM-v2.1.1

*Skin Cutaneous Melanoma*

---

## Description

A document describing the TCGA cancer code Note. Only the colData has changed.

## Details

```
> experiments( SKCM )
ExperimentList class object of length 0:
```

```
> rownames( SKCM )
CharacterList of length 0
```

```
> colnames( SKCM )
CharacterList of length 0
```

Sizes of each ExperimentList element:

```
[1] assay   size.Mb
<0 rows> (or 0-length row.names)
```

```
-----
Overall survival time-to-event summary (in years):
-----
```

```
Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)
```

```
249 observations deleted due to missingness
      n events median 0.95LCL 0.95UCL
[1,] 221    221   2.99    2.4    3.9
```

```
-----
Available sample meta-data:
-----
```

```
years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
```

15.00 48.00 58.00 58.24 71.00 90.00 8

vital\_status:

0 1  
247 223

days\_to\_death:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
79	518	1093	1789	2073	10870	249

days\_to\_last\_followup:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
-2.0	477.5	1146.0	1885.3	2658.8	11252.0	230

days\_to\_submitted\_specimen\_dx:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
-2	0	344	1017	1372	10847	14

melanoma\_ulceration:

no yes NA's  
146 167 157

melanoma\_primary\_known:

no yes  
47 423

Breslow\_thickness:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.000	1.300	3.000	5.585	6.950	75.000	111

gender:

female male  
180 290

date\_of\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1978	2003	2008	2006	2011	2013	11

radiation\_therapy:

no yes NA's  
420 49 1

race:

asian black or african american

white

	12	1	447
NA's			
	10		

ethnicity:

hispanic or latino	not hispanic or latino	NA's
11	446	13

Including an additional 1517 columns

---

STAD

*Stomach adenocarcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

```
> experiments( STAD )
ExperimentList class object of length 13:
 [1] STAD_CNASeq-20160128: RaggedExperiment with 31824 rows and 214 columns
 [2] STAD_CNASNP-20160128: RaggedExperiment with 443042 rows and 906 columns
 [3] STAD_CNVSNP-20160128: RaggedExperiment with 118389 rows and 904 columns
 [4] STAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 441 columns
 [5] STAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 84 rows and 441 columns
 [6] STAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 441 columns
 [7] STAD_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 430 columns
 [8] STAD_Mutation-20160128: RaggedExperiment with 148520 rows and 289 columns
 [9] STAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 450 columns
 [10] STAD_RNASeqGene-20160128: SummarizedExperiment with 26120 rows and 36 columns
 [11] STAD_RPPAArray-20160128: SummarizedExperiment with 195 rows and 357 columns
 [12] STAD_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 73 columns
 [13] STAD_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 397 columns

> rownames( STAD )
CharacterList of length 13
[["STAD_CNASeq-20160128"]] character(0)
[["STAD_CNASNP-20160128"]] character(0)
[["STAD_CNVSNP-20160128"]] character(0)
[["STAD_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["STAD_GISTIC_Peaks-20160128"]] chr1:10686864-11068052 ...
[["STAD_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["STAD_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["STAD_Mutation-20160128"]] character(0)
[["STAD_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["STAD_RNASeqGene-20160128"]] AADACL3 AADACL4 AB007962 ... VCY XKRY ZFY
```

```

...
<3 more elements>

> colnames( STAD )
CharacterList of length 13
[["STAD_CNASeq-20160128"]] TCGA-B7-5816-01A-21D-1598-02 ...
[["STAD_CNASNP-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_CNVSNP-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_GISTIC_AllByGene-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_GISTIC_Peaks-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_miRNASeqGene-20160128"]] TCGA-3M-AB46-01A-11R-A415-13 ...
[["STAD_Mutation-20160128"]] TCGA-B7-5816-01A-21D-1600-08 ...
[["STAD_RNASeq2GeneNorm-20160128"]] TCGA-3M-AB46-01A-11R-A414-31 ...
[["STAD_RNASeqGene-20160128"]] TCGA-BR-4191-01A-02R-1131-13 ...
...
<3 more elements>

```

Sizes of each ExperimentList element:

	assay	size.Mb
1	STAD_CNASeq-20160128	0.9 Mb
2	STAD_CNASNP-20160128	12.1 Mb
3	STAD_CNVSNP-20160128	3.4 Mb
4	STAD_GISTIC_AllByGene-20160128	4.9 Mb
5	STAD_GISTIC_Peaks-20160128	0.1 Mb
6	STAD_GISTIC_ThresholdedByGene-20160128	4.9 Mb
7	STAD_miRNASeqGene-20160128	0.1 Mb
8	STAD_Mutation-20160128	161.5 Mb
9	STAD_RNASeq2GeneNorm-20160128	1.3 Mb
10	STAD_RNASeqGene-20160128	1.7 Mb
11	STAD_RPPAArray-20160128	0 Mb
12	STAD_Methylation_methyl27-20160128	4.9 Mb
13	STAD_Methylation_methyl450-20160128	75 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

273 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
170.000 170.000  0.948  0.792  1.085

```

-----

Available sample meta-data:

-----

years\_to\_birth:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
30.00	58.00	67.00	65.73	73.00	90.00	9

vital\_status:

0	1
268	175

days\_to\_death:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.0	194.0	346.0	423.7	553.5	2197.0	273

days\_to\_last\_followup:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.0	335.5	547.5	673.7	912.0	3720.0	177

tumor\_tissue\_site:

stomach
443

pathology\_M\_stage:

m0	m1	mx
391	30	22

gender:

female	male
158	285

date\_of\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1996	2010	2011	2010	2012	2013	6

radiation\_therapy:

no	yes	NA's
323	77	43

residual\_tumor:

r0	r1	r2	rx	NA's
350	18	19	25	31

number\_of\_lymph\_nodes:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.000	0.000	3.000	5.635	8.000	57.000	51

race:

asian	89
black or african american	13
native hawaiian or other pacific islander	1
white	278
NA's	62

ethnicity:

hispanic or latino	5	NA's	120
not hispanic or latino	318		

Including an additional 1390 columns

### See Also

[STAD-v2.0.1](#)

---

STAD-v2.0.1

*Stomach adenocarcinoma*

---

### Description

A document describing the TCGA cancer code

### Details

```
> experiments( STAD )
ExperimentList class object of length 14:
 [1] STAD_CNASeq-20160128: RaggedExperiment with 31824 rows and 214 columns
 [2] STAD_CNASNP-20160128: RaggedExperiment with 443042 rows and 906 columns
 [3] STAD_CNVSNP-20160128: RaggedExperiment with 118389 rows and 904 columns
 [4] STAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 441 columns
 [5] STAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 84 rows and 441 columns
 [6] STAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 441 columns
 [7] STAD_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 430 columns
 [8] STAD_Mutation-20160128: RaggedExperiment with 148520 rows and 289 columns
 [9] STAD_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 450 columns
 [10] STAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 450 columns
 [11] STAD_RNASeqGene-20160128: SummarizedExperiment with 26120 rows and 271 columns
```



```
[12] STAD_RPPAArray-20160128: SummarizedExperiment with 195 rows and 357 columns
[13] STAD_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 73 columns
[14] STAD_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 397 columns
```

```
> rownames( STAD )
CharacterList of length 14
[["STAD_CNASeq-20160128"]] character(0)
[["STAD_CNASNP-20160128"]] character(0)
[["STAD_CNVSNP-20160128"]] character(0)
[["STAD_GISTIC_AllByGene-20160128"]] character(0)
[["STAD_GISTIC_Peaks-20160128"]] 1 37 38 2 3 39 40 ... 81 34 82 35 83 84 85
[["STAD_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["STAD_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["STAD_Mutation-20160128"]] character(0)
[["STAD_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["STAD_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
...
<4 more elements>
```

```
> colnames( STAD )
CharacterList of length 14
[["STAD_CNASeq-20160128"]] TCGA-B7-5816-01A-21D-1598-02 ...
[["STAD_CNASNP-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_CNVSNP-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_GISTIC_AllByGene-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_GISTIC_Peaks-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_miRNASeqGene-20160128"]] TCGA-3M-AB46-01A-11R-A415-13 ...
[["STAD_Mutation-20160128"]] TCGA-B7-5816-01A-21D-1600-08 ...
[["STAD_RNASeq2Gene-20160128"]] TCGA-3M-AB46-01A-11R-A414-31 ...
[["STAD_RNASeq2GeneNorm-20160128"]] TCGA-3M-AB46-01A-11R-A414-31 ...
...
<4 more elements>
```

Sizes of each ExperimentList element:

	assay	size.Mb
1	STAD_CNASeq-20160128	0.9 Mb
2	STAD_CNASNP-20160128	12.1 Mb
3	STAD_CNVSNP-20160128	3.4 Mb
4	STAD_GISTIC_AllByGene-20160128	87 Mb
5	STAD_GISTIC_Peaks-20160128	0.4 Mb
6	STAD_GISTIC_ThresholdedByGene-20160128	86.8 Mb
7	STAD_miRNASeqGene-20160128	3.7 Mb
8	STAD_Mutation-20160128	161.5 Mb
9	STAD_RNASeq2Gene-20160128	73 Mb
10	STAD_RNASeq2GeneNorm-20160128	73 Mb
11	STAD_RNASeqGene-20160128	57.4 Mb

```

12          STAD_RPPAArray-20160128    0.6 Mb
13  STAD_Methylation_methyl27-20160128  4.9 Mb
14  STAD_Methylation_methyl450-20160128 75.1 Mb

```

```

-----
Overall survival time-to-event summary (in years):
-----

```

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

      273 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
170.000 170.000   0.948   0.792   1.085

```

```

-----
Available sample meta-data:
-----

```

```

years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
 30.00  58.00   67.00   65.73  73.00   90.00     9

```

```

vital_status:
  0  1
268 175

```

```

days_to_death:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
  0.0   194.0   346.0   423.7  553.5  2197.0   273

```

```

days_to_last_followup:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
  0.0   335.5   547.5   673.7  912.0  3720.0   177

```

```

tumor_tissue_site:
stomach
  443

```

```

pathology_M_stage:
  m0  m1  mx
391  30  22

```

```

gender:

```

female male  
158 285

date\_of\_initial\_pathologic\_diagnosis:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
1996 2010 2011 2010 2012 2013 6

radiation\_therapy:  
no yes NA's  
323 77 43

residual\_tumor:  
r0 r1 r2 rx NA's  
350 18 19 25 31

number\_of\_lymph\_nodes:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
0.000 0.000 3.000 5.635 8.000 57.000 51

race:  
asian  
89  
black or african american  
13  
native hawaiian or other pacific islander  
1  
white  
278  
NA's  
62

ethnicity:  
hispanic or latino not hispanic or latino NA's  
5 318 120

Including an additional 1390 columns

---

STAD-v2.1.0

*Stomach adenocarcinoma*

---

## Description

A document describing the TCGA cancer code

**Details**

```

> experiments( STAD )
ExperimentList class object of length 14:
 [1] STAD_CNASeq-20160128: RaggedExperiment with 31824 rows and 214 columns
 [2] STAD_CNASNP-20160128: RaggedExperiment with 443042 rows and 906 columns
 [3] STAD_CNVSNP-20160128: RaggedExperiment with 118389 rows and 904 columns
 [4] STAD_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 441 columns
 [5] STAD_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 84 rows and 441 columns
 [6] STAD_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 441 columns
 [7] STAD_Mutation-20160128: RaggedExperiment with 148520 rows and 289 columns
 [8] STAD_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 450 columns
 [9] STAD_RNASeqGene-20160128: SummarizedExperiment with 26120 rows and 271 columns
[10] STAD_RPPAArray-20160128: SummarizedExperiment with 195 rows and 357 columns
[11] STAD_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 430 columns
[12] STAD_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18664 rows and 450 columns
[13] STAD_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 73 columns
[14] STAD_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 397 columns

> rownames( STAD )
CharacterList of length 14
[["STAD_CNASeq-20160128"]] character(0)
[["STAD_CNASNP-20160128"]] character(0)
[["STAD_CNVSNP-20160128"]] character(0)
[["STAD_GISTIC_AllByGene-20160128"]] character(0)
[["STAD_GISTIC_Peaks-20160128"]] 1 37 38 2 3 39 40 ... 81 34 82 35 83 84 85
[["STAD_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["STAD_Mutation-20160128"]] character(0)
[["STAD_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["STAD_RNASeqGene-20160128"]] AADACL3 AADACL4 AB007962 ... VCY XKRY ZFY
[["STAD_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<4 more elements>

> colnames( STAD )
CharacterList of length 14
[["STAD_CNASeq-20160128"]] TCGA-B7-5816-01A-21D-1598-02 ...
[["STAD_CNASNP-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_CNVSNP-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_GISTIC_AllByGene-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_GISTIC_Peaks-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_GISTIC_ThresholdedByGene-20160128"]] TCGA-3M-AB46-01A-11D-A40Z-01 ...
[["STAD_Mutation-20160128"]] TCGA-B7-5816-01A-21D-1600-08 ...
[["STAD_RNASeq2Gene-20160128"]] TCGA-3M-AB46-01A-11R-A414-31 ...
[["STAD_RNASeqGene-20160128"]] TCGA-B7-5816-01A-21R-1602-13 ...
[["STAD_RPPAArray-20160128"]] TCGA-3M-AB47-01A-11-A43D-20 ...
...
<4 more elements>

```

Sizes of each ExperimentList element:

	assay	size.Mb
1	STAD_CNASeq-20160128	0.9 Mb
2	STAD_CNASNP-20160128	12.1 Mb
3	STAD_CNVSNP-20160128	3.4 Mb
4	STAD_GISTIC_AllByGene-20160128	87 Mb
5	STAD_GISTIC_Peaks-20160128	0.4 Mb
6	STAD_GISTIC_ThresholdedByGene-20160128	86.8 Mb
7	STAD_Mutation-20160128	161.5 Mb
8	STAD_RNASeq2Gene-20160128	73 Mb
9	STAD_RNASeqGene-20160128	57.4 Mb
10	STAD_RPPAArray-20160128	0.6 Mb
11	STAD_miRNASeqGene-20160128	3.7 Mb
12	STAD_RNASeq2GeneNorm-20160128	66.5 Mb
13	STAD_Methylation_methyl27-20160128	4.9 Mb
14	STAD_Methylation_methyl450-20160128	75.1 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

Call: survfit(formula = survival::Surv(colDat\$days\_to\_death/365, colDat\$vital\_status) ~  
-1)

273 observations deleted due to missingness  
n events median 0.95LCL 0.95UCL  
[1,] 170 170 0.948 0.792 1.08

-----  
Available sample meta-data:  
-----

years\_to\_birth:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
30.00 58.00 67.00 65.73 73.00 90.00 9

vital\_status:  
0 1  
268 175

days\_to\_death:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
0.0 194.0 346.0 423.7 553.5 2197.0 273

days\_to\_last\_followup:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's

0.0 335.5 547.5 673.7 912.0 3720.0 177

tumor\_tissue\_site:

stomach

443

pathology\_M\_stage:

m0 m1 mx

391 30 22

gender:

female male

158 285

date\_of\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1996	2010	2011	2010	2012	2013	6

radiation\_therapy:

no yes NA's

323 77 43

residual\_tumor:

r0 r1 r2 rx NA's

350 18 19 25 31

number\_of\_lymph\_nodes:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.000	0.000	3.000	5.635	8.000	57.000	51

race:

asian

89

black or african american

13

native hawaiian or other pacific islander

1

white

278

NA's

62

ethnicity:

hispanic or latino not hispanic or latino

NA's

5

318

120

Including an additional 1390 columns

---

 TGCT

*Testicular Germ Cell Tumors*


---

## Description

A document describing the TCGA cancer code

## Details

```

> experiments( TGCT )
ExperimentList class object of length 10:
 [1] TGCT_CNASNP-20160128: RaggedExperiment with 137968 rows and 271 columns
 [2] TGCT_CNVSNP-20160128: RaggedExperiment with 25479 rows and 271 columns
 [3] TGCT_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 134 columns
 [4] TGCT_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 48 rows and 134 columns
 [5] TGCT_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 134 columns
 [6] TGCT_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 139 columns
 [7] TGCT_Mutation-20160128: RaggedExperiment with 14672 rows and 138 columns
 [8] TGCT_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 139 columns
 [9] TGCT_RPPAArray-20160128: SummarizedExperiment with 192 rows and 107 columns
 [10] TGCT_Methylation-20160128: SummarizedExperiment with 485577 rows and 139 columns

> rownames( TGCT )
CharacterList of length 10
[["TGCT_CNASNP-20160128"]] character(0)
[["TGCT_CNVSNP-20160128"]] character(0)
[["TGCT_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["TGCT_GISTIC_Peaks-20160128"]] chr1:1-48649489 ... chr22:18613558-22141824
[["TGCT_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["TGCT_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["TGCT_Mutation-20160128"]] character(0)
[["TGCT_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["TGCT_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["TGCT_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873

> colnames( TGCT )
CharacterList of length 10
[["TGCT_CNASNP-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_CNVSNP-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_GISTIC_AllByGene-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_GISTIC_Peaks-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_GISTIC_ThresholdedByGene-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_miRNASeqGene-20160128"]] TCGA-2G-AAEW-01A-11R-A439-13 ...

```

```

[["TGCT_Mutation-20160128"]] TCGA-2G-AAEW-01A-11D-A42Y-10 ...
[["TGCT_RNASeq2GeneNorm-20160128"]] TCGA-2G-AAEW-01A-11R-A430-07 ...
[["TGCT_RPPAArray-20160128"]] TCGA-2G-AAEW-01A-21-A45P-20 ...
[["TGCT_Methylation-20160128"]] TCGA-2G-AAEW-01A-11D-A42Z-05 ...

```

Sizes of each ExperimentList element:

		assay	size.Mb
1		TGCT_CNASNP-20160128	3.8 Mb
2		TGCT_CNVSNP-20160128	0.8 Mb
3		TGCT_GISTIC_AllByGene-20160128	4.9 Mb
4		TGCT_GISTIC_Peaks-20160128	0.1 Mb
5		TGCT_GISTIC_ThresholdedByGene-20160128	4.9 Mb
6		TGCT_miRNASeqGene-20160128	0.1 Mb
7		TGCT_Mutation-20160128	10 Mb
8		TGCT_RNASeq2GeneNorm-20160128	1.3 Mb
9		TGCT_RPPAArray-20160128	0 Mb
10		TGCT_Methylation-20160128	75 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

Call: survfit(formula = survival::Surv(colDat\$days\_to\_death/365, colDat\$vital\_status) ~  
-1)

```

130 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
4.0000 4.0000 1.5493 0.0466      NA

```

-----  
Available sample meta-data:  
-----

```

years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 14.00  26.00   31.00   31.99  37.00   67.00

```

vital\_status:

```

  0  1
130 4

```

days\_to\_death:

```

 17 513 618 6972 NA's
  1  1  1  1 130

```

days\_to\_last\_followup:



Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
3.0	688.2	1265.5	2092.7	2826.2	7437.0	4

tumor\_tissue\_site:

testes	134
--------	-----

pathology\_T\_stage:

t1	t2	t3	tx
76	51	6	1

pathology\_N\_stage:

n0	n1	n2	nx	NA's
46	11	2	65	10

pathology\_M\_stage:

m0	m1	m1a	m1b	NA's
115	2	1	1	15

gender:

male	134
------	-----

date\_of\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
1992	2006	2009	2008	2012	2013

radiation\_therapy:

no	yes	NA's
111	21	2

karnofsky\_performance\_score:

80	90	100	NA's
5	41	56	32

race:

asian	black or african american	white
4	6	119
NA's		
5		

ethnicity:

hispanic or latino	not hispanic or latino	NA's
12	111	11

Including an additional 762 columns

**See Also**[TGCT-v2.0.1](#)

TGCT-v2.0.1

*Testicular Germ Cell Tumors***Description**

A document describing the TCGA cancer code

**Details**

```

> experiments( TGCT )
ExperimentList class object of length 11:
 [1] TGCT_CNASNP-20160128: RaggedExperiment with 137968 rows and 271 columns
 [2] TGCT_CNVSNP-20160128: RaggedExperiment with 25479 rows and 271 columns
 [3] TGCT_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 134 columns
 [4] TGCT_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 48 rows and 134 columns
 [5] TGCT_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 134 columns
 [6] TGCT_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 139 columns
 [7] TGCT_Mutation-20160128: RaggedExperiment with 14672 rows and 138 columns
 [8] TGCT_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 139 columns
 [9] TGCT_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 139 columns
 [10] TGCT_RPPAArray-20160128: SummarizedExperiment with 192 rows and 107 columns
 [11] TGCT_Methylation-20160128: SummarizedExperiment with 485577 rows and 139 columns

> rownames( TGCT )
CharacterList of length 11
[["TGCT_CNASNP-20160128"]] character(0)
[["TGCT_CNVSNP-20160128"]] character(0)
[["TGCT_GISTIC_AllByGene-20160128"]] character(0)
[["TGCT_GISTIC_Peaks-20160128"]] 17 18 1 19 2 20 21 ... 44 45 47 46 48 15 16
[["TGCT_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["TGCT_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["TGCT_Mutation-20160128"]] character(0)
[["TGCT_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["TGCT_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["TGCT_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<1 more element>

> colnames( TGCT )
CharacterList of length 11
[["TGCT_CNASNP-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_CNVSNP-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_GISTIC_AllByGene-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_GISTIC_Peaks-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...

```

```

[["TGCT_GISTIC_ThresholdedByGene-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_miRNASeqGene-20160128"]] TCGA-2G-AAEW-01A-11R-A439-13 ...
[["TGCT_Mutation-20160128"]] TCGA-2G-AAEW-01A-11D-A42Y-10 ...
[["TGCT_RNASeq2Gene-20160128"]] TCGA-2G-AAEW-01A-11R-A430-07 ...
[["TGCT_RNASeq2GeneNorm-20160128"]] TCGA-2G-AAEW-01A-11R-A430-07 ...
[["TGCT_RPPAArray-20160128"]] TCGA-2G-AAEW-01A-21-A45P-20 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

		assay	size.Mb
1	TGCT_CNASNP-20160128		3.8 Mb
2	TGCT_CNVSNP-20160128		0.8 Mb
3	TGCT_GISTIC_AllByGene-20160128		28.8 Mb
4	TGCT_GISTIC_Peaks-20160128		0.1 Mb
5	TGCT_GISTIC_ThresholdedByGene-20160128		28.7 Mb
6	TGCT_miRNASeqGene-20160128		1.3 Mb
7	TGCT_Mutation-20160128		10 Mb
8	TGCT_RNASeq2Gene-20160128		24.3 Mb
9	TGCT_RNASeq2GeneNorm-20160128		24.3 Mb
10	TGCT_RPPAArray-20160128		0.2 Mb
11	TGCT_Methylation-20160128		75 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

130 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
4.0000 4.0000 1.5493 0.0466      NA

```

-----  
Available sample meta-data:  
-----

```

years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 14.00  26.00   31.00   31.99  37.00   67.00

```

```

vital_status:
  0  1
130 4

```

## days\_to\_death:

17	513	618	6972	NA's
1	1	1	1	130

## days\_to\_last\_followup:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
3.0	688.2	1265.5	2092.7	2826.2	7437.0	4

## tumor\_tissue\_site:

testes
134

## pathology\_T\_stage:

t1	t2	t3	tx
76	51	6	1

## pathology\_N\_stage:

n0	n1	n2	nx	NA's
46	11	2	65	10

## pathology\_M\_stage:

m0	m1	m1a	m1b	NA's
115	2	1	1	15

## gender:

male
134

## date\_of\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
1992	2006	2009	2008	2012	2013

## radiation\_therapy:

no	yes	NA's
111	21	2

## karnofsky\_performance\_score:

80	90	100	NA's
5	41	56	32

## race:

asian	black or african american	white
4	6	119
NA's		
5		

## ethnicity:

hispanic or latino	not hispanic or latino	NA's
12	111	11

Including an additional 762 columns

---

TGCT-v2.1.0

*Testicular Germ Cell Tumors*

---

## Description

A document describing the TCGA cancer code

## Details

```
> experiments( TGCT )
ExperimentList class object of length 11:
 [1] TGCT_CNASNP-20160128: RaggedExperiment with 137968 rows and 271 columns
 [2] TGCT_CNVSNP-20160128: RaggedExperiment with 25479 rows and 271 columns
 [3] TGCT_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 134 columns
 [4] TGCT_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 48 rows and 134 columns
 [5] TGCT_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 134 columns
 [6] TGCT_Mutation-20160128: RaggedExperiment with 14672 rows and 138 columns
 [7] TGCT_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 139 columns
 [8] TGCT_RPPAArray-20160128: SummarizedExperiment with 192 rows and 107 columns
 [9] TGCT_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 139 columns
 [10] TGCT_RNASeq2GeneNorm-20160128: SummarizedExperiment with 19036 rows and 139 columns
 [11] TGCT_Methylation-20160128: SummarizedExperiment with 485577 rows and 139 columns

> rownames( TGCT )
CharacterList of length 11
[["TGCT_CNASNP-20160128"]] character(0)
[["TGCT_CNVSNP-20160128"]] character(0)
[["TGCT_GISTIC_AllByGene-20160128"]] character(0)
[["TGCT_GISTIC_Peaks-20160128"]] 17 18 1 19 2 20 21 ... 44 45 47 46 48 15 16
[["TGCT_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["TGCT_Mutation-20160128"]] character(0)
[["TGCT_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["TGCT_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["TGCT_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["TGCT_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZEF1 ZZZ3 psiTPTE22
...
<1 more element>

> colnames( TGCT )
CharacterList of length 11
[["TGCT_CNASNP-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_CNVSNP-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
```

```

[["TGCT_GISTIC_AllByGene-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_GISTIC_Peaks-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_GISTIC_ThresholdedByGene-20160128"]] TCGA-2G-AAEW-01A-11D-A42X-01 ...
[["TGCT_Mutation-20160128"]] TCGA-2G-AAEW-01A-11D-A42Y-10 ...
[["TGCT_RNASeq2Gene-20160128"]] TCGA-2G-AAEW-01A-11R-A430-07 ...
[["TGCT_RPPAArray-20160128"]] TCGA-2G-AAEW-01A-21-A45P-20 ...
[["TGCT_miRNASeqGene-20160128"]] TCGA-2G-AAEW-01A-11R-A439-13 ...
[["TGCT_RNASeq2GeneNorm-20160128"]] TCGA-2G-AAEW-01 ... TCGA-ZM-AA0N-01
...
<1 more element>

```

Sizes of each ExperimentList element:

		assay size.Mb
1	TGCT_CNASNP-20160128	3.8 Mb
2	TGCT_CNVSNP-20160128	0.8 Mb
3	TGCT_GISTIC_AllByGene-20160128	28.8 Mb
4	TGCT_GISTIC_Peaks-20160128	0.1 Mb
5	TGCT_GISTIC_ThresholdedByGene-20160128	28.7 Mb
6	TGCT_Mutation-20160128	10 Mb
7	TGCT_RNASeq2Gene-20160128	24.3 Mb
8	TGCT_RPPAArray-20160128	0.2 Mb
9	TGCT_miRNASeqGene-20160128	1.3 Mb
10	TGCT_RNASeq2GeneNorm-20160128	22.6 Mb
11	TGCT_Methylation-20160128	75 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

130 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
[1,] 4      4  1.55 0.0466    NA

```

-----  
Available sample meta-data:  
-----

```

years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 14.00  26.00  31.00  31.99  37.00  67.00

```

```

vital_status:
 0  1

```

130 4

days\_to\_death:

17 513 618 6972 NA's

1 1 1 1 130

days\_to\_last\_followup:

Min. 1st Qu. Median Mean 3rd Qu. Max. NA's

3.0 688.2 1265.5 2092.7 2826.2 7437.0 4

tumor\_tissue\_site:

testes

134

pathology\_T\_stage:

t1 t2 t3 tx

76 51 6 1

pathology\_N\_stage:

n0 n1 n2 nx NA's

46 11 2 65 10

pathology\_M\_stage:

m0 m1 m1a m1b NA's

115 2 1 1 15

gender:

male

134

date\_of\_initial\_pathologic\_diagnosis:

Min. 1st Qu. Median Mean 3rd Qu. Max.

1992 2006 2009 2008 2012 2013

radiation\_therapy:

no yes NA's

111 21 2

karnofsky\_performance\_score:

80 90 100 NA's

5 41 56 32

race:

asian black or african american

4 6

NA's

5

white

119

```
ethnicity:
  hispanic or latino not hispanic or latino      NA's
                12                111                11
```

Including an additional 762 columns

---

THCA	<i>Thyroid carcinoma</i>
------	--------------------------

---

### Description

A document describing the TCGA cancer code

### Details

```
> experiments( THCA )
ExperimentList class object of length 12:
 [1] THCA_CNASeq-20160128: RaggedExperiment with 5953 rows and 203 columns
 [2] THCA_CNASNP-20160128: RaggedExperiment with 389998 rows and 1013 columns
 [3] THCA_CNVSNP-20160128: RaggedExperiment with 55117 rows and 1013 columns
 [4] THCA_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 499 columns
 [5] THCA_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 38 rows and 499 columns
 [6] THCA_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 499 columns
 [7] THCA_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 569 columns
 [8] THCA_Mutation-20160128: RaggedExperiment with 7458 rows and 405 columns
 [9] THCA_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 568 columns
 [10] THCA_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 4 columns
 [11] THCA_RPPAArray-20160128: SummarizedExperiment with 175 rows and 224 columns
 [12] THCA_Methylation-20160128: SummarizedExperiment with 485577 rows and 567 columns

> rownames( THCA )
CharacterList of length 12
[["THCA_CNASeq-20160128"]] character(0)
[["THCA_CNASNP-20160128"]] character(0)
[["THCA_CNVSNP-20160128"]] character(0)
[["THCA_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["THCA_GISTIC_Peaks-20160128"]] chr1:158681167-215338621 ...
[["THCA_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["THCA_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["THCA_Mutation-20160128"]] character(0)
[["THCA_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["THCA_RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
...
<2 more elements>

> colnames( THCA )
```



```

CharacterList of length 12
[["THCA_CNASeq-20160128"]] TCGA-BJ-A0Z2-01A-11D-A10R-02 ...
[["THCA_CNASNP-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_CNVSNP-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_GISTIC_AllByGene-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_GISTIC_Peaks-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_GISTIC_ThresholdedByGene-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_miRNASeqGene-20160128"]] TCGA-4C-A93U-01A-11R-A39B-13 ...
[["THCA_Mutation-20160128"]] TCGA-BJ-A0YZ-01A-11D-A10S-08 ...
[["THCA_RNASeq2GeneNorm-20160128"]] TCGA-4C-A93U-01A-11R-A39I-07 ...
[["THCA_RNASeqGene-20160128"]] TCGA-DJ-A1QE-01A-21R-A14Y-07 ...
...
<2 more elements>

```

Sizes of each ExperimentList element:

		assay size.Mb
1	THCA_CNASeq-20160128	0.2 Mb
2	THCA_CNASNP-20160128	10.7 Mb
3	THCA_CNVSNP-20160128	1.8 Mb
4	THCA_GISTIC_AllByGene-20160128	4.9 Mb
5	THCA_GISTIC_Peaks-20160128	0.1 Mb
6	THCA_GISTIC_ThresholdedByGene-20160128	4.9 Mb
7	THCA_miRNASeqGene-20160128	0.1 Mb
8	THCA_Mutation-20160128	14 Mb
9	THCA_RNASeq2GeneNorm-20160128	1.3 Mb
10	THCA_RNASeqGene-20160128	1.3 Mb
11	THCA_RPPAArray-20160128	0 Mb
12	THCA_Methylation-20160128	75.1 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

487 observations deleted due to missingness
  n  events  median 0.95LCL 0.95UCL
16.00  16.00   2.80   2.23   4.80

```

-----  
Available sample meta-data:  
-----

```

years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.

```

15.00 35.00 46.00 47.26 58.00 89.00

vital\_status:

0 1  
487 16

days\_to\_death:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
174	743	1021	1176	1631	2973	487

days\_to\_last\_followup:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0	535	943	1220	1513	5423	16

tumor\_tissue\_site:

thyroid  
503

pathology\_N\_stage:

n0	n1	n1a	n1b	nx
227	58	93	75	50

pathology\_M\_stage:

m0	m1	mx	NA's
280	9	213	1

date\_of\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
1993	2008	2010	2009	2011	2013

radiation\_therapy:

no	yes	NA's
181	306	16

radiation\_exposure:

no	yes	NA's
423	17	63

extrathyroidal\_extension:

minimal (t3)	moderate/advanced (t4a)	very advanced (t4b)	none
133	18		333
		1	18
			NA's

residual\_tumor:

r0	r1	r2	rx	NA's
----	----	----	----	------

```
385  52  4  30  32
```

```
number_of_lymph_nodes:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.000	0.000	1.000	3.658	5.000	41.000	114

```
multifocality:
```

multifocal	unifocal	NA's
227	266	10

```
tumor_size:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.300	1.700	2.600	2.975	4.000	8.200	100

Including an additional 1481 columns

### See Also

[THCA-v2.0.1](#)

---

THCA-v2.0.1

*Thyroid carcinoma*

---

### Description

A document describing the TCGA cancer code

### Details

```
> experiments( THCA )
```

```
ExperimentList class object of length 13:
```

```
[1] THCA_CNASeq-20160128: RaggedExperiment with 5953 rows and 203 columns
[2] THCA_CNASNP-20160128: RaggedExperiment with 389998 rows and 1013 columns
[3] THCA_CNVSNP-20160128: RaggedExperiment with 55117 rows and 1013 columns
[4] THCA_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 499 columns
[5] THCA_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 38 rows and 499 columns
[6] THCA_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 499 columns
[7] THCA_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 569 columns
[8] THCA_Mutation-20160128: RaggedExperiment with 7458 rows and 405 columns
[9] THCA_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 568 columns
[10] THCA_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 568 columns
[11] THCA_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 4 columns
[12] THCA_RPPAArray-20160128: SummarizedExperiment with 175 rows and 224 columns
[13] THCA_Methylation-20160128: SummarizedExperiment with 485577 rows and 567 columns
```

```
> rownames( THCA )
```

```
CharacterList of length 13
```

```

[["THCA_CNASeq-20160128"]] character(0)
[["THCA_CNASNP-20160128"]] character(0)
[["THCA_CNVSNP-20160128"]] character(0)
[["THCA_GISTIC_AllByGene-20160128"]] character(0)
[["THCA_GISTIC_Peaks-20160128"]] 1 10 11 12 2 13 3 14 ... 36 37 38 39 7 40 41
[["THCA_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["THCA_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["THCA_Mutation-20160128"]] character(0)
[["THCA_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["THCA_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
...
<3 more elements>

```

```

> colnames( THCA )
CharacterList of length 13
[["THCA_CNASeq-20160128"]] TCGA-BJ-A0Z2-01A-11D-A10R-02 ...
[["THCA_CNASNP-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_CNVSNP-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_GISTIC_AllByGene-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_GISTIC_Peaks-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_GISTIC_ThresholdedByGene-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_miRNASeqGene-20160128"]] TCGA-4C-A93U-01A-11R-A39B-13 ...
[["THCA_Mutation-20160128"]] TCGA-BJ-A0YZ-01A-11D-A10S-08 ...
[["THCA_RNASeq2Gene-20160128"]] TCGA-4C-A93U-01A-11R-A39I-07 ...
[["THCA_RNASeq2GeneNorm-20160128"]] TCGA-4C-A93U-01A-11R-A39I-07 ...
...
<3 more elements>

```

Sizes of each ExperimentList element:

		assay size.Mb
1	THCA_CNASeq-20160128	0.2 Mb
2	THCA_CNASNP-20160128	10.7 Mb
3	THCA_CNVSNP-20160128	1.8 Mb
4	THCA_GISTIC_AllByGene-20160128	97.8 Mb
5	THCA_GISTIC_Peaks-20160128	0.3 Mb
6	THCA_GISTIC_ThresholdedByGene-20160128	97.7 Mb
7	THCA_miRNASeqGene-20160128	4.8 Mb
8	THCA_Mutation-20160128	14 Mb
9	THCA_RNASeq2Gene-20160128	91.5 Mb
10	THCA_RNASeq2GeneNorm-20160128	91.5 Mb
11	THCA_RNASeqGene-20160128	3.2 Mb
12	THCA_RPPAArray-20160128	0.4 Mb
13	THCA_Methylation-20160128	75.1 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```
Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)
```

```
487 observations deleted due to missingness
  n events median 0.95LCL 0.95UCL
16.00  16.00   2.80   2.23   4.80
```

```
-----
Available sample meta-data:
-----
```

```
years_to_birth:
```

```
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 15.00  35.00  46.00  47.26  58.00  89.00
```

```
vital_status:
```

```
 0  1
487 16
```

```
days_to_death:
```

```
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
  174    743   1021   1176   1631   2973    487
```

```
days_to_last_followup:
```

```
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
    0    535    943   1220   1513   5423    16
```

```
tumor_tissue_site:
```

```
thyroid
 503
```

```
pathology_N_stage:
```

```
  n0  n1  n1a  n1b  nx
227  58  93  75  50
```

```
pathology_M_stage:
```

```
  m0  m1  mx  NA's
280   9 213   1
```

```
date_of_initial_pathologic_diagnosis:
```

```
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 1993   2008   2010   2009   2011   2013
```

```
radiation_therapy:
```

```
no yes NA's
181 306 16
```

```
radiation_exposure:
```

```
no yes NA's
423 17 63
```

```
extrathyroidal_extension:
```

```
minimal (t3) moderate/advanced (t4a) none
133 18 333
very advanced (t4b) NA's
1 18
```

```
residual_tumor:
```

```
r0 r1 r2 rx NA's
385 52 4 30 32
```

```
number_of_lymph_nodes:
```

```
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
0.000 0.000 1.000 3.658 5.000 41.000 114
```

```
multifocality:
```

```
multifocal unifocal NA's
227 266 10
```

```
tumor_size:
```

```
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
0.300 1.700 2.600 2.975 4.000 8.200 100
```

```
Including an additional 1481 columns
```

---

THCA-v2.1.0

*Thyroid carcinoma*

---

## Description

A document describing the TCGA cancer code

## Details

```
> experiments( THCA )
```

```
ExperimentList class object of length 13:
```

- [1] THCA\_CNASeq-20160128: RaggedExperiment with 5953 rows and 203 columns
- [2] THCA\_CNASNP-20160128: RaggedExperiment with 389998 rows and 1013 columns
- [3] THCA\_CNVSNP-20160128: RaggedExperiment with 55117 rows and 1013 columns
- [4] THCA\_GISTIC\_AllByGene-20160128: SummarizedExperiment with 24776 rows and 499 columns
- [5] THCA\_GISTIC\_Peaks-20160128: RangedSummarizedExperiment with 38 rows and 499 columns

```

[6] THCA_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 499 columns
[7] THCA_Mutation-20160128: RaggedExperiment with 7458 rows and 405 columns
[8] THCA_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 568 columns
[9] THCA_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 4 columns
[10] THCA_RPPAArray-20160128: SummarizedExperiment with 175 rows and 224 columns
[11] THCA_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 569 columns
[12] THCA_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18003 rows and 568 columns
[13] THCA_Methylation-20160128: SummarizedExperiment with 485577 rows and 567 columns

```

```

> rownames( THCA )
CharacterList of length 13
[["THCA_CNASeq-20160128"]] character(0)
[["THCA_CNASNP-20160128"]] character(0)
[["THCA_CNVSNP-20160128"]] character(0)
[["THCA_GISTIC_AllByGene-20160128"]] character(0)
[["THCA_GISTIC_Peaks-20160128"]] 1 10 11 12 2 13 3 14 ... 36 37 38 39 7 40 41
[["THCA_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["THCA_Mutation-20160128"]] character(0)
[["THCA_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["THCA_RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["THCA_RPPAArray-20160128"]] 14-3-3_epsilon 4E-BP1 ... p90RSK_pT359_S363
...
<3 more elements>

```

```

> colnames( THCA )
CharacterList of length 13
[["THCA_CNASeq-20160128"]] TCGA-BJ-A0Z2-01A-11D-A10R-02 ...
[["THCA_CNASNP-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_CNVSNP-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_GISTIC_AllByGene-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_GISTIC_Peaks-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_GISTIC_ThresholdedByGene-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["THCA_Mutation-20160128"]] TCGA-BJ-A0YZ-01A-11D-A10S-08 ...
[["THCA_RNASeq2Gene-20160128"]] TCGA-4C-A93U-01A-11R-A39I-07 ...
[["THCA_RNASeqGene-20160128"]] TCGA-DJ-A1QE-01A-21R-A14Y-07 ...
[["THCA_RPPAArray-20160128"]] TCGA-BJ-A0YZ-01A-21-A21L-20 ...
...
<3 more elements>

```

Sizes of each ExperimentList element:

		assay size.Mb
1	THCA_CNASeq-20160128	0.2 Mb
2	THCA_CNASNP-20160128	10.7 Mb
3	THCA_CNVSNP-20160128	1.8 Mb
4	THCA_GISTIC_AllByGene-20160128	97.8 Mb
5	THCA_GISTIC_Peaks-20160128	0.3 Mb
6	THCA_GISTIC_ThresholdedByGene-20160128	97.7 Mb

7	THCA_Mutation-20160128	14 Mb
8	THCA_RNASeq2Gene-20160128	91.5 Mb
9	THCA_RNASeqGene-20160128	3.2 Mb
10	THCA_RPPAArray-20160128	0.4 Mb
11	THCA_miRNASeqGene-20160128	4.8 Mb
12	THCA_RNASeq2GeneNorm-20160128	80.3 Mb
13	THCA_Methylation-20160128	75.1 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

Call: survfit(formula = survival::Surv(colDat\$days\_to\_death/365, colDat\$vital\_status) ~  
-1)

487 observations deleted due to missingness  
n events median 0.95LCL 0.95UCL  
[1,] 16 16 2.8 2.23 4.8

-----  
Available sample meta-data:  
-----

years\_to\_birth:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
15.00	35.00	46.00	47.26	58.00	89.00

vital\_status:

0	1
487	16

days\_to\_death:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
174	743	1021	1176	1631	2973	487

days\_to\_last\_followup:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0	535	943	1220	1513	5423	16

tumor\_tissue\_site:

thyroid
503

pathology\_N\_stage:

n0	n1	n1a	n1b	nx
----	----	-----	-----	----



227 58 93 75 50

pathology\_M\_stage:

m0	m1	mx	NA's
280	9	213	1

date\_of\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
1993	2008	2010	2009	2011	2013

radiation\_therapy:

no	yes	NA's
181	306	16

radiation\_exposure:

no	yes	NA's
423	17	63

extrathyroidal\_extension:

minimal (t3)	moderate/advanced (t4a)	very advanced (t4b)	none
133	18	NA's	333
		1	18

residual\_tumor:

r0	r1	r2	rx	NA's
385	52	4	30	32

number\_of\_lymph\_nodes:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.000	0.000	1.000	3.658	5.000	41.000	114

multifocality:

multifocal	unifocal	NA's
227	266	10

tumor\_size:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.300	1.700	2.600	2.975	4.000	8.200	100

Including an additional 1481 columns

---

THYM

*Thymoma*

---

**Description**

A document describing the TCGA cancer code

**Details**

```

> experiments( THYM )
ExperimentList class object of length 10:
 [1] THYM_CNASNP-20160128: RaggedExperiment with 105646 rows and 248 columns
 [2] THYM_CNVSNP-20160128: RaggedExperiment with 15571 rows and 248 columns
 [3] THYM_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 123 columns
 [4] THYM_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 16 rows and 123 columns
 [5] THYM_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 123 columns
 [6] THYM_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 126 columns
 [7] THYM_Mutation-20160128: RaggedExperiment with 3064 rows and 123 columns
 [8] THYM_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 122 columns
 [9] THYM_RPPAArray-20160128: SummarizedExperiment with 192 rows and 90 columns
 [10] THYM_Methylation-20160128: SummarizedExperiment with 485577 rows and 126 columns

> rownames( THYM )
CharacterList of length 10
[["THYM_CNASNP-20160128"]] character(0)
[["THYM_CNVSNP-20160128"]] character(0)
[["THYM_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["THYM_GISTIC_Peaks-20160128"]] chr1:208606110-249250621 ...
[["THYM_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["THYM_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["THYM_Mutation-20160128"]] character(0)
[["THYM_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["THYM_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["THYM_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873

> colnames( THYM )
CharacterList of length 10
[["THYM_CNASNP-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_CNVSNP-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_GISTIC_AllByGene-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_GISTIC_Peaks-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_GISTIC_ThresholdedByGene-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_miRNASeqGene-20160128"]] TCGA-3G-AB00-01A-22R-A42W-13 ...
[["THYM_Mutation-20160128"]] TCGA-3G-AB00-01A-22D-A423-09 ...
[["THYM_RNASeq2GeneNorm-20160128"]] TCGA-3G-AB00-01A-22R-A42C-07 ...
[["THYM_RPPAArray-20160128"]] TCGA-3G-AB00-01A-11-A45R-20 ...
[["THYM_Methylation-20160128"]] TCGA-3G-AB00-01A-22D-A424-05 ...

```

Sizes of each ExperimentList element:

		assay size.Mb
1	THYM_CNASNP-20160128	2.9 Mb
2	THYM_CNVSNP-20160128	0.5 Mb
3	THYM_GISTIC_AllByGene-20160128	4.9 Mb
4	THYM_GISTIC_Peaks-20160128	0 Mb
5	THYM_GISTIC_ThresholdedByGene-20160128	4.9 Mb

6	THYM_miRNASeqGene-20160128	0.1 Mb
7	THYM_Mutation-20160128	3.3 Mb
8	THYM_RNASeq2GeneNorm-20160128	1.3 Mb
9	THYM_RPPAArray-20160128	0 Mb
10	THYM_Methylation-20160128	75 Mb

-----  
 Overall survival time-to-event summary (in years):  
 -----

Call: survfit(formula = survival::Surv(colDat\$days\_to\_death/365, colDat\$vital\_status) ~  
 -1)

115 observations deleted due to missingness  
 n events median 0.95LCL 0.95UCL  
 9.00 9.00 2.34 1.04 NA

-----  
 Available sample meta-data:  
 -----

years\_to\_birth:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 17.00 49.50 60.00 58.15 68.50 84.00 1

vital\_status:  
 0 1  
 115 9

days\_to\_death:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 124 379 853 1423 2488 3488 115

days\_to\_last\_followup:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 14.0 725.2 1267.5 1486.3 1947.0 4575.0 10

tumor\_tissue\_site:  
 anterior mediastinum thymus  
 27 97

gender:  
 female male  
 60 64

date\_of\_initial\_pathologic\_diagnosis:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's

```

2000    2008    2010    2010    2012    2013    1

radiation_therapy:
no yes
81 43

race:
asian black or african american          white
    13                               6          103
NA's
    2

ethnicity:
hispanic or latino not hispanic or latino  NA's
    10                               100          14

```

Including an additional 685 columns

### See Also

[THYM-v2.0.1](#)

---

THYM-v2.0.1

*Thymoma*

---

### Description

A document describing the TCGA cancer code

### Details

```

> experiments( THYM )
ExperimentList class object of length 11:
 [1] THYM_CNASNP-20160128: RaggedExperiment with 105646 rows and 248 columns
 [2] THYM_CNVSNP-20160128: RaggedExperiment with 15571 rows and 248 columns
 [3] THYM_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 123 columns
 [4] THYM_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 16 rows and 123 columns
 [5] THYM_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 123 columns
 [6] THYM_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 126 columns
 [7] THYM_Mutation-20160128: RaggedExperiment with 3064 rows and 123 columns
 [8] THYM_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 122 columns
 [9] THYM_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 122 columns
[10] THYM_RPPAArray-20160128: SummarizedExperiment with 192 rows and 90 columns
[11] THYM_Methylation-20160128: SummarizedExperiment with 485577 rows and 126 columns

> rownames( THYM )

```

```

CharacterList of length 11
[["THYM_CNASNP-20160128"]] character(0)
[["THYM_CNVSNP-20160128"]] character(0)
[["THYM_GISTIC_AllByGene-20160128"]] character(0)
[["THYM_GISTIC_Peaks-20160128"]] 1 8 9 10 11 12 13 14 2 15 3 4 16 5 17 18
[["THYM_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["THYM_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["THYM_Mutation-20160128"]] character(0)
[["THYM_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["THYM_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["THYM_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
...
<1 more element>

```

```

> colnames( THYM )
CharacterList of length 11
[["THYM_CNASNP-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_CNVSNP-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_GISTIC_AllByGene-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_GISTIC_Peaks-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_GISTIC_ThresholdedByGene-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_miRNASeqGene-20160128"]] TCGA-3G-AB00-01A-22R-A42W-13 ...
[["THYM_Mutation-20160128"]] TCGA-3G-AB00-01A-22D-A423-09 ...
[["THYM_RNASeq2Gene-20160128"]] TCGA-3G-AB00-01A-22R-A42C-07 ...
[["THYM_RNASeq2GeneNorm-20160128"]] TCGA-3G-AB00-01A-22R-A42C-07 ...
[["THYM_RPPAArray-20160128"]] TCGA-3G-AB00-01A-11-A45R-20 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

		assay size.Mb
1	THYM_CNASNP-20160128	2.9 Mb
2	THYM_CNVSNP-20160128	0.5 Mb
3	THYM_GISTIC_AllByGene-20160128	26.7 Mb
4	THYM_GISTIC_Peaks-20160128	0.1 Mb
5	THYM_GISTIC_ThresholdedByGene-20160128	26.6 Mb
6	THYM_miRNASeqGene-20160128	1.2 Mb
7	THYM_Mutation-20160128	3.3 Mb
8	THYM_RNASeq2Gene-20160128	21.7 Mb
9	THYM_RNASeq2GeneNorm-20160128	21.7 Mb
10	THYM_RPPAArray-20160128	0.2 Mb
11	THYM_Methylation-20160128	75 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```
Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)
```

115 observations deleted due to missingness

n	events	median	0.95LCL	0.95UCL
9.00	9.00	2.34	1.04	NA

```
-----
Available sample meta-data:
-----
```

years\_to\_birth:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
17.00	49.50	60.00	58.15	68.50	84.00	1

vital\_status:

0	1
115	9

days\_to\_death:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
124	379	853	1423	2488	3488	115

days\_to\_last\_followup:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
14.0	725.2	1267.5	1486.3	1947.0	4575.0	10

tumor\_tissue\_site:

anterior mediastinum	thymus
27	97

gender:

female	male
60	64

date\_of\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
2000	2008	2010	2010	2012	2013	1

radiation\_therapy:

no	yes
81	43

race:

asian	black or african american	white
13	6	103

```

                NA's
                2

ethnicity:
  hispanic or latino not hispanic or latino      NA's
                10                100                14

```

Including an additional 685 columns

---

THYM-v2.1.0

*Thymoma*

---

## Description

A document describing the TCGA cancer code

## Details

```

> experiments( THYM )
ExperimentList class object of length 11:
 [1] THYM_CNASNP-20160128: RaggedExperiment with 105646 rows and 248 columns
 [2] THYM_CNVSNP-20160128: RaggedExperiment with 15571 rows and 248 columns
 [3] THYM_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 123 columns
 [4] THYM_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 16 rows and 123 columns
 [5] THYM_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 123 columns
 [6] THYM_Mutation-20160128: RaggedExperiment with 3064 rows and 123 columns
 [7] THYM_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 122 columns
 [8] THYM_RPPAArray-20160128: SummarizedExperiment with 192 rows and 90 columns
 [9] THYM_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 126 columns
[10] THYM_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18286 rows and 122 columns
[11] THYM_Methylation-20160128: SummarizedExperiment with 485577 rows and 126 columns

> rownames( THYM )
CharacterList of length 11
[["THYM_CNASNP-20160128"]] character(0)
[["THYM_CNVSNP-20160128"]] character(0)
[["THYM_GISTIC_AllByGene-20160128"]] character(0)
[["THYM_GISTIC_Peaks-20160128"]] 1 8 9 10 11 12 13 14 2 15 3 4 16 5 17 18
[["THYM_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["THYM_Mutation-20160128"]] character(0)
[["THYM_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["THYM_RPPAArray-20160128"]] 14-3-3_beta ... p90RSK_pT359_S363
[["THYM_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["THYM_RNASeq2GeneNorm-20160128"]] A1BG A2BP1 A2LD1 ... ZZEF1 ZZZ3 psiTPTE22
...
<1 more element>

```

```
> colnames( THYM )
CharacterList of length 11
[["THYM_CNASNP-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_CNVSNP-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_GISTIC_AllByGene-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_GISTIC_Peaks-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_GISTIC_ThresholdedByGene-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["THYM_Mutation-20160128"]] TCGA-3G-AB00-01A-22D-A423-09 ...
[["THYM_RNASeq2Gene-20160128"]] TCGA-3G-AB00-01A-22R-A42C-07 ...
[["THYM_RPPAArray-20160128"]] TCGA-3G-AB00-01A-11-A45R-20 ...
[["THYM_miRNASeqGene-20160128"]] TCGA-3G-AB00-01A-22R-A42W-13 ...
[["THYM_RNASeq2GeneNorm-20160128"]] TCGA-3G-AB00-01 ... TCGA-ZT-A80M-01
...
<1 more element>
```

Sizes of each ExperimentList element:

		assay size.Mb
1	THYM_CNASNP-20160128	2.9 Mb
2	THYM_CNVSNP-20160128	0.5 Mb
3	THYM_GISTIC_AllByGene-20160128	26.7 Mb
4	THYM_GISTIC_Peaks-20160128	0.1 Mb
5	THYM_GISTIC_ThresholdedByGene-20160128	26.6 Mb
6	THYM_Mutation-20160128	3.3 Mb
7	THYM_RNASeq2Gene-20160128	21.7 Mb
8	THYM_RPPAArray-20160128	0.2 Mb
9	THYM_miRNASeqGene-20160128	1.2 Mb
10	THYM_RNASeq2GeneNorm-20160128	19.3 Mb
11	THYM_Methylation-20160128	75 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```
Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)
```

```
115 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
[1,] 9      9  2.34  1.04  NA
```

-----  
Available sample meta-data:  
-----

```
years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
```



17.00 49.50 60.00 58.15 68.50 84.00 1

vital\_status:

0 1

115 9

days\_to\_death:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
124	379	853	1423	2488	3488	115

days\_to\_last\_followup:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
14.0	725.2	1267.5	1486.3	1947.0	4575.0	10

tumor\_tissue\_site:

anterior mediastinum	thymus
27	97

gender:

female	male
60	64

date\_of\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
2000	2008	2010	2010	2012	2013	1

radiation\_therapy:

no	yes
81	43

race:

asian	black or african american	white
13	6	103
NA's		
2		

ethnicity:

hispanic or latino	not hispanic or latino	NA's
10	100	14

Including an additional 685 columns

**Description**

A document describing the TCGA cancer code

**Details**

```
> experiments( UCEC )
ExperimentList class object of length 14:
 [1] UCEC_CNASeq-20160128: RaggedExperiment with 36400 rows and 213 columns
 [2] UCEC_CNASNP-20160128: RaggedExperiment with 619412 rows and 1083 columns
 [3] UCEC_CNVSNP-20160128: RaggedExperiment with 127094 rows and 1078 columns
 [4] UCEC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 539 columns
 [5] UCEC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 98 rows and 539 columns
 [6] UCEC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 539 columns
 [7] UCEC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 433 columns
 [8] UCEC_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 54 columns
 [9] UCEC_Mutation-20160128: RaggedExperiment with 184861 rows and 248 columns
[10] UCEC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 380 columns
[11] UCEC_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 269 columns
[12] UCEC_RPPAArray-20160128: SummarizedExperiment with 208 rows and 440 columns
[13] UCEC_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 118 columns
[14] UCEC_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 466 columns

> rownames( UCEC )
CharacterList of length 14
[["UCEC_CNASeq-20160128"]] character(0)
[["UCEC_CNASNP-20160128"]] character(0)
[["UCEC_CNVSNP-20160128"]] character(0)
[["UCEC_GISTIC_AllByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["UCEC_GISTIC_Peaks-20160128"]] chr1:13949775-15575840 ...
[["UCEC_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["UCEC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["UCEC_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["UCEC_Mutation-20160128"]] character(0)
[["UCEC_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
...
<4 more elements>

> colnames( UCEC )
CharacterList of length 14
[["UCEC_CNASeq-20160128"]] TCGA-A5-A0G5-01A-11D-A043-02 ...
[["UCEC_CNASNP-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_CNVSNP-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_GISTIC_AllByGene-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_GISTIC_Peaks-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_GISTIC_ThresholdedByGene-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_miRNASeqGene-20160128"]] TCGA-2E-A9G8-01A-11R-A404-13 ...
[["UCEC_mRNAArray-20160128"]] TCGA-A5-A0G2-01A-11R-A040-07 ...
[["UCEC_Mutation-20160128"]] TCGA-A5-A0G3-01A-11W-A062-09 ...
```

```
[[ "UCEC_RNASeq2GeneNorm-20160128" ]] TCGA-A5-A0G1-01A-11R-A118-07 ...
...
<4 more elements>
```

Sizes of each ExperimentList element:

		assay	size.Mb
1		UCEC_CNASeq-20160128	1 Mb
2		UCEC_CNASNP-20160128	16.9 Mb
3		UCEC_CNVSNP-20160128	3.7 Mb
4		UCEC_GISTIC_AllByGene-20160128	4.9 Mb
5		UCEC_GISTIC_Peaks-20160128	0.1 Mb
6		UCEC_GISTIC_ThresholdedByGene-20160128	4.9 Mb
7		UCEC_miRNASeqGene-20160128	0.1 Mb
8		UCEC_mRNAArray-20160128	1.1 Mb
9		UCEC_Mutation-20160128	73.1 Mb
10		UCEC_RNASeq2GeneNorm-20160128	1.3 Mb
11		UCEC_RNASeqGene-20160128	1.3 Mb
12		UCEC_RPPAArray-20160128	0.1 Mb
13		UCEC_Methylation_methyl27-20160128	4.9 Mb
14		UCEC_Methylation_methyl450-20160128	75.1 Mb

-----  
 Available sample meta-data:  
 -----

days\_to\_death:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
50.0	367.0	709.0	881.8	1063.0	3423.0	457

days\_to\_last\_followup:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
-6.0	543.0	948.5	1195.1	1753.2	6859.0	92

tumor\_tissue\_site:

endometrial	other	specify
547		1

date\_of\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1995	2007	2009	2009	2010	2013	9

days\_to\_last\_known\_alive:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
145	404	729	1405	2096	4144	535

radiation\_therapy:

```
no  yes  NA's
295 228  25
```

```
histological_type:
endometrioid endometrial adenocarcinoma
                                411
      mixed serous and endometrioid
                                22
      serous endometrial adenocarcinoma
                                115
```

```
residual_tumor:
  r0  r1  r2  rx  NA's
376  22  16  41   93
```

Including an additional 1779 columns

### See Also

[UCEC-v2.0.1](#)

---

UCEC-v2.0.1

*Uterine Corpus Endometrial Carcinoma*

---

### Description

A document describing the TCGA cancer code

### Details

```
> experiments( UCEC )
ExperimentList class object of length 16:
 [1] UCEC_CNASeq-20160128: RaggedExperiment with 36400 rows and 213 columns
 [2] UCEC_CNASNP-20160128: RaggedExperiment with 619412 rows and 1083 columns
 [3] UCEC_CNVSNP-20160128: RaggedExperiment with 127094 rows and 1078 columns
 [4] UCEC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 539 columns
 [5] UCEC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 98 rows and 539 columns
 [6] UCEC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 539 columns
 [7] UCEC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 433 columns
 [8] UCEC_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 54 columns
 [9] UCEC_Mutation-20160128: RaggedExperiment with 184861 rows and 248 columns
[10] UCEC_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 190 columns
[11] UCEC_RNASeq2GeneNorm_illumina-20160128: SummarizedExperiment with 20501 rows and 380 columns
[12] UCEC_RNASeq2GeneNorm_illumina-hiseq-20160128: SummarizedExperiment with 20501 rows and 190 columns
[13] UCEC_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 269 columns
[14] UCEC_RPPAArray-20160128: SummarizedExperiment with 208 rows and 440 columns
[15] UCEC_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 118 columns
```

[16] UCEC\_Methylation\_methyl450-20160128: SummarizedExperiment with 485577 rows and 466 columns

```
> rownames( UCEC )
CharacterList of length 16
[["UCEC_CNASeq-20160128"]] character(0)
[["UCEC_CNASNP-20160128"]] character(0)
[["UCEC_CNVSNP-20160128"]] character(0)
[["UCEC_GISTIC_AllByGene-20160128"]] character(0)
[["UCEC_GISTIC_Peaks-20160128"]] 51 52 1 2 3 4 5 53 ... 98 45 46 47 99 48 100
[["UCEC_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["UCEC_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["UCEC_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["UCEC_Mutation-20160128"]] character(0)
[["UCEC_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
...
<6 more elements>
```

```
> colnames( UCEC )
CharacterList of length 16
[["UCEC_CNASeq-20160128"]] TCGA-A5-A0G5-01A-11D-A043-02 ...
[["UCEC_CNASNP-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_CNVSNP-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_GISTIC_AllByGene-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_GISTIC_Peaks-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_GISTIC_ThresholdedByGene-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_miRNASeqGene-20160128"]] TCGA-2E-A9G8-01A-11R-A404-13 ...
[["UCEC_mRNAArray-20160128"]] TCGA-A5-A0G2-01A-11R-A040-07 ...
[["UCEC_Mutation-20160128"]] TCGA-A5-A0G3-01A-11W-A062-09 ...
[["UCEC_RNASeq2Gene-20160128"]] TCGA-2E-A9G8-01A-11R-A40A-07 ...
...
<6 more elements>
```

Sizes of each ExperimentList element:

	assay	size.Mb
1	UCEC_CNASeq-20160128	1 Mb
2	UCEC_CNASNP-20160128	16.9 Mb
3	UCEC_CNVSNP-20160128	3.7 Mb
4	UCEC_GISTIC_AllByGene-20160128	105.5 Mb
5	UCEC_GISTIC_Peaks-20160128	0.6 Mb
6	UCEC_GISTIC_ThresholdedByGene-20160128	105.3 Mb
7	UCEC_miRNASeqGene-20160128	3.7 Mb
8	UCEC_mRNAArray-20160128	9.6 Mb
9	UCEC_Mutation-20160128	73.1 Mb
10	UCEC_RNASeq2Gene-20160128	32.3 Mb
11	UCEC_RNASeq2GeneNorm_illumina-20160128	62 Mb
12	UCEC_RNASeq2GeneNorm_illuminahisec-20160128	32.3 Mb
13	UCEC_RNASeqGene-20160128	44.7 Mb

14	UCEC_RPPAArray-20160128	0.8 Mb
15	UCEC_Methylation_methyl27-20160128	4.9 Mb
16	UCEC_Methylation_methyl450-20160128	75.1 Mb

-----  
 Available sample meta-data:  
 -----

days\_to\_death:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
50.0	367.0	709.0	881.8	1063.0	3423.0	457

days\_to\_last\_followup:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
-6.0	543.0	948.5	1195.1	1753.2	6859.0	92

tumor\_tissue\_site:

endometrial	other	specify
547		1

date\_of\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1995	2007	2009	2009	2010	2013	9

days\_to\_last\_known\_alive:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
145	404	729	1405	2096	4144	535

radiation\_therapy:

no	yes	NA's
295	228	25

histological\_type:

endometrioid	endometrial adenocarcinoma
	411
mixed serous and endometrioid	
	22
serous endometrial adenocarcinoma	
	115

residual\_tumor:

r0	r1	r2	rx	NA's
376	22	16	41	93

Including an additional 1779 columns

UCEC-v2.1.0

*Uterine Corpus Endometrial Carcinoma***Description**

A document describing the TCGA cancer code

**Details**

```

> experiments( UCEC )
ExperimentList class object of length 17:
 [1] UCEC_CNASeq-20160128: RaggedExperiment with 36400 rows and 213 columns
 [2] UCEC_CNASNP-20160128: RaggedExperiment with 619412 rows and 1083 columns
 [3] UCEC_CNVSNP-20160128: RaggedExperiment with 127094 rows and 1078 columns
 [4] UCEC_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 539 columns
 [5] UCEC_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 98 rows and 539 columns
 [6] UCEC_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 539 columns
 [7] UCEC_mRNAArray-20160128: SummarizedExperiment with 17814 rows and 54 columns
 [8] UCEC_Mutation-20160128: RaggedExperiment with 184861 rows and 248 columns
 [9] UCEC_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 190 columns
 [10] UCEC_RNASeq2GeneNorm_illumina-20160128: SummarizedExperiment with 20501 rows and 380 columns
 [11] UCEC_RNASeq2GeneNorm_illumina-hiseq-20160128: SummarizedExperiment with 20501 rows and 190 columns
 [12] UCEC_RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 269 columns
 [13] UCEC_RPPAArray-20160128: SummarizedExperiment with 208 rows and 440 columns
 [14] UCEC_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 433 columns
 [15] UCEC_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18515 rows and 569 columns
 [16] UCEC_Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 118 columns
 [17] UCEC_Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 466 columns

> rownames( UCEC )
CharacterList of length 17
[["UCEC_CNASeq-20160128"]] character(0)
[["UCEC_CNASNP-20160128"]] character(0)
[["UCEC_CNVSNP-20160128"]] character(0)
[["UCEC_GISTIC_AllByGene-20160128"]] character(0)
[["UCEC_GISTIC_Peaks-20160128"]] 51 52 1 2 3 4 5 53 ... 98 45 46 47 99 48 100
[["UCEC_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["UCEC_mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SNRPD2 AQP7 CTSC
[["UCEC_Mutation-20160128"]] character(0)
[["UCEC_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["UCEC_RNASeq2GeneNorm_illumina-20160128"]] A1BG A1CF ... psiTPTE22 tAKR
...
<7 more elements>

> colnames( UCEC )
CharacterList of length 17
[["UCEC_CNASeq-20160128"]] TCGA-A5-A0G5-01A-11D-A043-02 ...

```

```

[["UCEC_CNASNP-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_CNVSNP-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_GISTIC_AllByGene-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_GISTIC_Peaks-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_GISTIC_ThresholdedByGene-20160128"]] TCGA-2E-A9G8-01A-11D-A402-01 ...
[["UCEC_mRNAArray-20160128"]] TCGA-A5-A0G2-01A-11R-A040-07 ...
[["UCEC_Mutation-20160128"]] TCGA-A5-A0G3-01A-11W-A062-09 ...
[["UCEC_RNASeq2Gene-20160128"]] TCGA-2E-A9G8-01A-11R-A40A-07 ...
[["UCEC_RNASeq2GeneNorm_illumina-20160128"]] TCGA-A5-A0G1-01A-11R-A118-07...
...
<7 more elements>

```

Sizes of each ExperimentList element:

	assay	size.Mb
1	UCEC_CNASeq-20160128	1 Mb
2	UCEC_CNASNP-20160128	16.9 Mb
3	UCEC_CNVSNP-20160128	3.7 Mb
4	UCEC_GISTIC_AllByGene-20160128	105.5 Mb
5	UCEC_GISTIC_Peaks-20160128	0.6 Mb
6	UCEC_GISTIC_ThresholdedByGene-20160128	105.3 Mb
7	UCEC_mRNAArray-20160128	9.6 Mb
8	UCEC_Mutation-20160128	73.1 Mb
9	UCEC_RNASeq2Gene-20160128	32.3 Mb
10	UCEC_RNASeq2GeneNorm_illumina-20160128	62 Mb
11	UCEC_RNASeq2GeneNorm_illuminahisec-20160128	32.3 Mb
12	UCEC_RNASeqGene-20160128	44.7 Mb
13	UCEC_RPPAArray-20160128	0.8 Mb
14	UCEC_miRNASeqGene-20160128	3.7 Mb
15	UCEC_RNASeq2GeneNorm-20160128	82.8 Mb
16	UCEC_Methylation_methyl27-20160128	4.9 Mb
17	UCEC_Methylation_methyl450-20160128	75.1 Mb

-----  
Available sample meta-data:  
-----

days\_to\_death:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
50.0	367.0	709.0	881.8	1063.0	3423.0	457

days\_to\_last\_followup:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
-6.0	543.0	948.5	1195.1	1753.2	6859.0	92

tumor\_tissue\_site:

endometrial other specify



```

                    547          1

date_of_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
  1995   2007   2009   2009   2010   2013     9

days_to_last_known_alive:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
  145   404   729   1405   2096   4144   535

radiation_therapy:
  no  yes NA's
  295 228  25

histological_type:
endometrioid endometrial adenocarcinoma
              411
  mixed serous and endometrioid
              22
  serous endometrial adenocarcinoma
              115

residual_tumor:
  r0  r1  r2  rx NA's
  376  22  16  41  93

```

Including an additional 1779 columns

---

UCS

*Uterine Carcinosarcoma*

---

## Description

A document describing the TCGA cancer code

## Details

```

> experiments( UCS )
ExperimentList class object of length 10:
 [1] UCS_CNASNP-20160128: RaggedExperiment with 54944 rows and 111 columns
 [2] UCS_CNVSNP-20160128: RaggedExperiment with 19298 rows and 111 columns
 [3] UCS_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 56 columns
 [4] UCS_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 56 rows and 56 columns
 [5] UCS_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 56 columns
 [6] UCS_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 56 columns
 [7] UCS_Mutation-20160128: RaggedExperiment with 11339 rows and 57 columns
 [8] UCS_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 57 columns

```

```
[9] UCS_RPPAArray-20160128: SummarizedExperiment with 192 rows and 48 columns
[10] UCS_Methylation-20160128: SummarizedExperiment with 485577 rows and 57 columns
```

```
> rownames( UCS )
CharacterList of length 10
[["UCS_CNASNP-20160128"]] character(0)
[["UCS_CNVSNP-20160128"]] character(0)
[["UCS_GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["UCS_GISTIC_Peaks-20160128"]] chr1:1-19401404 ... chr22:41958863-51304566
[["UCS_GISTIC_ThresholdedByGene-20160128"]] ACAP3 ...
[["UCS_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["UCS_Mutation-20160128"]] character(0)
[["UCS_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["UCS_RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363
[["UCS_Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
```

```
> colnames( UCS )
CharacterList of length 10
[["UCS_CNASNP-20160128"]] TCGA-N5-A4R8-10A-01D-A28T-01 ...
[["UCS_CNVSNP-20160128"]] TCGA-N5-A4R8-10A-01D-A28T-01 ...
[["UCS_GISTIC_AllByGene-20160128"]] TCGA-N5-A4RA-01A-11D-A28Q-01 ...
[["UCS_GISTIC_Peaks-20160128"]] TCGA-N5-A4RA-01A-11D-A28Q-01 ...
[["UCS_GISTIC_ThresholdedByGene-20160128"]] TCGA-N5-A4RA-01A-11D-A28Q-01 ...
[["UCS_miRNASeqGene-20160128"]] TCGA-N5-A4R8-01A-11R-A28Z-13 ...
[["UCS_Mutation-20160128"]] TCGA-N5-A4R8-01A-11D-A28R-08 ...
[["UCS_RNASeq2GeneNorm-20160128"]] TCGA-N5-A4R8-01A-11R-A28V-07 ...
[["UCS_RPPAArray-20160128"]] TCGA-N5-A4R8-01A-21-A41P-20 ...
[["UCS_Methylation-20160128"]] TCGA-N5-A4R8-01A-11D-A28S-05 ...
```

Sizes of each ExperimentList element:

		assay size.Mb
1	UCS_CNASNP-20160128	1.5 Mb
2	UCS_CNVSNP-20160128	0.6 Mb
3	UCS_GISTIC_AllByGene-20160128	4.9 Mb
4	UCS_GISTIC_Peaks-20160128	0.1 Mb
5	UCS_GISTIC_ThresholdedByGene-20160128	4.9 Mb
6	UCS_miRNASeqGene-20160128	0.1 Mb
7	UCS_Mutation-20160128	19.7 Mb
8	UCS_RNASeq2GeneNorm-20160128	1.3 Mb
9	UCS_RPPAArray-20160128	0 Mb
10	UCS_Methylation-20160128	75 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

Call: survfit(formula = survival::Surv(colDat\$days\_to\_death/365, colDat\$vital\_status) ~

-1)

22 observations deleted due to missingness

n	events	median	0.95LCL	0.95UCL
35.00	35.00	1.43	1.04	1.96

-----  
 Available sample meta-data:  
 -----

years\_to\_birth:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
51.00	62.00	68.00	69.72	76.00	90.00

vital\_status:

0	1
22	35

days\_to\_death:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
8.0	304.0	522.0	705.4	790.5	3115.0	22

days\_to\_last\_followup:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.0	591.2	828.0	1183.4	1647.5	4269.0	35

tumor\_tissue\_site:

uterus
57

gender:

female
57

date\_of\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
2002	2007	2009	2009	2011	2012

radiation\_therapy:

no	yes	NA's
29	25	3

histological\_type:

uterine carcinosarcoma/ malignant mixed mullerian tumor (mmt): nos	24
uterine carcinosarcoma/ mmt: heterologous type	20

uterine carcinosarcoma/mmt: homologous type  
13

race:

asian	black or african american	white
3	9	44
NA's		
1		

ethnicity:

hispanic or latino	not hispanic or latino	NA's
1	43	13

Including an additional 632 columns

### See Also

[UCS-v2.0.1](#)

---

UCS-v2.0.1

*Uterine Carcinosarcoma*

---

### Description

A document describing the TCGA cancer code

### Details

```
> experiments( UCS )
ExperimentList class object of length 11:
 [1] UCS_CNASNP-20160128: RaggedExperiment with 54944 rows and 111 columns
 [2] UCS_CNVSNP-20160128: RaggedExperiment with 19298 rows and 111 columns
 [3] UCS_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 56 columns
 [4] UCS_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 56 rows and 56 columns
 [5] UCS_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 56 columns
 [6] UCS_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 56 columns
 [7] UCS_Mutation-20160128: RaggedExperiment with 11339 rows and 57 columns
 [8] UCS_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 57 columns
 [9] UCS_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 57 columns
 [10] UCS_RPPAArray-20160128: SummarizedExperiment with 192 rows and 48 columns
 [11] UCS_Methylation-20160128: SummarizedExperiment with 485577 rows and 57 columns

> rownames( UCS )
CharacterList of length 11
[["UCS_CNASNP-20160128"]] character(0)
[["UCS_CNVSNP-20160128"]] character(0)
[["UCS_GISTIC_AllByGene-20160128"]] character(0)
```

```

[["UCS_GISTIC_Peaks-20160128"]] 26 1 2 3 27 4 28 29 ... 21 22 56 57 23 24 58
[["UCS_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["UCS_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["UCS_Mutation-20160128"]] character(0)
[["UCS_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["UCS_RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 ... ZZZ3 psiTPTE22 tAKR
[["UCS_RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363
...
<1 more element>

```

```

> colnames( UCS )
CharacterList of length 11
[["UCS_CNASNP-20160128"]] TCGA-N5-A4R8-10A-01D-A28T-01 ...
[["UCS_CNVSNP-20160128"]] TCGA-N5-A4R8-10A-01D-A28T-01 ...
[["UCS_GISTIC_AllByGene-20160128"]] TCGA-N5-A4RA-01A-11D-A28Q-01 ...
[["UCS_GISTIC_Peaks-20160128"]] TCGA-N5-A4RA-01A-11D-A28Q-01 ...
[["UCS_GISTIC_ThresholdedByGene-20160128"]] TCGA-N5-A4RA-01A-11D-A28Q-01 ...
[["UCS_miRNASeqGene-20160128"]] TCGA-N5-A4R8-01A-11R-A28Z-13 ...
[["UCS_Mutation-20160128"]] TCGA-N5-A4R8-01A-11D-A28R-08 ...
[["UCS_RNASeq2Gene-20160128"]] TCGA-N5-A4R8-01A-11R-A28V-07 ...
[["UCS_RNASeq2GeneNorm-20160128"]] TCGA-N5-A4R8-01A-11R-A28V-07 ...
[["UCS_RPPAArray-20160128"]] TCGA-N5-A4R8-01A-21-A41P-20 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

		assay size.Mb
1	UCS_CNASNP-20160128	1.5 Mb
2	UCS_CNVSNP-20160128	0.6 Mb
3	UCS_GISTIC_AllByGene-20160128	14.1 Mb
4	UCS_GISTIC_Peaks-20160128	0.1 Mb
5	UCS_GISTIC_ThresholdedByGene-20160128	13.9 Mb
6	UCS_miRNASeqGene-20160128	0.6 Mb
7	UCS_Mutation-20160128	19.7 Mb
8	UCS_RNASeq2Gene-20160128	11.5 Mb
9	UCS_RNASeq2GeneNorm-20160128	11.5 Mb
10	UCS_RPPAArray-20160128	0.1 Mb
11	UCS_Methylation-20160128	75 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

22 observations deleted due to missingness

n	events	median	0.95LCL	0.95UCL
35.00	35.00	1.43	1.04	1.96

-----  
 Available sample meta-data:  
 -----

years\_to\_birth:  
 Min. 1st Qu. Median Mean 3rd Qu. Max.  
 51.00 62.00 68.00 69.72 76.00 90.00

vital\_status:  
 0 1  
 22 35

days\_to\_death:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 8.0 304.0 522.0 705.4 790.5 3115.0 22

days\_to\_last\_followup:  
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
 0.0 591.2 828.0 1183.4 1647.5 4269.0 35

tumor\_tissue\_site:  
 uterus  
 57

gender:  
 female  
 57

date\_of\_initial\_pathologic\_diagnosis:  
 Min. 1st Qu. Median Mean 3rd Qu. Max.  
 2002 2007 2009 2009 2011 2012

radiation\_therapy:  
 no yes NA's  
 29 25 3

histological\_type:  
 uterine carcinosarcoma/ malignant mixed mullerian tumor (mmt): nos  
 24  
     uterine carcinosarcoma/ mmt: heterologous type  
     20  
     uterine carcinosarcoma/mmt: homologous type  
     13

```

race:
      asian black or african american      white
      3                9                44
      NA's
      1

ethnicity:
      hispanic or latino not hispanic or latino      NA's
      1                43                13

```

Including an additional 632 columns

---

UCS-v2.1.0

*Uterine Carcinosarcoma*

---

## Description

A document describing the TCGA cancer code

## Details

```

> experiments( UCS )
ExperimentList class object of length 11:
 [1] UCS_CNASNP-20160128: RaggedExperiment with 54944 rows and 111 columns
 [2] UCS_CNVSNP-20160128: RaggedExperiment with 19298 rows and 111 columns
 [3] UCS_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 56 columns
 [4] UCS_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 56 rows and 56 columns
 [5] UCS_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 56 columns
 [6] UCS_Mutation-20160128: RaggedExperiment with 11339 rows and 57 columns
 [7] UCS_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 57 columns
 [8] UCS_RPPAArray-20160128: SummarizedExperiment with 192 rows and 48 columns
 [9] UCS_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 56 columns
[10] UCS_RNASeq2GeneNorm-20160128: SummarizedExperiment with 18645 rows and 57 columns
[11] UCS_Methylation-20160128: SummarizedExperiment with 485577 rows and 57 columns

> rownames( UCS )
CharacterList of length 11
[["UCS_CNASNP-20160128"]] character(0)
[["UCS_CNVSNP-20160128"]] character(0)
[["UCS_GISTIC_AllByGene-20160128"]] character(0)
[["UCS_GISTIC_Peaks-20160128"]] 26 1 2 3 27 4 28 29 ... 21 22 56 57 23 24 58
[["UCS_GISTIC_ThresholdedByGene-20160128"]] character(0)
[["UCS_Mutation-20160128"]] character(0)
[["UCS_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["UCS_RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363
[["UCS_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["UCS_RNASeq2GeneNorm-20160128"]] A1BG A2BP1 A2LD1 ... ZZEF1 ZZZ3 psiTPTE22

```

```

...
<1 more element>

> colnames( UCS )
CharacterList of length 11
[["UCS_CNASNP-20160128"]] TCGA-N5-A4R8-10A-01D-A28T-01 ...
[["UCS_CNVSNP-20160128"]] TCGA-N5-A4R8-10A-01D-A28T-01 ...
[["UCS_GISTIC_AllByGene-20160128"]] TCGA-N5-A4RA-01A-11D-A28Q-01 ...
[["UCS_GISTIC_Peaks-20160128"]] TCGA-N5-A4RA-01A-11D-A28Q-01 ...
[["UCS_GISTIC_ThresholdedByGene-20160128"]] TCGA-N5-A4RA-01A-11D-A28Q-01 ...
[["UCS_Mutation-20160128"]] TCGA-N5-A4R8-01A-11D-A28R-08 ...
[["UCS_RNASeq2Gene-20160128"]] TCGA-N5-A4R8-01A-11R-A28V-07 ...
[["UCS_RPPAArray-20160128"]] TCGA-N5-A4R8-01A-21-A41P-20 ...
[["UCS_miRNASeqGene-20160128"]] TCGA-N5-A4R8-01A-11R-A28Z-13 ...
[["UCS_RNASeq2GeneNorm-20160128"]] TCGA-N5-A4R8-01 ... TCGA-QN-A5NN-01
...
<1 more element>

```

Sizes of each ExperimentList element:

		assay size.Mb
1	UCS_CNASNP-20160128	1.5 Mb
2	UCS_CNVSNP-20160128	0.6 Mb
3	UCS_GISTIC_AllByGene-20160128	14.1 Mb
4	UCS_GISTIC_Peaks-20160128	0.1 Mb
5	UCS_GISTIC_ThresholdedByGene-20160128	13.9 Mb
6	UCS_Mutation-20160128	19.7 Mb
7	UCS_RNASeq2Gene-20160128	11.5 Mb
8	UCS_RPPAArray-20160128	0.1 Mb
9	UCS_miRNASeqGene-20160128	0.6 Mb
10	UCS_RNASeq2GeneNorm-20160128	10.4 Mb
11	UCS_Methylation-20160128	75 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

22 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
[1,] 35 35 1.43 1.04 1.96

```

-----  
Available sample meta-data:  
-----



```

years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
  51.00  62.00  68.00  69.72  76.00  90.00

vital_status:
  0 1
 22 35

days_to_death:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.  NA's
   8.0  304.0  522.0  705.4  790.5 3115.0   22

days_to_last_followup:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.  NA's
   0.0  591.2  828.0 1183.4 1647.5 4269.0   35

tumor_tissue_site:
uterus
  57

gender:
female
  57

date_of_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.
  2002  2007  2009  2009  2011  2012

radiation_therapy:
  no  yes  NA's
  29  25   3

histological_type:
uterine carcinosarcoma/ malignant mixed mullerian tumor (mmt): nos
  24
      uterine carcinosarcoma/ mmt: heterologous type
      20
      uterine carcinosarcoma/mmt: homologous type
      13

race:
      asian black or african american
      3 9
      NA's
      1
      white
      44

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

**See Also**[UVM-v2.0.1](#)

**Description**

A document describing the TCGA cancer code

**Details**

```
> experiments( UVM )
ExperimentList class object of length 12:
 [1] UVM_CNASeq-20160128: RaggedExperiment with 6496 rows and 102 columns
 [2] UVM_CNASNP-20160128: RaggedExperiment with 69487 rows and 160 columns
 [3] UVM_CNVSNP-20160128: RaggedExperiment with 12973 rows and 160 columns
 [4] UVM_GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 80 columns
 [5] UVM_GISTIC_Peaks-20160128: RangedSummarizedExperiment with 21 rows and 80 columns
 [6] UVM_GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 80 columns
 [7] UVM_miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 80 columns
 [8] UVM_Mutation-20160128: RaggedExperiment with 2174 rows and 80 columns
 [9] UVM_RNASeq2Gene-20160128: SummarizedExperiment with 20501 rows and 80 columns
 [10] UVM_RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 80 columns
 [11] UVM_RPPAArray-20160128: SummarizedExperiment with 192 rows and 12 columns
 [12] UVM_Methylation-20160128: SummarizedExperiment with 485577 rows and 80 columns

> rownames( UVM )
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[["UVM_CNASNP-20160128"]] character(0)
[["UVM_CNVSNP-20160128"]] character(0)
[["UVM_GISTIC_AllByGene-20160128"]] character(0)
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[["UVM_GISTIC_ThresholdedByGene-20160128"]] character(0)
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[["UVM_Mutation-20160128"]] character(0)
[["UVM_RNASeq2Gene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
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[["UVM_Mutation-20160128"]] TCGA-RZ-AB0B-01A-11D-A39W-08 ...
[["UVM_RNASeq2Gene-20160128"]] TCGA-RZ-AB0B-01A-11R-A405-07 ...
[["UVM_RNASeq2GeneNorm-20160128"]] TCGA-RZ-AB0B-01A-11R-A405-07 ...
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<2 more elements>

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Sizes of each ExperimentList element:

		assay size.Mb
1	UVM_CNASeq-20160128	0.2 Mb
2	UVM_CNASNP-20160128	1.9 Mb
3	UVM_CNVSNP-20160128	0.4 Mb
4	UVM_GISTIC_AllByGene-20160128	18.5 Mb
5	UVM_GISTIC_Peaks-20160128	0.1 Mb
6	UVM_GISTIC_ThresholdedByGene-20160128	18.5 Mb
7	UVM_miRNASeqGene-20160128	0.8 Mb
8	UVM_Mutation-20160128	12.3 Mb
9	UVM_RNASeq2Gene-20160128	15.1 Mb
10	UVM_RNASeq2GeneNorm-20160128	15.1 Mb
11	UVM_RPPAArray-20160128	0.1 Mb
12	UVM_Methylation-20160128	75 Mb

-----  
Overall survival time-to-event summary (in years):  
-----

```

Call: survfit(formula = survival::Surv(colDat$days_to_death/365, colDat$vital_status) ~
-1)

```

```

57 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
23.00  23.00   1.66   1.14   3.05

```

-----  
Available sample meta-data:  
-----

```

years_to_birth:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 22.00  51.00   61.50   61.65  74.25   86.00

```

```

vital_status:
 0  1
57 23

```

```

days_to_death:

```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
40.0	393.5	606.0	693.9	1029.0	1581.0	57

days\_to\_last\_followup:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
4.0	495.0	821.0	861.9	1184.0	2600.0	23

tumor\_tissue\_site:

choroid	80
---------	----

pathology\_N\_stage:

n0	nx	NA's
52	27	1

pathology\_M\_stage:

m0	m1	m1b	mx	NA's
51	2	2	23	2

gender:

female	male
35	45

date\_of\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
2007	2011	2012	2012	2013	2013

radiation\_therapy:

no	yes	NA's
76	3	1

race:

white	NA's
55	25

ethnicity:

hispanic or latino	not hispanic or latino	NA's
1	52	27

Including an additional 448 columns

**Description**

A document describing the TCGA cancer code

**Details**

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 [11] UVM_RNASeq2GeneNorm-20160128: SummarizedExperiment with 17345 rows and 80 columns
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[["UVM_CNASeq-20160128"]] character(0)
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[["UVM_RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363
[["UVM_miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
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[["UVM_RNASeq2Gene-20160128"]] TCGA-RZ-AB0B-01A-11R-A405-07 ...
[["UVM_RPPAArray-20160128"]] TCGA-V3-A9ZX-01A-21-A41Z-20 ...
[["UVM_miRNASeqGene-20160128"]] TCGA-RZ-AB0B-01A-11R-A40B-13 ...
...
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<2 more elements>

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5	UVM_GISTIC_Peaks-20160128		0.1 Mb
6	UVM_GISTIC_ThresholdedByGene-20160128		18.5 Mb
7	UVM_Mutation-20160128		12.3 Mb
8	UVM_RNASeq2Gene-20160128		15.1 Mb
9	UVM_RPPAArray-20160128		0.1 Mb
10	UVM_miRNASeqGene-20160128		0.8 Mb
11	UVM_RNASeq2GeneNorm-20160128		12.8 Mb
12	UVM_Methylation-20160128		75 Mb

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-1)

57 observations deleted due to missingness  
n events median 0.95LCL 0.95UCL  
[1,] 23 23 1.66 1.14 3.05

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57	23

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days\_to\_last\_followup:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
------	---------	--------	------	---------	------	------

4.0 495.0 821.0 861.9 1184.0 2600.0 23

tumor\_tissue\_site:

choroid

80

pathology\_N\_stage:

n0 nx NA's

52 27 1

pathology\_M\_stage:

m0 m1 m1b mx NA's

51 2 2 23 2

gender:

female male

35 45

date\_of\_initial\_pathologic\_diagnosis:

Min. 1st Qu. Median Mean 3rd Qu. Max.

2007 2011 2012 2012 2013 2013

radiation\_therapy:

no yes NA's

76 3 1

race:

white NA's

55 25

ethnicity:

hispanic or latino not hispanic or latino

1

52

NA's

27

Including an additional 448 columns

# Index

## \* datasets

ACC, [6](#)  
ACC-v2.0.1, [9](#)  
ACC-v2.1.0, [12](#)  
BLCA, [15](#)  
BLCA-v2.0.1, [19](#)  
BLCA-v2.1.0, [22](#)  
BRCA, [25](#)  
BRCA-v2.0.1, [29](#)  
BRCA-v2.1.0, [32](#)  
CESC, [35](#)  
CESC-v2.0.1, [41](#)  
CESC-v2.1.0, [47](#)  
CHOL, [52](#)  
CHOL-v2.0.1, [55](#)  
CHOL-v2.1.0, [59](#)  
COAD, [62](#)  
COAD-v2.0.1, [64](#)  
COAD-v2.1.0, [67](#)  
DLBC, [72](#)  
DLBC-v2.0.1, [75](#)  
DLBC-v2.1.0, [77](#)  
ESCA, [80](#)  
ESCA-v2.0.1, [84](#)  
ESCA-v2.1.0, [87](#)  
GBM, [90](#)  
GBM-v2.0.1, [93](#)  
GBM-v2.1.0, [97](#)  
HNSC, [100](#)  
HNSC-v2.0.1, [103](#)  
HNSC-v2.1.0, [107](#)  
KICH, [110](#)  
KICH-v2.0.1, [114](#)  
KICH-v2.1.0, [117](#)  
KIRC, [120](#)  
KIRC-v2.0.1, [124](#)  
KIRC-v2.1.0, [127](#)  
KIRP, [131](#)  
KIRP-v2.0.1, [134](#)  
KIRP-v2.1.0, [138](#)  
LAML, [141](#)  
LAML-v2.0.1, [144](#)  
LAML-v2.1.0, [147](#)  
LGG, [149](#)  
LGG-v2.0.1, [152](#)  
LGG-v2.1.0, [155](#)  
LIHC, [158](#)  
LIHC-v2.0.1, [161](#)  
LIHC-v2.1.0, [165](#)  
LUAD, [168](#)  
LUAD-v2.0.1, [171](#)  
LUAD-v2.1.0, [175](#)  
LUSC, [178](#)  
LUSC-v2.0.1, [182](#)  
LUSC-v2.1.0, [185](#)  
MESO, [189](#)  
MESO-v2.0.1, [192](#)  
MESO-v2.1.0, [195](#)  
OV, [198](#)  
OV-v2.0.1, [201](#)  
OV-v2.1.0, [205](#)  
OV-v2.1.1, [208](#)  
PAAD, [210](#)  
PAAD-v2.0.1, [213](#)  
PAAD-v2.1.0, [217](#)  
PCPG, [220](#)  
PCPG-v2.0.1, [223](#)  
PCPG-v2.1.0, [226](#)  
PRAD, [229](#)  
PRAD-v2.0.1, [233](#)  
PRAD-v2.1.0, [236](#)  
READ, [239](#)  
READ-v2.0.1, [243](#)  
READ-v2.1.0, [246](#)  
SARC, [249](#)  
SARC-v2.0.1, [252](#)  
SARC-v2.1.0, [255](#)  
SKCM, [258](#)

- SKCM-v2.0.1, [261](#)
  - SKCM-v2.1.0, [264](#)
  - SKCM-v2.1.1, [267](#)
  - STAD, [269](#)
  - STAD-v2.0.1, [272](#)
  - STAD-v2.1.0, [275](#)
  - TGCT, [279](#)
  - TGCT-v2.0.1, [282](#)
  - TGCT-v2.1.0, [285](#)
  - THCA, [288](#)
  - THCA-v2.0.1, [291](#)
  - THCA-v2.1.0, [294](#)
  - THYM, [297](#)
  - THYM-v2.0.1, [300](#)
  - THYM-v2.1.0, [303](#)
  - UCEC, [305](#)
  - UCEC-v2.0.1, [308](#)
  - UCEC-v2.1.0, [311](#)
  - UCS, [313](#)
  - UCS-v2.0.1, [316](#)
  - UCS-v2.1.0, [319](#)
  - UVM, [322](#)
  - UVM-v2.0.1, [325](#)
  - UVM-v2.1.0, [327](#)
- 
- ACC (ACC), [6](#)
  - ACC-v2.0.1 (ACC-v2.0.1), [9](#)
  - ACC-v2.1.0 (ACC-v2.1.0), [12](#)
  - BLCA (BLCA), [15](#)
  - BLCA-v2.0.1 (BLCA-v2.0.1), [19](#)
  - BLCA-v2.1.0 (BLCA-v2.1.0), [22](#)
  - BRCA (BRCA), [25](#)
  - BRCA-v2.0.1 (BRCA-v2.0.1), [29](#)
  - BRCA-v2.1.0 (BRCA-v2.1.0), [32](#)
  - CESC (CESC), [35](#)
  - CESC-v2.0.1 (CESC-v2.0.1), [41](#)
  - CESC-v2.1.0 (CESC-v2.1.0), [47](#)
  - CHOL (CHOL), [52](#)
  - CHOL-v2.0.1 (CHOL-v2.0.1), [55](#)
  - CHOL-v2.1.0 (CHOL-v2.1.0), [59](#)
  - COAD (COAD), [62](#)
  - COAD-v2.0.1 (COAD-v2.0.1), [64](#)
  - COAD-v2.1.0 (COAD-v2.1.0), [67](#)
  - DLBC (DLBC), [72](#)
  - DLBC-v2.0.1 (DLBC-v2.0.1), [75](#)
  - DLBC-v2.1.0 (DLBC-v2.1.0), [77](#)
  - ESCA (ESCA), [80](#)
  - ESCA-v2.0.1 (ESCA-v2.0.1), [84](#)
  - ESCA-v2.1.0 (ESCA-v2.1.0), [87](#)
- 
- GBM (GBM), [90](#)
  - GBM-v2.0.1 (GBM-v2.0.1), [93](#)
  - GBM-v2.1.0 (GBM-v2.1.0), [97](#)
  - HNSC (HNSC), [100](#)
  - HNSC-v2.0.1 (HNSC-v2.0.1), [103](#)
  - HNSC-v2.1.0 (HNSC-v2.1.0), [107](#)
  - KICH (KICH), [110](#)
  - KICH-v2.0.1 (KICH-v2.0.1), [114](#)
  - KICH-v2.1.0 (KICH-v2.1.0), [117](#)
  - KIRC (KIRC), [120](#)
  - KIRC-v2.0.1 (KIRC-v2.0.1), [124](#)
  - KIRC-v2.1.0 (KIRC-v2.1.0), [127](#)
  - KIRP (KIRP), [131](#)
  - KIRP-v2.0.1 (KIRP-v2.0.1), [134](#)
  - KIRP-v2.1.0 (KIRP-v2.1.0), [138](#)
  - LAML (LAML), [141](#)
  - LAML-v2.0.1 (LAML-v2.0.1), [144](#)
  - LAML-v2.1.0 (LAML-v2.1.0), [147](#)
  - LGG (LGG), [149](#)
  - LGG-v2.0.1 (LGG-v2.0.1), [152](#)
  - LGG-v2.1.0 (LGG-v2.1.0), [155](#)
  - LIHC (LIHC), [158](#)
  - LIHC-v2.0.1 (LIHC-v2.0.1), [161](#)
  - LIHC-v2.1.0 (LIHC-v2.1.0), [165](#)
  - LUAD (LUAD), [168](#)
  - LUAD-v2.0.1 (LUAD-v2.0.1), [171](#)
  - LUAD-v2.1.0 (LUAD-v2.1.0), [175](#)
  - LUSC (LUSC), [178](#)
  - LUSC-v2.0.1 (LUSC-v2.0.1), [182](#)
  - LUSC-v2.1.0 (LUSC-v2.1.0), [185](#)
  - MESO (MESO), [189](#)
  - MESO-v2.0.1 (MESO-v2.0.1), [192](#)
  - MESO-v2.1.0 (MESO-v2.1.0), [195](#)
  - OV (OV), [198](#)
  - OV-v2.0.1 (OV-v2.0.1), [201](#)
  - OV-v2.1.0 (OV-v2.1.0), [205](#)
  - OV-v2.1.1 (OV-v2.1.1), [208](#)
  - PAAD (PAAD), [210](#)
  - PAAD-v2.0.1 (PAAD-v2.0.1), [213](#)
  - PAAD-v2.1.0 (PAAD-v2.1.0), [217](#)
  - PCPG (PCPG), [220](#)
  - PCPG-v2.0.1 (PCPG-v2.0.1), [223](#)
  - PCPG-v2.1.0 (PCPG-v2.1.0), [226](#)
  - PRAD (PRAD), [229](#)
  - PRAD-v2.0.1 (PRAD-v2.0.1), [233](#)
  - PRAD-v2.1.0 (PRAD-v2.1.0), [236](#)
  - READ (READ), [239](#)
  - READ-v2.0.1 (READ-v2.0.1), [243](#)

- READ-v2.1.0 (READ-v2.1.0), 246  
SARC (SARC), 249  
SARC-v2.0.1 (SARC-v2.0.1), 252  
SARC-v2.1.0 (SARC-v2.1.0), 255  
SKCM (SKCM), 258  
SKCM-v2.0.1 (SKCM-v2.0.1), 261  
SKCM-v2.1.0 (SKCM-v2.1.0), 264  
SKCM-v2.1.1 (SKCM-v2.1.1), 267  
STAD (STAD), 269  
STAD-v2.0.1 (STAD-v2.0.1), 272  
STAD-v2.1.0 (STAD-v2.1.0), 275  
TGCT (TGCT), 279  
TGCT-v2.0.1 (TGCT-v2.0.1), 282  
TGCT-v2.1.0 (TGCT-v2.1.0), 285  
THCA (THCA), 288  
THCA-v2.0.1 (THCA-v2.0.1), 291  
THCA-v2.1.0 (THCA-v2.1.0), 294  
THYM (THYM), 297  
THYM-v2.0.1 (THYM-v2.0.1), 300  
THYM-v2.1.0 (THYM-v2.1.0), 303  
UCEC (UCEC), 305  
UCEC-v2.0.1 (UCEC-v2.0.1), 308  
UCEC-v2.1.0 (UCEC-v2.1.0), 311  
UCS (UCS), 313  
UCS-v2.0.1 (UCS-v2.0.1), 316  
UCS-v2.1.0 (UCS-v2.1.0), 319  
UVM (UVM), 322  
UVM-v2.0.1 (UVM-v2.0.1), 325  
UVM-v2.1.0 (UVM-v2.1.0), 327
- ACC, 6  
ACC-v2.0.1, 9, 9  
ACC-v2.1.0, 12
- BLCA, 15  
BLCA-v2.0.1, 19, 19  
BLCA-v2.1.0, 22  
BRCA, 25  
BRCA-v2.0.1, 29, 29  
BRCA-v2.1.0, 32
- CESC, 35  
CESC-v2.0.1, 41, 41  
CESC-v2.1.0, 47  
CHOL, 52  
CHOL-v2.0.1, 55, 55  
CHOL-v2.1.0, 59  
COAD, 62  
COAD-v2.0.1, 64, 64
- COAD-v2.1.0, 67  
curatedTCGADData, 69  
curatedTCGADData-package, 4, 70
- DLBC, 72  
DLBC-v2.0.1, 75, 75  
DLBC-v2.1.0, 77
- ESCA, 80  
ESCA-v2.0.1, 83, 84  
ESCA-v2.1.0, 87  
ExperimentHub, 70
- GBM, 90  
GBM-v2.0.1, 93, 93  
GBM-v2.1.0, 97
- HNSC, 100  
HNSC-v2.0.1, 103, 103  
HNSC-v2.1.0, 107
- KICH, 110  
KICH-v2.0.1, 113, 114  
KICH-v2.1.0, 117  
KIRC, 120  
KIRC-v2.0.1, 124, 124  
KIRC-v2.1.0, 127  
KIRP, 131  
KIRP-v2.0.1, 134, 134  
KIRP-v2.1.0, 138
- LAML, 141  
LAML-v2.0.1, 144, 144  
LAML-v2.1.0, 147  
LGG, 149  
LGG-v2.0.1, 152, 152  
LGG-v2.1.0, 155  
LIHC, 158  
LIHC-v2.0.1, 161, 161  
LIHC-v2.1.0, 165  
LUAD, 168  
LUAD-v2.0.1, 171, 171  
LUAD-v2.1.0, 175  
LUSC, 178  
LUSC-v2.0.1, 182, 182  
LUSC-v2.1.0, 185
- MESO, 189  
MESO-v2.0.1, 192, 192  
MESO-v2.1.0, 195

MultiAssayExperiment, [69](#), [70](#)

OV, [198](#)

OV-v2.0.1, [201](#), [201](#)

OV-v2.1.0, [205](#)

OV-v2.1.1, [208](#)

PAAD, [210](#)

PAAD-v2.0.1, [213](#), [213](#)

PAAD-v2.1.0, [217](#)

PCPG, [220](#)

PCPG-v2.0.1, [223](#), [223](#)

PCPG-v2.1.0, [226](#)

PRAD, [229](#)

PRAD-v2.0.1, [232](#), [233](#)

PRAD-v2.1.0, [236](#)

READ, [239](#)

READ-v2.0.1, [242](#), [243](#)

READ-v2.1.0, [246](#)

SARC, [249](#)

SARC-v2.0.1, [252](#), [252](#)

SARC-v2.1.0, [255](#)

SKCM, [257](#)

SKCM-v2.0.1, [260](#), [261](#)

SKCM-v2.1.0, [264](#)

SKCM-v2.1.1, [267](#)

STAD, [269](#)

STAD-v2.0.1, [272](#), [272](#)

STAD-v2.1.0, [275](#)

TGCT, [279](#)

TGCT-v2.0.1, [282](#), [282](#)

TGCT-v2.1.0, [285](#)

THCA, [288](#)

THCA-v2.0.1, [291](#), [291](#)

THCA-v2.1.0, [294](#)

THYM, [297](#)

THYM-v2.0.1, [300](#), [300](#)

THYM-v2.1.0, [303](#)

UCEC, [305](#)

UCEC-v2.0.1, [308](#), [308](#)

UCEC-v2.1.0, [311](#)

UCS, [313](#)

UCS-v2.0.1, [316](#), [316](#)

UCS-v2.1.0, [319](#)

UVM, [322](#)

UVM-v2.0.1, [324](#), [325](#)

UVM-v2.1.0, [327](#)