

Package ‘curatedTCGAData’

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Type Package

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

Version 1.2.0

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

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Depends R (>= 3.4.0), MultiAssayExperiment

Imports AnnotationHub, ExperimentHub, S4Vectors, utils

Suggests BiocStyle, knitr, readr, rmarkdown, testthat

VignetteBuilder knitr

biocViews Homo_sapiens_Data, ReproducibleResearch, CancerData

LazyData true

RoxygenNote 6.0.1

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curatedTCGAData-package

curatedTCGAData-package

Description

The following are the TCGA cancer codes and full names.

Study Abbreviation	Study Name

1 ACC	Adrenocortical Carcinoma

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

Examples

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

ACC

Adrenocortical carcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( ACC )
ExperimentList class object of length 9:
 [1] CNASNP-20160128: RaggedExperiment with 79861 rows and 180 columns
 [2] CNVSNP-20160128: RaggedExperiment with 21052 rows and 180 columns
```

```
[3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 90 columns
[4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 90 columns
[5] Methylation-20160128: SummarizedExperiment with 485577 rows and 80 columns
[6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 80 columns
[7] Mutation-20160128: RaggedExperiment with 20166 rows and 90 columns
[8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 79 columns
[9] RPPAArray-20160128: SummarizedExperiment with 192 rows and 46 columns
```

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

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

Sizes of each ExperimentList element:

		assay size.Mb
1	CNASNP-20160128	2.2 Mb
2	CNVSNP-20160128	0.6 Mb
3	GISTIC_AllByGene-20160128	4.9 Mb
4	GISTIC_ThresholdedByGene-20160128	4.9 Mb
5	Methylation-20160128	75 Mb
6	miRNASeqGene-20160128	0.1 Mb
7	Mutation-20160128	12.6 Mb
8	RNASeq2GeneNorm-20160128	1.3 Mb
9	RPPAArray-20160128	0 Mb

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

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

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

 Available sample meta-data:

years_to_birth:

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

vital_status:

0	1
58	34

days_to_death:

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

days_to_last_followup:

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

tumor_tissue_site:

adrenal
92

pathologic_stage:

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

pathology_T_stage:

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

pathology_N_stage:

n0	n1	NA's
80	10	2

gender:

female	male
60	32

date_of_initial_pathologic_diagnosis:

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

radiation_therapy:

no	yes	NA's
71	18	3

```

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

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

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

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

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

```

Including an additional 806 columns

BLCA

Bladder Urothelial Carcinoma

Description

A document describing the TCGA cancer code

Details

```

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

```

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

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

Sizes of each ExperimentList element:

		assay size.Mb
1	CNASeq-20160128	1 Mb
2	CNASNP-20160128	13.1 Mb
3	CNVSNP-20160128	3 Mb
4	GISTIC_AllByGene-20160128	4.9 Mb
5	GISTIC_ThresholdedByGene-20160128	4.9 Mb
6	Methylation-20160128	75.1 Mb
7	miRNASeqGene-20160128	0.1 Mb
8	Mutation-20160128	56.1 Mb
9	RNASeq2GeneNorm-20160128	1.3 Mb
10	RNASeqGene-20160128	1.3 Mb
11	RPPAArray-20160128	0 Mb

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

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

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

 Available sample meta-data:

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

vital_status:
 0 1
 230 182

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

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

tumor_tissue_site:
 bladder
 412

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

pathology_M_stage:
 m0 m1 mx NA's
 196 11 202 3

gender:
 female male
 108 304

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

radiation_therapy:
 no yes NA's
 366 20 26


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

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

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

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

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

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

Including an additional 1695 columns

BRCA

Breast invasive carcinoma

Description

A document describing the TCGA cancer code

Details

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

```
[11] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 1212 columns
[12] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 878 columns
[13] RPPAArray-20160128: SummarizedExperiment with 226 rows and 937 columns
```

```
> rownames( BRCA )
CharacterList of length 13
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg000002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SLC39A6 SNRPD2 AQP7 CTSC
[["Mutation-20160128"]] character(0)
...
<3 more elements>
```

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

Sizes of each ExperimentList element:

		assay size.Mb
1	CNASeq-20160128	0.2 Mb
2	CNASNP-20160128	30.9 Mb
3	CNVSNP-20160128	8.2 Mb
4	GISTIC_AllByGene-20160128	5 Mb
5	GISTIC_ThresholdedByGene-20160128	5 Mb
6	Methylation_methyl27-20160128	4.9 Mb
7	Methylation_methyl450-20160128	75.1 Mb
8	miRNASeqGene-20160128	0.1 Mb
9	mRNAArray-20160128	1.2 Mb
10	Mutation-20160128	67.4 Mb
11	RNASeq2GeneNorm-20160128	1.4 Mb
12	RNASeqGene-20160128	1.4 Mb
13	RPPAArray-20160128	0.1 Mb

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

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

947 observations deleted due to missingness

n	events	median	0.95LCL	0.95UCL
151.00	151.00	3.48	2.83	4.50

Available sample meta-data:

years_to_birth:

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

vital_status:

0	1	NA's
945	152	1

days_to_death:

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

days_to_last_followup:

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

tumor_tissue_site:

breast	NA's
1097	1

pathology_M_stage:

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

gender:

female	male	NA's
1085	12	1

date_of_initial_pathologic_diagnosis:

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

days_to_last_known_alive:

735	2576	NA's
735	2576	NA's

```
1 1 1096
```

```
radiation_therapy:
```

```
no yes NA's
446 556 96
```

```
number_of_lymph_nodes:
```

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

```
race:
```

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

```
ethnicity:
```

```
hispanic or latino not hispanic or latino      NA's
                                     39      884      175
```

```
Including an additional 2667 columns
```

CESC

Cervical squamous cell carcinoma and endocervical adenocarcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( CESC )
ExperimentList class object of length 10:
 [1] CNASeq-20160128: RaggedExperiment with 7834 rows and 100 columns
 [2] CNASNP-20160128: RaggedExperiment with 267855 rows and 586 columns
 [3] CNVSNP-20160128: RaggedExperiment with 59450 rows and 586 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 295 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 295 columns
 [6] Methylation-20160128: SummarizedExperiment with 485577 rows and 312 columns
 [7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 312 columns
 [8] Mutation-20160128: RaggedExperiment with 46547 rows and 194 columns
 [9] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 309 columns
 [10] RPPAArray-20160128: SummarizedExperiment with 192 rows and 173 columns

> rownames( CESC )
CharacterList of length 10
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
```

```

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

```

```
> colnames( CESC )
```

```
CharacterList of length 10
```

```

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

```

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

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

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

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

```

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

```

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

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

vital_status:
 0 1
 235 72

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

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

tumor_tissue_site:
 cervical
 307

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

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

gender:
 female
 307

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

radiation_therapy:
 no yes NA's
 55 129 123

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

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

ethnicity:

hispanic or latino	not hispanic or latino	NA's				
24	171	112				
weight_kg_at_diagnosis:						
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
31.00	58.25	70.50	73.04	83.75	210.00	29
tumor_status:						
tumor free	with tumor	NA's				
201	80	26				
tobacco_smoking_year_stopped:						
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1949	1995	2003	2000	2010	2013	264
tobacco_smoking_pack_years_smoked:						
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.20	6.50	15.00	17.38	25.00	57.00	214
tobacco_smoking_history:						
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
1.000	1.000	1.000	1.829	2.000	5.000	44
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				
	29	3	NA's			
			275			
pregnancies_count_total:						
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.00	2.00	3.00	3.61	5.00	15.00	40
pregnancies_count_stillbirth:						
0	1	3	NA's			
106	5	1	195			
pregnancy_spontaneous_abortion_count:						
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.0000	0.0000	0.0000	0.5442	1.0000	6.0000	160
pregnancies_count_live_birth:						
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.000	1.250	2.000	2.844	4.000	11.000	45
pregnancy_therapeutic_abortion_count:						
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.0000	0.0000	0.0000	0.8525	1.0000	13.0000	185

pregnancies_count_ectopic:

0	1	2	NA's
104	11	1	191

lymph_node_location:

lymph_node_location_positive_pathology_name|lymph_node_location_positive_pathology_text
307

menopause_status:

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

lymphovascular_involvement:

absent	present	NA's
72	80	155

lymph_nodes_examined_he_count:

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

lymph_nodes_examined:

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

keratinization_squamous_cell:

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

initial_pathologic_dx_year:

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

hysterectomy_type:

hysterectomy_performed_type|hysterectomy_performed_text
307

history_hormonal_contraceptives_use:

current user	former user	never used	NA's
--------------	-------------	------------	------

	15	54	90	148		
height_cm_at_diagnosis:						
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
132	157	160	161	165	183	43
corpus_involvement:						
absent	present	NA's				
99	19	189				
chemo_concurrent_type:						
carboplatin	cisplatin		other		NA's	
7	104		2		194	
cervix_suv_results:						
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.00	8.70	12.00	13.22	16.92	28.80	290
cause_of_death:						
cardiopulmonary arrest			lung cancer		renal failure	
		1		1		1
		NA's				
		304				
age_at_diagnosis:						
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	
20.00	38.00	46.00	48.27	56.50	88.00	

Including an additional 1330 columns

CHOL

Cholangiocarcinoma

Description

A document describing the TCGA cancer code

Details

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

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

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

Sizes of each ExperimentList element:

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

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

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

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

Available sample meta-data:

```

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

vital_status:
  0 1
 18 18

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

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

tumor_tissue_site:
bile duct
  36

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

pathology_N_stage:
n0 n1 nx
26 5 5

pathology_M_stage:
m0 m1 mx
28 5 3

gender:
female  male
  20    16

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

radiation_therapy:
no NA's
  35  1

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

```

residual_tumor:

r0 r1 rx
28 5 3

race:

asian	black or african american	white
3	2	31

ethnicity:

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

Including an additional 622 columns

COAD

Colon adenocarcinoma

Description

A document describing the TCGA cancer code

Details

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

> rownames( COAD )
CharacterList of length 13
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SLC39A6 SNRPD2 AQP7 CTSC
```

```

[["Mutation-20160128"]] character(0)
...
<3 more elements>

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

```

Sizes of each ExperimentList element:

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

Available sample meta-data:

```

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

```

```

tumor_tissue_site:
colon NA's
  456    1

```

```

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

radiation_therapy:
  no  yes NA's
  378  9   70

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

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

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

```

Including an additional 2604 columns

curatedTCGAData

Create a MultiAssayExperiment from specific assays and cohorts

Description

Create a MultiAssayExperiment from specific assays and cohorts

Usage

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

Arguments

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

Details

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

Value

a [MultiAssayExperiment](#) of the specified assays and cancer codes

Examples

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

DLBC

*Lymphoid Neoplasm Diffuse Large B-cell Lymphoma***Description**

A document describing the TCGA cancer code

Details

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

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

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

```
[[ "RPPAArray-20160128" ]] TCGA-FA-8693-01A-21-A45K-20 ...
```

Sizes of each ExperimentList element:

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

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

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

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

Available sample meta-data:

years_to_birth:

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

vital_status:

0	1
39	9

days_to_death:

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

days_to_last_followup:

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

gender:

female	male
26	22


```

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

radiation_therapy:
  no  yes NA's
  40  7    1

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

race:
                                                                 asian black or african american
                                                                 18
                                                                                                     1
                                                                                                     white
                                                                                                     29

ethnicity:
  hispanic or latino not hispanic or latino
                                                                 12
                                                                                                     36

Including an additional 607 columns

```

ESCA

Esophageal carcinoma

Description

A document describing the TCGA cancer code

Details

```

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

> rownames( ESCA )
CharacterList of length 11

```

```

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

```

```

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

```

Sizes of each ExperimentList element:

		assay size.Mb
1	CNASeq-20160128	0.5 Mb
2	CNASNP-20160128	5.5 Mb
3	CNVSNP-20160128	1.7 Mb
4	GISTIC_AllByGene-20160128	4.9 Mb
5	GISTIC_ThresholdedByGene-20160128	4.9 Mb
6	Methylation-20160128	75 Mb
7	miRNASeqGene-20160128	0.1 Mb
8	Mutation-20160128	41.2 Mb
9	RNASeq2GeneNorm-20160128	1.3 Mb
10	RNASeqGene-20160128	1.7 Mb
11	RPPAArray-20160128	0 Mb

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

```

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

```

```

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

```

77.000 77.000 0.962 0.677 1.353

 Available sample meta-data:

years_to_birth:

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

vital_status:

0	1
108	77

days_to_death:

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

days_to_last_followup:

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

tumor_tissue_site:

esophagus
185

pathology_M_stage:

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

gender:

female	male
27	158

date_of_initial_pathologic_diagnosis:

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

radiation_therapy:

no	yes	NA's
124	43	18

karnofsky_performance_score:

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

histological_type:

esophagus adenocarcinoma, nos esophagus squamous cell carcinoma

89

96

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

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

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

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

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

Including an additional 940 columns

 GBM

Glioblastoma multiforme

Description

A document describing the TCGA cancer code

Details

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

[15] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 166 columns
 [16] RPPAArray-20160128: SummarizedExperiment with 208 rows and 244 columns

```
> rownames( GBM )
CharacterList of length 16
[["CNACGH_CGH_hg_244a-20160128"]] character(0)
[["CNACGH_CGH_hg_415k_g4124a-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg000002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNAArray-20160128"]] ebv-miR-BART1-3p ebv-miR-BART1-5p ... kshv-miR-K12-9*
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
...
<6 more elements>
```

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

Sizes of each ExperimentList element:

	assay	size.Mb
1	CNACGH_CGH_hg_244a-20160128	2.3 Mb
2	CNACGH_CGH_hg_415k_g4124a-20160128	1.7 Mb
3	CNASNP-20160128	16.4 Mb
4	CNVSNP-20160128	4.2 Mb
5	GISTIC_AllByGene-20160128	4.9 Mb
6	GISTIC_ThresholdedByGene-20160128	4.9 Mb
7	Methylation_methyl27-20160128	4.9 Mb
8	Methylation_methyl450-20160128	75 Mb
9	miRNAArray-20160128	0.1 Mb
10	miRNASeqGene-20160128	0.1 Mb
11	mRNAArray_huex-20160128	1.2 Mb
12	mRNAArray_TX_g4502a-20160128	1.2 Mb
13	mRNAArray_TX_ht_hg_u133a-20160128	0.8 Mb
14	Mutation-20160128	31 Mb
15	RNASeq2GeneNorm-20160128	1.3 Mb
16	RPPAArray-20160128	0 Mb

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

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

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

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

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

```
vital_status:
  0  1 NA's
104 491  4
```

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

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

```
tumor_tissue_site:
brain NA's
  595  4
```

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

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

```
radiation_therapy:
no yes NA's
  78 489  32
```

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

```

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

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

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

```

Including an additional 4368 columns

HNSC

Head and Neck squamous cell carcinoma

Description

A document describing the TCGA cancer code

Details

```

> experiments( HNSC )
ExperimentList class object of length 11:
 [1] CNASeq-20160128: RaggedExperiment with 32905 rows and 225 columns
 [2] CNASNP-20160128: RaggedExperiment with 499142 rows and 1090 columns
 [3] CNVSNP-20160128: RaggedExperiment with 110289 rows and 1089 columns
 [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 522 columns
 [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 522 columns
 [6] Methylation-20160128: SummarizedExperiment with 485577 rows and 580 columns
 [7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 532 columns
 [8] Mutation-20160128: RaggedExperiment with 51799 rows and 279 columns
 [9] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 566 columns
[10] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 294 columns
[11] RPPAArray-20160128: SummarizedExperiment with 160 rows and 212 columns

> rownames( HNSC )
CharacterList of length 11
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b

```

```

[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZ33 psiTPTE22 tAKR
[["RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZEF1 ZZ33 psiTPTE22 tAKR
...
<1 more element>

```

```

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

```

Sizes of each ExperimentList element:

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

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

```

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

```

```

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

```

Available sample meta-data:

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

```
vital_status:
  0  1
304 224
```

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

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

```
tumor_tissue_site:
head and neck
  528
```

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

```
gender:
female  male
  142   386
```

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

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

```
radiation_therapy:
  no  yes NA's
  163 303  62
```

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

```
number_pack_years_smoked:
```

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
	0.01685	25.00000	40.00000	45.75496	60.00000	300.00000	230
year_of_tobacco_smoking_onset:							
	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
	1936	1959	1968	1967	1975	2001	246
number_of_lymph_nodes:							
	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
	0.000	0.000	1.000	2.186	3.000	44.000	115
race:							
american indian or alaska native							asian
			2				11
black or african american							white
			48				452
			NA's				
			15				
ethnicity:							
hispanic or latino							NA's
			26				37
not hispanic or latino						465	

Including an additional 1426 columns

KICH

Kidney Chromophobe

Description

A document describing the TCGA cancer code

Details

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

> rownames( KICH )
CharacterList of length 9
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
```

```

[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

```

```
> colnames( KICH )
```

```
CharacterList of length 9
```

```

[["CNASNP-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["CNVSNP-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-KL-8323-01A-21D-2308-01 ...
[["Methylation-20160128"]] TCGA-KL-8323-01A-21D-2312-05 ...
[["miRNASeqGene-20160128"]] TCGA-KL-8323-01A-21R-2314-13 ...
[["Mutation-20160128"]] TCGA-KL-8323-01A-21D-2310-10 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-KL-8323-01A-21R-2315-07 ...
[["RPPAArray-20160128"]] TCGA-KL-8324-01A-21-A421-20 ...

```

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

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

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

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

```

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

```

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

```
years_to_birth:
```

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

vital_status:

0 1
56 10

days_to_death:

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

days_to_last_followup:

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

tumor_tissue_site:

kidney
66

pathologic_stage:

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

pathology_N_stage:

n0 n1 n2 nx
40 3 2 21

pathology_M_stage:

m0	m1	mx	NA's
34	2	9	21

gender:

female male
27 39

date_of_initial_pathologic_diagnosis:

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

radiation_therapy:

no
66

karnofsky_performance_score:

90	100	NA's
3	10	53

histological_type:

kidney chromophobe
66

number_pack_years_smoked:

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

```

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

```

```

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

```

```

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

```

Including an additional 718 columns

KIRC *Kidney renal clear cell carcinoma*

Description

A document describing the TCGA cancer code

Details

```

> experiments( KIRC )
ExperimentList class object of length 12:
 [1] CNASNP-20160128: RaggedExperiment with 488691 rows and 1059 columns
 [2] CNVSNP-20160128: RaggedExperiment with 85036 rows and 1059 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 528 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 528 columns
 [5] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 418 columns
 [6] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 480 columns
 [7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 326 columns
 [8] mRNAArray-20160128: SummarizedExperiment with 17814 rows and 72 columns
 [9] Mutation-20160128: RaggedExperiment with 26369 rows and 437 columns
[10] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 606 columns
[11] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 537 columns
[12] RPPAArray-20160128: SummarizedExperiment with 217 rows and 478 columns

> rownames( KIRC )
CharacterList of length 12
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SLC39A6 SNRPD2 AQP7 CTSC

```

```

[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
...
<2 more elements>

```

```

> colnames( KIRC )
CharacterList of length 12
[["CNASNP-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["CNVSNP-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-3Z-A93Z-01A-11D-A36W-01 ...
[["Methylation_methyl27-20160128"]] TCGA-A3-3306-11A-01D-0859-05 ...
[["Methylation_methyl450-20160128"]] TCGA-3Z-A93Z-01A-11D-A36Y-05 ...
[["miRNASeqGene-20160128"]] TCGA-3Z-A93Z-01A-11R-A37P-13 ...
[["mRNAArray-20160128"]] TCGA-A3-3306-01A-01R-0864-07 ...
[["Mutation-20160128"]] TCGA-A3-3308-01A-01D-0966-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-3Z-A93Z-01A-11R-A370-07 ...
...
<2 more elements>

```

Sizes of each ExperimentList element:

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

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

```

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

```

```

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

```

Available sample meta-data:

```

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

vital_status:
  0  1
360 177

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

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

tumor_tissue_site:
kidney
  537

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

pathology_N_stage:
  n0 n1 nx
240 17 280

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

gender:
female male
  191  346

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

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

radiation_therapy:
  no yes NA's
  142 2 393

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

```

```

histological_type:
kidney clear cell renal carcinoma
                    537

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

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

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

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

Including an additional 2250 columns

```

KIRP

Kidney renal papillary cell carcinoma

Description

A document describing the TCGA cancer code

Details

```

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

> rownames( KIRP )
CharacterList of length 12

```



```

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

```

```

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

```

Sizes of each ExperimentList element:

		assay size.Mb
1	CNASNP-20160128	8.2 Mb
2	CNVSNP-20160128	1.4 Mb
3	GISTIC_AllByGene-20160128	4.9 Mb
4	GISTIC_ThresholdedByGene-20160128	4.9 Mb
5	Methylation_methyl27-20160128	4.9 Mb
6	Methylation_methyl450-20160128	75 Mb
7	miRNASeqGene-20160128	0.1 Mb
8	mRNAArray-20160128	1.1 Mb
9	Mutation-20160128	10.6 Mb
10	RNASeq2GeneNorm-20160128	1.3 Mb
11	RNASeqGene-20160128	1.3 Mb
12	RPPAArray-20160128	0 Mb

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

```

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

```

247 observations deleted due to missingness

n	events	median	0.95LCL	0.95UCL
44.00	44.00	1.76	1.35	3.60

 Available sample meta-data:

years_to_birth:

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

vital_status:

0	1
247	44

days_to_death:

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

days_to_last_followup:

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

tumor_tissue_site:

kidney
291

pathologic_stage:

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

pathology_N_stage:

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

pathology_M_stage:

m0	m1	mx	NA's
95	9	172	15

gender:

female	male
77	214

date_of_initial_pathologic_diagnosis:

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

days_to_last_known_alive:

34	NA's
1	290

radiation_therapy:

no	yes	NA's
209	1	81

karnofsky_performance_score:

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

histological_type:

kidney papillary renal cell carcinoma	291
---------------------------------------	-----

number_pack_years_smoked:

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

year_of_tobacco_smoking_onset:

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

race:

american indian or alaska native	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 7:

- [1] CNASNP-20160128: RaggedExperiment with 874897 rows and 392 columns
- [2] CNVSNP-20160128: RaggedExperiment with 28324 rows and 380 columns
- [3] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 194 columns
- [4] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 194 columns
- [5] Mutation-20160128: RaggedExperiment with 2585 rows and 197 columns

```
[6] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 173 columns
[7] RNASeqGene-20160128: SummarizedExperiment with 19990 rows and 179 columns
```

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

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

Sizes of each ExperimentList element:

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

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

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

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

Available sample meta-data:

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

```

18.00  44.75  57.00  55.02  67.00  88.00

vital_status:
  0  1
67 133

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

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

tumor_tissue_site:
bone marrow      NA's
      199          1

gender:
female  male
   91   109

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

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

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

Including an additional 478 columns

```

LGG

*Brain Lower Grade Glioma***Description**

A document describing the TCGA cancer code

Details

```

> experiments( LGG )
ExperimentList class object of length 11:
 [1] CNASeq-20160128: RaggedExperiment with 6360 rows and 104 columns
 [2] CNASNP-20160128: RaggedExperiment with 411918 rows and 1015 columns

```

```

[3] CNVSNP-20160128: RaggedExperiment with 79791 rows and 1015 columns
[4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 513 columns
[5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 513 columns
[6] Methylation-20160128: SummarizedExperiment with 485577 rows and 530 columns
[7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 526 columns
[8] mRNAArray-20160128: SummarizedExperiment with 17814 rows and 27 columns
[9] Mutation-20160128: RaggedExperiment with 9885 rows and 286 columns
[10] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 530 columns
[11] RPPAArray-20160128: SummarizedExperiment with 201 rows and 435 columns

```

```

> rownames( LGG )
CharacterList of length 11
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SLC39A6 SNRPD2 AQP7 CTSC
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
...
<1 more element>

```

```

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

```

Sizes of each ExperimentList element:

		assay size.Mb
1	CNASeq-20160128	0.2 Mb
2	CNASNP-20160128	11.3 Mb
3	CNVSNP-20160128	2.4 Mb
4	GISTIC_AllByGene-20160128	4.9 Mb
5	GISTIC_ThresholdedByGene-20160128	4.9 Mb
6	Methylation-20160128	75.1 Mb
7	miRNASeqGene-20160128	0.1 Mb
8	mRNAArray-20160128	1.1 Mb
9	Mutation-20160128	4.2 Mb

10 RNASeq2GeneNorm-20160128 1.3 Mb
 11 RPPAArray-20160128 0.1 Mb

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

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

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

 Available sample meta-data:

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

vital_status:
 0 1 NA's
 389 126 1

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

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

tumor_tissue_site:
 central nervous system NA's
 515 1

gender:
 female male NA's
 230 285 1

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

radiation_therapy:
 no yes NA's
 186 296 34

karnofsky_performance_score:

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

histological_type:

astrocytoma	oligoastrocytoma	oligodendroglioma	NA's
194		130	191

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

LIHC

Liver hepatocellular carcinoma

Description

A document describing the TCGA cancer code

Details

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

> rownames( LIHC )
CharacterList of length 10
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
```



```

[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 tAKR
[["RNASeqGene-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZEF1 ZZZ3 psiTPTE22 tAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

```

```
> colnames( LIHC )
```

```
CharacterList of length 10
```

```

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

```

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

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

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

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

```

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

```

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

```
years_to_birth:
```

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

vital_status:

0	1
245	132

days_to_death:

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

days_to_last_followup:

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

tumor_tissue_site:

liver
377

pathology_N_stage:

n0	n1	nx	NA's
257	4	115	1

pathology_M_stage:

m0	m1	mx
272	4	101

gender:

female	male
122	255

date_of_initial_pathologic_diagnosis:

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

radiation_therapy:

no	yes	NA's
345	9	23

histological_type:

fibrolamellar carcinoma	3	hepatocellular carcinoma	367
hepatocholangiocarcinoma (mixed)	7		

residual_tumor:

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

race:

american indian or alaska native	2	asian	161
black or african american		white	


```

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

```

Sizes of each ExperimentList element:

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

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

```

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

```

```

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

```

Available sample meta-data:

```

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

```

vital_status:

0 1
332 188

days_to_death:

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

days_to_last_followup:

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

tumor_tissue_site:

lung
520

gender:

female	male
279	241

date_of_initial_pathologic_diagnosis:

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

days_to_last_known_alive:

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

radiation_therapy:

no	yes	NA's
413	61	46

karnofsky_performance_score:

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

number_pack_years_smoked:

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

year_of_tobacco_smoking_onset:

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

residual_tumor:

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

```

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

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

```

Including an additional 2607 columns

LUSC *Lung squamous cell carcinoma*

Description

A document describing the TCGA cancer code

Details

```

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

> rownames( LUSC )
CharacterList of length 15
[["CNACGH-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b

```

```

[["mRNAArray_huex-20160128"]] C9orf152 ELM02 RPS11 ... SLC39A6 CTSC AQP7
[["mRNAArray_TX_g4502a-20160128"]] ELM02 CREB3L1 RPS11 ... SNRPD2 AQP7 CTSC
...
<5 more elements>

```

```

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

```

Sizes of each ExperimentList element:

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

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

```

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

```

```

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

```

Available sample meta-data:

years_to_birth:

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

vital_status:

0	1
284	220

days_to_death:

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

days_to_last_followup:

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

tumor_tissue_site:

lung
504

pathology_N_stage:

n0	n1	n2	n3	nx
320	133	40	5	6

gender:

female	male
131	373

date_of_initial_pathologic_diagnosis:

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

days_to_last_known_alive:

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

radiation_therapy:

no	yes	NA's
387	53	64

karnofsky_performance_score:

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

histological_type:

lung basaloid squamous cell carcinoma


```

15
lung papillary squamous cell 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 8:

```

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

```

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

```
> colnames( MESO )
CharacterList of length 8
[["CNASNP-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["CNVSNP-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-3H-AB3K-01A-11D-A39Q-01 ...
[["Methylation-20160128"]] TCGA-3H-AB3K-01A-11D-A39S-05 ...
[["miRNASeqGene-20160128"]] TCGA-3H-AB3K-01A-11R-A404-13 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-3H-AB3K-01A-11R-A40A-07 ...
[["RPPAArray-20160128"]] TCGA-3H-AB3K-01A-21-A450-20 ...
```

Sizes of each ExperimentList element:

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

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

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

```
14 observations deleted due to missingness
n events median 0.95LCL 0.95UCL
73.00 73.00 1.25 1.11 1.67
```

Available sample meta-data:

years_to_birth:

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

vital_status:

0	1
13	74

days_to_death:

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

days_to_last_followup:

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

tumor_tissue_site:

pleura
87

pathology_N_stage:

n0	n1	n2	n3	nx
44	10	26	3	4

pathology_M_stage:

m0	m1	mx
57	3	27

gender:

female	male
16	71

date_of_initial_pathologic_diagnosis:

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

radiation_therapy:

no	yes	NA's
62	24	1

karnofsky_performance_score:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.00	80.00	90.00	77.65	90.00	100.00	70

histological_type:

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

residual_tumor:

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

race:

```
asian black or african american      white
           1                          1              85
```

ethnicity:

```
not hispanic or latino      NA's
           73                14
```

Including an additional 636 columns

OV

Ovarian serous cystadenocarcinoma

Description

A document describing the TCGA cancer code

Details

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

> rownames( OV )
CharacterList of length 17
[["CNACGH_CGH_hg_244a-20160128"]] character(0)
[["CNACGH_CGH_hg_415k_g4124a-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
```

```

[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNAArray-20160128"]] DarkCorner dmr_285 dmr_3 ... NegativeControl SCorner3
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
...
<7 more elements>

```

```

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

```

Sizes of each ExperimentList element:

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

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

```

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

```

```

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

```

 Available sample meta-data:

years_to_birth:

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

vital_status:

0	1
246	344

days_to_death:

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

days_to_last_followup:

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

tumor_tissue_site:

omentum	ovary	peritoneum	ovary	NA's
3	575		2	10

gender:

female	NA's
580	10

date_of_initial_pathologic_diagnosis:

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

radiation_therapy:

no	yes	NA's
556	5	29

karnofsky_performance_score:

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

histological_type:

serous	cystadenocarcinoma	NA's
	580	10

residual_tumor:

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

ethnicity:

hispanic or latino	not hispanic or latino	NA's

11

338

241

Including an additional 2869 columns

 PAAD

Pancreatic adenocarcinoma

Description

A document describing the TCGA cancer code

Details

```

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

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

> colnames( PAAD )
CharacterList of length 9
[["CNASNP-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["CNVSNP-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-2J-AAB1-01A-11D-A40V-01 ...
[["Methylation-20160128"]] TCGA-2J-AAB1-01A-11D-A40Y-05 ...
[["miRNASeqGene-20160128"]] TCGA-2J-AAB1-01A-11R-A41G-13 ...
[["Mutation-20160128"]] TCGA-2J-AAB1-01A-11D-A40W-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-2J-AAB1-01A-11R-A41B-07 ...
[["RPPAArray-20160128"]] TCGA-2J-AAB4-01A-21-A43K-20 ...

```

Sizes of each ExperimentList element:

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

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

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

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

Available sample meta-data:

years_to_birth:

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

vital_status:

0	1
85	100

days_to_death:

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

days_to_last_followup:

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

tumor_tissue_site:

pancreas
185

pathology_N_stage:

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

pathology_M_stage:
 m0 m1 mx
 85 5 95

gender:
 female male
 83 102

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

radiation_therapy:
 no yes NA's
 125 45 15

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

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

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

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

number_of_lymph_nodes:
 Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
 0.000 0.000 2.000 2.989 4.000 16.000 4

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

ethnicity:

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

Including an additional 960 columns

PCPG

Pheochromocytoma and Paraganglioma

Description

A document describing the TCGA cancer code

Details

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

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

> colnames( PCPG )
CharacterList of length 9
[["CNASNP-20160128"]] TCGA-P7-A5NX-10A-01D-A35A-01 ...
[["CNVSNP-20160128"]] TCGA-P7-A5NX-10A-01D-A35A-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-P7-A5NY-01A-12D-A35C-01 ...
[["Methylation-20160128"]] TCGA-P7-A5NX-01A-11D-A35E-05 ...
[["miRNASeqGene-20160128"]] TCGA-P7-A5NX-01A-11R-A35M-13 ...
[["Mutation-20160128"]] TCGA-P7-A5NX-01A-11D-A35D-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-P7-A5NX-01A-11R-A35K-07 ...
[["RPPAArray-20160128"]] TCGA-P7-A5NX-01A-21-A43B-20 ...
```

Sizes of each ExperimentList element:

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

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

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

173 observations deleted due to missingness

n	events	median	0.95LCL	0.95UCL	
6.00	6.00	1.24	0.26	NA	

Available sample meta-data:

years_to_birth:

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

vital_status:

0	1
173	6

days_to_death:

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

days_to_last_followup:

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

tumor_tissue_site:

adrenal gland	extra-adrenal site
147	32

gender:

female	male
101	78

```

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

```

```

radiation_therapy:
  no yes NA's
  172 5 2

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

Including an additional 894 columns

PRAD

Prostate adenocarcinoma

Description

A document describing the TCGA cancer code

Details

```

> experiments( PRAD )
ExperimentList class object of length 10:
[1] CNASeq-20160128: RaggedExperiment with 23398 rows and 230 columns
[2] CNASNP-20160128: RaggedExperiment with 573776 rows and 1029 columns

```

```
[3] CNVSNP-20160128: RaggedExperiment with 117345 rows and 1023 columns
[4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 492 columns
[5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 492 columns
[6] Methylation-20160128: SummarizedExperiment with 485577 rows and 549 columns
[7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 547 columns
[8] Mutation-20160128: RaggedExperiment with 12348 rows and 332 columns
[9] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 550 columns
[10] RPPAArray-20160128: SummarizedExperiment with 195 rows and 352 columns
```

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

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

Sizes of each ExperimentList element:

		assay size.Mb
1	CNASeq-20160128	0.7 Mb
2	CNASNP-20160128	15.6 Mb
3	CNVSNP-20160128	3.4 Mb
4	GISTIC_AllByGene-20160128	4.9 Mb
5	GISTIC_ThresholdedByGene-20160128	4.9 Mb
6	Methylation-20160128	75.1 Mb
7	miRNASeqGene-20160128	0.1 Mb
8	Mutation-20160128	21.5 Mb
9	RNASeq2GeneNorm-20160128	1.3 Mb
10	RPPAArray-20160128	0 Mb

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

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

```
488 observations deleted due to missingness
```

```
  n events median 0.95LCL 0.95UCL
10.00  10.00   3.02   1.99     NA
```

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

```
years_to_birth:
```

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

```
vital_status:
```

```
  0  1
488 10
```

```
days_to_death:
```

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

```
days_to_last_followup:
```

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

```
tumor_tissue_site:
```

```
prostate
 498
```

```
pathology_N_stage:
```

```
  n0  n1 NA's
346  79  73
```

```
gender:
```

```
male
 498
```

```
date_of_initial_pathologic_diagnosis:
```

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

```
radiation_therapy:
```

```
  no  yes NA's
395  59  44
```

```
histological_type:
```

```
prostate adenocarcinoma acinar type prostate adenocarcinoma, other subtype
```

483

15

residual_tumor:

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

number_of_lymph_nodes:

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

gleason_score:

6	7	8	9	10
45	248	64	137	4

psa_value:

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

days_to_psa:

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

race:

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

ethnicity:

not hispanic or latino	NA's
152	346

Including an additional 1126 columns

 READ

Rectum adenocarcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( READ )
```

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

- [1] CNASeq-20160128: RaggedExperiment with 56380 rows and 70 columns
- [2] CNASNP-20160128: RaggedExperiment with 156806 rows and 316 columns
- [3] CNVSNP-20160128: RaggedExperiment with 35765 rows and 316 columns
- [4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 165 columns
- [5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 165 columns
- [6] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 73 columns

```

[7] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 106 columns
[8] miRNASeqGene-20160128: SummarizedExperiment with 705 rows and 76 columns
[9] mRNAArray-20160128: SummarizedExperiment with 17814 rows and 72 columns
[10] Mutation-20160128: RaggedExperiment with 22075 rows and 69 columns
[11] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 72 columns
[12] RNASeqGene-20160128: SummarizedExperiment with 20502 rows and 72 columns
[13] RPPAArray-20160128: SummarizedExperiment with 208 rows and 131 columns

```

```

> rownames( READ )
CharacterList of length 13
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg000002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SLC39A6 SNRPD2 AQP7 CTSC
[["Mutation-20160128"]] character(0)
...
<3 more elements>

```

```

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

```

Sizes of each ExperimentList element:

		assay size.Mb
1	CNASeq-20160128	1.5 Mb
2	CNASNP-20160128	4.3 Mb
3	CNVSNP-20160128	1.1 Mb
4	GISTIC_AllByGene-20160128	4.9 Mb
5	GISTIC_ThresholdedByGene-20160128	4.9 Mb
6	Methylation_methyl27-20160128	4.9 Mb
7	Methylation_methyl450-20160128	75 Mb
8	miRNASeqGene-20160128	0.1 Mb
9	mRNAArray-20160128	1.1 Mb
10	Mutation-20160128	9.6 Mb
11	RNASeq2GeneNorm-20160128	1.3 Mb


```

12          RNASeqGene-20160128  1.3 Mb
13          RPPAArray-20160128   0 Mb

```

```

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

```

```

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

```

```

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

```

```

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

```

```

years_to_birth:

```

```

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

```

```

vital_status:

```

```

  0  1
141 28

```

```

days_to_death:

```

```

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

```

```

days_to_last_followup:

```

```

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

```

```

tumor_tissue_site:

```

```

rectum  NA's
  166     3

```

```

pathology_M_stage:

```

```

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

```

```

gender:

```

```

female  male
   77    92

```

```

date_of_initial_pathologic_diagnosis:

```

```

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

```

```

1999    2007    2009    2008    2010    2012

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

radiation_therapy:
  no  yes NA's
 114  22  33

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

tumor_stage:
stage iia    NA's
      1      168

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

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

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

```

Including an additional 2242 columns

SARC

Sarcoma

Description

A document describing the TCGA cancer code

Details

```

> experiments( SARC )
ExperimentList class object of length 9:
 [1] CNASNP-20160128: RaggedExperiment with 337377 rows and 516 columns
 [2] CNVSNP-20160128: RaggedExperiment with 106739 rows and 513 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 257 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 257 columns
 [5] Methylation-20160128: SummarizedExperiment with 485577 rows and 269 columns
 [6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 263 columns

```

```
[7] Mutation-20160128: RaggedExperiment with 20376 rows and 247 columns
[8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 265 columns
[9] RPPAArray-20160128: SummarizedExperiment with 192 rows and 226 columns
```

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

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

Sizes of each ExperimentList element:

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

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

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

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

 Available sample meta-data:

years_to_birth:

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

vital_status:

0	1
162	99

days_to_death:

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

days_to_last_followup:

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

gender:

female	male
142	119

date_of_initial_pathologic_diagnosis:

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

radiation_therapy:

no	yes	NA's
181	74	6

residual_tumor:

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

race:

asian	black or african american	white
6	18	228
NA's		
9		

ethnicity:

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

Including an additional 1413 columns

SKCM

*Skin Cutaneous Melanoma***Description**

A document describing the TCGA cancer code

Details

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

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

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

Sizes of each ExperimentList element:

	assay	size.Mb
1	CNASeq-20160128	0.9 Mb
2	CNASNP-20160128	12.3 Mb
3	CNVSNP-20160128	3.2 Mb
4	Methylation-20160128	75.1 Mb
5	miRNASeqGene-20160128	0.1 Mb
6	Mutation-20160128	299.6 Mb

7 RNASeq2GeneNorm-20160128 1.3 Mb
 8 RPPAArray-20160128 0 Mb

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

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

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

 Available sample meta-data:

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

vital_status:
 0 1
 247 223

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

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

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

melanoma_ulceration:
 no yes NA's
 146 167 157

melanoma_primary_known:
 no yes
 47 423

Breslow_thickness:

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

gender:

female	male
180	290

date_of_initial_pathologic_diagnosis:

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

radiation_therapy:

no	yes	NA's
420	49	1

race:

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

ethnicity:

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

Including an additional 1517 columns

STAD

*Stomach adenocarcinoma***Description**

A document describing the TCGA cancer code

Details

```
> experiments( STAD )
ExperimentList class object of length 12:
[1] CNASeq-20160128: RaggedExperiment with 31824 rows and 214 columns
[2] CNASNP-20160128: RaggedExperiment with 443042 rows and 906 columns
[3] CNVSNP-20160128: RaggedExperiment with 118389 rows and 904 columns
[4] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 441 columns
[5] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 441 columns
[6] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 73 columns
[7] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 397 columns
[8] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 430 columns
[9] Mutation-20160128: RaggedExperiment with 148520 rows and 289 columns
[10] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 450 columns
[11] RNASeqGene-20160128: SummarizedExperiment with 26120 rows and 36 columns
[12] RPPAArray-20160128: SummarizedExperiment with 195 rows and 357 columns
```

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

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

Sizes of each ExperimentList element:

	assay	size.Mb
1	CNASeq-20160128	0.9 Mb
2	CNASNP-20160128	12.1 Mb
3	CNVSNP-20160128	3.4 Mb
4	GISTIC_AllByGene-20160128	4.9 Mb
5	GISTIC_ThresholdedByGene-20160128	4.9 Mb
6	Methylation_methyl27-20160128	4.9 Mb
7	Methylation_methyl450-20160128	75 Mb
8	miRNASeqGene-20160128	0.1 Mb
9	Mutation-20160128	161.5 Mb
10	RNASeq2GeneNorm-20160128	1.3 Mb
11	RNASeqGene-20160128	1.7 Mb
12	RPPAArray-20160128	0 Mb

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

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


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

 Available sample meta-data:

years_to_birth:

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

vital_status:

0	1
268	175

days_to_death:

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

days_to_last_followup:

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

tumor_tissue_site:

stomach
443

pathology_M_stage:

m0	m1	mx
391	30	22

gender:

female	male
158	285

date_of_initial_pathologic_diagnosis:

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

radiation_therapy:

no	yes	NA's
323	77	43

residual_tumor:

r0	r1	r2	rx	NA's
----	----	----	----	------


```

[["Methylation-20160128"]] cg00000029 cg00000108 ... rs966367 rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["Mutation-20160128"]] character(0)
[["RNASeq2GeneNorm-20160128"]] A1BG A1CF A2BP1 A2LD1 ... ZZZ3 psiTPTE22 TAKR
[["RPPAArray-20160128"]] 14-3-3_beta 14-3-3_epsilon ... p90RSK_pT359_S363

```

```
> colnames( TGCT )
```

```
CharacterList of length 9
```

```

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

```

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

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

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

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

```

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

```

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

```
years_to_birth:
```

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

```
vital_status:
```

0 1
130 4

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

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

tumor_tissue_site:
testes
134

pathology_T_stage:
t1 t2 t3 tx
76 51 6 1

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

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

gender:
male
134

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

radiation_therapy:
no yes NA's
111 21 2

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

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

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

12

111

11

Including an additional 762 columns

 THCA

 Thyroid carcinoma

Description

A document describing the TCGA cancer code

Details

```

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

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

> colnames( THCA )
CharacterList of length 11
[["CNASeq-20160128"]] TCGA-BJ-A0Z2-01A-11D-A10R-02 ...
[["CNASNP-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["CNVSNP-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-4C-A93U-01A-11D-A396-01 ...
[["Methylation-20160128"]] TCGA-4C-A93U-01A-11D-A398-05 ...
[["miRNASeqGene-20160128"]] TCGA-4C-A93U-01A-11R-A39B-13 ...

```

```

[["Mutation-20160128"]] TCGA-BJ-A0YZ-01A-11D-A10S-08 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-4C-A93U-01A-11R-A39I-07 ...
[["RNASeqGene-20160128"]] TCGA-DJ-A1QE-01A-21R-A14Y-07 ...
...
<1 more element>

```

Sizes of each ExperimentList element:

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

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

```

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

```

```

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

```

Available sample meta-data:

years_to_birth:

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

vital_status:

0	1
487	16

days_to_death:

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

days_to_last_followup:

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

tumor_tissue_site:
thyroid
503

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

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

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

radiation_therapy:
no yes NA's
181 306 16

radiation_exposure:
no yes NA's
423 17 63

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

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

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

multifocality:
multifocal unifocal NA's
227 266 10

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

Including an additional 1481 columns

THYM

*Thymoma***Description**

A document describing the TCGA cancer code

Details

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

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

> colnames( THYM )
CharacterList of length 9
[["CNASNP-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["CNVSNP-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-3G-AB00-01A-22D-A422-01 ...
[["Methylation-20160128"]] TCGA-3G-AB00-01A-22D-A424-05 ...
[["miRNASeqGene-20160128"]] TCGA-3G-AB00-01A-22R-A42W-13 ...
[["Mutation-20160128"]] TCGA-3G-AB00-01A-22D-A423-09 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-3G-AB00-01A-22R-A42C-07 ...
[["RPPAArray-20160128"]] TCGA-3G-AB00-01A-11-A45R-20 ...
```

Sizes of each ExperimentList element:

		assay size.Mb
1	CNASNP-20160128	2.9 Mb
2	CNVSNP-20160128	0.5 Mb
3	GISTIC_AllByGene-20160128	4.9 Mb


```

4 GISTIC_ThresholdedByGene-20160128 4.9 Mb
5           Methylation-20160128 75 Mb
6           miRNASeqGene-20160128 0.1 Mb
7           Mutation-20160128 3.1 Mb
8           RNASeq2GeneNorm-20160128 1.3 Mb
9           RPPAArray-20160128 0 Mb

```

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

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

115 observations deleted due to missingness

n	events	median	0.95LCL	0.95UCL
9.00	9.00	2.34	1.04	NA

Available sample meta-data:

years_to_birth:

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

vital_status:

0	1
115	9

days_to_death:

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

days_to_last_followup:

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

tumor_tissue_site:

anterior mediastinum	thymus
27	97

gender:

female	male
60	64

date_of_initial_pathologic_diagnosis:

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

radiation_therapy:

no yes
81 43

race:

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

ethnicity:

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

Including an additional 685 columns

UCEC

Uterine Corpus Endometrial Carcinoma

Description

A document describing the TCGA cancer code

Details

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

> rownames( UCEC )
CharacterList of length 13
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
```

```

[["mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SLC39A6 SNRPD2 AQP7 CTSC
[["Mutation-20160128"]] character(0)
...
<3 more elements>

```

```

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

```

Sizes of each ExperimentList element:

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

Available sample meta-data:

days_to_death:

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

days_to_last_followup:

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

tumor_tissue_site:

endometrial other specify

```

                    547                1

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

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

radiation_therapy:
  no  yes NA's
  295 228  25

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

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

Including an additional 1779 columns

```

UCS

Uterine Carcinosarcoma

Description

A document describing the TCGA cancer code

Details

```

> experiments( UCS )
ExperimentList class object of length 9:
 [1] CNASNP-20160128: RaggedExperiment with 54944 rows and 111 columns
 [2] CNVSNP-20160128: RaggedExperiment with 19298 rows and 111 columns
 [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 56 columns
 [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 56 columns
 [5] Methylation-20160128: SummarizedExperiment with 485577 rows and 57 columns
 [6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 56 columns
 [7] Mutation-20160128: RaggedExperiment with 11339 rows and 57 columns
 [8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 57 columns
 [9] RPPAArray-20160128: SummarizedExperiment with 192 rows and 48 columns

> rownames( UCS )
CharacterList of length 9
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)

```

```

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

```

```
> colnames( UCS )
```

```
CharacterList of length 9
```

```

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

```

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

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

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

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

```

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

```

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

```
years_to_birth:
```

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

vital_status:

0 1
22 35

days_to_death:

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

days_to_last_followup:

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

tumor_tissue_site:

uterus
57

gender:

female
57

date_of_initial_pathologic_diagnosis:

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

radiation_therapy:

no	yes	NA's
29	25	3

histological_type:

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

race:

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

ethnicity:

hispanic or latino	not hispanic or latino	NA's
1	43	13

Including an additional 632 columns

Description

A document describing the TCGA cancer code

Details

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

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

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

Sizes of each ExperimentList element:

		assay size.Mb
1	CNASeq-20160128	0.2 Mb
2	CNASNP-20160128	1.9 Mb
3	CNVSNP-20160128	0.4 Mb
4	GISTIC_AllByGene-20160128	4.9 Mb
5	GISTIC_ThresholdedByGene-20160128	4.9 Mb

```

6           Methylation-20160128  75 Mb
7           miRNASeqGene-20160128 0.1 Mb
8           Mutation-20160128 12.3 Mb
9           RNASeq2GeneNorm-20160128 1.3 Mb
10          RPPAArray-20160128  0 Mb

```

```

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

```

```

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

```

```

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

```

```

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

```

```

years_to_birth:

```

```

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

```

```

vital_status:

```

```

 0  1
57 23

```

```

days_to_death:

```

```

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

```

```

days_to_last_followup:

```

```

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

```

```

tumor_tissue_site:

```

```

choroid
  80

```

```

pathology_N_stage:

```

```

 n0  nx NA's
 52  27   1

```

```

pathology_M_stage:

```

```

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

```


gender:

female	male
35	45

date_of_initial_pathologic_diagnosis:

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

radiation_therapy:

no	yes	NA's
76	3	1

race:

white	NA's
55	25

ethnicity:

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

Including an additional 448 columns

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