

Package ‘curatedTCGAData’

November 13, 2018

Type Package

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

Version 1.4.0

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

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Depends R (>= 3.5.0), MultiAssayExperiment

Imports AnnotationHub, ExperimentHub, S4Vectors, utils

Suggests BiocStyle, knitr, readr, rmarkdown, testthat

VignetteBuilder knitr

biocViews Homo_sapiens_Data, ReproducibleResearch, CancerData

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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

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Examples

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

ACC

*Adrenocortical carcinoma***Description**

A document describing the TCGA cancer code

Details

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

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

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

Sizes of each ExperimentList element:

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

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

years_to_birth:

```

```

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

```

```

vital_status:

```

```

 0 1
58 34

```

```

days_to_death:

```

```

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

```

```

days_to_last_followup:

```

```

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

```

```

tumor_tissue_site:

```

```

adrenal
 92

```

```

pathologic_stage:

```

```

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

```

```

pathology_T_stage:

```

```

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

```

```

pathology_N_stage:

```

```

n0  n1  NA's
80  10   2

gender:
female  male
  60    32

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

radiation_therapy:
no  yes  NA's
71  18   3

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

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

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

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

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

Including an additional 806 columns

```

BLCA

Bladder Urothelial Carcinoma

Description

A document describing the TCGA cancer code

Details

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

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

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

Sizes of each ExperimentList element:

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

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

vital_status:
 0  1
230 182

```

```

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

```

```

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

```

```

tumor_tissue_site:
bladder
 412

```

```

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

```

```

pathology_M_stage:
 m0  m1  mx NA's

```


196 11 202 3

gender:

female male
108 304

date_of_initial_pathologic_diagnosis:

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

radiation_therapy:

no yes NA's
366 20 26

karnofsky_performance_score:

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

histological_type:

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

number_pack_years_smoked:

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

number_of_lymph_nodes:

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

race:

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

ethnicity:

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

Including an additional 1695 columns

BRCA

Breast invasive carcinoma

Description

A document describing the TCGA cancer code

Details

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

```
> rownames( BRCA )
CharacterList of length 13
[["CNASeq-20160128"]] character(0)
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["mRNAArray-20160128"]] 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
  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-A370-07 ...
[["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	NA's
29		3	275

pregnancies_count_total:

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

pregnancies_count_stillbirth:

0	1	3	NA's
106	5	1	195

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

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

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

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

lymph_node_location:
 lymph_node_location_positive_pathology_name|lymph_node_location_positive_pathology_text
 307

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

lymphovascular_involvement:
 absent present NA's
 72 80 155

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

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

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


```

NA's
132

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

hysterectomy_type:
hysterectomy_performed_type|hysterectomy_performed_text
307

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

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

corpus_involvement:
absent present  NA's
  99     19   189

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

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

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

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

```

Including an additional 1330 columns

CHOL

Cholangiocarcinoma

Description

A document describing the TCGA cancer code

Details

```

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

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

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

Sizes of each ExperimentList element:

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

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

```

```

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

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

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

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

vital_status:
 0  1
18 18

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

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

tumor_tissue_site:
bile duct
      36

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

pathology_N_stage:
n0 n1 nx
26  5  5

pathology_M_stage:
m0 m1 mx
28  5  3

gender:
female  male
      20   16

date_of_initial_pathologic_diagnosis:

```

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

radiation_therapy:

no NA's

35 1

histological_type:

cholangiocarcinoma; distal cholangiocarcinoma; hilar/perihilar

2

4

cholangiocarcinoma; intrahepatic

30

residual_tumor:

r0 r1 rx

28 5 3

race:

asian black or african american

3

2

white

31

ethnicity:

hispanic or latino not hispanic or latino

2

33

NA's

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
...	Additional arguments passed on to the ExperimentHub constructor

Details

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

Value

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

Examples

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

DLBC

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

A document describing the TCGA cancer code

Details

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

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

```

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

```

```
> colnames( DLBC )
```

```
CharacterList of length 9
```

```

[["CNASNP-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["CNVSNP-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["GISTIC_AllByGene-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["GISTIC_ThresholdedByGene-20160128"]] TCGA-FA-8693-01A-11D-2389-01 ...
[["Methylation-20160128"]] TCGA-FA-8693-01A-11D-2399-05 ...
[["miRNASeqGene-20160128"]] TCGA-FA-8693-01A-11R-2401-13 ...
[["Mutation-20160128"]] TCGA-FA-8693-01A-11D-2397-10 ...
[["RNASeq2GeneNorm-20160128"]] TCGA-FA-8693-01A-11R-2404-07 ...
[["RPPAArray-20160128"]] TCGA-FA-8693-01A-21-A45K-20 ...

```

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

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

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

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

```

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

```

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

```
years_to_birth:
```

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

```
vital_status:
```

```
0 1
```


39 9

days_to_death:

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

days_to_last_followup:

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

gender:

female	male
26	22

date_of_initial_pathologic_diagnosis:

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

radiation_therapy:

no	yes	NA's
40	7	1

histological_type:

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

race:

asian black or african american	white
18	1
	29

ethnicity:

hispanic or latino	not hispanic or latino
12	36

Including an additional 607 columns

ESCA

Esophageal carcinoma

Description

A document describing the TCGA cancer code

Details

> experiments(ESCA)

ExperimentList class object of length 11:

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

```
> rownames( ESCA )
```

CharacterList of length 11

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

...

```
<1 more element>
```

```
> colnames( ESCA )
```

CharacterList of length 11

```
[[ "CNASeq-20160128" ]] TCGA-IG-A3I8-01A-11D-A248-26 ...
[[ "CNASNP-20160128" ]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[[ "CNVSNP-20160128" ]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[[ "GISTIC_AllByGene-20160128" ]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[[ "GISTIC_ThresholdedByGene-20160128" ]] TCGA-2H-A9GF-01A-11D-A37B-01 ...
[[ "Methylation-20160128" ]] TCGA-2H-A9GF-01A-11D-A37D-05 ...
[[ "miRNASeqGene-20160128" ]] TCGA-2H-A9GF-01A-11R-A37J-13 ...
[[ "Mutation-20160128" ]] TCGA-2H-A9GF-01A-11D-A37C-09 ...
[[ "RNASeq2GeneNorm-20160128" ]] TCGA-2H-A9GF-01A-11R-A37I-31 ...
[[ "RNASeqGene-20160128" ]] TCGA-2H-A9GF-01A-11R-A37I-31 ...
```

...

```
<1 more element>
```

Sizes of each ExperimentList element:

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

```

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

```

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

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

```

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

```

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

years_to_birth:

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

vital_status:

0	1
108	77

days_to_death:

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

days_to_last_followup:

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

tumor_tissue_site:

esophagus
185

pathology_M_stage:

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

gender:

female	male
27	158

```

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

radiation_therapy:
  no yes NA's
  124 43 18

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

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

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

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

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

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

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

Including an additional 940 columns

```

GBM

Glioblastoma multiforme

Description

A document describing the TCGA cancer code

Details

```
> experiments( GBM )
```

ExperimentList class object of length 16:

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

```
> rownames( GBM )
```

```
CharacterList of length 16
```

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

```
> colnames( GBM )
```

```
CharacterList of length 16
```

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

Sizes of each ExperimentList element:

```

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

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

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

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

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

Available sample meta-data:

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

vital_status:
0 1 NA's
104 491 4

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

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

tumor_tissue_site:
brain NA's
595 4

```

gender:
  female  male  NA's
    230    365     4

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

radiation_therapy:
  no  yes  NA's
  78  489  32

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

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

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

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

```

Including an additional 4368 columns

HNSC

Head and Neck squamous cell carcinoma

Description

A document describing the TCGA cancer code

Details

```

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

```

```

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

```

```

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

```

```

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

```

Sizes of each ExperimentList element:

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

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

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

305 observations deleted due to missingness

n	events	median	0.95LCL	0.95UCL
223.00	223.00	1.18	1.06	1.35

Available sample meta-data:

years_to_birth:

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

vital_status:

0	1
304	224

days_to_death:

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

days_to_last_followup:

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

tumor_tissue_site:

head and neck
528

pathology_M_stage:

m0	m1	mx	NA's
191	1	65	271

gender:

female	male
142	386

date_of_initial_pathologic_diagnosis:

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

days_to_last_known_alive:

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

```

98.0  483.0  848.5  1226.9  1647.5  3930.0  506

radiation_therapy:
  no  yes  NA's
163  303  62

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

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

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

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

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

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

```

Including an additional 1426 columns

KICH

Kidney Chromophobe

Description

A document describing the TCGA cancer code

Details

```

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

```

```

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

```

```

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

```

```

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

```

Sizes of each ExperimentList element:

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

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

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

-1)

57 observations deleted due to missingness

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

Available sample meta-data:

years_to_birth:

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

vital_status:

0	1
56	10

days_to_death:

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

days_to_last_followup:

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

tumor_tissue_site:

kidney
66

pathologic_stage:

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

pathology_N_stage:

n0	n1	n2	nx
40	3	2	21

pathology_M_stage:

m0	m1	mx	NA's
34	2	9	21

gender:

female	male
27	39

date_of_initial_pathologic_diagnosis:

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

radiation_therapy:

no
66

karnofsky_performance_score:

90 100 NA's
3 10 53

histological_type:

kidney chromophobe
66

number_pack_years_smoked:

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

year_of_tobacco_smoking_onset:

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

race:

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

ethnicity:

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

Including an additional 718 columns

KIRC

Kidney renal clear cell carcinoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( KIRC )
```

ExperimentList class object of length 12:

- [1] CNASNP-20160128: RaggedExperiment with 488691 rows and 1059 columns
- [2] CNVSNP-20160128: RaggedExperiment with 85036 rows and 1059 columns
- [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 528 columns
- [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 528 columns
- [5] Methylation_methyl27-20160128: SummarizedExperiment with 27578 rows and 418 columns
- [6] Methylation_methyl450-20160128: SummarizedExperiment with 485577 rows and 480 columns
- [7] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 326 columns
- [8] mRNAArray-20160128: SummarizedExperiment with 17814 rows and 72 columns

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

```
> rownames( KIRC )
CharacterList of length 12
[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 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)
[["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"]] 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( 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 not hispanic or latino NA's
 12 243 36

Including an additional 1686 columns

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

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                1

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

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

```

Including an additional 1764 columns

LIHC

Liver hepatocellular carcinoma

Description

A document describing the TCGA cancer code

Details

```

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

```



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

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

Sizes of each ExperimentList element:

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

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

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

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

 Available sample meta-data:

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

vital_status:
 0 1
 245 132

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

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

tumor_tissue_site:
 liver
 377

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

pathology_M_stage:
 m0 m1 mx
 272 4 101

gender:
 female male
 122 255

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

radiation_therapy:
 no yes NA's
 345 9 23

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

residual_tumor:

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

race:

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

ethnicity:

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

Including an additional 1218 columns

LUAD

Lung adenocarcinoma

Description

A document describing the TCGA cancer code

Details

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

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

```

[["Methylation_methyl27-20160128"]] cg00000292 cg00002426 ... cg27665659
[["Methylation_methyl450-20160128"]] cg00000029 cg00000108 ... rs9839873
[["miRNASeqGene-20160128"]] hsa-let-7a-1 hsa-let-7a-2 ... hsa-mir-99b
[["mRNAArray-20160128"]] ELM02 CREB3L1 RPS11 PNMA1 ... SLC39A6 SNRPD2 AQP7 CTSC
[["Mutation-20160128"]] character(0)
...
<3 more elements>

```

```

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

```

Sizes of each ExperimentList element:

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

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

```

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

```

```

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

```

 Available sample meta-data:

years_to_birth:

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

vital_status:

0	1
332	188

days_to_death:

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

days_to_last_followup:

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

tumor_tissue_site:

lung
520

gender:

female	male
279	241

date_of_initial_pathologic_diagnosis:

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

days_to_last_known_alive:

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

radiation_therapy:

no	yes	NA's
413	61	46

karnofsky_performance_score:

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

number_pack_years_smoked:

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

```

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

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

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

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

Including an additional 2607 columns

```

LUSC

Lung squamous cell carcinoma

Description

A document describing the TCGA cancer code

Details

```

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

> rownames( LUSC )

```

```

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

```

```

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

```

Sizes of each ExperimentList element:

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

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

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

```
289 observations deleted due to missingness
```

```
  n events median 0.95LCL 0.95UCL
215.00 215.00  1.51  1.25  1.88
```

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

```
years_to_birth:
```

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

```
vital_status:
```

```
  0  1
284 220
```

```
days_to_death:
```

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

```
days_to_last_followup:
```

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

```
tumor_tissue_site:
```

```
lung
504
```

```
pathology_N_stage:
```

```
  n0  n1  n2  n3  nx
320 133  40   5   6
```

```
gender:
```

```
female  male
  131    373
```

```
date_of_initial_pathologic_diagnosis:
```

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

```
days_to_last_known_alive:
```

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

```
radiation_therapy:
```



```

no  yes  NA's
387  53   64

```

karnofsky_performance_score:

```

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

```

histological_type:

```

          lung basaloid squamous cell carcinoma      15
          lung papillary squamous cell 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 cg000002426 ... 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:


```

[["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
NA's	162
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
                                1
                                asian
                                6
black or african american
                                20
                                white
                                148
NA's
                                4

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

```

Including an additional 894 columns

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

Description

A document describing the TCGA cancer code

Details

```

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

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

```

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):

```


9

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

Including an additional 1413 columns

SKCM

Skin Cutaneous Melanoma

Description

A document describing the TCGA cancer code

Details

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

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

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

Sizes of each ExperimentList element:

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

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

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

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

Available sample meta-data:

years_to_birth:

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

vital_status:

0	1
247	223

days_to_death:

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

days_to_last_followup:

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

days_to_submitted_specimen_dx:

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

melanoma_ulceration:

```

no yes NA's
146 167 157

melanoma_primary_known:
no yes
47 423

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

gender:
female male
  180   290

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

radiation_therapy:
no yes NA's
420 49  1

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

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

```

Including an additional 1517 columns

STAD

Stomach adenocarcinoma

Description

A document describing the TCGA cancer code

Details

```

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

```

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

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

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

Sizes of each ExperimentList element:

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

12 RPPAArray-20160128 0 Mb

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

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

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

 Available sample meta-data:

years_to_birth:

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

vital_status:

0	1
268	175

days_to_death:

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

days_to_last_followup:

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

tumor_tissue_site:

stomach
443

pathology_M_stage:

m0	m1	mx
391	30	22

gender:

female	male
158	285

date_of_initial_pathologic_diagnosis:

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

radiation_therapy:

no	yes	NA's
323	77	43

residual_tumor:

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

number_of_lymph_nodes:

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

race:

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

ethnicity:

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

Including an additional 1390 columns

TGCT

Testicular Germ Cell Tumors

Description

A document describing the TCGA cancer code

Details

```
> experiments( TGCT )
```

```
ExperimentList class object of length 9:
```

- [1] CNASNP-20160128: RaggedExperiment with 137968 rows and 271 columns
- [2] CNVSNP-20160128: RaggedExperiment with 25479 rows and 271 columns
- [3] GISTIC_AllByGene-20160128: SummarizedExperiment with 24776 rows and 134 columns
- [4] GISTIC_ThresholdedByGene-20160128: SummarizedExperiment with 24776 rows and 134 columns
- [5] Methylation-20160128: SummarizedExperiment with 485577 rows and 139 columns
- [6] miRNASeqGene-20160128: SummarizedExperiment with 1046 rows and 139 columns
- [7] Mutation-20160128: RaggedExperiment with 14672 rows and 138 columns
- [8] RNASeq2GeneNorm-20160128: SummarizedExperiment with 20501 rows and 139 columns

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

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

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

Sizes of each ExperimentList element:

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

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

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

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

```
-----
```

Available sample meta-data:

years_to_birth:

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

vital_status:

0	1
130	4

days_to_death:

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

days_to_last_followup:

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

tumor_tissue_site:

testes
134

pathology_T_stage:

t1	t2	t3	tx
76	51	6	1

pathology_N_stage:

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

pathology_M_stage:

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

gender:

male
134

date_of_initial_pathologic_diagnosis:

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

radiation_therapy:

no	yes	NA's
111	21	2

karnofsky_performance_score:

80	90	100	NA's
5	41	56	32

```

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

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

```

Including an additional 762 columns

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

Description

A document describing the TCGA cancer code

Details

```

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

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

> colnames( THCA )

```

```

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

```

Sizes of each ExperimentList element:

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

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

```

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

```

```

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

```

Available sample meta-data:

```

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

vital_status:
  0  1
487 16

```

days_to_death:

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

days_to_last_followup:

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

tumor_tissue_site:

thyroid	503
---------	-----

pathology_N_stage:

n0	n1	n1a	n1b	nx
227	58	93	75	50

pathology_M_stage:

m0	m1	mx	NA's
280	9	213	1

date_of_initial_pathologic_diagnosis:

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

radiation_therapy:

no	yes	NA's
181	306	16

radiation_exposure:

no	yes	NA's
423	17	63

extrathyroidal_extension:

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

residual_tumor:

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

number_of_lymph_nodes:

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

multifocality:

multifocal	unifocal	NA's
227	266	10

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

Including an additional 1481 columns

THYM

Thymoma

Description

A document describing the TCGA cancer code

Details

```
> experiments( THYM )
ExperimentList class object of length 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                103
      NA's
      2
```

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

Including an additional 685 columns

UCEC

Uterine Corpus Endometrial Carcinoma

Description

A document describing the TCGA cancer code

Details

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

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

```

[["CNASNP-20160128"]] character(0)
[["CNVSNP-20160128"]] character(0)
[["GISTIC_AllByGene-20160128"]] ACAP3 ACTRT2 ... WASIR1|ENSG00000185203.7
[["GISTIC_ThresholdedByGene-20160128"]] ACAP3 ... WASIR1|ENSG00000185203.7
[["Methylation_methyl27-20160128"]] cg00000292 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( 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 (mmt): nos	24
uterine carcinosarcoma/ mmt: heterologous type	20
uterine carcinosarcoma/mmt: homologous type	13

race:

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

ethnicity:

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

1

43

13

Including an additional 632 columns

UVM

Uveal Melanoma

Description

A document describing the TCGA cancer code

Details

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