

# Package ‘curatedOvarianData’

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**Type** Package

**Title** Clinically Annotated Data for the Ovarian Cancer Transcriptome

**Version** 1.39.0

**Date** 2015-03-05

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**Maintainer** Levi Waldron <lwaldron.research@gmail.com>

**Description** The curatedOvarianData package provides data for gene expression analysis in patients with ovarian cancer.

**Depends** R (>= 2.10.0), affy

**Imports** BiocGenerics

**Suggests** survival, RUnit, metafor, genefilter, logging, sva, xtable, futile.logger, BiocStyle

**License** Artistic-2.0

**URL** <http://bcb.dfci.harvard.edu/ovariancancer>

**biocViews** ExperimentData, RNASeqData, CancerData, OvarianCancerData, MicroarrayData

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

**git\_branch** devel

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curatedOvarianData-package

*Clinically Annotated Data for the Ovarian Cancer Transcriptome***Description**

The curatedOvarianData package provides manually curated clinical data, uniformly processed expression data, and convenience functions for gene expression analysis in patients with ovarian cancer.

**Details**

Package:	curatedOvarianData
Type:	Package
Version:	1.39.0
Date:	2015-03-05
License:	Artistic-2.0

Depends: R (>= 2.10.0), affy

Please see <http://bcb.dfci.harvard.edu/ovariancancer> for alterative versions of this package, differing in how redundant probe sets are dealt with. In the curatedOvarianData version, each gene is represented by the gene with maximum mean. In NormalizerVcuratedOvarianData, each gene is represented by the mean of the probesets after removing "noisy" probesets (see the Normalizer function of the Sleipnir library for computational biology), and in FULLVcuratedOvarianData, no collapsing of probe sets is done, but a map is provided to allow the user to do so by their method of choice through featureData(eset).

In the "Available sample meta-data" sections of each dataset, please refer to the following key.

For "sample\_type": tumor / metastatic / adjacentnormal / healthy / cellline: "healthy" should be only from individuals without cancer, "adjacentnormal" from individuals with cancer, "metastatic" for non-primary tumors.

For "histological\_type": ser=serous / endo=endometrioid / clearcell / mucinous, undifferentiated / other / mix. Other includes sarcomatoid, adenocarcinoma, dysgerminoma.

For "primarysite" and for "arrayedsite": ovlflother. ov=ovary;ft=fallopian tube

For "summarygrade": low = 1, 2, LMP. High= 3,4,23.

For "summarystage": early = 1,2, 12. late=3,4,23,34.

For "tumorstage": FIGO Stage (I-IV, but coded here as 1-4 to ensure correct ordering in factors). If multiple stages given (eg 34), use the highest.

For "substage": substage (abcd). For cases like ab, bc, use highest given.

For "grade": Grade (1-3): If multiple given, ie 12, 23, use highest given. Most ovarian cancer studies use FIGO grading, with a couple exceptions in this package (Yoshihara and Tothill).

For "pltx": (y/n): patient treated with platin.

For "tax": (y/n): patient treated with taxol.

For "neo": (y/n): patient treated with neoadjuvant treatment.

For "primary\_therapy\_outcome\_success": completeresponse|partialresponse|progressivedisease|stabledisease: response to any kind of therapy (including radiation only).

For "days\_to\_tumor\_recurrence": time to recurrence or last follow-up in days

For "recurrence\_status": recurrence censoring variable (recurrence / norecurrence)

For "days\_to\_death": time to death or last follow-up in days

For "vital\_status": Overall survival censoring variable (living / deceased)

For "os\_binary": dichotomized overall survival variable as defined by study authors (short / long).

For "relapse\_binary": dichotomized relapse variable as defined by study authors (short / long)

For "site\_of\_tumor\_first\_recurrence": (metastasis / locoregional / none / locoregional\_plus\_metastatic). none for no recurrence, na for unknown

For "primary\_therapy\_outcome\_success": (completeresponse / partialresponse / progressivedisease / stabledisease) Response to any kind of therapy (including radiation only).

For "debulking": amount of residual disease (optimal = <1cm, suboptimal=>1cm).

For "percent\_normal\_cells": Estimated percentage of normal cells. An integer 0-100, or can be >70, <70, etc.

For "percent\_stromal\_cells": Estimated percentage of stromal cells. An integer 0-100, or can be >70, <70, etc.

For "percent\_tumor\_cells": Estimated percentage of tumor cells. An integer 0-100, or can be >70, <70, etc.

For "batch": batch variable when available. Hybridization date when Affymetrix CEL files are available.

For "uncurated\_author\_metadata": Original uncurated data, with each field separated by ///.

### Author(s)

Benjamin F. Ganzfried, Steve Skates, Markus Riester, Victoria Wang, Thomas Risch, Benjamin Haibe-Kains, Curtis Huttenhower, Svitlana Tyekucheva, Jie Ding, Ina Jazic, Michael Birrer, Giovanni Parmigiani, Levi Waldron

Department of Biostatistics and Computational Biology, Dana-Farber Cancer Institute, Harvard School of Public Health

Maintainer: Levi Waldron <levi@jimmy.harvard.edu>

### Examples

```
##List all datasets:
data(package="curatedOvarianData")
##
##See the actual template used for syntax checking of clinical metadata:
template.file <- system.file("extdata/template_ov.csv", package = "curatedOvarianData")
template <- read.csv(template.file, as.is=TRUE)
head(template)
```

---

E.MTAB.386\_eset

*Angiogenic mRNA and microRNA gene expression signature predicts a novel subtype of serous ovarian cancer.*

---

### Description

Ovarian cancer is the fifth leading cause of cancer death for women in the U.S. and the seventh most fatal worldwide. Although ovarian cancer is notable for its initial sensitivity to platinum-based therapies, the vast majority of patients eventually develop recurrent cancer and succumb to increasingly platinum-resistant disease. Modern, targeted cancer drugs intervene in cell signaling, and identifying key disease mechanisms and pathways would greatly advance our treatment abilities. In order to shed light on the molecular diversity of ovarian cancer, we performed comprehensive transcriptional profiling on 129 advanced stage, high grade serous ovarian cancers. We implemented a, re-sampling based version of the ISIS class discovery algorithm (rISIS: robust ISIS) and applied it to the entire set of ovarian cancer transcriptional profiles. rISIS identified a previously undescribed patient stratification, further supported by micro-RNA expression profiles, and gene set enrichment analysis found strong biological support for the stratification by extracellular matrix, cell adhesion,

and angiogenesis genes. The corresponding "angiogenesis signature" was validated in ten published independent ovarian cancer gene expression datasets and is significantly associated with overall survival. The subtypes we have defined are of potential translational interest as they may be relevant for identifying patients who may benefit from the addition of anti-angiogenic therapies that are now being tested in clinical trials.

## Usage

```
data( E.MTAB.386_eset )
```

## Format

```
experimentData(eset):
  Experiment data
    Experimenter name: Bentink S, Haibe-Kains B, Risch T, Fan J-B, Hirsch MS, Holton K, Rubio R, April C, Ch
    Laboratory: Bentink, Matulonis 2012
    Contact information:
      Title: Angiogenic mRNA and microRNA gene expression signature predicts a novel subtype of serous ovarian
      URL:
      PMIDs: 22348002

    Abstract: A 212 word abstract is available. Use 'abstract' method.
    Information is available on: preprocessing
    notes:
      platform_title:
        Illumina humanRef-8 v2.0 expression beadchip
      platform_shorttitle:
        Illumina humanRef-8 v2.0
      platform_summary:
        illuminaHumanv2
      platform_manufacturer:
        Illumina
      platform_distribution:
        commercial
      platform_accession:
        GPL6104
      platform_technology:
        in situ oligonucleotide

    Preprocessing: default
    featureData(eset):
      An object of class 'AnnotatedDataFrame'
      featureNames: A2M A4GALT ... ZZEF1 (10357 total)
      varLabels: probeset gene
      varMetadata: labelDescription
```

**Details**

```

assayData: 10357 features, 129 samples
Platform type: illuminaHumanv2
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records    n.max n.start  events  median 0.95LCL 0.95UCL
129.00   129.00  129.00    73.00    3.51    2.68    4.13

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

unique_patient_ID:
  Length     Class      Mode
  129 character character

sample_type:
tumor
  129

histological_type:
ser
  129

primarysite:
ov
  129

summarygrade:
high
  129

summarystage:
early  late
  1    128

tumorstage:
  2    3    4
  1 109  19

substage:
  a     b     c  NA's
  5    12    93   19

age_at_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median  Mean 3rd Qu.  Max.
 21.00   50.00   66.00   60.71   72.00   95.00

```

```
days_to_death:
  Min. 1st Qu. Median   Mean 3rd Qu.   Max.
  3.9    516.9   917.1  1007.0  1401.0  2724.0

vital_status:
deceased   living
  73        56

debulking:
  optimal suboptimal      NA's
  98        28            3

uncurated_author_metadata:
  Length   Class      Mode
  129  character character
```

---

GSE12418\_eset

*Expression analysis of stage III serous ovarian adenocarcinoma distinguishes a sub-group of survivors.*

---

## Description

It is difficult to predict the clinical outcome for patients with ovarian cancer. However, the use of biomarkers as additional prognostic factors may improve the outcome for these patients. In order to find novel candidate biomarkers, differences in gene expressions were analysed in 54 stage III serous ovarian adenocarcinomas with oligonucleotide microarrays containing 27,000 unique probes. The microarray data was verified with quantitative real-time polymerase chain reaction for the genes TACC1, MUC5B and PRAME. Using hierarchical cluster analysis we detected a sub-group that included 60% of the survivors. The gene expressions in tumours from patients in this sub-group of survivors were compared with the remaining tumours, and 204 genes were found to be differently expressed. We conclude that the sub-group of survivors might represent patients with favourable tumour biology and sensitivity to treatment. A selection of the 204 genes might be used as a predictive model to distinguish patients within and outside of this group. Alternative chemotherapy strategies could then be offered as first-line treatment, which may lead to improvements in the clinical outcome for these patients.

## Usage

```
data( GSE12418_eset )
```

## Format

```
experimentData(eset):
Experiment data
  Experimenter name: Partheen K, Levan K, Osterberg L, Horvath G.Expression analysis of stage III serous
```

Laboratory: Partheen, Horvath 2006  
 Contact information:  
 Title: Expression analysis of stage III serous ovarian adenocarcinoma distinguishes a sub-group of sur  
 URL:  
 PMIDs: 16996261

Abstract: A 177 word abstract is available. Use 'abstract' method.  
 Information is available on: preprocessing  
 notes:  
 platform\_title:  
 SWEGENE H\_v2.1.1\_27k  
 platform\_shorttitle:  
 SWEGENE H\_v2.1.1\_27k  
 platform\_summary:  
 PartheenMetaData  
 platform\_manufacturer:  
 other  
 platform\_distribution:  
 non-commercial  
 platform\_accession:  
 GPL5886  
 platform\_technology:  
 spotted oligonucleotide

Preprocessing: default  
 featureData(eset):  
 An object of class 'AnnotatedDataFrame'  
 featureNames: A1CF A2M ... ZZZ3 (12681 total)  
 varLabels: probeset gene  
 varMetadata: labelDescription

## Details

assayData: 12681 features, 54 samples  
 Platform type: PartheenMetaData  
 Binary overall survival summary (definitions of long and short provided by study authors):  

long	short
20	34

-----

Available sample meta-data:

-----

alt\_sample\_name:  
 Length Class Mode  
 54 character character

```
sample_type:
tumor
54

histological_type:
ser
54

primarysite:
ov
54

summarystage:
late
54

tumorstage:
3
54

substage:
b c
19 35

age_at_initial_pathologic_diagnosis:
    Min. 1st Qu. Median     Mean 3rd Qu.    Max.
    35.00    51.25   59.50    59.56   69.75    84.00

pltx:
y
54

os_binary:
long short
20    34

debulking:
optimal suboptimal
13        41

uncurated_author_metadata:
Length     Class      Mode
54 character character
```

---

GSE12470_eset	<i>Gene expression profiling of advanced-stage serous ovarian cancers distinguishes novel subclasses and implicates ZEB2 in tumor progression and prognosis.</i>
---------------	--

---

## Description

To elucidate the mechanisms of rapid progression of serous ovarian cancer, gene expression profiles from 43 ovarian cancer tissues comprising eight early stage and 35 advanced stage tissues were carried out using oligonucleotide microarrays of 18,716 genes. By non-negative matrix factorization analysis using 178 genes, which were extracted as stage-specific genes, 35 advanced stage cases were classified into two subclasses with superior (n = 17) and poor (n = 18) outcome evaluated by progression-free survival (log rank test, P = 0.03). Of the 178 stage-specific genes, 112 genes were identified as showing different expression between the two subclasses. Of the 48 genes selected for biological function by gene ontology analysis or Ingenuity Pathway Analysis, five genes (ZEB2, CDH1, LTBP2, COL16A1, and ACTA2) were extracted as candidates for prognostic factors associated with progression-free survival. The relationship between high ZEB2 or low CDH1 expression and shorter progression-free survival was validated by real-time RT-PCR experiments of 37 independent advanced stage cancer samples. ZEB2 expression was negatively correlated with CDH1 expression in advanced stage samples, whereas ZEB2 knockdown in ovarian adenocarcinoma SKOV3 cells resulted in an increase in CDH1 expression. Multivariate analysis showed that high ZEB2 expression was independently associated with poor prognosis. Furthermore, the prognostic effect of E-cadherin encoded by CDH1 was verified using immunohistochemical analysis of an independent advanced stage cancer samples set (n = 74). These findings suggest that the expression of epithelial-mesenchymal transition-related genes such as ZEB2 and CDH1 may play important roles in the invasion process of advanced stage serous ovarian cancer.

## Usage

```
data( GSE12470_eset )
```

## Format

```
experimentData(eset):
  Experiment data
    Experimenter name: Yoshihara K, Tajima A, Komata D, Yamamoto T, Kodama S, Fujiwara H, Suzuki M, Onishi Y
    Laboratory: Yoshihara, Tanaka 2009
    Contact information:
      Title: Gene expression profiling of advanced-stage serous ovarian cancers distinguishes novel subclasses
      URL:
      PMIDs: 19486012

    Abstract: A 253 word abstract is available. Use 'abstract' method.
    Information is available on: preprocessing
    notes:
      platform_title:
        Agilent-012097 Human 1A Microarray (V2) G4110B (Feature Number version)
      platform_shorttitle:
```

```
    Agilent G4110B
  platform_summary:
    hgug4110b
  platform_manufacturer:
    Agilent
  platform_distribution:
    commercial
  platform_accession:
    GPL887
  platform_technology:
    in situ oligonucleotide

  Preprocessing: default
  featureData(eset):
  An object of class 'AnnotatedDataFrame'
  featureNames: A1BG A1CF ... ZZZ3 (16889 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

## Details

```
assayData: 16889 features, 53 samples
Platform type: hgug4110b
-----
Available sample meta-data:
-----
alt_sample_name:
  Length     Class      Mode
  53 character character

sample_type:
  healthy    tumor
  10        43

histological_type:
  ser NA's
  43    10

primarysite:
  ov
  53

summarystage:
  early   late  NA's
  8      35    10

tumorstage:
```

```
1 NA's
8 45
```

```
uncurated_author_metadata:
  Length      Class      Mode
  53 character character
```

---

GSE13876\_eset

*Survival-related profile, pathways, and transcription factors in ovarian cancer.*

---

### Description

Ovarian cancer has a poor prognosis due to advanced stage at presentation and either intrinsic or acquired resistance to classic cytotoxic drugs such as platinum and taxoids. Recent large clinical trials with different combinations and sequences of classic cytotoxic drugs indicate that further significant improvement in prognosis by this type of drugs is not to be expected. Currently a large number of drugs, targeting dysregulated molecular pathways in cancer cells have been developed and are introduced in the clinic. A major challenge is to identify those patients who will benefit from drugs targeting these specific dysregulated pathways. The aims of our study were (1) to develop a gene expression profile associated with overall survival in advanced stage serous ovarian cancer, (2) to assess the association of pathways and transcription factors with overall survival, and (3) to validate our identified profile and pathways/transcription factors in an independent set of ovarian cancers. According to a randomized design, profiling of 157 advanced stage serous ovarian cancers was performed in duplicate using approximately 35,000 70-mer oligonucleotide microarrays. A continuous predictor of overall survival was built taking into account well-known issues in microarray analysis, such as multiple testing and overfitting. A functional class scoring analysis was utilized to assess pathways/transcription factors for their association with overall survival. The prognostic value of genes that constitute our overall survival profile was validated on a fully independent, publicly available dataset of 118 well-defined primary serous ovarian cancers. Furthermore, functional class scoring analysis was also performed on this independent dataset to assess the similarities with results from our own dataset. An 86-gene overall survival profile discriminated between patients with unfavorable and favorable prognosis (median survival, 19 versus 41 mo, respectively; permutation p-value of log-rank statistic = 0.015) and maintained its independent prognostic value in multivariate analysis. Genes that composed the overall survival profile were also able to discriminate between the two risk groups in the independent dataset. In our dataset 17/167 pathways and 13/111 transcription factors were associated with overall survival, of which 16 and 12, respectively, were confirmed in the independent dataset. Our study provides new clues to genes, pathways, and transcription factors that contribute to the clinical outcome of serous ovarian cancer and might be exploited in designing new treatment strategies.

### Usage

```
data( GSE13876_eset )
```

## Format

```

experimentData(eset):
  Experiment data
    Experimenter name: Crijns AP, Fehrman RS, de Jong S, Gerbens F, Meersma GJ, Klip HG, Hollema H, Hofstra
    Laboratory: Crijns, van der Zee 2009
    Contact information:
    Title: Survival-related profile, pathways, and transcription factors in ovarian cancer.
    URL:
    PMIDs: 19192944

  Abstract: A 371 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
    platform_title:
      Operon human v3 ~35K 70-mer two-color oligonucleotide microarrays
    platform_shorttitle:
      Operon v3 two-color
    platform_summary:
      OperonHumanV3
    platform_manufacturer:
      other
    platform_distribution:
      non-commercial
    platform_accession:
      GPL7759
    platform_technology:
      spotted oligonucleotide

  Preprocessing: default
  featureData(eset):
    An object of class 'AnnotatedDataFrame'
    featureNames: A1BG A1CF ... ZZZ3 (20577 total)
    varLabels: probeset gene
    varMetadata: labelDescription

```

## Details

```

assayData: 20577 features, 157 samples
Platform type: OperonHumanV3
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records    n.max n.start  events  median 0.95LCL 0.95UCL
157.00    157.00  157.00   113.00    2.05    1.56    2.71
-----
Available sample meta-data:

```

-----

alt\_sample\_name:  
151 NA's  
1 156

unique\_patient\_ID:  
Min. 1st Qu. Median Mean 3rd Qu. Max.  
1 40 79 79 118 157

sample\_type:  
tumor  
157

histological\_type:  
ser  
157

primarysite:  
ov  
157

summarygrade:  
high low NA's  
85 59 13

summarystage:  
late  
157

grade:  
1 2 3 4 NA's  
14 45 82 3 13

age\_at\_initial\_pathologic\_diagnosis:  
Min. 1st Qu. Median Mean 3rd Qu. Max.  
21.00 50.00 60.00 57.95 67.00 84.00

days\_to\_death:  
Min. 1st Qu. Median Mean 3rd Qu. Max.  
30 360 630 1100 1470 7020

vital\_status:  
deceased living  
113 44

uncurated\_author\_metadata:  
Length Class Mode

```
157 character character
```

---

GSE14764_eset	<i>A prognostic gene expression index in ovarian cancer - validation across different independent data sets.</i>
---------------	--

---

## Description

Ovarian carcinoma has the highest mortality rate among gynaecological malignancies. In this project, we investigated the hypothesis that molecular markers are able to predict outcome of ovarian cancer independently of classical clinical predictors, and that these molecular markers can be validated using independent data sets. We applied a semi-supervised method for prediction of patient survival. Microarrays from a cohort of 80 ovarian carcinomas (TOC cohort) were used for the development of a predictive model, which was then evaluated in an entirely independent cohort of 118 carcinomas (Duke cohort). A 300-gene ovarian prognostic index (OPI) was generated and validated in a leave-one-out approach in the TOC cohort (Kaplan-Meier analysis,  $p = 0.0087$ ). In a second validation step, the prognostic power of the OPI was confirmed in an independent data set (Duke cohort,  $p = 0.0063$ ). In multivariate analysis, the OPI was independent of the post-operative residual tumour, the main clinico-pathological prognostic parameter with an adjusted hazard ratio of 6.4 (TOC cohort, CI 1.8-23.5,  $p = 0.0049$ ) and 1.9 (Duke cohort, CI 1.2-3.0,  $p = 0.0068$ ). We constructed a combined score of molecular data (OPI) and clinical parameters (residual tumour), which was able to define patient groups with highly significant differences in survival. The integrated analysis of gene expression data as well as residual tumour can be used for optimized assessment of the prognosis of platinum-taxol-treated ovarian cancer. As traditional treatment options are limited, this analysis may be able to optimize clinical management and to identify those patients who would be candidates for new therapeutic strategies.

## Usage

```
data( GSE14764_eset )
```

## Format

```
experimentData(eset):  
  Experiment data  
  Experimenter name: Denkert C, Budczies J, Darb-Esfahani S, Gy??rffy B et al. A prognostic gene expression index in ovarian cancer - validation across different independent data sets.  
  Laboratory: Denkert, Lage 2009  
  Contact information:  
  Title: A prognostic gene expression index in ovarian cancer - validation across different independent data sets.  
  URL:  
  PMIDs: 19294737  
  
  Abstract: A 254 word abstract is available. Use 'abstract' method.  
  Information is available on: preprocessing  
  notes:  
  platform_title:
```

```

[HG-U133A] Affymetrix Human Genome U133A Array
platform_shorttitle:
  Affymetrix HG-U133A
platform_summary:
  hgu133a
platform_manufacturer:
  Affymetrix
platform_distribution:
  commercial
platform_accession:
  GPL96
platform_technology:
  in situ oligonucleotide

Preprocessing: frma
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1CF A2M ... ZZZ3 (13104 total)
  varLabels: probeset gene
  varMetadata: labelDescription

```

## Details

```

assayData: 13104 features, 80 samples
Platform type: hgu133a
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records    n.max n.start  events  median 0.95LCL 0.95UCL
  80.00     80.00    80.00    21.00     4.52     4.19      NA

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

alt_sample_name:
  Min. 1st Qu. Median  Mean 3rd Qu.  Max.
  1.00   20.75  40.50  40.50  60.25  80.00

sample_type:
tumor
  80

histological_type:
  Length    Class      Mode
  80 character character

primarysite:

```

```
ov
80

summarygrade:
high  low
54    26

summarystage:
early late
9      71

tumorstage:
1   2   3   4
8   1   69  2

substage:
a    b    c  NA's
4    6    32   38

grade:
1   2   3
3 23 54

recurrence_status:
norecurrence   recurrence      NA's
50            26            4

days_to_death:
Min. 1st Qu. Median  Mean 3rd Qu.  Max.
210     660    1050   1011   1328   2190

vital_status:
deceased   living
21        59

batch:
Length     Class     Mode
80 character character

uncurated_author_metadata:
Length     Class     Mode
80 character character
```

## Description

Advanced-stage ovarian cancer patients are generally treated with platinum/taxane-based chemotherapy after primary debulking surgery. However, there is a wide range of outcomes for individual patients. Therefore, the clinicopathological factors alone are insufficient for predicting prognosis. Our aim is to identify a progression-free survival (PFS)-related molecular profile for predicting survival of patients with advanced-stage serous ovarian cancer. Advanced-stage serous ovarian cancer tissues from 110 Japanese patients who underwent primary surgery and platinum/taxane-based chemotherapy were profiled using oligonucleotide microarrays. We selected 88 PFS-related genes by a univariate Cox model ( $p < 0.01$ ) and generated the prognostic index based on 88 PFS-related genes after adjustment of regression coefficients of the respective genes by ridge regression Cox model using 10-fold cross-validation. The prognostic index was independently associated with PFS time compared to other clinical factors in multivariate analysis [hazard ratio (HR), 3.72; 95% confidence interval (CI), 2.66-5.43;  $p < 0.0001$ ]. In an external dataset, multivariate analysis revealed that this prognostic index was significantly correlated with PFS time (HR, 1.54; 95% CI, 1.20-1.98;  $p = 0.0008$ ). Furthermore, the correlation between the prognostic index and overall survival time was confirmed in the two independent external datasets (log rank test,  $p = 0.0010$  and 0.0008). The prognostic ability of our index based on the 88-gene expression profile in ridge regression Cox hazard model was shown to be independent of other clinical factors in predicting cancer prognosis across two distinct datasets. Further study will be necessary to improve predictive accuracy of the prognostic index toward clinical application for evaluation of the risk of recurrence in patients with advanced-stage serous ovarian cancer.

## Usage

```
data( GSE17260_eset )
```

## Format

```
experimentData(eset):
  Experiment data
  Experimenter name: Yoshihara K, Tajima A, Yahata T, Kodama S, Fujiwara H, Suzuki M, Onishi Y, Hatae M, S
  Laboratory: Yoshihara, Tanaka 2010
  Contact information:
  Title: Gene expression profile for predicting survival in advanced-stage serous ovarian cancer across
  URL:
  PMIDs: 20300634

  Abstract: A 257 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
  platform_title:
    Agilent-012391 Whole Human Genome Oligo Microarray G4112A
  platform_shorttitle:
    Agilent G4112A
  platform_summary:
    hgug4112a
  platform_manufacturer:
    Agilent
```

```
platform_distribution:
  commercial
platform_accession:
  GPL6848
platform_technology:
  in situ oligonucleotide

Preprocessing: default
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1BG A1BG-AS1 ... ZZZ3 (20106 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

## Details

```
assayData: 20106 features, 110 samples
Platform type: hgug4112a
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records  n.max n.start  events  median 0.95LCL 0.95UCL
  110.00  110.00  110.00    46.00    4.44    4.03      NA
-----
Available sample meta-data:
-----
alt_sample_name:
  Length     Class      Mode
  110 character character

sample_type:
  tumor
  110

histological_type:
  ser
  110

primarysite:
  ov
  110

summarygrade:
  high  low
  43   67
```

```
summarystage:  
late  
110  
  
tumorstage:  
3 4  
93 17  
  
substage:  
a b c NA's  
6 18 69 17  
  
grade:  
1 2 3  
26 41 43  
  
pltx:  
y  
110  
  
tax:  
y  
110  
  
days_to_tumor_recurrence:  
Min. 1st Qu. Median Mean 3rd Qu. Max.  
30.0 285.0 510.0 673.9 870.0 2250.0  
  
recurrence_status:  
norecurrence recurrence  
34 76  
  
days_to_death:  
Min. 1st Qu. Median Mean 3rd Qu. Max.  
30 660 915 1086 1530 2430  
  
vital_status:  
deceased living  
46 64  
  
debulking:  
optimal suboptimal  
57 53  
  
uncurated_author_metadata:  
Length Class Mode  
110 character character
```

---

GSE18520\_eset *A gene signature predictive for outcome in advanced ovarian cancer identifies a survival factor: microfibril-associated glycoprotein 2.*

---

## Description

Advanced stage papillary serous tumors of the ovary are responsible for the majority of ovarian cancer deaths, yet the molecular determinants modulating patient survival are poorly characterized. Here, we identify and validate a prognostic gene expression signature correlating with survival in a series of microdissected serous ovarian tumors. Independent evaluation confirmed the association of a prognostic gene microfibril-associated glycoprotein 2 (MAGP2) with poor prognosis, whereas in vitro mechanistic analyses demonstrated its ability to prolong tumor cell survival and stimulate endothelial cell motility and survival via the alpha(V)beta(3) integrin receptor. Increased MAGP2 expression correlated with microvessel density suggesting a proangiogenic role in vivo. Thus, MAGP2 may serve as a survival-associated target.

## Usage

```
data( GSE18520_eset )
```

## Format

```
experimentData(eset):
  Experiment data
    Experimenter name: Mok SC, Bonome T, Vathipadiekal V, Bell A, Johnson ME, Wong KK, Park DC, Hao K, Yip D
    Laboratory: Mok, Birrer 2009
    Contact information:
    Title: A gene signature predictive for outcome in advanced ovarian cancer identifies a survival factor
    URL:
    PMIDs: 19962670

  Abstract: A 110 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
    platform_title:
      [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
    platform_shorttitle:
      Affymetrix HG-U133Plus2
    platform_summary:
      hgu133plus2
    platform_manufacturer:
      Affymetrix
    platform_distribution:
      commercial
    platform_accession:
      GPL570
    platform_technology:
```

```
in situ oligonucleotide

Preprocessing: frma
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1BG A1BG-AS1 ... ZZZ3 (19816 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

## Details

```
assayData: 19816 features, 63 samples
Platform type: hgu133plus2
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

  10 observations deleted due to missingness
records  n.max n.start  events  median 0.95LCL 0.95UCL
  53.00   53.00   53.00   41.00    2.05   1.48   3.70

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

alt_sample_name:
  Min. 1st Qu. Median  Mean 3rd Qu.  Max.
  312.0   395.0  694.0  893.3 1040.0 2237.0

sample_type:
  healthy tumor
  10      53

histological_type:
  ser NA's
  53    10

primarysite:
  ov
  63

summarygrade:
  high NA's
  53    10

summarystage:
  late NA's
  53    10
```

```
tumorstage:  
 3 NA's  
 53 10  
  
grade:  
 3 NA's  
 53 10  
  
days_to_death:  
   Min. 1st Qu. Median     Mean 3rd Qu.     Max.    NA's  
   150     450     630    1212    1440    4500     10  
  
vital_status:  
deceased living    NA's  
 41       12       10  
  
debulking:  
optimal suboptimal    NA's  
 28       11       24  
  
percent_normal_cells:  
 0  
63  
  
percent_stromal_cells:  
 0  
63  
  
percent_tumor_cells:  
100  
63  
  
batch:  
  Length    Class    Mode  
 63 character character  
  
uncurated_author_metadata:  
  Length    Class    Mode  
 63 character character
```

## Description

To define a gene expression profile of BRCAness that correlates with chemotherapy response and outcome in epithelial ovarian cancer (EOC). A publicly available microarray data set including 61 patients with EOC with either sporadic disease or BRCA(1/2) germline mutations was used for development of the BRCAness profile. Correlation with platinum responsiveness was assessed in platinum-sensitive and platinum-resistant tumor biopsy specimens from six patients with BRCA germline mutations. Association with poly-ADP ribose polymerase (PARP) inhibitor responsiveness and with radiation-induced RAD51 foci formation (a surrogate of homologous recombination) was assessed in Capan-1 cell line clones. The BRCAness profile was validated in 70 patients enriched for sporadic disease to assess its association with outcome. The BRCAness profile accurately predicted platinum responsiveness in eight out of 10 patient-derived tumor specimens, and between PARP-inhibitor sensitivity and resistance in four out of four Capan-1 clones. [corrected] When applied to the 70 patients with sporadic disease, patients with the BRCA-like (BL) profile had improved disease-free survival (34 months v 15 months; log-rank  $P = .013$ ) and overall survival (72 months v 41 months; log-rank  $P = .006$ ) compared with patients with a non-BRCA-like (NBL) profile, respectively. The BRCAness profile maintained independent prognostic value in multivariate analysis, which controlled for other known clinical prognostic factors. The BRCAness profile correlates with responsiveness to platinum and PARP inhibitors and identifies a subset of sporadic patients with improved outcome. Additional evaluation of this profile as a predictive tool in patients with sporadic EOC is warranted.

## Usage

```
data( GSE19829.GPL570_eset )
```

## Format

```
experimentData(eset):
  Experiment data
    Experimenter name: Konstantinopoulos PA, Spentzos D, Karlan BY, Taniguchi T et al. Gene expression profile of BRCAness
    Laboratory: Konstantinopoulos, Cannistra 2010 hgu133plus2
    Contact information:
    Title: Gene expression profile of BRCAness that correlates with responsiveness to chemotherapy and with survival in epithelial ovarian cancer
    URL:
    PMIDs: 20547991

  Abstract: A 241 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
    platform_title:
      [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
    platform_shorttitle:
      Affymetrix HG-U133Plus2
    platform_summary:
      hgu133plus2
    platform_manufacturer:
      Affymetrix
    platform_distribution:
```

```

    commercial
platform_accession:
    GPL570
platform_technology:
    in situ oligonucleotide

Preprocessing: frma
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1BG A1BG-AS1 ... ZZZ3 (19816 total)
  varLabels: probeset gene
  varMetadata: labelDescription

```

## Details

```

assayData: 19816 features, 28 samples
Platform type: hgu133plus2
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records    n.max n.start  events  median 0.95LCL 0.95UCL
 28.00     28.00   28.00    17.00    3.95    2.71      NA
-----
Available sample meta-data:
-----
alt_sample_name:
  Length     Class      Mode
  28 character character

sample_type:
  tumor
  28

primarysite:
  ov
  28

days_to_death:
  Min. 1st Qu. Median    Mean 3rd Qu.    Max.
  150      540    1050    1291    1688    3450

vital_status:
  deceased   living
  17          11

batch:

```

2009-08-14

28

```
uncurated_author_metadata:
  Length      Class      Mode
  28 character character
```

---

GSE19829.GPL8300\_eset *Gene expression profile of BRCAness that correlates with responsiveness to chemotherapy and with outcome in patients with epithelial ovarian cancer.*

---

### Description

To define a gene expression profile of BRCAness that correlates with chemotherapy response and outcome in epithelial ovarian cancer (EOC). A publicly available microarray data set including 61 patients with EOC with either sporadic disease or BRCA(1/2) germline mutations was used for development of the BRCAness profile. Correlation with platinum responsiveness was assessed in platinum-sensitive and platinum-resistant tumor biopsy specimens from six patients with BRCA germline mutations. Association with poly-ADP ribose polymerase (PARP) inhibitor responsiveness and with radiation-induced RAD51 foci formation (a surrogate of homologous recombination) was assessed in Capan-1 cell line clones. The BRCAness profile was validated in 70 patients enriched for sporadic disease to assess its association with outcome. The BRCAness profile accurately predicted platinum responsiveness in eight out of 10 patient-derived tumor specimens, and between PARP-inhibitor sensitivity and resistance in four out of four Capan-1 clones. [corrected] When applied to the 70 patients with sporadic disease, patients with the BRCA-like (BL) profile had improved disease-free survival (34 months v 15 months; log-rank P = .013) and overall survival (72 months v 41 months; log-rank P = .006) compared with patients with a non-BRCA-like (NBL) profile, respectively. The BRCAness profile maintained independent prognostic value in multivariate analysis, which controlled for other known clinical prognostic factors. The BRCAness profile correlates with responsiveness to platinum and PARP inhibitors and identifies a subset of sporadic patients with improved outcome. Additional evaluation of this profile as a predictive tool in patients with sporadic EOC is warranted.

### Usage

```
data( GSE19829.GPL8300_eset )
```

### Format

```
experimentData(eset):
  Experiment data
  Experimenter name: Konstantinopoulos PA, Spentzos D, Karlan BY, Taniguchi T et al. Gene expression prot
  Laboratory: Konstantinopoulos, Cannistra 2010 hgu95
  Contact information:
  Title: Gene expression profile of BRCAness that correlates with responsiveness to chemotherapy and wit
```

URL:  
 PMIDs: 20547991

Abstract: A 241 word abstract is available. Use 'abstract' method.

Information is available on: preprocessing  
 notes:

platform\_title:  
 [HG\_U95Av2] Affymetrix Human Genome U95 Version 2 Array  
 platform\_shorttitle:  
 Affymetrix HG\_U95Av2  
 platform\_summary:  
 hgu95av2  
 platform\_manufacturer:  
 Affymetrix  
 platform\_distribution:  
 commercial  
 platform\_accession:  
 GPL8300  
 platform\_technology:  
 in situ oligonucleotide

Preprocessing: rma  
 featureData(eset):  
 An object of class 'AnnotatedDataFrame'  
 featureNames: AADAC AAK1 ... ZZZ3 (8995 total)  
 varLabels: probeset gene  
 varMetadata: labelDescription

## Details

assayData: 8995 features, 42 samples  
 Platform type: hgu95av2  
 Overall survival time-to-event summary (in years):  
 Call: survfit(formula = Surv(time, cens) ~ -1)

records	n.max	n.start	events	median	0.95LCL	0.95UCL
42.00	42.00	42.00	23.00	3.78	2.79	NA

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

alt\_sample\_name:  
 Length Class Mode  
 42 character character  
 sample\_type:  
 tumor

42

primarysite:

ov

42

days\_to\_death:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
30.0	727.5	1155.0	1089.0	1485.0	2040.0

vital\_status:

deceased	living
23	19

batch:

2001-09-14	2001-12-14	2002-08-20	2003-09-09	2003-09-18
7	4	14	13	4

uncurated\_author\_metadata:

Length	Class	Mode
42	character	character

GSE20565\_eset

*A genomic and transcriptomic approach for a differential diagnosis between primary and secondary ovarian carcinomas in patients with a previous history of breast cancer.*

## Description

The distinction between primary and secondary ovarian tumors may be challenging for pathologists. The purpose of the present work was to develop genomic and transcriptomic tools to further refine the pathological diagnosis of ovarian tumors after a previous history of breast cancer. Sixteen paired breast-ovary tumors from patients with a former diagnosis of breast cancer were collected. The genomic profiles of paired tumors were analyzed using the Affymetrix GeneChip Mapping 50 K Xba Array or Genome-Wide Human SNP Array 6.0 (for one pair), and the data were normalized with ITALICS (ITerative and Alternative normalIzation and Copy number calling for affymetrix Snp arrays) algorithm or Partek Genomic Suite, respectively. The transcriptome of paired samples was analyzed using Affymetrix GeneChip Human Genome U133 Plus 2.0 Arrays, and the data were normalized with gc-Robust Multi-array Average (gcRMA) algorithm. A hierarchical clustering of these samples was performed, combined with a dataset of well-identified primary and secondary ovarian tumors. In 12 of the 16 paired tumors analyzed, the comparison of genomic profiles confirmed the pathological diagnosis of primary ovarian tumor (n = 5) or metastasis of breast cancer (n = 7). Among four cases with uncertain pathological diagnosis, genomic profiles were clearly distinct between the ovarian and breast tumors in two pairs, thus indicating primary ovarian carcinomas, and showed common patterns in the two others, indicating metastases from breast cancer.

In all pairs, the result of the transcriptomic analysis was concordant with that of the genomic analysis. In patients with ovarian carcinoma and a previous history of breast cancer, SNP array analysis can be used to distinguish primary and secondary ovarian tumors. Transcriptomic analysis may be used when primary breast tissue specimen is not available.

### Usage

```
data( GSE20565_eset )
```

### Format

```
experimentData(eset):
  Experiment data
  Experimenter name: Meyniel JP, Cottu PH, Decraene C, Stern MH, Couturier J, Lebigot I, Nicolas A, Weber
  Laboratory: Meyniel, Sastre-Garau 2010
  Contact information:
  Title: A genomic and transcriptomic approach for a differential diagnosis between primary and secondary ovarian carcinomas
  URL:
  PMIDs: 20492709

  Abstract: A 277 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
  platform_title:
    [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
  platform_shorttitle:
    Affymetrix HG-U133Plus2
  platform_summary:
    hgu133plus2
  platform_manufacturer:
    Affymetrix
  platform_distribution:
    commercial
  platform_accession:
    GPL570
  platform_technology:
    in situ oligonucleotide

  Preprocessing: frma
  featureData(eset):
  An object of class 'AnnotatedDataFrame'
  featureNames: A1BG A1BG-AS1 ... ZZZ3 (19816 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

### Details

```
assayData: 19816 features, 140 samples
```

```
Platform type: hgu133plus2
-----
Available sample meta-data:
-----

alt_sample_name:
  Length     Class      Mode
  140 character character

sample_type:
  tumor
  140

histological_type:
  Length     Class      Mode
  140 character character

primarysite:
  other     ov
  44      96

summarygrade:
  high    low  NA's
  63     33   44

summarystage:
  early   late  NA's
  27     67   46

tumorstage:
  1      2      3      4  NA's
  18     9     52    15   46

substage:
  a      b      c  NA's
  14    10     55   61

grade:
  1      2      3  NA's
  6     27    63   44

batch:
  Length     Class      Mode
  140 character character

uncurated_author_metadata:
  Length     Class      Mode
  140 character character
```

---

GSE2109\_eset *IGC EXpression Project for Oncology*

---

## Description

EXpression Project for Oncology, International Genomics Consortium, [www.intgen.org](http://www.intgen.org)

## Usage

```
data( GSE2109_eset )
```

## Format

```
experimentData(eset):
  Experiment data
    Experimenter name: EXpression Project for Oncology, International Genomics Consortium, www.intgen.org
    Laboratory: exp0, IGC 2005
    Contact information:
    Title: IGC EXpression Project for Oncology
    URL:
    PMID: PMID unknown

  Abstract: A 8 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
    platform_title:
      [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
    platform_shorttitle:
      Affymetrix HG-U133Plus2
    platform_summary:
      hgu133plus2
    platform_manufacturer:
      Affymetrix
    platform_distribution:
      commercial
    platform_accession:
      GPL570
    platform_technology:
      in situ oligonucleotide

  Preprocessing: frma
  featureData(eset):
  An object of class 'AnnotatedDataFrame'
  featureNames: A1BG A1BG-AS1 ... ZZZ3 (19816 total)
  varLabels: probeset gene
```

```
varMetadata: labelDescription
```

### Details

```
assayData: 19816 features, 204 samples
Platform type: hgu133plus2
-----
```

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

```
alt_sample_name:
  Length     Class      Mode
  204 character character
```

```
sample_type:
  benign borderline      tumor
      2           8        194
```

```
histological_type:
  Length     Class      Mode
  204 character character
```

```
primarysite:
  other    ov  NA's
  23     178     3
```

```
summarygrade:
  high    low  NA's
  91     31     82
```

```
summarystage:
  early   late  NA's
  37     87     80
```

```
tumorstage:
  1     2     3     4  NA's
  20    14    58    18    94
```

```
substage:
  a     b     c  NA's
  17    22    79    86
```

```
grade:
  1     2     3     4  NA's
  11    20    83    8    82
```

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

```
25.00 45.00 55.00 58.82 65.00 85.00
```

batch:

Length	Class	Mode
204	character	character

uncurated\_author\_metadata:

Length	Class	Mode
204	character	character

---

GSE26193\_eset

*miR-141 and miR-200a act on ovarian tumorigenesis by controlling oxidative stress response.*

---

## Description

Although there is evidence that redox regulation has an essential role in malignancies, its impact on tumor prognosis remains unclear. Here we show crosstalk between oxidative stress and the miR-200 family of microRNAs that affects tumorigenesis and chemosensitivity. miR-141 and miR-200a target p38?? and modulate the oxidative stress response. Enhanced expression of these microRNAs mimics p38?? deficiency and increases tumor growth in mouse models, but it also improves the response to chemotherapeutic agents. High-grade human ovarian adenocarcinomas that accumulate miR-200a have low concentrations of p38?? and an associated oxidative stress signature. The miR200a-dependent stress signature correlates with improved survival of patients in response to treatment. Therefore, the role of miR-200a in stress could be a predictive marker for clinical outcome in ovarian cancer. In addition, although oxidative stress promotes tumor growth, it also sensitizes tumors to treatment, which could account for the limited success of antioxidants in clinical trials.

## Usage

```
data( GSE26193_eset )
```

## Format

```
experimentData(eset):  
  Experiment data  
    Experimenter name: Mateescu B, Batista L, Mariani O, Meyniel J, Cottu PH, Sastre-Garau X, Mechta-Grigoriou  
    Laboratory: Mateescu, Mechta-Grigoriou 2011  
    Contact information:  
    Title: miR-141 and miR-200a act on ovarian tumorigenesis by controlling oxidative stress response.  
    URL:  
    PMIDs: 22101765
```

Abstract: A 149 word abstract is available. Use 'abstract' method.  
Information is available on: preprocessing

```

notes:
platform_title:
[HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
platform_shorttitle:
Affymetrix HG-U133Plus2
platform_summary:
hgu133plus2
platform_manufacturer:
Affymetrix
platform_distribution:
commercial
platform_accession:
GPL570
platform_technology:
in situ oligonucleotide

Preprocessing: frma
featureData(eset):
An object of class 'AnnotatedDataFrame'
featureNames: A1BG A1BG-AS1 ... ZZZ3 (19816 total)
varLabels: probeset gene
varMetadata: labelDescription

```

## Details

```

assayData: 19816 features, 107 samples
Platform type: hgu133plus2
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records    n.max n.start  events  median 0.95LCL 0.95UCL
107.00  107.00  107.00    76.00    3.05    2.50    4.56

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

alt_sample_name:
  Length   Class    Mode
  107 character character

sample_type:
tumor
  107

histological_type:
clearcell      endo    mucinous     other      ser
          6          8          8          6         79

```

```
summarygrade:  
high  low  
67    40  
  
summarystage:  
early  late  
31     76  
  
tumorstage:  
1  2  3  4  
20 11 59 17  
  
substage:  
a   b   c  NA's  
16  12  62  17  
  
grade:  
1  2  3  
7 33 67  
  
days_to_tumor_recurrence:  
  Min. 1st Qu. Median  Mean 3rd Qu.  Max.  
  3.0   340.5  584.0 1108.0 1525.0 7386.0  
  
recurrence_status:  
norecurrence  recurrence  
  27          80  
  
days_to_death:  
  Min. 1st Qu. Median  Mean 3rd Qu.  Max.  
  3      668    1096   1520   2220   7386  
  
vital_status:  
deceased  living  
  76      31  
  
batch:  
  Length   Class   Mode  
  107   character  character  
  
uncurated_author_metadata:  
  Length   Class   Mode  
  107   character  character
```

---

GSE26712\_eset

*A gene signature predicting for survival in suboptimally debulked patients with ovarian cancer.*

## Description

Despite the existence of morphologically indistinguishable disease, patients with advanced ovarian tumors display a broad range of survival end points. We hypothesize that gene expression profiling can identify a prognostic signature accounting for these distinct clinical outcomes. To resolve survival-associated loci, gene expression profiling was completed for an extensive set of 185 (90 optimal/95 suboptimal) primary ovarian tumors using the Affymetrix human U133A microarray. Cox regression analysis identified probe sets associated with survival in optimally and suboptimally debulked tumor sets at a P value of <0.01. Leave-one-out cross-validation was applied to each tumor cohort and confirmed by a permutation test. External validation was conducted by applying the gene signature to a publicly available array database of expression profiles of advanced stage suboptimally debulked tumors. The prognostic signature successfully classified the tumors according to survival for suboptimally (P = 0.0179) but not optimally debulked (P = 0.144) patients. The suboptimal gene signature was validated using the independent set of tumors (odds ratio, 8.75; P = 0.0146). To elucidate signaling events amenable to therapeutic intervention in suboptimally debulked patients, pathway analysis was completed for the top 57 survival-associated probe sets. For suboptimally debulked patients, confirmation of the predictive gene signature supports the existence of a clinically relevant predictor, as well as the possibility of novel therapeutic opportunities. Ultimately, the prognostic classifier defined for suboptimally debulked tumors may aid in the classification and enhancement of patient outcome for this high-risk population.

## Usage

```
data( GSE26712_eset )
```

## Format

```
experimentData(eset):
  Experiment data
    Experimenter name: Bonome T, Levine DA, Shih J, Randonovich M, Pise-Masison CA, Bogomolniy F, Ozbum L, ...
    Laboratory: Bonome, Birrer 2008
    Contact information:
    Title: A gene signature predicting for survival in suboptimally debulked patients with ovarian cancer.
    URL:
    PMIDs: 18593951

  Abstract: A 238 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
    platform_title:
      [HG-U133A] Affymetrix Human Genome U133A Array
    platform_shorttitle:
      Affymetrix HG-U133A
    platform_summary:
      hgu133a
```

```
platform_manufacturer:
  Affymetrix
platform_distribution:
  commercial
platform_accession:
  GPL96
platform_technology:
  in situ oligonucleotide

Preprocessing: frma
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1CF A2M ... ZZZ3 (13104 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

## Details

```
assayData: 13104 features, 195 samples
Platform type: hgu133a
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

  10 observations deleted due to missingness
records  n.max n.start  events  median 0.95LCL 0.95UCL
  185.00  185.00  185.00  129.00    3.83    3.24    4.83

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

alt_sample_name:
  Length     Class      Mode
  195 character character

sample_type:
  healthy    tumor
  10        185

histological_type:
  ser NA's
  185    10

primarysite:
  ov
  195

summarygrade:
```

high NA's  
185 10

summarystage:  
late NA's  
185 10

tumorstage:  
3 4 NA's  
146 36 13

substage:  
b c NA's  
9 137 49

age\_at\_initial\_pathologic\_diagnosis:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
26.00 52.00 63.00 61.54 70.00 84.00 13

recurrence\_status:  
norecurrence recurrence  
42 153

days\_to\_death:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
21.9 660.6 1164.0 1429.0 1880.0 4982.0 10

vital\_status:  
deceased living NA's  
129 56 10

debulking:  
optimal suboptimal NA's  
90 95 10

percent\_normal\_cells:  
20-  
195

percent\_stromal\_cells:  
20-  
195

percent\_tumor\_cells:  
80+  
195

batch:

```
Length     Class      Mode
 195 character character

uncurated_author_metadata:
Length     Class      Mode
 195 character character
```

---

GSE30009_eset	<i>Multidrug resistance-linked gene signature predicts overall survival of patients with primary ovarian serous carcinoma.</i>
---------------	--

---

## Description

This study assesses the ability of multidrug resistance (MDR)-associated gene expression patterns to predict survival in patients with newly diagnosed carcinoma of the ovary. The scope of this research differs substantially from that of previous reports, as a very large set of genes was evaluated whose expression has been shown to affect response to chemotherapy. We applied a customized TaqMan low density array, a highly sensitive and specific assay, to study the expression profiles of 380 MDR-linked genes in 80 tumor specimens collected at initial surgery to debulk primary serous carcinoma. The RNA expression profiles of these drug resistance genes were correlated with clinical outcomes. Leave-one-out cross-validation was used to estimate the ability of MDR gene expression to predict survival. Although gene expression alone does not predict overall survival (OS;  $P = 0.06$ ), four covariates (age, stage, CA125 level, and surgical debulking) do ( $P = 0.03$ ). When gene expression was added to the covariates, we found an 11-gene signature that provides a major improvement in OS prediction (log-rank statistic  $P < 0.003$ ). The predictive power of this 11-gene signature was confirmed by dividing high- and low-risk patient groups, as defined by their clinical covariates, into four specific risk groups on the basis of expression levels. This study reveals an 11-gene signature that allows a more precise prognosis for patients with serous cancer of the ovary treated with carboplatin- and paclitaxel-based therapy. These 11 new targets offer opportunities for new therapies to improve clinical outcome in ovarian cancer.

## Usage

```
data( GSE30009_eset )
```

## Format

```
experimentData(eset):
Experiment data
  Experimenter name: Gillet JP, Calcagno AM, Varma S, Davidson B et al. Multidrug resistance-linked gene
  Laboratory: Gillet, Gottesman 2012
  Contact information:
  Title: Multidrug resistance-linked gene signature predicts overall survival of patients with primary ovarian carcinoma
  URL:
  PMIDs: 22492981
```

```

Abstract: A 244 word abstract is available. Use 'abstract' method.
Information is available on: preprocessing
notes:
platform_title:
  TaqMan qRT-PCR Homo sapiens Low-Density Array 380
platform_shorttitle:
  TaqMan qRT-PCR
platform_summary:
  NA
platform_manufacturer:
  TaqMan
platform_distribution:
  custom
platform_accession:
  GPL13728
platform_technology:
  qRT-PCR

Preprocessing: default
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: ABCA1 ABCA10 ... XRCC6 (359 total)
  varLabels: probeset gene
  varMetadata: labelDescription

```

## Details

```

assayData: 359 features, 103 samples
Platform type: NA
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records    n.max n.start  events  median 0.95LCL 0.95UCL
  103.00    103.00   103.00    57.00    3.42    2.92    5.34

```

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

```

alt_sample_name:
  Length     Class      Mode
  103 character character

sample_type:
borderline      tumor
  1           102

histological_type:
```

```

clearcell      ser
      1      102

summarygrade:
high  low NA's
 92    9    2

summarystage:
late
 103

tumorstage:
 3  4
82 21

substage:
  b   c NA's
 2   60  41

grade:
  1   2   3 NA's
  4   5   92   2

age_at_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median   Mean 3rd Qu.  Max.
 30.00   56.00   61.00   62.45   71.50   87.00

days_to_death:
  Min. 1st Qu.  Median   Mean 3rd Qu.  Max.
  24      598    1053    1156    1568   4748

vital_status:
deceased   living
  57       46

debulking:
  optimal suboptimal
    81       22

uncurated_author_metadata:
  Length   Class      Mode
 103   character character

```

## Description

Despite advances in radical surgery and chemotherapy delivery, ovarian cancer is the most lethal gynecologic malignancy. Standard therapy includes treatment with platinum-based combination chemotherapies yet there is no biomarker model to predict their responses to these agents. We here have developed and independently tested our multi-gene molecular predictors for forecasting patients' responses to individual drugs on a cohort of 55 ovarian cancer patients. To independently validate these molecular predictors, we performed microarray profiling on FFPE tumor samples of 55 ovarian cancer patients (UVA-55) treated with platinum-based adjuvant chemotherapy. Genome-wide chemosensitivity biomarkers were initially discovered from the in vitro drug activities and genomic expression data for carboplatin and paclitaxel, respectively. Multivariate predictors were trained with the cell line data and then evaluated with a historical patient cohort. For the UVA-55 cohort, the carboplatin, taxol, and combination predictors significantly stratified responder patients and non-responder patients ( $p = 0.019, 0.04, 0.014$ ) with sensitivity = 91%, 96%, 93 and NPV = 57%, 67%, 67% in pathologic clinical response. The combination predictor also demonstrated a significant survival difference between predicted responders and non-responders with a median survival of 55.4 months vs. 32.1 months. Thus, COXEN single- and combination-drug predictors successfully stratified platinum resistance and taxane response in an independent cohort of ovarian cancer patients based on their FFPE tumor samples.

## Usage

```
data( GSE30161_eset )
```

## Format

```
experimentData(eset):
Experiment data
  Experimenter name: Ferriss JS, Kim Y, Duska L, Birrer M, Levine DA, Moskaluk C, Theodorescu D, Lee JK
  Laboratory: Ferriss, Lee 2012
  Contact information:
    Title: Multi-gene expression predictors of single drug responses to adjuvant chemotherapy in ovarian cancer
    URL:
    PMIDs: 22348014

  Abstract: A 215 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
  platform_title:
    [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
  platform_shorttitle:
    Affymetrix HG-U133Plus2
  platform_summary:
    hgu133plus2
  platform_manufacturer:
    Affymetrix
  platform_distribution:
    commercial
  platform_accession:
```

```
GPL570
platform_technology:
  in situ oligonucleotide

Preprocessing: frma
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1BG A1BG-AS1 ... ZZZ3 (19816 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

## Details

```
assayData: 19816 features, 58 samples
Platform type: hgu133plus2
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records  n.max n.start  events  median 0.95LCL 0.95UCL
 58.00    58.00    58.00    36.00    4.19    2.70    6.17

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

alt_sample_name:
  Length     Class      Mode
  58 character character

sample_type:
  tumor
  58

histological_type:
  Length     Class      Mode
  58 character character

summarygrade:
  high   low  NA's
  33    21     4

summarystage:
  late
  58

tumorstage:
  3   4
  53   5
```

substage:  
a b c  
9 11 38

grade:  
1 2 3 NA's  
2 19 33 4

age\_at\_initial\_pathologic\_diagnosis:  
Min. 1st Qu. Median Mean 3rd Qu. Max.  
38.00 53.50 62.00 62.57 72.00 85.00

pltx:  
y  
58

tax:  
n y  
4 54

neo:  
n  
58

days\_to\_tumor\_recurrence:  
Min. 1st Qu. Median Mean 3rd Qu. Max.  
12.0 255.2 386.0 742.1 768.2 4208.0

recurrence\_status:  
norecurrence recurrence NA's  
6 48 4

days\_to\_death:  
Min. 1st Qu. Median Mean 3rd Qu. Max.  
49.0 585.2 1010.0 1375.0 2131.0 4208.0

vital\_status:  
deceased living  
36 22

debulking:  
optimal suboptimal NA's  
26 30 2

batch:  
2009-10-07 2009-10-08 2009-10-09 2009-10-20  
28 18 8 4

```
uncurated_author_metadata:  
  Length      Class      Mode  
  58 character character
```

---

GSE32062.GPL6480\_eset *High-risk ovarian cancer based on 126-gene expression signature is uniquely characterized by downregulation of antigen presentation pathway.*

---

## Description

High-grade serous ovarian cancers are heterogeneous not only in terms of clinical outcome but also at the molecular level. Our aim was to establish a novel risk classification system based on a gene expression signature for predicting overall survival, leading to suggesting novel therapeutic strategies for high-risk patients. In this large-scale cross-platform study of six microarray data sets consisting of 1,054 ovarian cancer patients, we developed a gene expression signature for predicting overall survival by applying elastic net and 10-fold cross-validation to a Japanese data set A (n = 260) and evaluated the signature in five other data sets. Subsequently, we investigated differences in the biological characteristics between high- and low-risk ovarian cancer groups. An elastic net analysis identified a 126-gene expression signature for predicting overall survival in patients with ovarian cancer using the Japanese data set A (multivariate analysis, P = 4 ?? 10(-20)). We validated its predictive ability with five other data sets using multivariate analysis (Tothill's data set, P = 1 ?? 10(-5); Bonome's data set, P = 0.0033; Dressman's data set, P = 0.0016; TCGA data set, P = 0.0027; Japanese data set B, P = 0.021). Through gene ontology and pathway analyses, we identified a significant reduction in expression of immune-response-related genes, especially on the antigen presentation pathway, in high-risk ovarian cancer patients. This risk classification based on the 126-gene expression signature is an accurate predictor of clinical outcome in patients with advanced stage high-grade serous ovarian cancer and has the potential to develop new therapeutic strategies for high-grade serous ovarian cancer patients.

## Usage

```
data( GSE32062.GPL6480_eset )
```

## Format

```
experimentData(eset):  
  Experiment data  
  Experimenter name: Yoshihara K, Tsunoda T, Shigemizu D, Fujiwara H et al. High-risk ovarian cancer base  
  Laboratory: Yoshihara, Tanaka 2012  
  Contact information:  
  Title: High-risk ovarian cancer based on 126-gene expression signature is uniquely characterized by do  
  URL:  
  PMIDs: 22241791
```

```

Abstract: A 255 word abstract is available. Use 'abstract' method.
Information is available on: preprocessing
notes:
  platform_title:
    Agilent-014850 Whole Human Genome Microarray 4x44K G4112F (Probe Name version)
  platform_shorttitle:
    Agilent G4112F
  platform_summary:
    hgug4112a
  platform_manufacturer:
    Agilent
  platform_distribution:
    commercial
  platform_accession:
    GPL6480
  platform_technology:
    in situ oligonucleotide

Preprocessing: default
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1BG A1BG-AS1 ... ZZZ3 (20106 total)
  varLabels: probeset gene
  varMetadata: labelDescription

```

## Details

```

assayData: 20106 features, 260 samples
Platform type: hgug4112a
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records    n.max n.start  events  median 0.95LCL 0.95UCL
260.00  260.00  260.00  121.00    4.93    4.11    6.58

```

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

```

alt_sample_name:
  Length     Class      Mode
  260 character character

sample_type:
tumor
  260

```

```
histological_type:
  ser
  260

summarygrade:
  high  low
  129  131

summarystage:
  late
  260

tumorstage:
  3    4
  204  56

substage:
  a    b    c  NA's
  4    20   180  56

grade:
  2    3
  131  129

pltx:
  y
  260

tax:
  y
  260

days_to_death:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  30      810     1245    1344     1710    3840

vital_status:
  deceased   living
  121        139

debulking:
  optimal  suboptimal
  103        157

uncurated_author_metadata:
  Length      Class      Mode
  260 character character
```

---

GSE32063_eset	<i>High-risk ovarian cancer based on 126-gene expression signature is uniquely characterized by downregulation of antigen presentation pathway.</i>
---------------	---

---

## Description

High-grade serous ovarian cancers are heterogeneous not only in terms of clinical outcome but also at the molecular level. Our aim was to establish a novel risk classification system based on a gene expression signature for predicting overall survival, leading to suggesting novel therapeutic strategies for high-risk patients. In this large-scale cross-platform study of six microarray data sets consisting of 1,054 ovarian cancer patients, we developed a gene expression signature for predicting overall survival by applying elastic net and 10-fold cross-validation to a Japanese data set A (n = 260) and evaluated the signature in five other data sets. Subsequently, we investigated differences in the biological characteristics between high- and low-risk ovarian cancer groups. An elastic net analysis identified a 126-gene expression signature for predicting overall survival in patients with ovarian cancer using the Japanese data set A (multivariate analysis, P = 4 ?? 10(-20)). We validated its predictive ability with five other data sets using multivariate analysis (Tothill's data set, P = 1 ?? 10(-5); Bonome's data set, P = 0.0033; Dressman's data set, P = 0.0016; TCGA data set, P = 0.0027; Japanese data set B, P = 0.021). Through gene ontology and pathway analyses, we identified a significant reduction in expression of immune-response-related genes, especially on the antigen presentation pathway, in high-risk ovarian cancer patients. This risk classification based on the 126-gene expression signature is an accurate predictor of clinical outcome in patients with advanced stage high-grade serous ovarian cancer and has the potential to develop new therapeutic strategies for high-grade serous ovarian cancer patients.

## Usage

```
data( GSE32063_eset )
```

## Format

```
experimentData(eset):
  Experiment data
  Experimenter name: Yoshihara K, Tsunoda T, Shigemizu D, Fujiwara H et al. High-risk ovarian cancer base
  Laboratory: Yoshihara, Tanaka 2012
  Contact information:
  Title: High-risk ovarian cancer based on 126-gene expression signature is uniquely characterized by do
  URL:
  PMIDs: 22241791

  Abstract: A 255 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
  platform_title:
  Agilent-014850 Whole Human Genome Microarray 4x44K G4112F (Probe Name vers
  ion)
```

```
platform_shorttitle:  
  Agilent G4112F  
platform_summary:  
  hgug4112a  
platform_manufacturer:  
  Agilent  
platform_distribution:  
  commercial  
platform_accession:  
  GPL6480  
platform_technology:  
  in situ oligonucleotide  
  
Preprocessing: default  
featureData(eset):  
An object of class 'AnnotatedDataFrame'  
  featureNames: A1BG A1BG-AS1 ... ZZZ3 (20106 total)  
  varLabels: probeset gene  
  varMetadata: labelDescription
```

## Details

```
assayData: 20106 features, 40 samples  
Platform type: hgug4112a  
Overall survival time-to-event summary (in years):  
Call: survfit(formula = Surv(time, cens) ~ -1)  
  
records    n.max n.start  events  median 0.95LCL 0.95UCL  
  40.00     40.00   40.00    22.00    4.44    3.29      NA  
  
-----  
Available sample meta-data:  
-----  
  
alt_sample_name:  
  Length     Class      Mode  
  40 character character  
  
sample_type:  
  tumor  
  40  
  
histological_type:  
  ser  
  40  
  
summarygrade:  
  high  low
```

```
17    23

summarystage:
late
40

tumorstage:
3   4
31  9

substage:
b   c  NA's
3   28   9

grade:
2   3
23 17

pltx:
y
40

tax:
y
40

days_to_death:
  Min. 1st Qu.  Median  Mean 3rd Qu.  Max.
  210     705    1155   1346    1792   3330

vital_status:
deceased   living
22        18

debulking:
optimal suboptimal
19        21

uncurated_author_metadata:
Length   Class   Mode
40   character character
```

## Description

Biomarkers that predict disease progression might assist the development of better therapeutic strategies for aggressive cancers, such as ovarian cancer. Here, we investigated the role of collagen type XI alpha 1 (COL11A1) in cell invasiveness and tumor formation and the prognostic impact of COL11A1 expression in ovarian cancer. Microarray analysis suggested that COL11A1 is a disease progression-associated gene that is linked to ovarian cancer recurrence and poor survival. Small interference RNA-mediated specific reduction in COL11A1 protein levels suppressed the invasive ability and oncogenic potential of ovarian cancer cells and decreased tumor formation and lung colonization in mouse xenografts. A combination of experimental approaches, including real-time RT-PCR, casein zymography and chromatin immunoprecipitation (ChIP) assays, showed that COL11A1 knockdown attenuated MMP3 expression and suppressed binding of Ets-1 to its putative MMP3 promoter-binding site, suggesting that the Ets-1-MMP3 axis is upregulated by COL11A1. Transforming growth factor (TGF)-beta (TGF-??1) treatment triggers the activation of smad2 signaling cascades, leading to activation of COL11A1 and MMP3. Pharmacological inhibition of MMP3 abrogated the TGF-??1-triggered, COL11A1-dependent cell invasiveness. Furthermore, the NF-YA-binding site on the COL11A1 promoter was identified as the major determinant of TGF-??1-dependent COL11A1 activation. Analysis of 88 ovarian cancer patients indicated that high COL11A1 mRNA levels are associated with advanced disease stage. The 5-year recurrence-free and overall survival rates were significantly lower (P=0.006 and P=0.018, respectively) among patients with high expression levels of tissue COL11A1 mRNA compared with those with low expression. We conclude that COL11A1 may promote tumor aggressiveness via the TGF-??1-MMP3 axis and that COL11A1 expression can predict clinical outcome in ovarian cancer patients.

## Usage

```
data( GSE44104_eset )
```

## Format

```
experimentData(eset):  
  Experiment data  
    Experimenter name: Wu Y, Chang T, Huang Y, Huang H, Chou C  
    Laboratory: Wu, Chou 2013  
    Contact information:  
      Title: COL11A1 promotes tumor progression and predicts poor clinical outcome in ovarian cancer.  
      URL:  
      PMIDs: 23934190  
  
  Abstract: A 260 word abstract is available. Use 'abstract' method.  
  Information is available on: preprocessing  
  notes:  
    platform_title:  
      [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array  
    platform_shorttitle:  
      Affymetrix HG-U133Plus2  
    platform_summary:  
      hgu133plus2  
    platform_manufacturer:
```

```

Affymetrix
platform_distribution:
  commercial
platform_accession:
  GPL570
platform_technology:
  in situ oligonucleotide

Preprocessing: frma
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1BG A1BG-AS1 ... ZZZ3 (19816 total)
  varLabels: probeset gene
  varMetadata: labelDescription

```

## Details

```

assayData: 19816 features, 60 samples
Platform type: hgu133plus2
Binary overall survival summary (definitions of long and short provided by study authors):

  long short
  44    16

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

alt_sample_name:
  Length     Class      Mode
  60 character character

sample_type:
  tumor
  60

histological_type:
  clearcell      endo  mucinous      ser
  12           11      9          28

summarystage:
  early  late
  25    35

tumorstage:
  1  2  3  4
  17  8 30  5

```

```
recurrence_status:  
norecurrence    recurrence  
        40            20  
  
os_binary:  
long short  
44    16  
  
relapse_binary:  
long short  
40    20  
  
batch:  
2010-09-07 2010-09-08 2010-10-14 2010-12-10 2010-12-14  
      2          18          16          4  
  
uncurated_author_metadata:  
Length      Class      Mode  
60 character character
```

---

GSE49997\_eset

*Validating the impact of a molecular subtype in ovarian cancer on outcomes: a study of the OVCAD Consortium.*

---

## Description

Most patients with epithelial ovarian cancer (EOC) are diagnosed at advanced stage and have a poor prognosis. However, a small proportion of these patients will survive, whereas others will die very quickly. Clinicopathological factors do not allow precise identification of these subgroups. Thus, we have validated a molecular subclassification as new prognostic factor in EOC. One hundred and ninety-four patients with Stage II-IV EOC were characterized by whole-genome expression profiling of tumor tissues and were classified using a published 112 gene set, derived from an International Federation of Gynecology and Obstetrics (FIGO) stage-directed supervised classification approach. The 194 tumor samples were classified into two subclasses comprising 95 (Subclass 1) and 99 (Subclass 2) tumors. All nine FIGO II tumors were grouped in Subclass 1 ( $P = 0.001$ ). Subclass 2 (54% of advanced-stage tumors) was significantly correlated with peritoneal carcinomatosis and non-optimal debulking. Patients with Subclass 2 tumors had a worse overall survival for both serous and non-serous histological subtypes, as revealed by univariate analysis (hazard ratios [HR] of 3.17 and 17.11, respectively;  $P = 0.001$ ) and in models corrected for relevant clinicopathologic parameters (HR 2.87 and 12.42, respectively;  $P = 0.023$ ). Significance analysis of microarrays revealed 2082 genes that were differentially expressed in advanced-grade serous tumors of both subclasses and the focal adhesion pathway as the most deregulated pathway. In the present validation study, we have shown that, in advanced-stage serous ovarian cancer, two approximately equally large molecular subtypes exist, independent of classical clinicopathological parameters and presenting with highly different whole-genome expression profiles and a markedly different overall survival. Similar results were obtained in a small cohort of patients with non-serous tumors.?? 2012 Japanese Cancer Association.

**Usage**

```
data( GSE49997_eset )
```

**Format**

```
experimentData(eset):
  Experiment data
    Experimenter name: Pils D1, Hager G, Tong D, Aust S, Heinze G, Kohl M, Schuster E, Wolf A, Sehouli J, Bra
    Laboratory: Pils, Zeilinger 2012
    Contact information:
    Title: Validating the impact of a molecular subtype in ovarian cancer on outcomes: a study of the OVCAD
    URL:
    PMIDs: 22497737

    Abstract: A 276 word abstract is available. Use 'abstract' method.
    Information is available on: preprocessing
    notes:
    platform_title:
      ABI Human Genome Survey Microarray Version 2
    platform_shorttitle:
      ABI Human Genome
    platform_summary:

    platform_manufacturer:
      Applied Biosystems
    platform_distribution:
      commercial
    platform_accession:
      GPL2986
    platform_technology:
      in situ oligonucleotide

    Preprocessing: default
    featureData(eset):
      An object of class 'AnnotatedDataFrame'
      featureNames: A1BG A1CF ... ZZZ3 (16048 total)
      varLabels: probeset gene
      varMetadata: labelDescription
```

**Details**

```
assayData: 16048 features, 204 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

10 observations deleted due to missingness
```

```
records    n.max n.start  events  median 0.95LCL 0.95UCL
194.00  194.00  194.00    57.00      NA     3.67      NA

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

alt_sample_name:
  Length     Class      Mode
  204 character character

sample_type:
  tumor
  204

histological_type:
  other    ser  NA's
  23     171    10

summarygrade:
  high    low  NA's
  143     50    11

summarystage:
  early   late  NA's
  9      185    10

tumorstage:
  2      3     4  NA's
  9     154    31    10

grade:
  2      3  NA's
  50    143    11

age_at_initial_pathologic_diagnosis:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.  NA's
  26.00  50.00  57.00   57.66  67.00  85.00    10

days_to_tumor_recurrence:
  Min. 1st Qu.  Median    Mean 3rd Qu.  Max.  NA's
  30.0   335.0  487.0   580.1  722.5  1461.0    10

recurrence_status:
  norecurrence   recurrence      NA's
  70                  124        10

days_to_death:
```

```

Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
30.0 517.0 745.5 782.9 1027.0 1491.0 10

vital_status:
deceased living NA's
57 137 10

debulking:
optimal suboptimal NA's
137 57 10

uncurated_author_metadata:
Length Class Mode
204 character character

```

GSE51088\_eset

*POSTN/TGFBI-associated stromal signature predicts poor prognosis in serous epithelial ovarian cancer.*

## Description

To identify molecular prognosticators and therapeutic targets for high-grade serous epithelial ovarian cancers (EOCs) using genetic analyses driven by biologic features of EOC pathogenesis. Ovarian tissue samples ( $n = 172$ ; 122 serous EOCs, 30 other EOCs, 20 normal/benign) collected prospectively from sequential patients undergoing gynecologic surgery were analyzed using RNA expression microarrays. Samples were classified based on expression of genes with potential relevance in ovarian cancer. Gene sets were defined using Rosetta Similarity Search Tool (ROAST) and analysis of variance (ANOVA). Gene copy number variations were identified by array comparative genomic hybridization. No distinct subgroups of EOC could be identified by unsupervised clustering, however, analyses based on genes correlated with periostin (POSTN) and estrogen receptor-alpha (ESR1) yielded distinct subgroups. When 95 high-grade serous EOCs were grouped by genes based on ANOVA comparing ESR1/WT1 and POSTN/TGFBI samples, overall survival (OS) was significantly shorter for 43 patients with tumors expressing genes associated with POSTN/TGFBI compared to 52 patients with tumors expressing genes associated with ESR1/WT1 (median 30 versus 49 months, respectively;  $P = 0.022$ ). Several targets with therapeutic potential were identified within each subgroup. BRCA germline mutations were more frequent in the ESR1/WT1 subgroup. Proliferation-associated genes and TP53 status (mutated or wild-type) did not correlate with survival. Findings were validated using independent ovarian cancer datasets. Two distinct molecular subgroups of high-grade serous EOCs based on POSTN/TGFBI and ESR1/WT1 expressions were identified with significantly different OS. Specific differentially expressed genes between these subgroups provide potential prognostic and therapeutic targets. Copyright ?? 2013 Elsevier Inc. All rights reserved.

## Usage

```
data( GSE51088_eset )
```

## Format

```

experimentData(eset):
  Experiment data
    Experimenter name: Karlan BY, Dering J, Walsh C, Orsulic S, Lester J, Anderson LA, Ginther CL, Fejzo M,
    Laboratory: Karlan, Slamon 2014
    Contact information:
    Title: POSTN/TGFBI-associated stromal signature predicts poor prognosis in serous epithelial ovarian cancer
    URL:
    PMIDs: 24368280

  Abstract: A 250 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
    platform_title:
      Agilent-012097 Human 1A Microarray (V2) G4110B (Probe Name version)
    platform_shorttitle:
      Agilent G4110B
    platform_summary:
      hgug4110b
    platform_manufacturer:
      Agilent
    platform_distribution:
      commercial
    platform_accession:
      GPL7264
    platform_technology:
      in situ oligonucleotide

  Preprocessing: default
  featureData(eset):
  An object of class 'AnnotatedDataFrame'
  featureNames: A1CF A2M ... ZZZ3 (8211 total)
  varLabels: probeset gene
  varMetadata: labelDescription

```

## Details

```

assayData: 8211 features, 172 samples
Platform type: hgug4110b
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

  20 observations deleted due to missingness
  records  n.max n.start  events  median 0.95LCL 0.95UCL
  152.00  152.00  152.00  112.00    4.13    3.50    4.92
  -----

```

```
Available sample meta-data:
-----
alt_sample_name:
  Length     Class      Mode
  172 character character

sample_type:
  benign borderline   healthy metastatic      tumor
  5           12          15          17          123

histological_type:
  Length     Class      Mode
  172 character character

summarygrade:
  high    low  NA's
  119     30     23

summarystage:
  early   late  NA's
  31     120    21

tumorstage:
  1      2      3      4  NA's
  22     9    103    17    21

substage:
  a      b      c  NA's
  17    22    94    39

grade:
  0      1      2      3  NA's
  8      8    14    119    23

age_at_initial_pathologic_diagnosis:
  Min. 1st Qu. Median   Mean 3rd Qu.   Max.
  26.0    49.0    57.5    58.6    68.0    91.0

neo:
  n
  172

recurrence_status:
  norecurrence   recurrence      NA's
  36            111            25

days_to_death:
```

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
vital_status:							
deceased	30	791	1491	1835	2344	7001	20
percent_normal_cells:							
30- NA's							
140	112	40	20				
percent_stromal_cells:							
30- NA's							
140	140	32	32				
percent_tumor_cells:							
70+ NA's							
140	140	32	32				
uncurated_author_metadata:							
Length	172	Class	character	Mode	character	character	character

GSE6008\_eset

*Lysophosphatidic acid-induced transcriptional profile represents serous epithelial ovarian carcinoma and worsened prognosis.*

## Description

Lysophosphatidic acid (LPA) governs a number of physiologic and pathophysiological processes. Malignant ascites fluid is rich in LPA, and LPA receptors are aberrantly expressed by ovarian cancer cells, implicating LPA in the initiation and progression of ovarian cancer. However, there is an absence of systematic data critically analyzing the transcriptional changes induced by LPA in ovarian cancer. In this study, gene expression profiling was used to examine LPA-mediated transcription by exogenously adding LPA to human epithelial ovarian cancer cells for 24 h to mimic long-term stimulation in the tumor microenvironment. The resultant transcriptional profile comprised a 39-gene signature that closely correlated to serous epithelial ovarian carcinoma. Hierarchical clustering of ovarian cancer patient specimens demonstrated that the signature is associated with worsened prognosis. Patients with LPA-signature-positive ovarian tumors have reduced disease-specific and progression-free survival times. They have a higher frequency of stage IIIc serous carcinoma and a greater proportion is deceased. Among the 39-gene signature, a group of seven genes associated with cell adhesion recapitulated the results. Out of those seven, claudin-1, an adhesion molecule and phenotypic epithelial marker, is the only independent biomarker of serous epithelial ovarian carcinoma. Knockdown of claudin-1 expression in ovarian cancer cells reduces LPA-mediated cellular adhesion, enhances suspended cells and reduces LPA-mediated migration. The data suggest

that transcriptional events mediated by LPA in the tumor microenvironment influence tumor progression through modulation of cell adhesion molecules like claudin-1 and, for the first time, report an LPA-mediated expression signature in ovarian cancer that predicts a worse prognosis.

## Usage

```
data( GSE6008_eset )
```

## Format

```
experimentData(eset):
Experiment data
  Experimenter name: Murph MM, Liu W, Yu S, Lu Y, Hall H, Hennessy BT, Lahad J, Schaner M, Helland A, Krist
  Laboratory: Murph, Mills 2009
  Contact information:
  Title: Lysophosphatidic acid-induced transcriptional profile represents serous epithelial ovarian can
  URL:
  PMID: 19440550

  Abstract: A 247 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
    platform_title:
      [HG-U133A] Affymetrix Human Genome U133A Array
    platform_shorttitle:
      Affymetrix HG-U133A
    platform_summary:
      hgu133a
    platform_manufacturer:
      Affymetrix
    platform_distribution:
      commercial
    platform_accession:
      GPL96
    platform_technology:
      in situ oligonucleotide

  Preprocessing: frma
featureData(eset):
  An object of class 'AnnotatedDataFrame'
  featureNames: A1CF A2M ... ZZZ3 (13104 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

## Details

assayData: 13104 features, 103 samples  
Platform type: hgu133a

```
-----  
Available sample meta-data:  
-----  
  
alt_sample_name:  
  Length     Class      Mode  
  103 character character  
  
sample_type:  
  healthy    tumor  
    4         99  
  
histological_type:  
  clearcell    endo  mucinous      ser      NA's  
    8          37      13        41        4  
  
primarysite:  
  ov  
103  
  
summarygrade:  
  high   low  NA's  
  38    36    29  
  
summarystage:  
  early  late  NA's  
  42    53    8  
  
tumorstage:  
  1     2     3     4  NA's  
  35    11    44    9    4  
  
substage:  
  a     b     c     d  NA's  
  19    2     54    1    27  
  
grade:  
  1     2     3  NA's  
  19    17    38    29  
  
batch:  
  Length     Class      Mode  
  103 character character  
  
uncurated_author_metadata:  
  Length     Class      Mode  
  103 character character
```

---

GSE6822_eset	<i>Classification of ovarian tumor samples</i>
--------------	--

---

### Description

Ouellet V, Provencher DM, Maugard CM, Le Page C, Ren F, Lussier C, Novak J, Ge B, Hudson TJ, Tonin PN, Mes-Masson A-M: Discrimination between serous low malignant potential and invasive epithelial ovarian tumors using molecular profiling. *Oncogene* 2005, 24:4672-4687.

### Usage

```
data( GSE6822_eset )
```

### Format

```
experimentData(eset):
  Experiment data
    Experimenter name: Ouellet V, Provencher DM, Maugard CM, Le Page C, Ren F, Lussier C, Novak J, Ge B, Hudson TJ, Tonin PN, Mes-Masson A-M
    Laboratory: Ouellet, Mes-Masson 2005
    Contact information:
    Title: Classification of ovarian tumor samples
    URL:
    PMID: PMID unknown

    Abstract: A 40 word abstract is available. Use 'abstract' method.
    Information is available on: preprocessing
    notes:
    platform_title:
      [Hu6800] Affymetrix Human Full Length HuGeneFL Array
    platform_shorttitle:
      Affymetrix Hu6800
    platform_summary:
      hu6800
    platform_manufacturer:
      Affymetrix
    platform_distribution:
      commercial
    platform_accession:
      GPL80
    platform_technology:
      in situ oligonucleotide

  Preprocessing: rma
  featureData(eset):
  An object of class 'AnnotatedDataFrame'
  featureNames: A2M AADAC ... ZYX (5251 total)
  varLabels: probeset gene
```

```
varMetadata: labelDescription
```

## Details

```
assayData: 5251 features, 66 samples
Platform type: hu6800
```

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

```
-----  
alt_sample_name:  
  Length   Class    Mode  
  66 character character
```

```
sample_type:  
borderline   cellline      tumor  
  6           2            58
```

```
histological_type:  
  Length   Class    Mode  
  66 character character
```

```
primarysite:  
ov  
66
```

```
summarygrade:  
high  low NA's  
  40    15   11
```

```
grade:  
  1    2    3 NA's  
  1   14   40   11
```

```
batch:  
  Length   Class    Mode  
  66 character character
```

```
uncurated_author_metadata:  
  Length   Class    Mode  
  66 character character
```

## Description

Gene expression profile was analyzed in 68 stage I and 15 borderline ovarian cancers to determine if different clinical features of stage I ovarian cancer such as histotype, grade, and survival are related to differential gene expression. Tumors were obtained directly at surgery and immediately frozen in liquid nitrogen until analysis. Glass arrays containing 16,000 genes were used in a dual-color assay labeling protocol. Unsupervised analysis identified eight major patient partitions, one of which was statistically associated to overall survival, grading, and histotype and another with grading and histotype. Supervised analysis allowed detection of gene profiles clearly associated to histotype or to degree of differentiation. No difference was found between borderline and grade 1 tumors. As to recurrence, a subset of genes able to differentiate relapsers from nonrelapsers was identified. Among these, cyclin E and minichromosome maintenance protein 5 were found particularly relevant, as their expression was inversely correlated to progression-free survival (P = 0.00033 and 0.017, respectively). Specific molecular signatures define different histotypes and prognosis of stage I ovarian cancer. Mucinous and clear cells histotypes can be distinguished from the others regardless of tumor grade. Cyclin E and minichromosome maintenance protein 5, whose expression was found previously to be related to a bad prognosis of advanced ovarian cancer, appear to be potential prognostic markers in stage I ovarian cancer too, independent of other pathologic and clinical variables.

## Usage

```
data( GSE8842_eset )
```

## Format

```
experimentData(eset):
  Experiment data
    Experimenter name: Marchini S, Mariani P, Chiorino G, Marrazzo E, Bonomi R, Fruscio R, Clivio L, Garbi A
    Laboratory: Marchini, D'Incalci 2008
    Contact information:
      Title: Analysis of gene expression in early-stage ovarian cancer.
      URL:
      PMIDs: 19047114

  Abstract: A 225 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
  platform_title:
    Agilent Human 1 cDNA Microarray (G4100A)
  platform_shorttitle:
    Agilent G4100A cDNA
  platform_summary:
    hgug4100a
  platform_manufacturer:
    Agilent
  platform_distribution:
    custom-commercial
  platform_accession:
```

```
GPL5689
platform_technology:
  spotted DNA/cDNA

Preprocessing: default
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A2M AADAC ... ZYX (6536 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

## Details

```
assayData: 6536 features, 83 samples
Platform type: hgug4100a
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records  n.max n.start  events  median 0.95LCL 0.95UCL
     83      83      83      15      NA      12      NA

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

alt_sample_name:
  Length     Class      Mode
  83 character character

sample_type:
borderline      tumor
  15          68

histological_type:
  Length     Class      Mode
  83 character character

primarysite:
ov
83

summarygrade:
high  low NA's
 35   33   15

summarystage:
early
83
```

```

tumorstage:
 1
83

substage:
 a  b  c
25  5  53

grade:
 1    2    3  NA's
13   20   35   15

age_at_initial_pathologic_diagnosis:
  Min. 1st Qu. Median   Mean 3rd Qu.   Max.
 21.00   43.00   50.00   51.25   61.00   87.00

recurrence_status:
norecurrence   recurrence
       62           21

days_to_death:
  Min. 1st Qu. Median   Mean 3rd Qu.   Max.
      0    1192    2248    2273    3048    5824

vital_status:
deceased   living
      15        68

uncurated_author_metadata:
  Length    Class     Mode
      83 character character

```

---

GSE9891\_eset

*Novel molecular subtypes of serous and endometrioid ovarian cancer linked to clinical outcome.*

---

### Description

The study aim to identify novel molecular subtypes of ovarian cancer by gene expression profiling with linkage to clinical and pathologic features. Microarray gene expression profiling was done on 285 serous and endometrioid tumors of the ovary, peritoneum, and fallopian tube. K-means clustering was applied to identify robust molecular subtypes. Statistical analysis identified differentially expressed genes, pathways, and gene ontologies. Laser capture microdissection, pathology review, and immunohistochemistry validated the array-based findings. Patient survival within k-means groups was evaluated using Cox proportional hazards models. Class prediction validated

k-means groups in an independent dataset. A semisupervised survival analysis of the array data was used to compare against unsupervised clustering results. Optimal clustering of array data identified six molecular subtypes. Two subtypes represented predominantly serous low malignant potential and low-grade endometrioid subtypes, respectively. The remaining four subtypes represented higher grade and advanced stage cancers of serous and endometrioid morphology. A novel subtype of high-grade serous cancers reflected a mesenchymal cell type, characterized by overexpression of N-cadherin and P-cadherin and low expression of differentiation markers, including CA125 and MUC1. A poor prognosis subtype was defined by a reactive stroma gene expression signature, correlating with extensive desmoplasia in such samples. A similar poor prognosis signature could be found using a semisupervised analysis. Each subtype displayed distinct levels and patterns of immune cell infiltration. Class prediction identified similar subtypes in an independent ovarian dataset with similar prognostic trends. Gene expression profiling identified molecular subtypes of ovarian cancer of biological and clinical importance.

## Usage

```
data( GSE9891_eset )
```

## Format

```
experimentData(eset):  
  Experiment data  
    Experimenter name: Tothill RW, Tinker AV, George J, Brown R, Fox SB, Lade S, Johnson DS, Trivett MK, Ete  
    Laboratory: Tothill, Bowtell 2008  
    Contact information:  
      Title: Novel molecular subtypes of serous and endometrioid ovarian cancer linked to clinical outcome.  
      URL:  
      PMIDs: 18698038  
  
    Abstract: A 243 word abstract is available. Use 'abstract' method.  
    Information is available on: preprocessing  
    notes:  
      platform_title:  
        [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array  
      platform_shorttitle:  
        Affymetrix HG-U133Plus2  
      platform_summary:  
        hgu133plus2  
      platform_manufacturer:  
        Affymetrix  
      platform_distribution:  
        commercial  
      platform_accession:  
        GPL570  
      platform_technology:  
        in situ oligonucleotide  
  
    Preprocessing: frma  
    featureData(eset):
```

```
An object of class 'AnnotatedDataFrame'
  featureNames: A1BG A1BG-AS1 ... ZZZ3 (19816 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

## Details

```
assayData: 19816 features, 285 samples
Platform type: hg133plus2
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

  7 observations deleted due to missingness
records  n.max n.start events  median 0.95LCL 0.95UCL
 278.00  278.00  278.00  113.00    3.95    3.53    5.01

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

alt_sample_name:
  Length     Class      Mode
  285 character character

sample_type:
borderline      tumor
      18        267

histological_type:
endo other    ser
  20      1    264

primarysite:
  ft other    ov
    8     34    243

arrayedsite:
  ft other    ov
    2     83    200

summarygrade:
high  low NA's
  163   116    6

summarystage:
early  late NA's
    42    240     3
```

tumorstage:  
1 2 3 4 NA's  
24 18 218 22 3

substage:  
a b c NA's  
26 19 212 28

grade:  
1 2 3 NA's  
19 97 163 6

age\_at\_initial\_pathologic\_diagnosis:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
22.00 53.00 59.00 59.62 68.00 80.00 3

pltx:  
n y NA's  
39 243 3

tax:  
n y NA's  
87 195 3

neo:  
n y NA's  
264 18 3

days\_to\_tumor\_recurrence:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
0.0 300.0 450.0 618.9 810.0 4980.0 10

recurrence\_status:  
norecurrence recurrence NA's  
94 188 3

days\_to\_death:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
0.0 547.5 855.0 955.1 1252.0 6420.0 7

vital\_status:  
deceased living NA's  
113 169 3

debulking:  
optimal suboptimal NA's  
160 88 37

```

batch:
  Length   Class   Mode
  285 character character

uncurated_author_metadata:
  Length   Class   Mode
  285 character character

```

---

PMID15897565_eset	<i>Patterns of gene expression that characterize long-term survival in advanced stage serous ovarian cancers.</i>
-------------------	---

---

## Description

A better understanding of the underlying biology of invasive serous ovarian cancer is critical for the development of early detection strategies and new therapeutics. The objective of this study was to define gene expression patterns associated with favorable survival. RNA from 65 serous ovarian cancers was analyzed using Affymetrix U133A microarrays. This included 54 stage III/IV cases (30 short-term survivors who lived <3 years and 24 long-term survivors who lived >7 years) and 11 stage I/II cases. Genes were screened on the basis of their level of and variability in expression, leaving 7,821 for use in developing a predictive model for survival. A composite predictive model was developed that combines Bayesian classification tree and multivariate discriminant models. Leave-one-out cross-validation was used to select and evaluate models. Patterns of genes were identified that distinguish short-term and long-term ovarian cancer survivors. The expression model developed for advanced stage disease classified all 11 early-stage ovarian cancers as long-term survivors. The MAL gene, which has been shown to confer resistance to cancer therapy, was most highly overexpressed in short-term survivors (3-fold compared with long-term survivors, and 29-fold compared with early-stage cases). These results suggest that gene expression patterns underlie differences in outcome, and an examination of the genes that provide this discrimination reveals that many are implicated in processes that define the malignant phenotype. Differences in survival of advanced ovarian cancers are reflected by distinct patterns of gene expression. This biological distinction is further emphasized by the finding that early-stage cancers share expression patterns with the advanced stage long-term survivors, suggesting a shared favorable biology.

## Usage

```
data( PMID15897565_eset )
```

## Format

```

experimentData(eset):
Experiment data
  Experimenter name: Berchuck A, Iversen ES, Lancaster JM, Pittman J, Luo J, Lee P, Murphy S, Dressman HK,
  Laboratory: Berchuck, Marks 2005
  Contact information:
  Title: Patterns of gene expression that characterize long-term survival in advanced stage serous ovarian

```

URL:  
PMIDs: 15897565

Abstract: A 258 word abstract is available. Use 'abstract' method.  
Information is available on: preprocessing  
notes:  
platform\_title:  
[HG-U133A] Affymetrix Human Genome U133A Array  
platform\_shorttitle:  
Affymetrix HG-U133A  
platform\_summary:  
hgu133a  
platform\_manufacturer:  
Affymetrix  
platform\_distribution:  
commercial  
platform\_accession:  
GPL96  
platform\_technology:  
in situ oligonucleotide  
warnings:  
These samples are a subset of PMID17290060.

Preprocessing: frma  
featureData(eset):  
An object of class 'AnnotatedDataFrame'  
featureNames: A1CF A2M ... ZZZ3 (13104 total)  
varLabels: probeset gene  
varMetadata: labelDescription

## Details

assayData: 13104 features, 63 samples  
Platform type: hgu133a  
Binary overall survival summary (definitions of long and short provided by study authors):

long	short	NA's
24	28	11

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

alt\_sample\_name:  
Min. 1st Qu. Median Mean 3rd Qu. Max.  
1761 1828 1907 2001 2032 2536

sample\_type:

```
tumor
63

histological_type:
ser
63

primarysite:
ov
63

summarygrade:
high  low  NA's
25    37    1

summarystage:
early  late
11     52

tumorstage:
1   2   3   4
1    4  48  4

grade:
1   2   3   4  NA's
2   35  24  1   1

age_at_initial_pathologic_diagnosis:
  Min. 1st Qu. Median   Mean 3rd Qu.   Max.
 33.00    52.50   59.00   59.21   67.00   79.00

os_binary:
long short  NA's
24    28    11

debulking:
optimal suboptimal      NA's
24        28        11

batch:
Length     Class     Mode
63 character character

uncurated_author_metadata:
Length     Class     Mode
63 character character
```

---

PMID17290060_eset	<i>An integrated genomic-based approach to individualized treatment of patients with advanced-stage ovarian cancer.</i>
-------------------	---

---

## Description

The purpose of this study was to develop an integrated genomic-based approach to personalized treatment of patients with advanced-stage ovarian cancer. We have used gene expression profiles to identify patients likely to be resistant to primary platinum-based chemotherapy and also to identify alternate targeted therapeutic options for patients with de novo platinum-resistant disease. A gene expression model that predicts response to platinum-based therapy was developed using a training set of 83 advanced-stage serous ovarian cancers and tested on a 36-sample external validation set. In parallel, expression signatures that define the status of oncogenic signaling pathways were evaluated in 119 primary ovarian cancers and 12 ovarian cancer cell lines. In an effort to increase chemotherapy sensitivity, pathways shown to be activated in platinum-resistant cancers were subject to targeted therapy in ovarian cancer cell lines. Gene expression profiles identified patients with ovarian cancer likely to be resistant to primary platinum-based chemotherapy with greater than 80% accuracy. In patients with platinum-resistant disease, we identified expression signatures consistent with activation of Src and Rb/E2F pathways, components of which were successfully targeted to increase response in ovarian cancer cell lines. We have defined a strategy for treatment of patients with advanced-stage ovarian cancer that uses therapeutic stratification based on predictions of response to chemotherapy, coupled with prediction of oncogenic pathway deregulation, as a method to direct the use of targeted agents.

## Usage

```
data( PMID17290060_eset )
```

## Format

```
experimentData(eset):
  Experiment data
  Experimenter name: Dressman HK, Berchuck A, Chan G, Zhai J, Bild A, Sayer R, Cragun J, Clarke J, Whitaker
  Laboratory: Dressman, Lancaster 2007
  Contact information:
  Title: An integrated genomic-based approach to individualized treatment of patients with advanced-stage
  URL:
  PMID: 17290060
```

Abstract: A 223 word abstract is available. Use 'abstract' method.

Information is available on: preprocessing

notes:

platform\_title:

[HG-U133A] Affymetrix Human Genome U133A Array

platform\_shorttitle:

Affymetrix HG-U133A

platform\_summary:

```
    hgu133a
platform_manufacturer:
  Affymetrix
platform_distribution:
  commercial
platform_accession:
  GPL96
platform_technology:
  in situ oligonucleotide
warnings:
  This paper has been retracted.

Preprocessing: frma
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1CF A2M ... ZZZ3 (13104 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

## Details

```
assayData: 13104 features, 117 samples
Platform type: hgu133a
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records    n.max n.start  events  median 0.95LCL 0.95UCL
117.00   117.00  117.00    67.00    5.26    2.79    7.48

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

alt_sample_name:
  Length     Class      Mode
  117 character character

sample_type:
tumor
  117

histological_type:
ser
  117

primarysite:
ov
  117
```

summarygrade:  
high low NA's  
57 57 3

summarystage:  
early late NA's  
1 115 1

tumorstage:  
2 3 4 NA's  
1 98 17 1

grade:  
1 2 3 4 NA's  
4 53 56 1 3

days\_to\_death:  
Min. 1st Qu. Median Mean 3rd Qu. Max.  
30 510 1020 1496 2220 5550

vital\_status:  
deceased living  
67 50

primary\_therapy\_outcome\_success:  
completeresponse progressivedisease  
85 32

debulking:  
optimal suboptimal  
63 54

batch:  
Length Class Mode  
117 character character

uncurated\_author\_metadata:  
Length Class Mode  
117 character character

## Description

Although few women with advanced serous ovarian cancer are cured, detection of the disease at an early stage is associated with a much higher likelihood of survival. We previously used gene expression array analysis to distinguish subsets of advanced cancers based on disease outcome. In the present study, we report on gene expression of early-stage cancers and validate our prognostic model for advanced-stage cancers. Frozen specimens from 39 stage I/II, 42 stage III/IV, and 20 low malignant potential cancers were obtained from four different sites. A linear discriminant model was used to predict survival based upon array data. We validated the late-stage survival model and show that three of the most differentially expressed genes continue to be predictive of outcome. Most early-stage cancers (38 of 39 invasive, 15 of 20 low malignant potential) were classified as long-term survivors (median probabilities 0.97 and 0.86). MAL, the most differentially expressed gene, was further validated at the protein level and found to be an independent predictor of poor survival in an unselected group of advanced serous cancers ( $P = 0.0004$ ). These data suggest that serous ovarian cancers detected at an early stage generally have a favorable underlying biology similar to advanced-stage cases that are long-term survivors. Conversely, most late-stage ovarian cancers seem to have a more virulent biology. This insight suggests that if screening approaches are to succeed it will be necessary to develop approaches that are able to detect these virulent cancers at an early stage.

## Usage

```
data( PMID19318476_eset )
```

## Format

```
experimentData(eset):  
  Experiment data  
    Experimenter name: Berchuck A, Iversen ES, Luo J, Clarke JP, Horne H, Levine DA, Boyd J, Alonso MA, Seco  
    Laboratory: Berchuck, Lancaster 2009  
    Contact information:  
      Title: Microarray analysis of early stage serous ovarian cancers shows profiles predictive of favorable  
      URL:  
      PMIDs: 19318476  
  
  Abstract: A 241 word abstract is available. Use 'abstract' method.  
  Information is available on: preprocessing  
  notes:  
  platform_title:  
    [HG-U133A] Affymetrix Human Genome U133A Array  
  platform_shorttitle:  
    Affymetrix HG-U133A  
  platform_summary:  
    hgu133a  
  platform_manufacturer:  
    Affymetrix  
  platform_distribution:  
    commercial  
  platform_accession:
```

```
GPL96
platform_technology:
  in situ oligonucleotide
warnings:
  These samples are a subset of PMID17290060.

Preprocessing: frma
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A1CF A2M ... ZZZ3 (13104 total)
  varLabels: probeset gene
  varMetadata: labelDescription
```

## Details

```
assayData: 13104 features, 42 samples
Platform type: hgu133a
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

records  n.max n.start  events  median 0.95LCL 0.95UCL
 42.00    42.00    42.00    22.00    2.79    2.30      NA
-----
Available sample meta-data:
-----
alt_sample_name:
  Length     Class      Mode
  42 character character

sample_type:
tumor
  42

histological_type:
ser
  42

summarygrade:
high  low NA's
  24   17    1

summarystage:
early  late NA's
  2     39    1

tumorstage:
```

```

1   2   3   4 NA's
1   1   29  10   1

substage:
a   b   c NA's
1   1   29  11

grade:
1   2   3 NA's
2   15  24   1

age_at_initial_pathologic_diagnosis:
Min. 1st Qu. Median   Mean 3rd Qu.   Max.   NA's
33.00 55.00 62.00 61.46 70.00 81.00       1

recurrence_status:
norecurrence   recurrence
6                  36

days_to_death:
Min. 1st Qu. Median   Mean 3rd Qu.   Max.
30.0 367.5 825.0 1105.0 1050.0 3420.0

vital_status:
deceased   living
22         20

debulking:
optimal suboptimal      NA's
20         21           1

batch:
Length   Class   Mode
42 character character

uncurated_author_metadata:
Length   Class   Mode
42 character character

```

---

TCGA.mirna.8x15kv2\_eset

*Integrated genomic analyses of ovarian carcinoma.*

---

## Description

A catalogue of molecular aberrations that cause ovarian cancer is critical for developing and deploying therapies that will improve patients' lives. The Cancer Genome Atlas project has analysed

messenger RNA expression, microRNA expression, promoter methylation and DNA copy number in 489 high-grade serous ovarian adenocarcinomas and the DNA sequences of exons from coding genes in 316 of these tumours. Here we report that high-grade serous ovarian cancer is characterized by TP53 mutations in almost all tumours (96%); low prevalence but statistically recurrent somatic mutations in nine further genes including NF1, BRCA1, BRCA2, RB1 and CDK12; 113 significant focal DNA copy number aberrations; and promoter methylation events involving 168 genes. Analyses delineated four ovarian cancer transcriptional subtypes, three microRNA subtypes, four promoter methylation subtypes and a transcriptional signature associated with survival duration, and shed new light on the impact that tumours with BRCA1/2 (BRCA1 or BRCA2) and CCNE1 aberrations have on survival. Pathway analyses suggested that homologous recombination is defective in about half of the tumours analysed, and that NOTCH and FOXM1 signalling are involved in serous ovarian cancer pathophysiology.

## Usage

```
data( TCGA.mirna.8x15kv2_eset )
```

## Format

```
experimentData(eset):
  Experiment data
    Experimenter name: Integrated genomic analyses of ovarian carcinoma. Nature 2011, 474:609-615.
    Laboratory: Cancer Genome Atlas Research Network 2011
    Contact information:
      Title: Integrated genomic analyses of ovarian carcinoma.
      URL:
      PMIDs: 21720365

  Abstract: A 179 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
    platform_title:
      [miRNA-8x15k2] Agilent Human miRNA G4470B
    platform_shorttitle:
      Agilent miRNA-8x15k2 G4470B
    platform_summary:
      NA
    platform_manufacturer:
      Agilent
    platform_distribution:
      commercial
    platform_accession:
      NA
    platform_technology:
      in situ oligonucleotide

  Preprocessing: default
  featureData(eset):
  An object of class 'AnnotatedDataFrame'
```

```
featureNames: ebv-miR-BART10 ebv-miR-BART10* ... kshv-miR-K12-9* (799
  total)
varLabels: probeset gene
varMetadata: labelDescription
```

## Details

```
assayData: 799 features, 554 samples
Platform type: NA
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

  10 observations deleted due to missingness
records  n.max n.start events  median 0.95LCL 0.95UCL
  544.00  544.00  544.00  286.00    3.71    3.42    4.03

-----
Available sample meta-data:
-----
alt_sample_name:
  Length     Class      Mode
  554 character character

unique_patient_ID:
  Length     Class      Mode
  554 character character

sample_type:
tumor
  554

histological_type:
ser
  554

primarysite:
other    ov
  4    550

summarygrade:
high   low  NA's
  474    68    12

summarystage:
early   late  NA's
  39    511     4
```

tumorstage:  
1 2 3 4 NA's  
16 23 426 85 4

substage:  
b c NA's  
31 434 89

grade:  
1 2 3 4 NA's  
6 62 473 1 12

age\_at\_initial\_pathologic\_diagnosis:  
Min. 1st Qu. Median Mean 3rd Qu. Max.  
26.00 51.00 59.00 59.81 69.00 89.00

pltx:  
n y NA's  
19 478 57

tax:  
n y NA's  
43 454 57

neo:  
n NA's  
497 57

days\_to\_tumor\_recurrence:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
8.0 235.2 436.0 618.7 797.0 5480.0 44

recurrence\_status:  
norecurrence recurrence  
268 286

days\_to\_death:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
8.0 346.0 867.5 997.7 1446.0 5480.0 10

vital\_status:  
deceased living NA's  
286 261 7

site\_of\_tumor\_first\_recurrence:  
locoregional locoregional\_plus\_metastatic  
145 3  
metastasis NA's

138

268

```

primary_therapy_outcome_success:
  completeresponse    partialresponse  progressivedisease    stabledisease
  308                  63              41                  30
  NA's
  112

debulking:
  optimal    suboptimal    NA's
  359        137          58

percent_normal_cells:
  Min. 1st Qu. Median    Mean 3rd Qu.    Max.    NA's
  0.000  0.000  0.000   2.375  0.000  55.000   10

percent_stromal_cells:
  Min. 1st Qu. Median    Mean 3rd Qu.    Max.    NA's
  0.00    5.00   10.00   12.78  19.00   70.00   16

percent_tumor_cells:
  Min. 1st Qu. Median    Mean 3rd Qu.    Max.    NA's
  0.00  75.00  85.00   80.72  90.00  100.00  13

uncurated_author_metadata:
  Length    Class    Mode
  554 character character

```

---

TCGA.RNASeqV2\_eset      *Integrated genomic analyses of ovarian carcinoma.*

---

## Description

A catalogue of molecular aberrations that cause ovarian cancer is critical for developing and deploying therapies that will improve patients' lives. The Cancer Genome Atlas project has analysed messenger RNA expression, microRNA expression, promoter methylation and DNA copy number in 489 high-grade serous ovarian adenocarcinomas and the DNA sequences of exons from coding genes in 316 of these tumours. Here we report that high-grade serous ovarian cancer is characterized by TP53 mutations in almost all tumours (96%); low prevalence but statistically recurrent somatic mutations in nine further genes including NF1, BRCA1, BRCA2, RB1 and CDK12; 113 significant focal DNA copy number aberrations; and promoter methylation events involving 168 genes. Analyses delineated four ovarian cancer transcriptional subtypes, three microRNA subtypes, four promoter methylation subtypes and a transcriptional signature associated with survival duration, and shed new light on the impact that tumours with BRCA1/2 (BRCA1 or BRCA2) and CCNE1 aberrations have on survival. Pathway analyses suggested that homologous recombination is defective in about half of the tumours analysed, and that NOTCH and FOXM1 signalling are involved in serous ovarian cancer pathophysiology.

**Usage**

```
data( TCGA.RNASeqV2_eset )
```

**Format**

```
experimentData(eset):
  Experiment data
    Experimenter name: Integrated genomic analyses of ovarian carcinoma. Nature 2011, 474:609-615.
    Laboratory: Cancer Genome Atlas Research Network 2011
    Contact information:
      Title: Integrated genomic analyses of ovarian carcinoma.
      URL:
      PMIDs: 21720365

    Abstract: A 179 word abstract is available. Use 'abstract' method.
    Information is available on: preprocessing
    notes:
      platform_title:
        [RNASeqV2] Illumina HiSeq RNA sequencing
      platform_shorttitle:
        Illumina HiSeq RNA sequencing
      platform_summary:
        NA
      platform_manufacturer:
        Illumina
      platform_distribution:
        sequencing
      platform_accession:
        NA
      platform_technology:
        RNA sequencing

    Preprocessing: default
  featureData(eset):
    An object of class 'AnnotatedDataFrame'
    featureNames: ? A1BG ... ZZZ3 (20502 total)
    varLabels: probeset gene
    varMetadata: labelDescription
```

**Details**

```
assayData: 20502 features, 261 samples
Platform type: NA
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

5 observations deleted due to missingness
```

```
records    n.max n.start  events  median 0.95LCL 0.95UCL
256.00   256.00  256.00  143.00    3.62    3.19    4.03

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

alt_sample_name:
  Length     Class      Mode
  261 character character

unique_patient_ID:
  Length     Class      Mode
  261 character character

sample_type:
tumor
  261

histological_type:
ser
  261

primarysite:
other    ov
  1    260

summarygrade:
high    low  NA's
226    29    6

summarystage:
early   late  NA's
18     242    1

tumorstage:
  2     3     4  NA's
18    209    33    1

substage:
  b     c  NA's
16    211    34

grade:
  1     2     3     4  NA's
  1    28    225    1     6

age_at_initial_pathologic_diagnosis:
```

```

      Min. 1st Qu. Median   Mean 3rd Qu.   Max.
34.00    51.00  58.00  58.84  66.00  87.00

pltx:
      n   y NA's
17  215  29

tax:
      n   y NA's
17  215  29

neo:
      n NA's
232  29

days_to_tumor_recurrence:
      Min. 1st Qu. Median   Mean 3rd Qu.   Max.   NA's
      9.0    225.0   426.5   585.3   755.0  5480.0    19

recurrence_status:
norecurrence   recurrence
      123        138

days_to_death:
      Min. 1st Qu. Median   Mean 3rd Qu.   Max.   NA's
      9.0    341.8   878.0  1018.0  1446.0  5480.0     5

vital_status:
deceased   living   NA's
      143        114        4

site_of_tumor_first_recurrence:
locoregional   metastasis   NA's
      82          56        123

primary_therapy_outcome_success:
completeresponse   partialresponse progressive disease   stable disease
      147                  30                  15                  15
      NA's
      54

debulking:
optimal   suboptimal   NA's
      171        60        30

percent_normal_cells:
      Min. 1st Qu. Median   Mean 3rd Qu.   Max.   NA's
      0.000    0.000    0.000   2.066   0.000  55.000     5

```

```

percent_stromal_cells:
  Min. 1st Qu. Median   Mean 3rd Qu.   Max.   NA's
  0.00    5.00 10.00  11.43 15.00  70.00      4

percent_tumor_cells:
  Min. 1st Qu. Median   Mean 3rd Qu.   Max.   NA's
  0.00  77.00 85.00  82.07 90.00 100.00      4

uncurated_author_metadata:
  Length    Class    Mode
  261 character character

```

---

TCGA\_eset

*Integrated genomic analyses of ovarian carcinoma.*

---

## Description

A catalogue of molecular aberrations that cause ovarian cancer is critical for developing and deploying therapies that will improve patients' lives. The Cancer Genome Atlas project has analysed messenger RNA expression, microRNA expression, promoter methylation and DNA copy number in 489 high-grade serous ovarian adenocarcinomas and the DNA sequences of exons from coding genes in 316 of these tumours. Here we report that high-grade serous ovarian cancer is characterized by TP53 mutations in almost all tumours (96%); low prevalence but statistically recurrent somatic mutations in nine further genes including NF1, BRCA1, BRCA2, RB1 and CDK12; 113 significant focal DNA copy number aberrations; and promoter methylation events involving 168 genes. Analyses delineated four ovarian cancer transcriptional subtypes, three microRNA subtypes, four promoter methylation subtypes and a transcriptional signature associated with survival duration, and shed new light on the impact that tumours with BRCA1/2 (BRCA1 or BRCA2) and CCNE1 aberrations have on survival. Pathway analyses suggested that homologous recombination is defective in about half of the tumours analysed, and that NOTCH and FOXM1 signalling are involved in serous ovarian cancer pathophysiology.

## Usage

```
data( TCGA_eset )
```

## Format

```

experimentData(eset):
Experiment data
  Experimenter name: Integrated genomic analyses of ovarian carcinoma. Nature 2011, 474:609-615.
  Laboratory: Cancer Genome Atlas Research Network 2011
  Contact information:
  Title: Integrated genomic analyses of ovarian carcinoma.
  URL:

```

PMIDs: 21720365

Abstract: A 179 word abstract is available. Use 'abstract' method.  
Information is available on: preprocessing  
notes:  
platform\_title:  
[HT\_HG-U133A] Affymetrix HT Human Genome U133A Array  
platform\_shorttitle:  
Affymetrix HT\_HG-U133A  
platform\_summary:  
hthgu133a  
platform\_manufacturer:  
Affymetrix  
platform\_distribution:  
commercial  
platform\_accession:  
GPL3921  
platform\_technology:  
in situ oligonucleotide  
warnings:  
The following samples are likely from specimens also used in GSE26712: TCG  
A.13.0725, TCGA.13.0885, TCGA.13.0887, TCGA.13.0890, TCGA.13.0886, TCGA.13  
.0714, TCGA.13.0727, TCGA.13.1817, TCGA.13.1499, TCGA.13.0883

Preprocessing: rma  
featureData(eset):  
An object of class 'AnnotatedDataFrame'  
featureNames: A1CF A2M ... ZZZ3 (13104 total)  
varLabels: probeset gene  
varMetadata: labelDescription

## Details

assayData: 13104 features, 578 samples  
Platform type: hthgu133a  
Overall survival time-to-event summary (in years):  
Call: survfit(formula = Surv(time, cens) ~ -1)  
  
21 observations deleted due to missingness  
records n.max n.start events median 0.95LCL 0.95UCL  
557.00 557.00 557.00 290.00 3.73 3.45 4.06

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

alt\_sample\_name:  
Length Class Mode

```
578 character character

unique_patient_ID:
  Length     Class      Mode
  578 character character

sample_type:
  healthy    tumor
    8        570

histological_type:
  ser NA's
  568    10

primarysite:
  other    ov  NA's
    4      564    10

summarygrade:
  high    low  NA's
  480    75    23

summarystage:
  early   late  NA's
    43    520    15

tumorstage:
  1      2      3      4  NA's
  16    27    436    84    15

substage:
  b      c  NA's
  31    448    99

grade:
  1      2      3      4  NA's
  6     69    479     1    23

age_at_initial_pathologic_diagnosis:
  Min. 1st Qu. Median     Mean 3rd Qu.  Max.  NA's
  26.00    51.00   59.00   59.70   68.25   89.00    10

pltx:
  n      y  NA's
  19    492    67

tax:
  n      y  NA's
```

43	468	67
----	-----	----

neo:

n	NA's
---	------

511	67
-----	----

days\_to\_tumor\_recurrence:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
8.0	238.2	443.5	623.7	812.0	5480.0	56

recurrence\_status:

norecurrence	recurrence
279	299

days\_to\_death:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
8	349	881	1010	1446	5480	21

vital\_status:

deceased	living	NA's
290	270	18

site\_of\_tumor\_first\_recurrence:

locoregional	locoregional_plus_metastatic
153	3
metastasis	NA's
143	279

primary\_therapy\_outcome\_success:

completeresponse	partialresponse	progressivedisease	stabledisease
318	65	41	30
NA's			
124			

debulking:

optimal	suboptimal	NA's
367	140	71

percent\_normal\_cells:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.000	0.000	0.000	2.385	0.000	55.000	19

percent\_stromal\_cells:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.00	5.00	10.00	12.85	20.00	70.00	25

percent\_tumor\_cells:

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

90

*TCGA\_eset*

0.00 75.00 85.00 80.64 90.00 100.00 22

batch:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
9.00	13.00	17.00	18.55	22.00	40.00	1

uncurated\_author\_metadata:

Length	Class	Mode
578	character	character

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