

Package ‘MetaGxOvarian’

May 7, 2024

Type Package

Title Transcriptomic Ovarian Cancer Datasets

Version 1.24.0

Date `r Sys.date()`

Description A collection of Ovarian Cancer Transcriptomic Datasets that are part of the MetaGxData package compendium.

License Artistic-2.0

Depends Biobase, AnnotationHub, ExperimentHub, SummarizedExperiment, R
(>= 3.6.0)

Imports stats, lattice, impute

Suggests testthat, xtable, rmarkdown, knitr, BiocStyle, markdown

Encoding UTF-8

VignetteBuilder knitr

NeedsCompilation no

biocViews ExpressionData, ExperimentHub, CancerData,
Homo_sapiens_Data, ArrayExpress, GEO, NCI, MicroarrayData,
ExperimentData

LazyData yes

RoxygenNote 7.1.1

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attention

days_to_death

Description

This is a note to inform package users that the `days_to_death` variable is also valid for living patients. In this case, the value in `days_to_death` is the number of days since the last follow-up appointment.

Format

A field included in various data files in the this package.

duplicates	<i>a list containing the names of patients that are believed to be duplicated across datasets</i>
------------	---

Description

The object is a list where each element is a patient ID that is believed to be a duplicate of a patient in another dataset. Patients are designated as duplicated if they have Spearman correlations greater than or equal to 0.98 with other patient expression profiles

Format

A list with 130 elements, each of which is a patient ID.

E.MTAB.386	<i>Angiogenic mRNA and microRNA gene expression signature predicts a novel subtype of serous ovarian cancer.</i>
------------	--

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.

Format

```
experimentData (eset) :
Experiment data
  Experimenter name: Bentink S, Haibe-Kains B, Risch T, Fan J-B, Hirsch MS, Holton
  Laboratory: Bentink, Matulonis 2012
  Contact information:
  Title: Angiogenic mRNA and microRNA gene expression signature predicts a novel su
```

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

version:

2015-09-22 19:06:44

featureData(eset):

An object of class 'AnnotatedDataFrame'

featureNames: ILMN_1343291 ILMN_1651228 ... ILMN_1815951 (12449
total)

varLabels: probeset gene EntrezGene.ID best_probe

varMetadata: labelDescription

Details

assayData: 12449 features, 129 samples

Platform type:

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

Call: survfit(formula = Surv(time, cens) ~ -1)

	n	events	median	0.95LCL	0.95UCL
	129.00	73.00	3.51	2.68	4.13

Available sample meta-data:

unique_patient_ID:

DFCI.1	DFCI.10	DFCI.100	DFCI.101	DFCI.102	DFCI.103	DFCI.104	DFCI.105
1	1	1	1	1	1	1	1
DFCI.106	DFCI.107	DFCI.108	DFCI.109	DFCI.11	DFCI.110	DFCI.111	DFCI.112
1	1	1	1	1	1	1	1
DFCI.113	DFCI.114	DFCI.115	DFCI.116	DFCI.117	DFCI.118	DFCI.119	DFCI.12

1	1	1	1	1	1	1	1
DFCI.120	DFCI.121	DFCI.122	DFCI.123	DFCI.124	DFCI.125	DFCI.126	DFCI.127
1	1	1	1	1	1	1	1
DFCI.128	DFCI.129	DFCI.13	DFCI.130	DFCI.131	DFCI.132	DFCI.14	DFCI.15
1	1	1	1	1	1	1	1
DFCI.16	DFCI.17	DFCI.18	DFCI.19	DFCI.2	DFCI.20	DFCI.21	DFCI.22
1	1	1	1	1	1	1	1
DFCI.23	DFCI.24	DFCI.25	DFCI.26	DFCI.27	DFCI.28	DFCI.29	DFCI.3
1	1	1	1	1	1	1	1
DFCI.30	DFCI.31	DFCI.32	DFCI.33	DFCI.34	DFCI.35	DFCI.36	DFCI.37
1	1	1	1	1	1	1	1
DFCI.38	DFCI.39	DFCI.4	DFCI.40	DFCI.41	DFCI.42	DFCI.44	DFCI.45
1	1	1	1	1	1	1	1
DFCI.46	DFCI.47	DFCI.48	DFCI.49	DFCI.50	DFCI.51	DFCI.52	DFCI.53
1	1	1	1	1	1	1	1
DFCI.54	DFCI.55	DFCI.56	DFCI.57	DFCI.58	DFCI.59	DFCI.6	DFCI.60
1	1	1	1	1	1	1	1
DFCI.61	DFCI.62	DFCI.63	DFCI.64	DFCI.65	DFCI.66	DFCI.67	DFCI.68
1	1	1	1	1	1	1	1
DFCI.69	DFCI.7	DFCI.70	(Other)				
1	1	1	30				

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:

Source.Name: DFCI-100///CH

Source.Name: DFCI-

Source.Name: DFCI-1

Source.Name: DFCI-103///

Source.Name: DFCI-104///C

Source.Name: DFCI-105///CH

Source.Name: DFCI-106///C

Source.Name: DFCI-107///C

Source.Name: DFCI-108///

Source.Name: DFCI-109///CH

Source.Name: DFCI-10/

Source.Name: DFCI-110//

Source.Name: DFCI-111///CH

Source.Name: DFCI-112///

Source.Name: DFCI-113///

Source.Name: DFCI-111
Source.Name: DFCI-115///C
Source.Name: DFCI-116///CH
Source.Name: DFCI-117//
Source.Name: DFCI-118///Characteristics.Age.: Age <has_measurement <Measurement <ha
Source.Name: DFCI-119///
Source.Name: DFCI-11///
Source.Name: DFCI-120///Characteristics.Age.: Age <has_measurement <Measurement
Source.Name: DFCI-121//
Source.Name: DFCI-12
Source.Name: DFCI-123///C
Source.Name: DFCI-124//
Source.Name: DFCI-125/
Source.Name: DFCI-1
Source.Name: DFCI-127///Characteristics.Age.: Age <has_measurement <Measureme
Source.Name: DFCI-128//
Source.Name: DFCI-129///Characteristics.Age.: Age <has_measurement <Measurement
Source.Name: DFCI-12//
Source.Name: DFCI-130///Characteristics.Age.: Age <has_measurement <Measurement <ha
Source.Name: DFCI-131///Characteristics.Age.: Age <has_measurement <Measureme
Source.Name: DFCI-132///Characteristics.Age.: Age <has_measurement <Measurement <h
Source.Name: DFCI-13//
Source.Name: DFCI-14/
Source.Name: DFCI-

Source.Name: DFCI-17//
Source.Name: DFCI-18//
Source.Name: DFCI-19//
Source.Name: DFCI-20//
Source.Name: DFCI-21//
Source.Name: DFCI-22///Characteristics.Age.: Age <has_measurement <Measurement
Source.Name: DFCI-23//
Source.Name: DFCI-24///CH
Source.Name: DFCI-25//
Source.Name: DFCI-26//
Source.Name: DFCI-27//
Source.Name: DFCI-28//
Source.Name: DFCI-29//
Source.Name: DFCI-30//
Source.Name: DFCI-31//
Source.Name: DFCI-32//
Source.Name: DFCI-33//
Source.Name: DFCI-34//
Source.Name: DFCI-35//
Source.Name: DFCI-36//
Source.Name: DFCI-37//

Source.Name: DFCI-38//

Source.Name: DFCI-39//

Source.Name: DFCI-

Source.Name: DFCI-40//

Source.Name: DFCI-41//

Source.Name: DFCI-42//

Source.Name: DFCI-44//

Source.Name: DFCI-

Source.Name: DFCI-46//

Source.Name: DFCI-47//

Source.Name: DFCI-

Source.Name: DFCI-49

Source.Name: DFCI-

Source.Name: DFCI-50//

Source.Name: DFCI-51//

Source.Name: DFCI-52//

Source.Name: DFCI-53//

Source.Name: DFCI-54//

Source.Name: DFCI-55//

Source.Name: DFCI-56//

Source.Name: DFCI-57//

Source.Name: DFCI-58//

Source.Name: DFCI-59

Source.Name: DFCI-60

Source.Name: DFCI-62///Characteristics.Age.: Age <has_measurement <Measurement
Source.Name: DFCI-62///Characteristics.Age.: Age <has_measurement <Measurement
Source.Name: DFCI-64
Source.Name: DFCI-65///
Source.Name: DFCI-65///
Source.Name: DFCI-68///
Source.Name: DFCI-69///
Source.Name: DFCI-70///
Source.Name: DFCI-71

Value

An expression set

GSE12418

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.

Format

```

experimentData(eset):
Experiment data
  Experimenter name: Partheen K, Levan K, Osterberg L, Horvath G.Expression analysis
  Laboratory: Partheen, Horvath 2006
  Contact information:
  Title: Expression analysis of stage III serous ovarian adenocarcinoma distinguish
  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
  version:
    2015-09-22 19:07:14

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 28 29 ... 29999 (11304 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

Details

```

assayData: 11304 features, 54 samples
Platform type:
-----
Available sample meta-data:
-----

```

alt_sample_name:

1035LA0	1047LB	1059LB0	1177DB	1178LB0	1180DB	1186DB0	123DC	1242LC0	1274LC
1	1	1	1	1	1	1	1	1	1
134LC	1426LB	1487DB	1528DC	1538DC	1567DB	1568DC	1574LC0	164DC	1658DC
1	1	1	1	1	1	1	1	1	1
1760LB	1805DB	193DC	198DC	202DC	211DC	26DC	272DC	405LB	436DC
1	1	1	1	1	1	1	1	1	1
452DC	454LC	45LA0	462DB	46LB0	47DC	480DC0	489DC	505DB	541DC
1	1	1	1	1	1	1	1	1	1
559DC	563LA	626DC	662DC	719DC	742LC0	755LC	759DC	76DC	789DC
1	1	1	1	1	1	1	1	1	1
83LC	918DB0	988LC0	99LC0						
1	1	1	1						

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:

title: 1035LA0///geo_accession: GSM311973///status: Public on Aug 12 2008///submitter: NCBI

title: 1047LB///geo_accession: GSM311974///status: Public on Aug 12 2008///submitter: NCBI

title: 1059LB0///geo_accession: GSM311975///status: Public on Aug 12 2008///submitter: NCBI

title: 1177DB///geo_accession: GSM311976///status: Public on Aug 12 2008///submitter: NCBI

title: 1178LB0///geo_accession: GSM311977///status: Public on Aug 12 2008///submitter: NCBI

title: 1180DB///geo_accession: GSM311978///status: Public on Aug 12 2008///submitter: NCBI

title: 1186DB0///geo_accession: GSM311979///status: Public on Aug 12 2008///submitter: NCBI

title: 123DC///geo_accession: GSM311945///status: Public on Aug 12 2008///submitter: NCBI

title: 1242LC0///geo_accession: GSM311980///status: Public on Aug 12 2008///submitter: NCBI

title: 1274LC///geo_accession: GSM311981///status: Public on Aug 12 2008///submitter: NCBI

title: 134LC///geo_accession: GSM311946///status: Public on Aug 12 2008///submitter: NCBI

title: 1426LB///geo_accession: GSM311982///status: Public on Aug 12 2008///submitter: NCBI

title: 1487DB///geo_accession: GSM311983///status: Public on Aug 12 2008///submitter: NCBI

title: 1528DC///geo_accession: GSM311984///status: Public on Aug 12 2008///submitter: NCBI

title: 1538DC///geo_accession: GSM311985///status: Public on Aug 12 2008///submitter: NCBI

title: 1567DB///geo_accession: GSM311986///status: Public on Aug 12 2008///submitter: NCBI

title: 1568DC///geo_accession: GSM311987///status: Public on Aug 12 2008///submitter: NCBI

title: 1574LC0///geo_accession: GSM311988///status: Public on Aug 12 2008///submitter: NCBI

title: 164DC///geo_accession: GSM311947///status: Public on Aug 12 2008///submitter: NCBI

title: 1658DC///geo_accession: GSM311989///status: Public on Aug 12 2008///submitter: NCBI

title: 1760LB///geo_accession: GSM311990///status: Public on Aug 12 2008///submitter: NCBI

title: 1805DB///geo_accession: GSM311991///status: Public on Aug 12 2008///submitter: NCBI

title: 193DC///geo_accession: GSM311948///status: Public on Aug 12 2008///submitter: NCBI

title: 198DC///geo_accession: GSM311949///status: Public on Aug 12 2008///submitter: NCBI

title: 202DC///geo_accession: GSM311950///status: Public on Aug 12 2008///submitter: NCBI

title: 211DC///geo_accession: GSM311951///status: Public on Aug 12 2008///submitter: NCBI

title: 26DC///geo_accession: GSM311938///status: Public on Aug 12 2008///submitter: NCBI

title: 272DC///geo_accession: GSM311952///status: Public on Aug 12 2008///submitter: NCBI

title: 405LB///geo_accession: GSM311953///status: Public on Aug 12 2008///submitter: NCBI

title: 436DC///geo_accession: GSM311954///status: Public on Aug 12 2008///submitter: NCBI

title: 452DC///geo_accession: GSM311955///status: Public on Aug 12 2008///submitter: NCBI

title: 454LC///geo_accession: GSM311956///status: Public on Aug 12 2008///submitter: NCBI

title: 45LA0///geo_accession: GSM311939///status: Public on Aug 12 2008///submitter: NCBI

title: 462DB///geo_accession: GSM311957///status: Public on Aug 12 2008///submitter: NCBI

title: 46LB0///geo_accession: GSM311940///status: Public on Aug 12 2008///submitter: NCBI

title: 47DC///geo_accession: GSM311941///status: Public on Aug 12 2008///submitter: NCBI

title: 480DC0///geo_accession: GSM311958///status: Public on Aug 12 2008///submitter: NCBI

title: 489DC///geo_accession: GSM311959///status: Public on Aug 12 2008///submitter: NCBI

title: 505DB///geo_accession: GSM311960///status: Public on Aug 12 2008///submitter: NCBI

title: 541DC///geo_accession: GSM311961///status: Public on Aug 12 2008///submitter: NCBI

title: 559DC///geo_accession: GSM311962///status: Public on Aug 12 2008///submitter: NCBI

title: 563LA///geo_accession: GSM311963///status: Public on Aug 12 2008///submitter: NCBI

title: 626DC///geo_accession: GSM311964///status: Public on Aug 12 2008///submitter: NCBI

title: 662DC///geo_accession: GSM311965///status: Public on Aug 12 2008///submitter: NCBI

title: 719DC///geo_accession: GSM311966///status: Public on Aug 12 2008///submitter: nci-geopharm
 title: 742LC0///geo_accession: GSM311967///status: Public on Aug 12 2008///submitter: nci-geopharm
 title: 755LC///geo_accession: GSM311968///status: Public on Aug 12 2008///submitter: nci-geopharm
 title: 759DC///geo_accession: GSM311969///status: Public on Aug 12 2008///submitter: nci-geopharm
 title: 76DC///geo_accession: GSM311942///status: Public on Aug 12 2008///submitter: nci-geopharm
 title: 789DC///geo_accession: GSM311970///status: Public on Aug 12 2008///submitter: nci-geopharm
 title: 83LC///geo_accession: GSM311943///status: Public on Aug 12 2008///submitter: nci-geopharm
 title: 918DB0///geo_accession: GSM311971///status: Public on Aug 12 2008///submitter: nci-geopharm
 title: 988LC0///geo_accession: GSM311972///status: Public on Aug 12 2008///submitter: nci-geopharm
 title: 99LC0///geo_accession: GSM311944///status: Public on Aug 12 2008///submitter: nci-geopharm

Value

An expression set

GSE12470

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

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.

Format

```

experimentData(eset):
Experiment data
  Experimenter name: Yoshihara K, Tajima A, Komata D, Yamamoto T, Kodama S, Fujiwara
  Laboratory: Yoshihara, Tanaka 2009
  Contact information:
  Title: Gene expression profiling of advanced-stage serous ovarian cancers distinguished by ZEB2
  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
  version:
    2015-09-22 19:08:17

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 3 5 ... 22571 (15999 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

Details

```

assayData: 15999 features, 53 samples
Platform type:
-----
Available sample meta-data:
-----

```



```

alt_sample_name:
Advanced serous ovarian cancer 10 Advanced serous ovarian cancer 11
1 1
Advanced serous ovarian cancer 15 Advanced serous ovarian cancer 17
1 1
Advanced serous ovarian cancer 18 Advanced serous ovarian cancer 2
1 1
Advanced serous ovarian cancer 20 Advanced serous ovarian cancer 23
1 1
Advanced serous ovarian cancer 24 Advanced serous ovarian cancer 25
1 1
Advanced serous ovarian cancer 27 Advanced serous ovarian cancer 36
1 1
Advanced serous ovarian cancer 37 Advanced serous ovarian cancer 38
1 1
Advanced serous ovarian cancer 39 Advanced serous ovarian cancer 42
1 1
Advanced serous ovarian cancer 43 Advanced serous ovarian cancer 45
1 1
Advanced serous ovarian cancer 46 Advanced serous ovarian cancer 49
1 1
Advanced serous ovarian cancer 50 Advanced serous ovarian cancer 51
1 1
Advanced serous ovarian cancer 52 Advanced serous ovarian cancer 53
1 1
Advanced serous ovarian cancer 54 Advanced serous ovarian cancer 55
1 1
Advanced serous ovarian cancer 56 Advanced serous ovarian cancer 57
1 1
Advanced serous ovarian cancer 58 Advanced serous ovarian cancer 6
1 1
Advanced serous ovarian cancer 60 Advanced serous ovarian cancer 61
1 1
Advanced serous ovarian cancer 62 Advanced serous ovarian cancer 64
1 1
Advanced serous ovarian cancer 7 Early serous ovarian cancer 28
1 1
Early serous ovarian cancer 32 Early serous ovarian cancer 33
1 1
Early serous ovarian cancer 35 Early serous ovarian cancer 5
1 1
Early serous ovarian cancer 65 Early serous ovarian cancer 8
1 1
Early serous ovarian cancer 9 Peritoneum normal 12
1 1
Peritoneum normal 15 Peritoneum normal 16
1 1

```

Peritoneum normal	18	Peritoneum normal	21
	1		1
Peritoneum normal	23	Peritoneum normal	3
	1		1
Peritoneum normal	30	Peritoneum normal	4
	1		1
Peritoneum normal	7		
	1		

```
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:
```

```
  title: Advanced serous ovarian cancer 10///geo_accession: GSM312155///status: Pub
  title: Advanced serous ovarian cancer 11///geo_accession: GSM312141///status: Pub
  title: Advanced serous ovarian cancer 15///geo_accession: GSM312156///status: Pub
  title: Advanced serous ovarian cancer 17///geo_accession: GSM312142///status: Pub
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 title: Advanced serous ovarian cancer 7///geo_accession: GSM312140///status: E
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 title: Early serous ovarian cancer 32///geo_accession: GSM312181///status: E
 title: Early serous ovarian cancer 33///geo_accession: GSM312182///status: E
 title: Early serous ovarian cancer 35///geo_accession: GSM312183///status: E
 title: Early serous ovarian cancer 5///geo_accession: GSM312176///status: E
 title: Early serous ovarian cancer 65///geo_accession: GSM312185///status: E
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 title: Early serous ovarian cancer 9///geo_accession: GSM312179///status: E
 title: Peritoneum normal 12///geo_accession: GSM312184///status: E
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 title: Peritoneum normal 23///geo_accession: GSM312190///status: E
 title: Peritoneum normal 30///geo_accession: GSM312191///status: E
 title: Peritoneum normal 3///geo_accession: GSM312192///status: E
 title: Peritoneum normal 4///geo_accession: GSM312193///status: E
 title: Peritoneum normal 7///geo_accession: GSM312194///status: E

duplicates:

GSE12470.GSE12470_GSM312135	GSE12470.GSE12470_GSM312136
1	1
GSE12470.GSE12470_GSM312145	GSE12470.GSE12470_GSM312146
1	1
NA's	
49	

Value

An expression set

GSE13876

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.

Format

```
experimentData (eset) :
```

```
Experiment data
```

```
  Experimenter name: Crijns AP, Fehrmann RS, de Jong S, Gerbens F, Meersma GJ, Klip
```

```
  Laboratory: Crijns, van der Zee 2009
```

```
  Contact information:
```

Title: Survival-related profile, pathways, and transcription factors in ovarian c
 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
version:
  2015-09-22 19:11:43
```

```
featureData(eset):
An object of class 'AnnotatedDataFrame'
featureNames: 1 2 ... 37629 (20939 total)
varLabels: probeset gene EntrezGene.ID best_probe
varMetadata: labelDescription
```

Details

```
assayData: 20939 features, 157 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)
```

	n	events	median	0.95LCL	0.95UCL
	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:

title: Ovarian tumor sample 105 / Ovarian tumor sample 106///geo_accession:

title: Ovarian tumor sample 10 / Ovarian tumor sample 11///geo_accession:

title: Ovarian tumor sample 111 / Ovarian tumor sample 112///geo_accession:

title: Ovarian tumor sample 115 / Ovarian tumor sample 117///geo_accession:

title: Ovarian tumor sample 126 / Ovarian tumor sample 127///geo_accession:

title: Ovarian tumor sample 13 / Ovarian tumor sample 14///geo_accession:

title: Ovarian tumor sample 165 / Ovarian tumor sample 166///geo_accession:

title: Ovarian tumor sample 193 / Ovarian tumor sample 194///geo_accession:

title: Ovarian tumor sample 230 / Ovarian tumor sample 231///geo_accession:

title: Ovarian tumor sample 237 / Ovarian tumor sample 238///geo_accession:

title: Ovarian tumor sample 250 / Ovarian tumor sample 251///geo_accession: GSM4058

title: Ovarian tumor sample 258 / Ovarian tumor sample 259///geo_accession:

title: Ovarian tumor sample 273 / Ovarian tumor sample 274///geo_accession: G

title: Ovarian tumor sample 284 / Ovarian tumor sample 285///geo_accession: G

title: Ovarian tumor sample 313 / Ovarian tumor sample 314///geo_accession: G

Value

An expression set

GSE14764

A prognostic gene expression index in ovarian cancer - validation across different independent data sets.

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.

Format

```
experimentData(eset):
```

```
Experiment data
```

```
  Experimenter name: Denkert C, Budczies J, Darb-Esfahani S, Gy??rffy B et al. A pr
```

```
  Laboratory: Denkert, Lage 2009
```

```
  Contact information:
```

```
  Title: A prognostic gene expression index in ovarian cancer - validation across c
```

```
  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
version:
  2015-09-22 19:13:08

```

```

featureData(eset):
An object of class 'AnnotatedDataFrame'
 featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
 (20967 total)
 varLabels: probeset gene EntrezGene.ID best_probe
 varMetadata: labelDescription

```

Details

```

assayData: 20967 features, 80 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

```

n	events	median	0.95LCL	0.95UCL
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:
  clearcell          endo          mix          other
           2           6           1           2
  ser undifferentiated
           68           1

```

```

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:

2004-09-29	2004-09-30	2004-10-01	2005-01-21	2005-01-25	2005-01-26	2005-01-28
1	2	6	4	7	8	10
2005-03-02	2006-07-26	2006-07-27	2006-07-28	2006-08-11	2006-08-18	2006-08-19
6	4	6	4	10	3	4
2006-08-21						
5						

uncurated_author_metadata:

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title: ovarian cancer: 09///geo_accession: GSM368669///status: Publi

```

duplicates:

```

GSE14764.GSE14764_GSM368667  GSE14764.GSE14764_GSM368668
                                1                               1
                                NA's
                                78

```

Value

An expression set

GSE17260

Gene expression profile for predicting survival in advanced-stage serous ovarian cancer across two independent datasets.

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.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Yoshihara K, Tajima A, Yahata T, Kodama S, Fujiwara H, Suzuki
  Laboratory: Yoshihara, Tanaka 2010
  Contact information:
  Title: Gene expression profile for predicting survival in advanced-stage serous o
  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
  version:
    2015-09-22 19:16:49
```

```
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A_23_P100001 A_23_P100011 ... A_32_P99902 (30936 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 30936 features, 110 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)
```

	n	events	median	0.95LCL	0.95UCL
	110.00	46.00	4.44	4.03	NA

 Available sample meta-data:

alt_sample_name:

Serous ovarian cancer 10	Serous ovarian cancer 100	Serous ovarian cancer 104
1	1	1
Serous ovarian cancer 106	Serous ovarian cancer 107	Serous ovarian cancer 108
1	1	1
Serous ovarian cancer 109	Serous ovarian cancer 11	Serous ovarian cancer 110
1	1	1
Serous ovarian cancer 111	Serous ovarian cancer 112	Serous ovarian cancer 113
1	1	1
Serous ovarian cancer 114	Serous ovarian cancer 115	Serous ovarian cancer 116
1	1	1
Serous ovarian cancer 117	Serous ovarian cancer 118	Serous ovarian cancer 119
1	1	1
Serous ovarian cancer 12	Serous ovarian cancer 120	Serous ovarian cancer 122
1	1	1
Serous ovarian cancer 123	Serous ovarian cancer 127	Serous ovarian cancer 129
1	1	1
Serous ovarian cancer 130	Serous ovarian cancer 131	Serous ovarian cancer 132
1	1	1
Serous ovarian cancer 134	Serous ovarian cancer 136	Serous ovarian cancer 137
1	1	1
Serous ovarian cancer 139	Serous ovarian cancer 140	Serous ovarian cancer 143
1	1	1
Serous ovarian cancer 144	Serous ovarian cancer 145	Serous ovarian cancer 146
1	1	1
Serous ovarian cancer 148	Serous ovarian cancer 149	Serous ovarian cancer 15
1	1	1
Serous ovarian cancer 150	Serous ovarian cancer 151	Serous ovarian cancer 154
1	1	1
Serous ovarian cancer 156	Serous ovarian cancer 157	Serous ovarian cancer 16
1	1	1
Serous ovarian cancer 160	Serous ovarian cancer 17	Serous ovarian cancer 171
1	1	1
Serous ovarian cancer 172	Serous ovarian cancer 173	Serous ovarian cancer 174
1	1	1
Serous ovarian cancer 176	Serous ovarian cancer 178	Serous ovarian cancer 18
1	1	1
Serous ovarian cancer 182	Serous ovarian cancer 183	Serous ovarian cancer 184
1	1	1
Serous ovarian cancer 185	Serous ovarian cancer 186	Serous ovarian cancer 2
1	1	1
Serous ovarian cancer 20	Serous ovarian cancer 22	Serous ovarian cancer 23
1	1	1
Serous ovarian cancer 25	Serous ovarian cancer 27	Serous ovarian cancer 31

	1		1		1
Serous ovarian cancer	36	Serous ovarian cancer	37	Serous ovarian cancer	38
	1		1		1
Serous ovarian cancer	4	Serous ovarian cancer	41	Serous ovarian cancer	42
	1		1		1
Serous ovarian cancer	43	Serous ovarian cancer	44	Serous ovarian cancer	45
	1		1		1
Serous ovarian cancer	49	Serous ovarian cancer	50	Serous ovarian cancer	51
	1		1		1
Serous ovarian cancer	52	Serous ovarian cancer	53	Serous ovarian cancer	54
	1		1		1
Serous ovarian cancer	55	Serous ovarian cancer	56	Serous ovarian cancer	57
	1		1		1
Serous ovarian cancer	58	Serous ovarian cancer	6	Serous ovarian cancer	60
	1		1		1
Serous ovarian cancer	61	Serous ovarian cancer	62	Serous ovarian cancer	64
	1		1		1
Serous ovarian cancer	66	Serous ovarian cancer	67	Serous ovarian cancer	68
	1		1		1
Serous ovarian cancer	69	Serous ovarian cancer	7	Serous ovarian cancer	72
	1		1		1
Serous ovarian cancer	77	Serous ovarian cancer	79	Serous ovarian cancer	80
	1		1		1
		(Other)			
	11				

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:

title: Serous ovarian cancer 100///geo_accession: GSM43

title: Serous ovarian cancer 104///geo_accession: GSM432222

title: Serous ovarian cancer 106///geo_accession: GSM432223///status: Public on Mar

title: Serous ovarian cancer 107///geo_accession: GSM432224

title: Serous ovarian cancer 108///geo_accession: GSM432225///status: Public on

title: Serous ovarian cancer 109///geo_accession: GSM432226///status: Public on Mar

title: Serous ovarian cancer 10///geo_accession: GSM43

title: Serous ovarian cancer 110///geo_accession: GSM432228///status: Public on Mar

title: Serous ovarian cancer 111///geo_accession: GSM432229///status: Public on Mar

title: Serous ovarian cancer 112///geo_accession: GSM43

title: Serous ovarian cancer 113///geo_accession: GSM432231

title: Serous ovarian cancer 114///geo_accession: GSM43223

title: Serous ovarian cancer 115///geo_accession: GSM432233

title: Serous ovarian cancer 116///geo_accession: GSM432234

title: Serous ovarian cancer 117///geo_accession: GSM43

title: Serous ovarian cancer 118///geo_accession: GSM43223

title: Serous ovarian cancer 119///geo_accession: GSM43

title: Serous ovarian cancer 11///geo_accession: GSM43

title: Serous ovarian cancer 120///geo_accession: GSM432

title: Serous ovarian cancer 122///geo_accession: GSM43224

title: Serous ovarian cancer 123///geo_accession: GSM432242

title: Serous ovarian cancer 127///geo_accession: GSM432243

title: Serous ovarian cancer 129///geo_accession: GSM43

title: Serous ovarian cancer 12///geo_accession: GSM4

title: Serous ovarian cancer 130///geo_accession: GSM432245

title: Serous ovarian cancer 131///geo_accession: GSM43

title: Serous ovarian cancer 132///geo_accession: GSM43

title: Serous ovarian cancer 134///geo_accession: GSM43

title: Serous ovarian cancer 136///geo_accession: GSM43

title: Serous ovarian cancer 182///geo_accession: GSM432276

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title: Serous ovarian cancer 187///geo_accession: GSM432276

title: Serous ovarian cancer 20///geo_accession: GSM432276

title: Serous ovarian cancer 22///geo_accession: GSM432282

title: Serous ovarian cancer 23///geo_accession: GSM432282

title: Serous ovarian cancer 25///geo_accession: GSM432282

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title: Serous ovarian cancer 28///geo_accession: GSM432280

title: Serous ovarian cancer 31///geo_accession: GSM432280

title: Serous ovarian cancer 36///geo_accession: GSM432280

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title: Serous ovarian cancer 38///geo_accession: GSM432280

title: Serous ovarian cancer 41///geo_accession: GSM432280

title: Serous ovarian cancer 42///geo_accession: GSM432292

title: Serous ovarian cancer 43///geo_accession: GSM432292

title: Serous ovarian cancer 44///geo_accession: GSM432292

title: Serous ovarian cancer 45///geo_accession: GSM432292

title: Serous ovarian cancer 49///geo_accession: GSM432296

title: Serous ovarian cancer 49///geo_accession: GSM432296

title: Serous ovarian cancer 50///geo_accession: GSM432296

title: Serous ovarian cancer 51///geo_accession: GSM432298
title: Serous ovarian cancer 52///geo_accession: GSM432299
title: Serous ovarian cancer 53///geo_accession: GSM432300
title: Serous ovarian cancer 54///geo_accession: GSM432301
title: Serous ovarian cancer 55///geo_accession: GSM432302
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title: Serous ovarian cancer 64///geo_accession: GSM432311
title: Serous ovarian cancer 66///geo_accession: GSM432313
title: Serous ovarian cancer 67///geo_accession: GSM432314
title: Serous ovarian cancer 68///geo_accession: GSM432315
title: Serous ovarian cancer 69///geo_accession: GSM432316
title: Serous ovarian cancer 70///geo_accession: GSM432317
title: Serous ovarian cancer 71///geo_accession: GSM432318
title: Serous ovarian cancer 72///geo_accession: GSM432319
title: Serous ovarian cancer 77///geo_accession: GSM432324
title: Serous ovarian cancer 79///geo_accession: GSM432326
title: Serous ovarian cancer 7///geo_accession: GSM432327
title: Serous ovarian cancer 80///geo_accession: GSM432319

Value

An expression set

GSE18520	<i>A gene signature predictive for outcome in advanced ovarian cancer identifies a survival factor: microfibril-associated glycoprotein 2.</i>
----------	--

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.

Format

```

experimentData(eset):
Experiment data
  Experimenter name: Mok SC, Bonome T, Vathipadiekal V, Bell A, Johnson ME, Wong KK
  Laboratory: Mok, Birrer 2009
  Contact information:
  Title: A gene signature predictive for outcome in advanced ovarian cancer identif
  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|Operon
  platform_distribution:
    commercial|non-commercial
  platform_accession:
    GPL570|GPL9216
  version:

```

2015-09-22 19:21:25

```
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFX-HUMISGF3A/M97935_MB_at
                (42447 total)
  varLabels:  probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 42447 features, 63 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)
```

```
  10 observations deleted due to missingness
      n events median 0.95LCL 0.95UCL
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
63

percent_normal_cells:

0
63

percent_stromal_cells:

0
63

percent_tumor_cells:

100
63

batch:

2004-03-12	2004-04-08	2004-04-09	2004-07-20	2004-08-12	2004-08-13	2004-09-30
20	6	9	11	10	1	6

uncurated_author_metadata:

title: Normal Ovary, 2008///geo_acc

title: Normal Ovary, 2061///geo_acc

title: Normal Ovary, 2064///geo_acc

title: Normal Ovary, 2085///geo_acc

title: Normal Ovary, 2225///geo_acc

title: Normal Ovary, 2226///geo_acc

title: Normal Ovary, 2228///geo_acc
title: Normal Ovary, 2230///geo_acc
title: Normal Ovary, 2234///geo_acc
title: Normal Ovary, 2237///geo_acc
title: Ovarian Tumor, 1109///geo_accession: GSM461390///status: Public on Oct 17 20
title: Ovarian Tumor, 1214///geo_accession: GSM461391///status: Public on Oct 1
title: Ovarian Tumor, 1231///geo_accession: GSM461367///status: Public on Oct 1
title: Ovarian Tumor, 1562///geo_accession: GSM461368///status: Public on Oct 17 20
title: Ovarian Tumor, 1660///geo_accession: GSM461369///status: Public on Oct 17 20
title: Ovarian Tumor, 1993///geo_accession: GSM461400///status: Public on Oct 17 20
title: Ovarian Tumor, 312///geo_accession: GSM461379///status: Public on Oct
title: Ovarian Tumor, 317///geo_accession: GSM461348///status: Public on Oct 17 20
title: Ovarian Tumor, 321///geo_accession: GSM461380///status: Public on Oct
title: Ovarian Tumor, 324///geo_accession: GSM461373///status: Public on Oct
title: Ovarian Tumor, 332///geo_accession: GSM461349///status: Public on Oct
title: Ovarian Tumor, 345///geo_accession: GSM461392///status: Public on Oct
title: Ovarian Tumor, 349///geo_accession: GSM461350///status: Public on Oct 17 20
title: Ovarian Tumor, 351///geo_accession: GSM461351///status: Public on Oct 17 20
title: Ovarian Tumor, 358///geo_accession: GSM461393///status: Public on Oct
title: Ovarian Tumor, 367///geo_accession: GSM461381///status: Public on Oct
title: Ovarian Tumor, 377///geo_accession: GSM461374///status: Public on Oct
title: Ovarian Tumor, 380///geo_accession: GSM461375///status: Public on Oct
title: Ovarian Tumor, 386///geo_accession: GSM461352///status: Public on Oct
title: Ovarian Tumor, 388///geo_accession: GSM461353///status: Public on Oct 17 20

title: Ovarian Tumor, 389///geo_accession: GSM461354///status: Public on Oct 17 2011

title: Ovarian Tumor, 394///geo_accession: GSM461382///status: Public on Oct 17 2011

title: Ovarian Tumor, 396///geo_accession: GSM461376///status: Public on Oct 17 2011

title: Ovarian Tumor, 402///geo_accession: GSM461355///status: Public on Oct 17 2011

title: Ovarian Tumor, 410///geo_accession: GSM461356///status: Public on Oct 17 2011

title: Ovarian Tumor, 412///geo_accession: GSM461357///status: Public on Oct 17 2011

title: Ovarian Tumor, 434///geo_accession: GSM461358///status: Public on Oct 17 2011

title: Ovarian Tumor, 443///geo_accession: GSM461377///status: Public on Oct 17 2011

title: Ovarian Tumor, 461///geo_accession: GSM461394///status: Public on Oct 17 2011

title: Ovarian Tumor, 467///geo_accession: GSM461359///status: Public on Oct 17 2011

title: Ovarian Tumor, 477///geo_accession: GSM461383///status: Public on Oct 17 2011

title: Ovarian Tumor, 486///geo_accession: GSM461395///status: Public on Oct 17 2011

title: Ovarian Tumor, 629///geo_accession: GSM461360///status: Public on Oct 17 2011

title: Ovarian Tumor, 631///geo_accession: GSM461396///status: Public on Oct 17 2011

title: Ovarian Tumor, 656///geo_accession: GSM461384///status: Public on Oct 17 2011

title: Ovarian Tumor, 662///geo_accession: GSM461370///status: Public on Oct 17 2011

title: Ovarian Tumor, 692///geo_accession: GSM461397///status: Public on Oct 17 2011

title: Ovarian Tumor, 694///geo_accession: GSM461385///status: Public on Oct 17 2011

title: Ovarian Tumor, 702///geo_accession: GSM461361///status: Public on Oct 17 2011

title: Ovarian Tumor, 714///geo_accession: GSM461362///status: Public on Oct 17 2011

title: Ovarian Tumor, 715///geo_accession: GSM461386///status: Public on Oct 17 2011

title: Ovarian Tumor, 718///geo_accession: GSM461398///status: Public on Oct 17 2011

title: Ovarian Tumor, 744///geo_accession: GSM461378///status: Public on Oct 17 2011

title: Ovarian Tumor, 765///geo_accession: GSM461363///status: Public on Oct 17 2011

title: Ovarian Tumor, 778///geo_accession: GSM461399///status: Public on Oct
 title: Ovarian Tumor, 780///geo_accession: GSM461364///status: Public on Oct
 title: Ovarian Tumor, 786///geo_accession: GSM461387///status: Public on Oct 17 2
 title: Ovarian Tumor, 794///geo_accession: GSM461388///status: Public on Oct
 title: Ovarian Tumor, 799///geo_accession: GSM461365///status: Public on Oct
 title: Ovarian Tumor, 800///geo_accession: GSM461371///status: Public on Oct
 title: Ovarian Tumor, 872///geo_accession: GSM461366///status: Public on Oct
 title: Ovarian Tumor, 934///geo_accession: GSM461372///status: Public on Oct 17 2
 title: Ovarian Tumor, 970///geo_accession: GSM461389///status: Public on Oct

duplicates:

	GSE18520.GSE18520_GSM462649	1
GSE18520.GSE18520_GSM462649///GSE18520.GSE18520_GSM462650		1
	GSE18520.GSE18520_GSM462650	1
		NA's
		60

Value

An expression set

GSE19829	<i>Gene expression profile of BRCAness that correlates with responsiveness to chemotherapy and with outcome in patients with epithelial ovarian cancer.</i>
----------	---

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.

Format

```

experimentData (eset) :
Experiment data
  Experimenter name: Konstantinopoulos PA, Spentzos D, Karlan BY, Taniguchi T et al
  Laboratory: Konstantinopoulos, Cannistra 2010 hgu95
  Contact information:
  Title: Gene expression profile of BRCAness that correlates with responsiveness to
  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:
    GPL570|GPL8300
  version:
    2015-09-22 19:26:29

featureData (eset) :
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-MurIL4_at (54253 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

Details

assayData: 54253 features, 70 samples

Platform type:

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

Call: survfit(formula = Surv(time, cens) ~ -1)

n	events	median	0.95LCL	0.95UCL
70.00	40.00	3.78	2.96	5.92

Available sample meta-data:

alt_sample_name:

Ovarian cancer_sample 1	Ovarian cancer_sample 10	Ovarian cancer_sample 11
1	1	1
Ovarian cancer_sample 12	Ovarian cancer_sample 13	Ovarian cancer_sample 14
1	1	1
Ovarian cancer_sample 15	Ovarian cancer_sample 16	Ovarian cancer_sample 17
1	1	1
Ovarian cancer_sample 18	Ovarian cancer_sample 19	Ovarian cancer_sample 2
1	1	1
Ovarian cancer_sample 20	Ovarian cancer_sample 21	Ovarian cancer_sample 22
1	1	1
Ovarian cancer_sample 23	Ovarian cancer_sample 24	Ovarian cancer_sample 25
1	1	1
Ovarian cancer_sample 26	Ovarian cancer_sample 27	Ovarian cancer_sample 28
1	1	1
Ovarian cancer_sample 29	Ovarian cancer_sample 3	Ovarian cancer_sample 30
1	1	1
Ovarian cancer_sample 31	Ovarian cancer_sample 32	Ovarian cancer_sample 33
1	1	1
Ovarian cancer_sample 34	Ovarian cancer_sample 35	Ovarian cancer_sample 36
1	1	1
Ovarian cancer_sample 37	Ovarian cancer_sample 38	Ovarian cancer_sample 39
1	1	1
Ovarian cancer_sample 4	Ovarian cancer_sample 40	Ovarian cancer_sample 41
1	1	1
Ovarian cancer_sample 42	Ovarian cancer_sample 43	Ovarian cancer_sample 44
1	1	1
Ovarian cancer_sample 45	Ovarian cancer_sample 46	Ovarian cancer_sample 47
1	1	1
Ovarian cancer_sample 48	Ovarian cancer_sample 49	Ovarian cancer_sample 5
1	1	1
Ovarian cancer_sample 50	Ovarian cancer_sample 51	Ovarian cancer_sample 52
1	1	1

```

Ovarian cancer_sample 53 Ovarian cancer_sample 54 Ovarian cancer_sample 55
      1                      1                      1
Ovarian cancer_sample 56 Ovarian cancer_sample 57 Ovarian cancer_sample 58
      1                      1                      1
Ovarian cancer_sample 59 Ovarian cancer_sample 60 Ovarian cancer_sample 60
      1                      1                      1
Ovarian cancer_sample 61 Ovarian cancer_sample 62 Ovarian cancer_sample 63
      1                      1                      1
Ovarian cancer_sample 64 Ovarian cancer_sample 65 Ovarian cancer_sample 66
      1                      1                      1
Ovarian cancer_sample 67 Ovarian cancer_sample 68 Ovarian cancer_sample 69
      1                      1                      1
Ovarian cancer_sample 7 Ovarian cancer_sample 70 Ovarian cancer_sample 8
      1                      1                      1
Ovarian cancer_sample 9
      1

```

batch:

```

2001-09-14 2001-12-14 2002-08-20 2003-09-09 2003-09-18 2009-08-14
              7           4           14           13           4           28

```

days_to_death:

```

  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  30.0   667.5  1125.0  1170.0  1522.0  3450.0

```

primarysite:

```

ov
70

```

sample_type:

```

tumor
  70

```

uncurated_author_metadata:

```

title: Ovarian cancer_sample 10///geo_accession: GSM495148///status: Pu
title: Ovarian cancer_sample 11///geo_accession: GSM495149///status: Pu
      title: Ovarian cancer_sample 12///geo_accession: GSM495150///statu
title: Ovarian cancer_sample 13///geo_accession: GSM495151///status: Pu
title: Ovarian cancer_sample 14///geo_accession: GSM495152///status: Pu
title: Ovarian cancer_sample 15///geo_accession: GSM495153///status: Pu
title: Ovarian cancer_sample 16///geo_accession: GSM495154///status: Pu

```

title: Ovarian cancer_sample 17///geo_accession: GSM495155///status: Pu
title: Ovarian cancer_sample 18///geo_accession: GSM495156///status: Pu
title: Ovarian cancer_sample 19///geo_accession: GSM495157///status: Pu
title: Ovarian cancer_sample 1///geo_accession: GSM495139///status: Pu
title: Ovarian cancer_sample 20///geo_accession: GSM495158///status: Pu
title: Ovarian cancer_sample 21///geo_accession: GSM495159///status: Pu
title: Ovarian cancer_sample 22///geo_accession: GSM495160///status: Pu
title: Ovarian cancer_sample 23///geo_accession: GSM495161///status: Pu
title: Ovarian cancer_sample 24///geo_accession: GSM495162///status: Pu
title: Ovarian cancer_sample 25///geo_accession: GSM495163///status: Pu
title: Ovarian cancer_sample 26///geo_accession: GSM495164///status: Pu
title: Ovarian cancer_sample 27///geo_accession: GSM495165///status: Pu
title: Ovarian cancer_sample 28///geo_accession: GSM495166///status: Pu
title: Ovarian cancer_sample 29///geo_accession: GSM495167///status: Public on Jul
title: Ovarian cancer_sample 2///geo_accession: GSM495140///status: Pu
title: Ovarian cancer_sample 30///geo_accession: GSM495168///status: Public o
title: Ovarian cancer_sample 31///geo_accession: GSM495169///status: Public o
title: Ovarian cancer_sample 32///geo_accession: GSM495170///status: Public on Jul
title: Ovarian cancer_sample 33///geo_accession: GSM495171///status: Public on Jul
title: Ovarian cancer_sample 34///geo_accession: GSM495172///status: Public o
title: Ovarian cancer_sample 35///geo_accession: GSM495173///status: Public on Jul
title: Ovarian cancer_sample 36///geo_accession: GSM495174///status: Public on Jul
title: Ovarian cancer_sample 37///geo_accession: GSM495175///status: Public on Jul
title: Ovarian cancer_sample 38///geo_accession: GSM495176///status: Public on Jul

title: Ovarian cancer_sample 39///geo_accession: GSM495177///status: Public on Jul
title: Ovarian cancer_sample 3///geo_accession: GSM495141///status
title: Ovarian cancer_sample 40///geo_accession: GSM495178///status: Public o
title: Ovarian cancer_sample 41///geo_accession: GSM495179///status: Public on Jul
title: Ovarian cancer_sample 42///geo_accession: GSM495180///status: Public o
title: Ovarian cancer_sample 43///geo_accession: GSM495181///status: Public on Jul
title: Ovarian cancer_sample 44///geo_accession: GSM495182///status: Public on
title: Ovarian cancer_sample 45///geo_accession: GSM495183///status: Public on
title: Ovarian cancer_sample 46///geo_accession: GSM495184///status: Public on Jul
title: Ovarian cancer_sample 47///geo_accession: GSM495185///status: Public on
title: Ovarian cancer_sample 48///geo_accession: GSM495186///status: Public on Jul
title: Ovarian cancer_sample 49///geo_accession: GSM495187///status: Public on
title: Ovarian cancer_sample 4///geo_accession: GSM495142///status
title: Ovarian cancer_sample 50///geo_accession: GSM495188///status: Public on Jul
title: Ovarian cancer_sample 51///geo_accession: GSM495189///status: Public on
title: Ovarian cancer_sample 52///geo_accession: GSM495190///status: Public on
title: Ovarian cancer_sample 53///geo_accession: GSM495191///status: Public on
title: Ovarian cancer_sample 54///geo_accession: GSM495192///status: Public on
title: Ovarian cancer_sample 55///geo_accession: GSM495193///status: Public on Jul
title: Ovarian cancer_sample 56///geo_accession: GSM495194///status: Public on J
title: Ovarian cancer_sample 57///geo_accession: GSM495195///status: Public on J
title: Ovarian cancer_sample 58///geo_accession: GSM495196///status: Public on Ju
title: Ovarian cancer_sample 59///geo_accession: GSM495197///status: Public
title: Ovarian cancer_sample 5///geo_accession: GSM495143///status: Pu

title: Ovarian cancer_sample 60///geo_accession: GSM495198///status: Public on Ju
 title: Ovarian cancer_sample 61///geo_accession: GSM495199///status: Public
 title: Ovarian cancer_sample 62///geo_accession: GSM495200///status: Public on Ju
 title: Ovarian cancer_sample 63///geo_accession: GSM495201///status: Public o
 title: Ovarian cancer_sample 64///geo_accession: GSM495202///status: Public on Jul
 title: Ovarian cancer_sample 65///geo_accession: GSM495203///status: Public o
 title: Ovarian cancer_sample 66///geo_accession: GSM495204///status: Public o
 title: Ovarian cancer_sample 67///geo_accession: GSM495205///status: Public on Ju
 title: Ovarian cancer_sample 68///geo_accession: GSM495206///status: Public on Ju
 title: Ovarian cancer_sample 69///geo_accession: GSM495207///status: Public on Ju
 title: Ovarian cancer_sample 6///geo_accession: GSM495144///status: Pu
 title: Ovarian cancer_sample 70///geo_accession: GSM495208///status: Public
 title: Ovarian cancer_sample 7///geo_accession: GSM495145///statu
 title: Ovarian cancer_sample 8///geo_accession: GSM495146///status: Pu
 title: Ovarian cancer_sample 9///geo_accession: GSM495147///status: E

vital_status:
 deceased living
 40 30

Value

An expression set

GSE20565

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.

Format

```

experimentData(eset) :
Experiment data
  Experimenter name: Meyniel JP, Cottu PH, Decraene C, Stern MH, Couturier J, Lebigot
  Laboratory: Meyniel, Sastre-Garau 2010
  Contact information:
  Title: A genomic and transcriptomic approach for a differential diagnosis between
  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:
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  platform_manufacturer:
    Affymetrix
  platform_distribution:
    commercial
  platform_accession:
    GPL570|GPL2005|GPL6801

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version:
  2015-09-22 19:33:01

featureData(eset):
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  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
  (42447 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

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Details

assayData: 42447 features, 140 samples

Platform type:

 Available sample meta-data:

alt_sample_name:

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Breast metastasis in the ovary_OC01_ARN0017	[HG-U133_Plus_2]	1
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Breast metastasis in the ovary_OC01_ARN0029	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0035	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0046	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0051	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0053	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0055	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0060	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0069	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0073	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0077	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0079	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0081	[HG-U133_Plus_2]	1

Breast metastasis in the ovary_OC01_ARN0083	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0092	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0097	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0098	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0099	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0102	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0104	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0112	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0120	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0121	[HG-U133_Plus_2]	1
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Ovarian carcinoma_OC01_ARN0115 [HG-U133_Plus_2]
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41

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tumor
  140

```

```

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clearcell      endo  mucinous  other  ser  NA's
           6      6          7      6    71   44

```

```

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
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batch:

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duplicates:

GSE20565.GSE20565_GSM516722	GSE20565.GSE20565_GSM516741
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138	

Value

An expression set

GSE2109

IGC EXpression Project for Oncology

Description

EXpression Project for Oncology, International Genomics Consortium, www.intgen.org

Format

```

experimentData(eset):
Experiment data
  Experimenter name: EXpression Project for Oncology, International Genomics Consor
  Laboratory: expO, IGC 2005
  Contact information:
  Title: IGC EXpression Project for Oncology
  URL:
  PMIDs: PMID unknown

Abstract: A 8 word abstract is available. Use 'abstract' method.
Information is available on: preprocessing
notes:
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  platform_accession:
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  version:
    2015-09-22 19:40:35

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  varMetadata: labelDescription

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Details

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assayData: 42447 features, 204 samples
Platform type:
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Available sample meta-data:
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Abdominal wall mass - 8176
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Omentum - 8174
Omentum - 1006
                      1
Omentum - 8186

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1	1
Ovary - 242929	(Other)

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105

sample_type:

tumor
204

histological_type:

clearcell	endo	mucinous	other
9	28	11	59
ser undifferentiated	NA's		
85	2	10	

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

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2005-03-15	2005-03-16	2005-03-17	2005-03-19	2005-03-22	2005-04-13	2005-04-26
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2005-04-29	2005-05-10	2005-06-01	2005-06-03	2005-06-08	2005-06-17	2005-08-05
2	2	5	3	3	6	3
2005-08-09	2005-08-11	2005-09-07	2005-09-09	2005-09-13	2005-11-02	2005-11-04

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2006-07-28	2006-09-12	2006-09-14	2006-10-10	2006-10-24	2006-10-31	2006-11-09
1	2	1	1	9	5	10
2006-11-21	2006-11-30	2006-12-07	2007-01-12	2007-02-09	2007-03-07	2007-03-09
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2007-03-15	2007-05-01	2007-05-03	2007-05-15	2007-05-18	2007-05-30	2007-06-12
4	2	3	4	2	2	1
2007-07-27	2007-09-05	2007-09-07	2007-09-11	2007-09-12	2008-02-15	2008-02-21
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duplicates:

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NA's
202

Value

An expression set

GSE26193

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 β and modulate the oxidative stress response. Enhanced expression of these microRNAs mimics p38 β 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.

Format

```

experimentData(eset):
Experiment data
  Experimenter name: Mateescu B, Batista L, Mariani O, Meyniel J, Cottu PH, Sastre-
  Laboratory: Mateescu, Mechta-Grigoriou 2011
  Contact information:
  Title: miR-141 and miR-200a act on ovarian tumorigenesis by controlling oxidative
  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
  version:
    2015-09-22 19:44:56

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
    (42447 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

Details

```

assayData: 42447 features, 107 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

```

	n	events	median	0.95LCL	0.95UCL
	107.00	76.00	3.05	2.50	4.56

```

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

```

```

alt_sample_name:
  Ovarian carcinoma 1  Ovarian carcinoma 10  Ovarian carcinoma 100
                        1                        1                        1
Ovarian carcinoma 101  Ovarian carcinoma 102  Ovarian carcinoma 103
                        1                        1                        1
Ovarian carcinoma 104  Ovarian carcinoma 105  Ovarian carcinoma 106
                        1                        1                        1
Ovarian carcinoma 107  Ovarian carcinoma 11   Ovarian carcinoma 12
                        1                        1                        1
  Ovarian carcinoma 13  Ovarian carcinoma 14   Ovarian carcinoma 15
                        1                        1                        1
  Ovarian carcinoma 16  Ovarian carcinoma 17   Ovarian carcinoma 18
                        1                        1                        1
  Ovarian carcinoma 19  Ovarian carcinoma 2   Ovarian carcinoma 20
                        1                        1                        1
  Ovarian carcinoma 21  Ovarian carcinoma 22   Ovarian carcinoma 23
                        1                        1                        1
  Ovarian carcinoma 24  Ovarian carcinoma 25   Ovarian carcinoma 26
                        1                        1                        1
  Ovarian carcinoma 27  Ovarian carcinoma 28   Ovarian carcinoma 29
                        1                        1                        1
    Ovarian carcinoma 3  Ovarian carcinoma 30   Ovarian carcinoma 31
                        1                        1                        1
  Ovarian carcinoma 32  Ovarian carcinoma 33   Ovarian carcinoma 34
                        1                        1                        1
  Ovarian carcinoma 35  Ovarian carcinoma 36   Ovarian carcinoma 37
                        1                        1                        1
  Ovarian carcinoma 38  Ovarian carcinoma 39   Ovarian carcinoma 4
                        1                        1                        1
  Ovarian carcinoma 40  Ovarian carcinoma 41   Ovarian carcinoma 42
                        1                        1                        1
  Ovarian carcinoma 43  Ovarian carcinoma 44   Ovarian carcinoma 45
                        1                        1                        1
  Ovarian carcinoma 46  Ovarian carcinoma 47   Ovarian carcinoma 48
                        1                        1                        1

```

Ovarian carcinoma	49	Ovarian carcinoma	5	Ovarian carcinoma	50
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Ovarian carcinoma	51	Ovarian carcinoma	52	Ovarian carcinoma	53
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Ovarian carcinoma	54	Ovarian carcinoma	55	Ovarian carcinoma	56
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Ovarian carcinoma	57	Ovarian carcinoma	58	Ovarian carcinoma	59
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Ovarian carcinoma	6	Ovarian carcinoma	60	Ovarian carcinoma	61
	1		1		1
Ovarian carcinoma	62	Ovarian carcinoma	63	Ovarian carcinoma	64
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Ovarian carcinoma	65	Ovarian carcinoma	66	Ovarian carcinoma	67
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Ovarian carcinoma	68	Ovarian carcinoma	69	Ovarian carcinoma	7
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Ovarian carcinoma	70	Ovarian carcinoma	71	Ovarian carcinoma	72
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Ovarian carcinoma	73	Ovarian carcinoma	74	Ovarian carcinoma	75
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Ovarian carcinoma	76	Ovarian carcinoma	77	Ovarian carcinoma	78
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Ovarian carcinoma	79	Ovarian carcinoma	8	Ovarian carcinoma	80
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Ovarian carcinoma	81	Ovarian carcinoma	82	Ovarian carcinoma	83
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Ovarian carcinoma	84	Ovarian carcinoma	85	Ovarian carcinoma	86
	1		1		1
Ovarian carcinoma	87	Ovarian carcinoma	88	Ovarian carcinoma	89
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Ovarian carcinoma	9	Ovarian carcinoma	90	Ovarian carcinoma	91
	1		1		1
		(Other)			
	8				

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:
2006-06-01 2006-06-27 2006-06-28 2006-06-29 2006-06-30 2006-07-20 2008-03-06
15 14 23 16 21 3 1
2009-03-18 2009-03-19
4 10

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Value

An expression set

GSE26712

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.

Format

```

experimentData(eset):
Experiment data
  Experimenter name: Bonome T, Levine DA, Shih J, Randonovich M, Pise-Masison CA, B
  Laboratory: Bonome, Birrer 2008
  Contact information:
  Title: A gene signature predicting for survival in suboptimally debulked patients
  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
version:
  2015-09-22 19:46:24

```

```

featureData(eset):
An object of class 'AnnotatedDataFrame'
 featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
 (20967 total)
 varLabels: probeset gene EntrezGene.ID best_probe
 varMetadata: labelDescription

```

Details

```

assayData: 20967 features, 195 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

```

```

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

```

```

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

```

```

alt_sample_name:
  Normal HOSE2008      Normal HOSE2061      Normal HOSE2064
                1                1                1
  Normal HOSE2085      Normal HOSE2225      Normal HOSE2226
                1                1                1
  Normal HOSE2228      Normal HOSE2230      Normal HOSE2234
                1                1                1
  Normal HOSE2237  Ovarian Cancer SO10  Ovarian Cancer SO100
                1                1                1
Ovarian Cancer SO103  Ovarian Cancer SO106  Ovarian Cancer SO108
                1                1                1
  Ovarian Cancer SO11  Ovarian Cancer SO113  Ovarian Cancer SO115
                1                1                1
Ovarian Cancer SO116  Ovarian Cancer SO117  Ovarian Cancer SO118
                1                1                1
  Ovarian Cancer SO12  Ovarian Cancer SO121  Ovarian Cancer SO122

```

1		1		1	
Ovarian Cancer	S0124	Ovarian Cancer	S0129	Ovarian Cancer	S013
1		1		1	
Ovarian Cancer	S0131	Ovarian Cancer	S0134	Ovarian Cancer	S0135
1		1		1	
Ovarian Cancer	S0137	Ovarian Cancer	S0141	Ovarian Cancer	S0143
1		1		1	
Ovarian Cancer	S0148	Ovarian Cancer	S0154	Ovarian Cancer	S016
1		1		1	
Ovarian Cancer	S0166	Ovarian Cancer	S017	Ovarian Cancer	S0173
1		1		1	
Ovarian Cancer	S0174	Ovarian Cancer	S018	Ovarian Cancer	S0181
1		1		1	
Ovarian Cancer	S0184	Ovarian Cancer	S0185	Ovarian Cancer	S0187
1		1		1	
Ovarian Cancer	S0189	Ovarian Cancer	S0190	Ovarian Cancer	S0193
1		1		1	
Ovarian Cancer	S0194	Ovarian Cancer	S0196	Ovarian Cancer	S0197
1		1		1	
Ovarian Cancer	S02	Ovarian Cancer	S0200	Ovarian Cancer	S0201
1		1		1	
Ovarian Cancer	S0203	Ovarian Cancer	S0205	Ovarian Cancer	S021
1		1		1	
Ovarian Cancer	S0211	Ovarian Cancer	S0214	Ovarian Cancer	S0216
1		1		1	
Ovarian Cancer	S0217	Ovarian Cancer	S0218	Ovarian Cancer	S0224
1		1		1	
Ovarian Cancer	S0225	Ovarian Cancer	S0227	Ovarian Cancer	S0228
1		1		1	
Ovarian Cancer	S0229	Ovarian Cancer	S023	Ovarian Cancer	S0230
1		1		1	
Ovarian Cancer	S0231	Ovarian Cancer	S0235	Ovarian Cancer	S0236
1		1		1	
Ovarian Cancer	S0237	Ovarian Cancer	S0241	Ovarian Cancer	S0242
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Ovarian Cancer	S0243	Ovarian Cancer	S0244	Ovarian Cancer	S0246
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Ovarian Cancer	S0247	Ovarian Cancer	S0249	Ovarian Cancer	S025
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Ovarian Cancer	S0250	Ovarian Cancer	S0256	Ovarian Cancer	S0257
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Ovarian Cancer	S0258	Ovarian Cancer	S0261	Ovarian Cancer	S0262
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Ovarian Cancer	S0263	Ovarian Cancer	S0265	Ovarian Cancer	S0267
1		1		1	
Ovarian Cancer	S0268	Ovarian Cancer	S0272	Ovarian Cancer	S0273
1		1		1	
Ovarian Cancer	S0278	Ovarian Cancer	S0279	Ovarian Cancer	S0282

	1		1		1
Ovarian Cancer SO283		Ovarian Cancer SO285		Ovarian Cancer SO290	
	1		1		1
(Other)					
	96				

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:

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2006-11-09						
10						

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duplicates:

GSE26712.GSE26712_GSM657526
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 GSE26712.GSE26712_GSM657526///GSE26712.GSE26712_GSM657527
 1
 GSE26712.GSE26712_GSM657527
 1
 NA's
 192

Value

An expression set

GSE30009

Multidrug resistance-linked gene signature predicts overall survival of patients with primary ovarian serous carcinoma.

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.

Format

```

experimentData(eset):
Experiment data
  Experimenter name: Gillet JP, Calcagno AM, Varma S, Davidson B et al. Multidrug r
  Laboratory: Gillet, Gottesman 2012
  Contact information:
  Title: Multidrug resistance-linked gene signature predicts overall survival of pa
  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
version:
  2015-09-22 19:46:26

```

```

featureData(eset):
An object of class 'AnnotatedDataFrame'
 featureNames: 5 6 ... 380 (363 total)
 varLabels: probeset gene EntrezGene.ID best_probe
 varMetadata: labelDescription

```

Details

```

assayData: 363 features, 103 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

```

	n	events	median	0.95LCL	0.95UCL
	103.00	57.00	3.42	2.92	5.34

```

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

```

```

alt_sample_name:
  Norwegian patient 1 Norwegian patient 10 Norwegian patient 11
                        1                        1                        1
Norwegian patient 12 Norwegian patient 13 Norwegian patient 14
                        1                        1                        1
Norwegian patient 15 Norwegian patient 16 Norwegian patient 17
                        1                        1                        1
Norwegian patient 18 Norwegian patient 19 Norwegian patient 2
                        1                        1                        1
Norwegian patient 20 Norwegian patient 21 Norwegian patient 22
                        1                        1                        1
Norwegian patient 23 Norwegian patient 3 Norwegian patient 4
                        1                        1                        1
  Norwegian patient 5 Norwegian patient 6 Norwegian patient 7
                        1                        1                        1
  Norwegian patient 8 Norwegian patient 9 US Patient 1
                        1                        1                        1
                US Patient 10 US Patient 11 US Patient 12

```

1	1	1
US Patient 13	US Patient 14	US Patient 15
1	1	1
US Patient 16	US Patient 17	US Patient 18
1	1	1
US Patient 19	US Patient 2	US Patient 20
1	1	1
US Patient 21	US Patient 22	US Patient 23
1	1	1
US Patient 24	US Patient 25	US Patient 26
1	1	1
US Patient 27	US Patient 28	US Patient 29
1	1	1
US Patient 3	US Patient 30	US Patient 31
1	1	1
US Patient 32	US Patient 33	US Patient 34
1	1	1
US Patient 35	US Patient 36	US Patient 37
1	1	1
US Patient 38	US Patient 39	US Patient 4
1	1	1
US Patient 40	US Patient 41	US Patient 42
1	1	1
US Patient 43	US Patient 44	US Patient 45
1	1	1
US Patient 46	US Patient 47	US Patient 48
1	1	1
US Patient 49	US Patient 5	US Patient 50
1	1	1
US Patient 51	US Patient 52	US Patient 53
1	1	1
US Patient 54	US Patient 55	US Patient 56
1	1	1
US Patient 57	US Patient 58	US Patient 59
1	1	1
US Patient 6	US Patient 60	US Patient 61
1	1	1
US Patient 62	US Patient 63	US Patient 64
1	1	1
US Patient 65	US Patient 66	US Patient 67
1	1	1
US Patient 68	US Patient 69	US Patient 7
1	1	1
US Patient 70	US Patient 71	US Patient 72
1	1	1
US Patient 73	US Patient 74	US Patient 75
1	1	1
US Patient 76	US Patient 77	US Patient 78

```

              1              1              1
            (Other)
              4

sample_type:
tumor
  103

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:

title: US Pati

title: US

title: US Patient 5

title: US Patient 51///geo_accession: GSM742615///status: Public on Apr 19 2012///s

title: US Patient 54///geo_accession: GSM7426

tit

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title: US Patient 59///geo_accession: GSM742623///status: Public o

title: US Patient 63///geo_accession:

title: US Patient

title: US Patient 66///geo_accession: GSM742630///status

ti

title: US Patient 70///geo_accession: GSM742634///status: Public on Apr 19 20

t

title: US Patien

title: US Patient 75///geo_accession: GSM7426

title:

title: US Patient 77///geo_ac

title: US Patient 78///

title: US Patient 79///g

Value

An expression set

GSE30161

Multi-gene expression predictors of single drug responses to adjuvant chemotherapy in ovarian carcinoma: predicting platinum resistance.

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.

Format

```
experimentData(eset) :
Experiment data
  Experimenter name: Ferriss JS, Kim Y, Duska L, Birrer M, Levine DA, Moskaluk C, Thaler HT
  Laboratory: Ferriss, Lee 2012
  Contact information:
  Title: Multi-gene expression predictors of single drug responses to adjuvant chemotherapy in ovarian carcinoma: predicting platinum resistance.
```

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

version:

2015-09-22 19:50:24

featureData(eset):

An object of class 'AnnotatedDataFrame'

featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
(42447 total)

varLabels: probeset gene EntrezGene.ID best_probe

varMetadata: labelDescription

Details

assayData: 42447 features, 58 samples

Platform type:

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

Call: survfit(formula = Surv(time, cens) ~ -1)

n	events	median	0.95LCL	0.95UCL
58.00	36.00	4.19	2.70	6.17

Available sample meta-data:

alt_sample_name:

OV_FFPE_1	OV_FFPE_10	OV_FFPE_11	OV_FFPE_12	OV_FFPE_13	OV_FFPE_14	OV_FFPE_15
1	1	1	1	1	1	1
OV_FFPE_16	OV_FFPE_17	OV_FFPE_18	OV_FFPE_19	OV_FFPE_2	OV_FFPE_20	OV_FFPE_21
1	1	1	1	1	1	1
OV_FFPE_22	OV_FFPE_23	OV_FFPE_24	OV_FFPE_25	OV_FFPE_26	OV_FFPE_27	OV_FFPE_28

OV_FFPE_29	OV_FFPE_3	OV_FFPE_30	OV_FFPE_31	OV_FFPE_32	OV_FFPE_33	OV_FFPE_34
1	1	1	1	1	1	1
OV_FFPE_35	OV_FFPE_36	OV_FFPE_37	OV_FFPE_38	OV_FFPE_39	OV_FFPE_4	OV_FFPE_40
1	1	1	1	1	1	1
OV_FFPE_41	OV_FFPE_42	OV_FFPE_43	OV_FFPE_44	OV_FFPE_45	OV_FFPE_46	OV_FFPE_47
1	1	1	1	1	1	1
OV_FFPE_48	OV_FFPE_49	OV_FFPE_5	OV_FFPE_50	OV_FFPE_51	OV_FFPE_52	OV_FFPE_53
1	1	1	1	1	1	1
OV_FFPE_54	OV_FFPE_55	OV_FFPE_56	OV_FFPE_57	OV_FFPE_58	OV_FFPE_6	OV_FFPE_7
1	1	1	1	1	1	1
OV_FFPE_8	OV_FFPE_9					
1	1					

sample_type:

tumor

58

histological_type:

clearcell	endo	mucinous	other
5	1	1	1
ser undifferentiated		NA's	
47	1	2	

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:

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title: OV_FFPE_9///geo_accession: GSM746869///status: Public on Aug 21 2012/

Value

An expression set

GSE32062

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, $P = 4 \times 10^{-20}$). We validated its predictive ability with five other data sets using multivariate analysis (Tohill's data set, $P = 1 \times 10^{-5}$; 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.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Yoshihara K, Tsunoda T, Shigemizu D, Fujiwara H et al. High-ri
  Laboratory: Yoshihara, Tanaka 2012
```

Contact information:

Title: High-risk ovarian cancer based on 126-gene expression signature is unique

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

version:

2015-09-22 19:55:29

featureData(eset):

An object of class 'AnnotatedDataFrame'

featureNames: A_23_P100001 A_23_P100011 ... A_32_P99902 (30936 total)

varLabels: probeset gene EntrezGene.ID best_probe

varMetadata: labelDescription

Details

assayData: 30936 features, 260 samples

Platform type:

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

Call: survfit(formula = Surv(time, cens) ~ -1)

	n	events	median	0.95LCL	0.95UCL
	260.00	121.00	4.93	4.11	6.58

Available sample meta-data:

alt_sample_name:

10d	115d	116d	117d	119d	11d	120d	122d	123d	125Rd
1	1	1	1	1	1	1	1	1	1
129d	12d	130d	132d	134d	139d	140d	143d	144d	145d

1	1	1	1	1	1	1	1	1	1
146d	148d	150d	155d	156d	15d	160d	16d	171d	173d
1	1	1	1	1	1	1	1	1	1
174d	178d	17d	183d	184d	185d	186d	18d	20d	22d
1	1	1	1	1	1	1	1	1	1
23d	249d	257d	25d	260d	262d	264d	266d	267d	268d
1	1	1	1	1	1	1	1	1	1
269d	27d	299d	2d	300d	301d	302d	303d	304d	305d2
1	1	1	1	1	1	1	1	1	1
306d	307d	310d	318d	319d	320d2	323d	327d	330d	331d
1	1	1	1	1	1	1	1	1	1
333d2	335d	337d	340d	342d	346d	347d	348d2	350d	352d
1	1	1	1	1	1	1	1	1	1
353d	355d	356d	357d	358d	360d	362d	363d	365d	366d
1	1	1	1	1	1	1	1	1	1
367d	368d2	36d	38d	41d2R	42d	43d	44d	456d (Other)	
1	1	1	1	1	1	1	1	1	161

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:

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duplicates:

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NA's	1
258	

Value

An expression set

GSE32063

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, $P = 4 \times 10^{-20}$). We validated its predictive ability with five other data sets using multivariate analysis (Tothill's data set, $P = 1 \times 10^{-5}$; 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.

Format

```

experimentData(eset):
Experiment data
  Experimenter name: Yoshihara K, Tsunoda T, Shigemizu D, Fujiwara H et al. High-risk
  Laboratory: Yoshihara, Tanaka 2012
  Contact information:
  Title: High-risk ovarian cancer based on 126-gene expression signature is unique
  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
    version:
      2015-09-22 19:58:23

featureData(eset):
An object of class 'AnnotatedDataFrame'

```

```
featureNames: A_23_P100001 A_23_P100011 ... A_32_P99902 (30936 total)
varLabels: probeset gene EntrezGene.ID best_probe
varMetadata: labelDescription
```

Details

```
assayData: 30936 features, 40 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)
```

```
      n events median 0.95LCL 0.95UCL
40.00  22.00   4.44   3.29      NA
```

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

```
alt_sample_name:
```

106	108	109R	110	111R	192	195R	196	197	198	200	203	205	206	207	213
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222	224	226	229	230	231	274	277	278	280	281	282	283	284	285	286
1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
287	288	289	291	292	294	297R	298R								
1	1	1	1	1	1	1	1								

```
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

plx:

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:

title: serous ovarian cancer 106///geo_accession: GSM795125///status: Public on M

title: serous ovarian cancer 108///geo_accession: GSM795126///status: Public o

title: serous ovarian cancer 109R///geo_accession: GSM795127///status: Public on M

title: serous ovarian cancer 110///geo_accession: GSM795128///status: Public on M

title: serous ovarian cancer 111R///geo_accession: GSM795129///status: Public on Ma

title: serous ovarian cancer 192///geo_accession: GSM7

title: serous ovarian cancer 195R///geo_accession: GSM79

title: serous ovarian cancer 196///geo_accession: GS

title: serous ovarian cancer 197///geo_accession: GSM7

title: serous ovarian cancer 198///geo_accession: GSM795

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title: serous ovarian cancer 203///geo_accession: GSM7951
title: serous ovarian cancer 205///geo_accession: GSM79
title: serous ovarian cancer 206///geo_accession: GSM7
title: serous ovarian cancer 207///geo_accession: GSM7951
title: serous ovarian cancer 213///geo_accession: GSM79
title: serous ovarian cancer 222///geo_accession: GSM7951
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title: serous ovarian cancer 226///geo_accession: GSM7
title: serous ovarian cancer 229///geo_accession: GS
title: serous ovarian cancer 230///geo_accession:
title: serous ovarian cancer 231///geo_accession: GS
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Value

An expression set

GSE44104

COL11A1 promotes tumor progression and predicts poor clinical outcome in ovarian cancer.

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- β) treatment triggers the activation of smad2 signaling cascades, leading to activation of COL11A1 and MMP3. Pharmacological inhibition of MMP3 abrogated the TGF- β -triggered, COL11A1-dependent cell invasiveness. Furthermore, the NF-YA-binding site on the COL11A1 promoter was identified as the major determinant of TGF- β -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- β -MMP3 axis and that COL11A1 expression can predict clinical outcome in ovarian cancer patients.

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 c
  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
  version:
    2015-09-22 20:02:05

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
    (42447 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

Details

```

assayData: 42447 features, 60 samples
Platform type:
-----
Available sample meta-data:
-----

alt_sample_name:
Tc_113 Tc_48 Tc_49 Tc_51 Tc_56 Tc_59 Tc_61 Tc_63 Tc_64 Tc_65 Tc_74

```

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Tc_94	Te_69	Te_77	Te_78	Te_79	Te_84	Te_87	Te_89	Te_90	Te_91	Te_92	
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Te_93	Tm_101	Tm_102	Tm_106	Tm_107	Tm_110	Tm_95	Tm_96	Tm_97	Tm_98	Ts_11	
1	1	1	1	1	1	1	1	1	1	1	1
Ts_14	Ts_15	Ts_17	Ts_19	Ts_2	Ts_20	Ts_21	Ts_23	Ts_24	Ts_26	Ts_28	
1	1	1	1	1	1	1	1	1	1	1	1
Ts_3	Ts_31	Ts_32	Ts_34	Ts_35	Ts_36	Ts_37	Ts_39	Ts_4	Ts_41	Ts_43	
1	1	1	1	1	1	1	1	1	1	1	1
Ts_45	Ts_46	Ts_47	Ts_5	Ts_8							
1	1	1	1	1							

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

20 2 18 16 4

uncurated_author_metadata:

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duplicates:

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60	character	character

Value

An expression set

GSE49997

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.

Format

```

experimentData(eset):
Experiment data
  Experimenter name: Pils D, Hager G, Tong D, Aust S, Heinze G, Kohl M, Schuster E
  Laboratory: Pils, Zeilinger 2012
  Contact information:
  Title: Validating the impact of a molecular subtype in ovarian cancer on outcomes
  URL:
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Abstract: A 276 word abstract is available. Use 'abstract' method.
Information is available on: preprocessing
notes:
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    ABI Human Genome Survey Microarray Version 2
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    2015-09-22 20:04:13

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An object of class 'AnnotatedDataFrame'
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Details

assayData: 18439 features, 204 samples
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 Overall survival time-to-event summary (in years):
 Call: survfit(formula = Surv(time, cens) ~ -1)

10 observations deleted due to missingness
 n events median 0.95LCL 0.95UCL
 194.00 57.00 NA 3.67 NA

 Available sample meta-data:

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 tumor
 204

histological_type:
 other ser NA's

```

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143 50 11

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9 185 10

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2 3 4 NA's
9 154 31 10

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50 143 11

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30.0 335.0 487.0 580.1 722.5 1461.0 10

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70 124 10

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Value

An expression set

GSE51088

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.

Format

```
experimentData (eset) :
```

```
Experiment data
```

```
  Experimenter name: Karlan BY, Dering J, Walsh C, Orsulic S, Lester J, Anderson LA
```

```
  Laboratory: Karlan, Slamon 2014
```

```
  Contact information:
```

```
  Title: POSTN/TGFBI-associated stromal signature predicts poor prognosis in serous
```

```
  URL:
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  PMIDs: 24368280
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Abstract: A 250 word abstract is available. Use 'abstract' method.
 Information is available on: preprocessing

notes:

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  Agilent-012097 Human 1A Microarray (V2) G4110B (Probe Name version)
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  Agilent G4110B
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  in situ oligonucleotide
version:
  2015-09-22 20:05:48
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featureData(eset):

An object of class 'AnnotatedDataFrame'

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featureNames: A_23_P100001 A_23_P100011 ... A_23_P99996 (18703 total)
varLabels: probeset gene EntrezGene.ID best_probe
varMetadata: labelDescription
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Details

assayData: 18703 features, 172 samples

Platform type:

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

Call: survfit(formula = Surv(time, cens) ~ -1)

20 observations deleted due to missingness

n	events	median	0.95LCL	0.95UCL
152.00	112.00	4.13	3.50	4.92

 Available sample meta-data:

alt_sample_name:

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Ov_Tumor_Ref_Mix vs. CS-OV-005 Ov_Tumor_Ref_Mix vs. CS-OV-006
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high low NA's
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summarystage:
early late NA's
   31  120  21

tumorstage:
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  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
   30   791   1491  1835  2344  7001  20

vital_status:
deceased  living      NA's
   112     40     20

```

percent_normal_cells:

30- NA's
140 32

percent_stromal_cells:

30- NA's
140 32

percent_tumor_cells:

70+ NA's
140 32

uncurated_author_metadata:

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Value

An expression set

GSE6008

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.

Format

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Experiment data
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  Laboratory: Murph, Mills 2009
  Contact information:
  Title: Lysophosphatidic acid-induced transcriptional profile represents serous ep
  URL:
  PMIDs: 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:
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  version:
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featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
    (20967 total)
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  varMetadata: labelDescription

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Details

```

assayData: 20967 features, 103 samples
Platform type:
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Available sample meta-data:

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histological_type:
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 8 37 13 41 4

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 103

summarygrade:
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 38 36 29

summarystage:
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 42 53 8

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 a b c d NA's
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Value

An expression set

GSE6822

Classification of ovarian tumor samples

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.

Format

experimentData (eset):
Experiment data
 Experimenter name: Ouellet V, Provencher DM, Maugard CM, Le Page C, Ren F, Lussier C
 Laboratory: Ouellet, Mes-Masson 2005
 Contact information:
 Title: Classification of ovarian tumor samples
 URL:
 PMIDs: PMID unknown

Abstract: A 40 word abstract is available. Use 'abstract' method.
Information is available on: preprocessing

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    Affymetrix
  platform_distribution:
    commercial
  platform_accession:
    GPL80
  version:
    2015-09-22 20:07:22

featureData(eset):
An object of class 'AnnotatedDataFrame'
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  varMetadata: labelDescription

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Details

assayData: 6407 features, 66 samples

Platform type:

 Available sample meta-data:

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Ovarian tumor AM127	Ovarian tumor AM137	Ovarian tumor AM138	Ovarian tumor AM144
1	1	1	1
Ovarian tumor AM178	Ovarian tumor AM179	Ovarian tumor AM182	Ovarian tumor AM195
1	1	1	1
Ovarian tumor AM196	Ovarian tumor AM198	Ovarian tumor AM200	Ovarian tumor AM201
1	1	1	1
Ovarian tumor AM202	Ovarian tumor AM203	Ovarian tumor AM204	Ovarian tumor AM207
1	1	1	1
Ovarian tumor AM208	Ovarian tumor AM209	Ovarian tumor AM225	Ovarian tumor AM226
1	1	1	1
Ovarian tumor AM228	Ovarian tumor AM233	Ovarian tumor AM250	Ovarian tumor AM252
1	1	1	1
Ovarian tumor AM253	Ovarian tumor AM255	Ovarian tumor AM256	Ovarian tumor AM259
1	1	1	1
Ovarian tumor AM261	Ovarian tumor AM263	Ovarian tumor AM268	Ovarian tumor AM269

Ovarian tumor AM287	1	Ovarian tumor AM288	1	Ovarian tumor AM289	1	Ovarian tumor AM290	1
Ovarian tumor AM292	1	Ovarian tumor AM293	1	Ovarian tumor AM294	1	Ovarian tumor AM311	1
Ovarian tumor AM313	1	Ovarian tumor AM315	1	Ovarian tumor AM317	1	Ovarian tumor AM333	1
Ovarian tumor AM335	1	Ovarian tumor AM339	1	Ovarian tumor AM341	1	Ovarian tumor AM344	1
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Ovarian tumor AM381	1	Ovarian tumor AM382	1	Ovarian tumor AM398	1	Ovarian tumor AM429	1
Ovarian tumor AM431	1	Ovarian tumor AM438	1				

sample_type:

tumor
66

histological_type:

clearcell	endo	mix	mucinous
11	7	3	1
ser undifferentiated			
41	3		

primarysite:

ov
66

summarygrade:

high	low	NA's
40	15	11

grade:

1	2	3	NA's
1	14	40	11

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2	2					

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duplicates:
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Value

An expression set

GSE8842

*Analysis of gene expression in early-stage ovarian cancer.***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.

Format

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Experiment data
  Experimenter name: Marchini S, Mariani P, Chiorino G, Marrazzo E, Bonomi R, Frusc
  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:
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    Agilent Human 1 cDNA Microarray (G4100A)
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    Agilent G4100A cDNA
  platform_summary:
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  platform_manufacturer:
    Agilent
  platform_distribution:
    custom-commerical
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                                1                                1
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  p90bis sample_Ovarian tumor
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sample_type:
borderline      tumor
          15          68

histological_type:
      clearcell      endo      mucinous      other
          16          17          17          1
      ser undifferentiated
          31          1

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.
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recurrence_status:

norecurrence	recurrence
62	21

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

An expression set

GSE9891

*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.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Tothill RW, Tinker AV, George J, Brown R, Fox SB, Lade S, John
  Laboratory: Tothill, Bowtell 2008
  Contact information:
  Title: Novel molecular subtypes of serous and endometrioid ovarian cancer linked
  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
version:
  2015-09-22 20:16:32

```

```

featureData(eset):
An object of class 'AnnotatedDataFrame'
 featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
 (42447 total)
 varLabels: probeset gene EntrezGene.ID best_probe
 varMetadata: labelDescription

```

Details

```

assayData: 42447 features, 285 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

```

```

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

```

```

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

```

```

alt_sample_name:
  X129    X146    X152  X20019  X20025  X20027  X20031  X20032  X20041  X20046
      1      1      1      1      1      1      1      1      1      1
X20074  X22002  X22012  X22013  X22020  X22023  X22027  X22029  X22031  X22037
      1      1      1      1      1      1      1      1      1      1
X22046  X22047  X22048  X22057  X22058  X2219   X2227  X23026  X23030  X23036
      1      1      1      1      1      1      1      1      1      1
X23043  X23052  X23053  X23055  X23066  X23070  X23074  X23077  X23084  X23098
      1      1      1      1      1      1      1      1      1      1
X23102  X23106  X23116  X23128  X23139  X23143  X23162  X23165  X23167  X23170
      1      1      1      1      1      1      1      1      1      1
X23172  X23177  X23178  X23182  X23187  X23197  X23202  X23204  X23210  X23212
      1      1      1      1      1      1      1      1      1      1
X23213  X23221  X26047    X261  X27006  X27098  X32013  X32022  X32032  X32034
      1      1      1      1      1      1      1      1      1      1
X32048  X32049  X32054  X32055  X32089  X32098  X32103  X32117  X34019  X34049
      1      1      1      1      1      1      1      1      1      1

```

X34066	X34078	X34080	X34085	X34086	X34090	X34102	X34103	X34111	X34113
1	1	1	1	1	1	1	1	1	1
X34117	X34125	X34165	X34168	X34172	X34186	X34202	X34207	X34801	(Other)
1	1	1	1	1	1	1	1	1	186

sample_type:
tumor
285

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:
2004-12-03 2004-12-23 2005-01-12 2005-01-17 2005-01-24 2005-01-31 2005-02-21
           3           4           7           7           8           10           10
2005-03-17 2005-05-05 2005-05-09 2005-05-25 2005-05-27 2005-05-30 2005-06-02
           2           1           1           2           3           3           6
2005-06-06 2005-06-08 2005-06-16 2005-06-17 2005-06-24 2005-07-06 2005-07-15
           4           5           3           5           6           2           9
2005-07-20 2005-07-29 2005-08-03 2005-08-05 2005-08-18 2005-08-24 2005-08-26
           7           5           6           3           4           8           4
2005-09-09 2005-09-14 2005-09-16 2005-09-21 2005-10-05 2005-10-26 2005-10-28
           4           6           6           4           5           2           4
2005-11-04 2005-11-09 2005-11-11 2005-11-23 2005-12-15 2005-12-21 2006-01-20
           6           3           7           4           7           8           3
2006-01-31 2006-02-08 2006-02-28 2006-04-05 2006-04-06 2006-04-12 2006-04-13
           7           3           3           7           3           7           4
2006-04-28 2006-05-03 2006-06-06 2006-06-07 2006-06-22 2006-07-07 2006-07-19
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uncurated_author_metadata:

```

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```
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```

```
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```

```
title: X34801///geo_accession: GSM249909///status: Public on Mar 01 2008//
```

Value

An expression set

```
loadOvarianDatasets
```

Function to load ovarian cancer SummarizedExperiment objects from the Experiment Hub

Description

This function returns ovarian cancer datasets from the hub and a vector of patients from the datasets that are duplicates based on a spearman correlation > 0.98

Usage

```
loadOvarianDatasets(  
  rescale = FALSE,  
  minNumberGenes = 0,  
  minNumberEvents = 0,  
  minSampleSize = 0,  
  keepCommonOnly = FALSE,  
  imputeMissing = FALSE,  
  removeDuplicates = FALSE  
)
```

Arguments

`rescale` apply centering and scaling to the expression sets (default FALSE)

`minNumberGenes` an integer specifying to remove expression sets with less genes than this number (default 0)

`minNumberEvents` an integer specifying how man survival events must be in the dataset to keep the dataset (default 0)

`minSampleSize`
 an integer specifying the minimum number of patients required in a summarizedExperiment (default 0)

`keepCommonOnly`
 remove entrezIDs not common to all datasets (default FALSE)

`imputeMissing`
 remove patients from datasets with missing expression values

`removeDuplicates`
 remove patients with a Spearman correlation greater than or equal to 0.98 with other patient expression profiles (default TRUE)

Value

a list with 2 elements. The First element named `summarizedExperiments` contains the datasets. The second element named `duplicates` contains a vector with patient IDs for the duplicate patients (those with Spearman correlation greater than or equal to 0.98 with other patient expression profiles).

Examples

```
experimentsAndDups = loadOvarianDatasets()
```

`loadOvarianEsets` *Function to load ovarian cancer expression sets from the Experiment Hub*

Description

This function returns ovarian cancer datasets from the hub and a vector of patients from the datasets that are most likely duplicates

Usage

```
loadOvarianEsets(
  removeDuplicates = TRUE,
  quantileCutoff = 0,
  rescale = FALSE,
  minNumberGenes = 0,
  minNumberEvents = 0,
  minSampleSize = 0,
  removeRetracted = TRUE,
  removeSubsets = TRUE,
  keepCommonOnly = FALSE,
  imputeMissing = FALSE
)
```

Arguments

<code>removeDuplicates</code>	remove patients with a Spearman correlation greater than or equal to 0.98 with other patient expression profiles (default TRUE)
<code>quantileCutoff</code>	A numeric between 0 and 1 specifying to remove genes with standard deviation below the required quantile (default 0)
<code>rescale</code>	apply centering and scaling to the expression sets (default FALSE)
<code>minNumberGenes</code>	an integer specifying to remove expression sets with less genes than this number (default 0)
<code>minNumberEvents</code>	an integer specifying how many survival events must be in the dataset to keep the dataset (default 0)
<code>minSampleSize</code>	an integer specifying the minimum number of patients required in an eset (default 0)
<code>removeRetracted</code>	remove datasets from retracted papers (default TRUE, currently just PMID17290060 dataset)
<code>removeSubsets</code>	remove datasets that are a subset of other datasets (default TRUE, currently just PMID19318476)
<code>keepCommonOnly</code>	remove probes not common to all datasets (default FALSE)
<code>imputeMissing</code>	remove patients from datasets with missing expression values

Value

a list with 2 elements. The first element named `esets` contains the datasets. The second element named `duplicates` contains a vector with patient IDs for the duplicate patients (those with Spearman correlation greater than or equal to 0.98 with other patient expression profiles).

Examples

```
esetsAndDups = loadOvarianEsets()
```

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.

Format

```

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

```

These samples are a subset of PMID17290060.
 version:
 2015-09-22 20:17:53

```
featureData(eset):
An object of class 'AnnotatedDataFrame'
 featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
 (20967 total)
 varLabels: probeset gene EntrezGene.ID best_probe
 varMetadata: labelDescription
```

Details

assayData: 20967 features, 63 samples
 Platform type:

 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
 7 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:

2002-09-20	2002-10-23	2002-11-12	2002-12-16	2002-12-21	2003-01-03	2003-05-30
15	9	10	1	3	11	13
2003-07-02						
1						

uncurated_author_metadata:

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1761///Cancer.Type: Early sta

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1762///Cancer.Type: Early sta

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1763///Cancer.Type: Early sta

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1764///Cancer.Type: Early sta

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1765///Cancer.Type: Early sta

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1772///Cancer.Type: Lon

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1773///Cancer.Type: Lon

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1774///Cancer.Type: Lon

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1775///Cancer.Type: Lon

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Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1777///Cancer.Type: Lon

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Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1781///Cancer.Type: Lon
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1828///Cancer.Type: SH
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1829///Cancer.Type: Shor
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1830///Cancer.Type: Shor
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1831///Cancer.Type: Shor
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1832///Cancer.Type: Shor
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1833///Cancer.Type: Shor
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1834///Cancer.Type: Shor
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1835///Cancer.Type: Shor
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1836///Cancer.Type: Shor
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1900///Cancer.Type: Lon
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1901///Cancer.Type: Lon
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1902///Cancer.Type: Lon
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1903///Cancer.Type: Early sta
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1904///Cancer.Type: Lon
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1905///Cancer.Type: Shor
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1906///Cancer.Type: Shor
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1907///Cancer.Type: Lon
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1908///Cancer.Type: Shor
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1909///Cancer.Type: Shor
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1989///Cancer.Type: Lon
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2003///Cancer.Type: Shor
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2004///Cancer.Type: Shor

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2005///Cancer.Type: Short
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2019///Cancer.Type: Long
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2020///Cancer.Type: Long
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2021///Cancer.Type: Long
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2026///Cancer.Type: Short
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2027///Cancer.Type: Short
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2028///Cancer.Type: Short
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2029///Cancer.Type: Short
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2030///Cancer.Type: Short
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2031///Cancer.Type: Long
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2032///Cancer.Type: Long
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2033///Cancer.Type: Long
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2390///Cancer.Type: Early stage
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2391///Cancer.Type: Early stage
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2392///Cancer.Type: Early stage
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2393///Cancer.Type: Early stage
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2394///Cancer.Type: Long
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2395///Cancer.Type: Long
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2396///Cancer.Type: Short
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2397///Cancer.Type: Short
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2398///Cancer.Type: Short
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2399///Cancer.Type: Short
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2400///Cancer.Type: Short
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2401///Cancer.Type: Short

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2402///Cancer.Type: SH

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2536///Cancer.Type: Early st

Value

An expression set

PMID17290060	<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.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Dressman HK, Berchuck A, Chan G, Zhai J, Bild A, Sayer R, Cra
  Laboratory: Dressman, Lancaster 2007
  Contact information:
  Title: An integrated genomic-based approach to individualized treatment of patien
  URL:
  PMIDs: 17290060
```

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

2895	2967	2981	2999	3018	3090	3102	3107	3142	860
1	1	1	1	1	1	1	1	1	1
872	922	D1805	D1837	D1859	D2098	D2208	D2332	D2342	D2358
1	1	1	1	1	1	1	1	1	1
D2421	D2432	D2433	D2480	D2557	D2559	D2560	D2572	D2575	D2576
1	1	1	1	1	1	1	1	1	1
D2581	D2603	D2611	D2629	D2640	D2648	D2668	D2689	D2691	D2700
1	1	1	1	1	1	1	1	1	1
D2726	D2727	D2733	D2738	D2749	D2776	D2792	M1054	M1055	M120
1	1	1	1	1	1	1	1	1	1
M1241	M1390	M1503	M1572	M17	M1891	M2070	M2097	M2184	(Other)
1	1	1	1	1	1	1	1	1	18

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 85
  progressivedisease 32

```

```

debulking:
  optimal 63
  suboptimal 54

```

```

batch:
2002-09-20 2002-10-23 2002-11-12 2002-12-16 2002-12-21 2003-01-03 2003-05-30
           10          8          9          1          3          11          10
2004-03-09 2004-03-16 2004-04-20 2004-05-18 2004-05-21 2004-05-27 2004-06-22
           16          6          5          15         7          7          1
2004-06-23
           8

```

```

uncurated_author_metadata:

```

```

  OVC.TumorID: 1024///Survival: 13///X0...alive...1...dead: 1/
  OVC.TumorID: 1447///Survival: 75///X0...alive...1...dead: 1/
  OVC.TumorID: 1451///Survival: 132///X0...alive...1...dead: 1/
  OVC.TumorID: 1504///Survival: 108///X0...alive...1...dead: 1/
  OVC.TumorID: 1526///Survival: 74///X0...alive...1...dead: 1/
  OVC.TumorID: 1552///Survival: 33///X0...alive...1...dead: 1/
  OVC.TumorID: 1578///Survival: 33///X0...alive...1...dead: 1/
  OVC.TumorID: 1590///Survival: 148///X0...alive...1...dead: 1/
  OVC.TumorID: 1615///Survival: 13///X0...alive...1...dead: 1/
  OVC.TumorID: 1623///Survival: 147///X0...alive...1...dead: 1/
  OVC.TumorID: 1665///Survival: 15///X0...alive...1...dead: 1/
  OVC.TumorID: 1674///Survival: 18///X0...alive...1...dead: 1/
  OVC.TumorID: 1675///Survival: 34///X0...alive...1...dead: 1/
  OVC.TumorID: 1774///Survival: 22///X0...alive...1...dead: 1/
  OVC.TumorID: 1784///Survival: 78///X0...alive...1...dead: 1/

```

OVC.TumorID: 1834///Survival: 118///X0...alive...1...dead: 1/
OVC.TumorID: 1846///Survival: 142///X0...alive...1...dead: 1/
OVC.TumorID: 1877///Survival: 119///X0...alive...1...dead: 1/
OVC.TumorID: 1913///Survival: 32///X0...alive...1...dead: 1/
OVC.TumorID: 1929///Survival: 134///X0...alive...1...dead: 1/
OVC.TumorID: 2046///Survival: 127///X0...alive...1...dead: 1/
OVC.TumorID: 2063///Survival: 16///X0...alive...1...dead: 1/
OVC.TumorID: 2064///Survival: 27///X0...alive...1...dead: 1///Ass
OVC.TumorID: 2075///Survival: 87///X0...alive...1...dead: 1/
OVC.TumorID: 2198///Survival: 91///X0...alive...1...dead: 1/
OVC.TumorID: 2204///Survival: 118///X0...alive...1...dead: 1/
OVC.TumorID: 2324///Survival: 98///X0...alive...1...dead: 1/
OVC.TumorID: 2419///Survival: 107///X0...alive...1...dead: 0/
OVC.TumorID: 2422///Survival: 20///X0...alive...1...dead: 1/
OVC.TumorID: 2424///Survival: 16///X0...alive...1...dead: 1/
OVC.TumorID: 2465///Survival: 17///X0...alive...1...dead: 1/
OVC.TumorID: 2476///Survival: 86///X0...alive...1...dead: 1/
OVC.TumorID: 2479///Survival: 95///X0...alive...1...dead: 0/
OVC.TumorID: 2505///Survival: 95///X0...alive...1...dead: 0/
OVC.TumorID: 2542///Survival: 36///X0...alive...1...dead: 1/
OVC.TumorID: 2573///Survival: 7///X0...alive...1...dead: 1/
OVC.TumorID: 2673///Survival: 74///X0...alive...1...dead: 0/
OVC.TumorID: 2739///Survival: 67///X0...alive...1...dead: 0/
OVC.TumorID: 2802///Survival: 24///X0...alive...1...dead: 1/

OVC.TumorID: 2849///Survival: 23///X0...alive...1...dead: 1//
OVC.TumorID: 2895///Survival: 9///X0...alive...1...dead: 1//
OVC.TumorID: 2967///Survival: 22///X0...alive...1...dead: 1//
OVC.TumorID: 2981///Survival: 6///X0...alive...1...dead: 1//
OVC.TumorID: 2999///Survival: 16///X0...alive...1...dead: 1//
OVC.TumorID: 3018///Survival: 16///X0...alive...1...dead: 1//
OVC.TumorID: 3090///Survival: 16///X0...alive...1...dead: 1//
OVC.TumorID: 3102///Survival: 10///X0...alive...1...dead: 1//
OVC.TumorID: 3107///Survival: 31///X0...alive...1...dead: 1//
OVC.TumorID: 3142///Survival: 18///X0...alive...1...dead: 1//
OVC.TumorID: 860///Survival: 17///X0...alive...1...dead: 1//
OVC.TumorID: 872///Survival: 185///X0...alive...1...dead: 0//
OVC.TumorID: 922///Survival: 183///X0...alive...1...dead: 1//
OVC.TumorID: D1805///Survival: 9///X0...alive...1...dead: 1//
OVC.TumorID: D1837///Survival: 83///X0...alive...1...dead: 0//
OVC.TumorID: D1859///Survival: 110///X0...alive...1...dead: 1//
OVC.TumorID: D2098///Survival: 42///X0...alive...1...dead: 1//
OVC.TumorID: D2208///Survival: 2///X0...alive...1...dead: 0//
OVC.TumorID: D2332///Survival: 27///X0...alive...1...dead: 1//
OVC.TumorID: D2342///Survival: 20///X0...alive...1...dead: 1//
OVC.TumorID: D2358///Survival: 9///X0...alive...1...dead: 1//
OVC.TumorID: D2421///Survival: 12///X0...alive...1...dead: 1//
OVC.TumorID: D2432///Survival: 34///X0...alive...1...dead: 1//
OVC.TumorID: D2433///Survival: 49///X0...alive...1...dead: 0//

OVC.TumorID: D2480///Survival: 34///X0...alive...1...dead: 1//
OVC.TumorID: D2557///Survival: 62///X0...alive...1...dead: 0//
OVC.TumorID: D2559///Survival: 5///X0...alive...1...dead: 1//
OVC.TumorID: D2560///Survival: 91///X0...alive...1...dead: 0//
OVC.TumorID: D2572///Survival: 37///X0...alive...1...dead: 0//
OVC.TumorID: D2575///Survival: 33///X0...alive...1...dead: 1//
OVC.TumorID: D2576///Survival: 17///X0...alive...1...dead: 1//
OVC.TumorID: D2581///Survival: 63///X0...alive...1...dead: 0//
OVC.TumorID: D2603///Survival: 42///X0...alive...1...dead: 0//
OVC.TumorID: D2611///Survival: 2///X0...alive...1...dead: 1//
OVC.TumorID: D2629///Survival: 36///X0...alive...1...dead: 0//
OVC.TumorID: D2640///Survival: 1///X0...alive...1...dead: 1//
OVC.TumorID: D2648///Survival: 35///X0...alive...1...dead: 1//
OVC.TumorID: D2668///Survival: 40///X0...alive...1...dead: 0//
OVC.TumorID: D2689///Survival: 45///X0...alive...1...dead: 0//
OVC.TumorID: D2691///Survival: 63///X0...alive...1...dead: 0//
OVC.TumorID: D2700///Survival: 74///X0...alive...1...dead: 0//
OVC.TumorID: D2726///Survival: 71///X0...alive...1...dead: 0//
OVC.TumorID: D2727///Survival: 53///X0...alive...1...dead: 0//
OVC.TumorID: D2733///Survival: 55///X0...alive...1...dead: 0//
OVC.TumorID: D2738///Survival: 68///X0...alive...1...dead: 0//
OVC.TumorID: D2749///Survival: 24///X0...alive...1...dead: 1//
OVC.TumorID: D2776///Survival: 10///X0...alive...1...dead: 1//
OVC.TumorID: D2792///Survival: 16///X0...alive...1...dead: 1//

OVC.TumorID: M1054///Survival: 101///X0...alive...1...dead: 0///Assigned

OVC.TumorID: M1055///Survival: 13///X0...alive...1...dead: 0///Assigned

OVC.TumorID: M120///Survival: 35///X0...alive...1...dead: 1///Assigned

OVC.TumorID: M1241///Survival: 95///X0...alive...1...dead: 0///Assigned.S

OVC.TumorID: M1390///Survival: 46///X0...alive...1...dead: 0///Assigned

OVC.TumorID: M1503///Survival: 53///X0...alive...1...dead: 1///Assigned

OVC.TumorID: M1572///Survival: 22///X0...alive...1...dead: 1///Assigned

OVC.TumorID: M17///Survival: 17///X0...alive...1...dead: 0///Assigned.Sta

OVC.TumorID: M1891///Survival: 12///X0...alive...1...dead: 0///Assigned.Stage: 4///

OVC.TumorID: M2070///Survival: 65///X0...alive...1...dead: 0///Assigned.S

OVC.TumorID: M2097///Survival: 58///X0...alive...1...dead: 0///Assigned

OVC.TumorID: M2184///Survival: 34///X0...alive...1...dead: 0///Assigned

Value

An expression set

PMID19318476	<i>Microarray analysis of early stage serous ovarian cancers shows profiles predictive of favorable outcome.</i>
--------------	--

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.

Format

```

experimentData(eset):
Experiment data
  Experimenter name: Berchuck A, Iversen ES, Luo J, Clarke JP, Horne H, Levine DA,
  Laboratory: Berchuck, Lancaster 2009
  Contact information:
  Title: Microarray analysis of early stage serous ovarian cancers shows profiles p
  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
  warnings:
    These samples are a subset of PMID17290060.
  version:
    2015-09-22 20:20:30

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
    (20967 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

Details

assayData: 20967 features, 42 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

n	events	median	0.95LCL	0.95UCL
42.00	22.00	2.79	2.30	NA

Available sample meta-data:

alt_sample_name:

D1462	D1805	D2171	D2208	D2247	D2332	D2432	D2480	D2559	D2560	D2575	D2576	D2611
1	1	1	1	1	1	1	1	1	1	1	1	1
D2629	D2640	D2648	D2736	D2749	D2776	D2792	M1025	M1054	M1055	M120	M1241	M1572
1	1	1	1	1	1	1	1	1	1	1	1	1
M17	M1777	M1891	M2184	M2515	M2807	M3035	M337	M3484	M359	M4161	M444	M503
1	1	1	1	1	1	1	1	1	1	1	1	1
M5668	M5775	M806										
1	1	1										

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:

2004-03-09	2004-03-16	2004-04-20	2004-05-18	2004-05-21	2004-05-27	2004-06-22
14	3	4	8	6	5	1
2004-06-23						
1						

uncurated_author_metadata:

Tumor: D2560///NEW.Response: CR///SHORT.LONG: NA///AgeDx: 60///DateDx: 5/14/1996///

Value

An expression set

TCGA.RNASeqV2

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.

Format

```

experimentData(eset):
Experiment data
  Experimenter name: Integrated genomic analyses of ovarian carcinoma. Nature 2011,
  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
  version:
    2015-09-22 20:27:26

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: ?|100133144 ?|100134869 ... ZZZ3|26009 (20471 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

Details

```

assayData: 20471 features, 261 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

      5 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
256.00 143.00   3.62   3.19   4.03

```



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

```
alt_sample_name:
```

```
TCGA-04-1348-01A-01R-1565-13 TCGA-04-1357-01A-01R-1565-13  
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TCGA-09-2045-01A-01R-1568-13 TCGA-09-2048-01A-01R-1568-13  
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TCGA-09-2051-01A-01R-1568-13 TCGA-09-2054-01A-01R-1568-13  
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TCGA-10-0936-01A-01R-1564-13 TCGA-13-0730-01A-01R-1564-13  
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TCGA-13-0799-01A-01R-1564-13 TCGA-13-0800-01A-01R-1564-13  
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TCGA-13-1481-01A-01R-1565-13 TCGA-13-1497-01A-01R-1565-13
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TCGA-23-1809-01A-01R-1566-13	1	TCGA-23-2077-01A-01R-1568-13	1
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TCGA-24-0975-01A-02R-1565-13	1	TCGA-24-1103-01A-01R-1565-13	1
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TCGA-24-1551	TCGA-24-1552	TCGA-24-1553	TCGA-24-1555	TCGA-24-1556	TCGA-24-1557
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TCGA-24-1558	TCGA-24-1560	TCGA-24-1562	(Other)		
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sample_type:

tumor

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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	progressivedisease	stabledisease
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:

age_at_initial_pathologic_diagnosis: 38///anatomic_organ_subdivision: Bilateral///b

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age_at_initial_pathologic_diagn  
age_at_initial_pathologic_diagnosis: 4  
age_at_initial_pathologic_diagnosi  
age_at_in  
age_at_initial_pathologic_diagnosis: 42///anatomic_organ_subdivi  
age_at_initial_pathologic_diagnosis: 4  
age_at_init  
age_at_initial_path  
age_at_initial_pathol  
a  
age_at_initial_patholog  
ag  
age_at_initial_p  
age_at_initial_pathologic_diagnosis: 45///anatomic_or  
age_at  
age_at_initial_pathologic_diagnosis: 45///anato  
age_at_initial_patholog
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age_at_initial_pathologic_diagnosis: 48///anatomic_organ_subdivision:

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age_at_initi

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age_at_initial_pathologic_diagnosis: 50///anatomic_organ_

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age_at_initial_pathol

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age_at_initial_pathologic_diagnosis: 50///anatom

age_at_initial_pathologi

age_at_initial_pathologic_diagnosis: 51///anatomic_organ_subdivision: Bilateral//

age_at_initial

age_at_initial_pathologic_diagno

age_at_in

age_at

age_at_initial_pathologic_diagnosis: 51///anatom

age_at_initial_pathologic_di

age_at_initial_p

age

age_at_initial_pathologic_c
age_at_initial_pathologic_diagn

age_at_
age_at_initial_pathologic_diagnosis:
age_at_initial_pathol
age_at_initial_pathologic_diagn
age_at_initial_pathologic_diagnosis: 53///anatomic_organ_sub
age_at_initial_pathologic_diagnosis:
age_at_initial_pathologic_diagnosis: 53///anatomic
age_at_initial_pathol

age_at_initial_pathologic_diagnosis: 54///anatomic_organ_subdivision
age_at_i
age_at_initia

age_at_init
age_at_initial_pathologic_diagnosis: 54///anatomic_organ_subdivisi
age

Value

An expression set

TCGAOVARIAN

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.

Format

```

experimentData(eset):
Experiment data
  Experimenter name: Integrated genomic analyses of ovarian carcinoma. Nature 2011,
  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:
    hthgul33a

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platform_manufacturer:
  Affymetrix
platform_distribution:
  commercial
platform_accession:
  GPL3921
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
version:
  2015-09-22 20:25:15

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-M27830_M_at (21260 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

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Details

```

assayData: 21260 features, 578 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

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  21 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
557.00 290.00   3.73   3.45   4.06

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Available sample meta-data:
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TCGA-01-0636-11A-01R-0362-01 TCGA-01-0637-11A-01R-0362-01
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TCGA-01-0639-11A-01R-0362-01 TCGA-01-0642-11A-02R-0362-01
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TCGA-04-1337-01A-01R-0434-01 TCGA-04-1338-01A-01R-0434-01

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	(Other)	NA's
	479	1

unique_patient_ID:

TCGA-01-0628	TCGA-01-0630	TCGA-01-0631	TCGA-01-0633	TCGA-01-0636	TCGA-01-0637
1	1	1	1	1	1
TCGA-01-0639	TCGA-01-0642	TCGA-04-1331	TCGA-04-1332	TCGA-04-1335	TCGA-04-1336
1	1	1	1	1	1
TCGA-04-1337	TCGA-04-1338	TCGA-04-1341	TCGA-04-1342	TCGA-04-1343	TCGA-04-1346
1	1	1	1	1	1
TCGA-04-1347	TCGA-04-1348	TCGA-04-1349	TCGA-04-1350	TCGA-04-1351	TCGA-04-1353

1	1	1	1	1	1
TCGA-04-1356	TCGA-04-1357	TCGA-04-1360	TCGA-04-1361	TCGA-04-1362	TCGA-04-1364
1	1	1	1	1	1
TCGA-04-1365	TCGA-04-1367	TCGA-04-1369	TCGA-04-1371	TCGA-04-1514	TCGA-04-1516
1	1	1	1	1	1
TCGA-04-1517	TCGA-04-1519	TCGA-04-1525	TCGA-04-1530	TCGA-04-1536	TCGA-04-1542
1	1	1	1	1	1
TCGA-04-1638	TCGA-04-1644	TCGA-04-1646	TCGA-04-1648	TCGA-04-1649	TCGA-04-1651
1	1	1	1	1	1
TCGA-04-1652	TCGA-04-1654	TCGA-04-1655	TCGA-09-0364	TCGA-09-0365	TCGA-09-0366
1	1	1	1	1	1
TCGA-09-0367	TCGA-09-0369	TCGA-09-1659	TCGA-09-1661	TCGA-09-1662	TCGA-09-1664
1	1	1	1	1	1
TCGA-09-1665	TCGA-09-1666	TCGA-09-1667	TCGA-09-1668	TCGA-09-1669	TCGA-09-1670
1	1	1	1	1	1
TCGA-09-1672	TCGA-09-1673	TCGA-09-1674	TCGA-09-1675	TCGA-09-2043	TCGA-09-2044
1	1	1	1	1	1
TCGA-09-2045	TCGA-09-2048	TCGA-09-2049	TCGA-09-2050	TCGA-09-2051	TCGA-09-2053
1	1	1	1	1	1
TCGA-09-2054	TCGA-09-2055	TCGA-09-2056	TCGA-10-0925	TCGA-10-0926	TCGA-10-0927
1	1	1	1	1	1
TCGA-10-0928	TCGA-10-0930	TCGA-10-0931	TCGA-10-0933	TCGA-10-0934	TCGA-10-0935
1	1	1	1	1	1
TCGA-10-0936	TCGA-10-0937	TCGA-10-0938	TCGA-13-0714	TCGA-13-0717	TCGA-13-0720
1	1	1	1	1	1
TCGA-13-0723	TCGA-13-0724	TCGA-13-0725	(Other)		
1	1	1	479		

sample_type:
 adjacentnormal 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	NA's
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
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:

age_at_initial_pathologic_diagnosis:

age_at

age_at_initial_pathologic_

age_at_initial_pathologic_diagnosis: 37///ar

age_at_initial_pathologic_diagnosis: 38///anatomic_organ_subdivision: Bilateral///b

age_at_initial_pathologic_diagnosis: 38///anatomic_organ_subdivision: Bil
age_at_initial_
age_at_in
age_at_initial_pathologic_diagnosis: 39///ana
age_at_initial_pathologic_dia
age_at_initial_pathologic_diagn
age_at_initial_pathologic_diagnosis: 4
age_at_initial_pathologic_diagnosis: 40///anatomic_organ_su
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age_at_initial_pathologic_dia
age_at_initial_pathologic_diagnosis: 4
age_at_initial_pathologic_diagnosis: 42///anatomic_organ_subdivi
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age_at_initial_pathologic_diagnosis: 46///anatomic_organ_subdivision

age_at_initial_pathologic_diagnosis: 46///anato

age_at_initial_pathologic_diagnosis: 47

age_at_initial_pathologic

age_at_initial_pathologic_diagnosis

age_at_initial_pathologic_diagnosis

age_at_initial_pathologic_diagnosis: 47///anatomic

age_at_initial_

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age_at_initial_pathologic_diagnosis: 47///anatomic_or
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age_at_initial_pathologic_diagnosis: 48///ana
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age_at_initial_pathologic_diagnosis
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age_at_initial_pathologic_di
```

```
age_at_initial_pathologic_diagnosis: 48///ana
```

```
duplicates:
  Length      Class      Mode
    578 character character
```

Value

An expression set