

Package ‘MetaGxOvarian’

May 30, 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
(\geq 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

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
  title: Advanced serous ovarian cancer 18///geo_accession: GSM312143///status: Pub
  title: Advanced serous ovarian cancer 20///geo_accession: GSM312144///status: Pub
  title: Advanced serous ovarian cancer 23///geo_accession: GSM312157///status: Pub
  title: Advanced serous ovarian cancer 24///geo_accession: GSM312145///status: Pub
  title: Advanced serous ovarian cancer 25///geo_accession: GSM312146///status: Pub
```

title: Advanced serous ovarian cancer 27///geo_accession: GSM312158///status: Pub
title: Advanced serous ovarian cancer 2///geo_accession: GSM312138///st
title: Advanced serous ovarian cancer 36///geo_accession: GSM312147///status: Pub
title: Advanced serous ovarian cancer 37///geo_accession: GSM312148///status: Pub
title: Advanced serous ovarian cancer 38///geo_accession: GSM312149///status: Pub
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title: Advanced serous ovarian cancer 42///geo_accession: GSM312160///status: Pub
title: Advanced serous ovarian cancer 43///geo_accession: GSM312150///status: Pub
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title: Advanced serous ovarian cancer 46///geo_accession: GSM312162///status: Pub
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title: Advanced serous ovarian cancer 51///geo_accession: GSM312165///status: Pub
title: Advanced serous ovarian cancer 52///geo_accession: GSM312167///status: Pub
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title: Advanced serous ovarian cancer 55///geo_accession: GSM312170///status: Publi
title: Advanced serous ovarian cancer 56///geo_accession: GSM312171///status: Pub
title: Advanced serous ovarian cancer 57///geo_accession: GSM312153///status: Pub
title: Advanced serous ovarian cancer 58///geo_accession: GSM312172///status: Pub
title: Advanced serous ovarian cancer 60///geo_accession: GSM312173///status: Pub
title: Advanced serous ovarian cancer 61///geo_accession: GSM312154///status: Pub
title: Advanced serous ovarian cancer 62///geo_accession: GSM312174///status: Pub
title: Advanced serous ovarian cancer 64///geo_accession: GSM312175///status: Pub

title: Advanced serous ovarian cancer 6///geo_accession: GSM312139///status: E
 title: Advanced serous ovarian cancer 7///geo_accession: GSM312140///status: E
 title: Early serous ovarian cancer 28///geo_accession: GSM312180///status: E
 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
 title: Early serous ovarian cancer 8///geo_accession: GSM312178///status: E
 title: Early serous ovarian cancer 9///geo_accession: GSM312179///status: E
 title: Peritoneum normal 12///geo_accession: GSM312184///status: E
 title: Peritoneum normal 15///geo_accession: GSM312186///status: E
 title: Peritoneum normal 16///geo_accession: GSM312187///status: E
 title: Peritoneum normal 18///geo_accession: GSM312188///status: E
 title: Peritoneum normal 21///geo_accession: GSM312189///status: E
 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:

```

title: ovarian cancer: 010///geo_accession: GSM368670///status: Public
title: ovarian cancer: 011///geo_accession: GSM368671///status: Public
title: ovarian cancer: 012///geo_accession: GSM368672///status: Public

```

title: ovarian cancer: 013///geo_accession: GSM368673///status: Public
title: ovarian cancer: 014///geo_accession: GSM368674///status: Public
title: ovarian cancer: 015///geo_accession: GSM368675///status: Public
title: ovarian cancer: 016///geo_accession: GSM368676///status: Public
title: ovarian cancer: 017///geo_accession: GSM368677///status: Public
title: ovarian cancer: 018///geo_accession: GSM368678///status: Public
title: ovarian cancer: 019///geo_accession: GSM368679///status: Public
title: ovarian cancer: 01///geo_accession: GSM368661///status: Public
title: ovarian cancer: 020///geo_accession: GSM368680///status: Public
title: ovarian cancer: 021///geo_accession: GSM368681///status: Public
title: ovarian cancer: 022///geo_accession: GSM368682///status: Public
title: ovarian cancer: 023///geo_accession: GSM368683///status: Public
title: ovarian cancer: 024///geo_accession: GSM368684///status: Public
title: ovarian cancer: 025///geo_accession: GSM368685///status: Public
title: ovarian cancer: 026///geo_accession: GSM368686///status: Public on Feb 09 20
title: ovarian cancer: 027///geo_accession: GSM368687///status: Public
title: ovarian cancer: 028///geo_accession: GSM368688///status: Public
title: ovarian cancer: 029///geo_accession: GSM368689///status: Public
title: ovarian cancer: 02///geo_accession: GSM368662///status: Public
title: ovarian cancer: 030///geo_accession: GSM368690///status: Public
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title: ovarian cancer: 033///geo_accession: GSM368693///status: Public
title: ovarian cancer: 034///geo_accession: GSM368694///status: Public

title: ovarian cancer: 035///geo_accession: GSM368695///status: Public

title: ovarian cancer: 036///geo_accession: GSM368696///status: Public

title: ovarian cancer: 037///geo_accession: GSM368697///status: Public

title: ovarian cancer: 038///geo_accession: GSM368698///status: Public

title: ovarian cancer: 039///geo_accession: GSM368699///status: Public

title: ovarian cancer: 03///geo_accession: GSM368663///status: Public on Feb

title: ovarian cancer: 040///geo_accession: GSM368700///status: Public

title: ovarian cancer: 041///geo_accession: GSM368701///status: Public

title: ovarian cancer: 042///geo_accession: GSM368702///status: Public

title: ovarian cancer: 043///geo_accession: GSM368703///status: Public

title: ovarian cancer: 044///geo_accession: GSM368704///status: Public

title: ovarian cancer: 045///geo_accession: GSM368705///status: Public

title: ovarian cancer: 046///geo_accession: GSM368706///status: Public

title: ovarian cancer: 047///geo_accession: GSM368707///status: Public

title: ovarian cancer: 048///geo_accession: GSM368708///status: Public

title: ovarian cancer: 049///geo_accession: GSM368709///status: Public

title: ovarian cancer: 04///geo_accession: GSM368664///status: Public

title: ovarian cancer: 050///geo_accession: GSM368710///status: Public

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title: ovarian cancer: 052///geo_accession: GSM368712///status: Public

title: ovarian cancer: 053///geo_accession: GSM368713///status: Public

title: ovarian cancer: 054///geo_accession: GSM368714///status: Public

title: ovarian cancer: 055///geo_accession: GSM368715///status: Public

title: ovarian cancer: 056///geo_accession: GSM368716///status: Public

title: ovarian cancer: 057///geo_accession: GSM368717///status: Pub
title: ovarian cancer: 058///geo_accession: GSM368718///status: Publ
title: ovarian cancer: 059///geo_accession: GSM368719///status: Pub
title: ovarian cancer: 05///geo_accession: GSM368665///status: Publi
title: ovarian cancer: 060///geo_accession: GSM368720///status: Publ
title: ovarian cancer: 061///geo_accession: GSM368721///status: Publ
title: ovarian cancer: 062///geo_accession: GSM368722///status: Publ
title: ovarian cancer: 063///geo_accession: GSM368723///status: Publ
title: ovarian cancer: 064///geo_accession: GSM368724///status: Publ
title: ovarian cancer: 065///geo_accession: GSM368725///status: Publ
title: ovarian cancer: 066///geo_accession: GSM368726///status: Pub
title: ovarian cancer: 067///geo_accession: GSM368727///status: Pub
title: ovarian cancer: 068///geo_accession: GSM368728///status: Publ
title: ovarian cancer: 069///geo_accession: GSM368729///status: Pub
title: ovarian cancer: 06///geo_accession: GSM368666///status: Publ
title: ovarian cancer: 070///geo_accession: GSM368730///status: Pub
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title: ovarian cancer: 072///geo_accession: GSM368732///status: Publ
title: ovarian cancer: 073///geo_accession: GSM368733///status: Public on Feb
title: ovarian cancer: 074///geo_accession: GSM368734///status: Publ
title: ovarian cancer: 075///geo_accession: GSM368735///status: Pub
title: ovarian cancer: 076///geo_accession: GSM368736///status: Publ
title: ovarian cancer: 077///geo_accession: GSM368737///status: Publ
title: ovarian cancer: 078///geo_accession: GSM368738///status: Pub

```

title: ovarian cancer: 079///geo_accession: GSM368739///status: Pub
title: ovarian cancer: 07///geo_accession: GSM368667///status: Publi
title: ovarian cancer: 080///geo_accession: GSM368740///status: Pub
title: ovarian cancer: 08///geo_accession: GSM368668///status: Publi
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 137///geo_accession: GSM432253
title: Serous ovarian cancer 139///geo_accession: GSM432254
title: Serous ovarian cancer 140///geo_accession: GSM432255
title: Serous ovarian cancer 143///geo_accession: GSM432256
title: Serous ovarian cancer 144///geo_accession: GSM432257
title: Serous ovarian cancer 145///geo_accession: GSM432258
title: Serous ovarian cancer 146///geo_accession: GSM432259
title: Serous ovarian cancer 148///geo_accession: GSM432260
title: Serous ovarian cancer 149///geo_accession: GSM432261
title: Serous ovarian cancer 150///geo_accession: GSM432262
title: Serous ovarian cancer 151///geo_accession: GSM432263
title: Serous ovarian cancer 154///geo_accession: GSM432264
title: Serous ovarian cancer 156///geo_accession: GSM432265
title: Serous ovarian cancer 157///geo_accession: GSM432266
title: Serous ovarian cancer 158///geo_accession: GSM432267
title: Serous ovarian cancer 160///geo_accession: GSM432268
title: Serous ovarian cancer 161///geo_accession: GSM432269
title: Serous ovarian cancer 166///geo_accession: GSM432270
title: Serous ovarian cancer 171///geo_accession: GSM432271
title: Serous ovarian cancer 172///geo_accession: GSM432272
title: Serous ovarian cancer 173///geo_accession: GSM432273
title: Serous ovarian cancer 174///geo_accession: GSM432274
title: Serous ovarian cancer 176///geo_accession: GSM432275
title: Serous ovarian cancer 178///geo_accession: GSM432276
title: Serous ovarian cancer 179///geo_accession: GSM432277

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

title: Serous ovarian cancer 183///geo_accession: GSM432276

title: Serous ovarian cancer 184///geo_accession: GSM432276

title: Serous ovarian cancer 185///geo_accession: GSM432276

title: Serous ovarian cancer 186///geo_accession: GSM432276

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

title: Serous ovarian cancer 27///geo_accession: GSM432282

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

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

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

title: Serous ovarian cancer 37///geo_accession: GSM432280

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
title: Serous ovarian cancer 56///geo_accession: GSM432303
title: Serous ovarian cancer 57///geo_accession: GSM432304
title: Serous ovarian cancer 58///geo_accession: GSM432305
title: Serous ovarian cancer 60///geo_accession: GSM432307
title: Serous ovarian cancer 61///geo_accession: GSM432308
title: Serous ovarian cancer 62///geo_accession: GSM432309
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
title: Ovarian Tumor, 394///geo_accession: GSM461382///status: Public on Oct
title: Ovarian Tumor, 396///geo_accession: GSM461376///status: Public on Oct
title: Ovarian Tumor, 402///geo_accession: GSM461355///status: Public on Oct
title: Ovarian Tumor, 410///geo_accession: GSM461356///status: Public on Oct 17 20
title: Ovarian Tumor, 412///geo_accession: GSM461357///status: Public on Oct 1
title: Ovarian Tumor, 434///geo_accession: GSM461358///status: Public on Oct
title: Ovarian Tumor, 443///geo_accession: GSM461377///status: Public on Oct 1
title: Ovarian Tumor, 461///geo_accession: GSM461394///status: Public on Oct
title: Ovarian Tumor, 467///geo_accession: GSM461359///status: Public on Oct
title: Ovarian Tumor, 477///geo_accession: GSM461383///status: Public on Oct
title: Ovarian Tumor, 486///geo_accession: GSM461395///status: Public on Oct
title: Ovarian Tumor, 629///geo_accession: GSM461360///status: Public on Oct 17 2
title: Ovarian Tumor, 631///geo_accession: GSM461396///status: Public on Oct
title: Ovarian Tumor, 656///geo_accession: GSM461384///status: Public on Oct
title: Ovarian Tumor, 662///geo_accession: GSM461370///status: Public on Oct
title: Ovarian Tumor, 692///geo_accession: GSM461397///status: Public on Oct
title: Ovarian Tumor, 694///geo_accession: GSM461385///status: Public on Oct
title: Ovarian Tumor, 702///geo_accession: GSM461361///status: Public on Oct
title: Ovarian Tumor, 714///geo_accession: GSM461362///status: Public on Oct
title: Ovarian Tumor, 715///geo_accession: GSM461386///status: Public on Oct
title: Ovarian Tumor, 718///geo_accession: GSM461398///status: Public on Oct
title: Ovarian Tumor, 744///geo_accession: GSM461378///status: Public on Oct
title: Ovarian Tumor, 765///geo_accession: GSM461363///status: Public on Oct

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///statu
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///statu
title: Ovarian cancer_sample 23///geo_accession: GSM495161///statu
title: Ovarian cancer_sample 24///geo_accession: GSM495162///statu
title: Ovarian cancer_sample 25///geo_accession: GSM495163///statu
title: Ovarian cancer_sample 26///geo_accession: GSM495164///status
title: Ovarian cancer_sample 27///geo_accession: GSM495165///status: Pu
title: Ovarian cancer_sample 28///geo_accession: GSM495166///stat
title: Ovarian cancer_sample 29///geo_accession: GSM495167///status: Public on Jul
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title: Ovarian cancer_sample 31///geo_accession: GSM495169///status: Public o
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 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:
    hgu133plus2
  platform_manufacturer:
    Affymetrix
  platform_distribution:
    commercial
  platform_accession:
    GPL570|GPL2005|GPL6801

```

```

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

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, 140 samples

Platform type:

 Available sample meta-data:

alt_sample_name:

```

Breast metastasis in the ovary_OC01_ARN0016 [HG-U133_Plus_2]
  1
Breast metastasis in the ovary_OC01_ARN0017 [HG-U133_Plus_2]
  1
Breast metastasis in the ovary_OC01_ARN0020 [HG-U133_Plus_2]
  1
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]

```


| | | |
|---|------------------|---|
| 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 |
| Breast metastasis in the ovary_OC01_ARN0123 | [HG-U133_Plus_2] | 1 |
| Breast metastasis in the ovary_OC01_ARN0126 | [HG-U133_Plus_2] | 1 |
| Breast metastasis in the ovary_OC01_ARN0141 | [HG-U133_Plus_2] | 1 |
| Breast metastasis in the ovary_OC01_ARN0142 | [HG-U133_Plus_2] | 1 |
| Breast metastasis in the ovary_OC01_ARN0143 | [HG-U133_Plus_2] | 1 |
| Breast metastasis in the ovary_OC01_ARN0145 | [HG-U133_Plus_2] | 1 |
| Breast metastasis in the ovary_OC01_ARN0146 | [HG-U133_Plus_2] | 1 |
| Breast metastasis in the ovary_OC01_ARN0153 | [HG-U133_Plus_2] | 1 |
| Breast metastasis in the ovary_OC01_ARN0162 | [HG-U133_Plus_2] | 1 |
| Breast metastasis in the ovary_OC01_ARN0201 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0001 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0002 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0004 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0005 | [HG-U133_Plus_2] | 1 |

| | | |
|--------------------------------|------------------|---|
| Ovarian carcinoma_OC01_ARN0007 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0008 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0009 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0010 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0011 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0012 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0013 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0015 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0022 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0023 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0025 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0028 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0030 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0032 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0034 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0036 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0037 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0038 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0039 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0041 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0042 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0045 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0049 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0057 | [HG-U133_Plus_2] | 1 |

| | | |
|--------------------------------|------------------|---|
| | | 1 |
| Ovarian carcinoma_OC01_ARN0058 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0061 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0062 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0063 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0064 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0066 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0067 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0070 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0072 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0075 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0076 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0080 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0084 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0085 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0089 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0091 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0093 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0095 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0096 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0100 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0101 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0103 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0105 | [HG-U133_Plus_2] | 1 |
| Ovarian carcinoma_OC01_ARN0106 | [HG-U133_Plus_2] | 1 |

```

1
Ovarian carcinoma_OC01_ARN0107 [HG-U133_Plus_2]
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Ovarian carcinoma_OC01_ARN0108 [HG-U133_Plus_2]
1
Ovarian carcinoma_OC01_ARN0109 [HG-U133_Plus_2]
1
Ovarian carcinoma_OC01_ARN0111 [HG-U133_Plus_2]
1
Ovarian carcinoma_OC01_ARN0113 [HG-U133_Plus_2]
1
Ovarian carcinoma_OC01_ARN0114 [HG-U133_Plus_2]
1
Ovarian carcinoma_OC01_ARN0115 [HG-U133_Plus_2]
1
Ovarian carcinoma_OC01_ARN0116 [HG-U133_Plus_2]
1
Ovarian carcinoma_OC01_ARN0118 [HG-U133_Plus_2]
1
Ovarian carcinoma_OC01_ARN0119 [HG-U133_Plus_2]
1
Ovarian carcinoma_OC01_ARN0124 [HG-U133_Plus_2]
1
Ovarian carcinoma_OC01_ARN0125 [HG-U133_Plus_2]
1
(Other)
41

```

```

sample_type:
tumor
  140

```

```

histological_type:
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 |
|---|----|----|------|
| 6 | 27 | 63 | 44 |

batch:

| 2006-06-01 | 2006-06-27 | 2006-06-28 | 2006-06-29 | 2006-06-30 | 2006-07-20 | 2008-03-06 |
|------------|------------|------------|------------|------------|------------|------------|
| | 21 | 18 | 37 | 20 | 36 | 7 |
| | | | | | | 1 |

uncurated_author_metadata:

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title: Breast metastasis in the ovary_OC01_ARN0055 [HG-U133_Plus_2]///geo_accession

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title: Breast metastasis in the ovary_OC01_ARN0079 [HG-U133_Plus_2]///geo_accession

title: Breast metastasis in the ovary_OC01_ARN0081 [HG-U133_Plus_2]///geo_accession

title: Breast metastasis in the ovary_OC01_ARN0083 [HG-U133_Plus_2]///geo_accession

title: Breast metastasis in the ovary_OC01_ARN0092 [HG-U133_Plus_2]///geo_accession

title: Breast metastasis in the ovary_OC01_ARN0097 [HG-U133_Plus_2]///geo_accession

title: Breast metastasis in the ovary_OC01_ARN0098 [HG-U133_Plus_2]///geo_accession

title: Breast metastasis in the ovary_OC01_ARN0099 [HG-U133_Plus_2]///geo_accession

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title: Breast metastasis in the ovary_OC01_ARN0104 [HG-U133_Plus_2]///geo_accession

title: Breast metastasis in the ovary_OC01_ARN0112 [HG-U133_Plus_2]///geo_accession

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title: Breast metastasis in the ovary_OC01_ARN0121 [HG-U133_Plus_2]///geo_accession

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title: Breast metastasis in the ovary_OC01_ARN0126 [HG-U133_Plus_2]///geo_accession

title: Breast metastasis in the ovary_OC01_ARN0141 [HG-U133_Plus_2]///geo_accession

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title: Breast metastasis in the ovary_OC01_ARN0153 [HG-U133_Plus_2]///geo_accession

title: Breast metastasis in the ovary_OC01_ARN0162 [HG-U133_Plus_2]///geo_accession

title: Breast metastasis in the ovary_OC01_ARN0201 [HG-U133_Plus_2]///geo_accession

title: Ovarian carcinoma_OC01_A

title: Ovarian carcinoma_OC01_ARN0002

title: Ovarian carcinoma_OC01_ARN

title: Ovarian carcinoma_OC01_A

title: Ovarian carcinoma_OC01_ARN

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title: Ovarian carcinoma_OC01_ARN0002
title: Ovarian carcinoma_OC01_ARN0003
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title: Ovarian carcinoma_OC01_ARN0049
title: Ovarian carcinoma_OC01_ARN0050

title: Ovarian carcinoma_OC01_ARN
 title: Ovarian carcinoma_OC01_ARN0109
 title: Ovarian carcinoma_OC01_ARN
 title: Ovarian carcinoma_OC01_ARN0113
 title: Ovarian carcinoma_OC01_ARN0114 [HC
 title: Ovarian carcinoma_OC01_ARN0115
 title: Ovarian carcinoma_OC01_A
 title: Ovarian carcinoma_OC01_ARN
 title: Ovarian carcinoma_OC01_ARN
 title: Ovarian carcinoma_OC01_ARN
 title: Ovarian carcinoma_OC01_ARN

duplicates:

| | |
|-----------------------------|-----------------------------|
| GSE20565.GSE20565_GSM516722 | GSE20565.GSE20565_GSM516741 |
| 1 | 1 |
| NA's | |
| 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:
  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 19:40:35

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, 204 samples
Platform type:
-----
Available sample meta-data:
-----

alt_sample_name:
Abdominal wall mass - 8176
                      1
Omentum - 8174
Omentum - 1006
                      1
Omentum - 8186

```

| | |
|----------------|----------------|
| 1 | 1 |
| Omentum - 8240 | Ovary - 101094 |
| 1 | 1 |
| Ovary - 101109 | Ovary - 101120 |
| 1 | 1 |
| Ovary - 101150 | Ovary - 1018 |
| 1 | 1 |
| Ovary - 1040 | Ovary - 1057 |
| 1 | 1 |
| Ovary - 112866 | Ovary - 112867 |
| 1 | 1 |
| Ovary - 118662 | Ovary - 118671 |
| 1 | 1 |
| Ovary - 1241 | Ovary - 1270 |
| 1 | 1 |
| Ovary - 129660 | Ovary - 129669 |
| 1 | 1 |
| Ovary - 1311 | Ovary - 1313 |
| 1 | 1 |
| Ovary - 1323 | Ovary - 133643 |
| 1 | 1 |
| Ovary - 133651 | Ovary - 1351 |
| 1 | 1 |
| Ovary - 151614 | Ovary - 151622 |
| 1 | 1 |
| Ovary - 161465 | Ovary - 161524 |
| 1 | 1 |
| Ovary - 161525 | Ovary - 161534 |
| 1 | 1 |
| Ovary - 1636 | Ovary - 1639 |
| 1 | 1 |
| Ovary - 1643 | Ovary - 170809 |
| 1 | 1 |
| Ovary - 174931 | Ovary - 174936 |
| 1 | 1 |
| Ovary - 180953 | Ovary - 184837 |
| 1 | 1 |
| Ovary - 187243 | Ovary - 187246 |
| 1 | 1 |
| Ovary - 187251 | Ovary - 187253 |
| 1 | 1 |
| Ovary - 191413 | Ovary - 191424 |
| 1 | 1 |
| Ovary - 195198 | Ovary - 199399 |
| 1 | 1 |
| Ovary - 199400 | Ovary - 202030 |
| 1 | 1 |
| Ovary - 202041 | Ovary - 20284 |

| | |
|----------------|----------------|
| 1 | 1 |
| Ovary - 20285 | Ovary - 20296 |
| 1 | 1 |
| Ovary - 20307 | Ovary - 20315 |
| 1 | 1 |
| Ovary - 20323 | Ovary - 20325 |
| 1 | 1 |
| Ovary - 20326 | Ovary - 20329 |
| 1 | 1 |
| Ovary - 207532 | Ovary - 209699 |
| 1 | 1 |
| Ovary - 209709 | Ovary - 209714 |
| 1 | 1 |
| Ovary - 209718 | Ovary - 211371 |
| 1 | 1 |
| Ovary - 211372 | Ovary - 211395 |
| 1 | 1 |
| Ovary - 211409 | Ovary - 21758 |
| 1 | 1 |
| Ovary - 219571 | Ovary - 219581 |
| 1 | 1 |
| Ovary - 219590 | Ovary - 219604 |
| 1 | 1 |
| Ovary - 21981 | Ovary - 22218 |
| 1 | 1 |
| Ovary - 226414 | Ovary - 226423 |
| 1 | 1 |
| Ovary - 228537 | Ovary - 228549 |
| 1 | 1 |
| Ovary - 231863 | Ovary - 234328 |
| 1 | 1 |
| Ovary - 234329 | Ovary - 235691 |
| 1 | 1 |
| Ovary - 235692 | Ovary - 235695 |
| 1 | 1 |
| Ovary - 23862 | Ovary - 23884 |
| 1 | 1 |
| Ovary - 23904 | Ovary - 23930 |
| 1 | 1 |
| Ovary - 23934 | Ovary - 23936 |
| 1 | 1 |
| Ovary - 23938 | Ovary - 241181 |
| 1 | 1 |
| Ovary - 241187 | Ovary - 241196 |
| 1 | 1 |
| Ovary - 241198 | Ovary - 241199 |
| 1 | 1 |
| Ovary - 242929 | (Other) |

1

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 |

batch:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|
| 2004-12-03 | 2004-12-04 | 2004-12-07 | 2005-02-11 | 2005-03-03 | 2005-03-10 | 2005-03-11 |
| 3 | 3 | 1 | 1 | 1 | 1 | 1 |
| 2005-03-15 | 2005-03-16 | 2005-03-17 | 2005-03-19 | 2005-03-22 | 2005-04-13 | 2005-04-26 |
| 3 | 1 | 2 | 4 | 2 | 1 | 5 |
| 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 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|
| 1 | 6 | 1 | 3 | 3 | 6 | 3 |
| 2005-11-15 | 2005-11-18 | 2005-12-02 | 2006-01-24 | 2006-01-26 | 2006-02-07 | 2006-02-28 |
| 3 | 1 | 4 | 2 | 1 | 1 | 1 |
| 2006-03-06 | 2006-03-14 | 2006-04-18 | 2006-04-20 | 2006-05-16 | 2006-06-08 | 2006-07-26 |
| 2 | 2 | 1 | 2 | 3 | 1 | 2 |
| 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 |
| 1 | 6 | 3 | 1 | 1 | 8 | 1 |
| 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 |
| 2 | 3 | 1 | 4 | 4 | 1 | 3 |
| 2008-02-27 | 2008-03-04 | 2008-05-13 | 2008-05-16 | 2008-05-23 | | |
| 2 | 1 | 4 | 4 | 5 | | |

uncurated_author_metadata:

title: Omentum -

title: Ovary - 170809///geo_accession: GSM137917///status: Public on Sep 28 2006///

duplicates:

| | |
|--------------------------|--------------------------|
| GSE2109.GSE2109_GSM76554 | GSE2109.GSE2109_GSM76567 |
| 1 | 1 |

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

uncurated_author_metadata:
title: Ovarian carcinoma 100///geo_accession: GSM643032///status: Public on M
title: Ovarian carcinoma 101///geo_accession: GSM643033///status: Public
title: Ovarian carcinoma 102///geo_accession: GSM643034///status: Public on M
title: Ovarian carcinoma 103///geo_accession: GSM643035///status: Public
title: Ovarian carcinoma 104///geo_accession: GSM643036///status: Public

title: Ovarian carcinoma 105///geo_accession: GSM643037///status: Public on Nov 01

title: Ovarian carcinoma 106///geo_accession: GSM643038///status: Public on Nov 01

title: Ovarian carcinoma 107///geo_accession: GSM643039///status: Public on Nov 01

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title: Ovarian carcinoma 19///geo_accession: GSM642951///status: Public on Nov 01

title: Ovarian carcinoma 1///geo_accession: GSM642933///status: Public on Nov 01

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title: Ovarian carcinoma 25///geo_accession: GSM642957///status: Public on Nov 01

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title: Ovarian carcinoma 27///geo_accession: GSM642959///status: Public on Nov 01

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title: Ovarian carcinoma 29///geo_accession: GSM642961///status: Public on Nov 01

title: Ovarian carcinoma 2///geo_accession: GSM642934///status: Public on Nov

title: Ovarian carcinoma 30///geo_accession: GSM642962///status: Public on Nov

title: Ovarian carcinoma 31///geo_accession: GSM642963///status: Public on Nov

title: Ovarian carcinoma 32///geo_accession: GSM642964///status: Public on Nov

title: Ovarian carcinoma 33///geo_accession: GSM642965///status: Public on Nov

title: Ovarian carcinoma 34///geo_accession: GSM642966///status: Public on Nov

title: Ovarian carcinoma 35///geo_accession: GSM642967///status: Public on Nov

title: Ovarian carcinoma 36///geo_accession: GSM642968///status: Public on Nov

title: Ovarian carcinoma 37///geo_accession: GSM642969///status: Public on Nov

title: Ovarian carcinoma 38///geo_accession: GSM642970///status: Public on Nov

title: Ovarian carcinoma 39///geo_accession: GSM642971///status: Public on Nov

title: Ovarian carcinoma 3///geo_accession: GSM642935///status: Public on Nov

title: Ovarian carcinoma 40///geo_accession: GSM642972///status: Public on Nov

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title: Ovarian carcinoma 50///geo_accession: GSM642982///status: Public on Nov

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title: Ovarian carcinoma 6///geo_accession: GSM642938///status: Public on Nov 01 2007

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title: Ovarian carcinoma 78///geo_accession: GSM643010///status: Public on Nov 11 2008
title: Ovarian carcinoma 79///geo_accession: GSM643011///status: Public on Nov 11 2008
title: Ovarian carcinoma 7///geo_accession: GSM642939///status: Public on Nov 11 2008
title: Ovarian carcinoma 80///geo_accession: GSM643012///status: Public on Nov 11 2008
title: Ovarian carcinoma 81///geo_accession: GSM643013///status: Public on Nov 11 2008
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title: Ovarian carcinoma 87///geo_accession: GSM643019///status: Public on Nov 11 2008
title: Ovarian carcinoma 88///geo_accession: GSM643020///status: Public on Nov 11 2008
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title: Ovarian carcinoma 8///geo_accession: GSM642940///status: Public on Nov 11 2008
title: Ovarian carcinoma 90///geo_accession: GSM643022///status: Public on Nov 11 2008
title: Ovarian carcinoma 91///geo_accession: GSM643023///status: Public on Nov 11 2008
title: Ovarian carcinoma 92///geo_accession: GSM643024///status: Public on Nov 11 2008

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 |
| 1 | | 1 | | 1 | |
| Ovarian Cancer | S0243 | Ovarian Cancer | S0244 | Ovarian Cancer | S0246 |
| 1 | | 1 | | 1 | |
| Ovarian Cancer | S0247 | Ovarian Cancer | S0249 | Ovarian Cancer | S025 |
| 1 | | 1 | | 1 | |
| Ovarian Cancer | S0250 | Ovarian Cancer | S0256 | Ovarian Cancer | S0257 |
| 1 | | 1 | | 1 | |
| Ovarian Cancer | S0258 | Ovarian Cancer | S0261 | Ovarian Cancer | S0262 |
| 1 | | 1 | | 1 | |
| 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:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|
| 2003-11-04 | 2003-11-05 | 2003-11-06 | 2003-11-07 | 2003-11-20 | 2003-11-21 | 2003-12-16 |
| 14 | 16 | 9 | 6 | 10 | 15 | 17 |
| 2003-12-23 | 2003-12-24 | 2004-04-20 | 2004-04-21 | 2004-04-27 | 2004-09-28 | 2005-07-27 |
| 12 | 11 | 20 | 17 | 9 | 14 | 15 |
| 2006-11-09 | | | | | | |
| 10 | | | | | | |

uncurated_author_metadata:

title: Norma
title: Norma
title: Norma
title: Norma
title: Norma
title: Norma
title: Norma
title: Norma
title: Norma
title: Norma

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title: Ovarian Cancer S0108///geo_accession: GSM657533///status: Public on Jan
title: Ovarian Cancer S010///geo_accession: GSM657529///status: Public on Ja
title: Ovarian Cancer S0113///geo_accession: GSM657535///status: Public on Jan 20
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title: Ovarian Cancer S0181///geo_accession: GSM657560///status: Public on Jan 20
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duplicates:

| | |
|---|------|
| GSE26712.GSE26712_GSM657526 | 1 |
| GSE26712.GSE26712_GSM657526///GSE26712.GSE26712_GSM657527 | 1 |
| GSE26712.GSE26712_GSM657527 | 1 |
| | 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

title: US Patient 57///geo_accession: GSM742621///status: Public o

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

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 |

| | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|
| 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| OV_FFPE_29 | OV_FFPE_3 | OV_FFPE_30 | OV_FFPE_31 | OV_FFPE_32 | OV_FFPE_33 | OV_FFPE_34 | OV_FFPE_34 |
| 1 | 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 | OV_FFPE_40 |
| 1 | 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 | OV_FFPE_47 |
| 1 | 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 | OV_FFPE_53 |
| 1 | 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 | OV_FFPE_7 |
| 1 | 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_6///geo_accession: GSM746866///status: Public on Aug 21 2012/

title: OV_FFPE_7///geo_accession: GSM746867///status: Public on Aug 21 2012/

title: OV_FFPE_8///geo_accession: GSM746868///status: Public on Aug 21 2012/

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:

title: serous ovarian cancer 10d///geo_accession: GSM794865///status: Public on Ma

title: serous ovarian cancer 115d///geo_accession: GSM794867///status: Public on Ma

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duplicates:

| | |
|-------------------------------------|-------------------------------------|
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| | 1 |
| 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 ovarian cancer
  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 19:58:23

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 |
| 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| 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

pltx:

y

40

tax:

y

40

days_to_death:

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

vital_status:

deceased living

22 18

debulking:

optimal suboptimal

19 21

uncurated_author_metadata:

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

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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

```

| | | | | | | | | | | |
|-------|--------|--------|--------|--------|--------|-------|-------|-------|-------|-------|
| 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| Tc_94 | Te_69 | Te_77 | Te_78 | Te_79 | Te_84 | Te_87 | Te_89 | Te_90 | Te_91 | Te_92 |
| 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| 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 |
| 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 |
| 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 |
| 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 |

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duplicates:

| Length | Class | Mode |
|--------|-----------|-----------|
| 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:
  PMIDs: 22497737

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

  platform_manufacturer:
    Applied Biosystems
  platform_distribution:
    commercial
  platform_accession:
    GPL2986
  platform_technology:
    in situ oligonucleotide
  version:
    2015-09-22 20:04:13

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 100027 100036 ... 10715781 (18439 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

Details

```

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

```

```

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

```

```

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

```

```

alt_sample_name:
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EOC P009 EOC P010 EOC P011 EOC P012 EOC P013 EOC P014 EOC P015 EOC P016
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EOC P017 EOC P018 EOC P019 EOC P020 EOC P021 EOC P022 EOC P023 EOC P024
      1      1      1      1      1      1      1      1      1
EOC P025 EOC P026 EOC P027 EOC P028 EOC P029 EOC P030 EOC P031 EOC P032
      1      1      1      1      1      1      1      1      1
EOC P033 EOC P034 EOC P035 EOC P036 EOC P037 EOC P038 EOC P039 EOC P040
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EOC P097 EOC P098 EOC P099 (Other)
      1      1      1      105

```

```

sample_type:
tumor
  204

```

```

histological_type:
other  ser  NA's

```

23 171 10

summarygrade:

high low NA's

143 50 11

summarystage:

early late NA's

9 185 10

tumorstage:

2 3 4 NA's

9 154 31 10

grade:

2 3 NA's

50 143 11

age_at_initial_pathologic_diagnosis:

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

days_to_tumor_recurrence:

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

recurrence_status:

| norecurrence | recurrence | NA's |
|--------------|------------|------|
| 70 | 124 | 10 |

days_to_death:

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

vital_status:

| deceased | living | NA's |
|----------|--------|------|
| 57 | 137 | 10 |

debulking:

| optimal | suboptimal | NA's |
|---------|------------|------|
| 137 | 57 | 10 |

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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:

PMIDs: 24368280

Abstract: A 250 word abstract is available. Use 'abstract' method.
 Information is available on: preprocessing

notes:

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  Agilent G4110B
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platform_technology:
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featureData(eset):

An object of class 'AnnotatedDataFrame'

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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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                                1                                1
Ov_Tumor_Ref_Mix vs. CS-OV-005 Ov_Tumor_Ref_Mix vs. CS-OV-006
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| Ov_Tumor_Ref_Mix vs. CS-OV-011 | | Ov_Tumor_Ref_Mix vs. CS-OV-012 | |
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| Ov_Tumor_Ref_Mix vs. CS-OV-013 | | Ov_Tumor_Ref_Mix vs. CS-OV-014 | |
| | 1 | | 1 |
| Ov_Tumor_Ref_Mix vs. CS-OV-015 | | Ov_Tumor_Ref_Mix vs. CS-OV-016 | |
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| Ov_Tumor_Ref_Mix vs. CS-OV-017 | | Ov_Tumor_Ref_Mix vs. CS-OV-018 | |
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histological_type:
clearcell    endo    mucinous    other    ser    NA's
      3         7         9         11         122         20

summarygrade:
high low NA's
  119  30  23

summarystage:
early late NA's
   31  120  21

tumorstage:
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 22  9 103 17 21

substage:
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grade:
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age_at_initial_pathologic_diagnosis:
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neo:
  n
 172

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norecurrence  recurrence    NA's
           36           111           25

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   30   791   1491   1835   2344   7001    20

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   112     40     20

```

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30- NA's
140 32

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30- NA's
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70+ NA's
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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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  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
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Details

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

```

```

-----
alt_sample_name:
  Ovarian_Tumor_ClearCell_CHTN-OC-004      Ovarian_Tumor_ClearCell_CHTN-OC-012
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  Ovarian_Tumor_ClearCell_CHTN-OC-028      Ovarian_Tumor_ClearCell_KU-OC-003
                                           1                               1
  Ovarian_Tumor_ClearCell_KU-OC-004        Ovarian_Tumor_ClearCell_KU-OC-005
                                           1                               1
  Ovarian_Tumor_ClearCell_KU-OC-006        Ovarian_Tumor_ClearCell_KU-OC-007
                                           1                               1
Ovarian_Tumor_Endometrioid_CHTN-OE-005    Ovarian_Tumor_Endometrioid_CHTN-OE-011
                                           1                               1
Ovarian_Tumor_Endometrioid_CHTN-OE-014    Ovarian_Tumor_Endometrioid_CHTN-OE-017
                                           1                               1
Ovarian_Tumor_Endometrioid_CHTN-OE-018    Ovarian_Tumor_Endometrioid_CHTN-OE-019
                                           1                               1
Ovarian_Tumor_Endometrioid_CHTN-OE-023    Ovarian_Tumor_Endometrioid_CHTN-OE-029
                                           1                               1
Ovarian_Tumor_Endometrioid_CHTN-OE-033    Ovarian_Tumor_Endometrioid_CHTN-OE-035
                                           1                               1
Ovarian_Tumor_Endometrioid_CHTN-OE-036    Ovarian_Tumor_Endometrioid_CHTN-OE-038
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Ovarian_Tumor_Endometrioid_CHTN-OE-039    Ovarian_Tumor_Endometrioid_CHTN-OE-040
                                           1                               1
Ovarian_Tumor_Endometrioid_CHTN-OE-042    Ovarian_Tumor_Endometrioid_CHTN-OE-046
                                           1                               1
Ovarian_Tumor_Endometrioid_CHTN-OE-047    Ovarian_Tumor_Endometrioid_CHTN-OE-048
                                           1                               1
Ovarian_Tumor_Endometrioid_CHTN-OE-053    Ovarian_Tumor_Endometrioid_CHTN-OE-054
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Ovarian_Tumor_Endometrioid_CHTN-OE-056    Ovarian_Tumor_Endometrioid_CHTN-OE-059
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Ovarian_Tumor_Endometrioid_CHTN-OE-076    Ovarian_Tumor_Endometrioid_CHTN-OE-077
                                           1                               1
Ovarian_Tumor_Endometrioid_CHTN-OE-080    Ovarian_Tumor_Endometrioid_CHTN-OE-082
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Ovarian_Tumor_Endometrioid_CHTN-OE-087    Ovarian_Tumor_Endometrioid_CHTN-OE-092
                                           1                               1
  Ovarian_Tumor_Endometrioid_JH-OE-2T      Ovarian_Tumor_Endometrioid_KU-OE-003
                                           1                               1
Ovarian_Tumor_Endometrioid_KU-OE-004      Ovarian_Tumor_Endometrioid_KU-OE-007
                                           1                               1
  Ovarian_Tumor_Endometrioid_UM-OE-1T      Ovarian_Tumor_Mucinous_CHTN-OM-007

```

| | |
|------------------------------------|------------------------------------|
| 1 | 1 |
| Ovarian_Tumor_Mucinous_CHTN-OM-017 | Ovarian_Tumor_Mucinous_CHTN-OM-023 |
| 1 | 1 |
| Ovarian_Tumor_Mucinous_CHTN-OM-029 | Ovarian_Tumor_Mucinous_CHTN-OM-032 |
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| Ovarian_Tumor_Mucinous_CHTN-OM-035 | Ovarian_Tumor_Mucinous_CHTN-OM-036 |
| 1 | 1 |
| Ovarian_Tumor_Mucinous_KU-OM-003 | Ovarian_Tumor_Mucinous_KU-OM-004 |
| 1 | 1 |
| Ovarian_Tumor_Mucinous_KU-OM-006 | Ovarian_Tumor_Mucinous_KU-OM-007 |
| 1 | 1 |
| Ovarian_Tumor_Mucinous_UM-OM-01 | Ovarian_Tumor_Mucinous_UM-OM-03 |
| 1 | 1 |
| Ovarian_Tumor_Serous_CHTN-OS-002 | Ovarian_Tumor_Serous_CHTN-OS-003 |
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| Ovarian_Tumor_Serous_CHTN-OS-009 | Ovarian_Tumor_Serous_CHTN-OS-010 |
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| 1 | 1 |
| Ovarian_Tumor_Serous_CHTN-OS-038 | Ovarian_Tumor_Serous_CHTN-OS-041 |
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| Ovarian_Tumor_Serous_CHTN-OS-044 | Ovarian_Tumor_Serous_CHTN-OS-046 |
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| Ovarian_Tumor_Serous_CHTN-OS-048 | Ovarian_Tumor_Serous_CHTN-OS-053 |
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| Ovarian_Tumor_Serous_CHTN-OS-055 | Ovarian_Tumor_Serous_CHTN-OS-068 |
| 1 | 1 |
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| Ovarian_Tumor_Serous_CU-OS-05 | Ovarian_Tumor_Serous_KU-OS-001 |
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| Ovarian_Tumor_Serous_KU-OS-002 | Ovarian_Tumor_Serous_KU-OS-003 |
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| Ovarian_Tumor_Serous_KU-OS-005 | Ovarian_Tumor_Serous_KU-OS-007 |
| 1 | 1 |
| Ovarian_Tumor_Serous_KU-OS-009 | Ovarian_Tumor_Serous_KU-OS-011 |
| 1 | 1 |
| Ovarian_Tumor_Serous_KU-OS-012 | Ovarian_Tumor_Serous_KU-OS-013 |
| 1 | 1 |
| Ovarian_Tumor_Serous_KU-OS-015 | Ovarian_Tumor_Serous_KU-OS-018 |
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| Ovarian_Tumor_Serous_KU-OS-021 | Ovarian_Tumor_Serous_KU-OS-022 |

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NA's
100
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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

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experimentData (eset) :
Experiment data
  Experimenter name: Ouellet V, Provencher DM, Maugard CM, Le Page C, Ren F, Lussie
  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

```

notes:
  platform_title:
    [Hu6800] Affymetrix Human Full Length HuGeneFL Array
  platform_shorttitle:
    Affymetrix Hu6800
  platform_summary:
    hu6800
  platform_manufacturer:
    Affymetrix
  platform_distribution:
    commercial
  platform_accession:
    GPL80
  version:
    2015-09-22 20:07:22

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A28102_at AB000114_at ... Z97074_at (6407 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

Details

assayData: 6407 features, 66 samples

Platform type:

 Available sample meta-data:

alt_sample_name:

| | | | |
|---------------------|---------------------|---------------------|---------------------|
| Ovarian tumor AM053 | Ovarian tumor AM122 | Ovarian tumor AM124 | Ovarian tumor AM125 |
| 1 | 1 | 1 | 1 |
| 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 AM354 | 1 | Ovarian tumor AM364 | 1 | Ovarian tumor AM367 | 1 | Ovarian tumor AM368 | 1 |
| 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 |

batch:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|
| 2000-12-21 | 2001-05-03 | 2001-05-29 | 2001-06-12 | 2001-09-25 | 2001-09-26 | 2001-09-27 |
| 1 | 1 | 3 | 3 | 1 | 5 | 8 |
| 2002-02-14 | 2002-04-17 | 2002-04-18 | 2002-07-18 | 2002-07-24 | 2002-10-20 | 2002-10-30 |
| 4 | 1 | 9 | 7 | 4 | 10 | 5 |
| 2002-11-01 | 2002-11-13 | | | | | |
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title: Ovarian tumor AM381///geo_accession:
title: Ovarian tumor AM382///geo_accession:
title: Ovarian tumor AM398///geo_accession: GSM157295///status: Public on Dec 31
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```

duplicates:

| Length | Class | Mode |
|--------|-----------|-----------|
| 66 | character | character |

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

```
experimentData(eset):
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:
  platform_title:
    Agilent Human 1 cDNA Microarray (G4100A)
  platform_shorttitle:
    Agilent G4100A cDNA
  platform_summary:
    hgug4100a
  platform_manufacturer:
    Agilent
  platform_distribution:
    custom-commerical
```


| | | | | | | | |
|---------|----------------|-------|---|---------|----------------|-------|---|
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| p183bis | sample_Ovarian | tumor | 1 | p209bis | sample_Ovarian | tumor | 1 |
| p212bis | sample_Ovarian | tumor | 1 | p213bis | sample_Ovarian | tumor | 1 |
| p243bis | sample_Ovarian | tumor | 1 | p246bis | sample_Ovarian | tumor | 1 |
| p261bis | sample_Ovarian | tumor | 1 | p284bis | sample_Ovarian | tumor | 1 |
| p293bis | sample_Ovarian | tumor | 1 | p310bis | sample_Ovarian | tumor | 1 |
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| p331bis | sample_Ovarian | tumor | 1 | p336bis | sample_Ovarian | tumor | 1 |
| p350bis | sample_Ovarian | tumor | 1 | p375bis | sample_Ovarian | tumor | 1 |
| p382bis | sample_Ovarian | tumor | 1 | p383bis | sample_Ovarian | tumor | 1 |
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| p398bis | sample_Ovarian | tumor | 1 | p39bis | sample_Ovarian | tumor | 1 |
| p401bis | sample_Ovarian | tumor | 1 | p414bis | sample_Ovarian | tumor | 1 |
| p421bis | sample_Ovarian | tumor | 1 | p429bis | sample_Ovarian | tumor | 1 |
| p433bis | sample_Ovarian | tumor | 1 | p448bis | sample_Ovarian | tumor | 1 |
| p455bis | sample_Ovarian | tumor | 1 | p459bis | sample_Ovarian | tumor | 1 |
| p462bis | sample_Ovarian | tumor | 1 | p482bis | sample_Ovarian | tumor | 1 |
| p487bis | sample_Ovarian | tumor | 1 | p497bis | sample_Ovarian | tumor | 1 |
| p502bis | sample_Ovarian | tumor | 1 | p540bis | sample_Ovarian | tumor | 1 |
| p541bis | sample_Ovarian | tumor | 1 | p549bis | sample_Ovarian | tumor | 1 |
| p550bis | sample_Ovarian | tumor | 1 | p567bis | sample_Ovarian | tumor | 1 |
| p56bis | sample_Ovarian | tumor | 1 | p573bis | sample_Ovarian | tumor | 1 |
| p586bis | sample_Ovarian | tumor | 1 | p597bis | sample_Ovarian | tumor | 1 |
| p616bis | sample_Ovarian | tumor | 1 | p63bis | sample_Ovarian | tumor | 1 |

```

p646bis sample_Ovarian tumor      p66bis sample_Ovarian tumor
                                1                                1
  p68bis sample_Ovarian tumor      p690bis sample_Ovarian tumor
                                1                                1
p692bis sample_Ovarian tumor      p725bis sample_Ovarian tumor
                                1                                1
  p73bis sample_Ovarian tumor      p760bis sample_Ovarian tumor
                                1                                1
p770bis sample_Ovarian tumor      p772bis sample_Ovarian tumor
                                1                                1
p775bis sample_Ovarian tumor      p793bis sample_Ovarian tumor
                                1                                1
  p79bis sample_Ovarian tumor      p84bis sample_Ovarian tumor
                                1                                1
  p90bis sample_Ovarian tumor
                                1

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. |
|-------|---------|--------|-------|---------|-------|
| 21.00 | 43.00 | 50.00 | 51.25 | 61.00 | 87.00 |

recurrence_status:

| norecurrence | recurrence |
|--------------|------------|
| 62 | 21 |

days_to_death:

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

vital_status:

| deceased | living |
|----------|--------|
| 15 | 68 |

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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
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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
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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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title: X23128///geo_accession: GSM249963///status: Public on Mar 01 2008/
title: X23139///geo_accession: GSM249962///status: Public on Mar 01 2008/
title: X23143///geo_accession: GSM249961///status: Public on Mar 01 2008/
title: X23162///geo_accession: GSM249960///status: Public on Mar 01 2008///su
title: X23165///geo_accession: GSM249959///status: Public on Mar 01 2008/

title: X23167///geo_accession: GSM249958///status: Public on Mar 01 2008//
title: X23170///geo_accession: GSM249957///status: Public on Mar 01 2008//
title: X23172///geo_accession: GSM249956///status: Public on Mar 01 2008//
title: X23177///geo_accession: GSM249720///status: Public on Mar 01 2008//
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title: X23204///geo_accession: GSM249949///status: Public on Mar 01 2008//
title: X23210///geo_accession: GSM249948///status: Public on Mar 01 2008//
title: X23212///geo_accession: GSM249947///status: Public on Mar 01 2008//su
title: X23213///geo_accession: GSM249946///status: Public on Mar 01 2008//
title: X23221///geo_accession: GSM249945///status: Public on Mar 01 2008//su
title: X26047///geo_accession: GSM249944///status: Public on Mar 01 2008//sub
title: X261///geo_accession: GSM249943///status: Public on Mar 01 2008//
title: X27006///geo_accession: GSM249942///status: Public on Mar 01 2008//
title: X27098///geo_accession: GSM249941///status: Public on Mar 01 2008//
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title: X32022///geo_accession: GSM249939///status: Public on Mar 01 2008//
title: X32032///geo_accession: GSM249938///status: Public on Mar 01 2008//su
title: X32034///geo_accession: GSM249937///status: Public on Mar 01 2008//subm
title: X32048///geo_accession: GSM249936///status: Public on Mar 01 2008//su
title: X32049///geo_accession: GSM249935///status: Public on Mar 01 2008//su

title: X32054///geo_accession: GSM249934///status: Public on Mar 01 2008//
title: X32055///geo_accession: GSM249933///status: Public on Mar 01 2008//
title: X32089///geo_accession: GSM249932///status: Public on Mar 01 2008///submiss
title: X32098///geo_accession: GSM249931///status: Public on Mar 01 2008///s
title: X32103///geo_accession: GSM249930///status: Public on Mar 01 2008//
title: X32117///geo_accession: GSM249715///status: Public on Mar 01 2008//
title: X34019///geo_accession: GSM249929///status: Public on Mar 01 2008//
title: X34049///geo_accession: GSM249928///status: Public on Mar 01 2008//
title: X34066///geo_accession: GSM249927///status: Public on Mar 01 2008//
title: X34078///geo_accession: GSM249926///status: Public on Mar 01 2008//
title: X34080///geo_accession: GSM249925///status: Public on Mar 01 2008//
title: X34085///geo_accession: GSM249924///status: Public on Mar 01 2008//
title: X34086///geo_accession: GSM249923///status: Public on Mar 01 2008//
title: X34090///geo_accession: GSM249922///status: Public on Mar 01 2008//
title: X34102///geo_accession: GSM249921///status: Public on Mar 01 2008///sub
title: X34103///geo_accession: GSM249920///status: Public on Mar 01 2008//
title: X34111///geo_accession: GSM249919///status: Public on Mar 01 2008//
title: X34113///geo_accession: GSM249918///status: Public on Mar 01 2008//
title: X34117///geo_accession: GSM249917///status: Public on Mar 01 2008//
title: X34125///geo_accession: GSM249916///status: Public on Mar 01 2008//
title: X34165///geo_accession: GSM249915///status: Public on Mar 01 2008//
title: X34168///geo_accession: GSM249914///status: Public on Mar 01 2008///su
title: X34172///geo_accession: GSM249913///status: Public on Mar 01 2008//
title: X34186///geo_accession: GSM249912///status: Public on Mar 01 2008//

```
title: X34202///geo_accession: GSM249911///status: Public on Mar 01 2008///sub
```

```
title: X34207///geo_accession: GSM249910///status: Public on Mar 01 2008///
```

```
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

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1776///Cancer.Type: Lon

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

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1778///Cancer.Type: Lon

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1779///Cancer.Type: Lon

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1780///Cancer.Type: Lon
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  
                               1                               1  
TCGA-04-1362-01A-01R-1565-13 TCGA-04-1364-01A-01R-1565-13  
                               1                               1  
TCGA-04-1365-01A-01R-1565-13 TCGA-04-1514-01A-01R-1566-13  
                               1                               1  
TCGA-04-1519-01A-01R-1565-13 TCGA-09-0364-01A-02R-1564-13  
                               1                               1  
TCGA-09-0366-01A-01R-1564-13 TCGA-09-0367-01A-01R-1564-13  
                               1                               1  
TCGA-09-0369-01A-01R-1564-13 TCGA-09-1662-01A-01R-1566-13  
                               1                               1  
TCGA-09-1666-01A-01R-1566-13 TCGA-09-1667-01C-01R-1566-13  
                               1                               1  
TCGA-09-1668-01B-01R-1566-13 TCGA-09-1669-01A-01R-1566-13  
                               1                               1  
TCGA-09-1670-01A-01R-1566-13 TCGA-09-1673-01A-01R-1566-13  
                               1                               1  
TCGA-09-1674-01A-01R-1566-13 TCGA-09-2044-01B-01R-1568-13  
                               1                               1  
TCGA-09-2045-01A-01R-1568-13 TCGA-09-2048-01A-01R-1568-13  
                               1                               1  
TCGA-09-2051-01A-01R-1568-13 TCGA-09-2054-01A-01R-1568-13  
                               1                               1  
TCGA-09-2056-01B-01R-1568-13 TCGA-10-0928-01A-02R-1564-13  
                               1                               1  
TCGA-10-0936-01A-01R-1564-13 TCGA-13-0730-01A-01R-1564-13  
                               1                               1  
TCGA-13-0799-01A-01R-1564-13 TCGA-13-0800-01A-01R-1564-13  
                               1                               1  
TCGA-13-0801-01A-01R-1564-13 TCGA-13-0890-01A-01R-1564-13  
                               1                               1  
TCGA-13-0893-01B-01R-1565-13 TCGA-13-0897-01A-01R-1564-13  
                               1                               1  
TCGA-13-0899-01A-01R-1564-13 TCGA-13-0913-01A-01R-1564-13  
                               1                               1  
TCGA-13-0916-01A-01R-1564-13 TCGA-13-0920-01A-01R-1564-13  
                               1                               1  
TCGA-13-0924-01A-01R-1564-13 TCGA-13-1403-01A-01R-1565-13  
                               1                               1  
TCGA-13-1405-01A-01R-1565-13 TCGA-13-1410-01A-01R-1565-13  
                               1                               1  
TCGA-13-1481-01A-01R-1565-13 TCGA-13-1497-01A-01R-1565-13
```

| | | | |
|------------------------------|---|------------------------------|---|
| TCGA-13-1498-01A-01R-1565-13 | 1 | TCGA-13-1505-01A-01R-1565-13 | 1 |
| TCGA-13-1506-01A-01R-1565-13 | 1 | TCGA-13-1507-01A-01R-1565-13 | 1 |
| TCGA-13-1511-01A-01R-1565-13 | 1 | TCGA-13-1512-01A-01R-1565-13 | 1 |
| TCGA-13-2060-01A-01R-1568-13 | 1 | TCGA-20-1682-01A-01R-1564-13 | 1 |
| TCGA-20-1683-01A-01R-1566-13 | 1 | TCGA-20-1684-01A-01R-1566-13 | 1 |
| TCGA-20-1685-01A-01R-1566-13 | 1 | TCGA-20-1687-01A-01R-1566-13 | 1 |
| TCGA-23-1023-01A-02R-1564-13 | 1 | TCGA-23-1026-01B-01R-1569-13 | 1 |
| TCGA-23-1027-01A-02R-1564-13 | 1 | TCGA-23-1029-01B-01R-1567-13 | 1 |
| TCGA-23-1109-01A-01R-1564-13 | 1 | TCGA-23-1111-01A-01R-1567-13 | 1 |
| TCGA-23-1114-01B-01R-1566-13 | 1 | TCGA-23-1120-01A-02R-1565-13 | 1 |
| TCGA-23-1122-01A-01R-1565-13 | 1 | TCGA-23-1123-01A-01R-1565-13 | 1 |
| TCGA-23-1809-01A-01R-1566-13 | 1 | TCGA-23-2077-01A-01R-1568-13 | 1 |
| TCGA-23-2081-01A-01R-1568-13 | 1 | TCGA-23-2084-01A-02R-1568-13 | 1 |
| TCGA-24-0975-01A-02R-1565-13 | 1 | TCGA-24-1103-01A-01R-1565-13 | 1 |
| TCGA-24-1413-01A-01R-1565-13 | 1 | TCGA-24-1416-01A-01R-1565-13 | 1 |
| TCGA-24-1417-01A-01R-1565-13 | 1 | TCGA-24-1418-01A-01R-1565-13 | 1 |
| TCGA-24-1419-01A-01R-1565-13 | 1 | TCGA-24-1423-01A-01R-1565-13 | 1 |
| TCGA-24-1424-01A-01R-1565-13 | 1 | TCGA-24-1427-01A-01R-1565-13 | 1 |
| TCGA-24-1428-01A-01R-1564-13 | 1 | TCGA-24-1430-01A-01R-1566-13 | 1 |
| TCGA-24-1436-01A-01R-1566-13 | 1 | TCGA-24-1467-01A-01R-1566-13 | 1 |
| TCGA-24-1469-01A-01R-1566-13 | 1 | TCGA-24-1474-01A-01R-1566-13 | 1 |
| TCGA-24-1544-01A-01R-1566-13 | 1 | TCGA-24-1548-01A-01R-1566-13 | 1 |
| TCGA-24-1549-01A-01R-1566-13 | 1 | TCGA-24-1550-01A-01R-1566-13 | 1 |
| TCGA-24-1551-01A-01R-1566-13 | 1 | TCGA-24-1552-01A-01R-1566-13 | 1 |

| | | |
|------------------------------|------------------------------|-----|
| | 1 | 1 |
| TCGA-24-1553-01A-01R-1566-13 | TCGA-24-1555-01A-01R-1566-13 | |
| | 1 | 1 |
| TCGA-24-1556-01A-01R-1566-13 | TCGA-24-1557-01A-01R-1566-13 | |
| | 1 | 1 |
| TCGA-24-1558-01A-01R-1566-13 | TCGA-24-1560-01A-01R-1566-13 | |
| | 1 | 1 |
| TCGA-24-1562-01A-01R-1566-13 | (Other) | |
| | 1 | 162 |

unique_patient_ID:

| | | | | | |
|--------------|--------------|--------------|--------------|--------------|--------------|
| TCGA-04-1348 | TCGA-04-1357 | TCGA-04-1362 | TCGA-04-1364 | TCGA-04-1365 | TCGA-04-1514 |
| 1 | 1 | 1 | 1 | 1 | 1 |
| TCGA-04-1519 | TCGA-09-0364 | TCGA-09-0366 | TCGA-09-0367 | TCGA-09-0369 | TCGA-09-1662 |
| 1 | 1 | 1 | 1 | 1 | 1 |
| TCGA-09-1666 | TCGA-09-1667 | TCGA-09-1668 | TCGA-09-1669 | TCGA-09-1670 | TCGA-09-1673 |
| 1 | 1 | 1 | 1 | 1 | 1 |
| TCGA-09-1674 | TCGA-09-2044 | TCGA-09-2045 | TCGA-09-2048 | TCGA-09-2051 | TCGA-09-2054 |
| 1 | 1 | 1 | 1 | 1 | 1 |
| TCGA-09-2056 | TCGA-10-0928 | TCGA-10-0936 | TCGA-13-0730 | TCGA-13-0799 | TCGA-13-0800 |
| 1 | 1 | 1 | 1 | 1 | 1 |
| TCGA-13-0801 | TCGA-13-0890 | TCGA-13-0893 | TCGA-13-0897 | TCGA-13-0899 | TCGA-13-0913 |
| 1 | 1 | 1 | 1 | 1 | 1 |
| TCGA-13-0916 | TCGA-13-0920 | TCGA-13-0924 | TCGA-13-1403 | TCGA-13-1405 | TCGA-13-1410 |
| 1 | 1 | 1 | 1 | 1 | 1 |
| TCGA-13-1481 | TCGA-13-1497 | TCGA-13-1498 | TCGA-13-1505 | TCGA-13-1506 | TCGA-13-1507 |
| 1 | 1 | 1 | 1 | 1 | 1 |
| TCGA-13-1511 | TCGA-13-1512 | TCGA-13-2060 | TCGA-20-1682 | TCGA-20-1683 | TCGA-20-1684 |
| 1 | 1 | 1 | 1 | 1 | 1 |
| TCGA-20-1685 | TCGA-20-1687 | TCGA-23-1023 | TCGA-23-1026 | TCGA-23-1027 | TCGA-23-1029 |
| 1 | 1 | 1 | 1 | 1 | 1 |
| TCGA-23-1109 | TCGA-23-1111 | TCGA-23-1114 | TCGA-23-1120 | TCGA-23-1122 | TCGA-23-1123 |
| 1 | 1 | 1 | 1 | 1 | 1 |
| TCGA-23-1809 | TCGA-23-2077 | TCGA-23-2081 | TCGA-23-2084 | TCGA-24-0975 | TCGA-24-1103 |
| 1 | 1 | 1 | 1 | 1 | 1 |
| TCGA-24-1413 | TCGA-24-1416 | TCGA-24-1417 | TCGA-24-1418 | TCGA-24-1419 | TCGA-24-1423 |
| 1 | 1 | 1 | 1 | 1 | 1 |
| TCGA-24-1424 | TCGA-24-1427 | TCGA-24-1428 | TCGA-24-1430 | TCGA-24-1436 | TCGA-24-1467 |
| 1 | 1 | 1 | 1 | 1 | 1 |
| TCGA-24-1469 | TCGA-24-1474 | TCGA-24-1544 | TCGA-24-1548 | TCGA-24-1549 | TCGA-24-1550 |
| 1 | 1 | 1 | 1 | 1 | 1 |
| TCGA-24-1551 | TCGA-24-1552 | TCGA-24-1553 | TCGA-24-1555 | TCGA-24-1556 | TCGA-24-1557 |
| 1 | 1 | 1 | 1 | 1 | 1 |
| TCGA-24-1558 | TCGA-24-1560 | TCGA-24-1562 | (Other) | | |
| | 1 | 1 | 1 | 162 | |

sample_type:

tumor

```

261

histological_type:
ser
261

primarysite:
other    ov
   1    260

summarygrade:
high low NA's
 226  29   6

summarystage:
early late NA's
   18  242   1

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

substage:
   b   c NA's
  16 211  34

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

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

pltx:
  n    y NA's
 17 215  29

tax:
  n    y NA's
 17 215  29

neo:
  n NA's
232  29

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

```

9.0 225.0 426.5 585.3 755.0 5480.0 19

recurrence_status:

| | |
|--------------|------------|
| norecurrence | recurrence |
| 123 | 138 |

days_to_death:

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

vital_status:

| | | |
|----------|--------|------|
| deceased | living | NA's |
| 143 | 114 | 4 |

site_of_tumor_first_recurrence:

| | | |
|--------------|------------|------|
| locoregional | metastasis | NA's |
| 82 | 56 | 123 |

primary_therapy_outcome_success:

| | | | |
|------------------|-----------------|--------------------|---------------|
| completeresponse | partialresponse | 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

age_at_initial_

```
age_at_in
age_at_initial_pathologic_diagn
age_at_initial_pathologic_diagnosis: 4
age_at_initial_pathologic_diagnosis
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
```

age_at_initial_pathologic

age_at_initial_pathologic_diagnosis

age_at_initial_pathologic_diagnosis: 45///anatomic_organ_subdivision:

age_at_initial_pathologic_dia

age_at_initial_pathologic_diagnosis: 46///anatomic_organ_subdivision:

age_at_initial_pathologic_diagnosis: 47

age_at_initial_pathologic_diagnosis

age_at_initial_pathologic_diagnosis: 47///anatomic

age_at_initial

age_at_initial_pathologic_diagnosis: 47///anatomic_or

age_at_initial_pathologic_diagnosis: 48///ana

age_at

age_

age_at_initial_pathologic_dia

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

```

```

platform_manufacturer:
  Affymetrix
platform_distribution:
  commercial
platform_accession:
  GPL3921
warnings:
  The following samples are likely from specimens also used in GSE26712: TCGA
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

```

Details

```

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

```

```

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

```

```

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

```

```

alt_sample_name:
TCGA-01-0628-11A-01R-0362-01 TCGA-01-0630-11A-01R-0362-01
                                1                                1
TCGA-01-0631-11A-01R-0362-01 TCGA-01-0633-11A-01R-0362-01
                                1                                1
TCGA-01-0636-11A-01R-0362-01 TCGA-01-0637-11A-01R-0362-01
                                1                                1
TCGA-01-0639-11A-01R-0362-01 TCGA-01-0642-11A-02R-0362-01
                                1                                1
TCGA-04-1331-01A-01R-0434-01 TCGA-04-1332-01A-01R-0434-01
                                1                                1
TCGA-04-1335-01A-01R-0434-01 TCGA-04-1336-01A-01R-0434-01
                                1                                1
TCGA-04-1337-01A-01R-0434-01 TCGA-04-1338-01A-01R-0434-01

```

| | | | |
|------------------------------|---|------------------------------|---|
| TCGA-04-1341-01A-01R-0434-01 | 1 | TCGA-04-1342-01A-01R-0434-01 | 1 |
| | 1 | | 1 |
| TCGA-04-1343-01A-01R-0434-01 | 1 | TCGA-04-1346-01A-01R-0434-01 | 1 |
| | 1 | | 1 |
| TCGA-04-1347-01A-01R-0434-01 | 1 | TCGA-04-1348-01A-01R-0453-01 | 1 |
| | 1 | | 1 |
| TCGA-04-1349-01A-01R-0453-01 | 1 | TCGA-04-1350-01A-01R-0453-01 | 1 |
| | 1 | | 1 |
| TCGA-04-1351-01A-01R-0453-01 | 1 | TCGA-04-1353-01A-01R-1048-01 | 1 |
| | 1 | | 1 |
| TCGA-04-1356-01A-01R-0453-01 | 1 | TCGA-04-1357-01A-01R-0453-01 | 1 |
| | 1 | | 1 |
| TCGA-04-1360-01A-01R-0453-01 | 1 | TCGA-04-1361-01A-01R-0453-01 | 1 |
| | 1 | | 1 |
| TCGA-04-1362-01A-01R-0453-01 | 1 | TCGA-04-1364-01A-01R-0453-01 | 1 |
| | 1 | | 1 |
| TCGA-04-1365-01A-01R-0453-01 | 1 | TCGA-04-1367-01A-01R-0453-01 | 1 |
| | 1 | | 1 |
| TCGA-04-1369-01A-02R-1048-01 | 1 | TCGA-04-1371-01A-01R-0453-01 | 1 |
| | 1 | | 1 |
| TCGA-04-1514-01A-01R-0502-01 | 1 | TCGA-04-1516-01A-01R-1048-01 | 1 |
| | 1 | | 1 |
| TCGA-04-1517-01A-01R-0538-01 | 1 | TCGA-04-1519-01A-01R-0538-01 | 1 |
| | 1 | | 1 |
| TCGA-04-1525-01A-01R-0538-01 | 1 | TCGA-04-1530-01A-02R-0502-01 | 1 |
| | 1 | | 1 |
| TCGA-04-1536-01A-01R-0538-01 | 1 | TCGA-04-1542-01A-01R-0502-01 | 1 |
| | 1 | | 1 |
| TCGA-04-1638-01A-01R-0582-01 | 1 | TCGA-04-1644-01B-01R-1048-01 | 1 |
| | 1 | | 1 |
| TCGA-04-1646-01A-01R-0582-01 | 1 | TCGA-04-1648-01A-01R-0582-01 | 1 |
| | 1 | | 1 |
| TCGA-04-1649-01A-01R-0582-01 | 1 | TCGA-04-1651-01A-01R-0582-01 | 1 |
| | 1 | | 1 |
| TCGA-04-1652-01A-01R-0582-01 | 1 | TCGA-04-1654-01A-02R-0653-01 | 1 |
| | 1 | | 1 |
| TCGA-04-1655-01A-01R-0564-01 | 1 | TCGA-09-0364-01A-02R-0362-01 | 1 |
| | 1 | | 1 |
| TCGA-09-0365-01A-02R-0362-01 | 1 | TCGA-09-0366-01A-01R-0362-01 | 1 |
| | 1 | | 1 |
| TCGA-09-0367-01A-01R-0362-01 | 1 | TCGA-09-0369-01A-01R-0362-01 | 1 |
| | 1 | | 1 |
| TCGA-09-1659-01B-01R-0538-01 | 1 | TCGA-09-1661-01B-01R-0538-01 | 1 |
| | 1 | | 1 |
| TCGA-09-1662-01A-01R-0538-01 | 1 | TCGA-09-1664-01A-01R-0582-01 | 1 |
| | 1 | | 1 |
| TCGA-09-1665-01B-01R-0538-01 | 1 | TCGA-09-1666-01A-01R-0538-01 | 1 |

| | | |
|------------------------------|------------------------------|------|
| | 1 | 1 |
| TCGA-09-1667-01C-01R-0538-01 | TCGA-09-1668-01B-01R-0538-01 | |
| | 1 | 1 |
| TCGA-09-1669-01A-01R-0538-01 | TCGA-09-1670-01A-01R-0564-01 | |
| | 1 | 1 |
| TCGA-09-1672-01A-01R-0564-01 | TCGA-09-1673-01A-01R-0564-01 | |
| | 1 | 1 |
| TCGA-09-1674-01A-01R-0564-01 | TCGA-09-1675-01B-01R-0564-01 | |
| | 1 | 1 |
| TCGA-09-2043-01A-01R-0709-01 | TCGA-09-2044-01B-01R-0709-01 | |
| | 1 | 1 |
| TCGA-09-2045-01A-01R-0709-01 | TCGA-09-2048-01A-01R-0709-01 | |
| | 1 | 1 |
| TCGA-09-2049-01D-01R-0709-01 | TCGA-09-2050-01A-01R-0709-01 | |
| | 1 | 1 |
| TCGA-09-2051-01A-01R-0709-01 | TCGA-09-2053-01C-01R-0668-01 | |
| | 1 | 1 |
| TCGA-09-2054-01A-01R-0668-01 | TCGA-09-2055-01B-01R-0709-01 | |
| | 1 | 1 |
| TCGA-09-2056-01B-01R-0668-01 | TCGA-10-0925-01B-01R-0653-01 | |
| | 1 | 1 |
| TCGA-10-0926-01A-01R-0404-01 | TCGA-10-0927-01A-02R-0404-01 | |
| | 1 | 1 |
| TCGA-10-0928-01A-02R-0404-01 | TCGA-10-0930-01A-02R-0404-01 | |
| | 1 | 1 |
| TCGA-10-0931-01A-01R-0404-01 | TCGA-10-0933-01A-01R-0404-01 | |
| | 1 | 1 |
| TCGA-10-0934-01A-02R-0404-01 | TCGA-10-0935-01A-02R-0404-01 | |
| | 1 | 1 |
| TCGA-10-0936-01A-01R-0404-01 | TCGA-10-0937-01A-02R-0404-01 | |
| | 1 | 1 |
| TCGA-10-0938-01A-02R-0404-01 | TCGA-13-0714-01A-01R-0362-01 | |
| | 1 | 1 |
| TCGA-13-0717-01A-01R-0362-01 | TCGA-13-0720-01A-01R-0362-01 | |
| | 1 | 1 |
| TCGA-13-0723-01A-02R-0362-01 | TCGA-13-0724-01A-01R-0362-01 | |
| | 1 | 1 |
| | (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
age_at_initial_pathologic_diagnosi
age_at_in
age_at_initial_patho
age_at_initial_pathologic_dia
age_at_initial_pathologic_diagnosis: 4
age_at_initial_pathologic_diagnosis: 42///anatomic_organ_subdivi
age_at_initial_pat
age_at_initial_pathologic_diagnosis: 42///anatomic_organ
age_at_initial_pathol
age_at_initial_pathologic_diagnosis: 4
age_at_ini

age
age_at_initial_pathologic_diagnosis: 4

age_at_initial
age_at_init
age_at_initi

age_at_initial_pathologic_diagn
age_at_initial_pathologic_diagnosis: 44///anatomic_o
age_at_initial_pathologic_diagn
age_at_initial_path
age_at_initial_patho
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

age_at_initial_patholo

age_at_initial_pathologic_diagnosis

age_at_initial_pathologic_diagnosis: 45///anatomic_organ_subdivision:

age_at_initial_pathologic_dia

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
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age_at_initial_pathologic_diagnosis: 48///ana
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duplicates:
  Length    Class      Mode
    578 character character
```

Value

An expression set