

# Package ‘MetaGxOvarian’

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**Type** Package

**Title** Transcriptomic Ovarian Cancer Datasets

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**Description** A collection of Ovarian Cancer Transcriptomic Datasets that are part of the MetaGx-Data package compendium.

**License** Artistic-2.0

**Depends** Biobase, stats, lattice, impute, AnnotationHub, ExperimentHub, SummarizedExperiment, R (>= 3.6.0)

**Suggests** testthat, xtable

**NeedsCompilation** no

**biocViews** ExpressionData, ExperimentHub, CancerData, Homo\_sapiens\_Data, ArrayExpress, GEO, NCI, MicroarrayData, ExperimentData

**LazyData** yes

**RoxygenNote** 7.0.2

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

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attention	<i>days_to_death</i>
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### 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 duplicates 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

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

## Description

Ovarian cancer is the fifth leading cause of cancer death for women in the U.S. and the seventh most fatal worldwide. Although ovarian cancer is notable for its initial sensitivity to platinum-based therapies, the vast majority of patients eventually develop recurrent cancer and succumb to increasingly platinum-resistant disease. Modern, targeted cancer drugs intervene in cell signaling, and identifying key disease mechanisms and pathways would greatly advance our treatment abilities. In order to shed light on the molecular diversity of ovarian cancer, we performed comprehensive transcriptional profiling on 129 advanced stage, high grade serous ovarian cancers. We implemented a, re-sampling based version of the ISIS class discovery algorithm (rISIS: robust ISIS) and applied it to the entire set of ovarian cancer transcriptional profiles. rISIS identified a previously undescribed patient stratification, further supported by micro-RNA expression profiles, and gene set enrichment analysis found strong biological support for the stratification by extracellular matrix, cell adhesion, and angiogenesis genes. The corresponding "angiogenesis signature" was validated in ten published independent ovarian cancer gene expression datasets and is significantly associated with overall survival. The subtypes we have defined are of potential translational interest as they may be relevant for identifying patients who may benefit from the addition of anti-angiogenic therapies that are now being tested in clinical trials.

## Format

```

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

Source.Name: DFCI-

Source.Name: DFCI-

Source.Name: DFCI-103

Source.Name: DFCI-104/

Source.Name: DFCI-105//

Source.Name: DFCI-106//

Source.Name: DFCI-107//

Source.Name: DFCI-108

Source.Name: DFCI-109//

Source.Name: DFCI-

Source.Name: DFCI-11

Source.Name: DFCI-111//

Source.Name: DFCI-112

Source.Name: DFCI-113

Source.Name: DFCI

Source.Name: DFCI-115/

Source.Name: DFCI-116//

Source.Name: DFCI-11

Source.Name: DFCI-118///Characteristics.Age.: Age <has\_measurement <Measurement

Source.Name: DFCI-119

Source.Name: DFCI-11

Source.Name: DFCI-120///Characteristics.Age.: Age <has\_measurement <Measureme

Source.Name: DFCI-12

Source.Name: DFCI

Source.Name: DFCI-123/

Source.Name: DFCI-12

Source.Name: DFCI-1

Source.Name: DFC

Source.Name: DFCI-127///Characteristics.Age.: Age <has\_measurement <Measure

Source.Name: DFCI-12



Source.Name: DFCI-  
Source.Name: DFCI-  
Source.Name: DFCI-  
Source.Name: DFCI-3  
Source.Name: DF  
Source.Name: DFCI-3  
Source.Name: DFCI-38  
Source.Name: DFCI-39  
Source.Name: DF  
Source.Name: DFCI-4  
Source.Name: DFCI-  
Source.Name: DFCI-  
Source.Name: DFCI-  
Source.Name: DF  
Source.Name: DFCI-4  
Source.Name: DFCI-  
Source.Name: DF  
Source.Name: DFCI-  
Source.Name: DF  
Source.Name: DFCI-  
Source.Name: DFCI-51  
Source.Name: DFCI-5  
Source.Name: DFCI-53  
Source.Name: DFCI-54  
Source.Name: DFCI-  
Source.Name: DFCI-56

Source.Name: DFCI-5

Source.Name: DFCI-

Source.Name: DFCI

Source.Name: DFCI

Source.Name: DFC

Source.Name: DFCI-62///Characteristics.Age.: Age &lt;has\_measurement &lt;Measure

Source.Name: DFC

Source.Name: DFCI

Source.Name: DFCI-65

Source.Name: DFC

Source.Name: DF

Source.Name: DFCI-6

Source.Name: DFCI-6

Source.Name:

Source.Name: DFCI-

Source.Name: DFCI

**Value**

An expression set

GSE12418

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

**Description**

It is difficult to predict the clinical outcome for patients with ovarian cancer. However, the use of biomarkers as additional prognostic factors may improve the outcome for these patients. In order to find novel candidate biomarkers, differences in gene expressions were analysed in 54 stage III serous ovarian adenocarcinomas with oligonucleotide microarrays containing 27,000 unique

probes. The microarray data was verified with quantitative real-time polymerase chain reaction for the genes TACC1, MUC5B and PRAME. Using hierarchical cluster analysis we detected a sub-group that included 60% of the survivors. The gene expressions in tumours from patients in this sub-group of survivors were compared with the remaining tumours, and 204 genes were found to be differently expressed. We conclude that the sub-group of survivors might represent patients with favourable tumour biology and sensitivity to treatment. A selection of the 204 genes might be used as a predictive model to distinguish patients within and outside of this group. Alternative chemotherapy strategies could then be offered as first-line treatment, which may lead to improvements in the clinical outcome for these patients.

## Format

```

experimentData(eset):
Experiment data
  Experimenter name: Partheen K, Levan K, Osterberg L, Horvath G.Expression anal
  Laboratory: Partheen, Horvath 2006
  Contact information:
  Title: Expression analysis of stage III serous ovarian adenocarcinoma distingui
  URL:
  PMIDs: 16996261

Abstract: A 177 word abstract is available. Use 'abstract' method.
Information is available on: preprocessing
notes:
  platform_title:
    SWEGENE H_v2.1.1.1_27k
  platform_shorttitle:
    SWEGENE H_v2.1.1.1_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///subm  
title: 1047LB///geo\_accession: GSM311974///status: Public on Aug 12 2008///s  
title: 1059LB0///geo\_accession: GSM311975///status: Public on Aug 12 2008///subm  
title: 1177DB///geo\_accession: GSM311976///status: Public on Aug 12 2  
title: 1178LB0///geo\_accession: GSM311977///status: Public on Aug 12 2008///subm  
title: 1180DB///geo\_accession: GSM311978///status: Public on Aug 12 2  
title: 1186DB0///geo\_accession: GSM311979///status: Public on Aug 12 2008  
title: 123DC///geo\_accession: GSM311945///status: Public on Aug 12  
title: 1242LC0///geo\_accession: GSM311980///status: Public on Aug 12 2008///sub  
title: 1274LC///geo\_accession: GSM311981///status: Public on Aug 12 2008///  
title: 134LC///geo\_accession: GSM311946///status: Public on Aug 12 2008///  
title: 1426LB///geo\_accession: GSM311982///status: Public on Aug 12 2008///s  
title: 1487DB///geo\_accession: GSM311983///status: Public on Aug 12 2  
title: 1528DC///geo\_accession: GSM311984///status: Public on Aug 12  
title: 1538DC///geo\_accession: GSM311985///status: Public on Aug 12  
title: 1567DB///geo\_accession: GSM311986///status: Public on Aug 12 2  
title: 1568DC///geo\_accession: GSM311987///status: Public on Aug 12  
title: 1574LC0///geo\_accession: GSM311988///status: Public on Aug 12 2008///sub  
title: 164DC///geo\_accession: GSM311947///status: Public on Aug 12  
title: 1658DC///geo\_accession: GSM311989///status: Public on Aug 12  
title: 1760LB///geo\_accession: GSM311990///status: Public on Aug 12 2008///s  
title: 1805DB///geo\_accession: GSM311991///status: Public on Aug 12 2  
title: 193DC///geo\_accession: GSM311948///status: Public on Aug 12  
title: 198DC///geo\_accession: GSM311949///status: Public on Aug 12

title: 202DC///geo\_accession: GSM311950///status: Public on Aug 12  
title: 211DC///geo\_accession: GSM311951///status: Public on Aug 12  
title: 26DC///geo\_accession: GSM311938///status: Public on Aug 12  
title: 272DC///geo\_accession: GSM311952///status: Public on Aug 12  
title: 405LB///geo\_accession: GSM311953///status: Public on Aug 12 2008///s  
title: 436DC///geo\_accession: GSM311954///status: Public on Aug 12  
title: 452DC///geo\_accession: GSM311955///status: Public on Aug 12  
title: 454LC///geo\_accession: GSM311956///status: Public on Aug 12 2008///  
title: 45LA0///geo\_accession: GSM311939///status: Public on Aug 12 2008///subm  
title: 462DB///geo\_accession: GSM311957///status: Public on Aug 12 2  
title: 46LB0///geo\_accession: GSM311940///status: Public on Aug 12 2008///subm  
title: 47DC///geo\_accession: GSM311941///status: Public on Aug 12  
title: 480DC0///geo\_accession: GSM311958///status: Public on Aug 12 200  
title: 489DC///geo\_accession: GSM311959///status: Public on Aug 12  
title: 505DB///geo\_accession: GSM311960///status: Public on Aug 12 2  
title: 541DC///geo\_accession: GSM311961///status: Public on Aug 12  
title: 559DC///geo\_accession: GSM311962///status: Public on Aug 12  
title: 563LA///geo\_accession: GSM311963///status: Public on Aug 12 2008///s  
title: 626DC///geo\_accession: GSM311964///status: Public on Aug 12  
title: 662DC///geo\_accession: GSM311965///status: Public on Aug 12  
title: 719DC///geo\_accession: GSM311966///status: Public on Aug 12  
title: 742LC0///geo\_accession: GSM311967///status: Public on Aug 12 2008///sub  
title: 755LC///geo\_accession: GSM311968///status: Public on Aug 12 2008///  
title: 759DC///geo\_accession: GSM311969///status: Public on Aug 12  
title: 76DC///geo\_accession: GSM311942///status: Public on Aug 12  
title: 789DC///geo\_accession: GSM311970///status: Public on Aug 12

title: 83LC//geo\_accession: GSM311943//status: Public on Aug 12 2008//  
 title: 918DB0//geo\_accession: GSM311971//status: Public on Aug 12 2008//  
 title: 988LC0//geo\_accession: GSM311972//status: Public on Aug 12 2008//sub  
 title: 99LC0//geo\_accession: GSM311944//status: Public on Aug 12 2008//sub

## 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, Fujii
  Laboratory: Yoshihara, Tanaka 2009
  Contact information:
  Title: Gene expression profiling of advanced-stage serous ovarian cancers dist
  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:  
title: Advanced serous ovarian cancer 11///geo\_accession: GSM312141///status:  
title: Advanced serous ovarian cancer 15///geo\_accession: GSM312156///status:  
title: Advanced serous ovarian cancer 17///geo\_accession: GSM312142///status:  
title: Advanced serous ovarian cancer 18///geo\_accession: GSM312143///status:  
title: Advanced serous ovarian cancer 20///geo\_accession: GSM312144///status:  
title: Advanced serous ovarian cancer 23///geo\_accession: GSM312157///status:  
title: Advanced serous ovarian cancer 24///geo\_accession: GSM312145///status:  
title: Advanced serous ovarian cancer 25///geo\_accession: GSM312146///status:  
title: Advanced serous ovarian cancer 27///geo\_accession: GSM312158///status:  
title: Advanced serous ovarian cancer 2///geo\_accession: GSM312138//  
title: Advanced serous ovarian cancer 36///geo\_accession: GSM312147///status:  
title: Advanced serous ovarian cancer 37///geo\_accession: GSM312148///status:  
title: Advanced serous ovarian cancer 38///geo\_accession: GSM312149///status:  
title: Advanced serous ovarian cancer 39///geo\_accession: GSM312159///status:  
title: Advanced serous ovarian cancer 42///geo\_accession: GSM312160///status:  
title: Advanced serous ovarian cancer 43///geo\_accession: GSM312150///status:  
title: Advanced serous ovarian cancer 45///geo\_accession: GSM312161///status:  
title: Advanced serous ovarian cancer 46///geo\_accession: GSM312162///status:  
title: Advanced serous ovarian cancer 49///geo\_accession: GSM312151///status:  
title: Advanced serous ovarian cancer 50///geo\_accession: GSM312163///status:  
title: Advanced serous ovarian cancer 51///geo\_accession: GSM312165///status:  
title: Advanced serous ovarian cancer 52///geo\_accession: GSM312167///status:

title: Advanced serous ovarian cancer 53///geo\_accession: GSM312168///status:  
title: Advanced serous ovarian cancer 54///geo\_accession: GSM312152///status:  
title: Advanced serous ovarian cancer 55///geo\_accession: GSM312170///status: Pu  
title: Advanced serous ovarian cancer 56///geo\_accession: GSM312171///status:  
title: Advanced serous ovarian cancer 57///geo\_accession: GSM312153///status:  
title: Advanced serous ovarian cancer 58///geo\_accession: GSM312172///status:  
title: Advanced serous ovarian cancer 60///geo\_accession: GSM312173///status:  
title: Advanced serous ovarian cancer 61///geo\_accession: GSM312154///status:  
title: Advanced serous ovarian cancer 62///geo\_accession: GSM312174///status:  
title: Advanced serous ovarian cancer 64///geo\_accession: GSM312175///status:  
title: Advanced serous ovarian cancer 6///geo\_accession: GSM312139///status  
title: Advanced serous ovarian cancer 7///geo\_accession: GSM312140///status  
title: Early serous ovarian cancer 28///geo\_accession: GSM312180///statu  
title: Early serous ovarian cancer 32///geo\_accession: GSM312181///statu  
title: Early serous ovarian cancer 33///geo\_accession: GSM312182///statu  
title: Early serous ovarian cancer 35///geo\_accession: GSM312183///statu  
title: Early serous ovarian cancer 5///geo\_accession: GSM312176///sta  
title: Early serous ovarian cancer 65///geo\_accession: GSM312185///statu  
title: Early serous ovarian cancer 8///geo\_accession: GSM312178///sta  
title: Early serous ovarian cancer 9///geo\_accession: GSM312179///sta  
title: Peritoneum normal 12///geo\_acces  
title: Peritoneum normal 15///geo\_acces  
title: Peritoneum normal 16///geo\_acces  
title: Peritoneum normal 18///geo\_acces  
title: Peritoneum normal 21///geo\_acces  
title: Peritoneum normal 23///geo\_accessi

title: Peritoneum normal 30///geo\_accession

title: Peritoneum normal 3///geo\_accession

title: Peritoneum normal 4///geo\_accession

title: Peritoneum normal 7///geo\_accession

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, K
  Laboratory: Crijns, van der Zee 2009
  Contact information:
  Title: Survival-related profile, pathways, and transcription factors in ovaria
  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\_accessio

title: Ovarian tumor sample 193 / Ovarian tumor sample 194///geo\_accessio

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: GSM4

title: Ovarian tumor sample 258 / Ovarian tumor sample 259///geo\_accession:

title: Ovarian tumor sample 273 / Ovarian tumor sample 274///geo\_accession:

title: Ovarian tumor sample 284 / Ovarian tumor sample 285///geo\_accession:

title: Ovarian tumor sample 313 / Ovarian tumor sample 314///geo\_accession

**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
  Laboratory: Denkert, Lage 2009
  Contact information:
  Title: A prognostic gene expression index in ovarian cancer - validation across
  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: Pu  
 title: ovarian cancer: 011///geo\_accession: GSM368671///status: Pu  
 title: ovarian cancer: 012///geo\_accession: GSM368672///status: Publ  
 title: ovarian cancer: 013///geo\_accession: GSM368673///status: Pu  
 title: ovarian cancer: 014///geo\_accession: GSM368674///status: P  
 title: ovarian cancer: 015///geo\_accession: GSM368675///status: Pub  
 title: ovarian cancer: 016///geo\_accession: GSM368676///status: Publi  
 title: ovarian cancer: 017///geo\_accession: GSM368677///status: Pu  
 title: ovarian cancer: 018///geo\_accession: GSM368678///status: Pu  
 title: ovarian cancer: 019///geo\_accession: GSM368679///status: Pu  
 title: ovarian cancer: 01///geo\_accession: GSM368661///status: P  
 title: ovarian cancer: 020///geo\_accession: GSM368680///status: P  
 title: ovarian cancer: 021///geo\_accession: GSM368681///status: Pu  
 title: ovarian cancer: 022///geo\_accession: GSM368682///status: Pu

title: ovarian cancer: 023///geo\_accession: GSM368683///status: Pu  
title: ovarian cancer: 024///geo\_accession: GSM368684///status: Public  
title: ovarian cancer: 025///geo\_accession: GSM368685///status: Pu  
title: ovarian cancer: 026///geo\_accession: GSM368686///status: Public on Feb 09  
title: ovarian cancer: 027///geo\_accession: GSM368687///status: Publ  
title: ovarian cancer: 028///geo\_accession: GSM368688///status: Publ  
title: ovarian cancer: 029///geo\_accession: GSM368689///status: Pub  
title: ovarian cancer: 02///geo\_accession: GSM368662///status: Pu  
title: ovarian cancer: 030///geo\_accession: GSM368690///status: Pu  
title: ovarian cancer: 031///geo\_accession: GSM368691///status: Pu  
title: ovarian cancer: 032///geo\_accession: GSM368692///status: Pu  
title: ovarian cancer: 033///geo\_accession: GSM368693///status: P  
title: ovarian cancer: 034///geo\_accession: GSM368694///status: Pu  
title: ovarian cancer: 035///geo\_accession: GSM368695///status: Pu  
title: ovarian cancer: 036///geo\_accession: GSM368696///status: P  
title: ovarian cancer: 037///geo\_accession: GSM368697///status: P  
title: ovarian cancer: 038///geo\_accession: GSM368698///status: Pub  
title: ovarian cancer: 039///geo\_accession: GSM368699///status: Pu  
title: ovarian cancer: 03///geo\_accession: GSM368663///status: Public on F  
title: ovarian cancer: 040///geo\_accession: GSM368700///status: Pu  
title: ovarian cancer: 041///geo\_accession: GSM368701///status: P  
title: ovarian cancer: 042///geo\_accession: GSM368702///status: Pub  
title: ovarian cancer: 043///geo\_accession: GSM368703///status: Pu  
title: ovarian cancer: 044///geo\_accession: GSM368704///status: P  
title: ovarian cancer: 045///geo\_accession: GSM368705///status:  
title: ovarian cancer: 046///geo\_accession: GSM368706///status:

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title: ovarian cancer: 049///geo\_accession: GSM368709///status: P  
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title: ovarian cancer: 055///geo\_accession: GSM368715///status: P  
title: ovarian cancer: 056///geo\_accession: GSM368716///status:  
title: ovarian cancer: 057///geo\_accession: GSM368717///status:  
title: ovarian cancer: 058///geo\_accession: GSM368718///status: P  
title: ovarian cancer: 059///geo\_accession: GSM368719///status:  
title: ovarian cancer: 05///geo\_accession: GSM368665///status: Pu  
title: ovarian cancer: 060///geo\_accession: GSM368720///status: P  
title: ovarian cancer: 061///geo\_accession: GSM368721///status: P  
title: ovarian cancer: 062///geo\_accession: GSM368722///status: P  
title: ovarian cancer: 063///geo\_accession: GSM368723///status: P  
title: ovarian cancer: 064///geo\_accession: GSM368724///status: P  
title: ovarian cancer: 065///geo\_accession: GSM368725///status: P  
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title: ovarian cancer: 068///geo\_accession: GSM368728///status: P  
title: ovarian cancer: 069///geo\_accession: GSM368729///status:  
title: ovarian cancer: 06///geo\_accession: GSM368666///status: P

title: ovarian cancer: 070///geo\_accession: GSM368730///status:  
 title: ovarian cancer: 071///geo\_accession: GSM368731///status:  
 title: ovarian cancer: 072///geo\_accession: GSM368732///status: P  
 title: ovarian cancer: 073///geo\_accession: GSM368733///status: Public on F  
 title: ovarian cancer: 074///geo\_accession: GSM368734///status: P  
 title: ovarian cancer: 075///geo\_accession: GSM368735///status:  
 title: ovarian cancer: 076///geo\_accession: GSM368736///status: P  
 title: ovarian cancer: 077///geo\_accession: GSM368737///status: P  
 title: ovarian cancer: 078///geo\_accession: GSM368738///status:  
 title: ovarian cancer: 079///geo\_accession: GSM368739///status:  
 title: ovarian cancer: 07///geo\_accession: GSM368667///status: Pu  
 title: ovarian cancer: 080///geo\_accession: GSM368740///status:  
 title: ovarian cancer: 08///geo\_accession: GSM368668///status: Pu  
 title: ovarian cancer: 09///geo\_accession: GSM368669///status: Pu

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
  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: GS

title: Serous ovarian cancer 104///geo\_accession: GSM432

title: Serous ovarian cancer 106///geo\_accession: GSM432223///status: Public on

title: Serous ovarian cancer 107///geo\_accession: GSM432

title: Serous ovarian cancer 108///geo\_accession: GSM432225///status: Public

title: Serous ovarian cancer 109///geo\_accession: GSM432226///status: Public on

title: Serous ovarian cancer 10///geo\_accession: GS  
title: Serous ovarian cancer 110///geo\_accession: GSM432228///status: Public on  
title: Serous ovarian cancer 111///geo\_accession: GSM432229///status: Public on  
title: Serous ovarian cancer 112///geo\_accession: GS  
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title: Serous ovarian cancer 68///geo\_accession: GS

title: Serous ovarian cancer 69///geo\_accession: GS

title: Serous ovarian cancer 6///geo\_accession: GS

title: Serous ovarian cancer 72///geo\_accession: GS

title: Serous ovarian cancer 77///geo\_accession: GSM4

title: Serous ovarian cancer 79///geo\_accession: GS

title: Serous ovarian cancer 7///geo\_accession: GS

title: Serous ovarian cancer 80///geo\_accession: GSM432

**Value**

An expression set

---

GSE18520

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

---

**Description**

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

MAGP2 expression correlated with microvessel density suggesting a proangiogenic role in vivo. Thus, MAGP2 may serve as a survival-associated target.

### Format

```

experimentData(eset):
Experiment data
  Experimenter name: Mok SC, Bonome T, Vathipadiekal V, Bell A, Johnson ME, Wong
  Laboratory: Mok, Birrer 2009
  Contact information:
  Title: A gene signature predictive for outcome in advanced ovarian cancer iden
  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 ... AFFX-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\_

title: Normal Ovary, 2061///geo\_

title: Normal Ovary, 2064///geo\_

title: Normal Ovary, 2085///geo\_

title: Normal Ovary, 2225///geo\_

title: Normal Ovary, 2226///geo\_

title: Normal Ovary, 2228///geo\_

title: Normal Ovary, 2230///geo\_

title: Normal Ovary, 2234///geo\_

title: Normal Ovary, 2237///geo\_

title: Ovarian Tumor, 1109///geo\_accession: GSM461390///status: Public on Oct 17

title: Ovarian Tumor, 1214///geo\_accession: GSM461391///status: Public on Oct 17

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title: Ovarian Tumor, 692///geo\_accession: GSM461397///status: Public on Oct 17 2011

title: Ovarian Tumor, 694///geo\_accession: GSM461385///status: Public on C  
 title: Ovarian Tumor, 702///geo\_accession: GSM461361///status: Public on C  
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 title: Ovarian Tumor, 715///geo\_accession: GSM461386///status: Public on C  
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 title: Ovarian Tumor, 744///geo\_accession: GSM461378///status: Public on C  
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 title: Ovarian Tumor, 794///geo\_accession: GSM461388///status: Public on C  
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 title: Ovarian Tumor, 800///geo\_accession: GSM461371///status: Public on C  
 title: Ovarian Tumor, 872///geo\_accession: GSM461366///status: Public on  
 title: Ovarian Tumor, 934///geo\_accession: GSM461372///status: Public on Oct 1  
 title: Ovarian Tumor, 970///geo\_accession: GSM461389///status: Public on C

duplicates:

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

## Value

An expression set

GSE19829

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

## Description

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

## Format

experimentData (eset) :

Experiment data

Experimenter name: Konstantinopoulos PA, Spentzos D, Karlan BY, Taniguchi T et

Laboratory: Konstantinopoulos, Cannistra 2010 hgu95

Contact information:

Title: Gene expression profile of BRCAness that correlates with responsiveness

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 6 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:
  title: Ovarian cancer_sample 11///geo_accession: GSM495149///status:
      title: Ovarian cancer_sample 12///geo_accession: GSM495150///st
  title: Ovarian cancer_sample 13///geo_accession: GSM495151///status:
  title: Ovarian cancer_sample 14///geo_accession: GSM495152///status:
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```

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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.*

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## 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 normalLization 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, Le
  Laboratory: Meyniel, Sastre-Garau 2010
  Contact information:
  Title: A genomic and transcriptomic approach for a differential diagnosis betw
  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:

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

Breast metastasis in the ovary_OC01_ARN0121	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0123	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0126	[HG-U133_Plus_2]	1
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Breast metastasis in the ovary_OC01_ARN0142	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0143	[HG-U133_Plus_2]	1
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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
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Ovarian carcinoma_OC01_ARN0022	[HG-U133_Plus_2]	1
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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
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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
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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
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title: Ovarian carcinoma\_OC01\_



## 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:

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 Available sample meta-data:  
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## alt\_sample\_name:

Abdominal wall mass - 8176	Omentum - 1006
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Omentum - 8174	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
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Ovary - 180953	Ovary - 184837
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Ovary - 199400	Ovary - 202030
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Ovary - 202041	Ovary - 20284
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Ovary - 20285	Ovary - 20296
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1	1
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1	1
Ovary - 207532	Ovary - 209699
1	1
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1	1
Ovary - 209718	Ovary - 211371

1			
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1			1
Ovary - 211409		Ovary - 21758	
1			1
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1			1
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1			1
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Ovary - 23904		Ovary - 23930	
1			1
Ovary - 23934		Ovary - 23936	
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Ovary - 23938		Ovary - 241181	
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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
           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:

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

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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 $\beta$  and modulate the oxidative stress response. Enhanced expression of these microRNAs mimics p38 $\beta$  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 $\beta$  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

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

Abstract: A 149 word abstract is available. Use 'abstract' method.
Information is available on: preprocessing
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  platform_distribution:
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  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 Nov 11 2009

title: Ovarian carcinoma 101///geo\_accession: GSM643033///status: Public on Nov 11 2009

title: Ovarian carcinoma 102///geo\_accession: GSM643034///status: Public on Nov 11 2009

title: Ovarian carcinoma 103///geo\_accession: GSM643035///status: Public on Nov 11 2009

title: Ovarian carcinoma 104///geo\_accession: GSM643036///status: Public on Nov 11 2009

title: Ovarian carcinoma 105///geo\_accession: GSM643037///status: Public on Nov 11 2009

title: Ovarian carcinoma 106///geo\_accession: GSM643038///status: Public on Nov 11 2009

title: Ovarian carcinoma 107///geo\_accession: GSM643039///status: Public on Nov 11 2009

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title: Ovarian carcinoma 12///geo\_accession: GSM642944///status: Public on Nov 11 2009

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title: Ovarian carcinoma 73///geo\_accession: GSM643005///status: Public on Nov 0

title: Ovarian carcinoma 74///geo\_accession: GSM643006///status: Public on Nov 0

title: Ovarian carcinoma 75///geo\_accession: GSM643007///status: Public on Nov 0

title: Ovarian carcinoma 76///geo\_accession: GSM643008///status: Public on Nov 0

title: Ovarian carcinoma 77///geo\_accession: GSM643009///status: Public on Nov 0

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title: Ovarian carcinoma 85///geo\_accession: GSM643017///status: Public

title: Ovarian carcinoma 86///geo\_accession: GSM643018///status: Public

title: Ovarian carcinoma 87///geo\_accession: GSM643019///status: Public

title: Ovarian carcinoma 88///geo\_accession: GSM643020///status: Public

title: Ovarian carcinoma 89///geo\_accession: GSM643021///status: Public

title: Ovarian carcinoma 8///geo\_accession: GSM642940///status: Public

title: Ovarian carcinoma 90///geo\_accession: GSM643022///status: Public

title: Ovarian carcinoma 91///geo\_accession: GSM643023///status: Public on

title: Ovarian carcinoma 92///geo\_accession: GSM643024///status: Public

## 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
  Laboratory: Bonome, Birrer 2008
  Contact information:
  Title: A gene signature predicting for survival in suboptimally debulked patie
  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:
    hg133a
  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 SO124	Ovarian Cancer SO129	Ovarian Cancer SO13
1	1	1
Ovarian Cancer SO131	Ovarian Cancer SO134	Ovarian Cancer SO135
1	1	1
Ovarian Cancer SO137	Ovarian Cancer SO141	Ovarian Cancer SO143
1	1	1
Ovarian Cancer SO148	Ovarian Cancer SO154	Ovarian Cancer SO16
1	1	1
Ovarian Cancer SO166	Ovarian Cancer SO17	Ovarian Cancer SO173
1	1	1
Ovarian Cancer SO174	Ovarian Cancer SO18	Ovarian Cancer SO181
1	1	1
Ovarian Cancer SO184	Ovarian Cancer SO185	Ovarian Cancer SO187
1	1	1
Ovarian Cancer SO189	Ovarian Cancer SO190	Ovarian Cancer SO193
1	1	1
Ovarian Cancer SO194	Ovarian Cancer SO196	Ovarian Cancer SO197
1	1	1
Ovarian Cancer SO2	Ovarian Cancer SO200	Ovarian Cancer SO201
1	1	1
Ovarian Cancer SO203	Ovarian Cancer SO205	Ovarian Cancer SO21
1	1	1
Ovarian Cancer SO211	Ovarian Cancer SO214	Ovarian Cancer SO216
1	1	1
Ovarian Cancer SO217	Ovarian Cancer SO218	Ovarian Cancer SO224
1	1	1
Ovarian Cancer SO225	Ovarian Cancer SO227	Ovarian Cancer SO228
1	1	1
Ovarian Cancer SO229	Ovarian Cancer SO23	Ovarian Cancer SO230
1	1	1
Ovarian Cancer SO231	Ovarian Cancer SO235	Ovarian Cancer SO236
1	1	1
Ovarian Cancer SO237	Ovarian Cancer SO241	Ovarian Cancer SO242
1	1	1
Ovarian Cancer SO243	Ovarian Cancer SO244	Ovarian Cancer SO246
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	S0283	Ovarian Cancer	S0285	Ovarian Cancer	S0290
	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: No

title: No

title: No

title: No

title: No

title: No

title: No

title: No

title: No

title: No

title: Ovarian Cancer S0100///geo\_accession: GSM657530///status: Public on Jan

title: Ovarian Cancer S0103///geo\_accession: GSM657531///status: Public on Jan

title: Ovarian Cancer S0106///geo\_accession: GSM657532///status: Public

title: Ovarian Cancer S0108///geo\_accession: GSM657533///status: Public on

title: Ovarian Cancer S010///geo\_accession: GSM657529///status: Public on

title: Ovarian Cancer S0113///geo\_accession: GSM657535///status: Public on Jan

title: Ovarian Cancer S0115///geo\_accession: GSM657536///status: Public

title: Ovarian Cancer S0116///geo\_accession: GSM657537///status: Public on

title: Ovarian Cancer S0117///geo\_accession: GSM657538///status: Public on

title: Ovarian Cancer S0118///geo\_accession: GSM657539///status: Public on Jan

title: Ovarian Cancer S011///geo\_accession: GSM657534///status: Public

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title: Ovarian Cancer S0122///geo\_accession: GSM657542///status: Public

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title: Ovarian Cancer S012///geo\_accession: GSM657540///status: Public

title: Ovarian Cancer S0131///geo\_accession: GSM657546///status: Public on Jan

title: Ovarian Cancer S0134///geo\_accession: GSM657547///status: Public

title: Ovarian Cancer S0135///geo\_accession: GSM657548///status: Public

title: Ovarian Cancer S0137///geo\_accession: GSM657549///status: Public on

title: Ovarian Cancer S013///geo\_accession: GSM657545///status: Public on Jan 20

title: Ovarian Cancer S0141///geo\_accession: GSM657550///status: Public on

title: Ovarian Cancer S0143///geo\_accession: GSM657551///status: Public on

title: Ovarian Cancer S0148///geo\_accession: GSM657552///status: Public on

title: Ovarian Cancer S0154///geo\_accession: GSM657553///status: Public on Ja

title: Ovarian Cancer S0166///geo\_accession: GSM657555///status: Public on Jan  
title: Ovarian Cancer S016///geo\_accession: GSM657554///status: Public on  
title: Ovarian Cancer S0173///geo\_accession: GSM657557///status: Public on  
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title: Ovarian Cancer S017///geo\_accession: GSM657556///status: Public on  
title: Ovarian Cancer S0181///geo\_accession: GSM657560///status: Public on Jan  
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title: Ovarian Cancer S0229///geo\_accession: GSM657585///status: Public on  
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title: Ovarian Cancer S0235///geo\_accession: GSM657589///status: Public on  
title: Ovarian Cancer S0236///geo\_accession: GSM657590///status: Public on Jan  
title: Ovarian Cancer S0237///geo\_accession: GSM657591///status: Public on  
title: Ovarian Cancer S023///geo\_accession: GSM657586///status: Public on Jan  
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title: Ovarian Cancer S0243///geo\_accession: GSM657594///status: Public on Jan  
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title: Ovarian Cancer S0263///geo\_accession: GSM657606///status: Public on

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 title: Ovarian Cancer S0290///geo\_accession: GSM657617///status: Public  
 title: Ovarian Cancer S0295///geo\_accession: GSM657618///status: Public on

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
  Laboratory: Gillet, Gottesman 2012
  Contact information:
  Title: Multidrug resistance-linked gene signature predicts overall survival of
  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 P

title:

title: US Patient

title: US Patient 51///geo\_accession: GSM742615///status: Public on Apr 19 2012/

title: US Patient 54///geo\_accession: GSM7

title: US Patient 57///geo\_accession: GSM742621///status: Publi

title: US Patient 59///geo\_accession: GSM742623///status: Publi

title: US Patient 63///geo\_acces

title: US Patie

title: US Patient 66///geo\_accession: GSM742630///sta

title: US Patient 70///geo\_accession: GSM742634///status: Public on Apr 19

title: US Pat

title: US Patient 75///geo\_accession: GSM7

titl

title: US Patient 77///geo

title: US Patient 78

title: US Patient 79/

**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

Laboratory: Ferriss, Lee 2012  
 Contact information:  
 Title: Multi-gene expression predictors of single drug responses to adjuvant c  
 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_20 OV_FFPE_21
    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
```

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

sample\_type:

tumor  
58

histological\_type:

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

summarygrade:

high	low	NA's
33	21	4

summarystage:

late  
58

tumorstage:

3	4
53	5

substage:

a	b	c
9	11	38

grade:

1	2	3	NA's
2	19	33	4

age\_at\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
38.00	53.50	62.00	62.57	72.00	85.00

pltx:

y  
58

tax:

n y  
4 54

neo:  
n  
58

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

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

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

vital\_status:  
deceased living  
36 22

debulking:  
optimal suboptimal NA's  
26 30 2

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

uncurated\_author\_metadata:  
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title: OV\_FFPE\_13///geo\_accession: GSM746873///status: Public on Aug 21 2012  
title: OV\_FFPE\_14///geo\_accession: GSM746874///status: Public on Aug 21 2012//  
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title: OV\_FFPE\_16///geo\_accession: GSM746876///status: Public on Aug 21 20  
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title: OV\_FFPE\_19///g

title: OV\_FFPE\_1///geo\_accession: GSM746861///status: Public on Aug 21 2012///s

title: OV\_FFPE\_20///geo\_accession: GSM746880///status: Public on Aug 21 2012///s

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title: OV\_FFPE\_36///geo\_accession: GSM746896///status: Public on Aug 21 2012///s

title: OV\_FFPE\_37///geo\_accession: GSM746897///status: Public on Aug 21 2012///s

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title: OV\_FFPE\_43///geo\_accession: GSM746903///st  
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title: OV\_FFPE\_57///geo\_accession: GSM746917///status: Public on Aug 21 2012///  
title: OV\_FFPE\_58///geo\_accession: GSM746918///status: Public on Aug 21 2012///  
title: OV\_FFPE\_5///geo\_accession: GSM746865///status: Public on Aug 21 2012///  
title: OV\_FFPE\_6///geo\_accession: GSM746866///status: Public on Aug 21 2012///  
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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
  Laboratory: Yoshihara, Tanaka 2012
  Contact information:
  Title: High-risk ovarian cancer based on 126-gene expression signature is unig
  URL:
  PMIDs: 22241791

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

```

```
platform_accession:
  GPL6480
version:
  2015-09-22 19:55:29
```

```
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	1	1	1	1	1	1	1	1	1	1
146d	1	1	1	1	1	1	1	1	1	1
174d	1	1	1	1	1	1	1	1	1	1
23d	1	1	1	1	1	1	1	1	1	1
269d	1	1	1	1	1	1	1	1	1	1
306d	1	1	1	1	1	1	1	1	1	1
333d2	1	1	1	1	1	1	1	1	1	1
353d	1	1	1	1	1	1	1	1	1	1
367d	1	1	1	1	1	1	1	1	1	1

```
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

title: serous ovarian cancer 115d///geo\_accession: GSM794867///status: Public on

title: serous ovarian cancer 116d///geo\_accession: GSM794868///status: Public on

title: serous ovarian cancer 117d///geo\_accession: GSM794869///status: Public

title: serous ovarian cancer 119d///geo\_accession: GSM794870///status: Public  
title: serous ovarian cancer 11d///geo\_accession: GSM794866///status: Public  
title: serous ovarian cancer 120d///geo\_accession: GSM794872///status: Public  
title: serous ovarian cancer 122d///geo\_accession: GSM794873///status: Public o  
title: serous ovarian cancer 123d///geo\_accession: GSM794874///status: Public on  
title: serous ovarian cancer 125Rd///geo\_accession: GSM794875///status: Public o  
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duplicates:

GSE32062.GSE32062.GPL6480_GSM794933	GSE32062.GSE32062.GPL6480_GSM794935
	1
	1
NA's	
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 (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
  Laboratory: Yoshihara, Tanaka 2012
  Contact information:
  Title: High-risk ovarian cancer based on 126-gene expression signature is uniq
  URL:
  PMIDs: 22241791

  Abstract: A 255 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
    platform_title:
      Agilent-014850 Whole Human Genome Microarray 4x44K G4112F (Probe Name vers
ion)
    platform_shorttitle:
      Agilent G4112F
    platform_summary:
      hgug4112a
    platform_manufacturer:
      Agilent
    platform_distribution:
      commercial
    platform_accession:
      GPL6480
    version:
      2015-09-22 19:58:23

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

```

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

## Details

assayData: 30936 features, 40 samples

Platform type:

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

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

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

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

alt\_sample\_name:

106	108	109R	110	111R	192	195R	196	197	198	200	203	205	206	207	213
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 o  
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title: serous ovarian cancer 109R///geo\_accession: GSM795127///status: Public o  
title: serous ovarian cancer 110///geo\_accession: GSM795128///status: Public o  
title: serous ovarian cancer 111R///geo\_accession: GSM795129///status: Public on  
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title: serous ovarian cancer 298R///geo\_accession: GSM

**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- $\beta$ 1) treatment triggers the activation of smad2 signaling cascades, leading to activation of COL11A1 and MMP3. Pharmacological inhibition of MMP3 abrogated the TGF- $\beta$ 1-triggered, COL11A1-dependent cell invasiveness. Furthermore, the NF-YA-binding site on the COL11A1 promoter was identified as the major determinant of TGF- $\beta$ 1-dependent COL11A1 activation. Analysis of 88 ovarian cancer patients indicated that high COL11A1 mRNA levels are associated with advanced disease stage. The 5-year recurrence-free and overall survival rates were significantly lower ( $P=0.006$  and  $P=0.018$ , respectively) among patients with high expression levels of tissue COL11A1 mRNA compared with those with low expression. We conclude that COL11A1 may promote tumor aggressiveness via the TGF- $\beta$ 1-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 i
```

```
  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:
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```
    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

## uncurated\_author\_metadata:

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     title: Ts\_8///geo\_accession: GSM1079031///status: Public on Jan 01

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.*

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## 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

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experimentData (eset) :
Experiment data
  Experimenter name: Pils D1, Hager G, Tong D, Aust S, Heinze G, Kohl M, Schuster
  Laboratory: Pils, Zeilinger 2012
  Contact information:
  Title: Validating the impact of a molecular subtype in ovarian cancer on outcome
  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

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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:
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143 50 11

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9 185 10

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2 3 4 NA's  
9 154 31 10

grade:  
2 3 NA's  
50 143 11

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norecurrence recurrence NA's  
70 124 10

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**Value**

An expression set

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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
  Laboratory: Karlan, Slamon 2014
  Contact information:
  Title: POSTN/TGFBI-associated stromal signature predicts poor prognosis in ser
  URL:
  PMIDs: 24368280

Abstract: A 250 word abstract is available. Use 'abstract' method.
Information is available on: preprocessing
notes:
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  platform_accession:
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  platform_technology:
    in situ oligonucleotide
  version:

```



Ov_Tumor_Ref_Mix vs. CS-OV-029	Ov_Tumor_Ref_Mix vs. CS-OV-030
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Ov_Tumor_Ref_Mix vs. CS-OV-031	Ov_Tumor_Ref_Mix vs. CS-OV-032
1	1
Ov_Tumor_Ref_Mix vs. CS-OV-033	Ov_Tumor_Ref_Mix vs. CS-OV-034
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Ov_Tumor_Ref_Mix vs. CS-OV-035	Ov_Tumor_Ref_Mix vs. CS-OV-036
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benign	borderline	healthy	metastatic	tumor
5	12	15	17	123

## 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:

1	2	3	4	NA's
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## substage:

a	b	c	NA's
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## grade:

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## Value

An expression set

---

GSE6008

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

---

## Description

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

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

### Format

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Experiment data
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  Laboratory: Murph, Mills 2009
  Contact information:
  Title: Lysophosphatidic acid-induced transcriptional profile represents serous
  URL:
  PMIDs: 19440550

Abstract: A 247 word abstract is available. Use 'abstract' method.
Information is available on: preprocessing
notes:
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  platform_accession:
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    2015-09-22 20:07:11

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

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

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38 36 29

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title: Ovarian\_Tumor\_Serous\_KU-OS-002///geo\_accession: GSM139

title: Ovarian\_Tumor\_Serous\_KU-OS-003///geo\_accession: GSM1394

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title: Ovarian\_Tumor\_Serous\_KU-OS-007///geo\_accession: GSM1394

title: Ovarian\_Tumor\_Serous\_KU-OS-009///geo\_accession: GSM1394

title: Ovarian\_Tumor\_Serous\_KU-OS-011///geo\_accession: GSM1394  
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 title: Ovarian\_Tumor\_Serous\_KU-OS-013///geo\_accession: GSM1394  
 title: Ovarian\_Tumor\_Serous\_KU-OS-015///geo\_accession: GSM1394  
 title: Ovarian\_Tumor\_Serous\_KU-OS-018///geo\_accession: GSM1394  
 title: Ovarian\_Tumor\_Serous\_KU-OS-021///geo\_accession: GSM1394  
 title: Ovarian\_Tumor\_Serous\_KU-OS-022///geo\_accession: GSM1394  
 title: Ovarian\_Tumor\_Serous\_UM-OS-02///geo\_accession: GSM1394  
 title: Ovarian\_Tumor\_Serous\_UM-OS-07///geo\_accession: GSM1394  
 title: Ovarian\_Tumor\_Serous\_UM-OS-09///geo\_accession: GSM1394  
 title: Ovarian\_Tumor\_Serous\_UM-OS-10///geo\_accession: GSM1394  
 title: Ovarian\_Tumor\_Serous\_UM-OS-11///geo\_accession: GSM1394

duplicates:

GSE6008.GSE6008\_GSM139476///GSE6008.GSE6008\_GSM139477  
 1  
 GSE6008.GSE6008\_GSM139476///GSE6008.GSE6008\_GSM139478  
 1  
 GSE6008.GSE6008\_GSM139477///GSE6008.GSE6008\_GSM139478  
 1  
 NA's  
 100

**Value**

An expression set

---

GSE6822

*Classification of ovarian tumor samples*

---

**Description**

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

**Format**

```

experimentData(eset):
Experiment data
  Experimenter name: Ouellet V, Provencher DM, Maugard CM, Le Page C, Ren F, Lus
  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
	1		1		1		1
Ovarian tumor	AM287	Ovarian tumor	AM288	Ovarian tumor	AM289	Ovarian tumor	AM290
	1		1		1		1
Ovarian tumor	AM292	Ovarian tumor	AM293	Ovarian tumor	AM294	Ovarian tumor	AM311
	1		1		1		1
Ovarian tumor	AM313	Ovarian tumor	AM315	Ovarian tumor	AM317	Ovarian tumor	AM333
	1		1		1		1
Ovarian tumor	AM335	Ovarian tumor	AM339	Ovarian tumor	AM341	Ovarian tumor	AM344
	1		1		1		1
Ovarian tumor	AM345	Ovarian tumor	AM347	Ovarian tumor	AM348	Ovarian tumor	AM349
	1		1		1		1
Ovarian tumor	AM354	Ovarian tumor	AM364	Ovarian tumor	AM367	Ovarian tumor	AM368
	1		1		1		1
Ovarian tumor	AM381	Ovarian tumor	AM382	Ovarian tumor	AM398	Ovarian tumor	AM429
	1		1		1		1
Ovarian tumor	AM431	Ovarian tumor	AM438				
	1		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					
2	2					

uncurated\_author\_metadata:

title: Ovarian tumor AM053///geo\_accession: GSM157230

title: Ovarian tumor AM122///geo\_accession: GSM157231///status: Public on Dec 31 2002

title: Ovarian tumor AM124///geo\_accession: GSM157232

title: Ovarian tumor AM125///geo\_accession: GSM157233

title: Ovarian tumor AM127///geo\_accession: GSM157234///status: Public on Dec 31 2002

title: Ovarian tumor AM137///geo\_accession: GSM157235

title: Ovarian tumor AM138///geo\_accession: GSM157236

title: Ovarian tumor AM144///geo\_accession: GSM157237

title: Ovarian tumor AM178///geo\_accession: GSM157238

title: Ovarian tumor AM179///geo\_accession: GSM157239

title: Ovarian tumor AM182///geo\_accession: GSM157240

title: Ovarian tumor AM195///geo\_accession: GSM157241

title: Ovarian tumor AM196///geo\_accession: GSM157242

title: Ovarian tumor AM198///geo\_accession: GSM157243

title: Ovarian tumor AM200///geo\_accession: GSM157244

title: Ovarian tumor AM201///geo\_accession: GSM157245

title: Ovarian tumor AM202///geo\_accession: GSM157246

title: Ovarian tumor AM203///geo\_accession: GSM157247

title: Ovarian tumor AM204///geo\_accession: GSM157248

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title: Ovarian tumor AM209///geo\_accession: GSM157251

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title: Ovarian tumor AM252///geo\_accession: GSM  
title: Ovarian tumor AM253///geo\_accession: GSM157  
title: Ovarian tumor AM255///geo\_accessio  
title: Ovarian tumor AM256///geo\_accessio  
title: Ovarian tumor AM259///geo\_accession: GSM15  
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title: Ovarian tumor AM263///geo\_accessio  
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title: Ovarian tumor AM269///geo\_accessio  
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title: Ovarian tumor AM290///geo\_accessio  
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title: Ovarian tumor AM294///geo\_accessio  
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title: Ovarian tumor AM315///geo\_accession:  
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title: Ovarian tumor AM333///geo\_accession: G  
title: Ovarian tumor AM335///geo\_accessio

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 title: Ovarian tumor AM344///geo\_accession: GS  
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 title: Ovarian tumor AM368///geo\_accession:  
 title: Ovarian tumor AM381///geo\_accession:  
 title: Ovarian tumor AM382///geo\_accession:  
 title: Ovarian tumor AM398///geo\_accession: GSM157295///status: Public on Dec  
 title: Ovarian tumor AM429///geo\_accession: GSM157296///status: Public on De  
 title: Ovarian tumor AM431///geo\_accession:  
 title: Ovarian tumor AM438///geo\_accession:

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, Fr
  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
  platform_accession:
    GPL5689
  platform_technology:
    spotted DNA/cDNA
  version:
    2015-09-22 20:07:40

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1 2 ... 8864 (7809 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

**Details**

assayData: 7809 features, 83 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
83	15	NA	12	NA

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

alt\_sample\_name:

p0102bis	sample_Ovarian	tumor	p0103bis	sample_Ovarian	tumor
		1			1
p0112bis	sample_Ovarian	tumor	p0114bis	sample_Ovarian	tumor
		1			1
p0125bis	sample_Ovarian	tumor	p0128bis	sample_Ovarian	tumor
		1			1
p0143bis	sample_Ovarian	tumor	p0146bis	sample_Ovarian	tumor
		1			1
p0188bis	sample_Ovarian	tumor	p0208bis	sample_Ovarian	tumor
		1			1
p0210bis	sample_Ovarian	tumor	p0217bis	sample_Ovarian	tumor
		1			1
p057bis	sample_Ovarian	tumor	p070bis	sample_Ovarian	tumor
		1			1
p080bis	sample_Ovarian	tumor	p091bis	sample_Ovarian	tumor
		1			1
p139bis	sample_Ovarian	tumor	p13bis	sample_Ovarian	tumor
		1			1
p141bis	sample_Ovarian	tumor	p166bis	sample_Ovarian	tumor
		1			1
p171bis	sample_Ovarian	tumor	p17bis	sample_Ovarian	tumor
		1			1
p183bis	sample_Ovarian	tumor	p209bis	sample_Ovarian	tumor
		1			1
p212bis	sample_Ovarian	tumor	p213bis	sample_Ovarian	tumor
		1			1
p243bis	sample_Ovarian	tumor	p246bis	sample_Ovarian	tumor
		1			1
p261bis	sample_Ovarian	tumor	p284bis	sample_Ovarian	tumor
		1			1
p293bis	sample_Ovarian	tumor	p310bis	sample_Ovarian	tumor
		1			1
p31bis	sample_Ovarian	tumor	p320bis	sample_Ovarian	tumor
		1			1
p331bis	sample_Ovarian	tumor	p336bis	sample_Ovarian	tumor
		1			1
p350bis	sample_Ovarian	tumor	p375bis	sample_Ovarian	tumor
		1			1

p382bis	sample_Ovarian	tumor	p383bis	sample_Ovarian	tumor
		1			1
p386bis	sample_Ovarian	tumor	p388bis	sample_Ovarian	tumor
		1			1
p398bis	sample_Ovarian	tumor	p39bis	sample_Ovarian	tumor
		1			1
p401bis	sample_Ovarian	tumor	p414bis	sample_Ovarian	tumor
		1			1
p421bis	sample_Ovarian	tumor	p429bis	sample_Ovarian	tumor
		1			1
p433bis	sample_Ovarian	tumor	p448bis	sample_Ovarian	tumor
		1			1
p455bis	sample_Ovarian	tumor	p459bis	sample_Ovarian	tumor
		1			1
p462bis	sample_Ovarian	tumor	p482bis	sample_Ovarian	tumor
		1			1
p487bis	sample_Ovarian	tumor	p497bis	sample_Ovarian	tumor
		1			1
p502bis	sample_Ovarian	tumor	p540bis	sample_Ovarian	tumor
		1			1
p541bis	sample_Ovarian	tumor	p549bis	sample_Ovarian	tumor
		1			1
p550bis	sample_Ovarian	tumor	p567bis	sample_Ovarian	tumor
		1			1
p56bis	sample_Ovarian	tumor	p573bis	sample_Ovarian	tumor
		1			1
p586bis	sample_Ovarian	tumor	p597bis	sample_Ovarian	tumor
		1			1
p616bis	sample_Ovarian	tumor	p63bis	sample_Ovarian	tumor
		1			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

uncurated\_author\_metadata:  
title: p0102bis sample\_Ovarian tumor///geo\_accession: GSM214010///stat  
title: p0103bis sample\_Ovarian tumor///geo\_accession: GSM214078///status: Publ  
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title: p0125bis sample\_Ovarian tumor///geo\_accession: GSM214009///status: Public

title: p0128bis sample\_Ovarian tumor///geo\_accession: GSM214030///status: Public

title: p0143bis sample\_Ovarian tumor///geo\_accession: GSM214012///status: Public

title: p0146bis sample\_Ovarian tumor///geo\_accession: GSM214033///status: Public

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title: p0208bis sample\_Ovarian tumor///geo\_accession: GSM214011///status: Public

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title: p0217bis sample\_Ovarian tumor///geo\_accession: GSM214008///status: Public

title: p057bis sample\_Ovarian tumor///geo\_accession: GSM214064///status: Public

title: p070bis sample\_Ovarian tumor///geo\_accession: GSM214032///status: Public

title: p080bis sample\_Ovarian tumor///geo\_accession: GSM214017///status: Public

title: p091bis sample\_Ovarian tumor///geo\_accession: GSM214024///status: Public

title: p139bis sample\_Ovarian tumor///geo\_accession: GSM214047///status: Public

title: p13bis sample\_Ovarian tumor///geo\_accession: GSM214043///status: Public

title: p141bis sample\_Ovarian tumor///geo\_accession: GSM214081///status: Public

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title: p212bis sample\_Ovarian tumor///geo\_accession: GSM214065///status: Public

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title: p261bis sample\_Ovarian tumor///geo\_accession: GSM214034///status: Public

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title: p310bis sample\_Ovarian tumor///geo\_accession: GSM214083///status: Public  
title: p31bis sample\_Ovarian tumor///geo\_accession: GSM214019///status  
title: p320bis sample\_Ovarian tumor///geo\_accession: GSM214020///statu  
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title: p79bis sample\_Ovarian tumor///geo\_accession: GSM214063///status: Pu

```

title: p84bis sample_Ovarian tumor///geo_accession: GSM214039///status: P
title: p90bis sample_Ovarian tumor///geo_accession: GSM214077///status: Public

```

## 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, J
  Laboratory: Tothill, Bowtell 2008
  Contact information:
  Title: Novel molecular subtypes of serous and endometrioid ovarian cancer link
  URL:
  PMIDs: 18698038

Abstract: A 243 word abstract is available. Use 'abstract' method.
Information is available on: preprocessing
notes:

```

```

platform_title:
  [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
platform_shorttitle:
  Affymetrix HG-U133Plus2
platform_summary:
  hgu133plus2
platform_manufacturer:
  Affymetrix
platform_distribution:
  commercial
platform_accession:
  GPL570
version:
  2015-09-22 20:16:32

```

```

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

```

## Details

```

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

```

```

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

```

```

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

```

```

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

```

X32048	X32049	X32054	X32055	X32089	X32098	X32103	X32117	X34019	X34049
1	1	1	1	1	1	1	1	1	1
X34066	X34078	X34080	X34085	X34086	X34090	X34102	X34103	X34111	X34113
1	1	1	1	1	1	1	1	1	1
X34117	X34125	X34165	X34168	X34172	X34186	X34202	X34207	X34801	(Other)
1	1	1	1	1	1	1	1	1	186

sample\_type:

tumor  
285

histological\_type:

endo	other	ser
20	1	264

primarysite:

ft	other	ov
8	34	243

arrayedsite:

ft	other	ov
2	83	200

summarygrade:

high	low	NA's
163	116	6

summarystage:

early	late	NA's
42	240	3

tumorstage:

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

substage:

a	b	c	NA's
26	19	212	28

grade:

1	2	3	NA's
19	97	163	6

age\_at\_initial\_pathologic\_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
22.00	53.00	59.00	59.62	68.00	80.00	3

pltx:

n	y	NA's
39	243	3

tax:

```

n      y NA's
87    195    3

```

```
neo:
```

```

n      y NA's
264    18    3

```

```
days_to_tumor_recurrence:
```

```

Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
0.0   300.0   450.0   618.9  810.0  4980.0    10

```

```
recurrence_status:
```

```

norecurrence  recurrence    NA's
           94           188           3

```

```
days_to_death:
```

```

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

```

```
vital_status:
```

```

deceased  living    NA's
      113     169     3

```

```
debulking:
```

```

optimal  suboptimal    NA's
      160           88           37

```

```
batch:
```

```

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

```

```
uncurated_author_metadata:
```

```

title: X129///geo_accession: GSM250001///status: Public on Mar 01 2008

```

```

title: X146///geo_accession: GSM250000///status: Public on Mar 01 2008

```

```

title: X152///geo_accession: GSM249999///status: Public on Mar 01 2008///su

```

title: X20019///geo\_accession: GSM249998///status: Public on Mar 01 2008///s

title: X20025///geo\_accession: GSM249997///status: Public on Mar 01 2008///s

title: X20027///geo\_accession: GSM249996///status: Public on Mar 01 2008///s

title: X20031///geo\_accession: GSM249995///status: Public on Mar 01 2008///s

title: X20032///geo\_accession: GSM249994///status: Public on Mar 01 2008///s

title: X20041///geo\_accession: GSM249993///status: Public on Mar 01 2008///s

title: X20046///geo\_accession: GSM249992///status: Public on Mar 01 2008///s

title: X20074///geo\_accession: GSM249991///status: Public on Mar 01 2008///s

title: X22002///geo\_accession: GSM249728///status: Public on Mar 01 2008///s

title: X22012///geo\_accession: GSM249990///status: Public on Mar 01 2008///s

title: X22013///geo\_accession: GSM249989///status: Public on Mar 01 2008///s

title: X22020///geo\_accession: GSM249988///status: Public on Mar 01 2008///s

title: X22023///geo\_accession: GSM249987///status: Public on Mar 01 2008///s

title: X22027///geo\_accession: GSM249725///status: Public on Mar 01 2008///s

title: X22029///geo\_accession: GSM249986///status: Public on Mar 01 2008///s

title: X22031///geo\_accession: GSM249985///status: Public on Mar 01 2008///s

title: X22037///geo\_accession: GSM249984///status: Public on Mar 01 2008///s

title: X22046///geo\_accession: GSM249983///status: Public on Mar 01 2008///s

title: X22047///geo\_accession: GSM249982///status: Public on Mar 01 2008///s

title: X22048///geo\_accession: GSM249981///status: Public on Mar 01 2008///s

title: X22057///geo\_accession: GSM249980///status: Public on Mar 01 2008///s

title: X22058///geo\_accession: GSM249979///status: Public on Mar 01 2008///s

title: X2219///geo\_accession: GSM249978///status: Public on Mar 01 2008///s

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title: X23030///geo\_accession: GSM249975///status: Public on Mar 01 2008///s

title: X23036///geo\_accession: GSM249727///status: Public on Mar 01 2008

title: X23043///geo\_accession: GSM249974///status: Public on Mar 01 2008

title: X23052///geo\_accession: GSM249721///status: Public on Mar 01 2008

title: X23053///geo\_accession: GSM249973///status: Public on Mar 01 2008

title: X23055///geo\_accession: GSM249972///status: Public on Mar 01 2008

title: X23066///geo\_accession: GSM249716///status: Public on Mar 01 2008

title: X23070///geo\_accession: GSM249971///status: Public on Mar 01 2008

title: X23074///geo\_accession: GSM249970///status: Public on Mar 01 2008

title: X23077///geo\_accession: GSM249969///status: Public on Mar 01 2008

title: X23084///geo\_accession: GSM249968///status: Public on Mar 01 2008

title: X23098///geo\_accession: GSM249967///status: Public on Mar 01 2008

title: X23102///geo\_accession: GSM249966///status: Public on Mar 01 2008

title: X23106///geo\_accession: GSM249965///status: Public on Mar 01 2008///submitted

title: X23116///geo\_accession: GSM249964///status: Public on Mar 01 2008///submitted

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

title: X23165///geo\_accession: GSM249959///status: Public on Mar 01 2008

title: X23167///geo\_accession: GSM249958///status: Public on Mar 01 2008

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title: X23172///geo\_accession: GSM249956///status: Public on Mar 01 2008

title: X23177///geo\_accession: GSM249720///status: Public on Mar 01 2008

title: X23178///geo\_accession: GSM249955///status: Public on Mar 01 2008

title: X23182///geo\_accession: GSM249954///status: Public on Mar 01 2008

title: X23187///geo\_accession: GSM249953///status: Public on Mar 01 2008

title: X23197///geo\_accession: GSM249951///status: Public on Mar 01 2008//  
title: X23202///geo\_accession: GSM249950///status: Public on Mar 01 2008//  
title: X23204///geo\_accession: GSM249949///status: Public on Mar 01 2008//  
title: X23210///geo\_accession: GSM249948///status: Public on Mar 01 2008//  
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title: X32034///geo\_accession: GSM249937///status: Public on Mar 01 2008//s  
title: X32048///geo\_accession: GSM249936///status: Public on Mar 01 2008//  
title: X32049///geo\_accession: GSM249935///status: Public on Mar 01 2008//  
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//subm  
title: X32098///geo\_accession: GSM249931///status: Public on Mar 01 2008//  
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
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
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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
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
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

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

`quantileCutoff`     A numeric between 0 and 1 specifying to remove genes with standard deviation below the required quantile (default 0)

`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 many survival events must be in the dataset to keep the dataset (default 0)

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

`removeRetracted`     remove datasets from retracted papers (default TRUE, currently just PMID17290060 dataset)

`removeSubsets`     remove datasets that are a subset of other datasets (default TRUE, currently just PMID19318476)

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

```
imputeMissing
    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()
```

---

PMID15897565	<i>Patterns of gene expression that characterize long-term survival in advanced stage serous ovarian cancers.</i>
--------------	---

---

### Description

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

### Format

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

Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1762///Cancer.Type: Early

Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1763///Cancer.Type: Early

Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1764///Cancer.Type: Early

Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1765///Cancer.Type: Early

Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1772///Cancer.Type:

Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1773///Cancer.Type:

Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1774///Cancer.Type:

Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1775///Cancer.Type:

Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1776///Cancer.Type:

Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1777///Cancer.Type:  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1778///Cancer.Type:  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1779///Cancer.Type:  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1780///Cancer.Type:  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1781///Cancer.Type:  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1828///Cancer.Type:  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1829///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1830///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1831///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1832///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1833///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1834///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1835///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1836///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1900///Cancer.Type:  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1901///Cancer.Type:  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1902///Cancer.Type:  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1903///Cancer.Type: Early  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1904///Cancer.Type:  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1905///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1906///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1907///Cancer.Type:  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1908///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1909///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1989///Cancer.Type:  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2003///Cancer.Type: S

Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2004///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2005///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2019///Cancer.Type:  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2020///Cancer.Type:  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2021///Cancer.Type:  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2026///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2027///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2028///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2029///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2030///Cancer.Type:  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2031///Cancer.Type:  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2032///Cancer.Type:  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2033///Cancer.Type:  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2390///Cancer.Type: Early  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2391///Cancer.Type: Early  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2392///Cancer.Type: Early  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2393///Cancer.Type: Early  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2394///Cancer.Type:  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2395///Cancer.Type:  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2396///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2397///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2398///Cancer.Type:  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2399///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2400///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2401///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2402///Cancer.Type:

Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2536///Cancer.Type: Early

### Value

An expression set

---

PMID17290060

*An integrated genomic-based approach to individualized treatment of patients with advanced-stage ovarian cancer.*

---

### 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, C
  Laboratory: Dressman, Lancaster 2007
  Contact information:
  Title: An integrated genomic-based approach to individualized treatment of pat
  URL:
  PMIDs: 17290060

Abstract: A 223 word abstract is available. Use 'abstract' method.
Information is available on: preprocessing
notes:
  platform_title:
    [HG-U133A] Affymetrix Human Genome U133A Array
  platform_shorttitle:
    Affymetrix HG-U133A

```

```

platform_summary:
  hgu133a
platform_manufacturer:
  Affymetrix
platform_distribution:
  commercial
platform_accession:
  GPL96
warnings:
  This paper has been retracted.
version:
  2015-09-22 20:19:16

```

```

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, 117 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
	117.00	67.00	5.26	2.79	7.48

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

alt_sample_name:	1024	1447	1451	1504	1526	1552	1578	1590	1615	1623
	1	1	1	1	1	1	1	1	1	1
	1665	1674	1675	1774	1784	1834	1846	1877	1913	1929
	1	1	1	1	1	1	1	1	1	1
	2046	2063	2064	2075	2198	2204	2324	2419	2422	2424
	1	1	1	1	1	1	1	1	1	1
	2465	2476	2479	2505	2542	2573	2673	2739	2802	2849
	1	1	1	1	1	1	1	1	1	1
	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	1
M1241	M1390	M1503	M1572	M17	M1891	M2070	M2097	M2184	(Other)	1
1	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	progressivedisease
85	32

debulking:

optimal	suboptimal
63	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  
2004-06-23  
8

6

5

15

7

7

1

## uncurated\_author\_metadata:

OVC.TumorID: 1024///Survival: 13///X0...alive...1...dead

OVC.TumorID: 1447///Survival: 75///X0...alive...1...dead:

OVC.TumorID: 1451///Survival: 132///X0...alive...1...dead

OVC.TumorID: 1504///Survival: 108///X0...alive...1...dea

OVC.TumorID: 1526///Survival: 74///X0...alive...1...dead:

OVC.TumorID: 1552///Survival: 33///X0...alive...1...dead:

OVC.TumorID: 1578///Survival: 33///X0...alive...1...dead:

OVC.TumorID: 1590///Survival: 148///X0...alive...1...dea

OVC.TumorID: 1615///Survival: 13///X0...alive...1...dead:

OVC.TumorID: 1623///Survival: 147///X0...alive...1...dea

OVC.TumorID: 1665///Survival: 15///X0...alive...1...dead:

OVC.TumorID: 1674///Survival: 18///X0...alive...1...dead

OVC.TumorID: 1675///Survival: 34///X0...alive...1...dead:

OVC.TumorID: 1774///Survival: 22///X0...alive...1...dead:

OVC.TumorID: 1784///Survival: 78///X0...alive...1...dead

OVC.TumorID: 1834///Survival: 118///X0...alive...1...dead

OVC.TumorID: 1846///Survival: 142///X0...alive...1...dea

OVC.TumorID: 1877///Survival: 119///X0...alive...1...dea

OVC.TumorID: 1913///Survival: 32///X0...alive...1...dead:

OVC.TumorID: 1929///Survival: 134///X0...alive...1...dea

OVC.TumorID: 2046///Survival: 127///X0...alive...1...dea

OVC.TumorID: 2063///Survival: 16///X0...alive...1...dead:

OVC.TumorID: 2064///Survival: 27///X0...alive...1...dead: 1///

OVC.TumorID: 2075///Survival: 87///X0...alive...1...dea

OVC.TumorID: 2198///Survival: 91///X0...alive...1...dead

OVC.TumorID: 2204///Survival: 118///X0...alive...1...dead

OVC.TumorID: 2324///Survival: 98///X0...alive...1...dead

OVC.TumorID: 2419///Survival: 107///X0...alive...1...dead

OVC.TumorID: 2422///Survival: 20///X0...alive...1...dead

OVC.TumorID: 2424///Survival: 16///X0...alive...1...dead:

OVC.TumorID: 2465///Survival: 17///X0...alive...1...dead:

OVC.TumorID: 2476///Survival: 86///X0...alive...1...dead:

OVC.TumorID: 2479///Survival: 95///X0...alive...1...dead:

OVC.TumorID: 2505///Survival: 95///X0...alive...1...dead

OVC.TumorID: 2542///Survival: 36///X0...alive...1...dead

OVC.TumorID: 2573///Survival: 7///X0...alive...1...dead: 1

OVC.TumorID: 2673///Survival: 74///X0...alive...1...dead:

OVC.TumorID: 2739///Survival: 67///X0...alive...1...dead

OVC.TumorID: 2802///Survival: 24///X0...alive...1...dead:

OVC.TumorID: 2849///Survival: 23///X0...alive...1...dead:

OVC.TumorID: 2895///Survival: 9///X0...alive...1...dead:

OVC.TumorID: 2967///Survival: 22///X0...alive...1...dead

OVC.TumorID: 2981///Survival: 6///X0...alive...1...dead:

OVC.TumorID: 2999///Survival: 16///X0...alive...1...dead:

OVC.TumorID: 3018///Survival: 16///X0...alive...1...dead:

OVC.TumorID: 3090///Survival: 16///X0...alive...1...dead:

OVC.TumorID: 3102///Survival: 10///X0...alive...1...dead: 1

OVC.TumorID: 3107///Survival: 31///X0...alive...1...dead:

OVC.TumorID: 3142///Survival: 18///X0...alive...1...dead

OVC.TumorID: 860///Survival: 17///X0...alive...1...dead:

OVC.TumorID: 872///Survival: 185///X0...alive...1...dead:  
OVC.TumorID: 922///Survival: 183///X0...alive...1...dea  
OVC.TumorID: D1805///Survival: 9///X0...alive...1...dead:  
OVC.TumorID: D1837///Survival: 83///X0...alive...1...dead:  
OVC.TumorID: D1859///Survival: 110///X0...alive...1...dead  
OVC.TumorID: D2098///Survival: 42///X0...alive...1...dead  
OVC.TumorID: D2208///Survival: 2///X0...alive...1...dead: 0  
OVC.TumorID: D2332///Survival: 27///X0...alive...1...dead  
OVC.TumorID: D2342///Survival: 20///X0...alive...1...dead:  
OVC.TumorID: D2358///Survival: 9///X0...alive...1...dead  
OVC.TumorID: D2421///Survival: 12///X0...alive...1...dead  
OVC.TumorID: D2432///Survival: 34///X0...alive...1...dea  
OVC.TumorID: D2433///Survival: 49///X0...alive...1...dead:  
OVC.TumorID: D2480///Survival: 34///X0...alive...1...dead:  
OVC.TumorID: D2557///Survival: 62///X0...alive...1...dead:  
OVC.TumorID: D2559///Survival: 5///X0...alive...1...dead:  
OVC.TumorID: D2560///Survival: 91///X0...alive...1...dead:  
OVC.TumorID: D2572///Survival: 37///X0...alive...1...dead  
OVC.TumorID: D2575///Survival: 33///X0...alive...1...dead:  
OVC.TumorID: D2576///Survival: 17///X0...alive...1...dead:  
OVC.TumorID: D2581///Survival: 63///X0...alive...1...dead  
OVC.TumorID: D2603///Survival: 42///X0...alive...1...dead:  
OVC.TumorID: D2611///Survival: 2///X0...alive...1...dead:  
OVC.TumorID: D2629///Survival: 36///X0...alive...1...dead  
OVC.TumorID: D2640///Survival: 1///X0...alive...1...dead: 1  
OVC.TumorID: D2648///Survival: 35///X0...alive...1...dead:

OVC.TumorID: D2668///Survival: 40///X0...alive...1...d  
OVC.TumorID: D2689///Survival: 45///X0...alive...1...dead:  
OVC.TumorID: D2691///Survival: 63///X0...alive...1...dead:  
OVC.TumorID: D2700///Survival: 74///X0...alive...1...dead:  
OVC.TumorID: D2726///Survival: 71///X0...alive...1...dead:  
OVC.TumorID: D2727///Survival: 53///X0...alive...1...dead  
OVC.TumorID: D2733///Survival: 55///X0...alive...1...dead:  
OVC.TumorID: D2738///Survival: 68///X0...alive...1...dead:  
OVC.TumorID: D2749///Survival: 24///X0...alive...1...dead:  
OVC.TumorID: D2776///Survival: 10///X0...alive...1...dead:  
OVC.TumorID: D2792///Survival: 16///X0...alive...1...dead:  
OVC.TumorID: M1054///Survival: 101///X0...alive...1...dead: 0///As  
OVC.TumorID: M1055///Survival: 13///X0...alive...1...dead: 0///Assig  
OVC.TumorID: M120///Survival: 35///X0...alive...1...dead: 1///Ass  
OVC.TumorID: M1241///Survival: 95///X0...alive...1...dead: 0///Assigne  
OVC.TumorID: M1390///Survival: 46///X0...alive...1...dead:  
OVC.TumorID: M1503///Survival: 53///X0...alive...1...dead: 1///Ass  
OVC.TumorID: M1572///Survival: 22///X0...alive...1...dead: 1///Assi  
OVC.TumorID: M17///Survival: 17///X0...alive...1...dead: 0///Assigned.  
OVC.TumorID: M1891///Survival: 12///X0...alive...1...dead: 0///Assigned.Stage: 4  
OVC.TumorID: M2070///Survival: 65///X0...alive...1...dead: 0///Assigne  
OVC.TumorID: M2097///Survival: 58///X0...alive...1...dead: 0///A  
OVC.TumorID: M2184///Survival: 34///X0...alive...1...dead: 0///Assi

**Value**

An expression set

PMID19318476

*Microarray analysis of early stage serous ovarian cancers shows profiles predictive of favorable outcome.***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 D

Laboratory: Berchuck, Lancaster 2009

Contact information:

Title: Microarray analysis of early stage serous ovarian cancers shows profile

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:

hg133a

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 20
  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
                                1                                1
TCGA-13-1498-01A-01R-1565-13 TCGA-13-1505-01A-01R-1565-13
                                1                                1
TCGA-13-1506-01A-01R-1565-13 TCGA-13-1507-01A-01R-1565-13
                                1                                1
TCGA-13-1511-01A-01R-1565-13 TCGA-13-1512-01A-01R-1565-13
                                1                                1
TCGA-13-2060-01A-01R-1568-13 TCGA-20-1682-01A-01R-1564-13
```

TCGA-20-1683-01A-01R-1566-13	1	TCGA-20-1684-01A-01R-1566-13	1
	1		1
TCGA-20-1685-01A-01R-1566-13	1	TCGA-20-1687-01A-01R-1566-13	1
	1		1
TCGA-23-1023-01A-02R-1564-13	1	TCGA-23-1026-01B-01R-1569-13	1
	1		1
TCGA-23-1027-01A-02R-1564-13	1	TCGA-23-1029-01B-01R-1567-13	1
	1		1
TCGA-23-1109-01A-01R-1564-13	1	TCGA-23-1111-01A-01R-1567-13	1
	1		1
TCGA-23-1114-01B-01R-1566-13	1	TCGA-23-1120-01A-02R-1565-13	1
	1		1
TCGA-23-1122-01A-01R-1565-13	1	TCGA-23-1123-01A-01R-1565-13	1
	1		1
TCGA-23-1809-01A-01R-1566-13	1	TCGA-23-2077-01A-01R-1568-13	1
	1		1
TCGA-23-2081-01A-01R-1568-13	1	TCGA-23-2084-01A-02R-1568-13	1
	1		1
TCGA-24-0975-01A-02R-1565-13	1	TCGA-24-1103-01A-01R-1565-13	1
	1		1
TCGA-24-1413-01A-01R-1565-13	1	TCGA-24-1416-01A-01R-1565-13	1
	1		1
TCGA-24-1417-01A-01R-1565-13	1	TCGA-24-1418-01A-01R-1565-13	1
	1		1
TCGA-24-1419-01A-01R-1565-13	1	TCGA-24-1423-01A-01R-1565-13	1
	1		1
TCGA-24-1424-01A-01R-1565-13	1	TCGA-24-1427-01A-01R-1565-13	1
	1		1
TCGA-24-1428-01A-01R-1564-13	1	TCGA-24-1430-01A-01R-1566-13	1
	1		1
TCGA-24-1436-01A-01R-1566-13	1	TCGA-24-1467-01A-01R-1566-13	1
	1		1
TCGA-24-1469-01A-01R-1566-13	1	TCGA-24-1474-01A-01R-1566-13	1
	1		1
TCGA-24-1544-01A-01R-1566-13	1	TCGA-24-1548-01A-01R-1566-13	1
	1		1
TCGA-24-1549-01A-01R-1566-13	1	TCGA-24-1550-01A-01R-1566-13	1
	1		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	1	TCGA-24-1555-01A-01R-1566-13	1
	1		1
TCGA-24-1556-01A-01R-1566-13	1	TCGA-24-1557-01A-01R-1566-13	1
	1		1
TCGA-24-1558-01A-01R-1566-13	1	TCGA-24-1560-01A-01R-1566-13	1
	1		1
TCGA-24-1562-01A-01R-1566-13	1	(Other)	1
	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	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	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	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	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	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	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	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	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	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	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	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	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	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	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	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	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/

age\_at\_initi

age\_at

age\_at\_initial\_pathologic\_di

age\_at\_initial\_pathologic\_diagnosis

age\_at\_initial\_pathologic\_diagn

age\_at

age\_at\_initial\_pathologic\_diagnosis: 42///anatomic\_organ\_subd

age\_at\_initial\_pathologic\_diagnosis

age\_at\_i

age\_at\_initial\_p

age\_at\_initial\_pat

age\_at\_initial\_patho

age\_at\_initia

age\_at\_initial\_pathologic\_diagnosis: 45///anatomic

age

age\_at\_initial\_pathologic\_diagnosis: 45///an

age\_at\_initial\_patho

age\_at\_initial\_path

age\_at\_initial\_pathologic\_diagno

age\_at\_initial\_pathologic\_diagnosis: 45///anatomic\_organ\_subdivisio

age\_at\_initial\_pathologic\_

age\_at\_initial\_pathologic\_diagnosis: 46///anatomic\_organ\_subdivisi

age\_at\_initial\_pathologic\_diagnosis:

age\_at\_initial\_pathologic\_diagno

age\_at\_initial\_pathologic\_diagnosis: 47///anato

age\_at\_initi

age\_at\_initial\_pathologic\_diagnosis: 47///anatomic\_

age\_at\_initial\_pathologic\_diagnosis: 48///

age

a

age\_at\_initial\_pathologic\_

age\_at\_in

age\_at\_initial\_pathologic\_diagnosis: 49///anatom

age\_at\_initial\_pathologic\_diagnosis: 50///anatomic\_org

age\_at\_initial\_pathologic\_dia

age\_at\_initial\_pat

age\_at\_initial\_pathologic\_diagnosis: 50///anatomic\_organ\_subdivision: Left///bo

age\_at\_initial\_pathologic\_diagnosis: 50///ana

age\_at\_initial\_pathol

age\_at\_initial\_pathologic\_diagnosis: 51///anatomic\_organ\_subdivision: Bilatera

age\_at\_init

age\_at\_initial\_pathologic\_dia

age\_at

age

age\_at\_initial\_pathologic\_diagnosis: 51///anatom

age\_at\_initial\_pathologic

age\_at\_initia

age\_at\_initial\_pathologi

age\_at\_initial\_pathologic\_di

age\_

age\_at\_initial\_pathologic\_diagnos

age\_at\_initial\_pat

age\_at\_initial\_pathologic\_di

age\_at\_initial\_pathologic\_diagnosis: 53///anatomic\_organ\_

age\_at\_initial\_pathologic\_diagnosi

age\_at\_initial\_pathologic\_diagnosis: 53///anato

age\_at\_initial\_pat

age\_at\_initial\_pathologic\_diagnosis: 54///anatomic\_organ\_subdivis

age\_a

age\_at\_ini

age\_at\_i

age\_at\_initial\_pathologic\_diagnosis: 54///anatomic\_organ\_subdiv

**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 20

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		

TCGA-04-1335-01A-01R-0434-01	1	TCGA-04-1336-01A-01R-0434-01	1
	1		1
TCGA-04-1337-01A-01R-0434-01	1	TCGA-04-1338-01A-01R-0434-01	1
	1		1
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
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TCGA-04-1349-01A-01R-0453-01	1	TCGA-04-1350-01A-01R-0453-01	1
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TCGA-04-1351-01A-01R-0453-01	1	TCGA-04-1353-01A-01R-1048-01	1
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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
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TCGA-04-1362-01A-01R-0453-01	1	TCGA-04-1364-01A-01R-0453-01	1
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	1		1
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TCGA-04-1514-01A-01R-0502-01	1	TCGA-04-1516-01A-01R-1048-01	1
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TCGA-04-1517-01A-01R-0538-01	1	TCGA-04-1519-01A-01R-0538-01	1
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TCGA-04-1525-01A-01R-0538-01	1	TCGA-04-1530-01A-02R-0502-01	1
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TCGA-04-1646-01A-01R-0582-01	1	TCGA-04-1648-01A-01R-0582-01	1
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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	
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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	
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TCGA-09-2051-01A-01R-0709-01	TCGA-09-2053-01C-01R-0668-01	
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TCGA-09-2054-01A-01R-0668-01	TCGA-09-2055-01B-01R-0709-01	
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	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	1
TCGA-04-1517	TCGA-04-1519	TCGA-04-1525	TCGA-04-1530	TCGA-04-1536	TCGA-04-1542	TCGA-04-1542
1	1	1	1	1	1	1
TCGA-04-1638	TCGA-04-1644	TCGA-04-1646	TCGA-04-1648	TCGA-04-1649	TCGA-04-1651	TCGA-04-1651
1	1	1	1	1	1	1
TCGA-04-1652	TCGA-04-1654	TCGA-04-1655	TCGA-09-0364	TCGA-09-0365	TCGA-09-0366	TCGA-09-0366
1	1	1	1	1	1	1
TCGA-09-0367	TCGA-09-0369	TCGA-09-1659	TCGA-09-1661	TCGA-09-1662	TCGA-09-1664	TCGA-09-1664
1	1	1	1	1	1	1
TCGA-09-1665	TCGA-09-1666	TCGA-09-1667	TCGA-09-1668	TCGA-09-1669	TCGA-09-1670	TCGA-09-1670
1	1	1	1	1	1	1
TCGA-09-1672	TCGA-09-1673	TCGA-09-1674	TCGA-09-1675	TCGA-09-2043	TCGA-09-2044	TCGA-09-2044
1	1	1	1	1	1	1
TCGA-09-2045	TCGA-09-2048	TCGA-09-2049	TCGA-09-2050	TCGA-09-2051	TCGA-09-2053	TCGA-09-2053
1	1	1	1	1	1	1
TCGA-09-2054	TCGA-09-2055	TCGA-09-2056	TCGA-10-0925	TCGA-10-0926	TCGA-10-0927	TCGA-10-0927
1	1	1	1	1	1	1
TCGA-10-0928	TCGA-10-0930	TCGA-10-0931	TCGA-10-0933	TCGA-10-0934	TCGA-10-0935	TCGA-10-0935
1	1	1	1	1	1	1
TCGA-10-0936	TCGA-10-0937	TCGA-10-0938	TCGA-13-0714	TCGA-13-0717	TCGA-13-0720	TCGA-13-0720
1	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

age\_at\_initial\_pathologic

age\_at\_initial\_pathologic\_diagnosis: 37//

age\_at\_initial\_pathologic\_diagnosis: 38///anatomic\_organ\_subdivision: Bilateral/

age\_at\_initial\_pathologic\_diagnosis: 38///anatomic\_organ\_subdivision:

age\_at\_initi

age\_at

age\_at\_initial\_pathologic\_diagnosis: 39///

age\_at\_initial\_pathologic\_

age\_at\_initial\_pathologic\_di

age\_at\_initial\_pathologic\_diagnosis

age\_at\_initial\_pathologic\_diagnosis: 40///anatomic\_organ

age\_at\_initial\_pathologic\_diagn

age\_at

age\_at\_initial\_pa

age\_at\_initial\_pathologic\_d

age\_at\_initial\_pathologic\_diagnosis

age\_at\_initial\_pathologic\_diagnosis: 42///anatomic\_organ\_subd

age\_at\_initial

age\_at\_initial\_pathologic\_diagnosis: 42///anatomic

age\_at\_initial\_pat

age\_at\_initial\_pathologic\_diagnosis

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age\_at\_initial\_pathologic\_diagnosis

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age\_at\_initial\_pathologic\_diagnosis: 44///anatom

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age\_at\_initial\_pathologic\_diagnosis: 45///anatomic

age

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age\_at\_initial\_patho

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age\_at\_initial\_pathologic\_diagnosis: 45///anatomic\_organ\_subdivisio

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age\_at\_initial\_pathologic\_diagnosis: 46///anatomic\_organ\_subdivis

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age\_at\_initial\_pathologic\_diagnosis:

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age\_at\_initial\_pathologic\_diagno

age\_at\_initial\_pathologic\_diagno

age\_at\_initial\_pathologic\_diagnosis: 47///anato

age\_at\_initi

age\_at\_initial\_pathologic\_diagnosis: 47///anatomic\_

age\_at\_initial\_pathologic\_diagnosis: 48///

age\_at\_initial\_pathologic\_diagno

age\_at\_initial\_pathologic

age\_at\_initial\_pathologic\_diagnosis: 48///

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

**Value**

An expression set