

# Package ‘MetaGxOvarian’

May 28, 2026

**Type** Package

**Title** Transcriptomic Ovarian Cancer Datasets

**Version** 1.33.0

**Date** `r Sys.date()`

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

**License** Artistic-2.0

**Depends** Biobase, AnnotationHub, ExperimentHub, SummarizedExperiment, R  
( $\geq$  3.6.0)

**Imports** stats, lattice, impute

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

**Encoding** UTF-8

**VignetteBuilder** knitr

**NeedsCompilation** no

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

**LazyData** yes

**RoxygenNote** 7.1.1

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

**git\_branch** devel

**git\_last\_commit** 432564f

**git\_last\_commit\_date** 2026-04-28

**Repository** Bioconductor 3.24

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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>
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---

### Description

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

### Format

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

---

E.MTAB.386	<i>Angiogenic mRNA and microRNA gene expression signature predicts a novel subtype of serous ovarian cancer.</i>
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### 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	1
DFCI.30	DFCI.31	DFCI.32	DFCI.33	DFCI.34	DFCI.35	DFCI.36	DFCI.37	DFCI.37
1	1	1	1	1	1	1	1	1
DFCI.38	DFCI.39	DFCI.4	DFCI.40	DFCI.41	DFCI.42	DFCI.44	DFCI.45	DFCI.45
1	1	1	1	1	1	1	1	1
DFCI.46	DFCI.47	DFCI.48	DFCI.49	DFCI.50	DFCI.51	DFCI.52	DFCI.53	DFCI.53
1	1	1	1	1	1	1	1	1
DFCI.54	DFCI.55	DFCI.56	DFCI.57	DFCI.58	DFCI.59	DFCI.6	DFCI.60	DFCI.60
1	1	1	1	1	1	1	1	1
DFCI.61	DFCI.62	DFCI.63	DFCI.64	DFCI.65	DFCI.66	DFCI.67	DFCI.68	DFCI.68
1	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-51

Source.Name: DFCI-52

Source.Name: DFCI-51

Source.Name: DFCI-51

Source.Name: DFCI-53

Source.Name: DFCI-54

Source.Name: DFCI-55

Source.Name: DFCI-56

Source.Name: DFCI-57

Source.Name: DFCI-58

Source.Name: DFCI-59

Source.Name: DFCI-60

Source.Name: DFCI-61

Source.Name: DFCI-62///Characteristics.Age.: Age <has\_measurement <Measurement

Source.Name: DFCI-63

Source.Name: DFCI-64

Source.Name: DFCI-65

Source.Name: DFCI-66

Source.Name: DFCI-67

Source.Name: DFCI-68

Source.Name: DFCI-69

Source.Name: DFCI-70

Source.Name: DFCI-71

Source.Name: DFCI-72

Source.Name: DFCI-73

Source.Name: DFCI-74

Source.Name: DFCI-75

Source.Name: DFCI-76

Source.Name: DFCI-77

Source.Name: DFCI-78

Source.Name: DFCI-79

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Source.Name: DFCI-84

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Source.Name: DFCI-86

Source.Name: DFCI-87

Source.Name: DFCI-88

Source.Name: DFCI-89

Source.Name: DFCI-90

Source.Name: DFCI-91

Source.Name: DFCI-92

Source.Name: DFCI-93

Source.Name: DFCI-94

Source.Name: DFCI-95

Source.Name: DFCI-96

Source.Name: DFCI-97

Source.Name: DFCI-98

Source.Name: DFCI-99

Source.Name: DFCI-100

**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 distingu

URL:

PMIDs: 16996261

Abstract: A 177 word abstract is available. Use 'abstract' method.

Information is available on: preprocessing

notes:

platform\_title:

SWEGENE H\_v2.1.1\_27k

platform\_shorttitle:

SWEGENE H\_v2.1.1\_27k

platform\_summary:

PartheenMetaData

platform\_manufacturer:

other

platform\_distribution:

non-commercial

platform\_accession:

GPL5886

version:

2015-09-22 19:07:14

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

**Details**

assayData: 11304 features, 54 samples

Platform type:

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

alt\_sample\_name:

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

sample\_type:

tumor

54

histological\_type:

ser

54

primarysite:

ov

54

summarystage:

late

54

tumorstage:

3

54

substage:

b c

19 35

age\_at\_initial\_pathologic\_diagnosis:

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

pltx:

y  
54

os\_binary:

long	short
20	34

debulking:

optimal	suboptimal
13	41

uncurated\_author\_metadata:

title: 1035LA0///geo\_accession: GSM311973///status: Public on Aug 12 2008///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///

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title: 1487DB///geo\_accession: GSM311983///status: Public on Aug 12 2

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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  
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title: 662DC///geo\_accession: GSM311965///status: Public on Aug 12  
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 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



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:
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title: Advanced serous ovarian cancer 18///geo_accession: GSM312143///status:
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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//
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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\_acces

title: Peritoneum normal 3///geo\_acc

title: Peritoneum normal 4///geo\_acc

title: Peritoneum normal 7///geo\_acc

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\_accessio

title: Ovarian tumor sample 10 / Ovarian tumor sample 11///geo\_accessi

title: Ovarian tumor sample 111 / Ovarian tumor sample 112///geo\_accessio

title: Ovarian tumor sample 115 / Ovarian tumor sample 117///geo\_accessio

title: Ovarian tumor sample 126 / Ovarian tumor sample 127///geo\_accessio

title: Ovarian tumor sample 13 / Ovarian tumor sample 14///geo\_accessio

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: GSM414141

title: Ovarian tumor sample 237 / Ovarian tumor sample 238///geo\_accession: GSM414142

title: Ovarian tumor sample 250 / Ovarian tumor sample 251///geo\_accession: GSM414143

title: Ovarian tumor sample 258 / Ovarian tumor sample 259///geo\_accession: GSM414144

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:  
title: ovarian cancer: 047///geo\_accession: GSM368707///status: P  
title: ovarian cancer: 048///geo\_accession: GSM368708///status:  
title: ovarian cancer: 049///geo\_accession: GSM368709///status: P  
title: ovarian cancer: 04///geo\_accession: GSM368664///status: Pu  
title: ovarian cancer: 050///geo\_accession: GSM368710///status: P  
title: ovarian cancer: 051///geo\_accession: GSM368711///status:  
title: ovarian cancer: 052///geo\_accession: GSM368712///status: Pu  
title: ovarian cancer: 053///geo\_accession: GSM368713///status:  
title: ovarian cancer: 054///geo\_accession: GSM368714///status: P  
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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  
 title: ovarian cancer: 066///geo\_accession: GSM368726///status:  
 title: ovarian cancer: 067///geo\_accession: GSM368727///status:  
 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, Suzu
```

```
  Laboratory: Yoshihara, Tanaka 2010
```

```
  Contact information:
```

```
  Title: Gene expression profile for predicting survival in advanced-stage serou
```

```
  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  
title: Serous ovarian cancer 113///geo\_accession: GSM432  
title: Serous ovarian cancer 114///geo\_accession: GSM43  
title: Serous ovarian cancer 115///geo\_accession: GSM432  
title: Serous ovarian cancer 116///geo\_accession: GSM432  
title: Serous ovarian cancer 117///geo\_accession: GS  
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title: Serous ovarian cancer 12///geo\_accession: G

title: Serous ovarian cancer 130///geo\_accession: GSM432  
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title: Serous ovarian cancer 143///geo\_accession: GSM43  
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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

title: Ovarian Tumor, 1231///geo\_accession: GSM461367///status: Public on Oct 17

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title: Ovarian Tumor, 692///geo\_accession: GSM461397///status: Public on Oct 1  
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title: Ovarian Tumor, 800///geo\_accession: GSM461371///status: Public on Oct 1  
title: Ovarian Tumor, 872///geo\_accession: GSM461366///status: Public on Oct 1  
title: Ovarian Tumor, 934///geo\_accession: GSM461372///status: Public on Oct 1  
title: Ovarian Tumor, 970///geo\_accession: GSM461389///status: Public on Oct 1

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
Ovarian cancer_sample 31 Ovarian cancer_sample 32 Ovarian cancer_sample 33
1
Ovarian cancer_sample 34 Ovarian cancer_sample 35 Ovarian cancer_sample 36
1
Ovarian cancer_sample 37 Ovarian cancer_sample 38 Ovarian cancer_sample 39
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Ovarian cancer_sample 4 Ovarian cancer_sample 40 Ovarian cancer_sample 41
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Ovarian cancer_sample 56 Ovarian cancer_sample 57 Ovarian cancer_sample 58
1
Ovarian cancer_sample 59 Ovarian cancer_sample 6 Ovarian cancer_sample 60
1
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1
Ovarian cancer_sample 64 Ovarian cancer_sample 65 Ovarian cancer_sample 66
1
Ovarian cancer_sample 67 Ovarian cancer_sample 68 Ovarian cancer_sample 69
1
Ovarian cancer_sample 7 Ovarian cancer_sample 70 Ovarian cancer_sample 8
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:  
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 title: Ovarian cancer\_sample 8///geo\_accession: GSM495146///status:  
 title: Ovarian cancer\_sample 9///geo\_accession: GSM495147///status:

vital\_status:  
 deceased    living  
           40        30

## Value

An expression set

---

GSE20565

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

---

## Description

The distinction between primary and secondary ovarian tumors may be challenging for pathologists. The purpose of the present work was to develop genomic and transcriptomic tools to further refine the pathological diagnosis of ovarian tumors after a previous history of breast cancer. Sixteen paired breast-ovary tumors from patients with a former diagnosis of breast cancer were collected. The genomic profiles of paired tumors were analyzed using the Affymetrix GeneChip Mapping 50 K Xba Array or Genome-Wide Human SNP Array 6.0 (for one pair), and the data were normalized with ITALICS (ITerative and Alternative normaLization and Copy number calling for affymetrix Snp arrays) algorithm or Partek Genomic Suite, respectively. The transcriptome of paired samples was analyzed using Affymetrix GeneChip Human Genome U133 Plus 2.0 Arrays, and the data were normalized with gc-Robust Multi-array Average (gcRMA) algorithm. A hierarchical clustering of these samples was performed, combined with a dataset of well-identified primary and secondary ovarian tumors. In 12 of the 16 paired tumors analyzed, the comparison of genomic profiles confirmed the pathological diagnosis of primary ovarian tumor (n = 5) or metastasis of breast cancer (n = 7). Among four cases with uncertain pathological diagnosis, genomic profiles were clearly distinct between the ovarian and breast tumors in two pairs, thus indicating primary ovarian carcinomas, and showed common patterns in the two others, indicating metastases from breast cancer. In all pairs, the result of the transcriptomic analysis was concordant with that of the genomic analysis. In patients with ovarian carcinoma and a previous history of breast cancer, SNP array analysis can be used to distinguish primary and secondary ovarian tumors. Transcriptomic analysis may be used when primary breast tissue specimen is not available.

## Format

```

experimentData(eset):
Experiment data
  Experimenter name: Meyniel JP, Cottu PH, Decraene C, Stern MH, Couturier J, 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):

```

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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

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assayData: 42447 features, 140 samples
Platform type:
```

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

```
-----
alt_sample_name:
Breast metastasis in the ovary_OC01_ARN0016 [HG-U133_Plus_2]
                                                    1
Breast metastasis in the ovary_OC01_ARN0017 [HG-U133_Plus_2]
                                                    1
Breast metastasis in the ovary_OC01_ARN0020 [HG-U133_Plus_2]
                                                    1
Breast metastasis in the ovary_OC01_ARN0029 [HG-U133_Plus_2]
                                                    1
Breast metastasis in the ovary_OC01_ARN0035 [HG-U133_Plus_2]
                                                    1
Breast metastasis in the ovary_OC01_ARN0046 [HG-U133_Plus_2]
                                                    1
Breast metastasis in the ovary_OC01_ARN0051 [HG-U133_Plus_2]
                                                    1
Breast metastasis in the ovary_OC01_ARN0053 [HG-U133_Plus_2]
                                                    1
Breast metastasis in the ovary_OC01_ARN0055 [HG-U133_Plus_2]
                                                    1
Breast metastasis in the ovary_OC01_ARN0060 [HG-U133_Plus_2]
                                                    1
Breast metastasis in the ovary_OC01_ARN0069 [HG-U133_Plus_2]
                                                    1
Breast metastasis in the ovary_OC01_ARN0073 [HG-U133_Plus_2]
                                                    1
Breast metastasis in the ovary_OC01_ARN0077 [HG-U133_Plus_2]
                                                    1
Breast metastasis in the ovary_OC01_ARN0079 [HG-U133_Plus_2]
                                                    1
Breast metastasis in the ovary_OC01_ARN0081 [HG-U133_Plus_2]
                                                    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]
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Breast metastasis in the ovary_OC01_ARN0098 [HG-U133_Plus_2]
                                                    1
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Breast metastasis in the ovary_OC01_ARN0099	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0102	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0104	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0112	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0120	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0121	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0123	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0126	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0141	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0142	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0143	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0145	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0146	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0153	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0162	[HG-U133_Plus_2]	1
Breast metastasis in the ovary_OC01_ARN0201	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0001	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0002	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0004	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0005	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0007	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0008	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0009	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0010	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0011	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0012	[HG-U133_Plus_2]	1

Ovarian carcinoma_OC01_ARN0013	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0015	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0022	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0023	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0025	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0028	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0030	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0032	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0034	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0036	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0037	[HG-U133_Plus_2]	1
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Ovarian carcinoma_OC01_ARN0042	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0045	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0049	[HG-U133_Plus_2]	1
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Ovarian carcinoma_OC01_ARN0063	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0064	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0066	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0067	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0070	[HG-U133_Plus_2]	1

Ovarian carcinoma_OC01_ARN0072	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0075	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0076	[HG-U133_Plus_2]	1
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Ovarian carcinoma_OC01_ARN0084	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0085	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0089	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0091	[HG-U133_Plus_2]	1
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Ovarian carcinoma_OC01_ARN0100	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0101	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0103	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0105	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0106	[HG-U133_Plus_2]	1
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Ovarian carcinoma_OC01_ARN0108	[HG-U133_Plus_2]	1
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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

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1
(Other)
41

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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

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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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**Description**

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

**Format**

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Experiment data
  Experimenter name: EXpression Project for Oncology, International Genomics Con
  Laboratory: expO, IGC 2005
  Contact information:
  Title: IGC EXpression Project for Oncology
  URL:
  PMIDs: PMID unknown

Abstract: A 8 word abstract is available. Use 'abstract' method.
Information is available on: preprocessing
notes:
  platform_title:
    [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
  platform_shorttitle:
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  platform_summary:
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    Affymetrix
  platform_distribution:
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  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
                      1
Omentum - 8174
Omentum - 1006
                      1
Omentum - 8186

```

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Omentum - 8240		Ovary - 101094
1		1
Ovary - 101109		Ovary - 101120
1		1
Ovary - 101150		Ovary - 1018
1		1
Ovary - 1040		Ovary - 1057
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Ovary - 112866		Ovary - 112867
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Ovary - 1241		Ovary - 1270
1		1
Ovary - 129660		Ovary - 129669
1		1
Ovary - 1311		Ovary - 1313
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1		1
Ovary - 133651		Ovary - 1351
1		1
Ovary - 151614		Ovary - 151622
1		1
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1		1
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Ovary - 191413		Ovary - 191424
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Ovary - 241198		Ovary - 241199
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Ovary - 242929		(Other)
1		105

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tumor  
204

histological\_type:  
clearcell                    endo                    mucinous                    other

	9	28	11	59
ser undifferentiated			NA's	
	85	2	10	

primarysite:  
 other ov NA's  
 23 178 3

summarygrade:  
 high low NA's  
 91 31 82

summarystage:  
 early late NA's  
 37 87 80

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

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

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

age\_at\_initial\_pathologic\_diagnosis:  
 Min. 1st Qu. Median Mean 3rd Qu. Max.  
 25.00 45.00 55.00 58.82 65.00 85.00

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 2005-03-15 2005-03-16 2005-03-17 2005-03-19 2005-03-22 2005-04-13 2005-04-26  
 3 1 2 4 2 1 5  
 2005-04-29 2005-05-10 2005-06-01 2005-06-03 2005-06-08 2005-06-17 2005-08-05  
 2 2 5 3 3 6 3  
 2005-08-09 2005-08-11 2005-09-07 2005-09-09 2005-09-13 2005-11-02 2005-11-04  
 1 6 1 3 3 6 3  
 2005-11-15 2005-11-18 2005-12-02 2006-01-24 2006-01-26 2006-02-07 2006-02-28  
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 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  
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 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

*GSE2109*

65

2	3	1	4	4	
2008-02-27	2008-03-04	2008-05-13	2008-05-16	2008-05-23	
2	1	4	4	5	

1

3

uncurated\_author\_metadata:

title: Omentu

title: Ovary - 170809///geo\_accession: GSM137917///status: Public on Sep 28 2006



duplicates:

GSE2109.GSE2109\_GSM76554 GSE2109.GSE2109\_GSM76567

NA's

1

1

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?? and modulate the oxidative stress response. Enhanced expression of these microRNAs mimics p38?? deficiency and increases tumor growth in mouse models, but it also improves the response to chemotherapeutic agents. High-grade human ovarian adenocarcinomas that accumulate miR-200a have low concentrations of p38?? and an associated oxidative stress signature. The miR200a-dependent stress signature correlates with improved survival of patients in response to treatment. Therefore, the role of miR-200a in stress could be a predictive marker for clinical outcome in ovarian cancer. In addition, although oxidative stress promotes tumor growth, it also sensitizes tumors to treatment, which could account for the limited success of antioxidants in clinical trials.

**Format**

```
experimentData(eset):
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```
Experiment data
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```
  Experimenter name: Mateescu B, Batista L, Mariani O, Meyniel J, Cottu PH, Sast
```

```
  Laboratory: Mateescu, Mechta-Grigoriou 2011
```

```
  Contact information:
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```
  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
```

```
notes:
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  platform_title:
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```
    [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:
```

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GPL570
platform_technology:
  in situ oligonucleotide
version:
  2015-09-22 19:44:56

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```
featureData(eset):
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```
An object of class 'AnnotatedDataFrame'
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featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
(42447 total)
```

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varLabels: probeset gene EntrezGene.ID best_probe
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varMetadata: labelDescription
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## Details

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assayData: 42447 features, 107 samples
```

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

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

**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:
    hgu133a
  platform_manufacturer:
    Affymetrix
  platform_distribution:
    commercial
  platform_accession:
    GPL96
  version:
    2015-09-22 19:46:24

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

```

**Details**

assayData: 20967 features, 195 samples

Platform type:

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

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

10 observations deleted due to missingness

n	events	median	0.95LCL	0.95UCL
185.00	129.00	3.83	3.24	4.83

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

alt\_sample\_name:

Normal HOSE2008	Normal HOSE2061	Normal HOSE2064
1	1	1
Normal HOSE2085	Normal HOSE2225	Normal HOSE2226
1	1	1
Normal HOSE2228	Normal HOSE2230	Normal HOSE2234
1	1	1
Normal HOSE2237	Ovarian Cancer S010	Ovarian Cancer S0100
1	1	1
Ovarian Cancer S0103	Ovarian Cancer S0106	Ovarian Cancer S0108
1	1	1
Ovarian Cancer S011	Ovarian Cancer S0113	Ovarian Cancer S0115
1	1	1
Ovarian Cancer S0116	Ovarian Cancer S0117	Ovarian Cancer S0118
1	1	1
Ovarian Cancer S012	Ovarian Cancer S0121	Ovarian Cancer S0122
1	1	1
Ovarian Cancer S0124	Ovarian Cancer S0129	Ovarian Cancer S013
1	1	1
Ovarian Cancer S0131	Ovarian Cancer S0134	Ovarian Cancer S0135
1	1	1
Ovarian Cancer S0137	Ovarian Cancer S0141	Ovarian Cancer S0143
1	1	1
Ovarian Cancer S0148	Ovarian Cancer S0154	Ovarian Cancer S016
1	1	1
Ovarian Cancer S0166	Ovarian Cancer S017	Ovarian Cancer S0173
1	1	1
Ovarian Cancer S0174	Ovarian Cancer S018	Ovarian Cancer S0181
1	1	1
Ovarian Cancer S0184	Ovarian Cancer S0185	Ovarian Cancer S0187
1	1	1
Ovarian Cancer S0189	Ovarian Cancer S0190	Ovarian Cancer S0193
1	1	1
Ovarian Cancer S0194	Ovarian Cancer S0196	Ovarian Cancer S0197
1	1	1
Ovarian Cancer S02	Ovarian Cancer S0200	Ovarian Cancer S0201
1	1	1
Ovarian Cancer S0203	Ovarian Cancer S0205	Ovarian Cancer S021

	1		1		1
Ovarian Cancer	S0211	Ovarian Cancer	S0214	Ovarian Cancer	S0216
	1		1		1
Ovarian Cancer	S0217	Ovarian Cancer	S0218	Ovarian Cancer	S0224
	1		1		1
Ovarian Cancer	S0225	Ovarian Cancer	S0227	Ovarian Cancer	S0228
	1		1		1
Ovarian Cancer	S0229	Ovarian Cancer	S023	Ovarian Cancer	S0230
	1		1		1
Ovarian Cancer	S0231	Ovarian Cancer	S0235	Ovarian Cancer	S0236
	1		1		1
Ovarian Cancer	S0237	Ovarian Cancer	S0241	Ovarian Cancer	S0242
	1		1		1
Ovarian Cancer	S0243	Ovarian Cancer	S0244	Ovarian Cancer	S0246
	1		1		1
Ovarian Cancer	S0247	Ovarian Cancer	S0249	Ovarian Cancer	S025
	1		1		1
Ovarian Cancer	S0250	Ovarian Cancer	S0256	Ovarian Cancer	S0257
	1		1		1
Ovarian Cancer	S0258	Ovarian Cancer	S0261	Ovarian Cancer	S0262
	1		1		1
Ovarian Cancer	S0263	Ovarian Cancer	S0265	Ovarian Cancer	S0267
	1		1		1
Ovarian Cancer	S0268	Ovarian Cancer	S0272	Ovarian Cancer	S0273
	1		1		1
Ovarian Cancer	S0278	Ovarian Cancer	S0279	Ovarian Cancer	S0282
	1		1		1
Ovarian Cancer	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  
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title: Ovarian Cancer S023///geo\_accession: GSM657586///status: Public on Jan  
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title: Ovarian Cancer S0244///geo\_accession: GSM657595///status: Public on  
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title: Ovarian Cancer S0256///geo\_accession: GSM657601///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:

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_2	OV_FFPE_20	OV_FFPE_21
1	1	1	1	1	1	1
OV_FFPE_22	OV_FFPE_23	OV_FFPE_24	OV_FFPE_25	OV_FFPE_26	OV_FFPE_27	OV_FFPE_28
1	1	1	1	1	1	1
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:

title: OV\_FFPE\_10///geo\_accession: GSM746870///status: Public on Aug

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title: OV\_FFPE\_19///g  
title: OV\_FFPE\_1///geo\_accession: GSM746861///status: Public on Aug 21 20  
title: OV\_FFPE\_20///geo\_accession: GSM746880///status: Public on Aug 21 2012//  
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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///  
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title: OV\_FFPE\_7///geo\_accession: GSM746867///status: Public on Aug 21 2012///

title: OV\_FFPE\_8///geo\_accession: GSM746868///status: Public on Aug 21 2012

title: OV\_FFPE\_9///geo\_accession: GSM746869///status: Public on Aug 21 2012

## Value

An expression set

---

GSE32062

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

---

## Description

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

## Format

experimentData (eset):

Experiment data

Experimenter name: Yoshihara K, Tsunoda T, Shigemizu D, Fujiwara H et al. High

Laboratory: Yoshihara, Tanaka 2012

Contact information:

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

URL:

PMIDs: 22241791

Abstract: A 255 word abstract is available. Use 'abstract' method.

Information is available on: preprocessing

notes:

```

platform_title:
  Agilent-014850 Whole Human Genome Microarray 4x44K G4112F (Probe Name vers
ion)
platform_shorttitle:
  Agilent G4112F
platform_summary:
  hgug4112a
platform_manufacturer:
  Agilent
platform_distribution:
  commercial
platform_accession:
  GPL6480
version:
  2015-09-22 19:55:29

```

```

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

```

## Details

```

assayData: 30936 features, 260 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

```

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

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

```

alt_sample_name:
  10d    115d    116d    117d    119d    11d    120d    122d    123d    125Rd
  1      1      1      1      1      1      1      1      1      1
  129d   12d    130d   132d   134d   139d   140d   143d   144d   145d
  1      1      1      1      1      1      1      1      1      1
  146d   148d   150d   155d   156d   15d    160d   16d    171d   173d
  1      1      1      1      1      1      1      1      1      1
  174d   178d   17d    183d   184d   185d   186d   18d    20d    22d
  1      1      1      1      1      1      1      1      1      1
  23d    249d   257d   25d    260d   262d   264d   266d   267d   268d
  1      1      1      1      1      1      1      1      1      1
  269d   27d    299d   2d     300d   301d   302d   303d   304d   305d2
  1      1      1      1      1      1      1      1      1      1
  306d   307d   310d   318d   319d   320d2  323d   327d   330d   331d
  1      1      1      1      1      1      1      1      1      1
  333d2  335d   337d   340d   342d   346d   347d   348d2  350d   352d

```

1	1	1	1	1	1	1	1	1	1	1
353d	355d	356d	357d	358d	360d	362d	363d	365d	366d	
1	1	1	1	1	1	1	1	1	1	1
367d	368d2	36d	38d	41d2R	42d	43d	44d	456d	(Other)	
1	1	1	1	1	1	1	1	1	1	161

sample\_type:

tumor  
260

histological\_type:

ser  
260

summarygrade:

high low  
129 131

summarystage:

late  
260

tumorstage:

3 4  
204 56

substage:

a	b	c	NA's
4	20	180	56

grade:

2 3  
131 129

pltx:

y  
260

tax:

y  
260

days\_to\_death:

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

vital\_status:

deceased living  
121 139

debulking:

optimal suboptimal

103 157

uncurated\_author\_metadata:

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NA's	

**Value**

An expression set

---

GSE32063

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

---

**Description**

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

**Format**

```
experimentData(eset):
```

```
Experiment data
```

```
  Experimenter name: Yoshihara K, Tsunoda T, Shigemizu D, Fujiwara H et al. High
```

```
  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:
```

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    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:

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**Value**

An expression set

---

GSE44104

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

---

**Description**

Biomarkers that predict disease progression might assist the development of better therapeutic strategies for aggressive cancers, such as ovarian cancer. Here, we investigated the role of collagen type XI alpha 1 (COL11A1) in cell invasiveness and tumor formation and the prognostic impact of COL11A1 expression in ovarian cancer. Microarray analysis suggested that COL11A1 is a disease progression-associated gene that is linked to ovarian cancer recurrence and poor survival. Small interference RNA-mediated specific reduction in COL11A1 protein levels suppressed the invasive ability and oncogenic potential of ovarian cancer cells and decreased tumor formation and lung colonization in mouse xenografts. A combination of experimental approaches, including real-time RT-PCR, casein zymography and chromatin immunoprecipitation (ChIP) assays, showed that COL11A1 knockdown attenuated MMP3 expression and suppressed binding of Ets-1 to its putative MMP3 promoter-binding site, suggesting that the Ets-1-MMP3 axis is upregulated by COL11A1. Transforming growth factor (TGF)-beta (TGF- $\beta$ ) treatment triggers the activation of smad2 signaling cascades, leading to activation of COL11A1 and MMP3. Pharmacological inhibition of MMP3 abrogated the TGF- $\beta$ -triggered, COL11A1-dependent cell invasiveness. Furthermore, the NF-YA-binding site on the COL11A1 promoter was identified as the major determinant of TGF- $\beta$ -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- $\beta$ -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:

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platform_title:
  [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
platform_shorttitle:
  Affymetrix HG-U133Plus2
platform_summary:
  hgu133plus2
platform_manufacturer:
  Affymetrix
platform_distribution:
  commercial
platform_accession:
  GPL570
platform_technology:
  in situ oligonucleotide
version:
  2015-09-22 20:02:05
  
```

featureData(eset):

An object of class 'AnnotatedDataFrame'

featureNames: 1007\_s\_at 1053\_at ... AFFX-HUMISGF3A/M97935\_MB\_at  
(42447 total)

varLabels: probeset gene EntrezGene.ID best\_probe

varMetadata: labelDescription

## Details

assayData: 42447 features, 60 samples

Platform type:

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 Available sample meta-data:  
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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
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Ts_3	Ts_31	Ts_32	Ts_34	Ts_35	Ts_36	Ts_37	Ts_39	Ts_4	Ts_41	Ts_43

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Ts_45	Ts_46	Ts_47	Ts_5	Ts_8						
1	1	1	1	1						

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tumor  
60

histological\_type:  
clearcell endo mucinous ser  
12 11 9 28

summarystage:  
early late  
25 35

tumorstage:  
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17 8 30 5

recurrence\_status:  
norecurrence recurrence  
40 20

os\_binary:  
long short  
44 16

relapse\_binary:  
long short  
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duplicates:
  Length      Class      Mode
      60 character character

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## Value

An expression set

---

GSE49997

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

---

## Description

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

## Format

```

experimentData (eset) :
Experiment data
  Experimenter name: Pils 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 outcomes
  URL:
  PMIDs: 22497737

```

Abstract: A 276 word abstract is available. Use 'abstract' method.

Information is available on: preprocessing notes:

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platform_title:
  ABI Human Genome Survey Microarray Version 2
platform_shorttitle:
  ABI Human Genome
platform_summary:

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

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

## Details

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

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

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

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alt_sample_name:
EOC P001 EOC P002 EOC P003 EOC P004 EOC P005 EOC P006 EOC P007 EOC P008
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EOC P009 EOC P010 EOC P011 EOC P012 EOC P013 EOC P014 EOC P015 EOC P016
      1      1      1      1      1      1      1      1      1
EOC P017 EOC P018 EOC P019 EOC P020 EOC P021 EOC P022 EOC P023 EOC P024
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EOC P025 EOC P026 EOC P027 EOC P028 EOC P029 EOC P030 EOC P031 EOC P032
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EOC P033 EOC P034 EOC P035 EOC P036 EOC P037 EOC P038 EOC P039 EOC P040
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EOC P041 EOC P042 EOC P043 EOC P044 EOC P045 EOC P046 EOC P047 EOC P048
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EOC P099	(Other)								
1	1	1	105						

sample\_type:

tumor  
204

histological\_type:

other ser NA's  
23 171 10

summarygrade:

high low NA's  
143 50 11

summarystage:

early late NA's  
9 185 10

tumorstage:

2 3 4 NA's  
9 154 31 10

grade:

2 3 NA's  
50 143 11

age\_at\_initial\_pathologic\_diagnosis:

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

days\_to\_tumor\_recurrence:

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

recurrence\_status:

norecurrence	recurrence	NA's
70	124	10

## days\_to\_death:

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

## vital\_status:

deceased	living	NA's
57	137	10

## debulking:

optimal	suboptimal	NA's
137	57	10

## uncurated\_author\_metadata:

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## Value

An expression set

---

GSE51088

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

---

## Description

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

## Format

experimentData (eset):

Experiment data

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

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_title:
  Agilent-012097 Human 1A Microarray (V2) G4110B (Probe Name version)
platform_shorttitle:
  Agilent G4110B
platform_summary:
  hgug4110b
platform_manufacturer:
  Agilent
platform_distribution:
  commercial
platform_accession:
  GPL7264
platform_technology:
  in situ oligonucleotide
version:
  2015-09-22 20:05:48
```

featureData(eset):

An object of class 'AnnotatedDataFrame'

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

## Details

assayData: 18703 features, 172 samples

Platform type:

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

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

20 observations deleted due to missingness

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

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

Ov_Tumor_Ref_Mix vs. CS-OV-001	Ov_Tumor_Ref_Mix vs. CS-OV-002
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Ov_Tumor_Ref_Mix vs. CS-OV-003	Ov_Tumor_Ref_Mix vs. CS-OV-004
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Ov_Tumor_Ref_Mix vs. CS-OV-005	Ov_Tumor_Ref_Mix vs. CS-OV-006
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Ov_Tumor_Ref_Mix vs. CS-OV-007	Ov_Tumor_Ref_Mix vs. CS-OV-008
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Ov_Tumor_Ref_Mix vs. CS-OV-009	Ov_Tumor_Ref_Mix vs. CS-OV-010
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Ov_Tumor_Ref_Mix vs. CS-OV-011	Ov_Tumor_Ref_Mix vs. CS-OV-012

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Ov_Tumor_Ref_Mix vs. CS-OV-015		Ov_Tumor_Ref_Mix vs. CS-OV-016	
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Ov_Tumor_Ref_Mix vs. CS-OV-023		Ov_Tumor_Ref_Mix vs. CS-OV-024	
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Ov_Tumor_Ref_Mix vs. CS-OV-025		Ov_Tumor_Ref_Mix vs. CS-OV-026	
	1		1
Ov_Tumor_Ref_Mix vs. CS-OV-027		Ov_Tumor_Ref_Mix vs. CS-OV-028	
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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	
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benign	borderline	healthy	metastatic	tumor
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## histological\_type:

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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
22 9 103 17 21

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

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

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26.0 49.0 57.5 58.6 68.0 91.0

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  n
172

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norecurrence recurrence NA's
36 111 25

days_to_death:
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112 40 20

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140 32

percent_tumor_cells:
70+ NA's
140 32

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**Value**

An expression set

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GSE6008

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

---

## Description

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

## Format

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

Abstract: A 247 word abstract is available. Use 'abstract' method.
Information is available on: preprocessing
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An object of class 'AnnotatedDataFrame'

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featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
(20967 total)
varLabels: probeset gene EntrezGene.ID best_probe
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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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alt_sample_name:
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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**

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Experiment data
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  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:
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    [Hu6800] Affymetrix Human Full Length HuGeneFL Array
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    Affymetrix Hu6800
  platform_summary:
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  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

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**Details**

assayData: 6407 features, 66 samples  
 Platform type:

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

Ovarian tumor AM053	Ovarian tumor AM122	Ovarian tumor AM124	Ovarian tumor AM125
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Ovarian tumor AM127	Ovarian tumor AM137	Ovarian tumor AM138	Ovarian tumor AM144
1	1	1	1
Ovarian tumor AM178	Ovarian tumor AM179	Ovarian tumor AM182	Ovarian tumor AM195
1	1	1	1
Ovarian tumor AM196	Ovarian tumor AM198	Ovarian tumor AM200	Ovarian tumor AM201
1	1	1	1
Ovarian tumor AM202	Ovarian tumor AM203	Ovarian tumor AM204	Ovarian tumor AM207
1	1	1	1
Ovarian tumor AM208	Ovarian tumor AM209	Ovarian tumor AM225	Ovarian tumor AM226
1	1	1	1
Ovarian tumor AM228	Ovarian tumor AM233	Ovarian tumor AM250	Ovarian tumor AM252
1	1	1	1
Ovarian tumor AM253	Ovarian tumor AM255	Ovarian tumor AM256	Ovarian tumor AM259
1	1	1	1
Ovarian tumor AM261	Ovarian tumor AM263	Ovarian tumor AM268	Ovarian tumor AM269
1	1	1	1
Ovarian tumor AM287	Ovarian tumor AM288	Ovarian tumor AM289	Ovarian tumor AM290
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Ovarian tumor AM292	Ovarian tumor AM293	Ovarian tumor AM294	Ovarian tumor AM311
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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
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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

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2002-11-01	2002-11-13					
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duplicates:

Length	Class	Mode
66	character	character

**Value**

An expression set

---

GSE8842

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

---

**Description**

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

**Format**

experimentData (eset):

Experiment data

Experimenter name: Marchini S, Mariani P, Chiorino G, Marrazzo E, Bonomi R, 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



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p183bis	sample_Ovarian	tumor	1	p209bis	sample_Ovarian	tumor	1
p212bis	sample_Ovarian	tumor	1	p213bis	sample_Ovarian	tumor	1
p243bis	sample_Ovarian	tumor	1	p246bis	sample_Ovarian	tumor	1
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		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
```

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days_to_death:
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    0     1192     2248     2273    3048     5824
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vital_status:
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deceased  living
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 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:

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

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title: X32048///geo\_accession: GSM249936///status: Public on Mar 01 2008  
title: X32049///geo\_accession: GSM249935///status: Public on Mar 01 2008

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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///

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title: X34207///geo\_accession: GSM249910///status: Public on Mar 01 2008///

title: X34801///geo\_accession: GSM249909///status: Public on Mar 01 200

## 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	<i>Function to load ovarian cancer expression sets from the Experiment Hub</i>
------------------	--

---

**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:  
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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:  
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Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1829///Cancer.Type: S  
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Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 1831///Cancer.Type: S  
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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: S  
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: S  
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: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2020///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2021///Cancer.Type: S  
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: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2031///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2032///Cancer.Type: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2033///Cancer.Type: S  
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: S  
Genome.ID..File.name....0074\_GenomeID\_h133a\_2802.cel: 2395///Cancer.Type: S  
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: S  
 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: S  
 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	1
2465	2476	2479	2505	2542	2573	2673	2739	2802	2849	
1	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	1
872	922	D1805	D1837	D1859	D2098	D2208	D2332	D2342	D2358	
1	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	1
D2581	D2603	D2611	D2629	D2640	D2648	D2668	D2689	D2691	D2700	
1	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	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           6           5           15           7           7           1  
 2004-06-23  
           8

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...dea  
OVC.TumorID: 2204///Survival: 118///X0...alive...1...dea  
OVC.TumorID: 2324///Survival: 98///X0...alive...1...dea  
OVC.TumorID: 2419///Survival: 107///X0...alive...1...dead  
OVC.TumorID: 2422///Survival: 20///X0...alive...1...dea  
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...dea  
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:
    hgu133a
  platform_manufacturer:
    Affymetrix
  platform_distribution:
    commercial
  platform_accession:
    GPL96
  warnings:
    These samples are a subset of PMID17290060.
  version:
    2015-09-22 20:20:30

```

```

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

```

## Details

```

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

```

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

```

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

```

```

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

```

```

sample_type:
tumor

```

42

histological\_type:

ser

42

summarygrade:

high low NA's

24 17 1

summarystage:

early late NA's

2 39 1

tumorstage:

1 2 3 4 NA's

1 1 29 10 1

substage:

a b c NA's

1 1 29 11

grade:

1 2 3 NA's

2 15 24 1

age\_at\_initial\_pathologic\_diagnosis:

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

recurrence\_status:

norecurrence recurrence

6 36

days\_to\_death:

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

vital\_status:

deceased living

22 20

debulking:

optimal suboptimal NA's

20 21 1

batch:

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

uncurated\_author\_metadata:

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

**Value**

An expression set

---

TCGA.RNASeqV2

*Integrated genomic analyses of ovarian carcinoma.*

---

**Description**

A catalogue of molecular aberrations that cause ovarian cancer is critical for developing and deploying therapies that will improve patients' lives. The Cancer Genome Atlas project has analysed messenger RNA expression, microRNA expression, promoter methylation and DNA copy number in 489 high-grade serous ovarian adenocarcinomas and the DNA sequences of exons from coding genes in 316 of these tumours. Here we report that high-grade serous ovarian cancer is characterized by TP53 mutations in almost all tumours (96%); low prevalence but statistically recurrent somatic

mutations in nine further genes including NF1, BRCA1, BRCA2, RB1 and CDK12; 113 significant focal DNA copy number aberrations; and promoter methylation events involving 168 genes. Analyses delineated four ovarian cancer transcriptional subtypes, three microRNA subtypes, four promoter methylation subtypes and a transcriptional signature associated with survival duration, and shed new light on the impact that tumours with BRCA1/2 (BRCA1 or BRCA2) and CCNE1 aberrations have on survival. Pathway analyses suggested that homologous recombination is defective in about half of the tumours analysed, and that NOTCH and FOXM1 signalling are involved in serous ovarian cancer pathophysiology.

### Format

```

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

```



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
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TCGA-13-2060-01A-01R-1568-13	TCGA-20-1682-01A-01R-1564-13
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TCGA-20-1683-01A-01R-1566-13	TCGA-20-1684-01A-01R-1566-13
1	1
TCGA-20-1685-01A-01R-1566-13	TCGA-20-1687-01A-01R-1566-13
1	1
TCGA-23-1023-01A-02R-1564-13	TCGA-23-1026-01B-01R-1569-13
1	1
TCGA-23-1027-01A-02R-1564-13	TCGA-23-1029-01B-01R-1567-13
1	1
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TCGA-23-1114-01B-01R-1566-13	TCGA-23-1120-01A-02R-1565-13
1	1
TCGA-23-1122-01A-01R-1565-13	TCGA-23-1123-01A-01R-1565-13
1	1
TCGA-23-1809-01A-01R-1566-13	TCGA-23-2077-01A-01R-1568-13
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TCGA-23-2081-01A-01R-1568-13	TCGA-23-2084-01A-02R-1568-13
1	1
TCGA-24-0975-01A-02R-1565-13	TCGA-24-1103-01A-01R-1565-13
1	1
TCGA-24-1413-01A-01R-1565-13	TCGA-24-1416-01A-01R-1565-13
1	1
TCGA-24-1417-01A-01R-1565-13	TCGA-24-1418-01A-01R-1565-13
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TCGA-24-1428-01A-01R-1564-13	TCGA-24-1430-01A-01R-1566-13
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1	1

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

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TCGA-13-0916	TCGA-13-0920	TCGA-13-0924	TCGA-13-1403	TCGA-13-1405	TCGA-13-1410
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TCGA-13-1511	TCGA-13-1512	TCGA-13-2060	TCGA-20-1682	TCGA-20-1683	TCGA-20-1684
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TCGA-20-1685	TCGA-20-1687	TCGA-23-1023	TCGA-23-1026	TCGA-23-1027	TCGA-23-1029
1	1	1	1	1	1
TCGA-23-1109	TCGA-23-1111	TCGA-23-1114	TCGA-23-1120	TCGA-23-1122	TCGA-23-1123
1	1	1	1	1	1
TCGA-23-1809	TCGA-23-2077	TCGA-23-2081	TCGA-23-2084	TCGA-24-0975	TCGA-24-1103
1	1	1	1	1	1
TCGA-24-1413	TCGA-24-1416	TCGA-24-1417	TCGA-24-1418	TCGA-24-1419	TCGA-24-1423
1	1	1	1	1	1
TCGA-24-1424	TCGA-24-1427	TCGA-24-1428	TCGA-24-1430	TCGA-24-1436	TCGA-24-1467
1	1	1	1	1	1
TCGA-24-1469	TCGA-24-1474	TCGA-24-1544	TCGA-24-1548	TCGA-24-1549	TCGA-24-1550
1	1	1	1	1	1
TCGA-24-1551	TCGA-24-1552	TCGA-24-1553	TCGA-24-1555	TCGA-24-1556	TCGA-24-1557
1	1	1	1	1	1
TCGA-24-1558	TCGA-24-1560	TCGA-24-1562		(Other)	
1	1	1		162	

## sample\_type:

tumor  
261

## histological\_type:

ser  
261

## primarysite:

other ov  
1 260

summarygrade:  
high low NA's  
226 29 6

summarystage:  
early late NA's  
18 242 1

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

substage:  
b c NA's  
16 211 34

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

age\_at\_initial\_pathologic\_diagnosis:  
Min. 1st Qu. Median Mean 3rd Qu. Max.  
34.00 51.00 58.00 58.84 66.00 87.00

pltx:  
n y NA's  
17 215 29

tax:  
n y NA's  
17 215 29

neo:  
n NA's  
232 29

days\_to\_tumor\_recurrence:  
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's  
9.0 225.0 426.5 585.3 755.0 5480.0 19

recurrence\_status:  
norecurrence recurrence  
123 138

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

vital\_status:

deceased	living	NA's
143	114	4

site_of_tumor_first_recurrence:			
locoregional	metastasis	NA's	
82	56	123	

primary_therapy_outcome_success:				
completeresponse	partialresponse	progressivedisease	stabledisease	
147	30	15	15	
NA's				
54				

debulking:		
optimal	suboptimal	NA's
171	60	30

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

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

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

uncurated\_author\_metadata:

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

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

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

age\_at\_initial\_pathologic

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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\_subdivis

## Value

An expression set

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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: TCG
    A.13.0725, TCGA.13.0885, TCGA.13.0887, TCGA.13.0890, TCGA.13.0886, TCGA.13
    .0714, TCGA.13.0727, TCGA.13.1817, TCGA.13.1499, TCGA.13.0883
  version:
    2015-09-22 20:25:15

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

```

**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:

```

```
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alt_sample_name:  
TCGA-01-0628-11A-01R-0362-01 TCGA-01-0630-11A-01R-0362-01  
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TCGA-01-0631-11A-01R-0362-01 TCGA-01-0633-11A-01R-0362-01  
1 1  
TCGA-01-0636-11A-01R-0362-01 TCGA-01-0637-11A-01R-0362-01  
1 1  
TCGA-01-0639-11A-01R-0362-01 TCGA-01-0642-11A-02R-0362-01  
1 1  
TCGA-04-1331-01A-01R-0434-01 TCGA-04-1332-01A-01R-0434-01  
1 1  
TCGA-04-1335-01A-01R-0434-01 TCGA-04-1336-01A-01R-0434-01  
1 1  
TCGA-04-1337-01A-01R-0434-01 TCGA-04-1338-01A-01R-0434-01  
1 1  
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1 1  
TCGA-04-1343-01A-01R-0434-01 TCGA-04-1346-01A-01R-0434-01  
1 1  
TCGA-04-1347-01A-01R-0434-01 TCGA-04-1348-01A-01R-0453-01  
1 1  
TCGA-04-1349-01A-01R-0453-01 TCGA-04-1350-01A-01R-0453-01  
1 1  
TCGA-04-1351-01A-01R-0453-01 TCGA-04-1353-01A-01R-1048-01  
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TCGA-04-1356-01A-01R-0453-01 TCGA-04-1357-01A-01R-0453-01  
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1 1  
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TCGA-04-1369-01A-02R-1048-01 TCGA-04-1371-01A-01R-0453-01  
1 1  
TCGA-04-1514-01A-01R-0502-01 TCGA-04-1516-01A-01R-1048-01  
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1 1  
TCGA-04-1638-01A-01R-0582-01 TCGA-04-1644-01B-01R-1048-01  
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1 1  
TCGA-04-1649-01A-01R-0582-01 TCGA-04-1651-01A-01R-0582-01  
1 1  
TCGA-04-1652-01A-01R-0582-01 TCGA-04-1654-01A-02R-0653-01
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TCGA-10-0936-01A-01R-0404-01	TCGA-10-0937-01A-02R-0404-01
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TCGA-10-0938-01A-02R-0404-01	TCGA-13-0714-01A-01R-0362-01
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TCGA-13-0717-01A-01R-0362-01	TCGA-13-0720-01A-01R-0362-01
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TCGA-13-0723-01A-02R-0362-01	TCGA-13-0724-01A-01R-0362-01
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(Other)	NA's
479	1

## unique\_patient\_ID:

TCGA-01-0628	TCGA-01-0630	TCGA-01-0631	TCGA-01-0633	TCGA-01-0636	TCGA-01-0637
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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
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TCGA-04-1365	TCGA-04-1367	TCGA-04-1369	TCGA-04-1371	TCGA-04-1514	TCGA-04-1516
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TCGA-04-1517	TCGA-04-1519	TCGA-04-1525	TCGA-04-1530	TCGA-04-1536	TCGA-04-1542
1	1	1	1	1	1
TCGA-04-1638	TCGA-04-1644	TCGA-04-1646	TCGA-04-1648	TCGA-04-1649	TCGA-04-1651
1	1	1	1	1	1
TCGA-04-1652	TCGA-04-1654	TCGA-04-1655	TCGA-09-0364	TCGA-09-0365	TCGA-09-0366
1	1	1	1	1	1
TCGA-09-0367	TCGA-09-0369	TCGA-09-1659	TCGA-09-1661	TCGA-09-1662	TCGA-09-1664
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TCGA-09-1665	TCGA-09-1666	TCGA-09-1667	TCGA-09-1668	TCGA-09-1669	TCGA-09-1670
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TCGA-09-1672	TCGA-09-1673	TCGA-09-1674	TCGA-09-1675	TCGA-09-2043	TCGA-09-2044
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TCGA-09-2045	TCGA-09-2048	TCGA-09-2049	TCGA-09-2050	TCGA-09-2051	TCGA-09-2053
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TCGA-09-2054	TCGA-09-2055	TCGA-09-2056	TCGA-10-0925	TCGA-10-0926	TCGA-10-0927
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TCGA-10-0928	TCGA-10-0930	TCGA-10-0931	TCGA-10-0933	TCGA-10-0934	TCGA-10-0935
1	1	1	1	1	1
TCGA-10-0936	TCGA-10-0937	TCGA-10-0938	TCGA-13-0714	TCGA-13-0717	TCGA-13-0720
1	1	1	1	1	1
TCGA-13-0723	TCGA-13-0724	TCGA-13-0725	(Other)		
1	1	1	479		

## sample\_type:

adjacentnormal	tumor
8	570

## histological\_type:

ser NA's
568 10

## primarysite:

other	ov	NA's
4	564	10

## summarygrade:

high	low	NA's
480	75	23

## summarystage:

early	late	NA's
43	520	15

## tumorstage:

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

## substage:

b	c	NA's
31	448	99

## grade:

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

## age\_at\_initial\_pathologic\_diagnosis:

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

## pltx:

n	y	NA's
19	492	67

## tax:

n	y	NA's
43	468	67

## neo:

n	NA's
511	67

## days\_to\_tumor\_recurrence:

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

## recurrence\_status:

norecurrence	recurrence
279	299

## days\_to\_death:

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

## vital\_status:

deceased	living	NA's
290	270	18

## site\_of\_tumor\_first\_recurrence:

locoregional	locoregional_plus_metastatic	NA's
153	3	
metastasis		NA's

143

279

primary\_therapy\_outcome\_success:

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

debulking:

optimal	suboptimal	NA's
367	140	71

percent\_normal\_cells:

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

percent\_stromal\_cells:

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

percent\_tumor\_cells:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.00	75.00	85.00	80.64	90.00	100.00	22

batch:

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

uncurated\_author\_metadata:

age\_at\_initial\_pathologic\_diagnosis

age

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

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

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

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

age

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

age\_at\_initial\_patho

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age\_at\_initial\_pathologic\_

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

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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

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age_at_initial_pathologic_diagnosis: 48//
```

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

**Value**

An expression set