

Package: MetaGxOvarian (via r-universe)

October 10, 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
(>= 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

Config/pak/sysreqs libicu-dev libpng-dev libssl-dev zlib1g-dev

Repository <https://bioc.r-universe.dev>

Date/Publication 2026-04-28 12:31:12 UTC

RemoteUrl <https://github.com/bioc/MetaGxOvarian>

RemoteRef HEAD

RemoteSha 432564fa061f127b861e98697efe559433b29b87

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GSE32062	106
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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 pateints. In this case, the value in `days_to_death` is the number of days since the last follow-up appointment.

Format

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

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

Description

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

Format

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

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

Description

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

Format

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

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
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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
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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
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DFCI.30	DFCI.31	DFCI.32	DFCI.33	DFCI.34	DFCI.35	DFCI.36	DFCI.37
1	1	1	1	1	1	1	1
DFCI.38	DFCI.39	DFCI.4	DFCI.40	DFCI.41	DFCI.42	DFCI.44	DFCI.45
1	1	1	1	1	1	1	1
DFCI.46	DFCI.47	DFCI.48	DFCI.49	DFCI.50	DFCI.51	DFCI.52	DFCI.53
1	1	1	1	1	1	1	1
DFCI.54	DFCI.55	DFCI.56	DFCI.57	DFCI.58	DFCI.59	DFCI.6	DFCI.60
1	1	1	1	1	1	1	1
DFCI.61	DFCI.62	DFCI.63	DFCI.64	DFCI.65	DFCI.66	DFCI.67	DFCI.68
1	1	1	1	1	1	1	1
DFCI.69	DFCI.7	DFCI.70	(Other)				
1	1	1	30				

sample_type:

tumor

129

histological_type:

ser

129

primarysite:

ov

129

summarygrade:

high

129

summarystage:

early late

1 128

tumorstage:

2 3 4

1 109 19

substage:

a b c NA's

5 12 93 19

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

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

vital_status:
deceased living
73 56

debulking:
optimal suboptimal NA's
98 28 3

uncurated_author_metadata:

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Source.Name: DFCI-71///Characteristics.Age.: Age <has_meas

Value

An expression set

GSE12418	<i>Expression analysis of stage III serous ovarian adenocarcinoma distinguishes a sub-group of survivors.</i>
----------	---

Description

It is difficult to predict the clinical outcome for patients with ovarian cancer. However, the use of biomarkers as additional prognostic factors may improve the outcome for these patients. In order to find novel candidate biomarkers, differences in gene expressions were analysed in 54 stage III serous ovarian adenocarcinomas with oligonucleotide microarrays containing 27,000 unique probes. The microarray data was verified with quantitative real-time polymerase chain reaction for the genes TACC1, MUC5B and PRAME. Using hierarchical cluster analysis we detected a sub-group that included 60% of the survivors. The gene expressions in tumours from patients in this sub-group of survivors were compared with the remaining tumours, and 204 genes were found to

be differently expressed. We conclude that the sub-group of survivors might represent patients with favourable tumour biology and sensitivity to treatment. A selection of the 204 genes might be used as a predictive model to distinguish patients within and outside of this group. Alternative chemotherapy strategies could then be offered as first-line treatment, which may lead to improvements in the clinical outcome for these patients.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Partheen K, Levan K, Osterberg L, Horvath G.Expression analysis of stage III serous
  Laboratory: Partheen, Horvath 2006
  Contact information:
  Title: Expression analysis of stage III serous ovarian adenocarcinoma distinguishes a sub-group of sur
  URL:
  PMIDs: 16996261

Abstract: A 177 word abstract is available. Use 'abstract' method.
Information is available on: preprocessing
notes:
  platform_title:
    SWEENEY H_v2.1.1_27k
  platform_shorttitle:
    SWEENEY 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///submission_date: Aug 12 2008

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

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

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

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

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

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

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

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Value

An expression set

GSE12470	<i>Gene expression profiling of advanced-stage serous ovarian cancers distinguishes novel subclasses and implicates ZEB2 in tumor progression and prognosis.</i>
----------	--

Description

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

high ZEB2 expression was independently associated with poor prognosis. Furthermore, the prognostic effect of E-cadherin encoded by CDH1 was verified using immunohistochemical analysis of an independent advanced stage cancer samples set (n = 74). These findings suggest that the expression of epithelial-mesenchymal transition-related genes such as ZEB2 and CDH1 may play important roles in the invasion process of advanced stage serous ovarian cancer.

Format

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

Abstract: A 253 word abstract is available. Use 'abstract' method.
Information is available on: preprocessing
notes:
  platform_title:
    Agilent-012097 Human 1A Microarray (V2) G4110B (Feature Number version)
  platform_shorttitle:
    Agilent G4110B
  platform_summary:
    hgug4110b
  platform_manufacturer:
    Agilent
  platform_distribution:
    commercial
  platform_accession:
    GPL887
  version:
    2015-09-22 19:08:17

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

Details

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

alt_sample_name:

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

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

```
sample_type:
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      10      43
```

```
histological_type:
ser NA's
43      10
```

```
primarysite:
ov
53
```

```
summarystage:
early late NA's
8      35      10
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```
tumorstage:
1 NA's
8      45
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```
uncurated_author_metadata:
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GSE12470.GSE12470_GSM312135 GSE12470.GSE12470_GSM312136

1 1

GSE12470.GSE12470_GSM312145 GSE12470.GSE12470_GSM312146

1 1

NA's

49

Value

An expression set

GSE13876	<i>Survival-related profile, pathways, and transcription factors in ovarian cancer.</i>
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Description

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

Format

experimentData(eset):
Experiment data
 Experimenter name: Crijns AP, Fehrmann RS, de Jong S, Gerbens F, Meersma GJ, Klip HG, Hollema H, Hofstra
 Laboratory: Crijns, van der Zee 2009
 Contact information:

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

URL:

PMIDs: 19192944

Abstract: A 371 word abstract is available. Use 'abstract' method.

Information is available on: preprocessing

notes:

platform_title:

Operon human v3 ~35K 70-mer two-color oligonucleotide microarrays

platform_shorttitle:

Operon v3 two-color

platform_summary:

OperonHumanV3

platform_manufacturer:

other

platform_distribution:

non-commercial

platform_accession:

GPL7759

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
title: Ovarian tumor sample 107 / Ovarian tumor sample 108
title: Ovarian tumor sample 109 / Ovarian tumor sample 110
title: Ovarian tumor sample 111 / Ovarian tumor sample 112

title: Ovarian tumor sample 105 / Ovarian tumor sample 106///geo_accession: GSM405628 / GSM405629/
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title: Ovarian tumor sample 111 / Ovarian tumor sample 112///geo_accession: GSM405634 / GSM405635/

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title: Ovaria

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title: Ovarian tumor sample 13 / Ovarian tumor sample 14///geo_accession: GSM405578 / GSM405580//

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title: Ovarian tumor sample 165 / Ovarian tumor sample 166///geo_accession: GSM405634 / GSM405635//

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title: Ovarian tumor sample 193 / Ovarian tumor sample 194///geo_accession: GSM405821 / GSM405823//

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title: Ovarian tumor sample 284 / Ovarian tumor sample 285///geo_accession: GSM405645 / GSM405647//

title: Ovarian

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title: Ovaria

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title: Ovari

title: Ovarian tumor

title: Ovarian

title: Ovari

title: Ovarian

title: Ovarian

title: Ovarian tumor sample 313 / Ovarian tumor sample 314///geo_accession: GSM405714 / GSM405715//

title: Ovari

title: Ovaria

title: Ovarian

title: Ovarian

title: Ovarian

title: Ovarian

title: Ovari

title: Ovarian tumor

Value

An expression set

GSE14764	<i>A prognostic gene expression index in ovarian cancer - validation across different independent data sets.</i>
----------	--

Description

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

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Denkert C, Budczies J, Darb-Esfahani S, Gy??rffy B et al. A prognostic gene expression
  Laboratory: Denkert, Lage 2009
  Contact information:
  Title: A prognostic gene expression index in ovarian cancer - validation across different independent c
  URL:
  PMIDs: 19294737

Abstract: A 254 word abstract is available. Use 'abstract' method.
Information is available on: preprocessing
notes:
  platform_title:
    [HG-U133A] Affymetrix Human Genome U133A Array
  platform_shorttitle:
    Affymetrix HG-U133A
```

```

platform_summary:
  hgu133a
platform_manufacturer:
  Affymetrix
platform_distribution:
  commercial
platform_accession:
  GPL96
version:
  2015-09-22 19:13:08

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

```

Details

```

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

```

n	events	median	0.95LCL	0.95UCL
80.00	21.00	4.52	4.19	NA

```

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

```

```

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

```

```

sample_type:
tumor
  80

```

```

histological_type:
  clearcell      endo      mix      other
           2           6           1           2
  ser undifferentiated
           68           1

```

```

primarysite:
ov

```

80

summarygrade:

high low

54 26

summarystage:

early late

9 71

tumorstage:

1 2 3 4

8 1 69 2

substage:

a b c NA's

4 6 32 38

grade:

1 2 3

3 23 54

recurrence_status:

norecurrence recurrence NA's

50 26 4

days_to_death:

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

210 660 1050 1011 1328 2190

vital_status:

deceased living

21 59

batch:

2004-09-29 2004-09-30 2004-10-01 2005-01-21 2005-01-25 2005-01-26 2005-01-28

1 2 6 4 7 8 10

2005-03-02 2006-07-26 2006-07-27 2006-07-28 2006-08-11 2006-08-18 2006-08-19

6 4 6 4 10 3 4

2006-08-21

5

uncurated_author_metadata:

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

Value

An expression set

GSE17260	<i>Gene expression profile for predicting survival in advanced-stage serous ovarian cancer across two independent datasets.</i>
----------	---

Description

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

prognostic index toward clinical application for evaluation of the risk of recurrence in patients with advanced-stage serous ovarian cancer.

Format

```
experimentData(eset):
```

```
Experiment data
```

```
  Experimenter name: Yoshihara K, Tajima A, Yahata T, Kodama S, Fujiwara H, Suzuki M, Onishi Y, Hatae M, S
```

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

```
  Contact information:
```

```
  Title: Gene expression profile for predicting survival in advanced-stage serous ovarian cancer across
```

```
  URL:
```

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  PMIDs: 20300634
```

```
Abstract: A 257 word abstract is available. Use 'abstract' method.
```

```
Information is available on: preprocessing
```

```
notes:
```

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  platform_title:
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    Agilent-012391 Whole Human Genome Oligo Microarray G4112A
```

```
  platform_shorttitle:
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```
    Agilent G4112A
```

```
  platform_summary:
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```
    hgug4112a
```

```
  platform_manufacturer:
```

```
    Agilent
```

```
  platform_distribution:
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```
    commercial
```

```
  platform_accession:
```

```
    GPL6848
```

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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:

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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
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Serous ovarian cancer 130	Serous ovarian cancer 131	Serous ovarian cancer 132
1	1	1
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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
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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

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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
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Serous ovarian cancer	55	Serous ovarian cancer	56	Serous ovarian cancer	57
	1		1		1
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	1		1		1
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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
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Serous ovarian cancer	77	Serous ovarian cancer	79	Serous ovarian cancer	80
	1		1		1
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	11				

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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

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Value

An expression set

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

Description

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

Format

```
experimentData(eset):
```

```
Experiment data
```

```
  Experimenter name: Mok SC, Bonome T, Vathipadiekal V, Bell A, Johnson ME, Wong KK, Park DC, Hao K, Yip D
```

```
  Laboratory: Mok, Birrer 2009
```

```
  Contact information:
```

```
  Title: A gene signature predictive for outcome in advanced ovarian cancer identifies a survival factor
```

```
  URL:
```

```
  PMIDs: 19962670
```

```
Abstract: A 110 word abstract is available. Use 'abstract' method.
```

```
Information is available on: preprocessing
```

```
notes:
```

```
  platform_title:
```

```
    [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
```

```
  platform_shorttitle:
```

```
    Affymetrix HG-U133Plus2
```

```
  platform_summary:
```

```
    hgu133plus2
```

```
  platform_manufacturer:
```

```
    Affymetrix|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

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1	
NA 's	
60	

Value

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

Description

To define a gene expression profile of BRCAness that correlates with chemotherapy response and outcome in epithelial ovarian cancer (EOC).A publicly available microarray data set including 61 patients with EOC with either sporadic disease or BRCA(1/2) germline mutations was used for development of the BRCAness profile. Correlation with platinum responsiveness was assessed in platinum-sensitive and platinum-resistant tumor biopsy specimens from six patients with BRCA

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

Format

```
experimentData(eset):
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```
Experiment data
```

```
  Experimenter name: Konstantinopoulos PA, Spentzos D, Karlan BY, Taniguchi T et al. Gene expression profile of BRCAness that correlates with responsiveness to chemotherapy and with overall survival in patients with sporadic epithelial ovarian cancer
```

```
  Laboratory: Konstantinopoulos, Cannistra 2010 hgu95
```

```
  Contact information:
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  Title: Gene expression profile of BRCAness that correlates with responsiveness to chemotherapy and with overall survival in patients with sporadic epithelial ovarian cancer
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  URL:
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  PMIDs: 20547991
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Abstract: A 241 word abstract is available. Use 'abstract' method.
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Information is available on: preprocessing
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notes:
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    [HG_U95Av2] Affymetrix Human Genome U95 Version 2 Array
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    Affymetrix
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  version:
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```
    2015-09-22 19:26:29
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featureData(eset):
```

```
An object of class 'AnnotatedDataFrame'
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```
  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:

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

```

Ovarian cancer_sample 53 Ovarian cancer_sample 54 Ovarian cancer_sample 55
                        1                        1                        1
Ovarian cancer_sample 56 Ovarian cancer_sample 57 Ovarian cancer_sample 58
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Ovarian cancer_sample 67 Ovarian cancer_sample 68 Ovarian cancer_sample 69
                        1                        1                        1
Ovarian cancer_sample 70 Ovarian cancer_sample 70 Ovarian cancer_sample 8
                        1                        1                        1
Ovarian cancer_sample 9
                        1

```

batch:

```

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

```

days_to_death:

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

primarysite:

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ov
70

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sample_type:

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tumor
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Value

An expression set

GSE20565	<i>A genomic and transcriptomic approach for a differential diagnosis between primary and secondary ovarian carcinomas in patients with a previous history of breast cancer.</i>
----------	--

Description

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

Format

```
experimentData(eset):
```

```
Experiment data
```

```
  Experimenter name: Meyniel JP, Cottu PH, Decraene C, Stern MH, Couturier J, Lebigot I, Nicolas A, Weber
```

```
  Laboratory: Meyniel, Sastre-Garau 2010
```

```
  Contact information:
```

```
  Title: A genomic and transcriptomic approach for a differential diagnosis between primary and secondary
```

```
  URL:
```

```
  PMIDs: 20492709
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```
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
```

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```

```
    Affymetrix HG-U133Plus2
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    hgu133plus2
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  platform_manufacturer:
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    Affymetrix
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    commercial
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    GPL570|GPL2005|GPL6801
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```

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

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

```

Details

```

assayData: 42447 features, 140 samples
Platform type:

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```

-----
Available sample meta-data:
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alt_sample_name:
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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]
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Breast metastasis in the ovary_OC01_ARN0053 [HG-U133_Plus_2]
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Breast metastasis in the ovary_OC01_ARN0055 [HG-U133_Plus_2]
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Breast metastasis in the ovary_OC01_ARN0060 [HG-U133_Plus_2]
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Breast metastasis in the ovary_OC01_ARN0069 [HG-U133_Plus_2]
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Breast metastasis in the ovary_OC01_ARN0077 [HG-U133_Plus_2]
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Breast metastasis in the ovary_OC01_ARN0081 [HG-U133_Plus_2]

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Breast metastasis in the ovary_OC01_ARN0083 [HG-U133_Plus_2]
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Breast metastasis in the ovary_OC01_ARN0092 [HG-U133_Plus_2]
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Breast metastasis in the ovary_OC01_ARN0104 [HG-U133_Plus_2]
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Breast metastasis in the ovary_OC01_ARN0123 [HG-U133_Plus_2]
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Breast metastasis in the ovary_OC01_ARN0126 [HG-U133_Plus_2]
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Breast metastasis in the ovary_OC01_ARN0141 [HG-U133_Plus_2]
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1
Breast metastasis in the ovary_OC01_ARN0143 [HG-U133_Plus_2]
1
Breast metastasis in the ovary_OC01_ARN0145 [HG-U133_Plus_2]
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Breast metastasis in the ovary_OC01_ARN0146 [HG-U133_Plus_2]
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Breast metastasis in the ovary_OC01_ARN0153 [HG-U133_Plus_2]
1
Breast metastasis in the ovary_OC01_ARN0162 [HG-U133_Plus_2]
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Breast metastasis in the ovary_OC01_ARN0201 [HG-U133_Plus_2]
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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]
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Ovarian carcinoma_OC01_ARN0008 [HG-U133_Plus_2]	
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	1
Ovarian carcinoma_OC01_ARN0010 [HG-U133_Plus_2]	
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Ovarian carcinoma_OC01_ARN0064 [HG-U133_Plus_2]	
	1
Ovarian carcinoma_OC01_ARN0066 [HG-U133_Plus_2]	
	1
Ovarian carcinoma_OC01_ARN0067 [HG-U133_Plus_2]	
	1
Ovarian carcinoma_OC01_ARN0070 [HG-U133_Plus_2]	
	1
Ovarian carcinoma_OC01_ARN0072 [HG-U133_Plus_2]	
	1
Ovarian carcinoma_OC01_ARN0075 [HG-U133_Plus_2]	
	1
Ovarian carcinoma_OC01_ARN0076 [HG-U133_Plus_2]	
	1
Ovarian carcinoma_OC01_ARN0080 [HG-U133_Plus_2]	
	1
Ovarian carcinoma_OC01_ARN0084 [HG-U133_Plus_2]	
	1
Ovarian carcinoma_OC01_ARN0085 [HG-U133_Plus_2]	
	1
Ovarian carcinoma_OC01_ARN0089 [HG-U133_Plus_2]	
	1
Ovarian carcinoma_OC01_ARN0091 [HG-U133_Plus_2]	
	1
Ovarian carcinoma_OC01_ARN0093 [HG-U133_Plus_2]	
	1
Ovarian carcinoma_OC01_ARN0095 [HG-U133_Plus_2]	
	1
Ovarian carcinoma_OC01_ARN0096 [HG-U133_Plus_2]	
	1
Ovarian carcinoma_OC01_ARN0100 [HG-U133_Plus_2]	
	1
Ovarian carcinoma_OC01_ARN0101 [HG-U133_Plus_2]	
	1
Ovarian carcinoma_OC01_ARN0103 [HG-U133_Plus_2]	
	1
Ovarian carcinoma_OC01_ARN0105 [HG-U133_Plus_2]	
	1
Ovarian carcinoma_OC01_ARN0106 [HG-U133_Plus_2]	

Ovarian carcinoma_OC01_ARN0107	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0108	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0109	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0111	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0113	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0114	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0115	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0116	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0118	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0119	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0124	[HG-U133_Plus_2]	1
Ovarian carcinoma_OC01_ARN0125	[HG-U133_Plus_2]	1
	(Other)	41
sample_type:		
tumor		
140		
histological_type:		
clearcell	endo	mucinous
6	6	7
		other
		6
		ser
		71
		NA's
		44
primarysite:		
other	ov	
44	96	
summarygrade:		
high	low	NA's
63	33	44
summarystage:		
early	late	NA's
27	67	46

tumorstage:

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

substage:

a	b	c	NA's
14	10	55	61

grade:

1	2	3	NA's
6	27	63	44

batch:

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

uncurated_author_metadata:

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title: Breast metastasis in the ovary_OC01_ARN0102 [HG-U133_Plus_2]///geo_accession: GSM516757///status: public

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title: Ovarian carcinoma_OC01_ARN0125 [HG-U133_Plus_2]///geo_accession: GSE2109

duplicates:
GSE20565.GSE20565_GSM516722 GSE20565.GSE20565_GSM516741
1 1
NA's
138

Value

An expression set

GSE2109	<i>IGC EXpression Project for Oncology</i>
---------	--

Description

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

Format

```

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

Abstract: A 8 word abstract is available. Use 'abstract' method.
Information is available on: preprocessing
notes:
  platform_title:
    [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
  platform_shorttitle:
    Affymetrix HG-U133Plus2
  platform_summary:
    hgu133plus2
  platform_manufacturer:
    Affymetrix
  platform_distribution:
    commercial
  platform_accession:
    GPL570
  version:
    2015-09-22 19:40:35

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

```

Details

```

assayData: 42447 features, 204 samples
Platform type:
-----
Available sample meta-data:
-----

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

```

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

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

1 105

sample_type:

tumor

204

histological_type:

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

primarysite:

other ov NA's

23 178 3

summarygrade:

high low NA's

91 31 82

summarystage:

early late NA's

37 87 80

tumorstage:

1 2 3 4 NA's

20 14 58 18 94

substage:

a b c NA's

17 22 79 86

grade:

1 2 3 4 NA's

11 20 83 8 82

age_at_initial_pathologic_diagnosis:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
25.00	45.00	55.00	58.82	65.00	85.00

batch:

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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
3	1	4	2	1	1	1
2006-03-06	2006-03-14	2006-04-18	2006-04-20	2006-05-16	2006-06-08	2006-07-26
2	2	1	2	3	1	2
2006-07-28	2006-09-12	2006-09-14	2006-10-10	2006-10-24	2006-10-31	2006-11-09
1	2	1	1	9	5	10
2006-11-21	2006-11-30	2006-12-07	2007-01-12	2007-02-09	2007-03-07	2007-03-09
1	6	3	1	1	8	1
2007-03-15	2007-05-01	2007-05-03	2007-05-15	2007-05-18	2007-05-30	2007-06-12
4	2	3	4	2	2	1
2007-07-27	2007-09-05	2007-09-07	2007-09-11	2007-09-12	2008-02-15	2008-02-21
2	3	1	4	4	1	3
2008-02-27	2008-03-04	2008-05-13	2008-05-16	2008-05-23		
2	1	4	4	5		

uncurated_author_metadata:

title: Omentum - 8240///geo_accession: GSM38095///status

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

duplicates:
GSE2109.GSE2109_GSM76554 GSE2109.GSE2109_GSM76567 NA's
1 1 202

Value

An expression set

GSE26193	<i>miR-141 and miR-200a act on ovarian tumorigenesis by controlling oxidative stress response.</i>
----------	--

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):
```

```
Experiment data
```

```
  Experimenter name: Mateescu B, Batista L, Mariani O, Meyniel J, Cottu PH, Sastre-Garau X, Mechta-Grigor
```

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

```
  Contact information:
```

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

```
  URL:
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```
  PMIDs: 22101765
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Abstract: A 149 word abstract is available. Use 'abstract' method.
```

```
Information is available on: preprocessing
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```
notes:
```

```
  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:
```

```
    hgu133plus2
```

```
  platform_manufacturer:
```

```
    Affymetrix
```

```
  platform_distribution:
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    commercial
```

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  platform_accession:
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```
    GPL570
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  platform_technology:
```

```
    in situ oligonucleotide
```

```
version:
```

```
  2015-09-22 19:44:56
```

```
featureData(eset):
```

```
An object of class 'AnnotatedDataFrame'
```

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

```
  varLabels: probeset gene EntrezGene.ID best_probe
```

```
  varMetadata: labelDescription
```

Details

assayData: 42447 features, 107 samples

Platform type:

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

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

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

Available sample meta-data:

alt_sample_name:

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

Ovarian carcinoma 49	Ovarian carcinoma 5	Ovarian carcinoma 50
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Ovarian carcinoma 51	Ovarian carcinoma 52	Ovarian carcinoma 53
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
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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
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4 10

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Value

An expression set

GSE26712

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

Description

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

Format

```
experimentData(eset):
```

```
Experiment data
```

```
  Experimenter name: Bonome T, Levine DA, Shih J, Randonovich M, Pise-Masison CA, Bogomolnii F, Ozbun L,
```

```
  Laboratory: Bonome, Birrer 2008
```

```
  Contact information:
```

```
  Title: A gene signature predicting for survival in suboptimally debulked patients with ovarian cancer.
```

```
  URL:
```

```
  PMIDs: 18593951
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```
Abstract: A 238 word abstract is available. Use 'abstract' method.
```

```
Information is available on: preprocessing
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```
notes:
```

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    [HG-U133A] Affymetrix Human Genome U133A Array
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hgu133a
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  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
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Ovarian Cancer	S0203	Ovarian Cancer	S0205	Ovarian Cancer	S021
	1		1		1
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Ovarian Cancer	S0217	Ovarian Cancer	S0218	Ovarian Cancer	S0224
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Ovarian Cancer	S0231	Ovarian Cancer	S0235	Ovarian Cancer	S0236
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Ovarian Cancer	S0237	Ovarian Cancer	S0241	Ovarian Cancer	S0242
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Ovarian Cancer	S0243	Ovarian Cancer	S0244	Ovarian Cancer	S0246
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Ovarian Cancer	S0247	Ovarian Cancer	S0249	Ovarian Cancer	S025
	1		1		1
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Ovarian Cancer	S0278	Ovarian Cancer	S0279	Ovarian Cancer	S0282

	1		1		1
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	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
----------	--------	------

1295610

debulking:
optimal suboptimal NA's
909510

percent_normal_cells:
20-
195

percent_stromal_cells:
20-
195

percent_tumor_cells:
80+
195

batch:
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		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 resistance-linked gene

Laboratory: Gillet, Gottesman 2012

Contact information:

Title: Multidrug resistance-linked gene signature predicts overall survival of patients with primary o

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:

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NA
platform_manufacturer:
  TaqMan
platform_distribution:
  custom
platform_accession:
  GPL13728
version:
  2015-09-22 19:46:26

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

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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:
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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

```

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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
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US Patient 24	US Patient 25	US Patient 26
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US Patient 32	US Patient 33	US Patient 34
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US Patient 57	US Patient 58	US Patient 59
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US Patient 65	US Patient 66	US Patient 67
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US Patient 68	US Patient 69	US Patient 7
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US Patient 70	US Patient 71	US Patient 72
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US Patient 73	US Patient 74	US Patient 75
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US Patient 76	US Patient 77	US Patient 78

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(Other)			
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tumor			
103			
histological_type:			
clearcell	ser		
1	102		
summarygrade:			
high	low	NA's	
92	9	2	
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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		

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Value

An expression set

GSE30161	<i>Multi-gene expression predictors of single drug responses to adjuvant chemotherapy in ovarian carcinoma: predicting platinum resistance.</i>
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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, Theodorescu D, Lee JK
 Laboratory: Ferriss, Lee 2012
 Contact information:
 Title: Multi-gene expression predictors of single drug responses to adjuvant chemotherapy in ovarian 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:

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OV_FFPE_22	OV_FFPE_23	OV_FFPE_24	OV_FFPE_25	OV_FFPE_26	OV_FFPE_27	OV_FFPE_28

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	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							
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OV_FFPE_8	OV_FFPE_9												
	1		1										

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tumor
58

histological_type:
clearcell endo mucinous other
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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

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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:
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36 22

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

Value

An expression set

GSE32062	<i>High-risk ovarian cancer based on 126-gene expression signature is uniquely characterized by downregulation of antigen presentation pathway.</i>
----------	---

Description

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

Format

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

```

Contact information:
Title: High-risk ovarian cancer based on 126-gene expression signature is uniquely characterized by do
URL:
PMIDs: 22241791

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

alt_sample_name:
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129d   12d   130d   132d   134d   139d   140d   143d   144d   145d
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146d	148d	150d	155d	156d	15d	160d	16d	171d	173d
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23d	249d	257d	25d	260d	262d	264d	266d	267d	268d
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269d	27d	299d	2d	300d	301d	302d	303d	304d	305d2
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306d	307d	310d	318d	319d	320d2	323d	327d	330d	331d
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333d2	335d	337d	340d	342d	346d	347d	348d2	350d	352d
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353d	355d	356d	357d	358d	360d	362d	363d	365d	366d
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367d	368d2	36d	38d	41d2R	42d	43d	44d	456d	(Other)
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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.
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vital_status:

deceased	living
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debulking:

optimal	suboptimal
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NA's
258

Value

An expression set

GSE32063	<i>High-risk ovarian cancer based on 126-gene expression signature is uniquely characterized by downregulation of antigen presentation pathway.</i>
----------	---

Description

High-grade serous ovarian cancers are heterogeneous not only in terms of clinical outcome but also at the molecular level. Our aim was to establish a novel risk classification system based on

a gene expression signature for predicting overall survival, leading to suggesting novel therapeutic strategies for high-risk patients. In this large-scale cross-platform study of six microarray data sets consisting of 1,054 ovarian cancer patients, we developed a gene expression signature for predicting overall survival by applying elastic net and 10-fold cross-validation to a Japanese data set A (n = 260) and evaluated the signature in five other data sets. Subsequently, we investigated differences in the biological characteristics between high- and low-risk ovarian cancer groups. An elastic net analysis identified a 126-gene expression signature for predicting overall survival in patients with ovarian cancer using the Japanese data set A (multivariate analysis, $P = 4 \times 10^{-20}$). 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

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experimentData(eset):
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```
Experiment data
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  Experimenter name: Yoshihara K, Tsunoda T, Shigemizu D, Fujiwara H et al. High-risk ovarian cancer base
```

```
  Laboratory: Yoshihara, Tanaka 2012
```

```
  Contact information:
```

```
  Title: High-risk ovarian cancer based on 126-gene expression signature is uniquely characterized by do
```

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  URL:
```

```
  PMIDs: 22241791
```

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

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  Information is available on: preprocessing
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```
  notes:
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    platform_title:
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```
      Agilent-014850 Whole Human Genome Microarray 4x44K G4112F (Probe Name vers
ion)
```

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    platform_shorttitle:
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```
      Agilent G4112F
```

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    platform_summary:
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      hgug4112a
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    platform_manufacturer:
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      Agilent
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    platform_distribution:
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      commercial
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    platform_accession:
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      GPL6480
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    version:
```

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      2015-09-22 19:58:23
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featureData(eset):
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An object of class 'AnnotatedDataFrame'
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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:

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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:
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19 21

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Value

An expression set

GSE44104	<i>COL11A1 promotes tumor progression and predicts poor clinical outcome in ovarian cancer.</i>
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Description

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

Format

```

experimentData(eset):
Experiment data
  Experimenter name: Wu Y, Chang T, Huang Y, Huang H, Chou C
  Laboratory: Wu, Chou 2013
  Contact information:
  Title: COL11A1 promotes tumor progression and predicts poor clinical outcome in ovarian cancer.
  URL:
  PMIDs: 23934190

Abstract: A 260 word abstract is available. Use 'abstract' method.
Information is available on: preprocessing
notes:
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  platform_technology:
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  version:
    2015-09-22 20:02:05

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An object of class 'AnnotatedDataFrame'
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    (42447 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription

```

Details

```

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

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Tc_113 Tc_48 Tc_49 Tc_51 Tc_56 Tc_59 Tc_61 Tc_63 Tc_64 Tc_65 Tc_74

```

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Ts_14	Ts_15	Ts_17	Ts_19	Ts_2	Ts_20	Ts_21	Ts_23	Ts_24	Ts_26	Ts_28
1	1	1	1	1	1	1	1	1	1	1
Ts_3	Ts_31	Ts_32	Ts_34	Ts_35	Ts_36	Ts_37	Ts_39	Ts_4	Ts_41	Ts_43
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1	1	1	1	1						

sample_type:

tumor

60

histological_type:

clearcell	endo	mucinous	ser
12	11	9	28

summarystage:

early	late
25	35

tumorstage:

1	2	3	4
17	8	30	5

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norecurrence	recurrence
40	20

os_binary:

long	short
44	16

relapse_binary:

long	short
40	20

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2010-09-07	2010-09-08	2010-10-14	2010-12-10	2010-12-14
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duplicates:
Length Class Mode
60 character character

Value

An expression set

GSE49997	<i>Validating the impact of a molecular subtype in ovarian cancer on outcomes: a study of the OVCAD Consortium.</i>
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Description

Most patients with epithelial ovarian cancer (EOC) are diagnosed at advanced stage and have a poor prognosis. However, a small proportion of these patients will survive, whereas others will die very quickly. Clinicopathological factors do not allow precise identification of these subgroups. Thus, we have validated a molecular subclassification as new prognostic factor in EOC. One hundred and ninety-four patients with Stage II-IV EOC were characterized by whole-genome expression profiling of tumor tissues and were classified using a published 112 gene set, derived from an International Federation of Gynecology and Obstetrics (FIGO) stage-directed supervised classification approach. The 194 tumor samples were classified into two subclasses comprising 95 (Subclass 1) and 99 (Subclass 2) tumors. All nine FIGO II tumors were grouped in Subclass 1 (P = 0.001). Subclass 2 (54% of advanced-stage tumors) was significantly correlated with peritoneal carcinomatosis

and non-optimal debulking. Patients with Subclass 2 tumors had a worse overall survival for both serous and non-serous histological subtypes, as revealed by univariate analysis (hazard ratios [HR] of 3.17 and 17.11, respectively; $P < 0.001$) and in models corrected for relevant clinicopathologic parameters (HR 2.87 and 12.42, respectively; $P = 0.023$). Significance analysis of microarrays revealed 2082 genes that were differentially expressed in advanced-grade serous tumors of both subclasses and the focal adhesion pathway as the most deregulated pathway. In the present validation study, we have shown that, in advanced-stage serous ovarian cancer, two approximately equally large molecular subtypes exist, independent of classical clinicopathological parameters and presenting with highly different whole-genome expression profiles and a markedly different overall survival. Similar results were obtained in a small cohort of patients with non-serous tumors. 2012 Japanese Cancer Association.

Format

```
experimentData(eset):
```

```
Experiment data
```

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  Experimenter name: Pils D1, Hager G, Tong D, Aust S, Heinze G, Kohl M, Schuster E, Wolf A, Sehouli J, Bra
```

```
  Laboratory: Pils, Zeilinger 2012
```

```
  Contact information:
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  Title: Validating the impact of a molecular subtype in ovarian cancer on outcomes: a study of the OVCAD
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  URL:
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```
  PMIDs: 22497737
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Abstract: A 276 word abstract is available. Use 'abstract' method.
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Information is available on: preprocessing
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notes:
```

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  platform_title:
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    ABI Human Genome Survey Microarray Version 2
```

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  platform_shorttitle:
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  platform_summary:
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    in situ oligonucleotide
```

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  version:
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    2015-09-22 20:04:13
```

```
featureData(eset):
```

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An object of class 'AnnotatedDataFrame'
```

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  featureNames: 100027 100036 ... 10715781 (18439 total)
```

```
  varLabels: probeset gene EntrezGene.ID best_probe
```

```
  varMetadata: labelDescription
```

Details

assayData: 18439 features, 204 samples

Platform type:

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

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

10 observations deleted due to missingness

n	events	median	0.95LCL	0.95UCL
194.00	57.00	NA	3.67	NA

Available sample meta-data:

alt_sample_name:

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EOC P009	EOC P010	EOC P011	EOC P012	EOC P013	EOC P014	EOC P015	EOC P016
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EOC P017	EOC P018	EOC P019	EOC P020	EOC P021	EOC P022	EOC P023	EOC P024
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EOC P097	EOC P098	EOC P099	(Other)				
1	1	1	105				

sample_type:

tumor
204

histological_type:

other ser NA's

23 171 10

summarygrade:

high low NA's

143 50 11

summarystage:

early late NA's

9 185 10

tumorstage:

2 3 4 NA's

9 154 31 10

grade:

2 3 NA's

50 143 11

age_at_initial_pathologic_diagnosis:

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

days_to_tumor_recurrence:

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

recurrence_status:

norecurrence	recurrence	NA's
70	124	10

days_to_death:

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

vital_status:

deceased	living	NA's
57	137	10

debulking:

optimal	suboptimal	NA's
137	57	10

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Value

An expression set

GSE51088	<i>POSTN/TGFBI-associated stromal signature predicts poor prognosis in serous epithelial ovarian cancer.</i>
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Description

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

Format

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

```

Abstract: A 250 word abstract is available. Use 'abstract' method.
Information is available on: preprocessing
notes:
  platform_title:
    Agilent-012097 Human 1A Microarray (V2) G4110B (Probe Name version)
  platform_shorttitle:
    Agilent G4110B
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  platform_accession:
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  platform_technology:
    in situ oligonucleotide
  version:
    2015-09-22 20:05:48

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```

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

```

```

-----
Available sample meta-data:
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Ov_Tumor_Ref_Mix vs. CS-OV-003 Ov_Tumor_Ref_Mix vs. CS-OV-004
                                1                                1
Ov_Tumor_Ref_Mix vs. CS-OV-005 Ov_Tumor_Ref_Mix vs. CS-OV-006

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Ov_Tumor_Ref_Mix vs. CS-OV-013		Ov_Tumor_Ref_Mix vs. CS-OV-014	
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  benign borderline healthy metastatic tumor
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histological_type:
clearcell      endo mucinous      other      ser      NA's
      3         7         9        11      122      20

summarygrade:
high low NA's
 119  30  23

summarystage:
early late NA's
   31  120  21

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

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

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

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

neo:
n
172

recurrence_status:
norecurrence recurrence NA's
          36          111      25

days_to_death:
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
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vital_status:
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   112     40    20

```

percent_normal_cells:

30- NA's
140 32

percent_stromal_cells:

30- NA's
140 32

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70+ NA's
140 32

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Value

An expression set

GSE6008	<i>Lysophosphatidic acid-induced transcriptional profile represents serous epithelial ovarian carcinoma and worsened prognosis.</i>
---------	---

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

Abstract: A 247 word abstract is available. Use 'abstract' method.
Information is available on: preprocessing
notes:
  platform_title:
    [HG-U133A] Affymetrix Human Genome U133A Array
  platform_shorttitle:
    Affymetrix HG-U133A
  platform_summary:
    hgu133a
  platform_manufacturer:
    Affymetrix
  platform_distribution:
    commercial
  platform_accession:
    GPL96
  version:
    2015-09-22 20:07:11

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
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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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  Ovarian_Tumor_ClearCell_CHTN-OC-028      Ovarian_Tumor_ClearCell_KU-OC-003
                                           1
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  Ovarian_Tumor_ClearCell_KU-OC-006        Ovarian_Tumor_ClearCell_KU-OC-007
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Ovarian_Tumor_Endometrioid_CHTN-OE-087 Ovarian_Tumor_Endometrioid_CHTN-OE-092
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  Ovarian_Tumor_Endometrioid_KU-OE-004      Ovarian_Tumor_Endometrioid_KU-OE-007
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  Ovarian_Tumor_Endometrioid_UM-OE-1T      Ovarian_Tumor_Mucinous_CHTN-OM-007

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Ovarian_Tumor_Mucinous_CHTN-OM-035		Ovarian_Tumor_Mucinous_CHTN-OM-036	
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Ovarian_Tumor_Mucinous_KU-OM-003		Ovarian_Tumor_Mucinous_KU-OM-004	
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Ovarian_Tumor_Serous_CHTN-OS-011		Ovarian_Tumor_Serous_CHTN-OS-018	
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Ovarian_Tumor_Serous_KU-OS-012		Ovarian_Tumor_Serous_KU-OS-013	
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healthy	tumor
4	99

histological_type:

clearcell	endo	mucinous	ser	NA's
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primarysite:

ov
103

summarygrade:

high	low	NA's
38	36	29

summarystage:

early	late	NA's
42	53	8

tumorstage:

1	2	3	4	NA's
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substage:

a	b	c	d	NA's
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grade:

1	2	3	NA's
19	17	38	29

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GSE6008.GSE6008_GSM139477///GSE6008.GSE6008_GSM139478
1
NA 's
100

Value

An expression set

GSE6822	<i>Classification of ovarian tumor samples</i>
---------	--

Description

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

Format

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

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

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

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

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Details

assayData: 6407 features, 66 samples

Platform type:

Available sample meta-data:

alt_sample_name:

Ovarian tumor AM053	Ovarian tumor AM122	Ovarian tumor AM124	Ovarian tumor AM125
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Ovarian tumor AM127	Ovarian tumor AM137	Ovarian tumor AM138	Ovarian tumor AM144
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Ovarian tumor AM431	Ovarian tumor AM438		
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sample_type:

tumor

66

histological_type:

clearcell

endo

mix

mucinous

11

7

3

1

ser undifferentiated

41

3

primarysite:

ov

66

summarygrade:

high low NA's

40 15 11

grade:

1 2 3 NA's

1 14 40 11

batch:

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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, Fruscio R, Clivio L, Garbi A

Laboratory: Marchini, D'Incalci 2008

Contact information:

Title: Analysis of gene expression in early-stage ovarian cancer.

URL:

PMIDs: 19047114

Abstract: A 225 word abstract is available. Use 'abstract' method.

Information is available on: preprocessing

notes:

platform_title:

Agilent Human 1 cDNA Microarray (G4100A)

platform_shorttitle:

Agilent G4100A cDNA

platform_summary:

hgug4100a

platform_manufacturer:

Agilent

platform_distribution:

custom-commercial

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platform_accession:
  GPL5689
platform_technology:
  spotted DNA/cDNA
version:
  2015-09-22 20:07:40
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```
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1 2 ... 8864 (7809 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 7809 features, 83 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)
```

n	events	median	0.95LCL	0.95UCL
83	15	NA	12	NA

Available sample meta-data:

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p0143bis sample_Ovarian tumor	1	p0146bis sample_Ovarian tumor
p0188bis sample_Ovarian tumor	1	p0208bis sample_Ovarian tumor
p0210bis sample_Ovarian tumor	1	p0217bis sample_Ovarian tumor
p057bis sample_Ovarian tumor	1	p070bis sample_Ovarian tumor
p080bis sample_Ovarian tumor	1	p091bis sample_Ovarian tumor
p139bis sample_Ovarian tumor	1	p13bis sample_Ovarian tumor
p141bis sample_Ovarian tumor	1	p166bis sample_Ovarian tumor

p171bis sample_Ovarian tumor	p17bis sample_Ovarian tumor
1	1
p183bis sample_Ovarian tumor	p209bis sample_Ovarian tumor
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p646bis sample_Ovarian tumor	1	p66bis sample_Ovarian tumor	1
p68bis sample_Ovarian tumor	1	p690bis sample_Ovarian tumor	1
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p73bis sample_Ovarian tumor	1	p760bis sample_Ovarian tumor	1
p770bis sample_Ovarian tumor	1	p772bis sample_Ovarian tumor	1
p775bis sample_Ovarian tumor	1	p793bis sample_Ovarian tumor	1
p79bis sample_Ovarian tumor	1	p84bis sample_Ovarian tumor	1
p90bis sample_Ovarian tumor	1		

sample_type:

borderline	tumor
15	68

histological_type:

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

primarysite:

ov
83

summarygrade:

high	low	NA's
35	33	15

summarystage:

early
83

tumorstage:

1
83

substage:

a	b	c
25	5	53

grade:

1	2	3	NA's
13	20	35	15

age_at_initial_pathologic_diagnosis:

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

recurrence_status:

norecurrence	recurrence
62	21

days_to_death:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
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deceased	living
15	68

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Value

An expression set

GSE9891

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

The study aim to identify novel molecular subtypes of ovarian cancer by gene expression profiling with linkage to clinical and pathologic features. Microarray gene expression profiling was done on 285 serous and endometrioid tumors of the ovary, peritoneum, and fallopian tube. K-means clustering was applied to identify robust molecular subtypes. Statistical analysis identified differentially expressed genes, pathways, and gene ontologies. Laser capture microdissection, pathology review, and immunohistochemistry validated the array-based findings. Patient survival within k-means groups was evaluated using Cox proportional hazards models. Class prediction validated k-means groups in an independent dataset. A semisupervised survival analysis of the array data was used to compare against unsupervised clustering results. Optimal clustering of array data identified six molecular subtypes. Two subtypes represented predominantly serous low malignant potential and low-grade endometrioid subtypes, respectively. The remaining four subtypes represented higher grade and advanced stage cancers of serous and endometrioid morphology. A novel subtype of high-grade serous cancers reflected a mesenchymal cell type, characterized by overexpression of N-cadherin and P-cadherin and low expression of differentiation markers, including CA125 and MUC1. A poor prognosis subtype was defined by a reactive stroma gene expression signature, correlating with extensive desmoplasia in such samples. A similar poor prognosis signature could be found using a semisupervised analysis. Each subtype displayed distinct levels and patterns of immune cell infiltration. Class prediction identified similar subtypes in an independent ovarian dataset with similar prognostic trends. Gene expression profiling identified molecular subtypes of ovarian cancer of biological and clinical importance.

Format

```
experimentData(eset):
```

```
Experiment data
```

```
  Experimenter name: Tothill RW, Tinker AV, George J, Brown R, Fox SB, Lade S, Johnson DS, Trivett MK, Ete
```

```
  Laboratory: Tothill, Bowtell 2008
```

```
  Contact information:
```

```
  Title: Novel molecular subtypes of serous and endometrioid ovarian cancer linked to clinical outcome.
```

```
  URL:
```

```
  PMIDs: 18698038
```

```
Abstract: A 243 word abstract is available. Use 'abstract' method.
```

```
Information is available on: preprocessing
```

```
notes:
```

```
  platform_title:
```

```
    [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
```

```
  platform_shorttitle:
```

```
    Affymetrix HG-U133Plus2
```

```
  platform_summary:
```

```
    hgu133plus2
```

```
platform_manufacturer:
  Affymetrix
platform_distribution:
  commercial
platform_accession:
  GPL570
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
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X23102 X23106 X23116 X23128 X23139 X23143 X23162 X23165 X23167 X23170
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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

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

Value

An expression set

loadOvarianDatasets	<i>Function to load ovarian cancer SummarizedExperiment objects 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 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 nueric 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 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 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 (defeault 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 eset 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 P, Murphy S, Dressman HK,
```

```
  Laboratory: Berchuck, Marks 2005
```

```
  Contact information:
```

```
  Title: Patterns of gene expression that characterize long-term survival in advanced stage serous ovari
```

```
  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:
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```
    Affymetrix HG-U133A
```

```
  platform_summary:
```

```
    hgu133a
```

```
  platform_manufacturer:
```

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    Affymetrix
```

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  platform_distribution:
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    commercial
```

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  platform_accession:
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    GPL96
```

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warnings:
```

```
  These samples are a subset of PMID17290060.
```

```
version:
```

```
  2015-09-22 20:17:53
```

```
featureData(eset):
```

```
An object of class 'AnnotatedDataFrame'
```

```
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  (20967 total)
```

```
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```

```
  varMetadata: labelDescription
```

Details

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Platform type:

Available sample meta-data:

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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:

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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 stage///AgeDx: 72///	1
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1762///Cancer.Type: Early stage///AgeDx: 52///	1
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1763///Cancer.Type: Early stage///AgeDx: 58///	1
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1764///Cancer.Type: Early stage///AgeDx: 48///	1
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1765///Cancer.Type: Early stage///AgeDx: 45///	1
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1772///Cancer.Type: Long///AgeDx: 33///STA	1
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1773///Cancer.Type: Long///AgeDx: 68///STA	1
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1774///Cancer.Type: Long///AgeDx: 56///STA	1
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1775///Cancer.Type: Long///AgeDx: 60///STA	1
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1776///Cancer.Type: Long///AgeDx: 40///STA	1
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1777///Cancer.Type: Long///AgeDx: 78///STA	1
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1778///Cancer.Type: Long///AgeDx: 66///STA	1
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1779///Cancer.Type: Long///AgeDx: 53///STA	1
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1780///Cancer.Type: Long///AgeDx: 63///STA	1
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1781///Cancer.Type: Long///AgeDx: 73///STA	1
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1828///Cancer.Type: Short///AgeDx: 59///ST	1
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1829///Cancer.Type: Short///AgeDx: 65///STA	1
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1830///Cancer.Type: Short///AgeDx: 79///STA	1
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1831///Cancer.Type: Short///AgeDx: 70///STA	1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1832///Cancer.Type: Short///AgeDx: 59///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1833///Cancer.Type: Short///AgeDx: 55///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1834///Cancer.Type: Short///AgeDx: 48///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1835///Cancer.Type: Short///AgeDx: 54///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1836///Cancer.Type: Short///AgeDx: 57///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1900///Cancer.Type: Long///AgeDx: 62///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1901///Cancer.Type: Long///AgeDx: 50///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1902///Cancer.Type: Long///AgeDx: 67///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1903///Cancer.Type: Early stage///AgeDx: 73///S
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1904///Cancer.Type: Long///AgeDx: 70///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1905///Cancer.Type: Short///AgeDx: 70///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1906///Cancer.Type: Short///AgeDx: 75///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1907///Cancer.Type: Long///AgeDx: 73///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1908///Cancer.Type: Short///AgeDx: 59///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1909///Cancer.Type: Short///AgeDx: 65///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1989///Cancer.Type: Long///AgeDx: 67///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2003///Cancer.Type: Short///AgeDx: 49///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2004///Cancer.Type: Short///AgeDx: 55///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2005///Cancer.Type: Short///AgeDx: 47///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2019///Cancer.Type: Long///AgeDx: 48///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2020///Cancer.Type: Long///AgeDx: 58///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2021///Cancer.Type: Long///AgeDx: 62///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2026///Cancer.Type: Short///AgeDx: 46///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2027///Cancer.Type: Short///AgeDx: 65///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2028///Cancer.Type: Short///AgeDx: 71///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2029///Cancer.Type: Short///AgeDx: 68///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2030///Cancer.Type: Short///AgeDx: 54///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2031///Cancer.Type: Long///AgeDx: 63///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2032///Cancer.Type: Long///AgeDx: 58///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2033///Cancer.Type: Long///AgeDx: 57///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2390///Cancer.Type: Early stage///AgeDx: 66///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2391///Cancer.Type: Early stage///AgeDx: 77///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2392///Cancer.Type: Early stage///AgeDx: 46///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2393///Cancer.Type: Early stage///AgeDx: 49///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2394///Cancer.Type: Long///AgeDx: 62///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2395///Cancer.Type: Long///AgeDx: 40///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2396///Cancer.Type: Short///AgeDx: 73///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2397///Cancer.Type: Short///AgeDx: 57///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2398///Cancer.Type: Short///AgeDx: 37///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2399///Cancer.Type: Short///AgeDx: 62///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2400///Cancer.Type: Short///AgeDx: 62///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2401///Cancer.Type: Short///AgeDx: 57///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2402///Cancer.Type: Short///AgeDx: 57///STA
1

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2536///Cancer.Type: Early stage///AgeDx: 42///STA
1

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, Cragun J, Clarke J, Whitake``Laboratory: Dressman, Lancaster 2007``Contact information:``Title: An integrated genomic-based approach to individualized treatment of patients with advanced-stage``URL:``PMIDs: 17290060``Abstract: A 223 word abstract is available. Use 'abstract' method.``Information is available on: preprocessing``notes:``platform_title:``[HG-U133A] Affymetrix Human Genome U133A Array``platform_shorttitle:``Affymetrix HG-U133A``platform_summary:``hgu133a``platform_manufacturer:``Affymetrix``platform_distribution:`

```

commercial
platform_accession:
  GPL96
warnings:
  This paper has been retracted.
version:
  2015-09-22 20:19:16

```

```

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

```

Details

```

assayData: 20967 features, 117 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

```

n	events	median	0.95LCL	0.95UCL
117.00	67.00	5.26	2.79	7.48

```

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

```

```

alt_sample_name:
  1024    1447    1451    1504    1526    1552    1578    1590    1615    1623
    1         1         1         1         1         1         1         1         1         1
  1665    1674    1675    1774    1784    1834    1846    1877    1913    1929
    1         1         1         1         1         1         1         1         1         1
  2046    2063    2064    2075    2198    2204    2324    2419    2422    2424
    1         1         1         1         1         1         1         1         1         1
  2465    2476    2479    2505    2542    2573    2673    2739    2802    2849
    1         1         1         1         1         1         1         1         1         1
  2895    2967    2981    2999    3018    3090    3102    3107    3142     860
    1         1         1         1         1         1         1         1         1         1
    872     922   D1805   D1837   D1859   D2098   D2208   D2332   D2342   D2358
    1         1         1         1         1         1         1         1         1         1
  D2421   D2432   D2433   D2480   D2557   D2559   D2560   D2572   D2575   D2576
    1         1         1         1         1         1         1         1         1         1
  D2581   D2603   D2611   D2629   D2640   D2648   D2668   D2689   D2691   D2700
    1         1         1         1         1         1         1         1         1         1
  D2726   D2727   D2733   D2738   D2749   D2776   D2792   M1054   M1055   M1200
    1         1         1         1         1         1         1         1         1         1

```

M1241	M1390	M1503	M1572	M17	M1891	M2070	M2097	M2184	(Other)
1	1	1	1	1	1	1	1	1	18

sample_type:
tumor
117

histological_type:
ser
117

primarysite:
ov
117

summarygrade:
high low NA's
57 57 3

summarystage:
early late NA's
1 115 1

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

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

days_to_death:
Min. 1st Qu. Median Mean 3rd Qu. Max.
30 510 1020 1496 2220 5550

vital_status:
deceased living
67 50

primary_therapy_outcome_success:
completeresponse 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: 1///Assigned.Stage: 4///GRA

OVC.TumorID: 1447///Survival: 75///X0...alive...1...dead: 1///Assigned.Stage: 3///GRA

OVC.TumorID: 1451///Survival: 132///X0...alive...1...dead: 1///Assigned.Stage: 3///GR

OVC.TumorID: 1504///Survival: 108///X0...alive...1...dead: 1///Assigned.Stage: 3///GF

OVC.TumorID: 1526///Survival: 74///X0...alive...1...dead: 1///Assigned.Stage: 3///GRA

OVC.TumorID: 1552///Survival: 33///X0...alive...1...dead: 1///Assigned.Stage: 3///GRA

OVC.TumorID: 1578///Survival: 33///X0...alive...1...dead: 1///Assigned.Stage: 4///GRA

OVC.TumorID: 1590///Survival: 148///X0...alive...1...dead: 0///Assigned.Stage: 3///GF

OVC.TumorID: 1615///Survival: 13///X0...alive...1...dead: 1///Assigned.Stage: 3///GRA

OVC.TumorID: 1623///Survival: 147///X0...alive...1...dead: 0///Assigned.Stage: 3///GF

OVC.TumorID: 1665///Survival: 15///X0...alive...1...dead: 1///Assigned.Stage: 3///GRA

OVC.TumorID: 1674///Survival: 18///X0...alive...1...dead: 1///Assigned.Stage: 3///GRA

OVC.TumorID: 1675///Survival: 34///X0...alive...1...dead: 1///Assigned.Stage: 3///GRAD

OVC.TumorID: 1774///Survival: 22///X0...alive...1...dead: 1///Assigned.Stage: 3///GRAD

OVC.TumorID: 1784///Survival: 78///X0...alive...1...dead: 1///Assigned.Stage: 3///GRA

OVC.TumorID: 1834///Survival: 118///X0...alive...1...dead: 1///Assigned.Stage: 3///GR

OVC.TumorID: 1846///Survival: 142///X0...alive...1...dead: 0///Assigned.Stage: 3///GF

OVC.TumorID: 1877///Survival: 119///X0...alive...1...dead: 1///Assigned.Stage: 3///GF

OVC.TumorID: 1913///Survival: 32///X0...alive...1...dead: 1///Assigned.Stage: 3///GRA

OVC.TumorID: 1929///Survival: 134///X0...alive...1...dead: 0///Assigned.Stage: 3///GF

OVC.TumorID: 2046///Survival: 127///X0...alive...1...dead: 0///Assigned.Stage: 3///GRAD

OVC.TumorID: 2063///Survival: 16///X0...alive...1...dead: 1///Assigned.Stage: 3///GRAD

OVC.TumorID: 2064///Survival: 27///X0...alive...1...dead: 1///Assigned.Stage: 3///GRADE:

OVC.TumorID: 2075///Survival: 87///X0...alive...1...dead: 1///Assigned.Stage: 3///GR

OVC.TumorID: 2198///Survival: 91///X0...alive...1...dead: 1///Assigned.Stage: 3///GR

OVC.TumorID: 2204///Survival: 118///X0...alive...1...dead: 0///Assigned.Stage: 3///GR

OVC.TumorID: 2324///Survival: 98///X0...alive...1...dead: 1///Assigned.Stage: 3///GR

OVC.TumorID: 2419///Survival: 107///X0...alive...1...dead: 0///Assigned.Stage: 3///GR

OVC.TumorID: 2422///Survival: 20///X0...alive...1...dead: 1///Assigned.Stage: 3///GR

OVC.TumorID: 2424///Survival: 16///X0...alive...1...dead: 1///Assigned.Stage: 3///GRAD

OVC.TumorID: 2465///Survival: 17///X0...alive...1...dead: 1///Assigned.Stage: 3///GRAD

OVC.TumorID: 2476///Survival: 86///X0...alive...1...dead: 1///Assigned.Stage: 3///GRAD

OVC.TumorID: 2479///Survival: 95///X0...alive...1...dead: 0///Assigned.Stage: 3///GRAD

OVC.TumorID: 2505///Survival: 95///X0...alive...1...dead: 0///Assigned.Stage: 3///GR

OVC.TumorID: 2542///Survival: 36///X0...alive...1...dead: 1///Assigned.Stage: 3///GR

OVC.TumorID: 2573///Survival: 7///X0...alive...1...dead: 1///Assigned.Stage: 3///GRADE

OVC.TumorID: 2673///Survival: 74///X0...alive...1...dead: 0///Assigned.Stage: 3///GRAD

OVC.TumorID: 2739///Survival: 67///X0...alive...1...dead: 0///Assigned.Stage: 3///GR

OVC.TumorID: 2802///Survival: 24///X0...alive...1...dead: 1///Assigned.Stage: 3///GR

OVC.TumorID: 2849///Survival: 23///X0...alive...1...dead: 1///Assigned.Stage: 3///GRAD

OVC.TumorID: 2895///Survival: 9///X0...alive...1...dead: 1///Assigned.Stage: 3///GRAD

OVC.TumorID: 2967///Survival: 22///X0...alive...1...dead: 1///Assigned.Stage: 3///GR

OVC.TumorID: 2981///Survival: 6///X0...alive...1...dead: 1///Assigned.Stage: 3///GRAD

OVC.TumorID: 2999///Survival: 16///X0...alive...1...dead: 1///Assigned.Stage: 3///GRAD

OVC.TumorID: 3018///Survival: 16///X0...alive...1...dead: 1///Assigned.Stage: 3///GRADE
OVC.TumorID: 3090///Survival: 16///X0...alive...1...dead: 1///Assigned.Stage: 4///GRADE
OVC.TumorID: 3102///Survival: 10///X0...alive...1...dead: 1///Assigned.Stage: 3///GRADE
OVC.TumorID: 3107///Survival: 31///X0...alive...1...dead: 1///Assigned.Stage: 3///GRADE
OVC.TumorID: 3142///Survival: 18///X0...alive...1...dead: 1///Assigned.Stage: 3///GRADE
OVC.TumorID: 860///Survival: 17///X0...alive...1...dead: 1///Assigned.Stage: 4///GRADE
OVC.TumorID: 872///Survival: 185///X0...alive...1...dead: 0///Assigned.Stage: 3///GRADE
OVC.TumorID: 922///Survival: 183///X0...alive...1...dead: 0///Assigned.Stage: 3///GRADE
OVC.TumorID: D1805///Survival: 9///X0...alive...1...dead: 1///Assigned.Stage: 4///GRADE
OVC.TumorID: D1837///Survival: 83///X0...alive...1...dead: 0///Assigned.Stage: 3///GRADE
OVC.TumorID: D1859///Survival: 110///X0...alive...1...dead: 1///Assigned.Stage: 3///GRADE
OVC.TumorID: D2098///Survival: 42///X0...alive...1...dead: 1///Assigned.Stage: 3///GRADE
OVC.TumorID: D2208///Survival: 2///X0...alive...1...dead: 0///Assigned.Stage: 4///GRADE
OVC.TumorID: D2332///Survival: 27///X0...alive...1...dead: 1///Assigned.Stage: 3///GRADE
OVC.TumorID: D2342///Survival: 20///X0...alive...1...dead: 1///Assigned.Stage: 3///GRADE
OVC.TumorID: D2358///Survival: 9///X0...alive...1...dead: 1///Assigned.Stage: 4///GRADE
OVC.TumorID: D2421///Survival: 12///X0...alive...1...dead: 1///Assigned.Stage: 3///GRADE
OVC.TumorID: D2432///Survival: 34///X0...alive...1...dead: 1///Assigned.Stage: 3///GRADE
OVC.TumorID: D2433///Survival: 49///X0...alive...1...dead: 0///Assigned.Stage: 3///GRADE
OVC.TumorID: D2480///Survival: 34///X0...alive...1...dead: 1///Assigned.Stage: 3///GRADE
OVC.TumorID: D2557///Survival: 62///X0...alive...1...dead: 0///Assigned.Stage: 3///GRADE
OVC.TumorID: D2559///Survival: 5///X0...alive...1...dead: 1///Assigned.Stage: 4///GRADE
OVC.TumorID: D2560///Survival: 91///X0...alive...1...dead: 0///Assigned.Stage: 3///GRADE
OVC.TumorID: D2572///Survival: 37///X0...alive...1...dead: 0///Assigned.Stage: 3///GRADE

OVC.TumorID: D2575///Survival: 33///X0...alive...1...dead: 1///Assigned.Stage: 4///GRADE: 3

OVC.TumorID: D2576///Survival: 17///X0...alive...1...dead: 1///Assigned.Stage: 3///GRADE: 3

OVC.TumorID: D2581///Survival: 63///X0...alive...1...dead: 0///Assigned.Stage: 3///GRADE: 3

OVC.TumorID: D2603///Survival: 42///X0...alive...1...dead: 0///Assigned.Stage: 3///GRADE: 3

OVC.TumorID: D2611///Survival: 2///X0...alive...1...dead: 1///Assigned.Stage: 3///GRADE: 3

OVC.TumorID: D2629///Survival: 36///X0...alive...1...dead: 0///Assigned.Stage: 4///GRADE: 3

OVC.TumorID: D2640///Survival: 1///X0...alive...1...dead: 1///Assigned.Stage: 3///GRADE: 3

OVC.TumorID: D2648///Survival: 35///X0...alive...1...dead: 1///Assigned.Stage: 3///GRADE: 3

OVC.TumorID: D2668///Survival: 40///X0...alive...1...dead: 1///Assigned.Stage: 3///GRADE: 3

OVC.TumorID: D2689///Survival: 45///X0...alive...1...dead: 0///Assigned.Stage: 3///GRADE: 3

OVC.TumorID: D2691///Survival: 63///X0...alive...1...dead: 0///Assigned.Stage: 3///GRADE: 3

OVC.TumorID: D2700///Survival: 74///X0...alive...1...dead: 0///Assigned.Stage: 3///GRADE: 3

OVC.TumorID: D2726///Survival: 71///X0...alive...1...dead: 0///Assigned.Stage: 3///GRADE: 3

OVC.TumorID: D2727///Survival: 53///X0...alive...1...dead: 0///Assigned.Stage: 3///GRADE: 3

OVC.TumorID: D2733///Survival: 55///X0...alive...1...dead: 0///Assigned.Stage: 3///GRADE: 3

OVC.TumorID: D2738///Survival: 68///X0...alive...1...dead: 0///Assigned.Stage: 3///GRADE: 3

OVC.TumorID: D2749///Survival: 24///X0...alive...1...dead: 1///Assigned.Stage: 3///GRADE: 3

OVC.TumorID: D2776///Survival: 10///X0...alive...1...dead: 1///Assigned.Stage: 3///GRADE: 3

OVC.TumorID: D2792///Survival: 16///X0...alive...1...dead: 1///Assigned.Stage: 3///GRADE: 3

OVC.TumorID: M1054///Survival: 101///X0...alive...1...dead: 0///Assigned.Stage: 3///GRADE: 3

OVC.TumorID: M1055///Survival: 13///X0...alive...1...dead: 0///Assigned.Stage: 3///GRADE: 3

OVC.TumorID: M120///Survival: 35///X0...alive...1...dead: 1///Assigned.Stage: 3///GRADE: 3

OVC.TumorID: M1241///Survival: 95///X0...alive...1...dead: 0///Assigned.Stage: 4///GRADE: 3

OVC.TumorID: M1390///Survival: 46///X0...alive...1...dead: 0///Assigned.Stage: 4///GRADE: 3

OVC.TumorID: M1503///Survival: 53///X0...alive...1...dead: 1///Assigned.Stage: 3///GRADE: 2

OVC.TumorID: M1572///Survival: 22///X0...alive...1...dead: 1///Assigned.Stage: 3///GRADE: 3

OVC.TumorID: M17///Survival: 17///X0...alive...1...dead: 0///Assigned.Stage: 4///GRADE: 2 ///

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

OVC.TumorID: M2070///Survival: 65///X0...alive...1...dead: 0///Assigned.Stage: 3///GRADE: 3 /

OVC.TumorID: M2097///Survival: 58///X0...alive...1...dead: 0///Assigned.Stage: 2///GRADE:

OVC.TumorID: M2184///Survival: 34///X0...alive...1...dead: 0///Assigned.Stage: 3///GRADE: 3

Value

An expression set

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

Description

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

Format

```

experimentData(eset):
Experiment data
  Experimenter name: Berchuck A, Iversen ES, Luo J, Clarke JP, Horne H, Levine DA, Boyd J, Alonso MA, Seco
  Laboratory: Berchuck, Lancaster 2009
  Contact information:
  Title: Microarray analysis of early stage serous ovarian cancers shows profiles predictive of favorabl
  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: D1462///NEW.Respo

Tumor: D1805///NEW.Resp

Tumor: D2171///NEW.Respo

Tumor: D2208///NEW.Response: NR///SH

Tumor: D2247///NEW

Tumor: D2332///NEW.

Tumor: D2432///NEW

Tumor: D2480///NEW.

Tumor: D2559///NE

Tumor: D2560///NEW.Response: CR///SHORT.LONG: NA///AgeDx: 60///DateDx: 5/14/1996///Status: 12/9/03, AV

Tumor: D2575///NI

Tumor: D2576///NEW

Tumor: D2611///NE

Tumor: D2629///NEW.Response: NR///SHORT.LO

Tumor: D2640///NEW

Tumor: D2648///NEW

Tumor: D2736///NEW

Tumor: D2749///NEW.Response

Tumor: D2776///NEW.Response

Tumor: D2792///NEW

Tumor: M1025///NEW.Response

Tumor: M1054///NEW.Response

Tumor: M1055///NEW.Response

Tumor: M120///NEW.Response

Tumor: M1241///NEW.Response

Tumor: M1572///NEW.Response

Tumor: M1777///NEW.Response

Tumor: M17///NEW.Response

Tumor: M1891///NEW.Response

Tumor: M2184///NEW.Response

Tumor: M2515///NEW.Response: CR///S

Tumor: M2807///NEW.Response

Tumor: M3035///NEW.Response

Tumor: M337///NEW.Response

Tumor: M3484///NEW.Response

Tumor: M359///NEW.Response

Tumor: M4161///NEW.Response

Tumor: M444///NEW.Response

Tumor: M503///NEW.Respons

Tumor: M5668///NEW.Respon

Tumor: M5775///NEW.Respons

Tumor: M806///NEW.Resp

Value

An expression set

TCGA.RNASeqV2	<i>Integrated genomic analyses of ovarian carcinoma.</i>
---------------	--

Description

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

Format

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

  Abstract: A 179 word abstract is available. Use 'abstract' method.
```

```

Information is available on: preprocessing
notes:
  platform_title:
    [RNASeqV2] Illumina HiSeq RNA sequencing
  platform_shorttitle:
    Illumina HiSeq RNA sequencing
  platform_summary:
    NA
  platform_manufacturer:
    Illumina
  platform_distribution:
    sequencing
  platform_accession:
    NA
  platform_technology:
    RNA sequencing
  version:
    2015-09-22 20:27:26

```

```

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

```

Details

```

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

```

```

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

```

```

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

```

```

alt_sample_name:
TCGA-04-1348-01A-01R-1565-13 TCGA-04-1357-01A-01R-1565-13
                                1                                1
TCGA-04-1362-01A-01R-1565-13 TCGA-04-1364-01A-01R-1565-13
                                1                                1
TCGA-04-1365-01A-01R-1565-13 TCGA-04-1514-01A-01R-1566-13
                                1                                1
TCGA-04-1519-01A-01R-1565-13 TCGA-09-0364-01A-02R-1564-13

```

TCGA-09-0366-01A-01R-1564-13	1	TCGA-09-0367-01A-01R-1564-13	1
TCGA-09-0369-01A-01R-1564-13	1	TCGA-09-1662-01A-01R-1566-13	1
TCGA-09-1666-01A-01R-1566-13	1	TCGA-09-1667-01C-01R-1566-13	1
TCGA-09-1668-01B-01R-1566-13	1	TCGA-09-1669-01A-01R-1566-13	1
TCGA-09-1670-01A-01R-1566-13	1	TCGA-09-1673-01A-01R-1566-13	1
TCGA-09-1674-01A-01R-1566-13	1	TCGA-09-2044-01B-01R-1568-13	1
TCGA-09-2045-01A-01R-1568-13	1	TCGA-09-2048-01A-01R-1568-13	1
TCGA-09-2051-01A-01R-1568-13	1	TCGA-09-2054-01A-01R-1568-13	1
TCGA-09-2056-01B-01R-1568-13	1	TCGA-10-0928-01A-02R-1564-13	1
TCGA-10-0936-01A-01R-1564-13	1	TCGA-13-0730-01A-01R-1564-13	1
TCGA-13-0799-01A-01R-1564-13	1	TCGA-13-0800-01A-01R-1564-13	1
TCGA-13-0801-01A-01R-1564-13	1	TCGA-13-0890-01A-01R-1564-13	1
TCGA-13-0893-01B-01R-1565-13	1	TCGA-13-0897-01A-01R-1564-13	1
TCGA-13-0899-01A-01R-1564-13	1	TCGA-13-0913-01A-01R-1564-13	1
TCGA-13-0916-01A-01R-1564-13	1	TCGA-13-0920-01A-01R-1564-13	1
TCGA-13-0924-01A-01R-1564-13	1	TCGA-13-1403-01A-01R-1565-13	1
TCGA-13-1405-01A-01R-1565-13	1	TCGA-13-1410-01A-01R-1565-13	1
TCGA-13-1481-01A-01R-1565-13	1	TCGA-13-1497-01A-01R-1565-13	1
TCGA-13-1498-01A-01R-1565-13	1	TCGA-13-1505-01A-01R-1565-13	1
TCGA-13-1506-01A-01R-1565-13	1	TCGA-13-1507-01A-01R-1565-13	1
TCGA-13-1511-01A-01R-1565-13	1	TCGA-13-1512-01A-01R-1565-13	1
TCGA-13-2060-01A-01R-1568-13	1	TCGA-20-1682-01A-01R-1564-13	1
TCGA-20-1683-01A-01R-1566-13	1	TCGA-20-1684-01A-01R-1566-13	1
TCGA-20-1685-01A-01R-1566-13	1	TCGA-20-1687-01A-01R-1566-13	1

	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
TCGA-23-1109-01A-01R-1564-13	TCGA-23-1111-01A-01R-1567-13	
	1	1
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	
	1	1
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	
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TCGA-24-1413-01A-01R-1565-13	TCGA-24-1416-01A-01R-1565-13	
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	1	1
TCGA-24-1544-01A-01R-1566-13	TCGA-24-1548-01A-01R-1566-13	
	1	1
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TCGA-24-1551-01A-01R-1566-13	TCGA-24-1552-01A-01R-1566-13	
	1	1
TCGA-24-1553-01A-01R-1566-13	TCGA-24-1555-01A-01R-1566-13	
	1	1
TCGA-24-1556-01A-01R-1566-13	TCGA-24-1557-01A-01R-1566-13	
	1	1
TCGA-24-1558-01A-01R-1566-13	TCGA-24-1560-01A-01R-1566-13	
	1	1
TCGA-24-1562-01A-01R-1566-13	(Other)	
	1	162

unique_patient_ID:

TCGA-04-1348 TCGA-04-1357 TCGA-04-1362 TCGA-04-1364 TCGA-04-1365 TCGA-04-1514

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

sample_type:

tumor

261

histological_type:

ser

261

primarysite:

other ov

1 260

summarygrade:

high low NA's

226 29 6

summarystage:

early late NA's

18 242 1

tumorstage:

2 3 4 NA's

18 209 33 1

substage:

b c NA's

16 211 34

grade:

1 2 3 4 NA's

1 28 225 1 6

age_at_initial_pathologic_diagnosis:

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

pltx:

n y NA's

17 215 29

tax:

n y NA's

17 215 29

neo:

n NA's

232 29

days_to_tumor_recurrence:

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

recurrence_status:

norecurrence recurrence

123 138

days_to_death:

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

vital_status:

deceased living NA's


```
age_at_initial_pathologic_diagnosis: 43///anatomic_organ_subdivision:
age_at_initial_pathologic_diagnosis: 43///anatomic_organ_subdivision:
age_at_initial_pathologic_diagnosis: 43///anatomic_organ_subdivision:
age_at_initial_pathologic_diagnosis: 44///anatomic_organ_subdivision:
age_at_initial_pathologic_diagnosis: 44///anatomic_organ_subdivision:
age_at_initial_pathologic_diagnosis: 44///anatomic_organ_subdivision:
age_at_initial_pathologic_diagnosis: 44///anatomic_organ_subdivision:
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age_at_initial_pathologic_diagnosis: 45///anatomic_organ_subdivision:
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age_at_initial_pathologic_diagnosis: 45///anatomic_organ_subdivision: Bilateral//
age_at_initial_pathologic_diagnosis: 45///anatomic_organ_subdivision: Right///bcr_patient_u
age_at_initial_pathologic_diagnosis: 46///anatomic_organ_subdivision: Bilateral///bcr_patient_u
```

age_at_in
age_at_initial_pathologic_diagnos
age_at_initial_pathologic_diagnosis: 47///anatomic_organ_subdivision: E
age_at_initial_pathologic_diagnosis: 47///anatomic_organ_subdivision
age_at_initial_pathologic_diagnosis: 47///anatomic_organ_subdivision: Bilatera
age_at_initial_pathologic_diagnosis: 47///anatomic_organ
age_at_initial_pathologic_diagnosis: 47///anatomic_organ_subdivision: NA///bcr_pa
age_at_initial_pathologic_di
age_at_initial_pathologic_diagnosis: 48///an
age_at_initial_patho
age_at_initial_pathologic_diagnosis: 48///anatomic_organ_subdivision: NA///
age_at_initial_pathologic
age_at_initial_pathologic
age_at_initial_pathologic_diagnosis: 49///a
age_at_initial_pathologic_diagnosis: 49///anatom
age_at_initial_pathologic_diagnosis: 49///anato
age_at_initial_pathologic_diagnosis: 49///anatomic_organ_subdivi
age_at_initial_pathologic_diagnosis: 49///anatomic_o
age_at_initial_pathologic_diagnosis: 49///anatomic_organ_subdivision: Left///b
age_at_initial_pathologic_diagnosi
age_at_initial_pathologic_diagnosis: 50///anatomic_organ_subdivision: Bilateral///b
age_at_initial_pathologi
age_at_initial_pathologic_diagnosis: 50///anatomic_organ_subdivisi

```
age_at_initial_pathologic_diagnosis: 50///anatomic_organ_subdivision: Left///bcr_patient_uuid: 9c74d8e6-4f31-4901-a012-333333333333
age_at_initial_pathologic_diagnosis: 50///anatomic_organ_subdivision: NA///bcr_patient_uuid: 9c74d8e6-4f31-4901-a012-333333333333
age_at_initial_pathologic_diagnosis: 51///anatomic_organ_subdivision: Bilateral///bcr_patient_uuid: 9c74d8e6-4f31-4901-a012-333333333333
age_at_initial_pathologic_diagnosis: 51///anatomic_organ_subdivision: Bilateral///bcr_patient_uuid: 9c74d8e6-4f31-4901-a012-333333333333
age_at_initial_pathologic_diagnosis: 51///anatomic_organ_subdivision: Bilateral///bcr_patient_uuid: 9c74d8e6-4f31-4901-a012-333333333333
age_at_initial_pathologic_diagnosis: 51///anatomic_organ_subdivision: Bilateral///bcr_patient_uuid: 9c74d8e6-4f31-4901-a012-333333333333
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Value

An expression set

TCGAOVARIAN	<i>Integrated genomic analyses of ovarian carcinoma.</i>
-------------	--

Description

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

Format

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

Abstract: A 179 word abstract is available. Use 'abstract' method.
Information is available on: preprocessing
notes:
  platform_title:
    [HT_HG-U133A] Affymetrix HT Human Genome U133A Array
  platform_shorttitle:
    Affymetrix HT_HG-U133A
  platform_summary:
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  platform_manufacturer:
    Affymetrix
  platform_distribution:
    commercial
  platform_accession:
    GPL3921
  warnings:
    The following samples are likely from specimens also used in GSE26712: TCG
    A.13.0725, TCGA.13.0885, TCGA.13.0887, TCGA.13.0890, TCGA.13.0886, TCGA.13
    .0714, TCGA.13.0727, TCGA.13.1817, TCGA.13.1499, TCGA.13.0883
  version:
    2015-09-22 20:25:15
```

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

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

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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	metastasis	NA's
153	3		
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
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duplicates:
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578 character character

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