Package 'MetaGxOvarian'

December 10, 2024

Type Package **Title** Transcriptomic Ovarian Cancer Datasets **Version** 1.27.0 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 git_url https://git.bioconductor.org/packages/MetaGxOvarian git_branch devel git_last_commit 7e4535f git_last_commit_date 2024-10-29 Repository Bioconductor 3.21 **Date/Publication** 2024-12-10 Author Michael Zon [aut], Vandana Sandhu [aut], Christopher Eeles [ctb], Benjamin Haibe-Kains [aut, cre] Maintainer Benjamin Haibe-Kains

benjamin.haibe.kains@utoronto.ca> 2 attention

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PMID17290060
PMID19318476
TCGA.RNASeqV2
TCGAOVARIAN

attention

days_to_death

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.

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duplicates	a list containing the names of patients that are believed to be dulicates
	across datasets

Description

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

Format

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

E.MTAB.386	Angiogenic mRNA and microRNA gene expression signature predicts
	a novel subtype of serous ovarian cancer.

Description

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

Format

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

```
URL:
    PMIDs: 22348002
    Abstract: A 212 word abstract is available. Use 'abstract' method.
    Information is available on: preprocessing
    notes:
     platform_title:
        Illumina humanRef-8 v2.0 expression beadchip
     platform shorttitle:
        Illumina humanRef-8 v2.0
     platform_summary:
        illuminaHumanv2
     platform_manufacturer:
        Illumina
     platform_distribution:
        commercial
     platform_accession:
        GPL6104
     version:
        2015-09-22 19:06:44
   featureData(eset):
  An object of class 'AnnotatedDataFrame'
    featureNames: ILMN_1343291 ILMN_1651228 ... ILMN_1815951 (12449
      total)
    varLabels: probeset gene EntrezGene.ID best_probe
    varMetadata: labelDescription
Details
  assayData: 12449 features, 129 samples
  Platform type:
  Overall survival time-to-event summary (in years):
  Call: survfit(formula = Surv(time, cens) ~ -1)
        n events median 0.95LCL 0.95UCL
   129.00 73.00 3.51 2.68 4.13
   _____
  Available sample meta-data:
  unique_patient_ID:
    DFCI.1 DFCI.10 DFCI.100 DFCI.101 DFCI.102 DFCI.103 DFCI.104 DFCI.105
            DFCI.106 DFCI.107 DFCI.108 DFCI.109 DFCI.11 DFCI.110 DFCI.111 DFCI.112
                1 1
                                1
                                        1
  DFCI.113 DFCI.114 DFCI.115 DFCI.116 DFCI.117 DFCI.118 DFCI.119 DFCI.12
```

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```
1
                    1
                       1
                               1
DFCI.120 DFCI.121 DFCI.122 DFCI.123 DFCI.124 DFCI.125 DFCI.126 DFCI.127
   DFCI.128 DFCI.129 DFCI.13 DFCI.130 DFCI.131 DFCI.132 DFCI.14 DFCI.15
   1 1
           1 1 1 1
DFCI.16 DFCI.17 DFCI.18 DFCI.19 DFCI.2 DFCI.20 DFCI.21 DFCI.22
   DFCI.23 DFCI.24 DFCI.25 DFCI.26 DFCI.27 DFCI.28 DFCI.29 DFCI.3
      1 1 1 1 1 1
DFCI.30 DFCI.31 DFCI.32 DFCI.33 DFCI.34 DFCI.35 DFCI.36 DFCI.37
    DFCI.38 DFCI.39 DFCI.4 DFCI.40 DFCI.41 DFCI.42 DFCI.44 DFCI.45
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                 1
                      1
    1
      1
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                                           1
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   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
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
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-1

Source.Name: DFCI-103//

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Source.Name: DFCI-105///Ch

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Source.Name: DFCI-107///

Source.Name: DFCI-108///

Source.Name: DFCI-109///Ch

Source.Name: DFCI-10,

Source.Name: DFCI-110//

Source.Name: DFCI-111///Ch

Source.Name: DFCI-112///

Source.Name: DFCI-113//

Source.Name: DFCI-11

Source.Name: DFCI-115///0

Source.Name: DFCI-116///Ch

Source.Name: DFCI-117/

```
Source.Name: DFCI-119///
                                                             Source.Name: DFCI-11//
  Source.Name: DFCI-120///Characteristics.Age.: Age <has_measurement <Measurement
                                                             Source.Name: DFCI-121/
                                                                Source.Name: DFCI-12
                                                           Source.Name: DFCI-123///0
                                                             Source.Name: DFCI-124/
                                                              Source.Name: DFCI-125/
                                                                 Source.Name: DFCI-1
     Source.Name: DFCI-127///Characteristics.Age.: Age <has_measurement <Measurement
                                                             Source.Name: DFCI-128/
  Source.Name: DFCI-129///Characteristics.Age.: Age <has_measurement <Measurement
                                                              Source.Name: DFCI-12/
Source.Name: DFCI-130///Characteristics.Age.: Age <has_measurement <Measurement <ha
      Source.Name: DFCI-131///Characteristics.Age.: Age <has_measurement <Measurement
Source.Name: DFCI-132///Characteristics.Age.: Age <has_measurement <Measurement <h
                                                              Source.Name: DFCI-13/
                                                               Source.Name: DFCI-14/
                                                                  Source.Name: DFCI-
```

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Source.Name: DFC

Source.Name: DFCI-17/

Source.Name: DFCI-18/

Source.Name: DFCI-19/

Source.Name: DE

Source.Name: DFCI-20/

Source.Name: DFCI-

Source.Name: DFCI-22///Characteristics.Age.: Age <has_measurement <Measurement

Source.Name: DFCI-23///

Source.Name: DFCI-24///Ch

Source.Name: DFCI-25///

Source.Name: DFCI-20

Source.Name: DFCI-27/

Source.Name: DFCI-2

Source.Name: DFCI-29/

Source.Name: DFCI-2

Source.Name: DFCI-30

Source.Name: DFCI-31/

Source.Name: DFCI-32

Source.Name: DFCI-33,

Source.Name: DFCI-34/

Source.Name: DFCI-35/

Source.Name: DFCI-

Source.Name: DFCI-37/

Source.Name: DFCI-38///
Source.Name: DFCI-39///
Source.Name: DFCI-

Source.Name: DFCI-41,

Source.Name: DFCI-40/

Source.Name: DFCI-42,

Source.Name: DFCI-44,

Source.Name: DFCI-

Source.Name: DFCI-46/

Source.Name: DFCI-47,

Source.Name: DFCI-

Source.Name: DFCI-49

Source.Name: DFCI-

Source.Name: DFCI-50,

Source.Name: DFCI-51//

Source.Name: DFCI-52/

Source.Name: DFCI-53///

Source.Name: DFCI-54//

Source.Name: DFCI-55/

Source.Name: DFCI-56///

Source.Name: DFCI-57/

Source.Name: DFCI-58,

Source.Name: DFCI-59

Source.Name: DFCI-60

Source.Name: DFCI-6

Source.Name: DFCI-62///Characteristics.Age.: Age <has_measurement <Measurement

Source.Name: DFCI-6

Source.Name: DFCI-64

Source.Name: DFCI-65//

Source.Name: DFCI-6

Source.Name: DFCI-

Source.Name: DFCI-68/

Source.Name: DFCI-69/

Source.Name: DF0

Source.Name: DFCI-70,

Source.Name: DFCI-71

Value

An expression set

GSE12418

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

Description

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

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

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Partheen K, Levan K, Osterberg L, Horvath G. Expression analysis
  Laboratory: Partheen, Horvath 2006
  Contact information:
  Title: Expression analysis of stage III serous ovarian adenocarcinoma distinguish
  URL:
  PMIDs: 16996261
  Abstract: A 177 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
  platform_title:
      SWEGENE H_v2.1.1_27k
  platform_shorttitle:
      SWEGENE H_v2.1.1_27k
   platform_summary:
      PartheenMetaData
   platform_manufacturer:
      other
   platform_distribution:
      non-commercial
   platform_accession:
      GPL5886
   version:
      2015-09-22 19:07:14
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 28 29 ... 29999 (11304 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

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

```
alt_sample_name:
1035LA0 1047LB 1059LB0 1177DB 1178LB0 1180DB 1186DB0 123DC 1242LC0 1274LC
                       1 1
             1
       1
                                    1 1
                                              1 1
                                                           1
 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
                                  47DC 480DC0
 452DC
       454LC
              45LA0
                    462DB
                           46LB0
                                              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
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.
 35.00 51.25 59.50 59.56 69.75
                                  84.00
pltx:
У
54
os_binary:
```

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```
long short
   20
         34
debulking:
   optimal suboptimal
        13
uncurated author metadata:
title: 1035LA0///geo_accession: GSM311973///status: Public on Aug 12 2008///submiss
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title: 1178LB0///geo_accession: GSM311977///status: Public on Aug 12 2008///submiss
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 title: 1574LC0///geo_accession: GSM311988///status: Public on Aug 12 2008///submis
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```

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           title: 272DC///geo_accession: GSM311952///status: Public on Aug 12 200
   title: 405LB///geo_accession: GSM311953///status: Public on Aug 12 2008///subr
           title: 436DC///geo_accession: GSM311954///status: Public on Aug 12 200
           title: 452DC///geo_accession: GSM311955///status: Public on Aug 12 200
    title: 454LC///geo_accession: GSM311956///status: Public on Aug 12 2008///suk
title: 45LAO///geo_accession: GSM311939///status: Public on Aug 12 2008///submiss
          title: 462DB///geo_accession: GSM311957///status: Public on Aug 12 2008
title: 46LB0///geo_accession: GSM311940///status: Public on Aug 12 2008///submiss
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       title: 480DC0///geo_accession: GSM311958///status: Public on Aug 12 2008/
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           title: 626DC///geo_accession: GSM311964///status: Public on Aug 12 200
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```

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

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

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```
title: 719DC///geo_accession: GSM311966///status: Public on Aug 12 2008///submissed title: 742LCO///geo_accession: GSM311967///status: Public on Aug 12 2008///submissed title: 755LC///geo_accession: GSM311968///status: Public on Aug 12 2008///submissed title: 759DC///geo_accession: GSM311969///status: Public on Aug 12 2008///submissed title: 76DC///geo_accession: GSM311942///status: Public on Aug 12 2008///submissed title: 83LC///geo_accession: GSM311970///status: Public on Aug 12 2008///submissed title: 918DBO///geo_accession: GSM311971///status: Public on Aug 12 2008///submissed title: 99LCO///geo_accession: GSM311972///status: Public on Aug 12 2008///submissed title: 99LCO///geo_accession: GSM311944///status: Public on Aug 12 2008///submissed title: 99LCO///geo_accession:
```

Value

An expression set

GSE12470

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

Description

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

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

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Yoshihara K, Tajima A, Komata D, Yamamoto T, Kodama S, Fujiwan
  Laboratory: Yoshihara, Tanaka 2009
  Contact information:
  Title: Gene expression profiling of advanced-stage serous ovarian cancers disting
  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:
      hquq4110b
   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:
```

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

1

Peritoneum normal 21

Peritoneum normal 3

Peritoneum normal 18

Peritoneum normal 23

```
Peritoneum normal 30
                                                Peritoneum normal 4
              Peritoneum normal 7
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healthy
        tumor
     10
           43
histological_type:
 ser NA's
  43
     10
primarysite:
ΟV
53
summarystage:
early late NA's
    8
        35
tumorstage:
   1 NA's
   8 45
uncurated_author_metadata:
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title: Advanced serous ovarian cancer 27///geo_accession: GSM312158///status: Puk

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   title: Early serous ovarian cancer 32///geo_accession: GSM312181///status:
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      title: Early serous ovarian cancer 5///geo_accession: GSM312176///status
   title: Early serous ovarian cancer 65///geo_accession: GSM312185///status:
      title: Early serous ovarian cancer 8///geo_accession: GSM312178///status
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                                  title: Peritoneum normal 23///geo_accession:
                                    title: Peritoneum normal 30///geo_accession
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                                       title: Peritoneum normal 7///geo_access
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GSE13876 21

Value

An expression set

GSE13876

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

Description

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

Format

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

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

GSE13876 23

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: 2 3 4 NA's 1 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 uncurated_author_metadata:

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

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

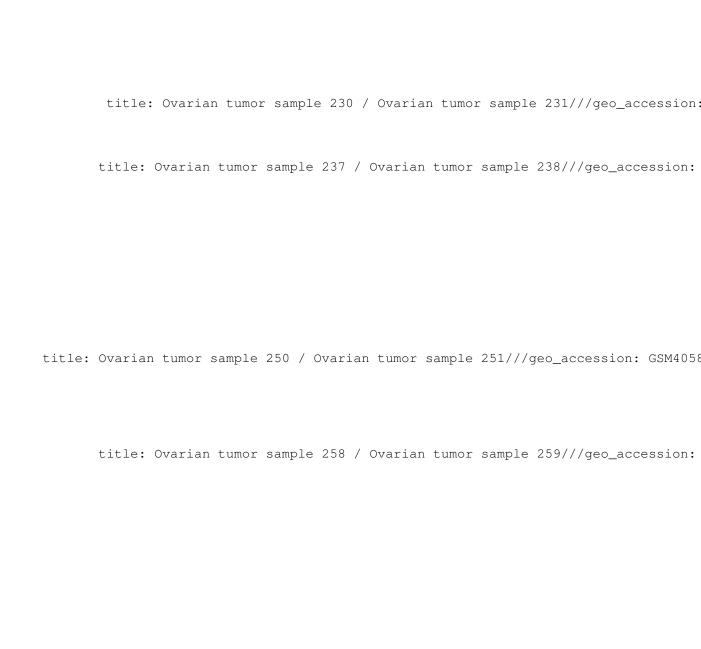
title: Ovarian tumor sample 111 / Ovarian tumor sample 112///geo_accession:
title: Ovarian tumor sample 115 / Ovarian tumor sample 117///geo_accession:

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

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

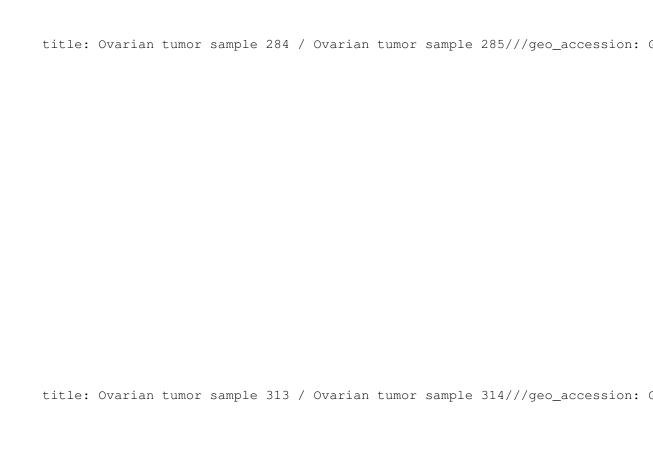
GSE13876 25





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

GSE13876 27



Value

An expression set

GSE14764

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

Description

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

Format

```
experimentData(eset):
Experiment data

Experimenter name: Denkert C, Budczies J, Darb-Esfahani S, Gy??rffy B et al. A production Laboratory: Denkert, Lage 2009

Contact information:

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

GSE14764 29

```
platform_summary:
        hgu133a
     platform_manufacturer:
        Affymetrix
     platform_distribution:
        commercial
     platform_accession:
        GPL96
     version:
        2015-09-22 19:13:08
  featureData(eset):
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      (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)
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                  4.52 4.19 NA
    _____
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                                         Max.
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                                          80.00
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     80
  histological_type:
         clearcell
                             endo
                                              mix
                                                            other
                               6
                                               1
              ser undifferentiated
  primarysite:
  OV
```

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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
days_to_death:
  Min. 1st Qu. Median Mean 3rd Qu. Max.
   210 660 1050 1011 1328
                                    2190
vital_status:
deceased living
   21 59
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
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2006-08-21
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GSE14764 31

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GSE14764 33

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NA's 78

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duplicates:
GSE14764_GSM368667 GSE14764_GSE14764_GSM368668

1
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title: ovarian cancer: 079///qeo_accession: GSM368739///status: Puk

Value

An expression set

GSE17260

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

Description

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

GSE17260 35

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

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Yoshihara K, Tajima A, Yahata T, Kodama S, Fujiwara H, Suzuki
  Laboratory: Yoshihara, Tanaka 2010
  Contact information:
  Title: Gene expression profile for predicting survival in advanced-stage serous
  URL:
  PMIDs: 20300634
  Abstract: A 257 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
  platform_title:
      Agilent-012391 Whole Human Genome Oligo Microarray G4112A
   platform_shorttitle:
      Agilent G4112A
   platform_summary:
      hgug4112a
   platform_manufacturer:
      Agilent
   platform_distribution:
      commercial
   platform_accession:
      GPL6848
   version:
      2015-09-22 19:16:49
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A_23_P100001 A_23_P100011 ... A_32_P99902 (30936 total)
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  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
```

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Serous ovarian cancer 109 Serous ovarian cancer 11 Serous ovarian cancer 110
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Serous ovarian cancer 12 Serous ovarian cancer 120 Serous ovarian cancer 122
Serous ovarian cancer 123 Serous ovarian cancer 127 Serous ovarian cancer 129
Serous ovarian cancer 130 Serous ovarian cancer 131 Serous ovarian cancer 132
Serous ovarian cancer 134 Serous ovarian cancer 136 Serous ovarian cancer 137
                       1
Serous ovarian cancer 139 Serous ovarian cancer 140 Serous ovarian cancer 143
Serous ovarian cancer 144 Serous ovarian cancer 145 Serous ovarian cancer 146
Serous ovarian cancer 148 Serous ovarian cancer 149 Serous ovarian cancer 15
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Serous ovarian cancer 156 Serous ovarian cancer 157 Serous ovarian cancer 16
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Serous ovarian cancer 176 Serous ovarian cancer 178 Serous ovarian cancer 18
Serous ovarian cancer 182 Serous ovarian cancer 183 Serous ovarian cancer 184
Serous ovarian cancer 185 Serous ovarian cancer 186
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Serous ovarian cancer 25 Serous ovarian cancer 27 Serous ovarian cancer 31
```

```
Serous ovarian cancer 36
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                                                      Serous ovarian cancer 38
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                           Serous ovarian cancer 41
                                                      Serous ovarian cancer 42
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                           Serous ovarian cancer 44
                                                      Serous ovarian cancer 45
 Serous ovarian cancer 49
                           Serous ovarian cancer 50
                                                      Serous ovarian cancer 51
 Serous ovarian cancer 52
                           Serous ovarian cancer 53
                                                      Serous ovarian cancer 54
                                                                              1
 Serous ovarian cancer 55
                           Serous ovarian cancer 56
                                                      Serous ovarian cancer 57
                                                                              1
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                                                                              1
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                                                      Serous ovarian cancer 72
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 Serous ovarian cancer 77
                           Serous ovarian cancer 79
                                                      Serous ovarian cancer 80
                                                                              1
                   (Other)
                       11
sample_type:
tumor
  110
histological_type:
ser
110
primarysite:
OV
110
summarygrade:
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high low 43

late 110

> 3 4

67

summarystage:

tumorstage:

```
93 17
substage:
         c NA's
  a b
     18
         69 17
grade:
1 2 3
26 41 43
pltx:
 У
110
tax:
 У
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
days_to_death:
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    30 660 915 1086 1530
                                      2430
vital_status:
deceased living
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debulking:
  optimal suboptimal
      57 53
uncurated_author_metadata:
                         title: Serous ovarian cancer 100///geo_accession: GSM43
                     title: Serous ovarian cancer 104///geo_accession: GSM432222
title: Serous ovarian cancer 106///geo_accession: GSM432223///status: Public on Man
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title: Serous ovarian cancer 107///geo_accession: GSM432224

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

GSE17260 39

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                             title: Serous ovarian cancer 10///geo_accession: GSM43
title: Serous ovarian cancer 110///geo_accession: GSM432228///status: Public on Man
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                            title: Serous ovarian cancer 112///geo_accession: GSM43
                        title: Serous ovarian cancer 113///geo_accession: GSM432231
                         title: Serous ovarian cancer 114///geo_accession: GSM43223
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    title: Serous ovarian cancer 149///geo_accession: GSM43
title: Serous ovarian cancer 150///geo_accession: GSM432260
   title: Serous ovarian cancer 151///geo_accession: GSM43
     title: Serous ovarian cancer 154///geo_accession: GSM
    title: Serous ovarian cancer 156///geo_accession: GSM43
    title: Serous ovarian cancer 157///geo_accession: GSM43
    title: Serous ovarian cancer 15///geo_accession: GSM43
title: Serous ovarian cancer 160///geo_accession: GSM432260
     title: Serous ovarian cancer 16///geo_accession: GSM43
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      title: Serous ovarian cancer 174///geo_accession: GSM
   title: Serous ovarian cancer 176///geo_accession: GSM432
      title: Serous ovarian cancer 178///geo_accession: GSN
     title: Serous ovarian cancer 17///geo_accession: GSM43
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GSE17260 41

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  title: Serous ovarian cancer 2///geo_accession: GSM432280
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       title: Serous ovarian cancer 36///geo_accession: GSN
     title: Serous ovarian cancer 37///geo_accession: GSM43
     title: Serous ovarian cancer 38///geo_accession: GSM43
     title: Serous ovarian cancer 41///geo_accession: GSM43
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   title: Serous ovarian cancer 4///geo_accession: GSM43229
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title: Serous ovarian cancer 50///geo_accession: GSM4

```
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   title: Serous ovarian cancer 54///geo_accession: GSM43
   title: Serous ovarian cancer 55///geo_accession: GSM43
title: Serous ovarian cancer 56///geo_accession: GSM432303
    title: Serous ovarian cancer 57///geo_accession: GSM43
   title: Serous ovarian cancer 58///geo_accession: GSM43
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    title: Serous ovarian cancer 68///geo_accession: GSM43
    title: Serous ovarian cancer 69///geo_accession: GSM43
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    title: Serous ovarian cancer 7///geo_accession: GSM43
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title: Serous ovarian cancer 80///geo_accession: GSM432319

title: Serous ovarian cancer 51///geo_accession: GSM432298

GSE18520 43

Value

An expression set

GSE18520

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

Description

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

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Mok SC, Bonome T, Vathipadiekal V, Bell A, Johnson ME, Wong KF
  Laboratory: Mok, Birrer 2009
  Contact information:
  Title: A gene signature predictive for outcome in advanced ovarian cancer identified
  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:
  ΟV
  63
  summarygrade:
  high NA's
   53 10
  summarystage:
  late NA's
```

53 10

GSE18520 45

```
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
2004 - 03 - 12 \ 2004 - 04 - 08 \ 2004 - 04 - 09 \ 2004 - 07 - 20 \ 2004 - 08 - 12 \ 2004 - 08 - 13 \ 2004 - 09 - 30
        20 6 9 11 10 1 6
uncurated_author_metadata:
                                                 title: Normal Ovary, 2008///geo_acc
                                                 title: Normal Ovary, 2061///geo_acc
                                                 title: Normal Ovary, 2064///geo_acc
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title: Normal Ovary, 2085///geo_acc

title: Normal Ovary, 2225///geo_acc

title: Normal Ovary, 2226///geo_acc

```
title: Normal Ovary, 2230///geo_acc
                                                title: Normal Ovary, 2234///geo_acc
                                                title: Normal Ovary, 2237///geo_acc
title: Ovarian Tumor, 1109///geo_accession: GSM461390///status: Public on Oct 17 20
    title: Ovarian Tumor, 1214///geo_accession: GSM461391///status: Public on Oct 1
    title: Ovarian Tumor, 1231///geo_accession: GSM461367///status: Public on Oct 1
title: Ovarian Tumor, 1562///geo_accession: GSM461368///status: Public on Oct 17 20
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title: Ovarian Tumor, 1993///geo_accession: GSM461400///status: Public on Oct 17 20
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title: Normal Ovary, 2228///geo_acc

GSE18520 47

```
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      title: Ovarian Tumor, 402///geo_accession: GSM461355///status: Public on Oct
title: Ovarian Tumor, 410///geo_accession: GSM461356///status: Public on Oct 17 20
    title: Ovarian Tumor, 412///geo_accession: GSM461357///status: Public on Oct 1
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     title: Ovarian Tumor, 477///geo_accession: GSM461383///status: Public on Oct
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 title: Ovarian Tumor, 629///geo_accession: GSM461360///status: Public on Oct 17 2
     title: Ovarian Tumor, 631///geo_accession: GSM461396///status: Public on Oct
     title: Ovarian Tumor, 656///geo_accession: GSM461384///status: Public on Oct
     title: Ovarian Tumor, 662///geo_accession: GSM461370///status: Public on Oct
     title: Ovarian Tumor, 692///geo_accession: GSM461397///status: Public on Oct
     title: Ovarian Tumor, 694///geo_accession: GSM461385///status: Public on Oct
     title: Ovarian Tumor, 702///geo_accession: GSM461361///status: Public on Oct
     title: Ovarian Tumor, 714///geo_accession: GSM461362///status: Public on Oct
     title: Ovarian Tumor, 715///geo_accession: GSM461386///status: Public on Oct
     title: Ovarian Tumor, 718///geo_accession: GSM461398///status: Public on Oct
     title: Ovarian Tumor, 744///geo_accession: GSM461378///status: Public on Oct
     title: Ovarian Tumor, 765///geo_accession: GSM461363///status: Public on Oct
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     title: Ovarian Tumor, 786///geo_accession: GSM461387///status: Public on Oct 17 2
         title: Ovarian Tumor, 794///geo_accession: GSM461388///status: Public on Oct
          title: Ovarian Tumor, 799///geo_accession: GSM461365///status: Public on Oct
         title: Ovarian Tumor, 800///geo_accession: GSM461371///status: Public on Oct
          title: Ovarian Tumor, 872///geo_accession: GSM461366///status: Public on Oct
     title: Ovarian Tumor, 934///geo_accession: GSM461372///status: Public on Oct 17 2
         title: Ovarian Tumor, 970///geo_accession: GSM461389///status: Public on Oct
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                                  GSE18520.GSE18520 GSM462649
   GSE18520.GSE18520_GSM462649///GSE18520.GSE18520_GSM462650
                                  GSE18520.GSE18520 GSM462650
                                                          NA's
                                                            60
Value
   An expression set
 GSE19829
                      Gene expression profile of BRCAness that correlates with respon-
```

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

ovarian cancer.

siveness to chemotherapy and with outcome in patients with epithelial

GSE19829 49

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

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Konstantinopoulos PA, Spentzos D, Karlan BY, Taniguchi T et al
 Laboratory: Konstantinopoulos, Cannistra 2010 hqu95
  Contact information:
  Title: Gene expression profile of BRCAness that correlates with responsiveness to
  HRT. .
  PMIDs: 20547991
 Abstract: A 241 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
  platform_title:
      [HG_U95Av2] Affymetrix Human Genome U95 Version 2 Array
  platform shorttitle:
      Affymetrix HG_U95Av2
  platform_summary:
      hgu95av2
  platform_manufacturer:
      Affymetrix
  platform distribution:
      commercial
  platform_accession:
      GPL570 | GPL8300
   version:
      2015-09-22 19:26:29
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-MurIL4_at (54253 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 54253 features, 70 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)
      n events median 0.95LCL 0.95UCL
         40.00 3.78 2.96 5.92
  70.00
Available sample meta-data:
alt_sample_name:
 Ovarian cancer_sample 1 Ovarian cancer_sample 10 Ovarian cancer_sample 11
Ovarian cancer_sample 12 Ovarian cancer_sample 13 Ovarian cancer_sample 14
Ovarian cancer_sample 15 Ovarian cancer_sample 16 Ovarian cancer_sample 17
Ovarian cancer_sample 18 Ovarian cancer_sample 19 Ovarian cancer_sample 2
Ovarian cancer_sample 20 Ovarian cancer_sample 21 Ovarian cancer_sample 22
Ovarian cancer_sample 23 Ovarian cancer_sample 24 Ovarian cancer_sample 25
Ovarian cancer_sample 26 Ovarian cancer_sample 27 Ovarian cancer_sample 28
Ovarian cancer_sample 29 Ovarian cancer_sample 3 Ovarian cancer_sample 30
Ovarian cancer_sample 31 Ovarian cancer_sample 32 Ovarian cancer_sample 33
Ovarian cancer_sample 34 Ovarian cancer_sample 35 Ovarian cancer_sample 36
Ovarian cancer_sample 37 Ovarian cancer_sample 38 Ovarian cancer_sample 39
Ovarian cancer_sample 4 Ovarian cancer_sample 40 Ovarian cancer_sample 41
                                                1
Ovarian cancer_sample 42 Ovarian cancer_sample 43 Ovarian cancer_sample 44
Ovarian cancer_sample 45 Ovarian cancer_sample 46 Ovarian cancer_sample 47
Ovarian cancer_sample 48 Ovarian cancer_sample 49 Ovarian cancer_sample 5
                                                1
Ovarian cancer_sample 50 Ovarian cancer_sample 51 Ovarian cancer_sample 52
```

GSE19829 51

Ovarian cancer_sample 53 Ovarian cancer_sample 54 Ovarian cancer_sample 55

```
Ovarian cancer_sample 56 Ovarian cancer_sample 57 Ovarian cancer_sample 58
Ovarian cancer_sample 59 Ovarian cancer_sample 6 Ovarian cancer_sample 60
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Ovarian cancer_sample 64 Ovarian cancer_sample 65 Ovarian cancer_sample 66
Ovarian cancer_sample 67 Ovarian cancer_sample 68 Ovarian cancer_sample 69
 Ovarian cancer_sample 7 Ovarian cancer_sample 70 Ovarian cancer_sample 8
                                                                         1
 Ovarian cancer_sample 9
batch:
2001-09-14 2001-12-14 2002-08-20 2003-09-09 2003-09-18 2009-08-14
                           14
                                   13
days_to_death:
  Min. 1st Qu. Median Mean 3rd Qu.
   30.0 667.5 1125.0 1170.0 1522.0 3450.0
primarysite:
ΟV
70
sample_type:
tumor
   70
uncurated_author_metadata:
            title: Ovarian cancer_sample 10///geo_accession: GSM495148///status: Pu
            title: Ovarian cancer_sample 11///geo_accession: GSM495149///status: Pu
                 title: Ovarian cancer_sample 12///geo_accession: GSM495150///statu
            title: Ovarian cancer_sample 13///geo_accession: GSM495151///status: Pu
            title: Ovarian cancer_sample 14///geo_accession: GSM495152///status: Pu
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                title: Ovarian cancer_sample 22///geo_accession: GSM495160///statu
                title: Ovarian cancer_sample 23///geo_accession: GSM495161///statu
                title: Ovarian cancer_sample 24///geo_accession: GSM495162///statu
                title: Ovarian cancer_sample 25///geo_accession: GSM495163///statu
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GSE19829 53

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     title: Ovarian cancer_sample 45///geo_accession: GSM495183///status: Public or
title: Ovarian cancer_sample 46///geo_accession: GSM495184///status: Public on Jul
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title: Ovarian cancer_sample 48///geo_accession: GSM495186///status: Public on Jul
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                 title: Ovarian cancer_sample 4///geo_accession: GSM495142///status
title: Ovarian cancer_sample 50///geo_accession: GSM495188///status: Public on Jul
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     title: Ovarian cancer_sample 52///geo_accession: GSM495190///status: Public or
     title: Ovarian cancer_sample 53///geo_accession: GSM495191///status: Public or
     title: Ovarian cancer_sample 54///geo_accession: GSM495192///status: Public or
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   title: Ovarian cancer_sample 56///geo_accession: GSM495194///status: Public on 3
   title: Ovarian cancer_sample 57///geo_accession: GSM495195///status: Public on 3
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       title: Ovarian cancer_sample 59///geo_accession: GSM495197///status: Public
             title: Ovarian cancer_sample 5///geo_accession: GSM495143///status: Pu
```

```
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      title: Ovarian cancer_sample 63///geo_accession: GSM495201///status: Public of
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      title: Ovarian cancer_sample 65///geo_accession: GSM495203///status: Public of
      title: Ovarian cancer_sample 66///geo_accession: GSM495204///status: Public o
  title: Ovarian cancer_sample 67///geo_accession: GSM495205///status: Public on Ju
  title: Ovarian cancer_sample 68///geo_accession: GSM495206///status: Public on Ju
  title: Ovarian cancer_sample 69///geo_accession: GSM495207///status: Public on Ju
             title: Ovarian cancer_sample 6///geo_accession: GSM495144///status: Pu
       title: Ovarian cancer_sample 70///geo_accession: GSM495208///status: Public
                  title: Ovarian cancer_sample 7///geo_accession: GSM495145///statu
             title: Ovarian cancer_sample 8///geo_accession: GSM495146///status: Pu
              title: Ovarian cancer_sample 9///geo_accession: GSM495147///status: F
vital_status:
deceased
           living
      40
               30
```

Value

An expression set

GSE20565

A genomic and transcriptomic approach for a differential diagnosis between primary and secondary ovarian carcinomas in patients with a previous history of breast cancer. GSE20565 55

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, Lebiq
  Laboratory: Meyniel, Sastre-Garau 2010
  Contact information:
  Title: A genomic and transcriptomic approach for a differential diagnosis between
  URT:
  PMIDs: 20492709
 Abstract: A 277 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
  platform title:
      [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
  platform_shorttitle:
      Affymetrix HG-U133Plus2
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  platform_manufacturer:
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  platform_distribution:
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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
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Details

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assayData: 42447 features, 140 samples
Platform type:
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Available sample meta-data:
alt_sample_name:
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Breast metastasis in the ovary_OC01_ARN0017 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0020 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0029 [HG-U133_Plus_2]
                                                          1
Breast metastasis in the ovary_OC01_ARN0035 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0046 [HG-U133_Plus_2]
Breast metastasis in the ovary OC01 ARN0051 [HG-U133 Plus 2]
Breast metastasis in the ovary_OC01_ARN0053 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0055 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0060 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0069 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0073 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0077 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0079 [HG-U133_Plus_2]
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]
Breast metastasis in the ovary_OC01_ARN0092 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0097 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0098 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0099 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0102 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0104 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0112 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0120 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0121 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0123 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0126 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0141 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0142 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0143 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0145 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0146 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0153 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0162 [HG-U133_Plus_2]
Breast metastasis in the ovary_OC01_ARN0201 [HG-U133_Plus_2]
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             Ovarian carcinoma_OC01_ARN0002 [HG-U133_Plus_2]
             Ovarian carcinoma_OC01_ARN0004 [HG-U133_Plus_2]
             Ovarian carcinoma_OC01_ARN0005 [HG-U133_Plus_2]
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Ovarian carcinoma_OC01_ARN0008 [HG-U133_Plus_2]
Ovarian carcinoma_OC01_ARN0009 [HG-U133_Plus_2]
Ovarian carcinoma_OC01_ARN0010 [HG-U133_Plus_2]
Ovarian carcinoma_OC01_ARN0011 [HG-U133_Plus_2]
Ovarian carcinoma_OC01_ARN0012 [HG-U133_Plus_2]
Ovarian carcinoma_OC01_ARN0013 [HG-U133_Plus_2]
Ovarian carcinoma_OC01_ARN0015 [HG-U133_Plus_2]
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Ovarian carcinoma_OC01_ARN0041 [HG-U133_Plus_2]
Ovarian carcinoma OC01 ARN0042 [HG-U133 Plus 2]
Ovarian carcinoma_OC01_ARN0045 [HG-U133_Plus_2]
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Ovarian carcinoma_OC01_ARN0064 [HG-U133_Plus_2]
Ovarian carcinoma_OC01_ARN0066 [HG-U133_Plus_2]
Ovarian carcinoma_OC01_ARN0067 [HG-U133_Plus_2]
Ovarian carcinoma_OC01_ARN0070 [HG-U133_Plus_2]
Ovarian carcinoma_OC01_ARN0072 [HG-U133_Plus 2]
Ovarian carcinoma_OC01_ARN0075 [HG-U133_Plus_2]
Ovarian carcinoma_OC01_ARN0076 [HG-U133_Plus_2]
Ovarian carcinoma_OC01_ARN0080 [HG-U133_Plus_2]
Ovarian carcinoma OC01 ARN0084 [HG-U133 Plus 2]
Ovarian carcinoma_OC01_ARN0085 [HG-U133_Plus_2]
Ovarian carcinoma_OC01_ARN0089 [HG-U133_Plus_2]
Ovarian carcinoma_OC01_ARN0091 [HG-U133_Plus_2]
Ovarian carcinoma_OC01_ARN0093 [HG-U133_Plus_2]
Ovarian carcinoma_OC01_ARN0095 [HG-U133_Plus_2]
Ovarian carcinoma_OC01_ARN0096 [HG-U133_Plus_2]
Ovarian carcinoma_OC01_ARN0100 [HG-U133_Plus_2]
Ovarian carcinoma OC01 ARN0101 [HG-U133 Plus 2]
Ovarian carcinoma_OC01_ARN0103 [HG-U133_Plus_2]
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            Ovarian carcinoma_OC01_ARN0111 [HG-U133_Plus_2]
            Ovarian carcinoma_OC01_ARN0113 [HG-U133_Plus_2]
            Ovarian carcinoma_OC01_ARN0114 [HG-U133_Plus_2]
            Ovarian carcinoma_OC01_ARN0115 [HG-U133_Plus_2]
            Ovarian carcinoma_OC01_ARN0116 [HG-U133_Plus_2]
            Ovarian carcinoma_OC01_ARN0118 [HG-U133_Plus_2]
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                                                     NA's
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                                            71
       6
              6
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primarysite:
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        96
summarygrade:
high low NA's
 63 33 44
summarystage:
early late NA's
      67 46
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tumor 140

44

27

GSE20565 61

tumorstage:

1

2

3

4 NA's

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9
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  18
               15
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  а
       b
  14
       10
            55
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        2
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      27
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title: Ovarian carcinoma_OC01_A

title: Ovarian carcinoma_OC01_ARM

GSE20565 63

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title: Ovarian carcinoma_OC01_ARM

title: Ovarian carcinoma_OC01_ARN005

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title: Ovarian carcinoma_OC01_ARM

title: Ovarian carcinoma_OC01_ARM

GSE2109 65

title: Ovarian carcinoma_OC01_ARM

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                       NA's
                        138
An expression set
```

Description

GSE2109

Value

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

IGC EXpression Project for Oncology

Format

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experimentData(eset):
Experiment data
  Experimenter name: EXpression Project for Oncology, International Genomics Consor
 Laboratory: expO, IGC 2005
  Contact information:
  Title: IGC EXpression Project for Oncology
  URL:
  PMIDs: PMID unknown
  Abstract: A 8 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
  platform_title:
      [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
   platform_shorttitle:
      Affymetrix HG-U133Plus2
   platform_summary:
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   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
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Details

GSE2109 67

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Ovary - 20323	Ovary - 20325
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1 Ovary - 241187	1 Ovary - 241196
1 Ovary - 241198	1 Ovary - 241199
1 Ovary - 242929	1 (Other)

GSE2109 69

105

1

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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
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2006-11-21	2006-11-30	2006-12-07	2007-01-12	2007-02-09	2007-03-07	2007-03-09
1	6	3	1	1	8	1
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4	2	3	4	2	2	1
2007-07-27	2007-09-05	2007-09-07	2007-09-11	2007-09-12	2008-02-15	2008-02-21
2	3	1	4	4	1	3
2008-02-27	2008-03-04	2008-05-13	2008-05-16	2008-05-23		
2	1	4	4	5		

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title: Omentum -



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

GSE2109 73

NA's 202

Value

An expression set

GSE26193

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

Description

Although there is evidence that redox regulation has an essential role in malignancies, its impact on tumor prognosis remains unclear. Here we show crosstalk between oxidative stress and the miR-200 family of microRNAs that affects tumorigenesis and chemosensitivity. miR-141 and miR-200a target p38?? and modulate the oxidative stress response. Enhanced expression of these microR-NAs mimics p38?? deficiency and increases tumor growth in mouse models, but it also improves

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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

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experimentData(eset):
Experiment data
  Experimenter name: Mateescu B, Batista L, Mariani O, Meyniel J, Cottu PH, Sastre-
  Laboratory: Mateescu, Mechta-Grigoriou 2011
  Contact information:
  Title: miR-141 and miR-200a act on ovarian tumorigenesis by controlling oxidative
  URL:
  PMIDs: 22101765
  Abstract: A 149 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
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   platform_accession:
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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
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Details

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assayData: 42447 features, 107 samples
Platform type:
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Call: survfit(formula = Surv(time, cens) ~ -1)
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107.00
        76.00
                3.05 2.50 4.56
Available sample meta-data:
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Ovarian carcinoma 101 Ovarian carcinoma 102 Ovarian carcinoma 103
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Ovarian carcinoma 107 Ovarian carcinoma 11
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 Ovarian carcinoma 19
                      Ovarian carcinoma 2
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                   1
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GSE26193 77

Ovarian carcinoma	49 1	Ovariar	n carcinoma	a 5	Ovarian	carcinoma	50 1
Ovarian carcinoma	_	Ovarian	carcinoma	_	Ovarian	carcinoma	_
Ovarian carcinoma	_	Ovarian	carcinoma	_	Ovarian	carcinoma	
Ovarian carcinoma	_	Ovarian	carcinoma		Ovarian	carcinoma	
Ovarian carcinoma	_	Ovarian	carcinoma		Ovarian	carcinoma	
Ovarian carcinoma	_	Ovarian	carcinoma		Ovarian	carcinoma	64
Ovarian carcinoma	_	Ovarian	carcinoma	_	Ovarian	carcinoma	
Ovarian carcinoma	68	Ovarian	carcinoma	69	Ovariar	n carcinoma	
Ovarian carcinoma		Ovarian	carcinoma		Ovarian	carcinoma	
Ovarian carcinoma		Ovarian	carcinoma		Ovarian	carcinoma	
Ovarian carcinoma		Ovarian	carcinoma		Ovarian	carcinoma	
Ovarian carcinoma		Ovariar	n carcinoma		Ovarian	carcinoma	
Ovarian carcinoma		Ovarian	carcinoma		Ovarian	carcinoma	
Ovarian carcinoma		Ovarian	carcinoma		Ovarian	carcinoma	
Ovarian carcinoma		Ovarian	carcinoma		Ovarian	carcinoma	
Ovarian carcinoma		Ovarian	carcinoma		Ovarian	carcinoma	
(Othe				1			1
	8						
<pre>sample_type: tumor 107</pre>							
histological_type: clearcell endo	o m:	ucinous 8	other 6		ser 79		
summarygrade: high low 67 40							

summarystage:

early late

```
31 76
tumorstage:
1 2 3 4
20 11 59 17
substage:
 a b c NA's
 16 12 62 17
grade:
1 2 3
7 33 67
days_to_tumor_recurrence:
  Min. 1st Qu. Median Mean 3rd Qu.
                                     Max.
   3.0 340.5 584.0 1108.0 1525.0 7386.0
recurrence_status:
norecurrence recurrence
        27
                   80
days_to_death:
  Min. 1st Qu. Median Mean 3rd Qu. Max.
     3 668 1096 1520 2220
                                     7386
vital_status:
deceased living
    76 31
batch:
2006-06-01 2006-06-27 2006-06-28 2006-06-29 2006-06-30 2006-07-20 2008-03-06
      15 14
                      23 16 21
                                                   3
2009-03-18 2009-03-19
       4
            10
uncurated_author_metadata:
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GSE26193 79

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title: Ovarian carcinoma 52///geo_accession: GSM642984///status: Publ

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title: Ovarian carcinoma 73///geo_accession: GSM643005///status: Public on No

GSE26712 83

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 the apeutic 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, F
  Laboratory: Bonome, Birrer 2008
  Contact information:
  Title: A gene signature predicting for survival in suboptimally debulked patients
  URL:
  PMIDs: 18593951
 Abstract: A 238 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
  platform_title:
      [HG-U133A] Affymetrix Human Genome U133A Array
  platform_shorttitle:
      Affymetrix HG-U133A
  platform_summary:
```

hgu133a

```
platform_manufacturer:
        Affymetrix
     platform_distribution:
        commercial
     platform_accession:
       GPL96
     version:
        2015-09-22 19:46:24
  featureData(eset):
  An object of class 'AnnotatedDataFrame'
    featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
      (20967 total)
    varLabels: probeset gene EntrezGene.ID best_probe
    varMetadata: labelDescription
Details
  assayData: 20967 features, 195 samples
  Platform type:
  Overall survival time-to-event summary (in years):
  Call: survfit(formula = Surv(time, cens) ~ -1)
     10 observations deleted due to missingness
        n events median 0.95LCL 0.95UCL
   185.00 129.00 3.83 3.24 4.83
  Available sample meta-data:
  ______
  alt_sample_name:
       Normal HOSE2008 Normal HOSE2061 Normal HOSE2064
                           1
              1
       Normal HOSE2085 Normal HOSE2225 Normal HOSE2226
                  1
                                1
       Normal HOSE2228
                         Normal HOSE2230 Normal HOSE2234
       Normal HOSE2237 Ovarian Cancer SO10 Ovarian Cancer SO100
                   1
                                1
  Ovarian Cancer S0103 Ovarian Cancer S0106 Ovarian Cancer S0108
                   1
                                    1
   Ovarian Cancer SO11 Ovarian Cancer SO113 Ovarian Cancer SO115
                                      1
  Ovarian Cancer SO116 Ovarian Cancer SO117 Ovarian Cancer SO118
   Ovarian Cancer SO12 Ovarian Cancer SO121 Ovarian Cancer SO122
```

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```
Ovarian Cancer S0124 Ovarian Cancer S0129 Ovarian Cancer S013
Ovarian Cancer S0131 Ovarian Cancer S0134 Ovarian Cancer S0135
Ovarian Cancer S0137 Ovarian Cancer S0141 Ovarian Cancer S0143
Ovarian Cancer S0148 Ovarian Cancer S0154 Ovarian Cancer S016
                  1
Ovarian Cancer S0166 Ovarian Cancer S017 Ovarian Cancer S0173
Ovarian Cancer S0174 Ovarian Cancer S018 Ovarian Cancer S0181
Ovarian Cancer SO184 Ovarian Cancer SO185 Ovarian Cancer SO187
                  1
Ovarian Cancer S0189 Ovarian Cancer S0190 Ovarian Cancer S0193
                  1
Ovarian Cancer S0194 Ovarian Cancer S0196 Ovarian Cancer S0197
 Ovarian Cancer SO2 Ovarian Cancer SO200 Ovarian Cancer SO201
Ovarian Cancer SO203 Ovarian Cancer SO205 Ovarian Cancer SO21
Ovarian Cancer SO211 Ovarian Cancer SO214 Ovarian Cancer SO216
                  1
                                       1
Ovarian Cancer SO217 Ovarian Cancer SO218 Ovarian Cancer SO224
Ovarian Cancer SO225 Ovarian Cancer SO227 Ovarian Cancer SO228
Ovarian Cancer SO229 Ovarian Cancer SO23 Ovarian Cancer SO230
Ovarian Cancer SO231 Ovarian Cancer SO235 Ovarian Cancer SO236
Ovarian Cancer SO237 Ovarian Cancer SO241 Ovarian Cancer SO242
Ovarian Cancer SO243 Ovarian Cancer SO244 Ovarian Cancer SO246
Ovarian Cancer SO247 Ovarian Cancer SO249 Ovarian Cancer SO25
Ovarian Cancer SO250 Ovarian Cancer SO256 Ovarian Cancer SO257
Ovarian Cancer SO258 Ovarian Cancer SO261 Ovarian Cancer SO262
Ovarian Cancer SO263 Ovarian Cancer SO265 Ovarian Cancer SO267
Ovarian Cancer SO268 Ovarian Cancer SO272 Ovarian Cancer SO273
                  1
Ovarian Cancer SO278 Ovarian Cancer SO279 Ovarian Cancer SO282
```

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Ovarian Cancer SO283 Ovarian Cancer SO285 Ovarian Cancer SO290
            (Other)
              96
sample_type:
healthy tumor 10 185
histological_type:
 ser NA's
185 10
primarysite:
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
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
```

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```
129 56 10
debulking:
   optimal suboptimal
                           NA's
        90 95
                             10
percent_normal_cells:
20-
195
percent_stromal_cells:
20-
195
percent_tumor_cells:
80+
195
2003 - 11 - 04 \ 2003 - 11 - 05 \ 2003 - 11 - 06 \ 2003 - 11 - 07 \ 2003 - 11 - 20 \ 2003 - 11 - 21 \ 2003 - 12 - 16
       14 16 9 6 10 15 17
2003 - 12 - 23 \ 2003 - 12 - 24 \ 2004 - 04 - 20 \ 2004 - 04 - 21 \ 2004 - 04 - 27 \ 2004 - 09 - 28 \ 2005 - 07 - 27
                  11
                         20
                                        17
                                                     9
                                                                          15
                                                              14
2006-11-09
        10
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                                                                        title: Norma
                                                                        title: Norma
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title: Norma

title: Norma

title: Norma

title: Norma

title: Norma

title: Norma

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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

platform_summary:

```
experimentData(eset):

Experiment data

Experimenter name: Gillet JP, Calcagno AM, Varma S, Davidson B et al. Multidrug no Laboratory: Gillet, Gottesman 2012

Contact information:

Title: Multidrug resistance-linked gene signature predicts overall survival of particles. 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
```

GSE30009 93

```
platform_manufacturer:
        TaqMan
     platform_distribution:
        custom
     platform_accession:
        GPL13728
     version:
        2015-09-22 19:46:26
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    featureNames: 5 6 ... 380 (363 total)
    varLabels: probeset gene EntrezGene.ID best_probe
    varMetadata: labelDescription
Details
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  Platform type:
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  Call: survfit(formula = Surv(time, cens) ~ -1)
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   103.00 57.00 3.42 2.92 5.34
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                                         1
  Norwegian patient 12 Norwegian patient 13 Norwegian patient 14
  Norwegian patient 15 Norwegian patient 16 Norwegian patient 17
  Norwegian patient 18 Norwegian patient 19 Norwegian patient 2
  Norwegian patient 20 Norwegian patient 21 Norwegian patient 22
  Norwegian patient 23 Norwegian patient 3 Norwegian patient 4
   Norwegian patient 5 Norwegian patient 6 Norwegian patient 7
   Norwegian patient 8 Norwegian patient 9
                                                  US Patient 1
         US Patient 10 US Patient 11 US Patient 12
```

		1			1	1
US	Patient	13 1	US	Patient	14 1	US Patient 15
US	Patient	16	US	Patient	17	US Patient 18
US	Patient	19	U	S Patient	_	US Patient 20
US	Patient	21	US	Patient	22	US Patient 23
US	Patient	24	US	Patient	25	US Patient 26
US	Patient	27	US	Patient	28	US Patient 29
US	S Patient		US	Patient	30	US Patient 31
US	Patient	32	US	Patient	33	US Patient 34
US	Patient	35	US	Patient	36	US Patient 37
US	Patient	38	US	Patient	39	US Patient 4
US	Patient	40	US	Patient	41	US Patient 42
US	Patient	43	US	Patient	44	US Patient 45
US	Patient	46	US	Patient	47	US Patient 48
US	Patient	49	U	S Patient		US Patient 50
US	Patient	51	US	Patient	52	US Patient 53
US	Patient	54	US	Patient	55	US Patient 56
US	Patient	57 1	US	Patient	58	US Patient 59
US	S Patient		US	Patient	60	US Patient 61
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US	Patient	1 68	US	Patient		US Patient 7
US	Patient	1 70	US	Patient	1 71	US Patient 72
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US	Patient	1 76	US	Patient	1 77	1 US Patient 78

GSE30009 95

1

1

1

(Other)

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tumor
 103
histological_type:
clearcell ser
  1
            102
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high low NA's
 92 9 2
summarystage:
late
103
tumorstage:
3 4
82 21
substage:
  b c NA's
  2 60 41
grade:
  1 2 3 NA's
  4 5 92 2
age_at_initial_pathologic_diagnosis:
  Min. 1st Qu. Median Mean 3rd Qu. Max.
 30.00 56.00 61.00
                      62.45 71.50
                                   87.00
days_to_death:
  Min. 1st Qu. Median Mean 3rd Qu.
                                   Max.
    24 598 1053 1156 1568
                                    4748
vital_status:
deceased living
    57
debulking:
  optimal suboptimal
      81 22
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uncurated_author_metadata:

GSE30009 97

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title: US Patient 54///geo_accession: GSM7426

GSE30009 99

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title:

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title: US Patient 78//

title: US Patient 79///g

Value

An expression set

GSE30161

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

Description

Despite advances in radical surgery and chemotherapy delivery, ovarian cancer is the most lethal gynecologic malignancy. Standard therapy includes treatment with platinum-based combination chemotherapies yet there is no biomarker model to predict their responses to these agents. We here have developed and independently tested our multi-gene molecular predictors for forecasting patients' responses to individual drugs on a cohort of 55 ovarian cancer patients. To independently validate these molecular predictors, we performed microarray profiling on FFPE tumor samples of 55 ovarian cancer patients (UVA-55) treated with platinum-based adjuvant chemotherapy. Genomewide 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,Th
  Laboratory: Ferriss, Lee 2012
  Contact information:
  Title: Multi-gene expression predictors of single drug responses to adjuvant cher
```

GSE30161 101

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URL:
    PMIDs: 22348014
    Abstract: A 215 word abstract is available. Use 'abstract' method.
    Information is available on: preprocessing
    notes:
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        [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
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        Affymetrix HG-U133Plus2
     platform_summary:
        hgu133plus2
     platform_manufacturer:
        Affymetrix
     platform_distribution:
        commercial
     platform_accession:
        GPL570
     version:
        2015-09-22 19:50:24
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      (42447 total)
    varLabels: probeset gene EntrezGene.ID best_probe
    varMetadata: labelDescription
Details
  assayData: 42447 features, 58 samples
  Platform type:
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  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_16 OV_FFPE_17 OV_FFPE_18 OV_FFPE_19 OV_FFPE_2 OV_FFPE_20 OV_FFPE_21
                    1
                              1
                                         1
                                                             1
                                                   1
  OV_FFPE_22 OV_FFPE_23 OV_FFPE_24 OV_FFPE_25 OV_FFPE_26 OV_FFPE_27 OV_FFPE_28
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                          1
OV_FFPE_48 OV_FFPE_49 OV_FFPE_5 OV_FFPE_50 OV_FFPE_51 OV_FFPE_52 OV_FFPE_53
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    1 1
                1 1 1 1 1
OV_FFPE_8 OV_FFPE_9
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tumor
 58
histological_type:
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        47
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                   1
summarygrade:
high low NA's
33 21 4
summarystage:
late
58
tumorstage:
3 4
53 5
substage:
a b c
9 11 38
grade:
 1 2 3 NA's
  2 19 33 4
age_at_initial_pathologic_diagnosis:
 Min. 1st Qu. Median Mean 3rd Qu. Max. 38.00 53.50 62.00 62.57 72.00 85.00
```

GSE30161 103

```
pltx:
У
58
tax:
n y
4 54
neo:
n
58
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norecurrence recurrence
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                               4
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debulking:
  optimal suboptimal NA's
      26 30
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GSE30161 105

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```

Value

An expression set

GSE32062

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

Description

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

Format

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

GSE32062 107

```
Contact information:
    Title: High-risk ovarian cancer based on 126-gene expression signature is uniquely
    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)
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      10d 115d
                   116d 117d 119d
                                           11d 120d 122d 123d 125Rd
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       1
                    1
                            1
                                   1
                                            1
                                                   1
                                                           1
```

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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174d	178d	17d	183d	184d	185d	186d	18d	20d	22d
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23d	249d	257d	25d	260d	262d	264d	266d	267d	268d
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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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sample_type:

tumor

260

histological_type:

ser

260

summarygrade:

high low

129 131

summarystage:

late

260

tumorstage:

3 4

204 56

substage:

a b c NA's 4 20 180 56

grade:

2 3

131 129

pltx:

У

GSE32062 109

```
260
tax:
260
days_to_death:
  Min. 1st Qu. Median
                          Mean 3rd Qu.
           810
                  1245
                           1344 1710
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title: serous ovarian cancer $22d///geo_accession$: GSM794905///status: Public on N title: serous ovarian cancer 23d///geo_accession: GSM794906///status: Public or title: serous ovarian cancer 249d///geo_accession: GSM794907///status: Public or title: serous ovarian cancer 257d///geo_accession: GSM794909///status: Public on Ma title: serous ovarian cancer 25d///geo_accession: GSM794908///status: Public of title: serous ovarian cancer 260d///geo_accession: GSM794910///status: Public on N title: serous ovarian cancer 262d///geo_accession: GSM794911///status: Public on Ma title: serous ovarian cancer 264d///geo_accession: GSM794912///status: Public on Ma title: serous ovarian cancer 266d///geo_accession: GSM794913///status: Public on Ma title: serous ovarian cancer 267d///geo_accession: GSM794914///status: Public or title: serous ovarian cancer 268d///geo_accession: GSM794915///status: Public or title: serous ovarian cancer 269d///geo_accession: GSM794916///status: Public on Ma title: serous ovarian cancer 27d///geo_accession: GSM794917///status: Public on title: serous ovarian cancer 299d///geo_accession: GSM794918///status: Public o title: serous ovarian cancer 2d///geo_accession: GSM794903///status: Public on title: serous ovarian cancer 300d///geo_accession: GSM794919///status: Public on title: serous ovarian cancer 301d///geo_accession: GSM794920///status: Public on Ma title: serous ovarian cancer 302d///geo_accession: GSM794921///status: Public or title: serous ovarian cancer 303d///geo_accession: GSM794922///status: Public or title: serous ovarian cancer 304d///geo_accession: GSM794923///status: Public on Ma title: serous ovarian cancer 305d2///geo_accession: GSM794924///status: Public on title: serous ovarian cancer 306d///geo_accession: GSM794925///status: Public on Ma title: serous ovarian cancer 307d///geo_accession: GSM794926///status: Public on Ma title: serous ovarian cancer 310d///geo_accession: GSM794927///status: Public

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 title: serous ovarian cancer 368d2///geo_accession: GSM794957///status: Public on
      title: serous ovarian cancer 36d///geo_accession: GSM794950///status: Public
    title: serous ovarian cancer 38d///geo_accession: GSM794958///status: Public of
title: serous ovarian cancer 41d2R///geo_accession: GSM794960///status: Public on N
  title: serous ovarian cancer 42d///geo_accession: GSM794961///status: Public on N
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  title: serous ovarian cancer 456d///geo_accession: GSM794965///status: Public or
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                               NA's
                                258
```

Value

An expression set

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

Description

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

a gene expression signature for predicting overall survival, leading to suggesting novel therapeutic strategies for high-risk patients. In this large-scale cross-platform study of six microarray data sets consisting of 1,054 ovarian cancer patients, we developed a gene expression signature for predicting overall survival by applying elastic net and 10-fold cross-validation to a Japanese data set A (n = 260) and evaluated the signature in five other data sets. Subsequently, we investigated differences in the biological characteristics between high- and low-risk ovarian cancer groups. An elastic net analysis identified a 126-gene expression signature for predicting overall survival in patients with ovarian cancer using the Japanese data set A (multivariate analysis, P = 4 ?? 10(-20)). We validated its predictive ability with five other data sets using multivariate analysis (Tothill's data set, P = 1 ?? 10(-5); Bonome's data set, P = 0.0033; Dressman's data set, P = 0.0016; TCGA data set, P = 0.0027; Japanese data set B, P = 0.021). Through gene ontology and pathway analyses, we identified a significant reduction in expression of immune-response-related genes, especially on the antigen presentation pathway, in high-risk ovarian cancer patients. This risk classification based on the 126-gene expression signature is an accurate predictor of clinical outcome in patients with advanced stage high-grade serous ovarian cancer and has the potential to develop new therapeutic strategies for high-grade serous ovarian cancer patients.

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Yoshihara K, Tsunoda T, Shigemizu D, Fujiwara H et al. High-ri
 Laboratory: Yoshihara, Tanaka 2012
  Contact information:
  Title: High-risk ovarian cancer based on 126-gene expression signature is uniquely
  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:
      hquq4112a
  platform_manufacturer:
      Agilent
  platform_distribution:
      commercial
  platform_accession:
      GPL6480
   version:
      2015-09-22 19:58:23
featureData(eset):
An object of class 'AnnotatedDataFrame'
```

GSE32063 115

varLabels: probeset gene EntrezGene.ID best_probe

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

```
varMetadata: labelDescription
Details
  assayData: 30936 features, 40 samples
  Platform type:
  Overall survival time-to-event summary (in years):
  Call: survfit(formula = Surv(time, cens) ~ -1)
      n events median 0.95LCL 0.95UCL
   40.00 22.00 4.44 3.29 NA
  _____
  Available sample meta-data:
  ______
  alt_sample_name:
   106 108 109R 110 111R 192 195R 196 197 198 200 203 205 206 207 213
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                      1 1 1 1
                                      1 1
                                              1 1 1 1
                                                                1
   222 224 226 229 230 231 274 277 278 280 281 282 283 284 285 286
    1 1 1 1 1
                       1 1 1
                                   1 1 1 1 1
                                                       1 1 1
   287 288 289 291 292 294 297R 298R
       1
           1
               1
                   1
                       1
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  tumor
    40
  histological_type:
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   40
  summarygrade:
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  17 23
  summarystage:
  late
   40
  tumorstage:
  3 4
  31 9
  substage:
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28

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 2 3
23 17
pltx:
40
tax:
 У
40
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                                           Max.
    210
           705 1155
                          1346
                                  1792
                                           3330
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debulking:
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GSE32063 117

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Value

An expression set

GSE44104

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

Description

Biomarkers that predict disease progression might assist the development of better therapeutic strategies for aggressive cancers, such as ovarian cancer. Here, we investigated the role of collagen type XI alpha 1 (COL11A1) in cell invasiveness and tumor formation and the prognostic impact of COL11A1 expression in ovarian cancer. Microarray analysis suggested that COL11A1 is a disease progression-associated gene that is linked to ovarian cancer recurrence and poor survival. Small interference RNA-mediated specific reduction in COL11A1 protein levels suppressed the invasive ability and oncogenic potential of ovarian cancer cells and decreased tumor formation and lung colonization in mouse xenografts. A combination of experimental approaches, including realtime 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.

GSE44104 119

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 o
 URL:
 PMIDs: 23934190
 Abstract: A 260 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
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      Affymetrix HG-U133Plus2
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      hgu133plus2
   platform_manufacturer:
      Affymetrix
  platform distribution:
      commercial
  platform accession:
     GPL570
  platform_technology:
     in situ oligonucleotide
   version:
      2015-09-22 20:02:05
featureData(eset):
An object of class 'AnnotatedDataFrame'
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  varMetadata: labelDescription
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Details

120

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 Te_93 Tm_101 Tm_102 Tm_106 Tm_107 Tm_110
                        Tm_95 Tm_96 Tm_97 Tm_98 Ts_11
  1 1 1 1 1
                        1
                            1
                                1
                                     1
                                         1
Ts_14 Ts_15 Ts_17 Ts_19 Ts_2 Ts_20 Ts_21 Ts_23 Ts_24 Ts_26 Ts_28
  Ts_3 Ts_31 Ts_32 Ts_34 Ts_35 Ts_36 Ts_37 Ts_39 Ts_4 Ts_41 Ts_43
  1 1 1 1
                 1 1 1 1 1 1 1
Ts_45 Ts_46 Ts_47 Ts_5 Ts_8
  1 1 1 1 1
sample_type:
tumor
 60
histological_type:
clearcell endo mucinous
                    ser
         11 9
   12
                    28
summarystage:
early late
 25 35
tumorstage:
1 2 3 4
17 8 30 5
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recurrence_status:

norecurrence recurrence 40 20

os_binary: long short 44 16

relapse_binary: long short 40 20

2010-09-07 2010-09-08 2010-10-14 2010-12-10 2010-12-14 20 2 18 16

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GSE44104 121

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GSE49997 123

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```

Value

An expression set

Length

Class

60 character character

Mode

GSE49997

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

Description

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

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

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Pils D1, Hager G, Tong D, Aust S, Heinze G, Kohl M, Schuster F
 Laboratory: Pils, Zeilinger 2012
  Contact information:
  Title: Validating the impact of a molecular subtype in ovarian cancer on outcomes
  URT:
 PMIDs: 22497737
 Abstract: A 276 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
  platform_title:
      ABI Human Genome Survey Microarray Version 2
  platform_shorttitle:
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      Applied Biosystems
  platform_distribution:
      commercial
  platform_accession:
      GPL2986
  platform_technology:
      in situ oligonucleotide
   version:
      2015-09-22 20:04:13
featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 100027 100036 ... 10715781 (18439 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
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GSE49997 125

Details

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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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histological_type:
other ser NA's
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23 171 10

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143
    50 11
summarystage:
early late NA's
 9 185 10
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  2 3 4 NA's
  9 154 31 10
grade:
 2 3 NA's
 50 143 11
age_at_initial_pathologic_diagnosis:
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  30.0 335.0 487.0 580.1 722.5 1461.0 10
recurrence_status:
norecurrence recurrence NA's
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GSE49997 127

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GSE49997 129

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GSE51088 131

Value

An expression set

GSE51088

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

Description

To identify molecular prognosticators and therapeutic targets for high-grade serous epithelial ovarian cancers (EOCs) using genetic analyses driven by biologic features of EOC pathogenesis. Ovarian tissue samples (n = 172; 122 serous EOCs, 30 other EOCs, 20 normal/benign) collected prospectively from sequential patients undergoing gynecologic surgery were analyzed using RNA expression microarrays. Samples were classified based on expression of genes with potential relevance in ovarian cancer. Gene sets were defined using Rosetta Similarity Search Tool (ROAST) and analysis of variance (ANOVA). Gene copy number variations were identified by array comparative genomic hybridization. No distinct subgroups of EOC could be identified by unsupervised clustering, however, analyses based on genes correlated with periostin (POSTN) and estrogen receptoralpha (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 the rapeutic 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

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experimentData(eset):
Experiment data
   Experimenter name: Karlan BY, Dering J, Walsh C, Orsulic S, Lester J, Anderson LA
   Laboratory: Karlan, Slamon 2014
   Contact information:
   Title: POSTN/TGFBI-associated stromal signature predicts poor prognosis in serous
   URL:
   PMIDs: 24368280
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        Agilent-012097 Human 1A Microarray (V2) G4110B (Probe Name version)
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    featureNames: A_23_P100001 A_23_P100011 ... A_23_P99996 (18703 total)
    varLabels: probeset gene EntrezGene.ID best_probe
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Details
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  Call: survfit(formula = Surv(time, cens) ~ -1)
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        n events median 0.95LCL 0.95UCL
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GSE51088 135

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GSE51088 137

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GSE51088 139

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Value

An expression set

GSE6008

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

Description

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

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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.

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Experiment data
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  Laboratory: Murph, Mills 2009
  Contact information:
  Title: Lysophosphatidic acid-induced transcriptional profile represents serous ex
  URL:
  PMIDs: 19440550
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  Information is available on: preprocessing
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   platform_accession:
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      2015-09-22 20:07:11
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Details

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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-033 Ovarian_Tumor_Endometrioid_CHTN-OE-035
Ovarian_Tumor_Endometrioid_CHTN-OE-036 Ovarian_Tumor_Endometrioid_CHTN-OE-038
Ovarian_Tumor_Endometrioid_CHTN-OE-039 Ovarian_Tumor_Endometrioid_CHTN-OE-040
Ovarian Tumor Endometrioid CHTN-OE-042 Ovarian Tumor Endometrioid CHTN-OE-046
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GSE6008 145

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GSE6008 147

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GSE6822 149

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Value

An expression set

GSE6822

Classification of ovarian tumor samples

Description

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

Format

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experimentData(eset):
Experiment data
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   Contact information:
   Title: Classification of ovarian tumor samples
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[Hu6800] Affymetrix Human Full Length HuGeneFL Array

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platform_shorttitle:
 Affymetrix Hu6800

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        commercial
     platform_accession:
        GPL80
      version:
        2015-09-22 20:07:22
   featureData(eset):
  An object of class 'AnnotatedDataFrame'
     featureNames: A28102_at AB000114_at ... Z97074_at (6407 total)
     varLabels: probeset gene EntrezGene.ID best_probe
     varMetadata: labelDescription
Details
   assayData: 6407 features, 66 samples
  Platform type:
   Available sample meta-data:
   alt_sample_name:
   Ovarian tumor AM053 Ovarian tumor AM122 Ovarian tumor AM124 Ovarian tumor AM125
                                                        1
                   1
                                    1
   Ovarian tumor AM127 Ovarian tumor AM137 Ovarian tumor AM138 Ovarian tumor AM144
   Ovarian tumor AM178 Ovarian tumor AM179 Ovarian tumor AM182 Ovarian tumor AM195
   Ovarian tumor AM196 Ovarian tumor AM198 Ovarian tumor AM200 Ovarian tumor AM201
                                       1
   Ovarian tumor AM202 Ovarian tumor AM203 Ovarian tumor AM204 Ovarian tumor AM207
                                       1
   Ovarian tumor AM208 Ovarian tumor AM209 Ovarian tumor AM225 Ovarian tumor AM226
                    1
                                     1
                                                         1
   Ovarian tumor AM228 Ovarian tumor AM233 Ovarian tumor AM250 Ovarian tumor AM252
                    1
                                       1
                                                         1
   Ovarian tumor AM253 Ovarian tumor AM255 Ovarian tumor AM256 Ovarian tumor AM259
                                        1
   Ovarian tumor AM261 Ovarian tumor AM263 Ovarian tumor AM268 Ovarian tumor AM269
```

GSE6822 151

```
Ovarian tumor AM287 Ovarian tumor AM288 Ovarian tumor AM289 Ovarian tumor AM290
                                   1
Ovarian tumor AM292 Ovarian tumor AM293 Ovarian tumor AM294 Ovarian tumor AM311
Ovarian tumor AM313 Ovarian tumor AM315 Ovarian tumor AM317 Ovarian tumor AM333
                                   1
Ovarian tumor AM335 Ovarian tumor AM339 Ovarian tumor AM341 Ovarian tumor AM344
                1
                                   1
                                                      1
Ovarian tumor AM345 Ovarian tumor AM347 Ovarian tumor AM348 Ovarian tumor AM349
                                   1
                                                       1
Ovarian tumor AM354 Ovarian tumor AM364 Ovarian tumor AM367 Ovarian tumor AM368
                                                       1
                 1
                                    1
Ovarian tumor AM381 Ovarian tumor AM382 Ovarian tumor AM398 Ovarian tumor AM429
                                                      1
                1
Ovarian tumor AM431 Ovarian tumor AM438
                 1
sample_type:
tumor
  66
histological_type:
      clearcell
                                                       mucinous
                           endo
                                            mix
             11
                                             3
            ser undifferentiated
             41
primarysite:
OV
66
summarygrade:
high low NA's
     15 11
  40
grade:
      2 3 NA's
    14
          40 11
2000-12-21 2001-05-03 2001-05-29 2001-06-12 2001-09-25 2001-09-26 2001-09-27
           1
                             3
                                       3
                                                  1
                                                            5
2002-02-14 2002-04-17 2002-04-18 2002-07-18 2002-07-24 2002-10-20 2002-10-30
       4
                 1
2002-11-01 2002-11-13
```

uncurated_author_metadata: title: Ovarian tumor AM053///geo_accession: title: Ovarian tumor AM122///geo_accession: GSM157231///status: Public on Dec 31 20 title: Ovarian tumor AM124///geo_accession: title: Ovarian tumor AM125///geo_accession: title: Ovarian tumor AM127///geo_accession: GSM157234///status: Public title: Ovarian tumor AM137///geo_accession: GSM157238 title: Ovarian tumor AM138///geo_accession: GSM157239 title: Ovarian tumor AM144///geo_accession: GSM157 title: Ovarian tumor AM178///geo_accession: title: Ovarian tumor AM179///geo_accession: GSM157242 title: Ovarian tumor AM182///geo_accession: GSM157 title: Ovarian tumor AM195///geo_accession: title: Ovarian tumor AM196///geo_accession: GSM157245 title: Ovarian tumor AM198///geo_accession: GSM1 title: Ovarian tumor AM200///geo_accession: GSM157 title: Ovarian tumor AM201///geo_accession: GSM1 title: Ovarian tumor AM202///geo_accession: GSM1 title: Ovarian tumor AM203///geo_accession: GSM157 title: Ovarian tumor AM204///geo_accession: GSM1 title: Ovarian tumor AM207///geo_accession: GSM1 title: Ovarian tumor AM208///geo_accession: GSM1 title: Ovarian tumor AM209///geo_accession: GSM1 title: Ovarian tumor AM225///geo_accession: GSM15 title: Ovarian tumor AM226///geo_accession: GSM15 GSE6822 153

```
title: Ovarian tumor AM233///geo_accession: GSM15
                            title: Ovarian tumor AM250///geo_accession:
                     title: Ovarian tumor AM252///geo_accession: GSM157
                  title: Ovarian tumor AM253///geo_accession: GSM157261
                           title: Ovarian tumor AM255///geo_accession:
                           title: Ovarian tumor AM256///geo_accession:
                   title: Ovarian tumor AM259///geo_accession: GSM15726
                           title: Ovarian tumor AM261///geo_accession:
                           title: Ovarian tumor AM263///geo_accession:
                           title: Ovarian tumor AM268///geo_accession:
                           title: Ovarian tumor AM269///geo_accession:
title: Ovarian tumor AM287///geo_accession: GSM157269///status: Public
title: Ovarian tumor AM288///geo_accession: GSM157270///status: Public
                           title: Ovarian tumor AM289///geo_accession:
                           title: Ovarian tumor AM290///geo_accession:
title: Ovarian tumor AM292///geo_accession: GSM157273///status: Public
                           title: Ovarian tumor AM293///geo_accession:
                           title: Ovarian tumor AM294///geo_accession:
                     title: Ovarian tumor AM311///geo_accession: GSM157
                         title: Ovarian tumor AM313///geo_accession: GS
                         title: Ovarian tumor AM315///geo_accession: GS
                       title: Ovarian tumor AM317///geo_accession: GSM1
                       title: Ovarian tumor AM333///geo_accession: GSM1
```

title: Ovarian tumor AM228///geo_accession: GSM15

```
title: Ovarian tumor AM335///geo_accession:
                                       title: Ovarian tumor AM339///geo_accession:
                                      title: Ovarian tumor AM341///geo_accession: 0
                                  title: Ovarian tumor AM344///geo_accession: GSM15
                                       title: Ovarian tumor AM345///geo_accession:
             title: Ovarian tumor AM347///geo_accession: GSM157286///status: Public
                                       title: Ovarian tumor AM348///geo_accession:
                                       title: Ovarian tumor AM349///geo_accession:
                                   title: Ovarian tumor AM354///geo_accession: GSM1
                            title: Ovarian tumor AM364///geo_accession: GSM157290/
                                       title: Ovarian tumor AM367///geo_accession:
                                       title: Ovarian tumor AM368///geo_accession:
                                       title: Ovarian tumor AM381///geo_accession:
                                       title: Ovarian tumor AM382///geo_accession:
 title: Ovarian tumor AM398///geo_accession: GSM157295///status: Public on Dec 31
   title: Ovarian tumor AM429///geo_accession: GSM157296///status: Public on Dec 3
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                                        title: Ovarian tumor AM438///geo_accession:
duplicates:
  Length
             Class
                        Mode
      66 character character
```

Value

An expression set

GSE8842 155

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 dualcolor assay labeling protocol. Unsupervised analysis identified eight major patient partitions, one of which was statistically associated to overall survival, grading, and histotype and another with grading and histotype. Supervised analysis allowed detection of gene profiles clearly associated to histotype or to degree of differentiation. No difference was found between borderline and grade 1 tumors. As to recurrence, a subset of genes able to differentiate relapsers from nonrelapsers was identified. Among these, cyclin E and minichromosome maintenance protein 5 were found particularly relevant, as their expression was inversely correlated to progression-free survival (P = 0.00033 and 0.017, respectively). Specific molecular signatures define different histotypes and prognosis of stage I ovarian cancer. Mucinous and clear cells histotypes can be distinguished from the others regardless of tumor grade. Cyclin E and minichromosome maintenance protein 5, whose expression was found previously to be related to a bad prognosis of advanced ovarian cancer, appear to be potential prognostic markers in stage I ovarian cancer too, independent of other pathologic and clinical variables.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Marchini S, Mariani P, Chiorino G, Marrazzo E, Bonomi R, Frusc
 Laboratory: Marchini, D'Incalci 2008
  Contact information:
  Title: Analysis of gene expression in early-stage ovarian cancer.
  URL:
  PMIDs: 19047114
  Abstract: A 225 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
  platform_title:
      Agilent Human 1 cDNA Microarray (G4100A)
  platform_shorttitle:
      Agilent G4100A cDNA
  platform_summary:
      hgug4100a
  platform_manufacturer:
      Agilent
  platform distribution:
      custom-commerical
```

```
platform_accession:
        GPL5689
     platform_technology:
        spotted DNA/cDNA
     version:
        2015-09-22 20:07:40
   featureData(eset):
  An object of class 'AnnotatedDataFrame'
    featureNames: 1 2 ... 8864 (7809 total)
    varLabels: probeset gene EntrezGene.ID best_probe
    varMetadata: labelDescription
Details
  assayData: 7809 features, 83 samples
  Platform type:
  Overall survival time-to-event summary (in years):
  Call: survfit(formula = Surv(time, cens) ~ -1)
        n events median 0.95LCL 0.95UCL
       83
           15 NA 12 NA
  Available sample meta-data:
  alt_sample_name:
  p0102bis sample_Ovarian tumor p0103bis sample_Ovarian tumor
  p0112bis sample_Ovarian tumor p0114bis sample_Ovarian tumor
  p0125bis sample_Ovarian tumor p0128bis sample_Ovarian tumor
  p0143bis sample_Ovarian tumor p0146bis sample_Ovarian tumor
  p0188bis sample Ovarian tumor p0208bis sample Ovarian tumor
  p0210bis sample_Ovarian tumor p0217bis sample_Ovarian tumor
   p057bis sample_Ovarian tumor p070bis sample_Ovarian tumor
   p080bis sample_Ovarian tumor p091bis sample_Ovarian tumor
   p139bis sample_Ovarian tumor p13bis sample_Ovarian tumor
   p141bis sample_Ovarian tumor p166bis sample_Ovarian tumor
```

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p171bis	sample_Ovarian	tumor 1	p17bis	sample_Ovarian	tumor 1
p183bis	sample_Ovarian	tumor 1	p209bis	sample_Ovarian	tumor 1
p212bis	sample_Ovarian	tumor 1	p213bis	sample_Ovarian	tumor 1
p243bis	sample_Ovarian	tumor 1	p246bis	sample_Ovarian	tumor 1
p261bis	sample_Ovarian	tumor 1	p284bis	sample_Ovarian	tumor 1
p293bis	sample_Ovarian	tumor 1	p310bis	sample_Ovarian	tumor 1
p31bis	sample_Ovarian	tumor 1	p320bis	sample_Ovarian	tumor 1
p331bis	sample_Ovarian	tumor 1	p336bis	sample_Ovarian	tumor 1
p350bis	sample_Ovarian	tumor 1	p375bis	sample_Ovarian	tumor 1
p382bis	sample_Ovarian	tumor 1	p383bis	sample_Ovarian	tumor 1
p386bis	sample_Ovarian	tumor 1	p388bis	sample_Ovarian	tumor 1
p398bis	sample_Ovarian	tumor 1	p39bis	sample_Ovarian	tumor 1
p401bis	sample_Ovarian	tumor 1	p414bis	sample_Ovarian	tumor 1
p421bis	sample_Ovarian	tumor 1	p429bis	sample_Ovarian	tumor 1
p433bis	sample_Ovarian	tumor 1	p448bis	sample_Ovarian	tumor 1
p455bis	sample_Ovarian	tumor 1	p459bis	sample_Ovarian	tumor 1
p462bis	sample_Ovarian	tumor 1	p482bis	sample_Ovarian	tumor 1
p487bis	sample_Ovarian	tumor 1	p497bis	sample_Ovarian	tumor 1
p502bis	sample_Ovarian	tumor 1	p540bis	sample_Ovarian	tumor 1
p541bis	sample_Ovarian	tumor 1	p549bis	sample_Ovarian	tumor 1
p550bis	sample_Ovarian	tumor 1	p567bis	sample_Ovarian	tumor 1
p56bis	sample_Ovarian	tumor 1	p573bis	sample_Ovarian	tumor 1
p586bis	sample_Ovarian	tumor 1	p597bis	sample_Ovarian	tumor 1
p616bis	sample_Ovarian	tumor 1	p63bis	sample_Ovarian	tumor 1

p66bis sample_Ovarian tumor

p646bis sample_Ovarian tumor

```
p690bis sample_Ovarian tumor
  p68bis sample_Ovarian tumor
 p692bis sample_Ovarian tumor
                              p725bis sample_Ovarian tumor
                              p760bis sample_Ovarian tumor
  p73bis sample_Ovarian tumor
 p770bis sample_Ovarian tumor
                               p772bis sample_Ovarian tumor
 p775bis sample_Ovarian tumor
                              p793bis sample_Ovarian tumor
  p79bis sample_Ovarian tumor
                               p84bis sample_Ovarian tumor
  p90bis sample_Ovarian tumor
sample_type:
borderline
                tumor
       15
                   68
histological_type:
       clearcell
                                        mucinous
                                                             other
                             endo
                                                17
             ser undifferentiated
              31
primarysite:
ΟV
83
summarygrade:
high low NA's
  35
     33 15
summarystage:
early
   83
tumorstage:
1
83
substage:
 a b c
25 5 53
grade:
```

GSE8842 159

```
1
       2
           3 NA's
           35 15
  13
      20
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
                      2.1
days_to_death:
  Min. 1st Qu. Median
                          Mean 3rd Qu.
                                          Max.
     0 1192 2248
                          2273 3048
                                          5824
vital_status:
deceased living
     15
uncurated_author_metadata:
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                      title: p0114bis sample_Ovarian tumor///geo_accession: GSM214
         title: p0125bis sample_Ovarian tumor///geo_accession: GSM214009///status:
               title: p0128bis sample_Ovarian tumor///geo_accession: GSM214030///s
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                title: p0188bis sample_Ovarian tumor///geo_accession: GSM214041//
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             title: p0217bis sample_Ovarian tumor///geo_accession: GSM214008///sta
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```

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            title: p13bis sample_Ovarian tumor///geo_accession: GSM214043///status:
  title: p141bis sample_Ovarian tumor///geo_accession: GSM214081///status: Public
    title: p166bis sample_Ovarian tumor///geo_accession: GSM214013///status: Public
           title: p171bis sample_Ovarian tumor///geo_accession: GSM214014///status
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          title: p183bis sample_Ovarian tumor///geo_accession: GSM214015///status:
title: p209bis sample_Ovarian tumor///geo_accession: GSM214090///status: Public or
     title: p212bis sample_Ovarian tumor///geo_accession: GSM214065///status: Publ
        title: p213bis sample_Ovarian tumor///geo_accession: GSM214018///status: F
        title: p243bis sample_Ovarian tumor///geo_accession: GSM214042///status: F
    title: p246bis sample_Ovarian tumor///geo_accession: GSM214055///status: Public
           title: p261bis sample_Ovarian tumor///geo_accession: GSM214034///status:
                         title: p284bis sample_Ovarian tumor///geo_accession: GSM21
    title: p293bis sample_Ovarian tumor///geo_accession: GSM214035///status: Publi
title: p310bis sample_Ovarian tumor///geo_accession: GSM214083///status: Public on
         title: p31bis sample_Ovarian tumor///geo_accession: GSM214019///status: F
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GSE8842 161

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      title: p487bis sample_Ovarian tumor///geo_accession: GSM214026///status: Publ
             title: p497bis sample_Ovarian tumor///geo_accession: GSM214052///statu
       title: p502bis sample_Ovarian tumor///geo_accession: GSM214070///status: Puk
   title: p540bis sample_Ovarian tumor///geo_accession: GSM214085///status: Public
 title: p541bis sample_Ovarian tumor///geo_accession: GSM214082///status: Public or
title: p549bis sample_Ovarian tumor///geo_accession: GSM214086///status: Public on
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     title: p567bis sample_Ovarian tumor///geo_accession: GSM214054///status: Publi
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     title: p573bis sample_Ovarian tumor///geo_accession: GSM214060///status: Publ
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     title: p79bis sample_Ovarian tumor///geo_accession: GSM214063///status: Publi
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```

Value

An expression set

GSE9891 163

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 kmeans groups was evaluated using Cox proportional hazards models. Class prediction validated k-means groups in an independent dataset. A semisupervised survival analysis of the array data was used to compare against unsupervised clustering results. Optimal clustering of array data identified six molecular subtypes. Two subtypes represented predominantly serous low malignant potential and low-grade endometrioid subtypes, respectively. The remaining four subtypes represented higher grade and advanced stage cancers of serous and endometrioid morphology. A novel subtype of high-grade serous cancers reflected a mesenchymal cell type, characterized by overexpression of N-cadherin and P-cadherin and low expression of differentiation markers, including CA125 and MUC1. A poor prognosis subtype was defined by a reactive stroma gene expression signature, correlating with extensive desmoplasia in such samples. A similar poor prognosis signature could be found using a semisupervised analysis. Each subtype displayed distinct levels and patterns of immune cell infiltration. Class prediction identified similar subtypes in an independent ovarian dataset with similar prognostic trends. Gene expression profiling identified molecular subtypes of ovarian cancer of biological and clinical importance.

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Tothill RW, Tinker AV, George J, Brown R, Fox SB, Lade S, John
 Laboratory: Tothill, Bowtell 2008
 Contact information:
 Title: Novel molecular subtypes of serous and endometrioid ovarian cancer linked
 URL:
 PMIDs: 18698038
 Abstract: A 243 word abstract is available. Use 'abstract' method.
 Information is available on: preprocessing
  notes:
  platform_title:
      [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
  platform_shorttitle:
      Affymetrix HG-U133Plus2
  platform_summary:
     hgu133plus2
```

```
platform_manufacturer:
      Affymetrix
    platform_distribution:
      commercial
    platform accession:
      GPL570
    version:
      2015-09-22 20:16:32
  featureData(eset):
  An object of class 'AnnotatedDataFrame'
   featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
     (42447 total)
   varLabels: probeset gene EntrezGene.ID best_probe
   varMetadata: labelDescription
Details
  assayData: 42447 features, 285 samples
  Platform type:
  Overall survival time-to-event summary (in years):
  Call: survfit(formula = Surv(time, cens) ~ -1)
    7 observations deleted due to missingness
      n events median 0.95LCL 0.95UCL
   278.00 113.00 3.95 3.53 5.01
  Available sample meta-data:
  ______
  alt_sample_name:
    X129 X146 X152 X20019 X20025 X20027 X20031 X20032 X20041 X20046
         1
                X20074 X22002 X22012 X22013 X22020 X22023 X22027 X22029 X22031 X22037
      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
  X23043 X23052 X23053 X23055 X23066 X23070 X23074 X23077 X23084 X23098
                                             1
      1
         1
               1
                     1
                           1
                                 1
                                      1
                                                    1
   X23102 X23106 X23116 X23128 X23139 X23143 X23162 X23165 X23167 X23170
                           1
      1
           1
               1
                     1
                                    1
                                       1
                                              1
                                                    1
  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
   X32048 X32049 X32054 X32055 X32089 X32098 X32103 X32117 X34019 X34049
                     1
      1
          1
                1
                            1
                                  1
                                        1
                                              1
                                                    1
```

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```
X34066 X34078 X34080 X34085 X34086 X34090 X34102 X34103 X34111 X34113
 X34117 X34125 X34165 X34168 X34172 X34186 X34202 X34207 X34801 (Other)
      1 1 1 1 1 1 1
                                             1
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
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 6
2005-06-06 2005-06-08 2005-06-16 2005-06-17 2005-06-24 2005-07-06 2005-07-15
                                            2
     4
             5
                     3
                            5 6
2005-07-20 2005-07-29 2005-08-03 2005-08-05 2005-08-18 2005-08-24 2005-08-26
                            3
             5
                    6
                                    4
                                            8
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
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
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
```

uncurated_author_metadata:

GSE9891 167

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       title: X20027///geo_accession: GSM249996///status: Public on Mar 01 2008
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          title: X23053///geo_accession: GSM249973///status: Public on Mar 01 2008/
         title: X23055///geo_accession: GSM249972///status: Public on Mar 01 2008/
              title: X23066///geo_accession: GSM249716///status: Public on Mar 01 2
            title: X23070///geo_accession: GSM249971///status: Public on Mar 01 200
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          title: X23077///geo_accession: GSM249969///status: Public on Mar 01 2008/
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              title: X23102///geo_accession: GSM249966///status: Public on Mar 01 2
title: X23106///geo_accession: GSM249965///status: Public on Mar 01 2008///submissi
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          title: X23128///geo_accession: GSM249963///status: Public on Mar 01 2008/
          title: X23139///geo_accession: GSM249962///status: Public on Mar 01 2008/
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       title: X23213///geo_accession: GSM249946///status: Public on Mar 01 2008
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title: X32034///geo_accession: GSM249937///status: Public on Mar 01 2008///subr
    title: X32048///geo_accession: GSM249936///status: Public on Mar 01 2008//
  title: X32049///geo_accession: GSM249935///status: Public on Mar 01 2008///su
```

title: X23167///geo_accession: GSM249958///status: Public on Mar 01 2008/

title: X23170///geo_accession: GSM249957///status: Public on Mar 01 2008/

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             title: X32055///geo_accession: GSM249933///status: Public on Mar 01 2
title: X32089///geo_accession: GSM249932///status: Public on Mar 01 2008///submiss
      title: X32098///geo_accession: GSM249931///status: Public on Mar 01 2008///s
        title: X32103///geo_accession: GSM249930///status: Public on Mar 01 2008/
                 title: X32117///geo_accession: GSM249715///status: Public on Mar
         title: X34019///geo_accession: GSM249929///status: Public on Mar 01 2008/
           title: X34049///geo_accession: GSM249928///status: Public on Mar 01 200
        title: X34066///geo_accession: GSM249927///status: Public on Mar 01 2008/
        title: X34078///geo_accession: GSM249926///status: Public on Mar 01 2008/
         title: X34080///geo_accession: GSM249925///status: Public on Mar 01 2008/
       title: X34085///geo_accession: GSM249924///status: Public on Mar 01 2008//
          title: X34086///geo_accession: GSM249923///status: Public on Mar 01 2008
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    title: X34102///geo_accession: GSM249921///status: Public on Mar 01 2008///suk
         title: X34103///geo_accession: GSM249920///status: Public on Mar 01 2008/
        title: X34111///geo_accession: GSM249919///status: Public on Mar 01 2008/
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        title: X34125///geo_accession: GSM249916///status: Public on Mar 01 2008/
         title: X34165///geo_accession: GSM249915///status: Public on Mar 01 2008/
     title: X34168///geo_accession: GSM249914///status: Public on Mar 01 2008///su
         title: X34172///geo_accession: GSM249913///status: Public on Mar 01 2008/
        title: X34186///geo_accession: GSM249912///status: Public on Mar 01 2008/
```

loadOvarianDatasets 171

```
title: X34202///geo_accession: GSM249911///status: Public on Mar 01 2008///suk
title: X34207///geo_accession: GSM249910///status: Public on Mar 01 2008///
title: X34801///geo_accession: GSM249909///status: Public on Mar 01 2008///
```

Value

An expression set

loadOvarianDatasets

Function to load ovarian cancer SummarizedExperiment objects from the Experiment Hub

Description

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

Usage

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

Arguments

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

minNumberGenes

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

minNumberEvents

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

172 loadOvarianEsets

Value

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

Examples

```
experimentsAndDups = loadOvarianDatasets()
```

loadOvarianEsets

Function to load ovarian cancer expression sets from the Experiment Hub

Description

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

Usage

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

PMID15897565 173

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

Examples

```
esetsAndDups = loadOvarianEsets()
```

PMID15897565

Patterns of gene expression that characterize long-term survival in advanced stage serous ovarian cancers.

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 29fold compared with early-stage cases). These results suggest that gene expression patterns underlie differences in outcome, and an examination of the genes that provide this discrimination reveals that many are implicated in processes that define the malignant phenotype. Differences in survival of advanced ovarian cancers are reflected by distinct patterns of gene expression. This biological distinction is further emphasized by the finding that early-stage cancers share expression patterns with the advanced stage long-term survivors, suggesting a shared favorable biology.

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Berchuck A, Iversen ES, Lancaster JM, Pittman J, Luo J, Lee P,
  Laboratory: Berchuck, Marks 2005
  Contact information:
  Title: Patterns of gene expression that characterize long-term survival in advance
  URT:
  PMIDs: 15897565
 Abstract: A 258 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
  platform_title:
      [HG-U133A] Affymetrix Human Genome U133A Array
  platform_shorttitle:
      Affymetrix HG-U133A
  platform_summary:
      hqu133a
  platform_manufacturer:
      Affymetrix
  platform_distribution:
      commercial
  platform_accession:
      GPL96
   warnings:
```

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```
These samples are a subset of PMID17290060.
     version:
        2015-09-22 20:17:53
   featureData(eset):
  An object of class 'AnnotatedDataFrame'
    featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
      (20967 total)
    varLabels: probeset gene EntrezGene.ID best_probe
    varMetadata: labelDescription
Details
  assayData: 20967 features, 63 samples
  Platform type:
  _____
  Available sample meta-data:
  alt_sample_name:
     Min. 1st Qu. Median Mean 3rd Qu. Max.
     1761 1828 1907 2001 2032
                                          2536
  sample_type:
  tumor
     63
  histological_type:
  ser
   63
  primarysite:
  ΟV
  63
  summarygrade:
  high low NA's
    25 37 1
  summarystage:
  early late
     11 52
  tumorstage:
   1 2 3 4
   7 4 48 4
```

grade:

```
2
            3
                  4 NA's
       35
            24
                  1 1
age_at_initial_pathologic_diagnosis:
  Min. 1st Qu. Median
                           Mean 3rd Qu.
                                           Max.
  33.00 52.50 59.00
                          59.21 67.00
                                           79.00
os_binary:
 long short NA's
   24
         28
             11
debulking:
   optimal suboptimal
                            NA's
        24
                   28
                              11
batch:
2002 - 09 - 20 \ 2002 - 10 - 23 \ 2002 - 11 - 12 \ 2002 - 12 - 16 \ 2002 - 12 - 21 \ 2003 - 01 - 03 \ 2003 - 05 - 30
                    9
                             10
                                          1
                                                     3
2003-07-02
uncurated author metadata:
 Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1761///Cancer.Type: Early st
 Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1762///Cancer.Type: Early st
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1763///Cancer.Type: Early sta
 Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1764///Cancer.Type: Early st
 Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1765///Cancer.Type: Early st
      Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1772///Cancer.Type: Lor
      Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1773///Cancer.Type: Lor
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      Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1779///Cancer.Type: Lor
```

```
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1781///Cancer.Type: Lor
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    Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1829///Cancer.Type: Short
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    Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1831///Cancer.Type: Short
    Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1832///Cancer.Type: Short
    Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1833///Cancer.Type: Short
    Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1834///Cancer.Type: Short
    Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1835///Cancer.Type: Short
    Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1836///Cancer.Type: Short
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      Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1901///Cancer.Type: Lor
      Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1902///Cancer.Type: Lor
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1903///Cancer.Type: Early sta
      Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1904///Cancer.Type: Lor
    Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1905///Cancer.Type: Short
    Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1906///Cancer.Type: Short
     Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1907///Cancer.Type: Lor
    Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1908///Cancer.Type: Short
    Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1909///Cancer.Type: Short
     Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1989///Cancer.Type: Lor
    Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2003///Cancer.Type: Shore
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```

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1780///Cancer.Type: Lor

```
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    Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2026///Cancer.Type: Short
    Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2027///Cancer.Type: Short
    Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2028///Cancer.Type: Short
    Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2029///Cancer.Type: Short
      Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2030///Cancer.Type: Sh
      Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2031///Cancer.Type: Lor
      Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2032///Cancer.Type: Lor
     Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2033///Cancer.Type: Lor
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2390///Cancer.Type: Early st
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2391///Cancer.Type: Early st
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2392///Cancer.Type: Early sta
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2393///Cancer.Type: Early sta
     Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2394///Cancer.Type: Lor
     Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2395///Cancer.Type: Lor
    Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2396///Cancer.Type: Short
    Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2397///Cancer.Type: Short
      Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2398///Cancer.Type: Sh
    Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2399///Cancer.Type: Short
    Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2400///Cancer.Type: Short
    Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2401///Cancer.Type: Short
```

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PMID17290060 179

```
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2402///Cancer.Type: Sh
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2536///Cancer.Type: Early st
```

Value

An expression set

PMID17290060

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, Crag Laboratory: Dressman, Lancaster 2007
Contact information:
Title: An integrated genomic-based approach to individualized treatment of patier 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:
        hqu133a
      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
    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
           2476 2479 2505 2542 2573 2673 2739
                                                                    2802 2849
      2465
              1
                     1
                                                                       1
        1
                             1
                                      1
                                               1
                                                       1
                                                               1
                                                                                1
```

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```
    2895
    2967
    2981
    2999
    3018
    3090
    3102
    3107
    3142
    860

    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
                     D2557
                          D2559
          D2433
                D2480
                                          D2575 D2576
D2421
    D2432
                                D2560
                                      D2572
                                    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
                    D2749 D2776
                                    M1054
                                          M1055
D2726
    D2727 D2733 D2738
                               D2792
                                                M120
          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

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```
primary_therapy_outcome_success:
  completeresponse progressivedisease
                85
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
                   8
                               9
                                          1
                                                     3
2004-03-09 2004-03-16 2004-04-20 2004-05-18 2004-05-21 2004-05-27 2004-06-22
                              5
                                        15
                                                     7
                    6
2004-06-23
uncurated_author_metadata:
                        OVC.TumorID: 1024///Survival: 13///X0...alive...1...dead: 1
                       OVC.TumorID: 1447///Survival: 75///X0...alive...1...dead: 1/
                       OVC.TumorID: 1451///Survival: 132///X0...alive...1...dead: 1
                        OVC.TumorID: 1504///Survival: 108///X0...alive...1...dead:
                       OVC.TumorID: 1526///Survival: 74///X0...alive...1...dead: 1/
                       OVC.TumorID: 1552///Survival: 33///X0...alive...1...dead: 1/
                       OVC.TumorID: 1578///Survival: 33///X0...alive...1...dead: 1/
                        OVC.TumorID: 1590///Survival: 148///X0...alive...1...dead:
                       OVC.TumorID: 1615///Survival: 13///X0...alive...1...dead: 1/
                        OVC.TumorID: 1623///Survival: 147///X0...alive...1...dead:
                       OVC.TumorID: 1665///Survival: 15///X0...alive...1...dead: 1/
                        OVC.TumorID: 1674///Survival: 18///X0...alive...1...dead: 1
                      OVC.TumorID: 1675///Survival: 34///X0...alive...1...dead: 1/
                      OVC.TumorID: 1774///Survival: 22///X0...alive...1...dead: 1/
```

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

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

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

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

OVC.TumorID: D2433///Survival: 49///X0...alive...1...dead: 0//

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

OVC.TumorID: D2480///Survival: 34///X0...alive...1...dead: 1/

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```
OVC.TumorID: M1054///Survival: 101///X0...alive...1...dead: 0///Assigned OVC.TumorID: M1055///Survival: 13///X0...alive...1...dead: 0///Assigned OVC.TumorID: M120///Survival: 35///X0...alive...1...dead: 1///Assigned.S OVC.TumorID: M1241///Survival: 95///X0...alive...1...dead: 0///Assigned.S OVC.TumorID: M1390///Survival: 46///X0...alive...1...dead: 0//OVC.TumorID: M1503///Survival: 53///X0...alive...1...dead: 1///Assigned OVC.TumorID: M1572///Survival: 22///X0...alive...1...dead: 1///Assigned OVC.TumorID: M17///Survival: 17///X0...alive...1...dead: 0///Assigned.Stage: 4///OVC.TumorID: M2070///Survival: 65///X0...alive...1...dead: 0///Assigned.S OVC.TumorID: M2070///Survival: 58///X0...alive...1...dead: 0///Assigned.S OVC.TumorID: M2097///Survival: 58///X0...alive...1...dead: 0///Assigned.S OVC.TumorID: M2184///Survival: 34///X0...alive...1...dead: 0///Assigned.S OVC.TumorID: M2184//Survival: 34///X0...alive...1...dead: 0///Assigned.S OVC.TumorID: M2184//Survival: 34//X0...alive...1...dead: 0//As
```

Value

An expression set

PMID19318476

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

Description

Although few women with advanced serous ovarian cancer are cured, detection of the disease at an early stage is associated with a much higher likelihood of survival. We previously used gene expression array analysis to distinguish subsets of advanced cancers based on disease outcome. In the present study, we report on gene expression of early-stage cancers and validate our prognostic model for advanced-stage cancers. Frozen specimens from 39 stage I/II, 42 stage III/IV, and 20 low malignant potential cancers were obtained from four different sites. A linear discriminant model was used to predict survival based upon array data. We validated the late-stage survival model and show that three of the most differentially expressed genes continue to be predictive of outcome. Most early-stage cancers (38 of 39 invasive, 15 of 20 low malignant potential) were classified as

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long-term survivors (median probabilities 0.97 and 0.86). MAL, the most differentially expressed gene, was further validated at the protein level and found to be an independent predictor of poor survival in an unselected group of advanced serous cancers (P = 0.0004). These data suggest that serous ovarian cancers detected at an early stage generally have a favorable underlying biology similar to advanced-stage cases that are long-term survivors. Conversely, most late-stage ovarian cancers seem to have a more virulent biology. This insight suggests that if screening approaches are to succeed it will be necessary to develop approaches that are able to detect these virulent cancers at an early stage.

Format

```
experimentData(eset):
Experiment data
 Experimenter name: Berchuck A, Iversen ES, Luo J, Clarke JP, Horne H, Levine DA,
  Laboratory: Berchuck, Lancaster 2009
  Contact information:
 Title: Microarray analysis of early stage serous ovarian cancers shows profiles
  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
```

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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
  D2629 D2640 D2648 D2736 D2749 D2776 D2792 M1025 M1054 M1055 M120 M1241 M1572
  M17 M1777 M1891 M2184 M2515 M2807 M3035 M337 M3484 M359 M4161 M444 M503
  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 29 10 1
  1
substage:
  a b c NA's
  1 1 29 11
grade:
```

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```
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
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
uncurated_author_metadata:
```

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

Value

An expression set

TCGA.RNASeqV2

Integrated genomic analyses of ovarian carcinoma.

Description

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

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Integrated genomic analyses of ovarian carcinoma. Nature 2011,
 Laboratory: Cancer Genome Atlas Research Network 2011
  Contact information:
  Title: Integrated genomic analyses of ovarian carcinoma.
  URL:
  PMIDs: 21720365
  Abstract: A 179 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
  platform_title:
      [RNASeqV2] Illumina HiSeq RNA sequencing
   platform_shorttitle:
      Illumina HiSeq RNA sequencing
   platform_summary:
      NA
   platform_manufacturer:
      Illumina
   platform distribution:
      sequencing
  platform_accession:
  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 TCGA-04-1362-01A-01R-1565-13 TCGA-04-1364-01A-01R-1565-13 1 TCGA-04-1365-01A-01R-1565-13 TCGA-04-1514-01A-01R-1566-13 1 TCGA-04-1519-01A-01R-1565-13 TCGA-09-0364-01A-02R-1564-13 1 TCGA-09-0366-01A-01R-1564-13 TCGA-09-0367-01A-01R-1564-13 1 TCGA-09-0369-01A-01R-1564-13 TCGA-09-1662-01A-01R-1566-13 1 TCGA-09-1666-01A-01R-1566-13 TCGA-09-1667-01C-01R-1566-13 1 TCGA-09-1668-01B-01R-1566-13 TCGA-09-1669-01A-01R-1566-13 1 TCGA-09-1670-01A-01R-1566-13 TCGA-09-1673-01A-01R-1566-13 1 TCGA-09-1674-01A-01R-1566-13 TCGA-09-2044-01B-01R-1568-13 1 TCGA-09-2045-01A-01R-1568-13 TCGA-09-2048-01A-01R-1568-13 1 TCGA-09-2051-01A-01R-1568-13 TCGA-09-2054-01A-01R-1568-13 1 TCGA-09-2056-01B-01R-1568-13 TCGA-10-0928-01A-02R-1564-13 1 TCGA-10-0936-01A-01R-1564-13 TCGA-13-0730-01A-01R-1564-13 1 TCGA-13-0799-01A-01R-1564-13 TCGA-13-0800-01A-01R-1564-13 1 TCGA-13-0801-01A-01R-1564-13 TCGA-13-0890-01A-01R-1564-13 1 TCGA-13-0893-01B-01R-1565-13 TCGA-13-0897-01A-01R-1564-13 1 TCGA-13-0899-01A-01R-1564-13 TCGA-13-0913-01A-01R-1564-13 1 TCGA-13-0916-01A-01R-1564-13 TCGA-13-0920-01A-01R-1564-13 1 TCGA-13-0924-01A-01R-1564-13 TCGA-13-1403-01A-01R-1565-13 1 TCGA-13-1405-01A-01R-1565-13 TCGA-13-1410-01A-01R-1565-13 1 TCGA-13-1481-01A-01R-1565-13 TCGA-13-1497-01A-01R-1565-13

```
TCGA-13-1498-01A-01R-1565-13 TCGA-13-1505-01A-01R-1565-13
                          1
TCGA-13-1506-01A-01R-1565-13 TCGA-13-1507-01A-01R-1565-13
TCGA-13-1511-01A-01R-1565-13 TCGA-13-1512-01A-01R-1565-13
                          1
TCGA-13-2060-01A-01R-1568-13 TCGA-20-1682-01A-01R-1564-13
                          1
TCGA-20-1683-01A-01R-1566-13 TCGA-20-1684-01A-01R-1566-13
                          1
TCGA-20-1685-01A-01R-1566-13 TCGA-20-1687-01A-01R-1566-13
                          1
TCGA-23-1023-01A-02R-1564-13 TCGA-23-1026-01B-01R-1569-13
                          1
TCGA-23-1027-01A-02R-1564-13 TCGA-23-1029-01B-01R-1567-13
                          1
TCGA-23-1109-01A-01R-1564-13 TCGA-23-1111-01A-01R-1567-13
                          1
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TCGA-24-1551-01A-01R-1566-13 TCGA-24-1552-01A-01R-1566-13
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TCGA-24-1558-01A-01R-1566-13 TCGA-24-1560-01A-01R-1566-13
TCGA-24-1562-01A-01R-1566-13
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TCGA-09-1674 TCGA-09-2044 TCGA-09-2045 TCGA-09-2048 TCGA-09-2051 TCGA-09-2054
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       TCGA-13-1481 TCGA-13-1497 TCGA-13-1498 TCGA-13-1505 TCGA-13-1506 TCGA-13-1507
       TCGA-13-1511 TCGA-13-1512 TCGA-13-2060 TCGA-20-1682 TCGA-20-1683 TCGA-20-1684
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                                  1 1 1
TCGA-23-1809 TCGA-23-2077 TCGA-23-2081 TCGA-23-2084 TCGA-24-0975 TCGA-24-1103
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TCGA-24-1413 TCGA-24-1416 TCGA-24-1417 TCGA-24-1418 TCGA-24-1419 TCGA-24-1423
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TCGA-24-1424 TCGA-24-1427 TCGA-24-1428 TCGA-24-1430 TCGA-24-1436 TCGA-24-1467
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TCGA-24-1469 TCGA-24-1474 TCGA-24-1544 TCGA-24-1548 TCGA-24-1549 TCGA-24-1550
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        1
                                      1
TCGA-24-1558 TCGA-24-1560 TCGA-24-1562
                                 (Other)
                                     162
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sample_type:
tumor

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261
histological_type:
ser
261
primarysite:
other ov
  1 260
summarygrade:
high low NA's
226 29 6
summarystage:
early late NA's
  18 242 1
tumorstage:
 2 3 4 NA's
18 209 33 1
substage:
  b c NA's
 16 211 34
grade:
  1 2 3 4 NA's
  1 28 225
             1 6
age_at_initial_pathologic_diagnosis:
  Min. 1st Qu. Median Mean 3rd Qu. Max.
  34.00 51.00 58.00 58.84 66.00 87.00
pltx:
 n y NA's
 17 215 29
tax:
 n y NA's
 17 215 29
neo:
 n NA's
```

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

232 29

days_to_tumor_recurrence:

9.0 225.0 426.5 585.3 755.0 5480.0 19

recurrence_status:

norecurrence recurrence

123 138

days_to_death:

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

vital_status:

deceased living NA's 143 114 4

site_of_tumor_first_recurrence:

locoregional metastasis NA's 82 56 123

primary_therapy_outcome_success:

completeresponse partialresponse progressivedisease stabledisease 147 30 15

NA's 54

debulking:

optimal suboptimal NA's 171 60 30

percent_normal_cells:

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

percent_stromal_cells:

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

percent_tumor_cells:

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

uncurated_author_metadata:

 $\verb|age_at_initial_pathologic_diagnosis: 38///anatomic_organ_subdivision: Bilateral//kapatomic_organ_subdivision: Bilateral//k$

age_at_initial_

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                               age_at_initial_pathologic_diagnosi
                                                         age_at_ir
age_at_initial_pathologic_diagnosis: 42///anatomic_organ_subdivi
                          age_at_initial_pathologic_diagnosis: 4
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                                              age_at_initial_path
                                            age_at_initial_pathol
                                          age_at_initial_patholog
                                                 age_at_initial_p
           age_at_initial_pathologic_diagnosis: 45///anatomic_or
                                                            age_at
                 age_at_initial_pathologic_diagnosis: 45///anato
```

age_at_ir

age_at_initial_patholog

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                                          age_at_initial_pathologic_dia
age_at_initial_pathologic_diagnosis: 46///anatomic_organ_subdivision:
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                                   age_at_initial_pathologic_diagnosis
                    age_at_initial_pathologic_diagnosis: 47///anatomic
                                                        age_at_initial_
                age_at_initial_pathologic_diagnosis: 47///anatomic_org
                         age_at_initial_pathologic_diagnosis: 48///ana
```

age_at_initial_patholo

age_at

age_at_initial_pathologic_dia

age_

age_at_initi

age

age_at_initial_pathologic_diagnosis: 49///anatomic_

age_at_initial_pathologic_diagno

age_at_initial_pathologic_diagnosis: 50///anatomic_organ_

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age_at_initial_pathologic_diagnosis: 50///anatomic_organ_subdivision: Left///bcr_gage_at_initial_pathologic_diagnosis: 50///anatomage_at_initial_pathologic_diagnosis: 50///anatomage_at_initial_pathologic_diagnosis: 51///anatomic_organ_subdivision: Bilateral//age_at_initial_pathologic_diagnosic age_at_initial_pathologic_diagnosic age_at_initial_patholog
```

age_at_initial_pathologic_c

age_at_initial_pathologic_diagr

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age_at_
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                                                age_at_initial_pathol
                                      age_at_initial_pathologic_diagr
        age_at_initial_pathologic_diagnosis: 53///anatomic_organ_suk
                               age_at_initial_pathologic_diagnosis:
                  age_at_initial_pathologic_diagnosis: 53///anatomic
                                                age_at_initial_pathol
age_at_initial_pathologic_diagnosis: 54///anatomic_organ_subdivision
                                                             age_at_i
                                                        age_at_initia
                                                          age_at_init
  age_at_initial_pathologic_diagnosis: 54///anatomic_organ_subdivisi
                                                                   age
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Value

An expression set

TCGAOVARIAN

Integrated genomic analyses of ovarian carcinoma.

Description

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

Format

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experimentData(eset):
Experiment data
  Experimenter name: Integrated genomic analyses of ovarian carcinoma. Nature 2011,
 Laboratory: Cancer Genome Atlas Research Network 2011
  Contact information:
  Title: Integrated genomic analyses of ovarian carcinoma.
  URL:
  PMIDs: 21720365
  Abstract: A 179 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
  platform_title:
      [HT_HG-U133A] Affymetrix HT Human Genome U133A Array
  platform_shorttitle:
      Affymetrix HT_HG-U133A
  platform_summary:
      hthgu133a
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     platform distribution:
        commercial
     platform accession:
        GPL3921
     warnings:
        The following samples are likely from specimens also used in GSE26712: TCG
  A.13.0725, TCGA.13.0885, TCGA.13.0887, TCGA.13.0890, TCGA.13.0886, TCGA.13
   .0714, TCGA.13.0727, TCGA.13.1817, TCGA.13.1499, TCGA.13.0883
     version:
        2015-09-22 20:25:15
   featureData(eset):
  An object of class 'AnnotatedDataFrame'
    featureNames: 1007_s_at 1053_at ... AFFX-M27830_M_at (21260 total)
    varLabels: probeset gene EntrezGene.ID best_probe
    varMetadata: labelDescription
Details
  assayData: 21260 features, 578 samples
  Platform type:
  Overall survival time-to-event summary (in years):
  Call: survfit(formula = Surv(time, cens) ~ -1)
     21 observations deleted due to missingness
        n events median 0.95LCL 0.95UCL
   557.00 290.00 3.73 3.45 4.06
    ______
  Available sample meta-data:
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  TCGA-04-1335-01A-01R-0434-01 TCGA-04-1336-01A-01R-0434-01
  TCGA-04-1337-01A-01R-0434-01 TCGA-04-1338-01A-01R-0434-01
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TCGA-13-0723-01A-02R-0362-01 TCGA-13-0724-01A-01R-0362-01
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TCGA-01-0639 TCGA-01-0642 TCGA-04-1331 TCGA-04-1332 TCGA-04-1335 TCGA-04-1336
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     TCGA-04-1517 TCGA-04-1519 TCGA-04-1525 TCGA-04-1530 TCGA-04-1536 TCGA-04-1542
     1 1 1 1 1 1
TCGA-04-1638 TCGA-04-1644 TCGA-04-1646 TCGA-04-1648 TCGA-04-1649 TCGA-04-1651
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TCGA-09-2045 TCGA-09-2048 TCGA-09-2049 TCGA-09-2050 TCGA-09-2051 TCGA-09-2053
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                                 1 1
TCGA-13-0723 TCGA-13-0724 TCGA-13-0725 (Other)
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adjacentnormal
             tumor
               570
histological_type:
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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

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    1    2    3    4 NA's
 16 27 436 84 15
substage:
  b c NA's
  31 448 99
grade:
  1 2 3 4 NA's
   6 69 479 1 23
age_at_initial_pathologic_diagnosis:
  Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
  26.00 51.00 59.00 59.70 68.25 89.00 10
pltx:
 n y NA's
 19 492 67
tax:
 n y NA's
 43 468 67
neo:
 n NA's
 511 67
days_to_tumor_recurrence:
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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:
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                       153
                 metastasis
                                                   NA's
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143 279

primary_therapy_outcome_success:

completeresponse partialresponse progressivedisease stabledisease 318 65 41 30

NA's 124

-

debulking:
 optimal suboptimal NA's

367 140 71

percent_normal_cells:

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

percent_stromal_cells:

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

percent_tumor_cells:

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

batch:

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

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age_at

age_at_initial_pathologic_

age_at_initial_pathologic_diagnosis: 37///ar

age_at_initial_pathologic_diagnosis: 38///anatomic_organ_subdivision: Bilateral///k

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                                    age_at_initial_pathologic_diagnosis: 4
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age_at_ini

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                       age_at_initial_pathologic_diagr
                                   age_at_initial_path
                                  age_at_initial_patho
                                 age_at_initial_pathol
                               age_at_initial_patholog
                                                     ag
                                      age_at_initial_p
age_at_initial_pathologic_diagnosis: 45///anatomic_or
```

age

age_at_initial_pathologic_diagnosis: 4

```
age_at
                       age_at_initial_pathologic_diagnosis: 45///anato
                                                age_at_initial_patholog
                                                 age_at_initial_patholo
                                   age_at_initial_pathologic_diagnosis
age_at_initial_pathologic_diagnosis: 45///anatomic_organ_subdivision:
                                          age_at_initial_pathologic_dia
 age_at_initial_pathologic_diagnosis: 46///anatomic_organ_subdivision
                       age_at_initial_pathologic_diagnosis: 46///anato
                               age_at_initial_pathologic_diagnosis: 47
                                              age_at_initial_pathologic
                                   age_at_initial_pathologic_diagnosis
                                   age_at_initial_pathologic_diagnosis
```

age_at_initial_pathologic_diagnosis: 47///anatomic

age_at_initial_

age_at_initial_pathologic_diagnosis: 47///anatomic_org

age_at_initial_pathologic_diagnosis: 48///ana

age_at_initial_pathologic_diagnosis

age_at_initial_pathologic_di

age_at_initial_pathologic_diagnosis: 48///ana

duplicates:

Length Class Mode 578 character character

Value

An expression set