Package ‘MetaGxOvarian’

March 21, 2024

Type Package

Title Transcriptomic Ovarian Cancer Datasets

Version 1.22.0

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 RELEASE_3_18

git_last_commit 77bbd05

git_last_commit_date 2023-10-24

Repository Bioconductor 3.18

Date/Publication 2024-03-21

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  Christopher Eeles [ctb],
  Benjamin Haibe-Kains [aut, cre]

Maintainer Benjamin Haibe-Kains <benjamin.haibe.kains@utoronto.ca>
Description

This is a note to inform package users that the `days_to_death` variable is also valid for living patients. In this case, the value in `days_to_death` is the number of days since the last follow-up appointment.

Format

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

**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 K, Rubio R, April C, Chen J, ...
Laboratory: Bentink, Matulonis 2012
Contact information:
Title: Angiogenic mRNA and microRNA gene expression signature predicts a novel subtype of serous ovarian cancer.
```
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:

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  1   1   1   1   1   1   1   1
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URL: PMIDs: 22348002
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a b c NA's
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Source.Name: DFCI-33

Source.Name: DFCI-34

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Source.Name: DFCI-37
An expression set

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

It is difficult to predict the clinical outcome for patients with ovarian cancer. However, the use of biomarkers as additional prognostic factors may improve the outcome for these patients. In order to find novel candidate biomarkers, differences in gene expressions were analysed in 54 stage III serous ovarian adenocarcinomas with oligonucleotide microarrays containing 27,000 unique probes. The microarray data was verified with quantitative real-time polymerase chain reaction for the genes TACC1, MUC5B and PRAME. Using hierarchical cluster analysis we detected a sub-group that included 60% of the survivors. The gene expressions in tumours from patients in this sub-group of survivors were compared with the remaining tumours, and 204 genes were found to
be differently expressed. We conclude that the sub-group of survivors might represent patients with favourable tumour biology and sensitivity to treatment. A selection of the 204 genes might be used as a predictive model to distinguish patients within and outside of this group. Alternative chemotherapy strategies could then be offered as first-line treatment, which may lead to improvements in the clinical outcome for these patients.

Format

experimentData(eset):
Experiment data
Laboratory: Partheen, Horvath 2006
Contact information:
Title: Expression analysis of stage III serous ovarian adenocarcinoma distinguishes a sub-group of survivors.
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:
-----------------------------
sample_type: tumor
histological_type: ser
primarysite: ov
summarystage: late
tumorstage: 3
substage: b c
age_at_initial_pathologic_diagnosis:
 Min. 1st Qu. Median Mean 3rd Qu. Max.
35.00 51.25 59.50 59.56 69.75 84.00
pltx: y
os_binary:
long short
20 34

debulking:
optimal suboptimal
13 41

uncurated_author_metadata:


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title: 626DC///geo_accession: GSM311964///status: Public on Aug 12 2008///submission_date: Aug 12 2008

Value

An expression set

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

eperimentData(eset):
Experiment data
Laboratory: Yoshihara, Tanaka 2009
Contact information:
Title: Gene expression profiling of advanced-stage serous ovarian cancers distinguishing novel subclasses and implicates ZEB2 in tumor progression and prognosis.
URL:
PMIDs: 19486012

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

featureData(eset):
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featureNames: 3 5 ... 22571 (15999 total)
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varMetadata: labelDescription

Details

assayData: 15999 features, 53 samples
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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 HG, Hollema H, Hofstra RM, te Meerman ... Zee AG.

Laboratory: Crijns, van der Zee 2009

Contact information:
Title: Survival-related profile, pathways, and transcription factors in ovarian cancer.
URL:
PMIDs: 19192944

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Information is available on: preprocessing
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version:
    2015-09-22 19:11:43

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submission_date: May 19 2009

data_row_count: 37632

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status: Public on May ...

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Value

An expression set

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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

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Laboratory: Denkert, Lage 2009

Contact information:

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

URL:

PMIDs: 19294737

Abstract: A 254 word abstract is available. Use 'abstract' method.

Information is available on: preprocessing

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[HG-U133A] Affymetrix Human Genome U133A Array

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

Format

experimentData(eset):
Experiment data
Laboratory: Yoshihara, Tanaka 2010
Contact information:
Title: Gene expression profile for predicting survival in advanced-stage serous ovarian cancer across two independent datasets.
URL:
PMIDs: 20300634

Abstract: A 257 word abstract is available. Use 'abstract' method.
Information is available on: preprocessing
notes:
platform_title:
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platform_shorttitle:
  Agilent G4112A
platform_summary:
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platform_manufacturer:
  Agilent
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platform_accession:
  GPL6848
version:
  2015-09-22 19:16:49

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

Details

assayData: 30936 features, 110 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

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**Histological Type:**
- ser: 110

**Primary Site:**
- ov: 110

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**Summary Stage:**
- late: 110

**Tumor Stage:**
- 3, 4
93 17

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tax:
Y
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debulking:
optimal suboptimal
| 57   | 53    |

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relation: Reanalyzed by: GSM795127

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relation:

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**Value**

An expression set

---

**GSE18520**


**Description**

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

**Format**

experimentData(eset):

Experiment data  
Experimenter name: Mok SC, Bonome T, Vathipadiekal V, Bell A, Johnson ME, Wong KK, Park DC, Hao K, Yip DK, Donninger H, ...  
Laboratory: Mok, Birrer 2009  
Contact information:  
Title: A gene signature predictive for outcome in advanced ovarian cancer identifies a survival factor: microfibril-associated glycoprotein 2.  
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  
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platform_manufacturer:  
Affymetrix|Operon  
platform_distribution:  
commercial|non-commercial  
platform_accession:  
GPL570|GPL9216  
version:
2015-09-22 19:21:25

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Details

assayData: 42447 features, 63 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

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histological_type:
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     53     10

primarysite:
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summarygrade:
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     53     10

summarystage:
   late  NA's
     53     10
tumorstage:
  3 NA's
  53  10

grade:
  3 NA's
  53  10

days_to_death:
  Min. 1st Qu. Median  Mean  3rd Qu.  Max.  NA's
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debulking:
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percent_normal_cells:
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  63

percent_tumor_cells:
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batch:
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uncurated_author_metadata:
  title: Normal Ovary, 2008///geo_accession: GSM462643///status: Public on Oct 17 2009///submission_date: Oct 16...2, the dimensions of the data set were reduced from 200 to 5 by PC analysis. The number of PCs was set at 5 capturing 90...
An expression set

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

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

Format

experimentData(eset):
Experiment data
Experimenter name: Konstantinopoulos PA, Spentzos D, Karlan BY, Taniguchi T et al.
Laboratory: Konstantinopoulos, Cannistra 2010 hgu95
Contact information:
Title: Gene expression profile of BRCAness that correlates with responsiveness to chemotherapy and with outcome in patients with epithelial ovarian cancer.
URL:
PMIDs: 20547991

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Information is available on: preprocessing
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[HG_U95Av2] Affymetrix Human Genome U95 Version 2 Array
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platform_accession: GPL570|GPL8300
version: 2015-09-22 19:26:29

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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)

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

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

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Information is available on: preprocessing
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| histological_type: | clearcell | endo | mucinous | other | ser | NA's |
| | 6 | 6 | 7 | 6 | 71 | 44 |
| primarysite: | other | ov | 44 | 96 |
| summarygrade: | high | low | NA's |
| | 63 | 33 | 44 |
| summarystage: | early | late | NA's |
| | 27 | 67 | 46 |
tumorstage:
1  2  3  4  NA's
18  9  52  15  46

substage:
a  b  c  NA's
14  10  55  61

grade:
1  2  3  NA's
6  27  63  44

batch:
21  18  37  20  36  7  1

uncurated_author_metadata:
title: Breast metastasis in the ovary_OC01_ARN0016 [HG-U133_Plus_2]///geo_accession: GSM516692///status: Public on Apr...

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title: Ovarian carcinoma_OC01_ARN0065

...
Value

An expression set

duplicates:
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NA's
138

Description

Format

experimentData(eset):
Experiment data
Experimenter name: EXpression Project for Oncology, International Genomics Consortium
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
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   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)
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varMetadata: labelDescription

Details

assayData: 42447 features, 204 samples
Platform type:
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Available sample meta-data:
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other  ov  NA's
        23  178     3
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high  low  NA's
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early  late  NA's
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       20  14  58  18  94
substage:
a  b  c  NA's
      17  22  79  86
grade:
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       11  20  83   8  82
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Min.  1st Qu.  Median  Mean  3rd Qu.  Max.
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miR-141 and miR-200a act on ovarian tumorigenesis by controlling oxidative stress response.

Although there is evidence that redox regulation has an essential role in malignancies, its impact on tumor prognosis remains unclear. Here we show crosstalk between oxidative stress and the miR-200 family of microRNAs that affects tumorigenesis and chemosensitivity. miR-141 and miR-200a target p38 and modulate the oxidative stress response. Enhanced expression of these microRNAs mimics p38 deficiency and increases tumor growth in mouse models, but it also improves
the response to chemotherapeutic agents. High-grade human ovarian adenocarcinomas that accumulate miR-200a have low concentrations of p38α and an associated oxidative stress signature. The miR200a-dependent stress signature correlates with improved survival of patients in response to treatment. Therefore, the role of miR-200a in stress could be a predictive marker for clinical outcome in ovarian cancer. In addition, although oxidative stress promotes tumor growth, it also sensitizes tumors to treatment, which could account for the limited success of antioxidants in clinical trials.

Format

experimentData(eset):
Experiment data
Experimenter name: Mateescu B, Batista L, Mariani O, Meyniel J, Cottu PH, Sastre-P, Mateescu, Mehta-Grigoriou 2011
Contact information:
Title: miR-141 and miR-200a act on ovarian tumorigenesis by controlling oxidative stress response.
PMIDs: 22101765
Abstract: A 149 word abstract is available. Use 'abstract' method.
Information is available on: preprocessing
notes:
platform_title:
[HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
platform_shorttitle:
Affymetrix HG-U133Plus2
platform_summary:
Affymetrix HG-U133Plus2
platform_manufacturer:
Affymetrix
platform_distribution:
commercial
platform_accession:
GPL570
platform_technology:
in situ oligonucleotide
version:
2015-09-22 19:44:56

featureData(eset):
An object of class 'AnnotatedDataFrame'
featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at (42447 total)
varLabels: probeset gene EntrezGene.ID best_probe
varMetadata: labelDescription
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assayData: 42447 features, 107 samples
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mucinous 8
other 6
ser 79

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low 40

summarystage:
early  late
   31    76

tumorstage:
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  20  11  59  17

substage:
  a  b  c  NA's
  16  12  62  17

grade:
  1  2  3
  7  33  67

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An expression set

Description

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

Format

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Title: A gene signature predicting for survival in suboptimally debulked patients with ovarian cancer.
URL:
PMIDs: 18593951

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Information is available on: preprocessing
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Affymetrix HG-U133A
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hgu133a
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version: 2015-09-22 19:46:24

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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
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Details

assayData: 20967 features, 195 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

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**GSE30009**  
*Multidrug resistance-linked gene signature predicts overall survival of patients with primary ovarian serous carcinoma.*

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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.

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Contact information:
Title: Multidrug resistance-linked gene signature predicts overall survival of patients with primary ovarian serous carcinoma.
URL: 22492981
PMIDs: 22492981

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Information is available on: preprocessing
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platform_summary:
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version: 2015-09-22 19:46:26

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featureNames: 5 6 ... 380 (363 total)
varLabels: probeset gene EntrezGene.ID best_probe
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Details

assayData: 363 features, 103 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

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Value

An expression set

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### GSE30161

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

**Description**

Despite advances in radical surgery and chemotherapy delivery, ovarian cancer is the most lethal gynecologic malignancy. Standard therapy includes treatment with platinum-based combination chemotherapies yet there is no biomarker model to predict their responses to these agents. We here have developed and independently tested our multi-gene molecular predictors for forecasting patients’ responses to individual drugs on a cohort of 55 ovarian cancer patients. To independently validate these molecular predictors, we performed microarray profiling on FFPE tumor samples of 55 ovarian cancer patients (UVA-55) treated with platinum-based adjuvant chemotherapy. Genome-wide chemosensitivity biomarkers were initially discovered from the in vitro drug activities and genomic expression data for carboplatin and paclitaxel, respectively. Multivariate predictors were trained with the cell line data and then evaluated with a historical patient cohort. For the UVA-55 cohort, the carboplatin, taxol, and combination predictors significantly stratified responder patients and non-responder patients (p = 0.019, 0.04, 0.014) with sensitivity = 91%, 96%, 93 and NPV = 57%, 67%, 67% in pathologic clinical response. The combination predictor also demonstrated a significant survival difference between predicted responders and non-responders with a median survival of 55.4 months vs. 32.1 months. Thus, COXEN single- and combination-drug predictors successfully stratified platinum resistance and taxane response in an independent cohort of ovarian cancer patients based on their FFPE tumor samples.

**Format**

```r
experimentData(eset):
Experiment data
  Laboratory: Ferriss, Lee 2012
  Contact information:
  Title: Multi-gene expression predictors of single drug responses to adjuvant chemotherapy in ovarian carcinoma: predicting platinum resistance.
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Abstract: A 215 word abstract is available. Use 'abstract' method.
Information is available on: preprocessing

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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 

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

Details 

assayData: 42447 features, 58 samples 
Platform type: 
Overall survival time-to-event summary (in years): 
Call: survfit(formula = Surv(time, cens) ~ -1) 

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\text{n} & \text{events} & \text{median} & \text{0.95LCL} & \text{0.95UCL} \\
58.00 & 36.00 & 4.19 & 2.70 & 6.17 \\
\end{array}
\]

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  ser  undifferentiated  NA's
  47        1        2

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summarystage:
  late
  58

tumorstage:
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substage:
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  9  11  38

grade:
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  2  19  33  4

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An expression set

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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 = 4.4 × 10^{-20}). We validated its predictive ability with five other data sets using multivariate analysis (Tothill’s data set, P = 1.1 × 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

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Experiment data
  Laboratory: Yoshihara, Tanaka 2012
Contact information:
Title: High-risk ovarian cancer based on 126-gene expression signature is uniquely characterized by downregulation of antigen presentation pathway.
URL: 
PMIDs: 22241791

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Information is available on: preprocessing
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2015-09-22 19:55:29

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varLabels: probeset gene EntrezGene.ID best_probe
varMetadata: labelDescription

Details

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

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debulking:
  optimal suboptimal
  103    157

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

Description

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

Format

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  Contact information:
  Title: High-risk ovarian cancer based on 126-gene expression signature is uniquely characterized by downregulation of antigen presentation pathway.
  URL:
  PMIDs: 22241791

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Information is available on: preprocessing
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varMetadata: labelDescription

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

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An expression set

| GSE44104 | COL11A1 promotes tumor progression and predicts poor clinical outcome in ovarian cancer. |

Description

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

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Laboratory: Wu, Chou 2013
Contact information:
Title: COL11A1 promotes tumor progression and predicts poor clinical outcome in ovarian cancer.
URL:
PMIDs: 23934190

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

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; $P \leq 0.001$) and in models corrected for relevant clinicopathologic parameters (HR 2.87 and 12.42, respectively; $P \leq 0.023$). 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

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Laboratory: Pils, Zeilinger 2012
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URL:
PMIDs: 22497737

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Value

An expression set

GSE51088

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

Description

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

Format

experimentData(eset):

Experiment data

Experiment 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 epithelial ovarian cancer
URL:
PMIDs: 24368280
Abstract: A 250 word abstract is available. Use 'abstract' method.

Information is available on: preprocessing

notes:

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

Details

assayData: 18703 features, 172 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

20 observations deleted due to missingness
 n  events  median  0.95LCL  0.95UCL
 152.00  112.00   4.13     3.50    4.92

Available sample meta-data:

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Ov_Tumor_Ref_Mix vs. CS-OV-001  Ov_Tumor_Ref_Mix vs. CS-OV-002
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Ov_Tumor_Ref_Mix vs. CS-OV-003  Ov_Tumor_Ref_Mix vs. CS-OV-004
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Lysophosphatidic acid-induced transcriptional profile represents serous epithelial ovarian carcinoma and worsened prognosis.

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

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Information is available on: preprocessing
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GSE6822

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Description


Format

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PMIDs: PMID unknown

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Information is available on: preprocessing
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Available sample meta-data:
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submission_date: Jan 22
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Value

An expression set
Description

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

Format

experimentData(eset):
Experiment data
  Experimenter name: Marchini S, Mariani P, Chiorino G, Marrazzo E, Bonomi R, Fruscio R, Clivio L, Garbi A, Torri V, ... M, D'Incalci M.
  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)
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    Agilent G4100A cDNA
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    hgu4100a
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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)

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**age_at_initial_pathologic_diagnosis:**

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**recurrence_status:**

- no recurrence
- recurrence

| 62 | 21 |

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- deceased
- living

| 15 | 68 |

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Value

An expression set
GSE9891

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

Description

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

Format

experimentData(eset):

Experiment data


Laboratory: Tothill, Bowtell 2008

Contact information:

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

URL:

PMIDs: 18698038

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

Information is available on: preprocessing

notes:

platform_title:

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

platform_shorttitle:

Affymetrix HG-U133Plus2

platform_summary:

hgu133plus2
platform_manufacturer: Affymetrix
platform_distribution: commercial
platform_accession: GPL570
version: 2015-09-22 20:16:32

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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
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163 116 6

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**substage:**
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26 19 212 28

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1 2 3 NA's

19 97 163 6

**age_at_initial_pathologic_diagnosis:**

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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)

Value

An expression set
minSampleSize
   an integer specifying the minimum number of patients required in a summarizedExperiment (default 0)
keepCommonOnly
   remove entrezIDs not common to all datasets (default FALSE)
imputeMissing
   remove patients from datasets with missing expression values
removeDuplicates
   remove patients with a Spearman correlation greater than or equal to 0.98 with other patient expression profiles (default TRUE)

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

Examples
   experimentsAndDups = loadOvarianDatasets()

loadOvarianEsets

Function to load ovarian cancer expression sets from the Experiment Hub

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

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

removeDuplicates

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

quantileCutoff

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

rescale

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

minNumberGenes

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

minNumberEvents

an integer specifying how 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 (default TRUE, currently just PMID19318476)

keepCommonOnly

remove probes not common to all datasets (default FALSE)

imputeMissing

remove patients from datasets with missing expression values

Value

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

Examples

esetsAndDups = loadOvarianEsets()
Description

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

Format

experimentData(eset):

Experiment data
Experimenter name: Berchuck A, Iversen ES, Lancaster JM, Pittman J, Luo J, Lee P, Murphy S, Dressman HK, Febbo PG, West ...
Laboratory: Berchuck, Marks 2005
Contact information:
Title: Patterns of gene expression that characterize long-term survival in advanced stage serous ovarian cancers.
URL:
PMIDs: 15897565

Abstract: A 258 word abstract is available. Use 'abstract' method.
Information is available on: preprocessing
notes:
platform_title:
[HG-U133A] Affymetrix Human Genome U133A Array
platform_shorttitle:
Affymetrix HG-U133A
platform_summary:
hgu133a
platform_manufacturer:
Affymetrix
platform_distribution:
commercial
platform_accession:
GPL96
warnings:
These samples are a subset of PMID17290060.

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

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

Details

assayData: 20967 features, 63 samples
Platform type:
---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
               Min. 1st Qu. Median Mean 3rd Qu. Max.
1761     1828    1907  2001   2032   2536

sample_type:
tumor
  63

histological_type:
ser
  63

primarysite:
ov
  63

summarygrade:
high  low  NA's
  25   37    1

summarystage:
early  late
  11   52

tumorstage:
  1  2  3  4
  7  4  48  4

grade:
1 2 3 4 NA's
2 35 24 1 1

age_at_initial_pathologic_diagnosis:
  Min. 1st Qu. Median  Mean  3rd Qu. Max.
  33.00  52.50  59.00  59.21  67.00  79.00

os_binary:
  long short NA's
  24  28  11

debulking:
  optimal suboptimal NA's
  24  28  11

batch:
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  2003-07-02
  1

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Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1903///Cancer.Type: Early stage///AgeDx: 73///STAGE: IIC///GRADE: 3///Debulking: ///X: NA

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1904///Cancer.Type: Long///AgeDx: 70///STAGE: IIIC///GRADE: 3///Debulking: O///X: NA

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Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2020///Cancer.Type: Long
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Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2026///Cancer.Type: Short
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Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2028///Cancer.Type: Short
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2029///Cancer.Type: Short
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2030///Cancer.Type: Short
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Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2404///Cancer.Type: Early stage
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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**

```markdown
experimentData(eSet):
Experiment data
```

**Abstract:** A 223 word abstract is available. Use 'abstract' method.

**Information is available on:** preprocessing
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    [HG-U133A] Affymetrix Human Genome U133A Array
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    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:
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alt_sample_name:

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  85 32

debulking:
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  63 54

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2004-06-23
  8

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

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

Format

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Laboratory: Berchuck, Lancaster 2009
Contact information:
URL:
PMIDs: 19318476

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Information is available on: preprocessing
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version:
    2015-09-22 20:20:30

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An object of class 'AnnotatedDataFrame'
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varMetadata: labelDescription
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Platform type:

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An expression set

Integrated genomic analyses of ovarian carcinoma.

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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Experiment data
Laboratory: Cancer Genome Atlas Research Network 2011
Contact information:
Title: Integrated genomic analyses of ovarian carcinoma.
URL:
PMIDs: 21720365

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Information is available on: preprocessing
notes:

notes:
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Illumina HiSeq RNA sequencing
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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
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Details

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

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days_to_death:
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   9.0  341.8   878.0  1018.0  1446.0  5480.0 5

vital_status:
deceased  living  NA's
143     114      4

site_of_tumor_first_recurrence:
   locoregional  metastasis  NA's
   82         56        123

primary_therapy_outcome_success:
   completeresponse  partialresponse  progressivedisease  stabledisease
   147          30       15         15          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

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

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:

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unique_patient_id: TCGA-61-2008

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bcr_patient_uuid: ...
year_of_form_completion: 2009
Extract.Name: TCGA-61-1725-01A-01R-1567-13
unique_patient_id: TCGA-61-1725

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anatomic_organ_subdivision: Bilateral
bcr_patient_uuid: ...
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unique_patient_id: TCGA-61-2109

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year_of_form_completion: 2010
unique_patient_id: TCGA-59-2363

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anatomic_organ_subdivision: Bilateral
bcr_patient_uuid: ...
year_of_form_completion: 2009
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unique_patient_id: TCGA-09-2051

age_at_initial_pathologic_diagnosis: 42
anatomic_organ_subdivision: NA
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age_at_initial_pathologic_diagnosis: 43
anatomic_organ_subdivision: Bilateral
bcr_patient_uuid: ...
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unique_patient_id: TCGA-29-1694

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unique_patient_id: TCGA-24-1846

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unique_patient_id: TCGA-13-0800
Value

An expression set

TCGAOVARIAN  Integrated genomic analyses of ovarian carcinoma.

Description

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

Format

experimentData(eset):
Experiment data
  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
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platform_distribution: commercial
platform_accession: GPL3921
warnings:
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
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Available sample meta-data:

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anatomic_organ_subdivision: Bilateral
bcr_patient_uuid: ... 2009
unique_patient_ID: TCGA-20-1685
batch: 18
Extract.Name: TCGA-20-1685-01A-01R-0564-01

age_at_initial_pathologic_diagnosis: 45
anatomic_organ_subdivision: Bilateral
bcr_patient_uuid: ... 2009
unique_patient_ID: TCGA-04-1514
batch: 15
Extract.Name: TCGA-04-1514-01A-01R-0502-01

age_at_initial_pathologic_diagnosis: 45
anatomic_organ_subdivision: Bilateral
bcr_patient_uuid: ... 2009
unique_patient_ID: TCGA-29-1711
batch: 18
Extract.Name: TCGA-29-1711-01A-01R-0564-01

age_at_initial_pathologic_diagnosis: 45
anatomic_organ_subdivision: Left
bcr_patient_uuid: ... 2009
unique_patient_ID: TCGA-23-2077
batch: 22
Extract.Name: TCGA-23-2077-01A-01R-0668-01

age_at_initial_pathologic_diagnosis: 45
anatomic_organ_subdivision: NA
bcr_patient_uuid: ... 2009
unique_patient_ID: TCGA-23-1118
batch: 12
Extract.Name: TCGA-23-1118-01A-01R-0434-01

age_at_initial_pathologic_diagnosis: 45
anatomic_organ_subdivision: NA
bcr_patient_uuid: ... 2009
unique_patient_ID: TCGA-23-1021
batch: 12
Extract.Name: TCGA-23-1021-01B-01R-0434-01

age_at_initial_pathologic_diagnosis: 45
anatomic_organ_subdivision: NA
bcr_patient_uuid: ... 2009
unique_patient_ID: TCGA-23-1026
batch: 12
Extract.Name: TCGA-23-1026-01B-01R-0434-01

age_at_initial_pathologic_diagnosis: 46
anatomic_organ_subdivision: Right
bcr_patient_uuid: ... 2009
unique_patient_ID: TCGA-23-2084
batch: 22
Extract.Name: TCGA-23-2084-01A-02R-0668-01

age_at_initial_pathologic_diagnosis: 46
anatomic_organ_subdivision: Bilateral
bcr_patient_uuid: ... 2009
unique_patient_ID: TCGA-61-2002
batch: 22
Extract.Name: TCGA-61-2002-01A-01R-0668-01

age_at_initial_pathologic_diagnosis: 46
anatomic_organ_subdivision: Bilateral
bcr_patient_uuid: ... 2009
unique_patient_ID: TCGA-20-1687
batch: 18
Extract.Name: TCGA-20-1687-01A-01R-0564-01

age_at_initial_pathologic_diagnosis: 46
anatomic_organ_subdivision: Bilateral
bcr_patient_uuid: ... 2009
unique_patient_ID: TCGA-24-1546
batch: 17
Extract.Name: TCGA-24-1546-01A-01R-0538-01

age_at_initial_pathologic_diagnosis: 46
anatomic_organ_subdivision: Bilateral
bcr_patient_uuid: ... 2010
unique_patient_ID: TCGA-24-2019
batch: 22

age_at_initial_pathologic_diagnosis: 46
anatomic_organ_subdivision: Bilateral
bcr_patient_uuid: ... 2009
unique_patient_ID: TCGA-23-2079
batch: 22
Extract.Name: TCGA-23-2079-01A-01R-0668-01

age_at_initial_pathologic_diagnosis: 46
anatomic_organ_subdivision: NA
bcr_patient_uuid: ... 2009
unique_patient_ID: TCGA-04-1350
batch: 13
Extract.Name: TCGA-04-1350-01A-01R-0453-01

age_at_initial_pathologic_diagnosis: 46
anatomic_organ_subdivision: NA
bcr_patient_uuid: ... 2009
unique_patient_ID: TCGA-30-1867
batch: 21
Extract.Name: TCGA-30-1867-01A-01R-0653-01

age_at_initial_pathologic_diagnosis: 46
anatomic_organ_subdivision: Right
bcr_patient_uuid: ... 2009
unique_patient_ID: TCGA-23-1029
batch: 19
Extract.Name: TCGA-23-1029-01B-01R-0582-01

age_at_initial_pathologic_diagnosis: 47
anatomic_organ_subdivision: Bilateral
bcr_patient_uuid: ... 2009
unique_patient_ID: TCGA-61-1724
batch: 21
Extract.Name: TCGA-61-1724-01A-01R-0653-01

age_at_initial_pathologic_diagnosis: 47
anatomic_organ_subdivision: Bilateral
bcr_patient_uuid: ... 2009
unique_patient_ID: TCGA-04-1525
batch: 17
Extract.Name: TCGA-04-1525-01A-01R-0538-01

age_at_initial_pathologic_diagnosis: 47
anatomic_organ_subdivision: Bilateral
bcr_patient_uuid: ... 2009
unique_patient_ID: TCGA-29-1777
batch: 19
Extract.Name: TCGA-29-1777-01A-01R-0582-01

age_at_initial_pathologic_diagnosis: 47
anatomic_organ_subdivision: Bilateral
bcr_patient_uuid: ... 2009
unique_patient_ID: TCGA-31-1944
batch: 21
Extract.Name: TCGA-31-1944-01A-01R-0653-01

age_at_initial_pathologic_diagnosis: 47
anatomic_organ_subdivision: Bilateral
bcr_patient_uuid: ... 2009
unique_patient_ID: TCGA-57-1584
batch: 17
Extract.Name: TCGA-57-1584-01A-01R-0538-01

age_at_initial_pathologic_diagnosis: 47
anatomic_organ_subdivision: Bilateral
bcr_patient_uuid: ... 2009
unique_patient_ID: TCGA-29-1705
batch: 18
Extract.Name: TCGA-29-1705-01A-01R-0564-01
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age_at_initial_pathologic_diagnosis: 48//anatomic_organ_subdivision: Left

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