

The Impact of Molecular Testing on Therapeutic Decisions in Ovarian Cancer

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Director Gynecologic Medical Oncology
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Ovarian Cancer

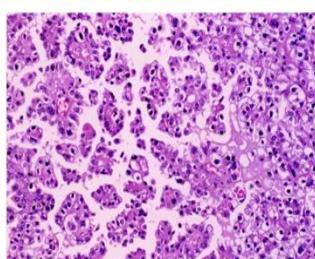
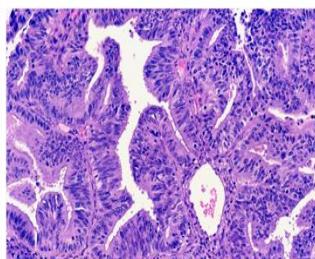
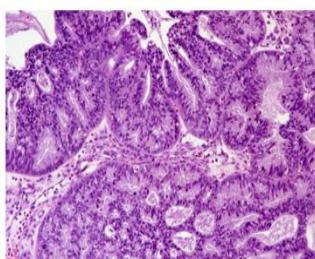
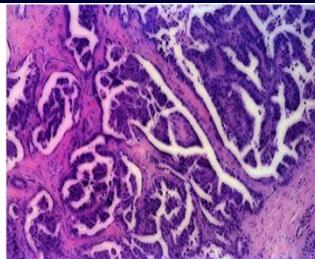
The Clinical Problem

- 250,000 women diagnosed yearly worldwide
- 75% patients present with advanced stage disease
- 80% respond to chemotherapy
- Vast majority of patients relapse and eventually develop drug resistant disease
- Minimal increase in overall survival over last 30 years
- 14,000 deaths yearly
- Highest case fatality rate for gynecologic cancers in the world
- All ovarian cancers treated with surgery/chemotherapy

Impact of Molecular Analysis

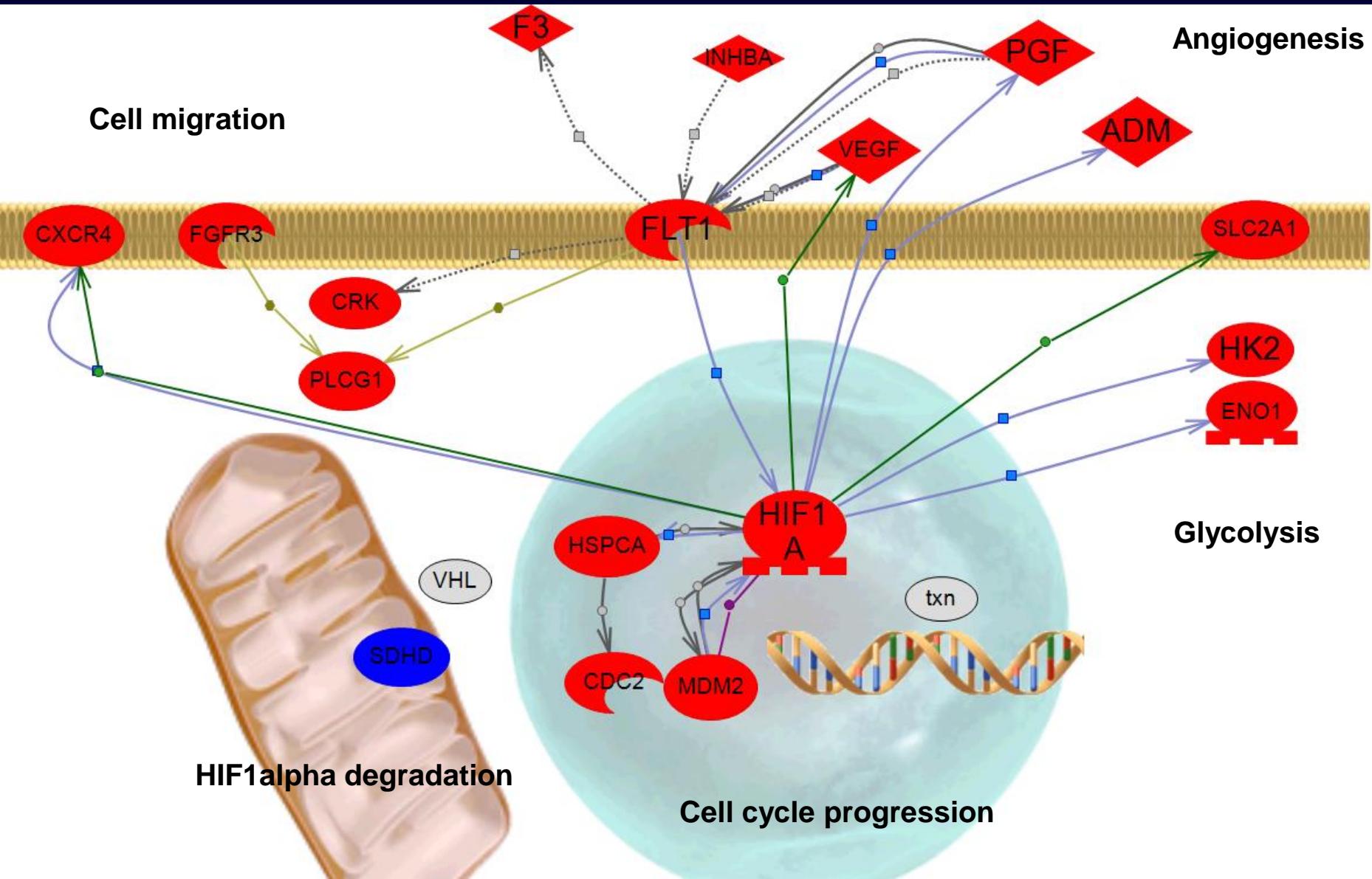
Identifying Unique Diseases
and Their Pathways

Ovarian Cancers



- **Serous**
 - A disease of genomic instability
- **Mucinous**
 - A disease of aberrant RAS pathway signaling
- **Endometrioid**
 - A disease of aberrant PTEN, PI-3K, AKT signaling
- **Clear cell**
 - A disease of ARID1A

Clear Cell Ovarian Cancer Has Unique Targetable Pathways

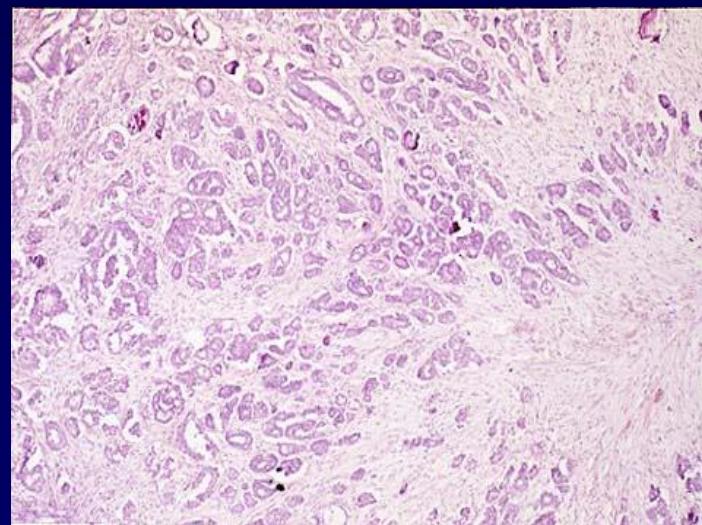
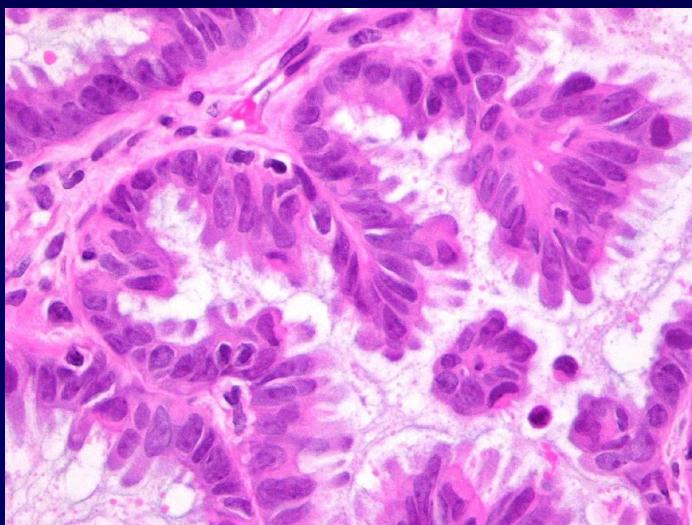
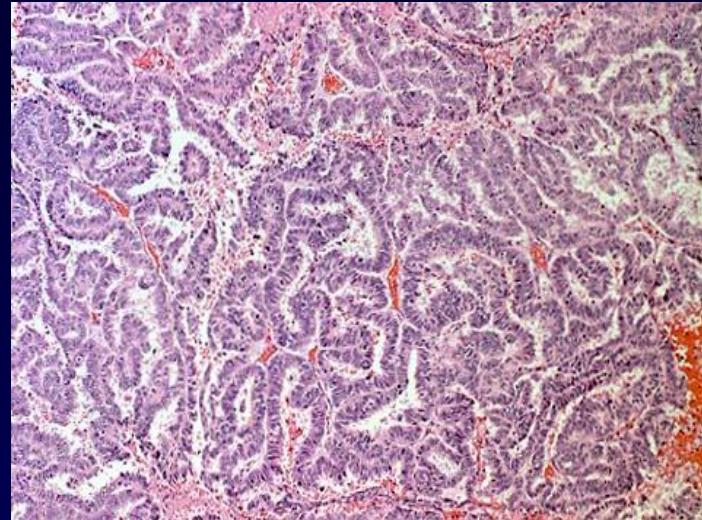
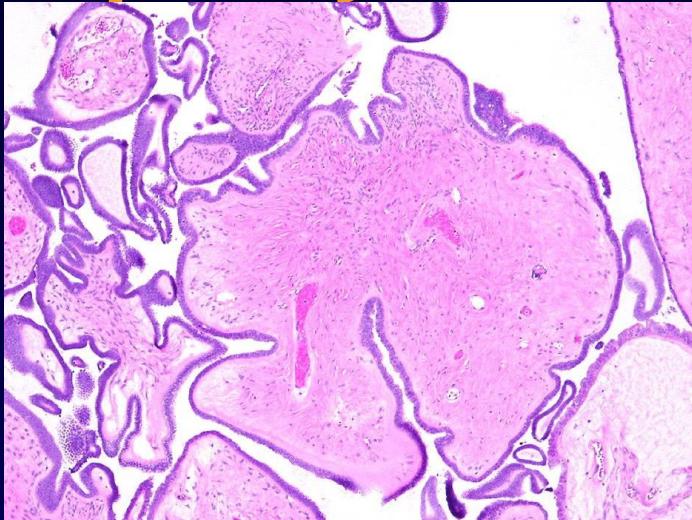


Clear Cell Specific Trials

GOG0254 A Phase II Evaluation of SU11248 (Sunitinib Malate) in the Treatment of Persistent or Recurrent Clear Cell Ovarian Carcinoma
(John K Chan)

GOG0268 A Phase II Evaluation of Temsirolimus (CCI-779) (NCI Supplied Agent: 683864, IND #61010) in Combination With Carboplatin and Paclitaxel Followed by Temsirolimus Consolidation as First-line Therapy in the Treatment of Clear Cell Carcinoma of the Ovary
(John H Farley)

Papillary Serous Ovarian Cancer

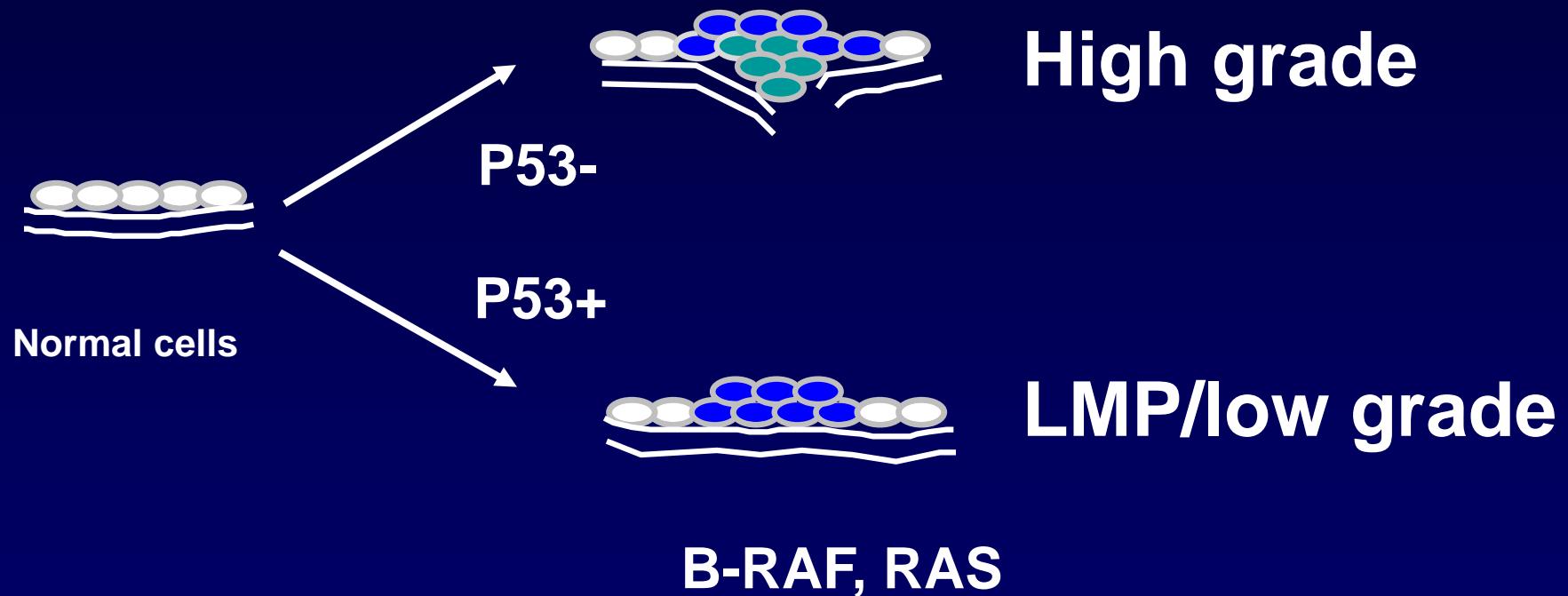


(40x Magnification)
Low-malignant potential (LMP)

(40x Magnification)
Invasive carcinoma

Ovarian Cancer

Papillary serous ovarian tumors



A Phase II Trial of AZD6244 in Women With Recurrent Low-Grade Serous Carcinoma of the Ovary or Peritoneum: A Gynecologic Oncology Group Study

MAPK Pathway Inhibition Is Effective for Low Grade Tumors

| | 1 prior chemo treatment, % | >3 prior chemo treatment, % | Stable disease, % | Median PFS, months |
|--------------------|----------------------------|-----------------------------|-------------------|--------------------|
| MDACC ¹ | 28 | 14 | 60 | 7.25 |
| GOG239 | 19 | 57 | 65 | 11 |

- Exhibits considerable activity with minimal toxicity in recurrent low-grade serous tumors
 - The 15% response rate is 5 times that observed for cytotoxic chemotherapy in the setting of recurrent low-grade serous tumors
- These results warrant further evaluation of inhibitors of the MAPK pathway in low-grade serous ovarian cancers

1. Gershenson DM, et al. *Gynecol Oncol*. 2009;114(1):48-52.

pERK Correlates Better With Response

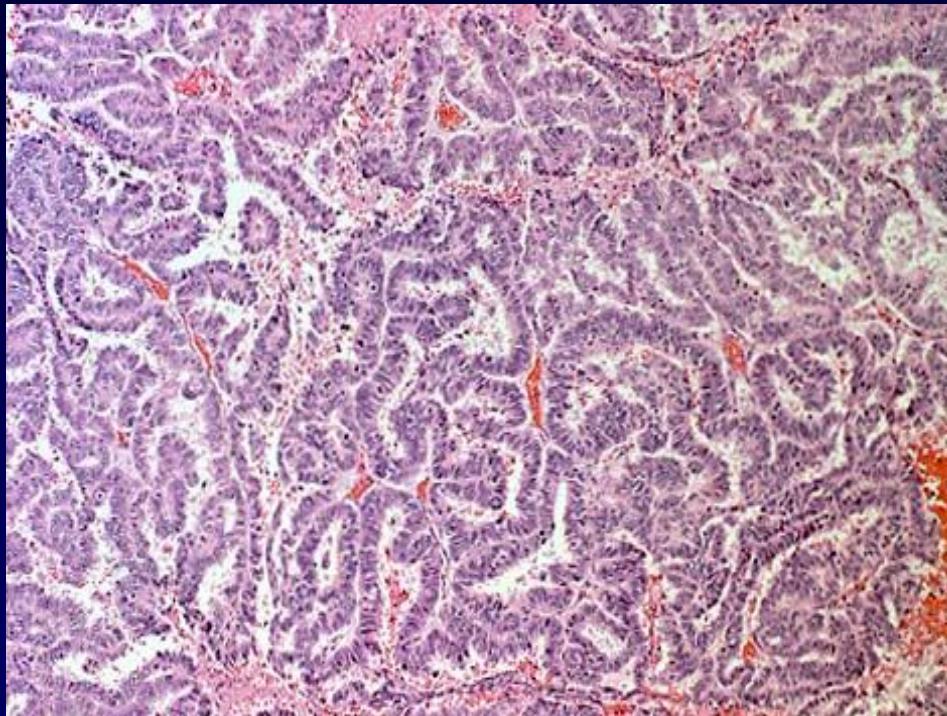
- Tumor response by pERK positivity

| | N | pERK Score | | P value (Fishers Exact Test) |
|--------------------------|----|---------------|---------------|------------------------------------|
| | | ≤108 n (%) | >108 n (%) | |
| Total | 33 | 20 (60.6%) | 13 (39.4%) | |
| Response (CR,PR) | | | | |
| No | 26 | 16 (80.0%) | 10 (76.9%) | 1.000 |
| Yes | 7 | 4 (20.0%) | 3 (23.1%) | |
| Response category | | | | |
| Complete response | 1 | 0 (0.0%) | 1 (7.7%) | 0.078 |
| Partial response | 6 | 4 (20.0%) | 2 (15.4%) | |
| Stable disease | 19 | 9 (45.0%) | 10 (76.9%) | |
| Increasing disease | 6 | 6 (30.0%) | 0 (0.0%) | |
| Indeterminate | 1 | 1 (5.0%) | 0 (0.0%) | |

†Fishers Exact Test

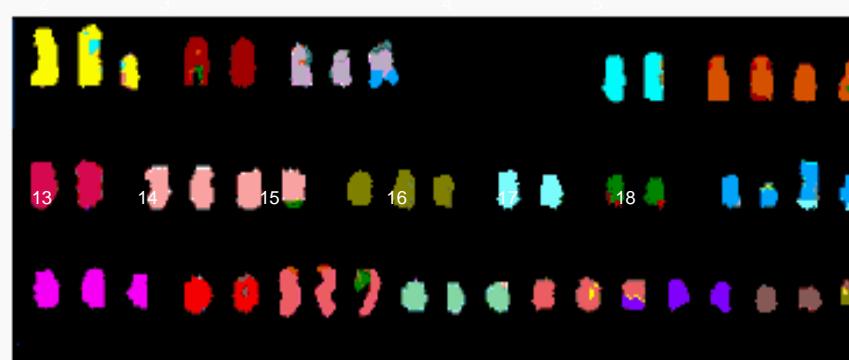
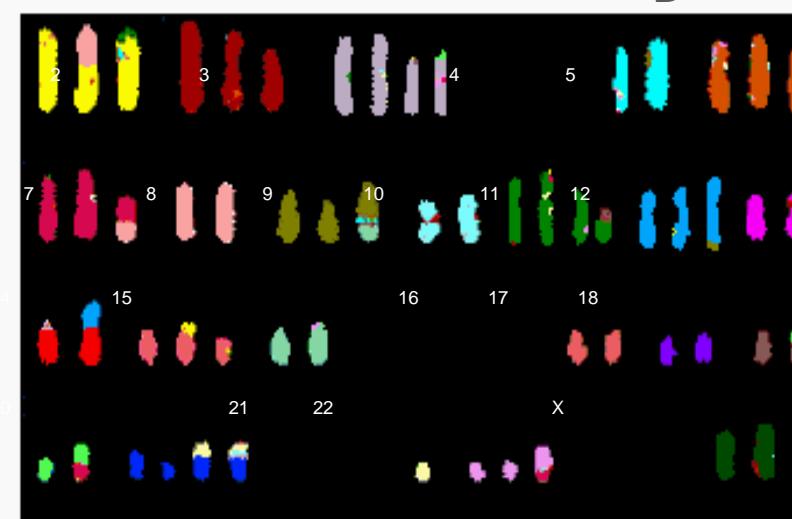
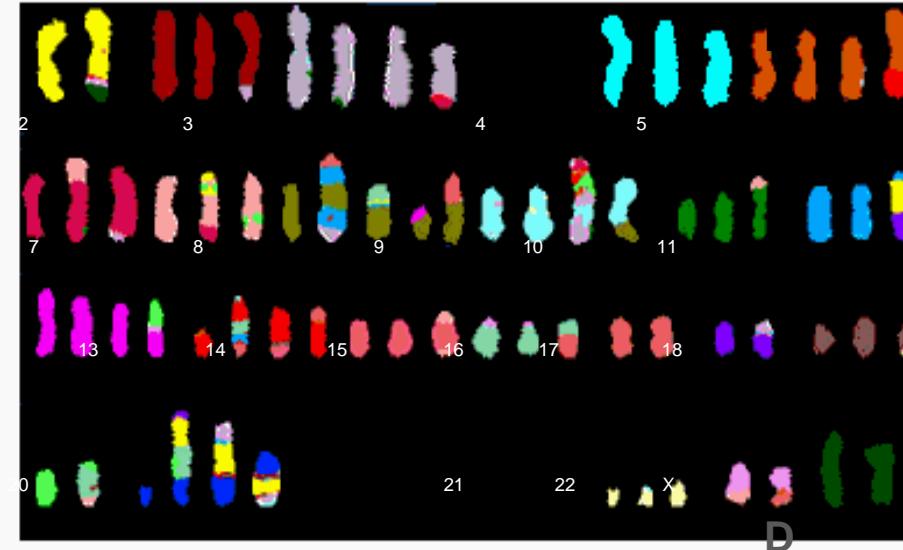
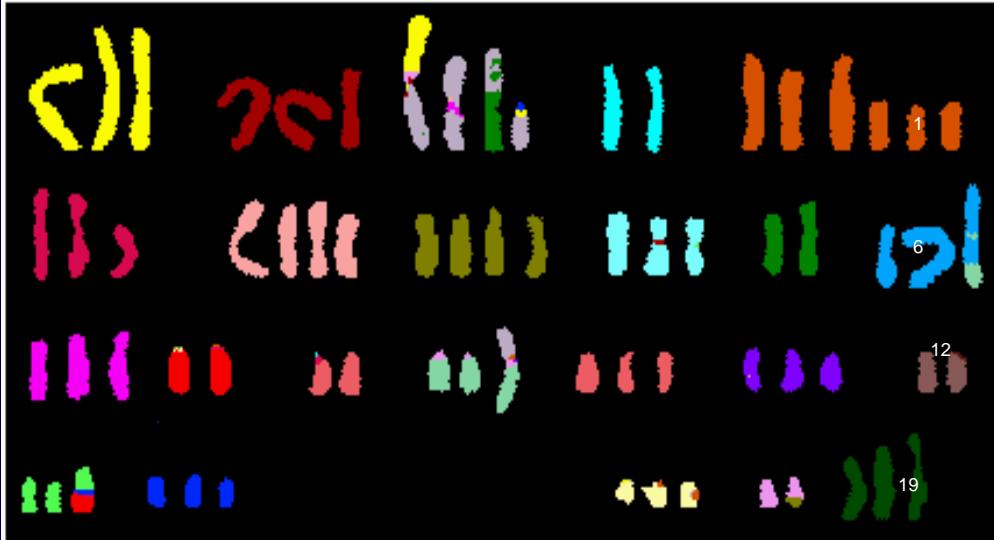
Note: Percentages are column percentages, except for the Total row, which are row percentages

What About High Grade Serous Cancers?



The Cancer Genome Atlas (TCGA) Overview

- Large amounts of genomic/epigenomic abnormalities
 - Few high frequent mutations except p53 and *BRCA*
 - Multiple areas of chromosomal gain
 - Containing 100s of genes
 - Multiple areas of relatively common chromosomal loss
 - Containing 100s of gene
 - Many hypermethylated genes
 - 4 transcriptional cluster patterns
 - Transcriptional subtypes not linked strongly to survival
 - 3 microRNA subtypes
 - Loosely linked to transcriptional cluster



**In a Tumor With Genomic
Instability Can We Identify
Prognostic or Predictive
Signatures?**

Prognostic Gene Signatures of Ovarian Cancer

OPEN ACCESS Freely available online

PLOS one

Angiogenic mRNA and microRNA Gene Expression Signature Predicts a Novel Subtype of Serous Ovarian Cancer

Cancer Research

A Gene Signature Predicting for Survival in Suboptimal Debulked Patients with Ovarian Cancer
Tomas Bonome, Douglas A. Levine, Joanna Shih, et al.

OPEN ACCESS Freely available online

PLOS MEDICINE

Survival-Related Profile, Pathways, and Transcription Factors in Ovarian Cancer
Anne P. G. Crijns¹*, Rudolf S. N. Fehrmann^{1,2,3,4}, Steven de Jong², Frans Gerbens³, Gert Jan Meersma¹, Harry G. Klijn¹, Harry Hollema⁵, Robert M. W. Hofstra², Gerard J. te Meerman³, Elisabeth G. E. de Vries¹, Ate G. J. van der Zee^{1*}

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PLOS one

Gene Expression Profile for Predicting Survival in Advanced-Stage Serous Ovarian Cancer Across Two Independent Datasets

Clinical Cancer Research

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High-Risk Ovarian Cancer Based on 126-Gene Expression Signature Is Uniquely Characterized by Downregulation of Antigen Presentation Pathway

Published Online First January 12, 2013; DOI: 10.1158/0732-183X.CCR-11-3725
Cancer Res 2012; 72: 12–18.

Cancer Cell Article

Cell PRESS

A Gene Signature Predictive for Outcome in Advanced Ovarian Cancer Identifies a Survival Factor: Microfibril-Associated Glycoprotein 2

The Journal of Molecular Diagnostics
Volume 14, Issue 3, May–June 2012, Pages 214–222

ELSEVIER

Regular article
Genes with Bimodal Expression Are Robust Diagnostic Targets that Define Distinct Subtypes of Epithelial Ovarian Cancer with Different Overall Survival

Dawn N. Kernagis, Allison H.S. Hall, Michael B. Datto

Molecular and Cellular Pathobiology

Cancer Research

Activation of NF-κB Signaling by Inhibitor of NF-κB Kinase β Increases Aggressiveness of Ovarian Cancer
Lidia Hernandez¹, Sarah C. Hsu¹, Ben Davidson², Michael J. Birrer³, Elise C. Kohn¹, and Christina M. Annunziata¹

JNCI JOURNAL OF THE NATIONAL CANCER INSTITUTE

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Oxford Journals | Medicine | JNCI J Natl Cancer Inst | Volume 104, Issue 9 | Pp. 670-681

Published Online First January 12, 2013; DOI: 10.1093/jncnjnl1078
doi: 10.1093/jncnjnl1078
JNCI J Natl Cancer Inst (2012) 104: 670-681
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Nominations for the eighth biennial Carcinogenesis awards now open. Click for more information.

A DNA Repair Pathway–Focused Score for Prediction of Outcomes in Ovarian Cancer Treated With Platinum-Based Chemotherapy
Josephine Kang, Alan D. D'Andrea and David Kozonko

BJC British Journal of Cancer

Journal home > Archive > Genetics and Genomics > Full text

Genetics and Genomics
British Journal of Cancer (2011) 105, 304–311. doi:10.1038/bjc.2011.219
Published online 7 June 2011

A seven-gene prognostic model for platinum-treated ovarian carcinomas
R Sabatier^{1,2}, P Finetti¹, J Bonneterre³, J Jacquemier^{1,2}, J Adelaide⁴, E Lambaudie², P Viens^{2,5}, D Birnbaum⁴ and F Bertuccio^{1,2,5}

THE JOURNAL OF Pathology

Original Paper
A prognostic gene expression index in ovarian cancer—validation across different independent data sets[†]

VOLUME 28 • NUMBER 22 • AUGUST 1 2010

JOURNAL OF CLINICAL ONCOLOGY

ORIGINAL REPORT

Gene Expression Profile of BRCA-ness That Correlates With Responsiveness to Chemotherapy and With Outcome in Patients With Epithelial Ovarian Cancer
Panagiota A. Konstantinopoulos, Dimitrios Spentzos, Beth Y. Karlan, Toshiyasu Tamiguchi, Elena Fountzilas, Nancy Francoeur, Douglas A. Levine, and Stephen A. Camann

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NATURE | ARTICLE

日本語要約

Integrated genomic analyses of ovarian carcinoma

Prognostic Gene Signatures of Ovarian Cancer

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Angiogenic mRNA and microRNA Gene Expression Signature Predicts a Novel Subtype of Serous Ovarian Cancer

Cancer Cell Article

A Gene Signature Predictive for Outcome in Advanced Ovarian Cancer Identifies a Survival

BJC
British Journal of Cancer

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British Journal of Cancer (2011) 105, 304–311. doi:10.1038/bjc.2011.219
www.bjcancer.com
Published online 7 June 2011

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A seven-gene prognostic model for platinum-treated ovarian carcinomas

Objectives:

1. Assess the reproducibility of published prognostic gene expression models
2. Evaluate published models using publicly available data
3. Improve on models using all publicly available data

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PLOS one

Gene Expression Profile for Predicting Survival in Advanced-Stage Serous Ovarian Cancer Across Two Independent Datasets

Molecular and Cellular Pathobiology

Cancer Research

Activation of NF-κB Signaling by Inhibitor of NF-κB Kinase β Increases Aggressiveness of Ovarian Cancer

Lidia Hernandez¹, Sarah C. Hsu¹, Ben Davidson², Michael J. Birrer³, Elise C. Kohn¹, and Christina M. Annunziata¹

Responsiveness to Chemotherapy and With Outcome in Patients With Epithelial Ovarian Cancer

Panagiotis A. Konstantinopoulos, Dimitrios Spentzos, Beth Y. Karlan, Toshiyasu Taniguchi, Elena Fountzilas, Nancy Francoeur, Douglas A. Levine, and Stephen A. Cannistra

Clinical Cancer Research

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« Previous | Next Article » Table of Contents

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Oncogene Res Repn 1, 2012 45

JNCI JOURNAL OF THE NATIONAL CANCER INSTITUTE

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Oxford Journals | Medicine | JNCI J Natl Cancer Inst | Volume 104, Issue 9 | Pp. 670-681

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doi: 10.1093/jncnjdsf177

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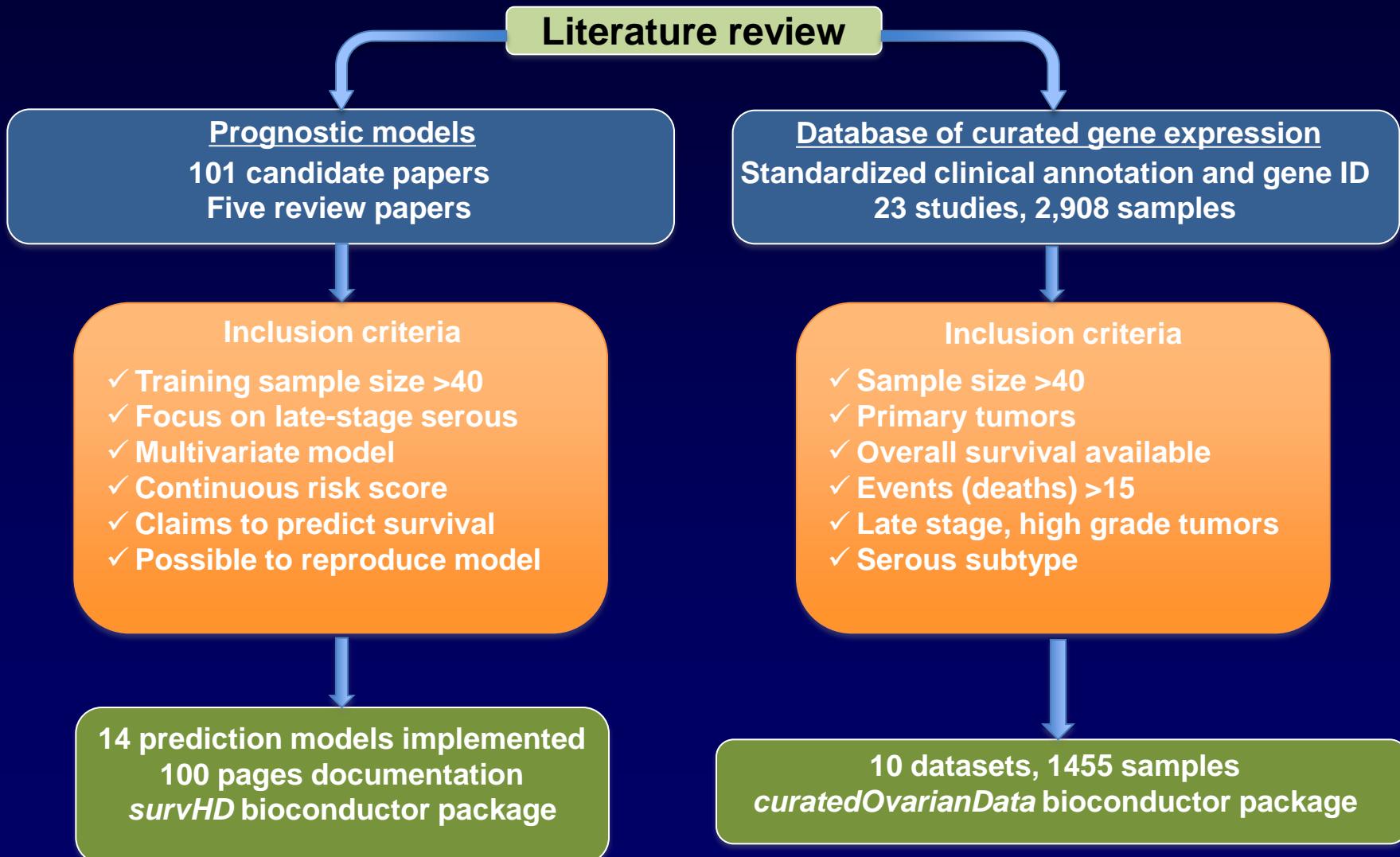
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日本語要約

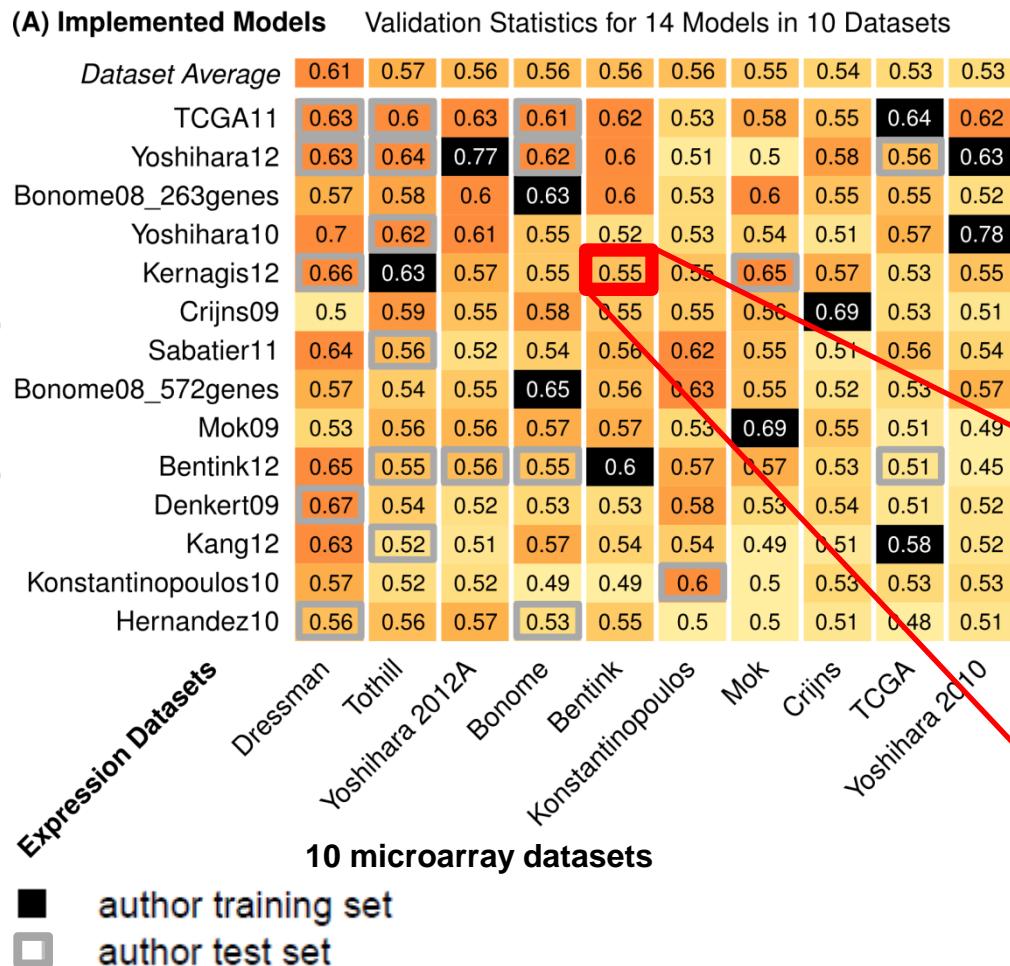
Integrated genomic analyses of ovarian carcinoma

Meta-Analysis Overview



Assessment of Prognostic Signatures

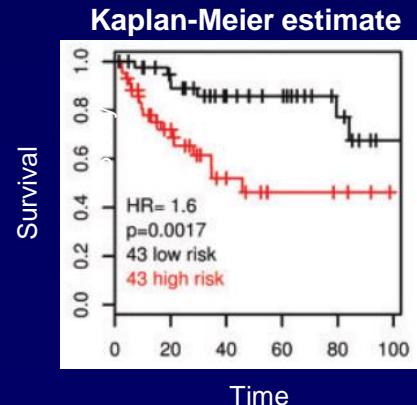
14 prognostic signatures



$$C\text{-Index} = \Pr(g(Z_1) > g(Z_2) \mid T_2 > T_1)$$

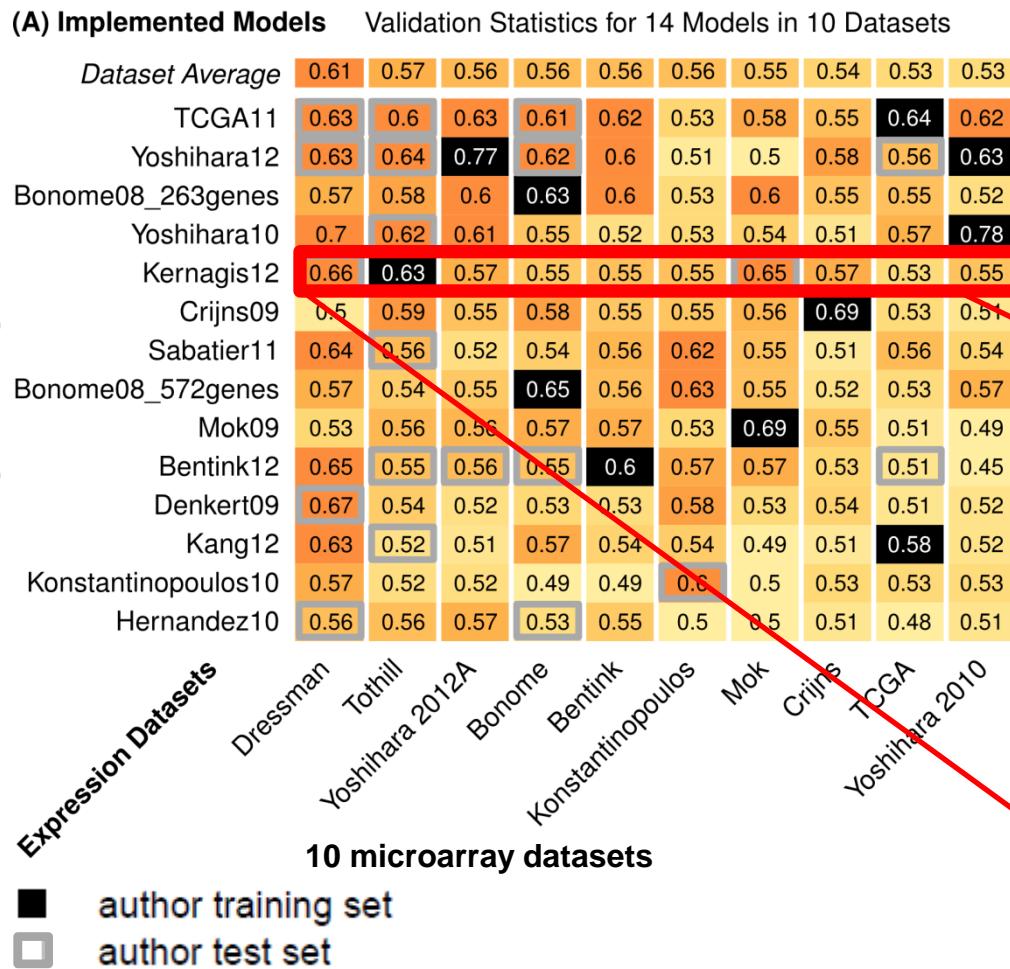
T_1, T_2 = times to death of two patients
 $g(Z_1), g(Z_2)$ = predicted risk scores

$C = 0.5$ expectation for random prediction
 $C = 1$ if the exact order of all deaths is predicted



Assessment of Prognostic Signatures

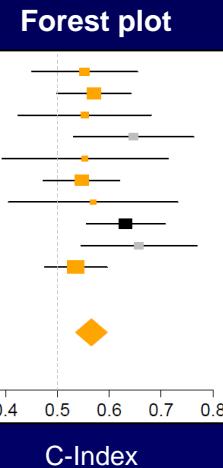
14 prognostic signatures



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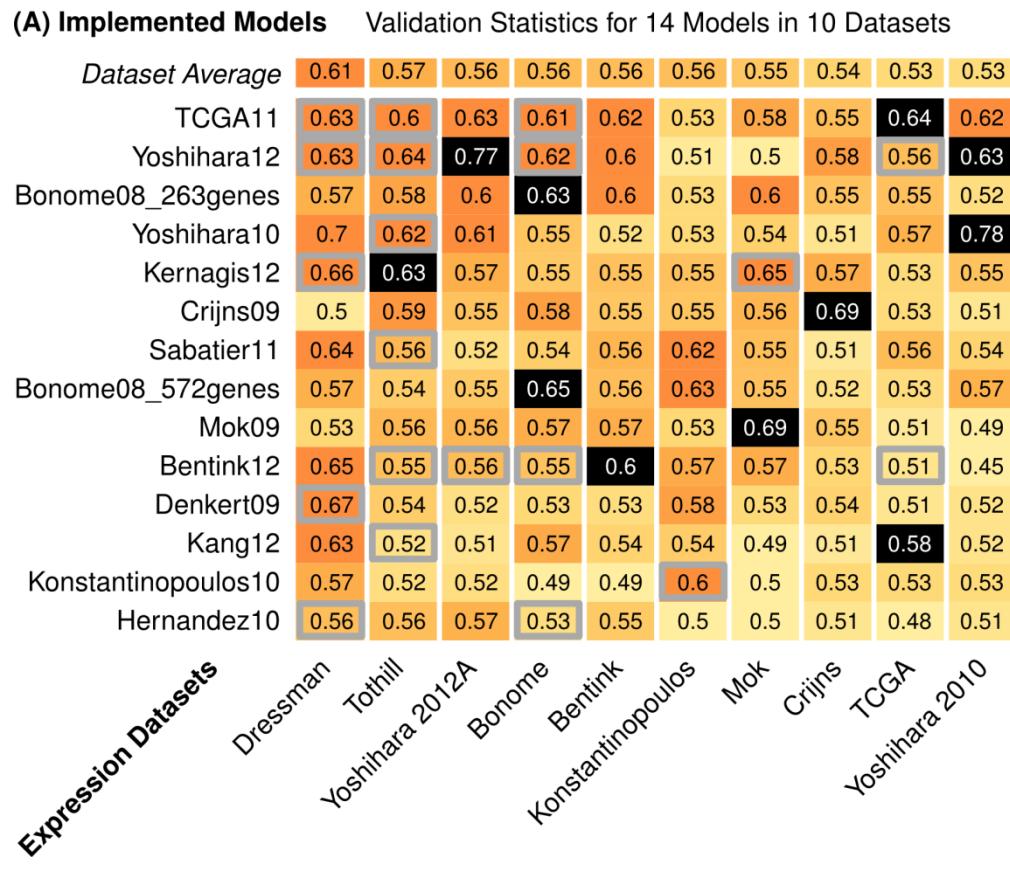
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Assessment of Prognostic Models

1



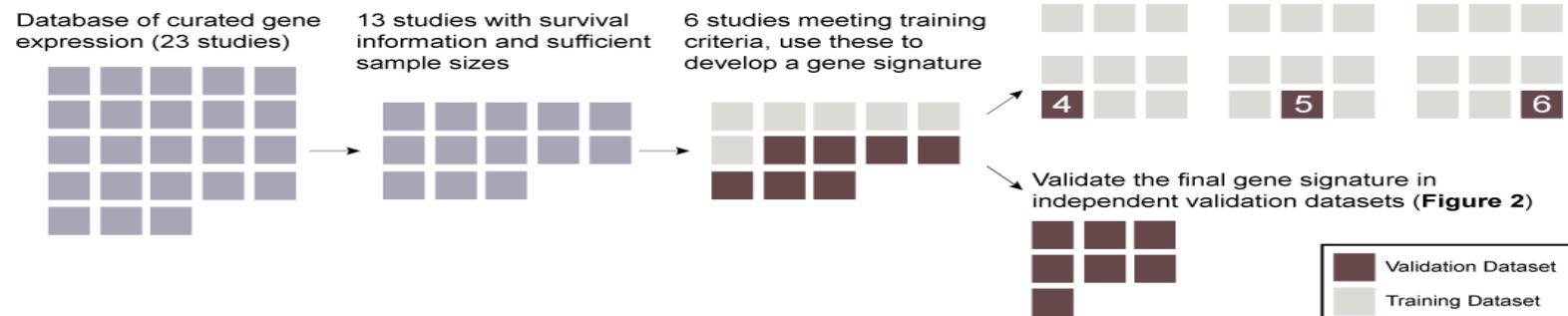
Conclusions:

- **Most models make better predictions than random**
- **Large, consortium studies performed best**
- **Validation datasets can be biased**
- **None of these models are ready for the clinic**

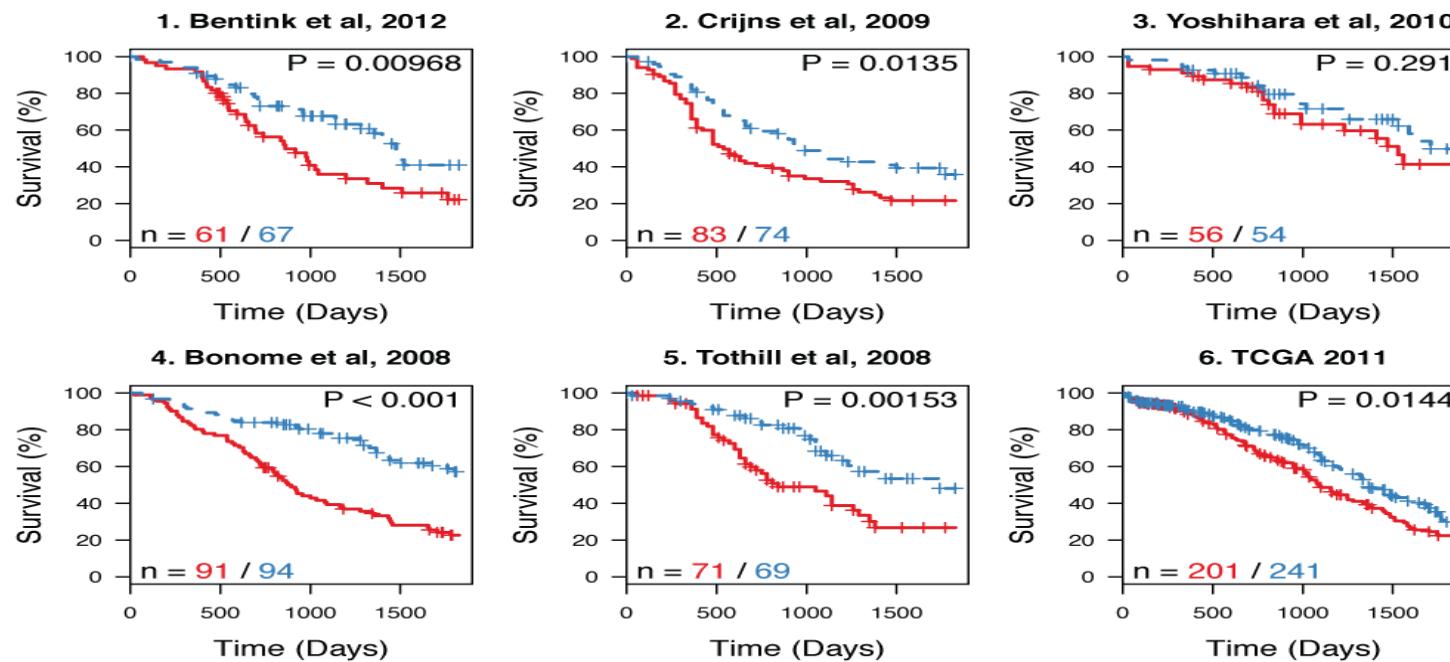
Application of Large Database for the Generation of Clinically Relevant Signatures

Patient Survival

A) Overview

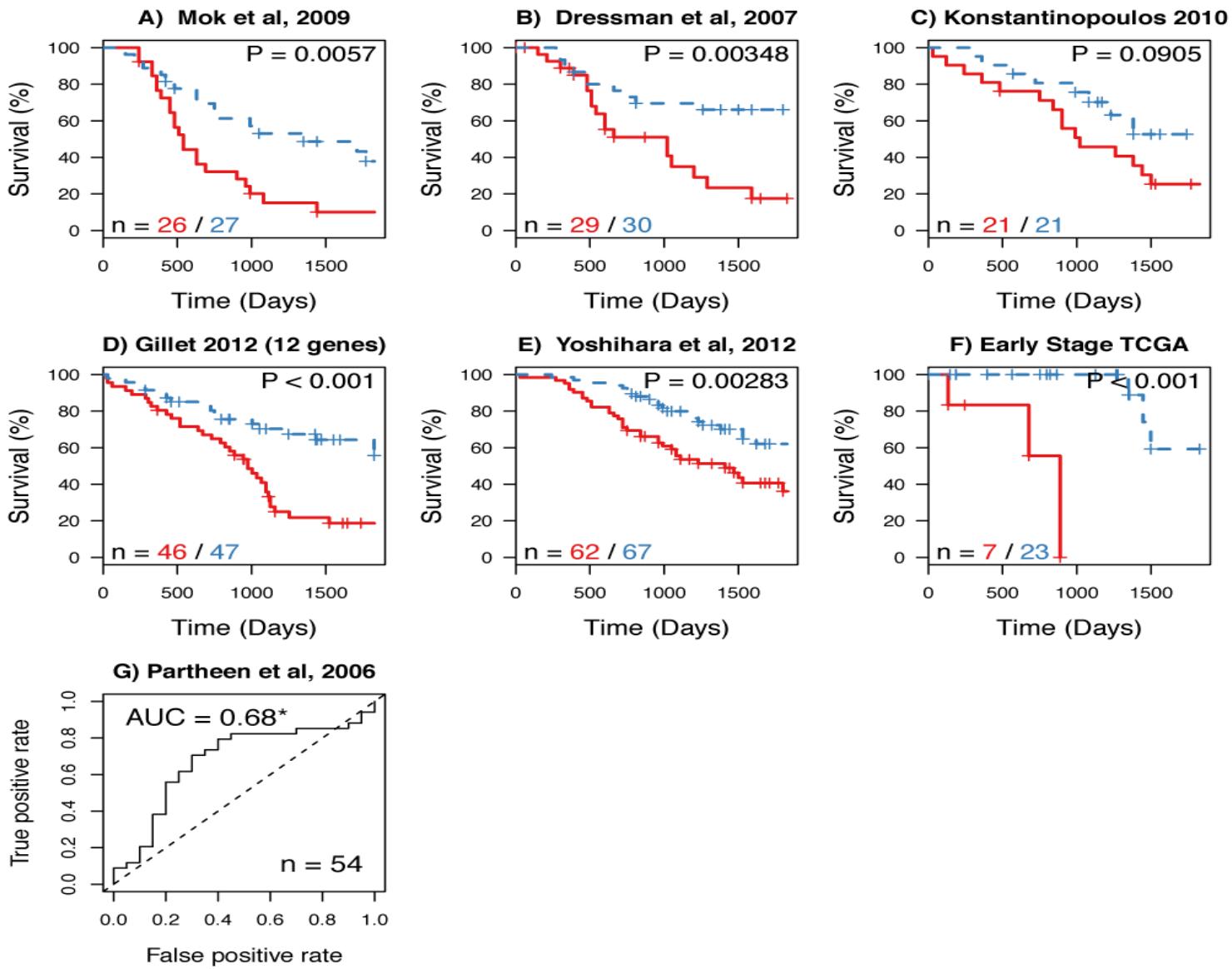


B) Kaplan-Meier analysis of datasets 1 to 6



Riester M, et al. *J Natl Cancer Inst.* 2014;106(5).

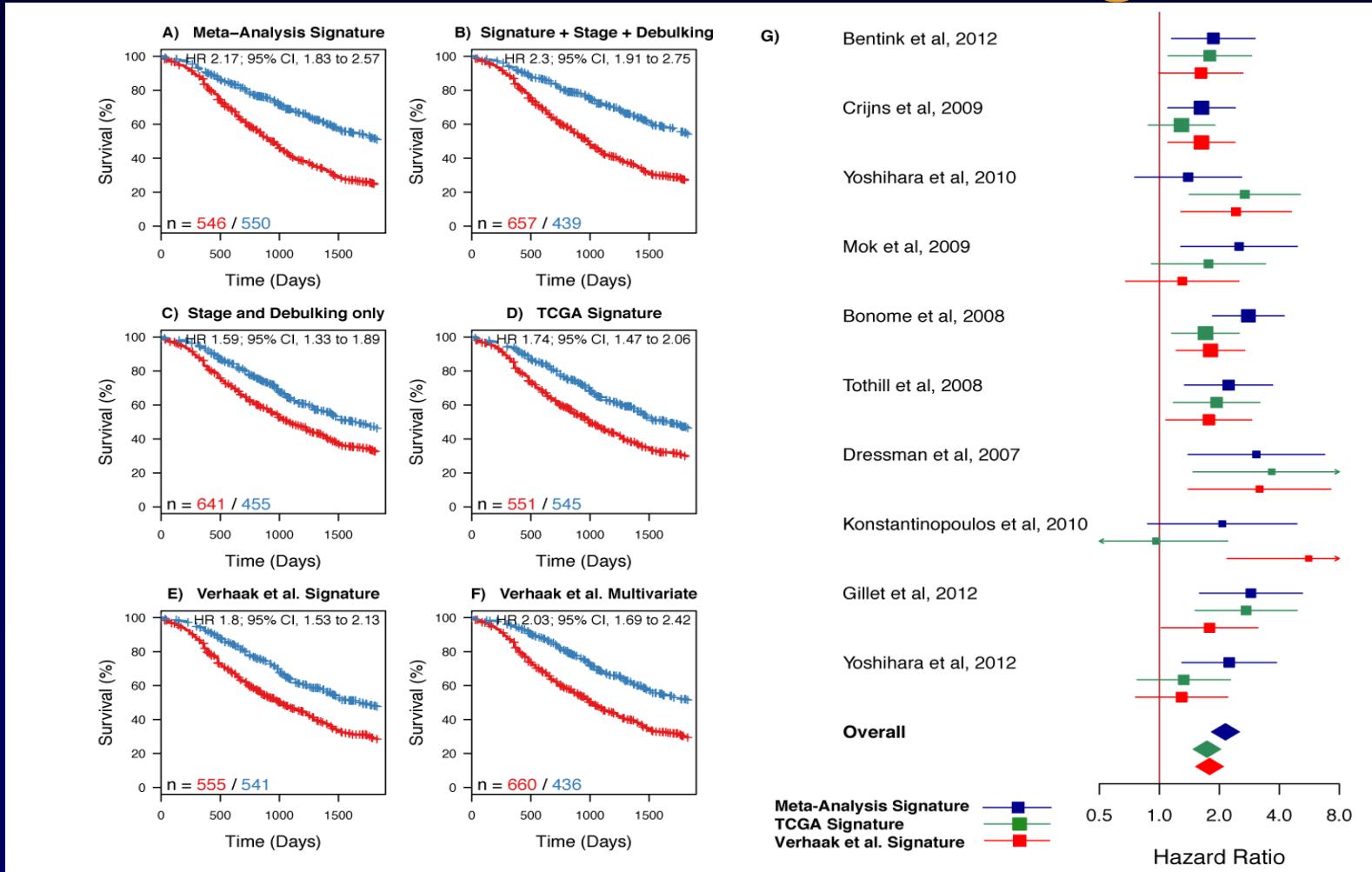
Bentink S, et al. *PLoS One.* 2012;7(2):e30269. Crijns AP, et al. *PLoS Med.* 2009;6(2):e24. Yoshihara K, et al. *PLoS One.* 2010;5(3):e9615. Bonome T, et al. *Cancer Res.* 2008;68(13):5478-5486. Tothill RW, et al. *Clin Cancer Res.* 2008;14(16):5198-5208. Cancer Genome Atlas Research Network. *Nature.* 2011;474(7353):609-615.



Riester M, et al. *J Natl Cancer Inst.* 2014;106(5).

Mok SC, et al. *Cancer Cell.* 2009;16(6):521-532. Dressman HK, et al. *J Clin Oncol.* 2007;25(5):517-525. Konstantinopoulos PA, et al. *J Clin Oncol.* 2010;28(22):3555-3561. Gillet JP, et al. *Clin Cancer Res.* 2012;18(11):3197-3206. Yoshihara K, et al. *Clin Cancer Res.* 2012;18(5):1374-1385. Partheen K, et al. *Eur J Cancer.* 2006;42(16):2846-2854.

Survival Signature Performs Better Than Known Clinical Factors and Signatures



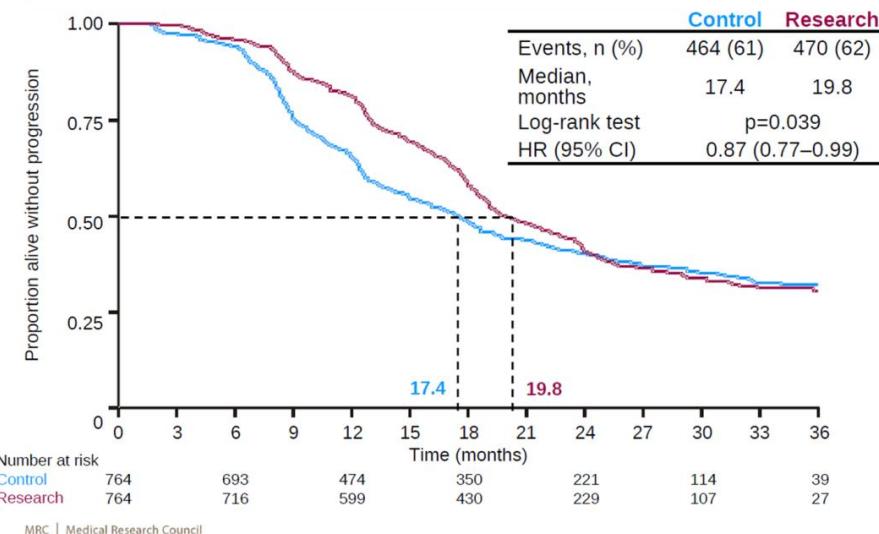
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Survival Signatures Still Not Clinically Relevant

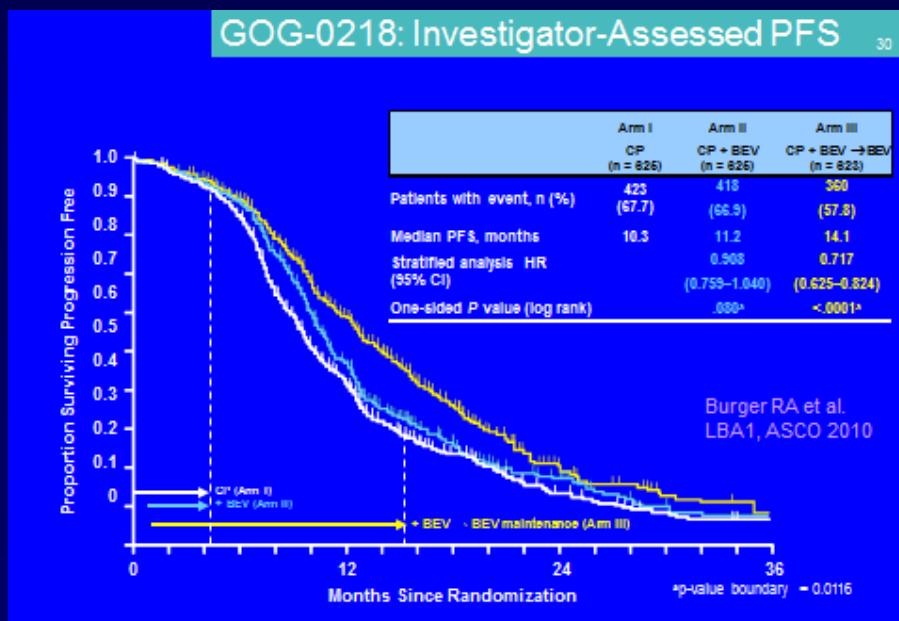
**Can We Generate Clinically
Relevant Signatures?
Predictive Signatures**

ARTICLE



Effect of Bevacizumab on Progression-Free Survival in Ovarian Cancer

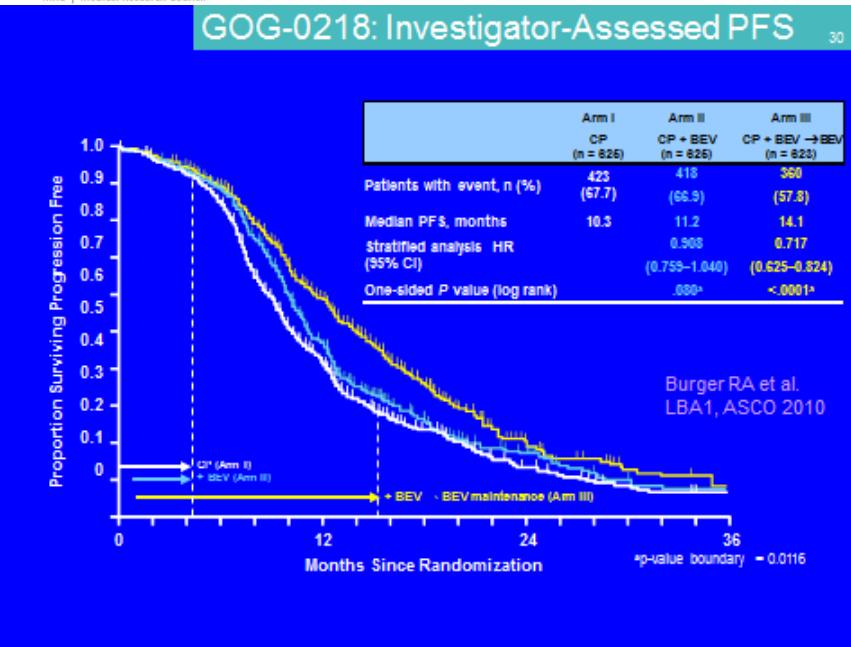
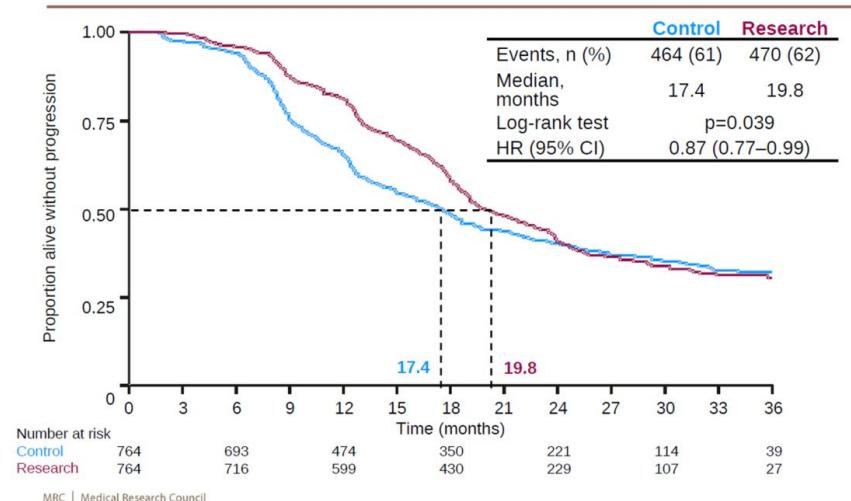
Perren TJ, Jacobus Pfisterer, M.D., Gudrun Kauraine, M.D., Gunnar Kristensen, M.D., Michaela M. Andrés Cervantes, M.D., Daniel Bois, M.D., Jalid Sehouli, M.D., Barbara, M.D., Fiona Collinson, M.D., Alain Lortholary, M.D., Arto Ariza, M.D., Arto Leminen, M.D., Qian, Ph.D., Mahesh K.B. Parmar, Ph.D., and the ICON7 Investigators*



ARTICLE

Bevacizumab in the Maintenance of Ovarian Cancer

Perren TJ, Michael A. Bookman, M.D., Mark Monk, M.D., Helen Huang, M.S., James Comesley, M.D., Jeffrey Fowler, M.D., Michael J. Birrer, M.D., Ph.D., and the Gynecologic Oncology Group*



- European Medicines Agency (EMA) granted bevacizumab a license for first line treatment of stage IIIB, IIIC and IV ovarian cancer in 2011
- Bevacizumab currently licensed for the treatment of recurrent platinum resistant ovarian cancer in the USA

Methods

Discovery

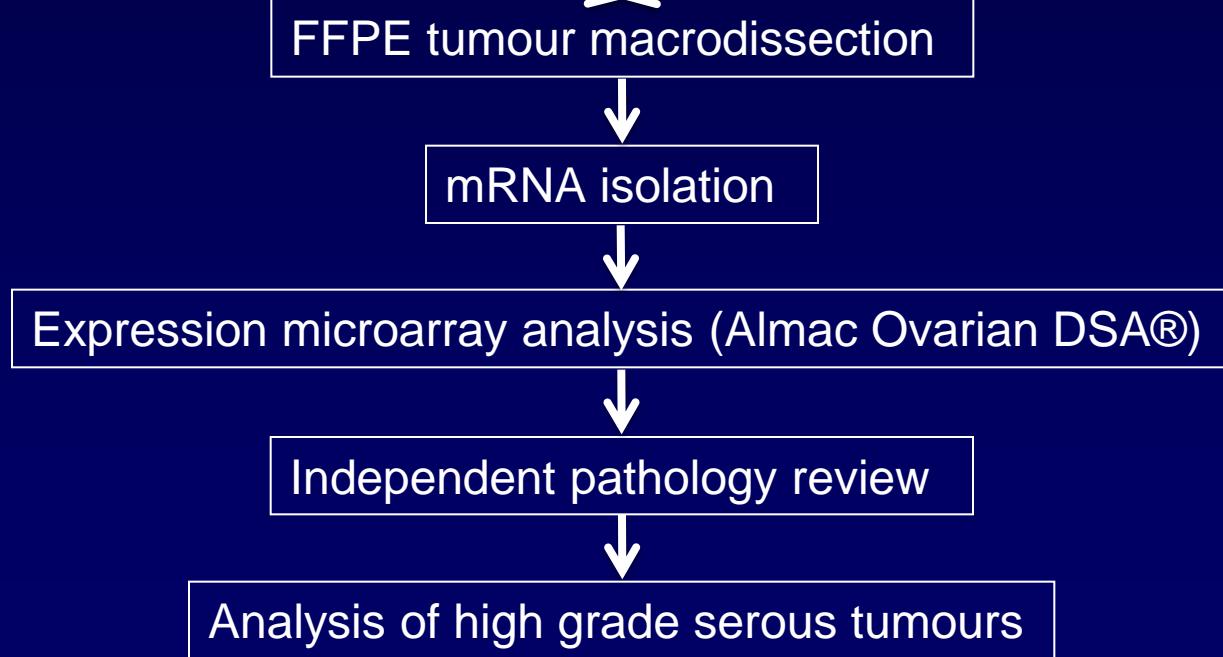
Edinburgh:
387 ovarian cancers

Validation 1 (in silico)

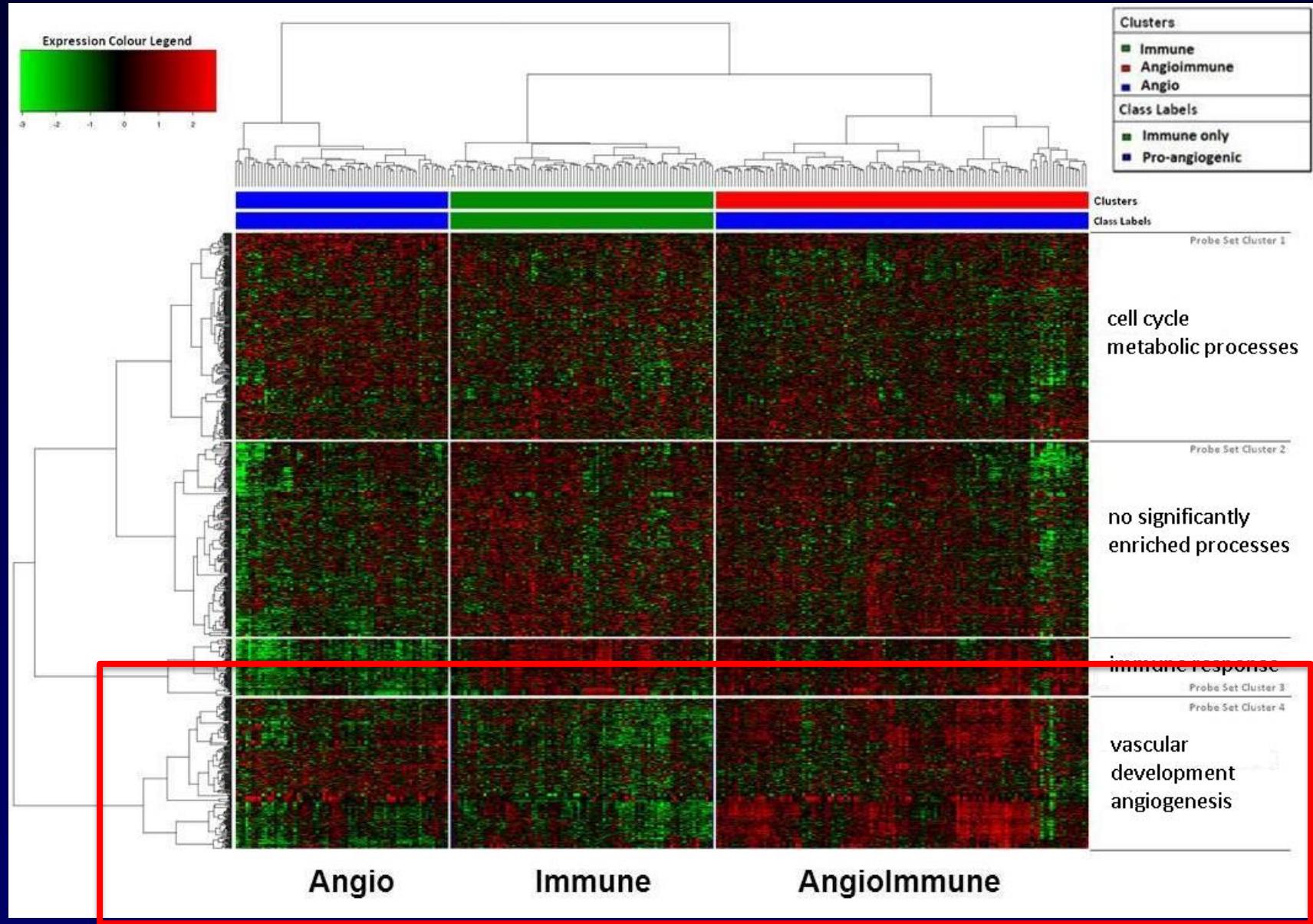
Australia (Tothill):
285 ovarian cancers

Validation 2

ICON7:
375 ovarian cancers

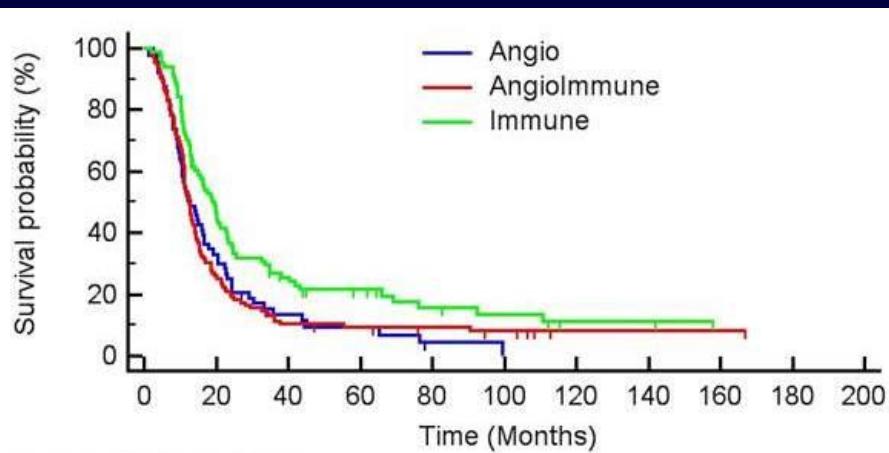


Edinburgh Dataset; Unsupervised Hierarchical Clustering

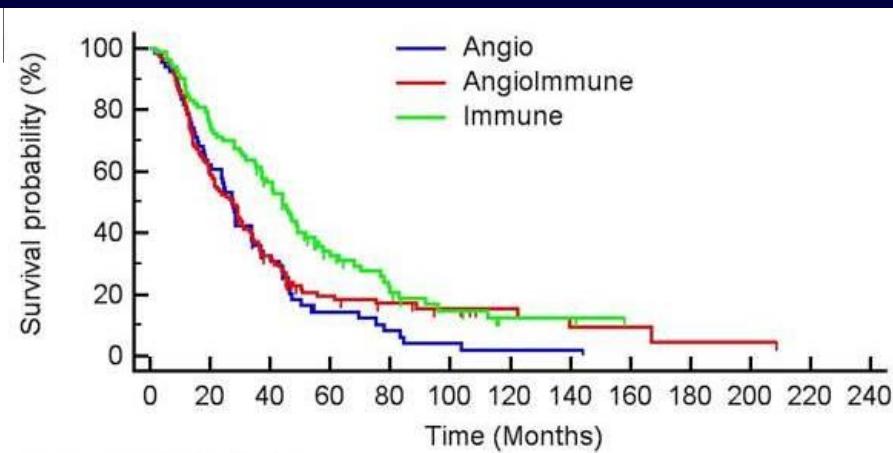


Edinburgh Dataset; Survival Analysis

Progression-free survival



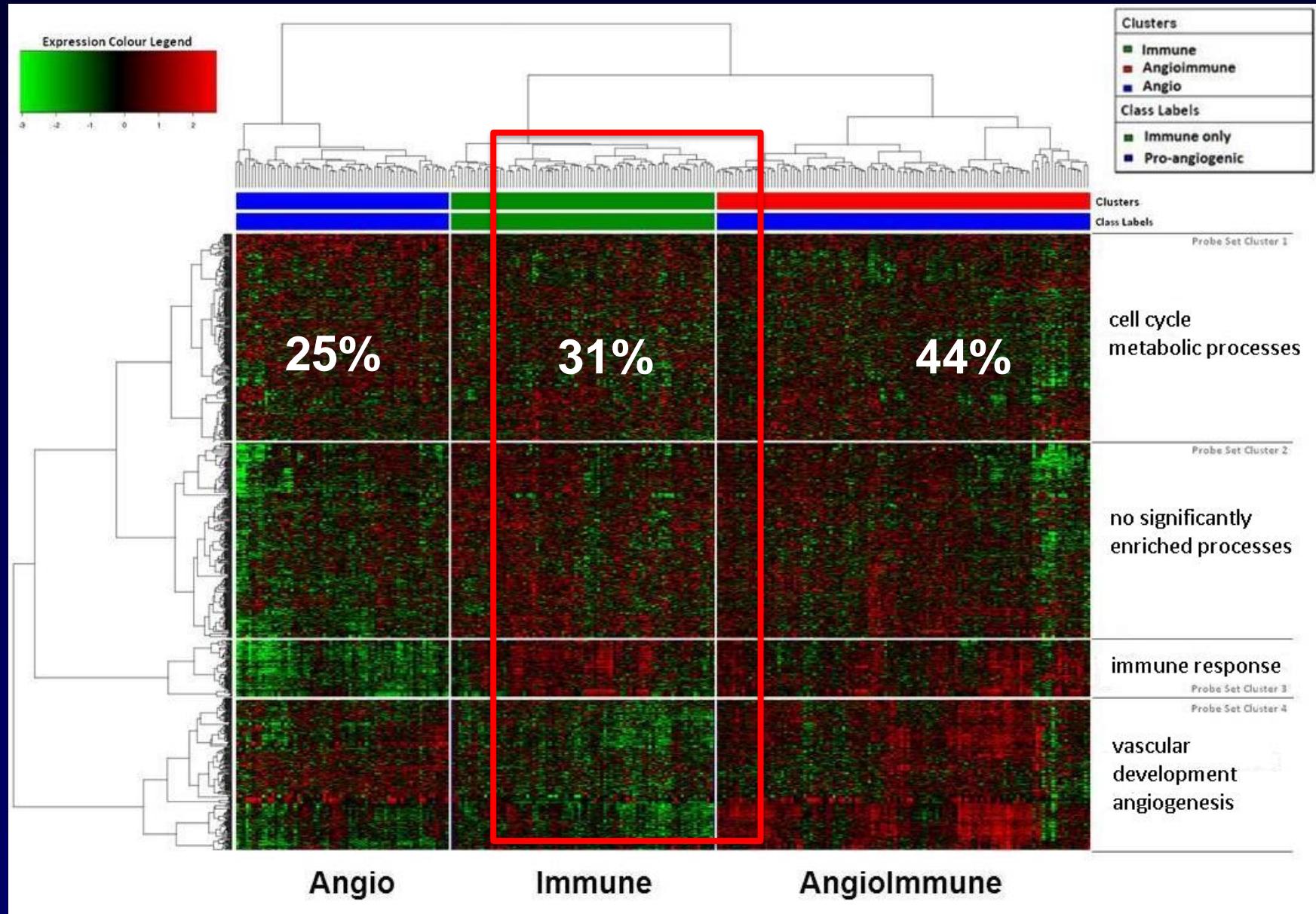
Overall survival



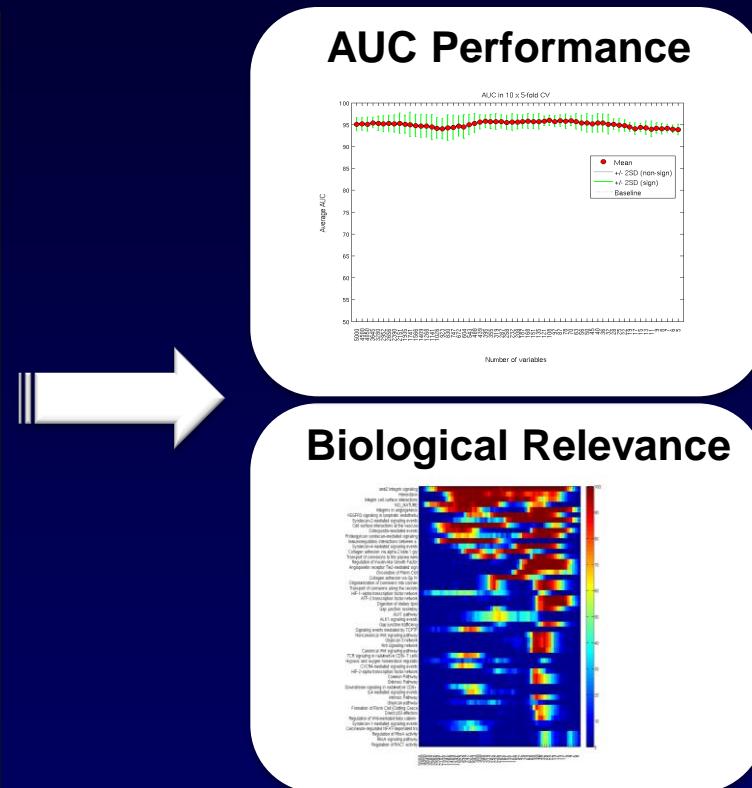
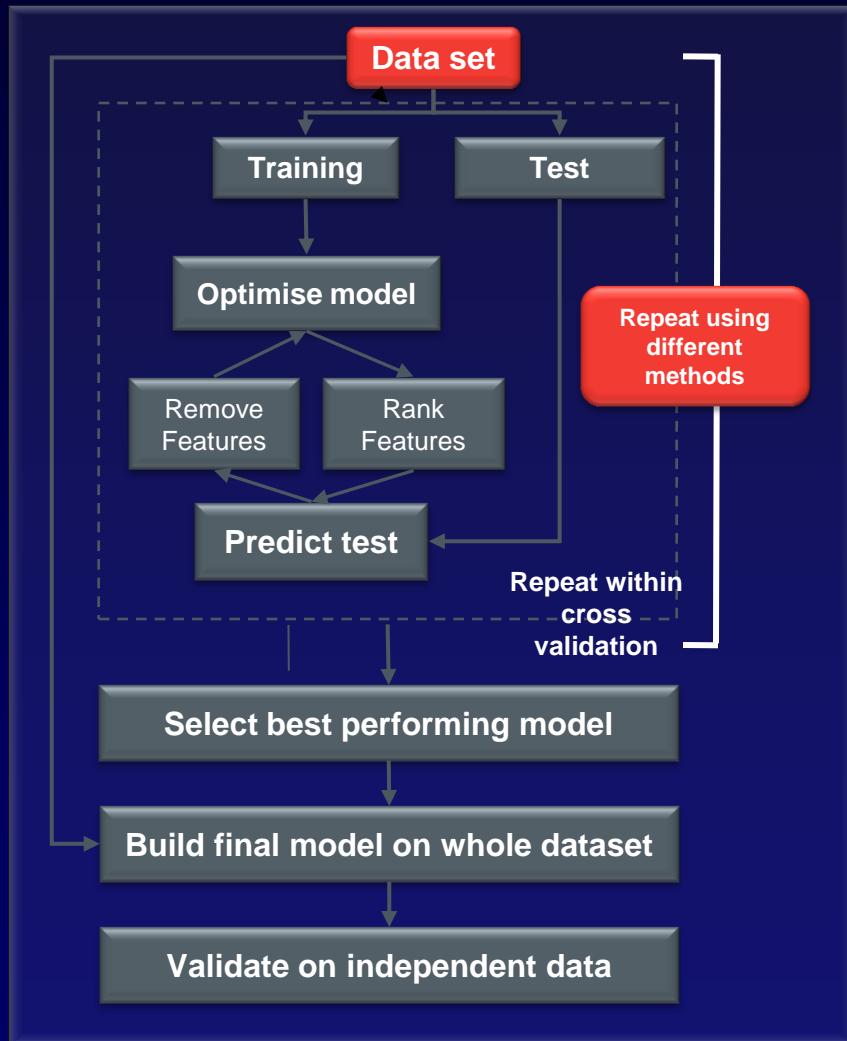
| | HR | 95% CI | P value |
|-----------------------|------|-----------|---------|
| Immune vs angioimmune | 0.60 | 0.44-0.82 | .002 |
| Immune vs angio | 0.64 | 0.45-0.92 | .02 |

| | HR | 95% CI | P value |
|-----------------------|------|-----------|---------|
| Immune vs angioimmune | 0.58 | 0.41-0.82 | .001 |
| Immune vs angio | 0.55 | 0.37-0.80 | .001 |

Edinburgh Dataset; Unsupervised Hierarchical Clustering



Edinburgh Dataset; Immune Subgroup Signature Generation

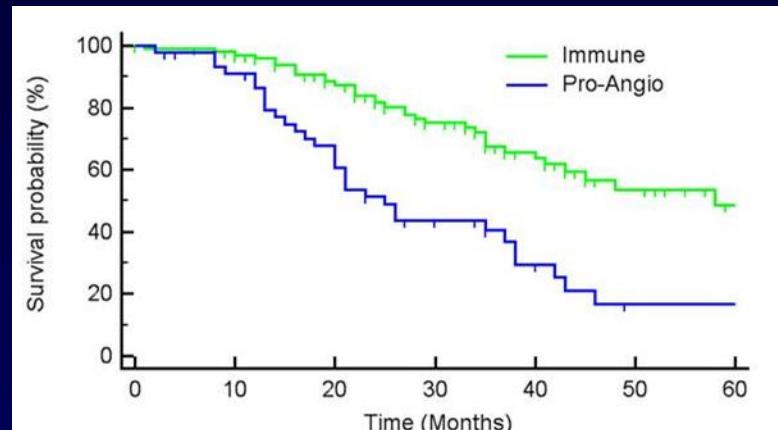
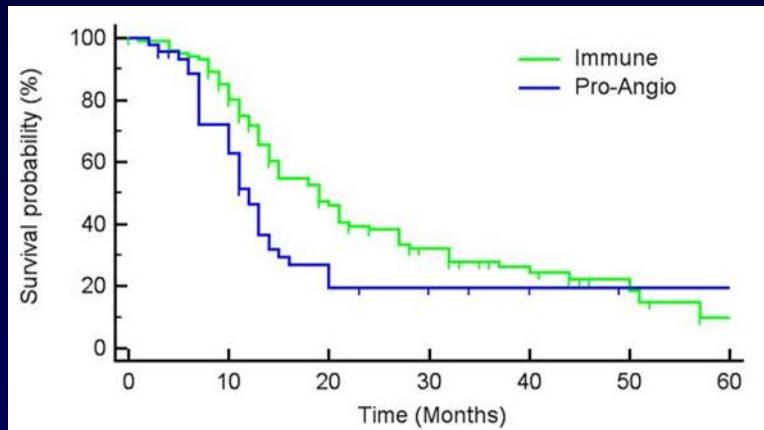


63-gene signature developed to distinguish Immune subgroup patients from those in the angio and angioimmune subgroups.

Application of Signature to Tothill Dataset

PFS

OS



Univariate: $HR = 0.661 [0.439-0.996]$, $P = .048$

Multivariable: $HR = 0.645 [0.423-0.982]$, $P = .041$

$HR = 0.357 [0.219-0.582]$, $P < .001$

$HR = 0.343 [0.206-0.571]$, $P < .001$

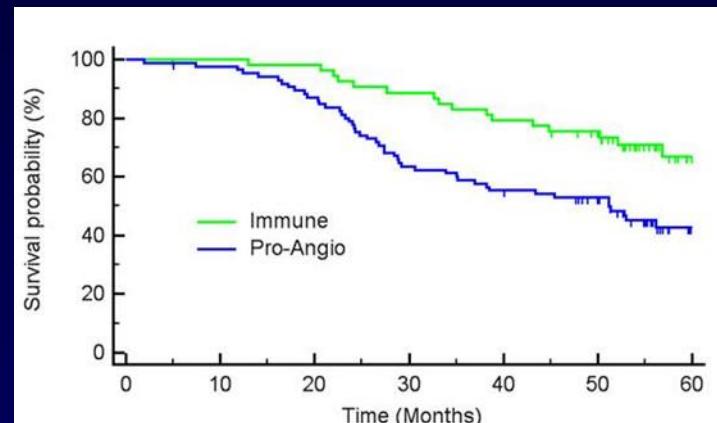
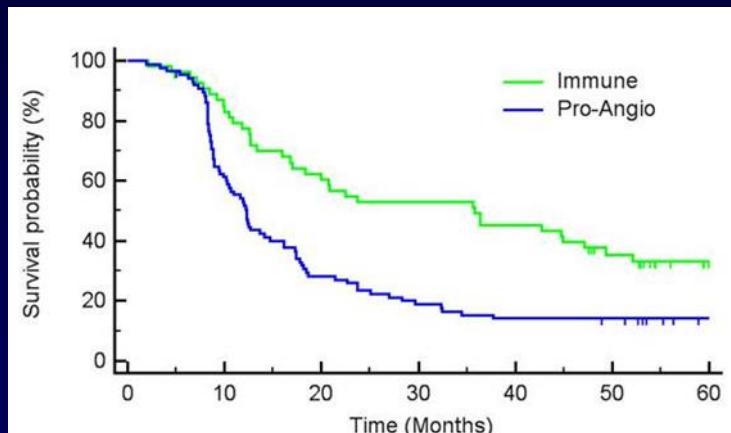
Application of the 63-gene Immune Signature to the ICON7 Translational Specimens

- The immune molecular subtype is characterised by absence of angiogenic biology
- We hypothesized that this group would not benefit from anti-angiogenic agents
- The Immune assay was therefore applied to translational research samples from the ICON7 study (carboplatin and paclitaxel +/- bevacizumab)
- 88% power to detect interaction >2 in the predicted direction for PFS ($\alpha = 0.1$, one-tail)

Immune Signature Prognostic Within the Control Arm of ICON7

PFS

OS



Univariate: HR = 0.47 [0.32-0.71], $P < .001$

Multivariable: HR = 0.52 [0.33-0.81], $P = .004$

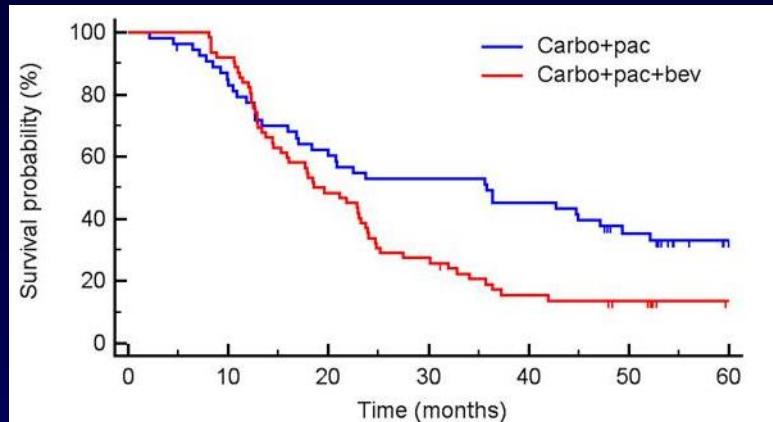
HR = 0.45 [0.26-0.79], $P = .005$

HR = 0.53 [0.29-0.96], $P = .04$

Immune Subgroup Patients Have Inferior Progression-Free Survival When Treated With Bevacizumab

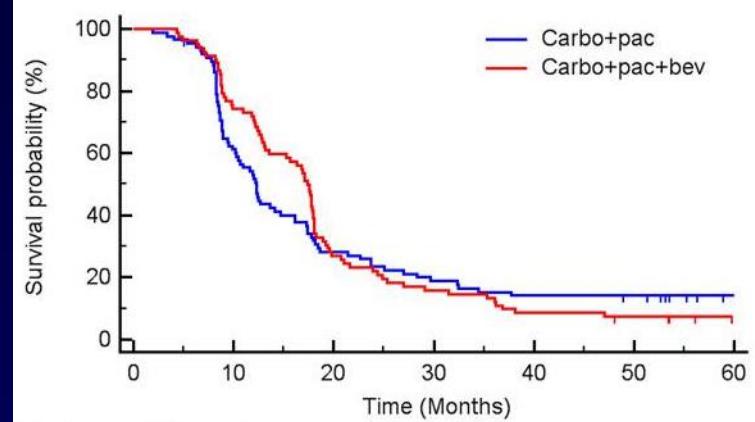
Immune subgroup:

41% of ICON7 TR patients



Nonimmune (proangiogenic) subgroup:

59% of ICON7 TR patients

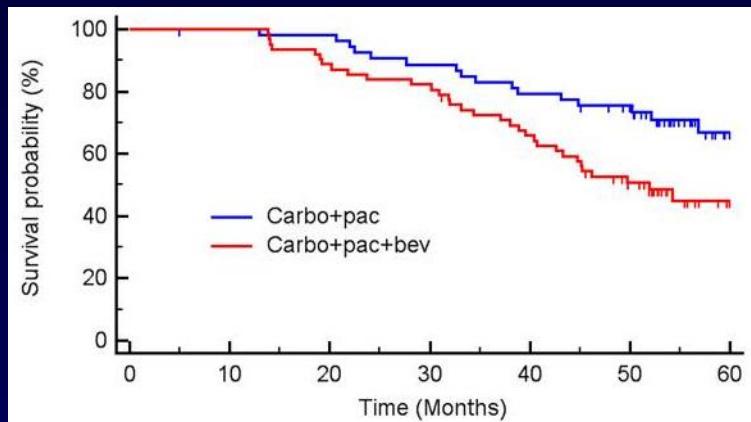


Test for interaction, $P = .015$

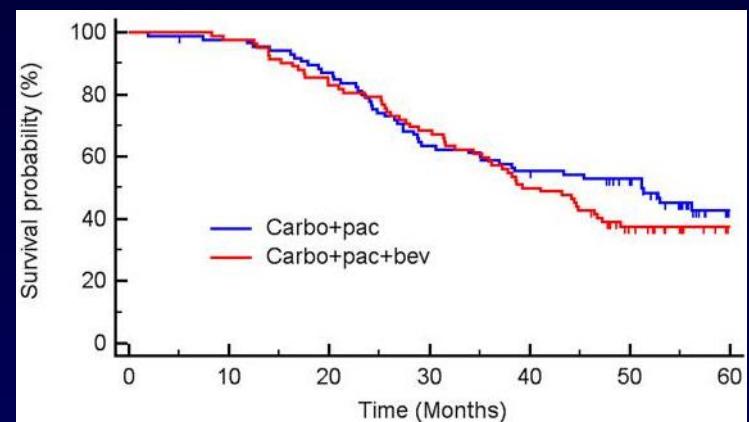
| | Immune subgroup | Proangiogenic subgroup |
|--------------------------------------|--------------------------------------|--------------------------------------|
| Nonproportionality test | $P = .048$ | $P = .003$ |
| Restricted mean PFS in months (se) | C/P 29.7 (2.2) C/P/Bev 23.8 (1.8) | C/P 18.3 (1.5) C/P/Bev 19.3 (1.3) |
| Diff in restricted mean PFS (95% CI) | -5.9 (-11.5 to -0.3) | 1.0 (-2.9 to 4.9) |
| Median PFS in months | C/P 35.8 C/P/Bev 18.5 | C/P 12.3 C/P/Bev 17.4 |

Immune Subgroup Patients Have Inferior Overall Survival When Treated With Bevacizumab

Immune subgroup



Non-immune (pro-angiogenic) subgroup



Test for nonproportionality negative in both molecular subgroups

Immune subgroup

Univariate

HR 2.00 (1.11-3.61), $P = .022$

Proangiogenic subgroup

HR 1.19 (0.80-1.78), $P = .386$

Test for interaction, $P = .075$

Multivariate

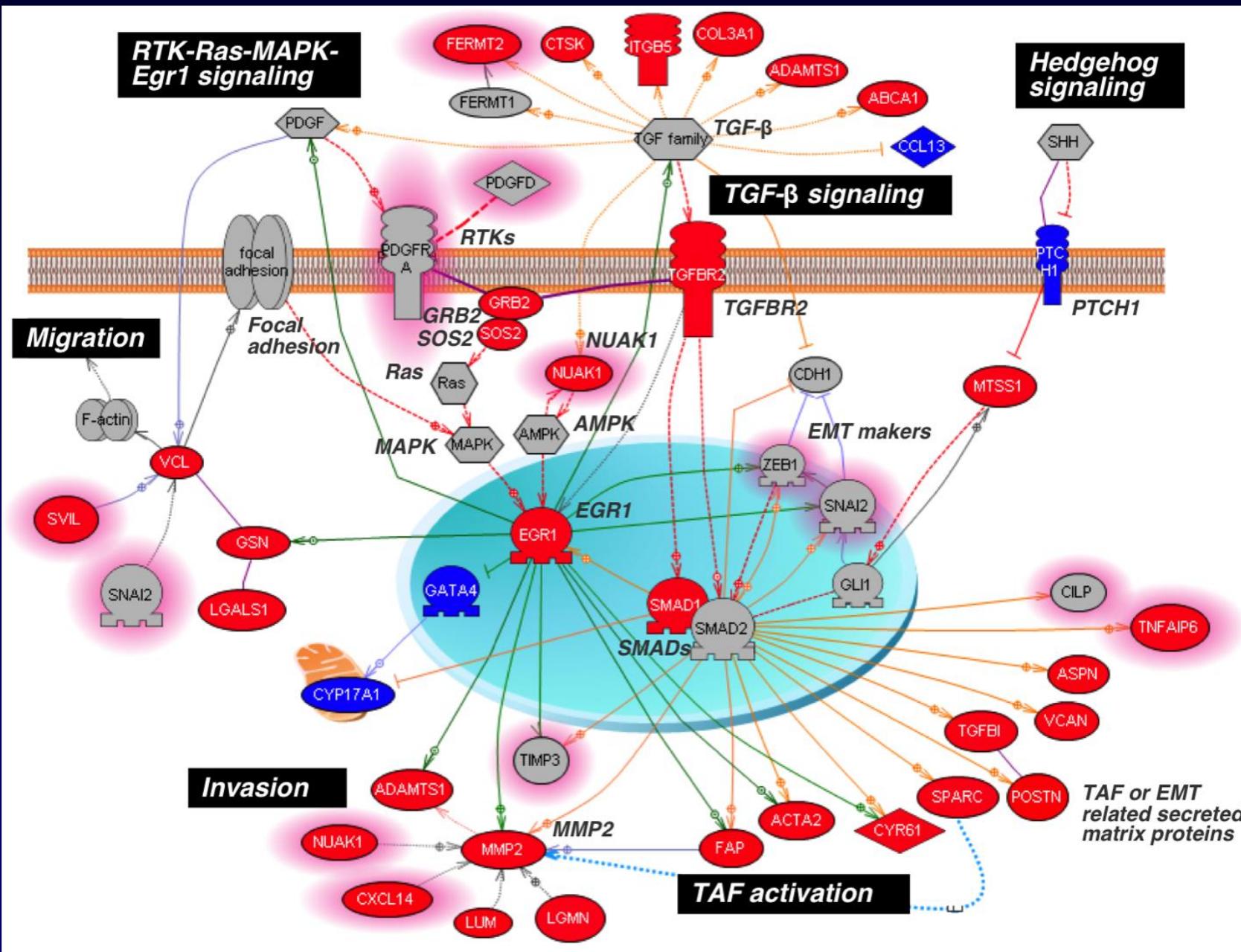
HR 2.37 (1.27-4.41), $P = .007$

HR 1.10 (0.73-1.66), $P = .637$

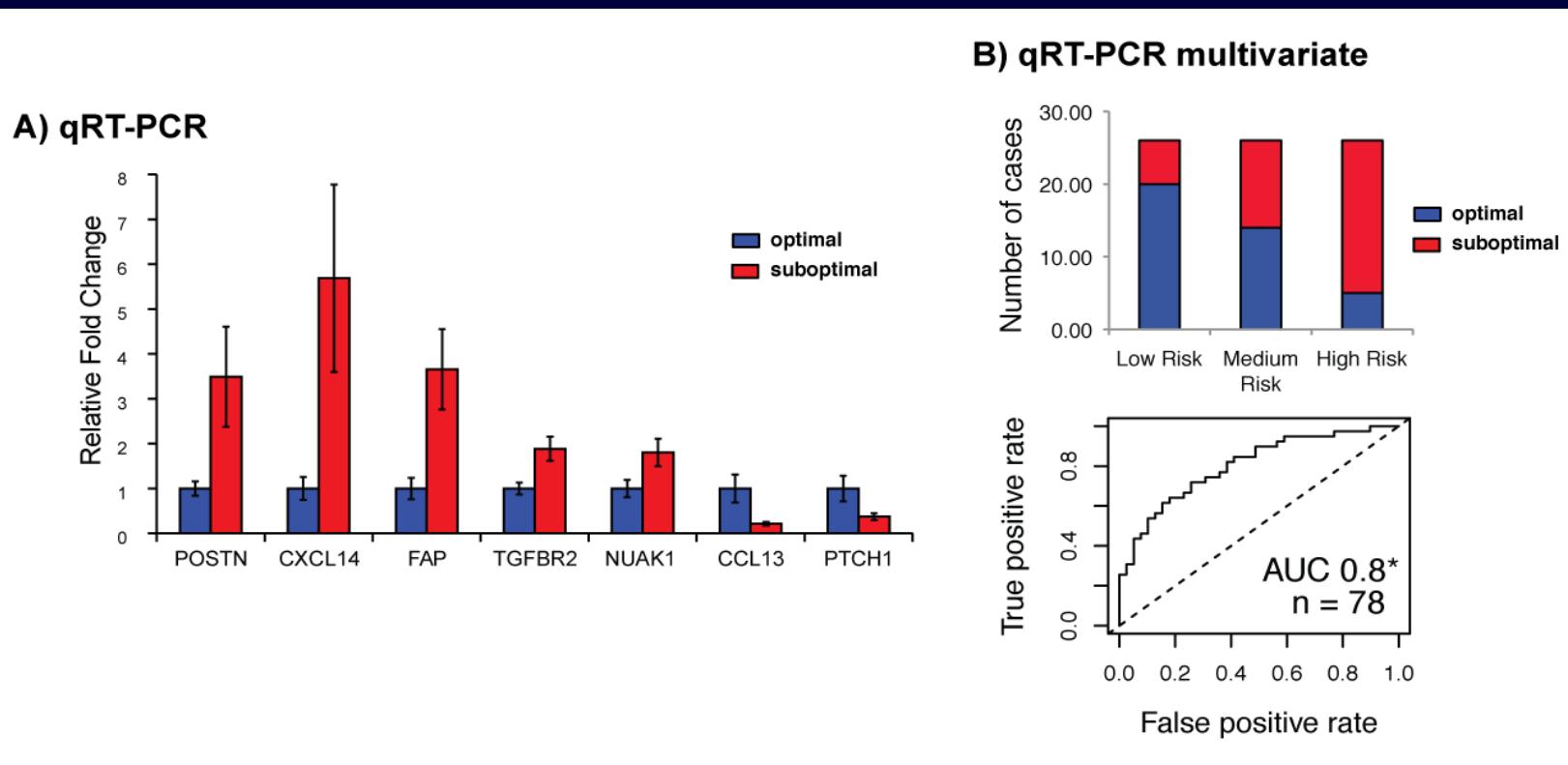
Test for interaction, $P = .020$

Establishment of Debulking Signature

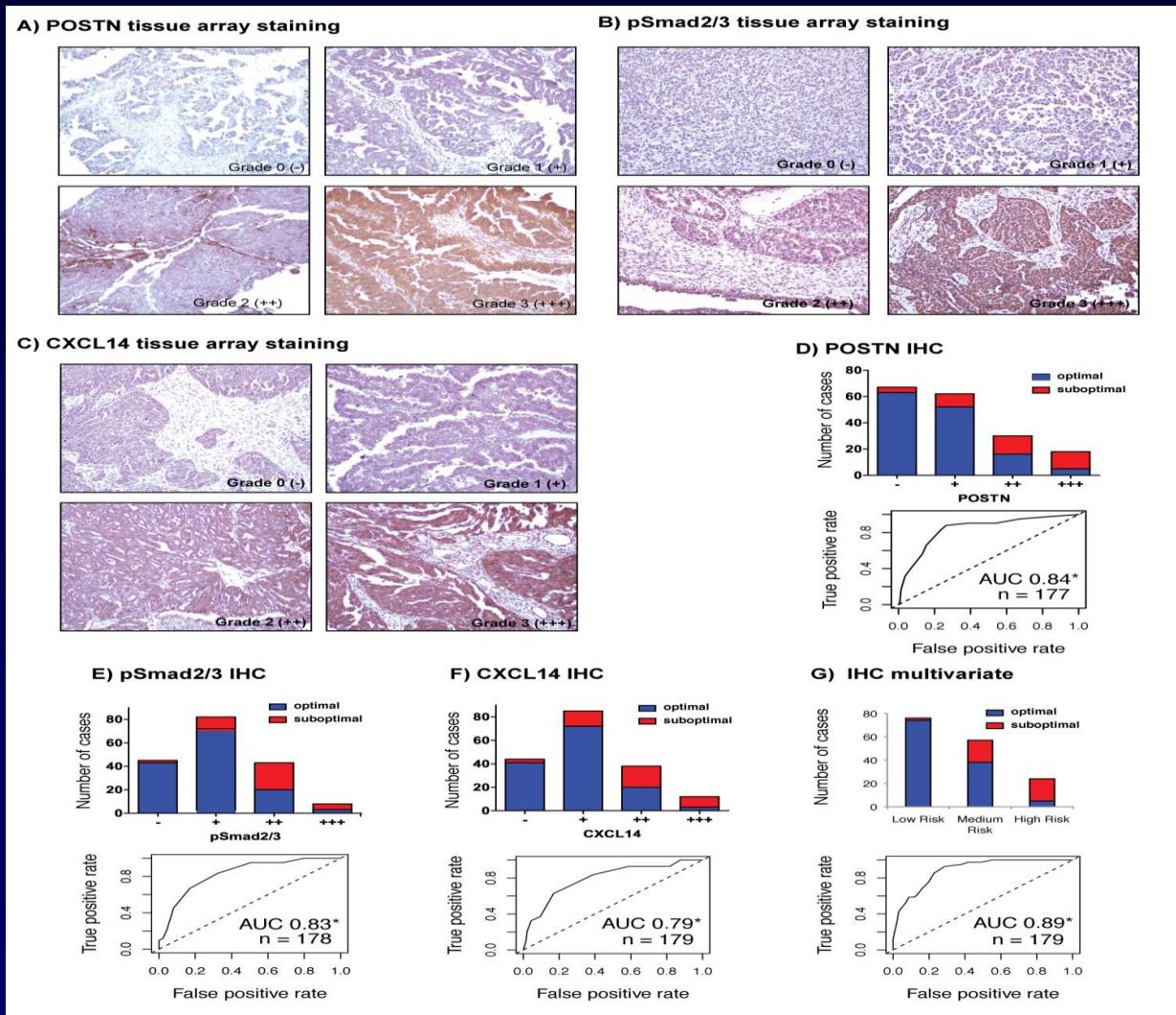
- Based upon the biologic basis of disease spread
- Analyzed 1525 microarrays of primary ovarian cancers
- 22% suboptimal (>1CM)
- Supervised analysis/signature identification
- Generate pathway



qRT-PCR of 7 Pathway Genes Validates Signature and Provides an AUC of .8



Expression of Three Proteins Provides 93% Accuracy for Determining Sub-optimal Debulking Status



Genomic Instability/HRD

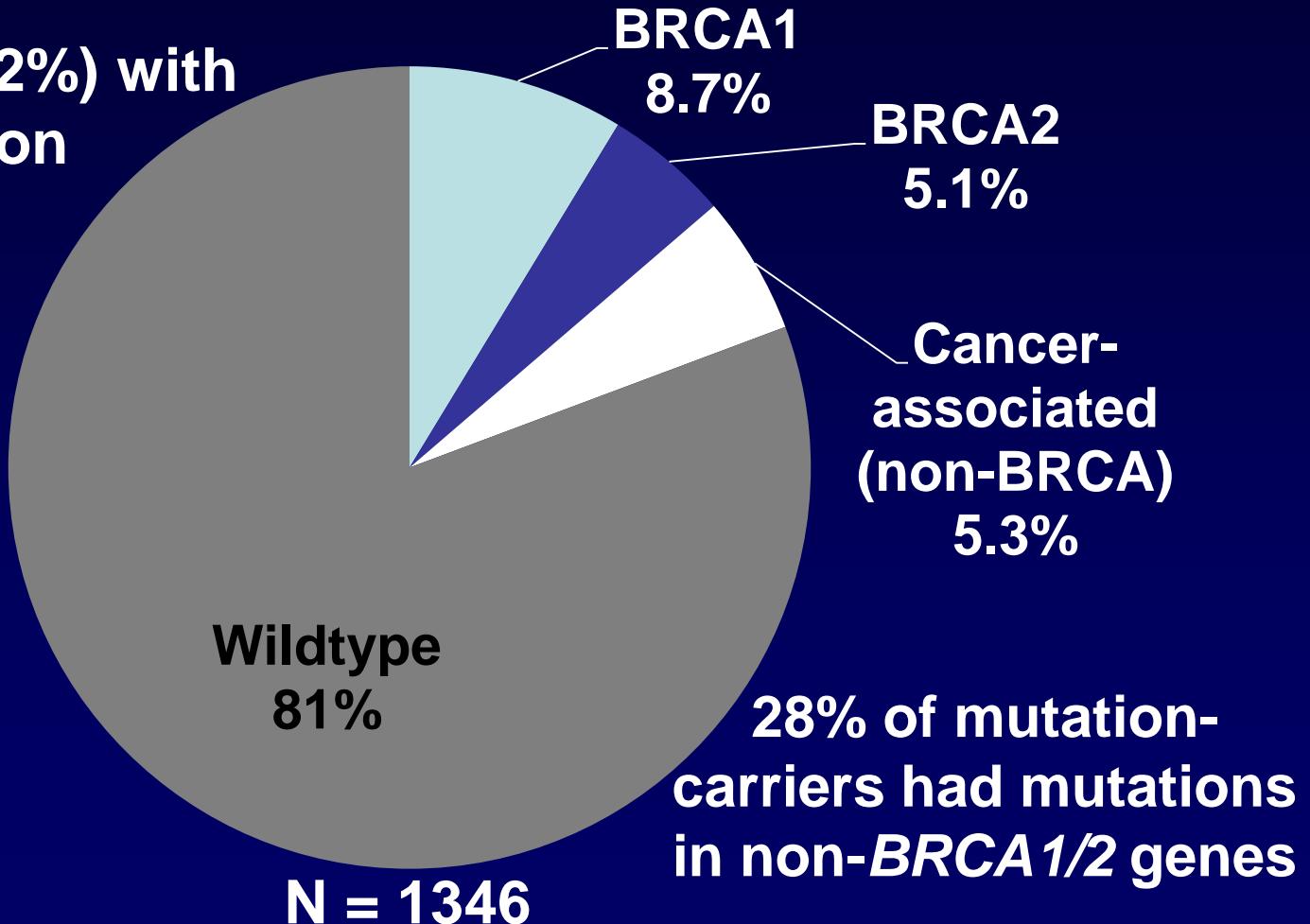
**Does It Provide Prognostic
Versus Predictive Biomarkers?**

Background: GOG 218 and GOG 262

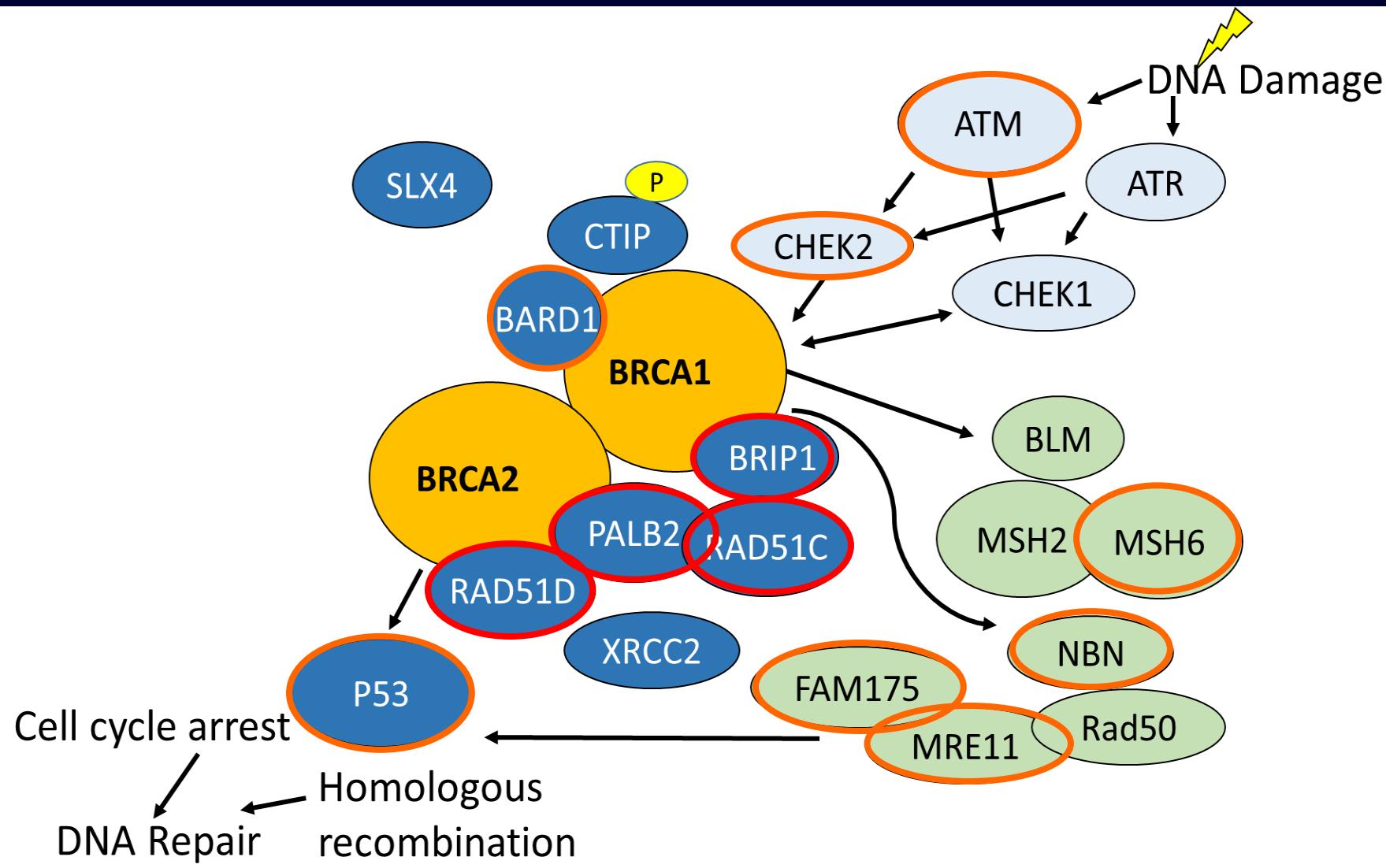
| | | GOG 218 | GOG 262 |
|--------------------------------|----------|-----------------------------------|--|
| Chemotherapy arms | | Carbo/Taxol +/- Bev, Bev maint | Carbo/Taxol q 3wk vs. Dose-dense, + Bev |
| Age | <40 | 22 (2.8%) | 19 (2.7%) |
| | 40-49 | 108 (13.9%) | 86 (12.4%) |
| | 50-59 | 242 (31.1%) | 210 (30.3%) |
| | 60-69 | 262 (33.7%) | 233 (33.7%) |
| | 70-79 | 136 (17.5%) | 120 (17.3%) |
| | >80 | 8 (1.0%) | 24 (3.5%) |
| Race | White | 688 (88.4%) | 592 (85.5%) |
| | Black | 28 (3.6%) | 38 (5.5%) |
| | Hispanic | 32 (4.1%) | 27 (3.9%) |
| Stage/debulking | Stage IV | 184 (23.7%) | 217 (31.4%) |
| | Optimal | 333 (42.8%) | 0 (not allowed) |
| Neoadjuvant | | 0 (not allowed) | 88 (12.7%) |
| High grade serous histology | | 632 (81.2%) | 556 (80.3%) |

Summary of Mutation-Carriers: GOG 218 and GOG 262

258/1346 (19.2%) with
loss of function
mutations

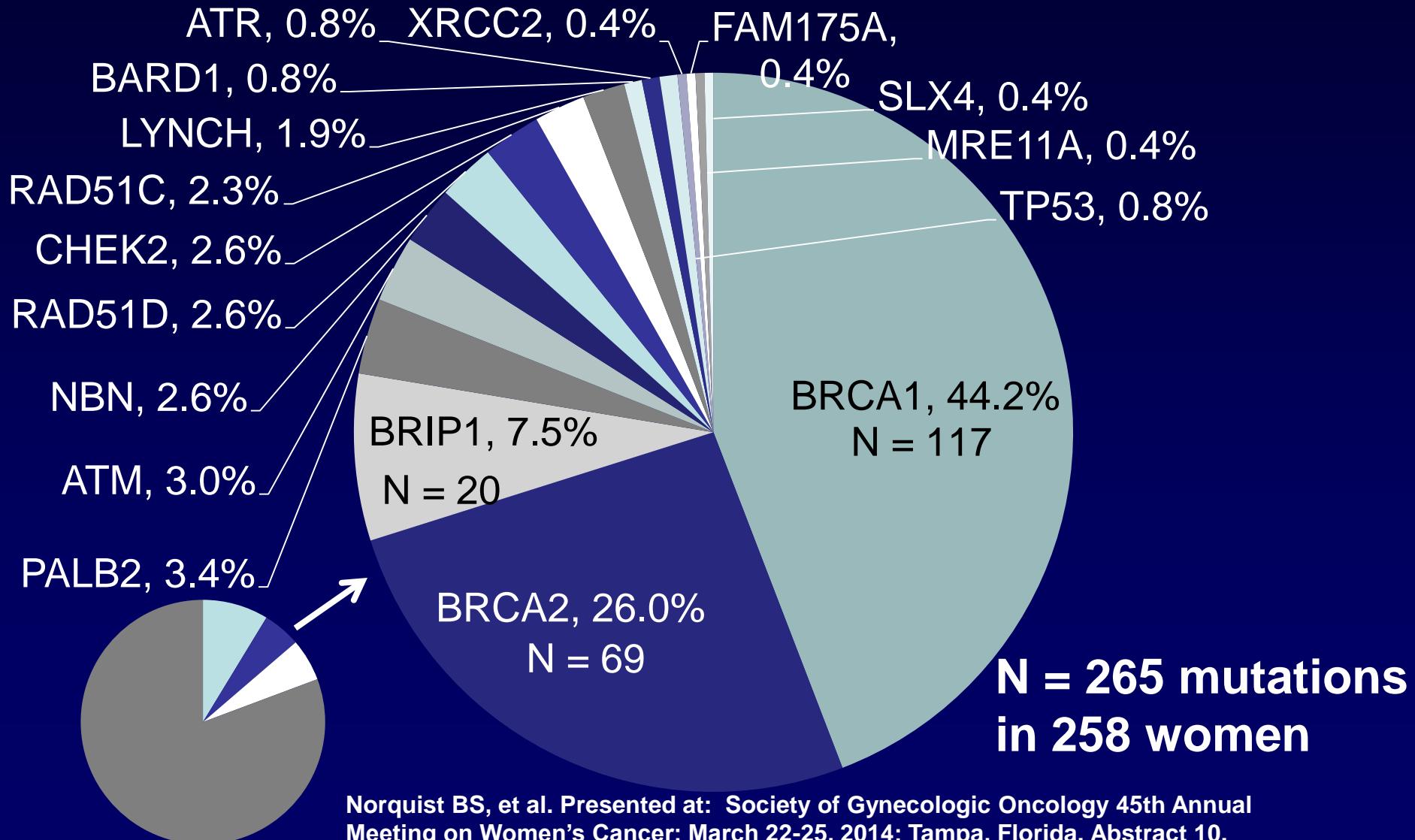


There Is More to DNA-Repair Than *BRCA1/2*

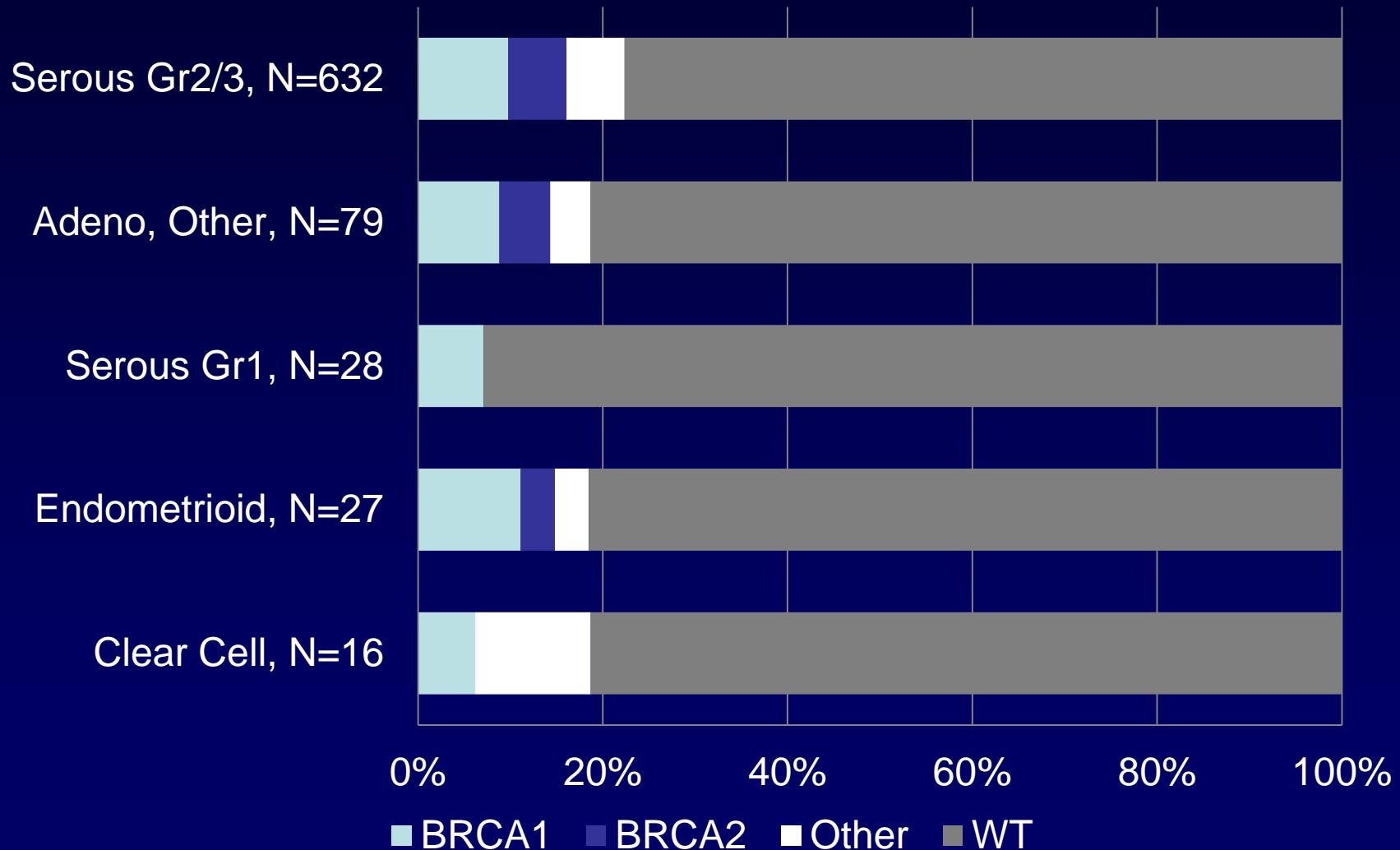


Orange: Walsh T, et al. *Proc Natl Acad Sci U S A*. 2011;108(44):18032-18037. Red: Meindl A, et al. *Nat Genet*. 2010;42(5):410-414. Loveday C, et al. *Nat Genet*. 2011;43(9):879-882. Rafnar T, et al. *Nat Genet*. 2011;43(11):1104-1107. Casadei S, et al. *Cancer Res*. 2011;71(6):2222-2229.

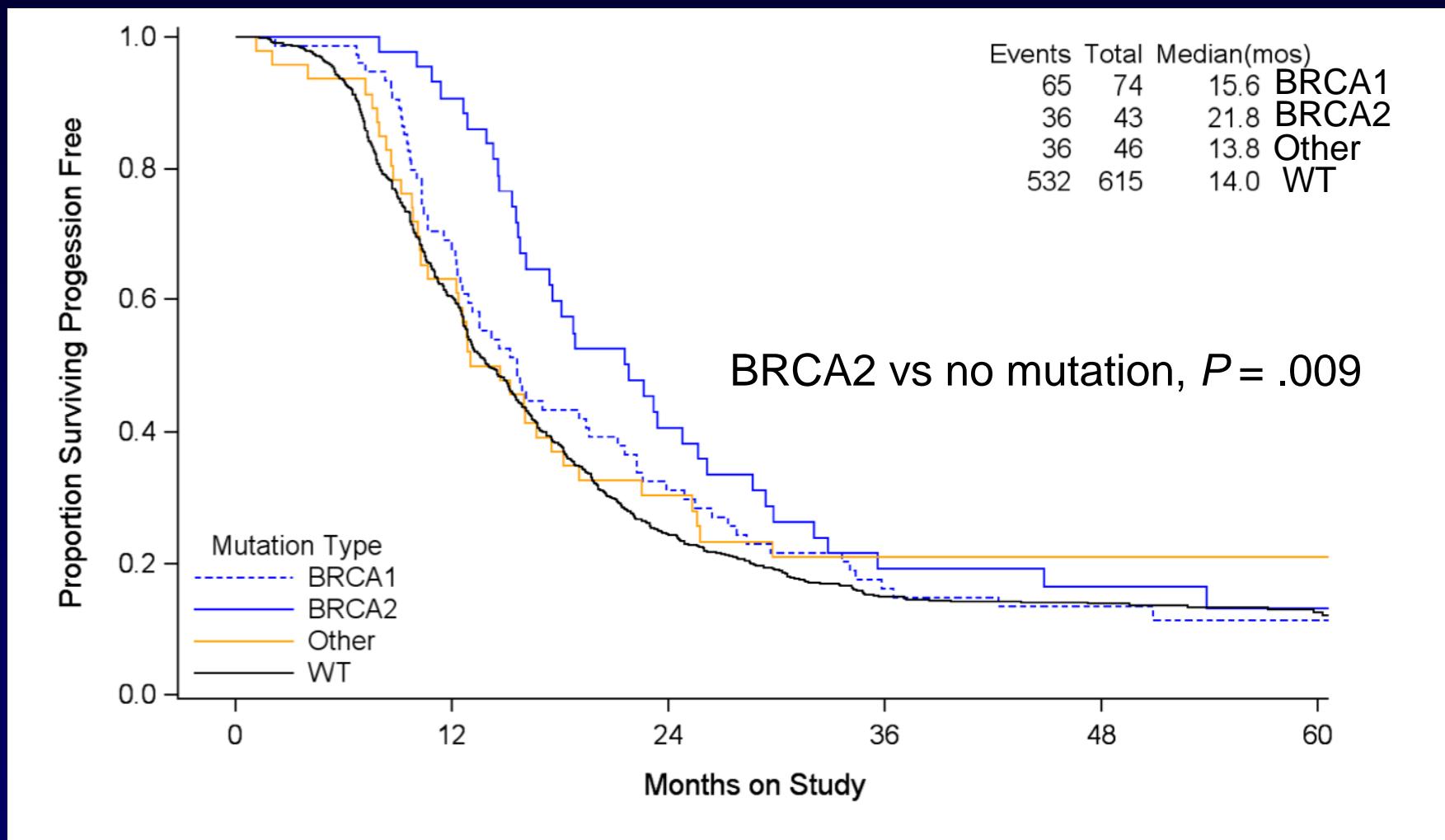
Summary of Cancer-Associated Mutations: GOG 218 and GOG 262



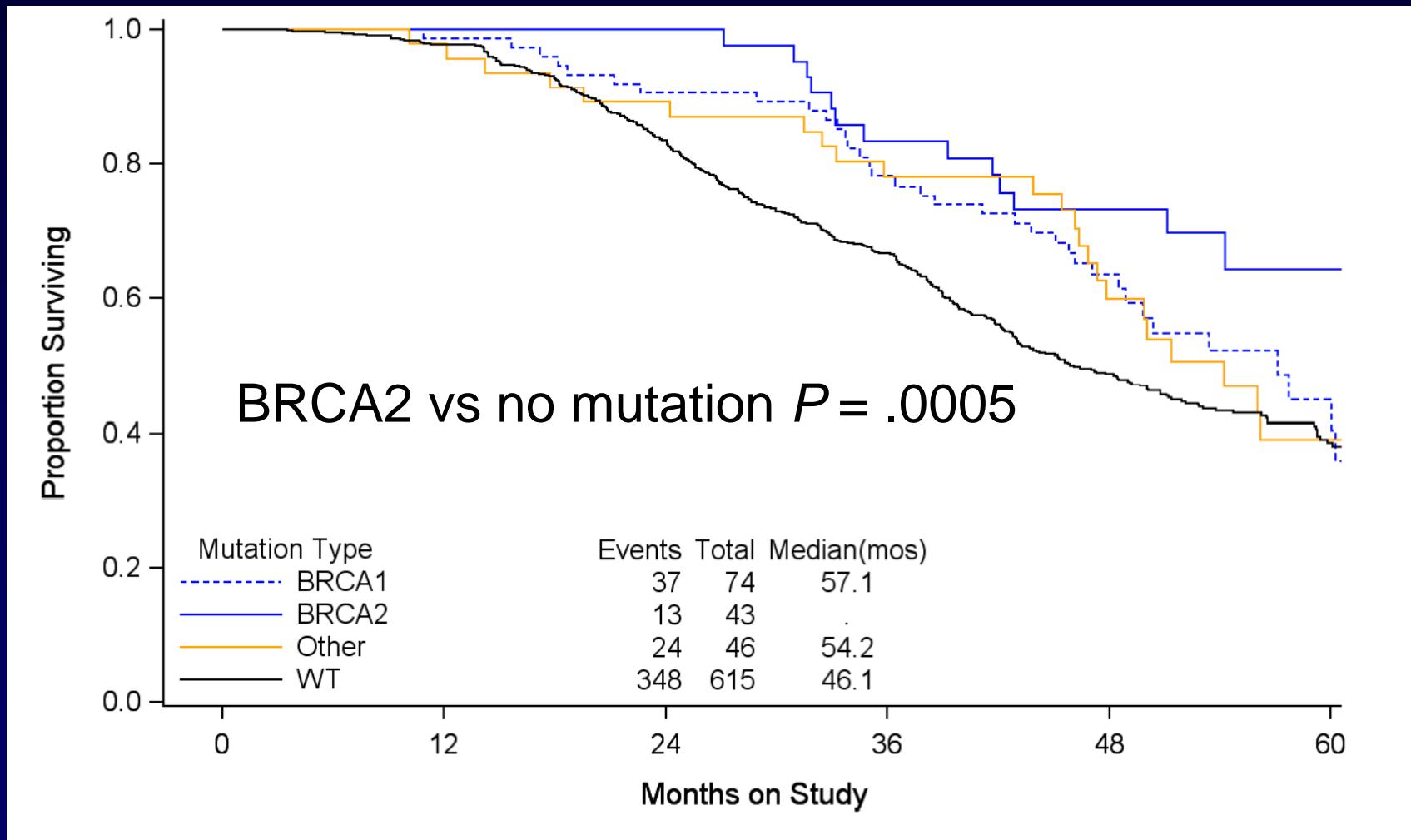
Mutation Status by Histology



Progression-Free Survival, GOG 218



Overall Survival, GOG 218

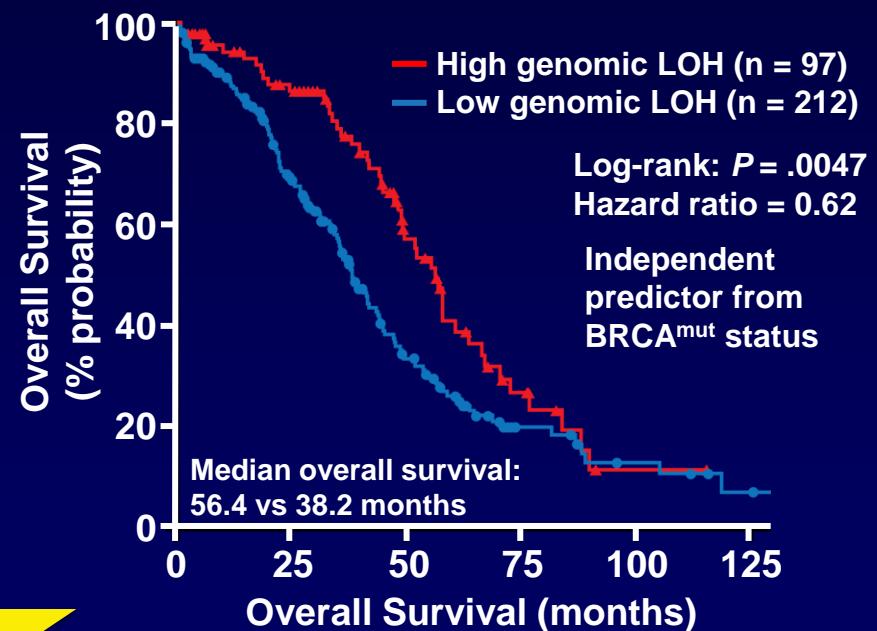
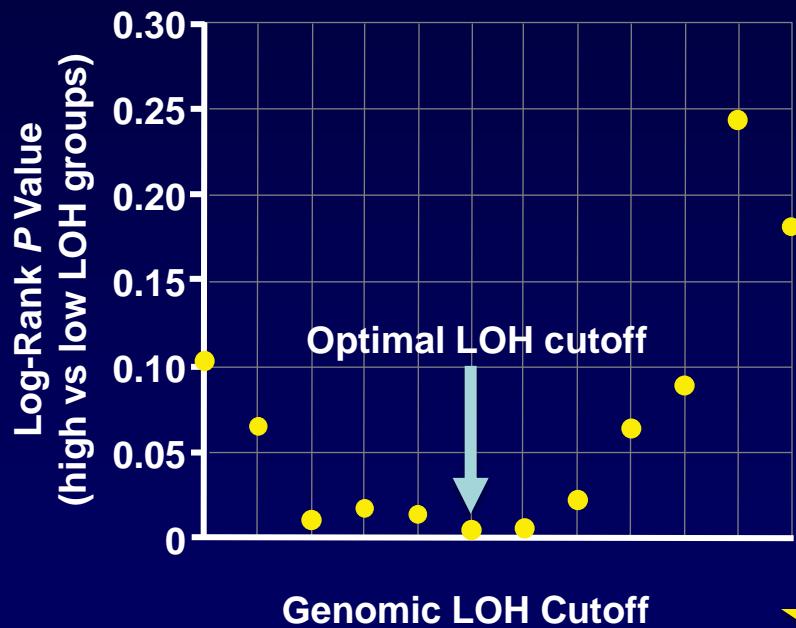


Genomic Instability/HRD

**This Prognostic Signature May
Be Predictive**

Diagnostic Development: Cutoff Defined for BRCA-Like Signature, Being Tested and Refined

TCGA and AOCS overall survival data used to develop LOH cutoff to identify high-grade ovarian cancer patient tumors with BRCA-like signature



Prospective testing of prespecified cutoff in ARIEL2 and ARIEL3

ARIEL2 Goal: Assess Rucaparib Sensitivity in Prospectively Defined Molecular Subgroups

Key Eligibility

- High-grade serous or endometrioid ovarian cancer
- ≥1 prior platinum chemotherapy
- Platinum-sensitive, relapsed, measurable disease
- Adequate tumor tissue (screening biopsy and archival)
- No prior PARPi

600 mg BID
rucaparib
continuously until
progression by
RECIST

Cap on known
germline BRCA^{mut}

Primary Endpoint

- PFS (RECIST) in:
 - BRCA^{mut}
 - BRCA-like (excludes BRCA^{mut})
 - Biomarker negative

Secondary Endpoints

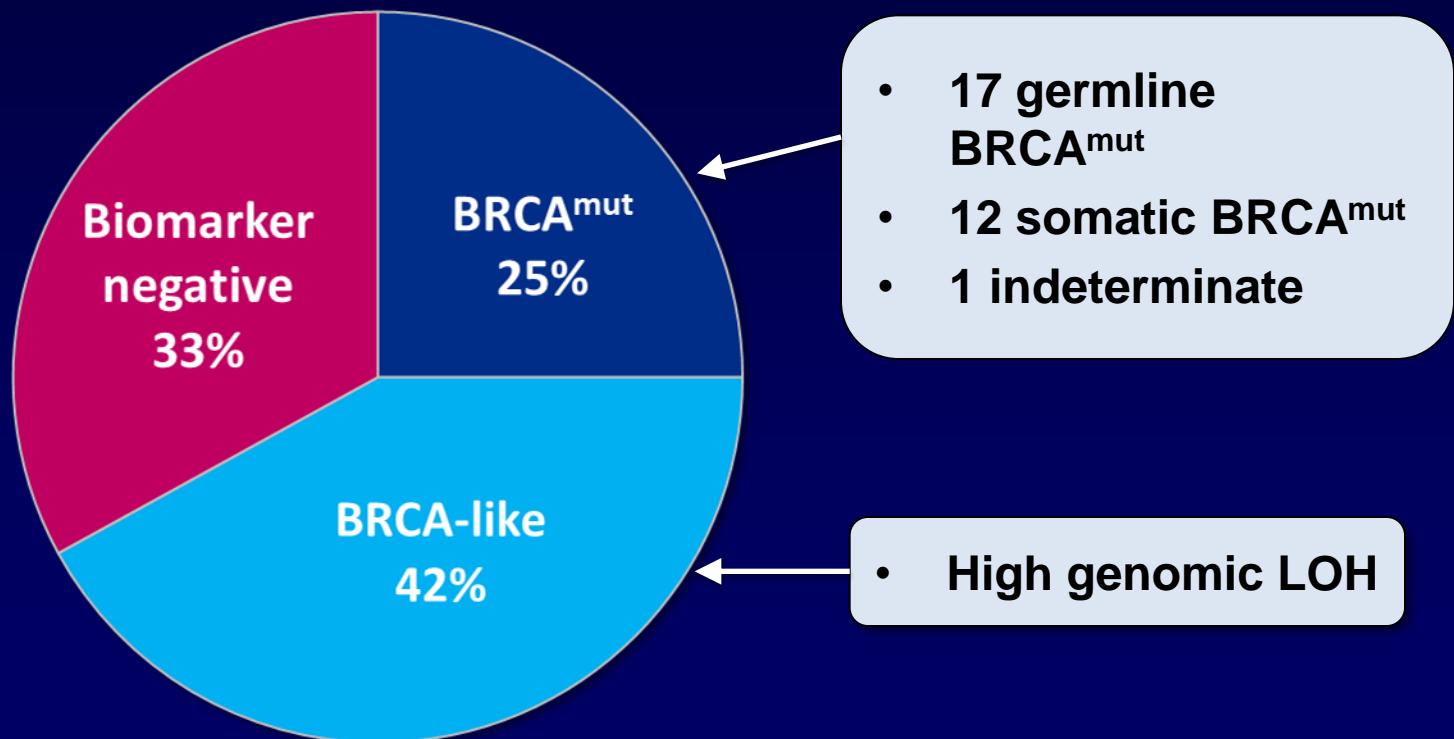
- ORR (RECIST & CA-125)
- Safety
- Pharmacokinetics

CA-125, cancer antigen 125 test; ORR, overall response rate; RECIST, Response Evaluation Criteria In Solid Tumors

Swisher E, et al. Presented at: 26th EORTC-NCI-AACR Symposium on Molecular Targets and Cancer Therapeutics; November 18-21, 2014; Barcelona, Spain.

The Majority of BRCA^{wt} Patient Tumors Exhibit BRCA-Like Signature

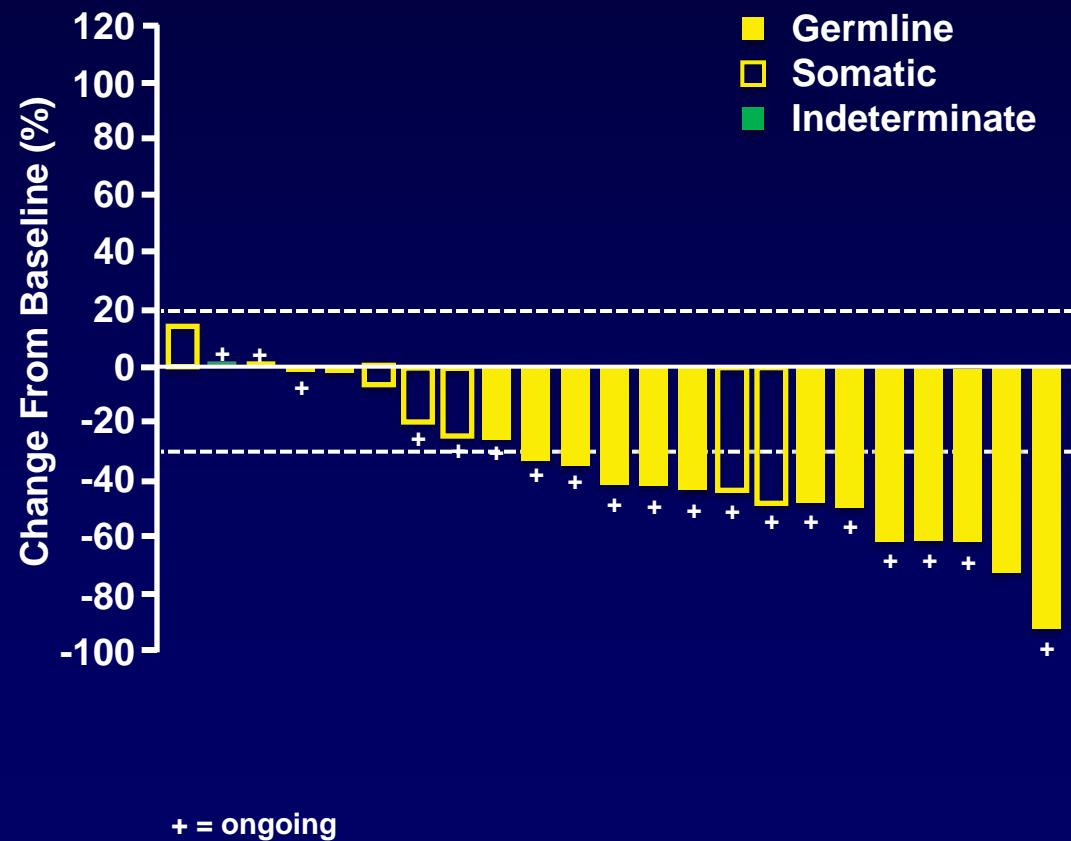
Tumor BRCA/BRCA-like status as determined by HRD Test (N = 121)



Greatest Rucaparib Activity Observed in BRCA^{mut} Patients...

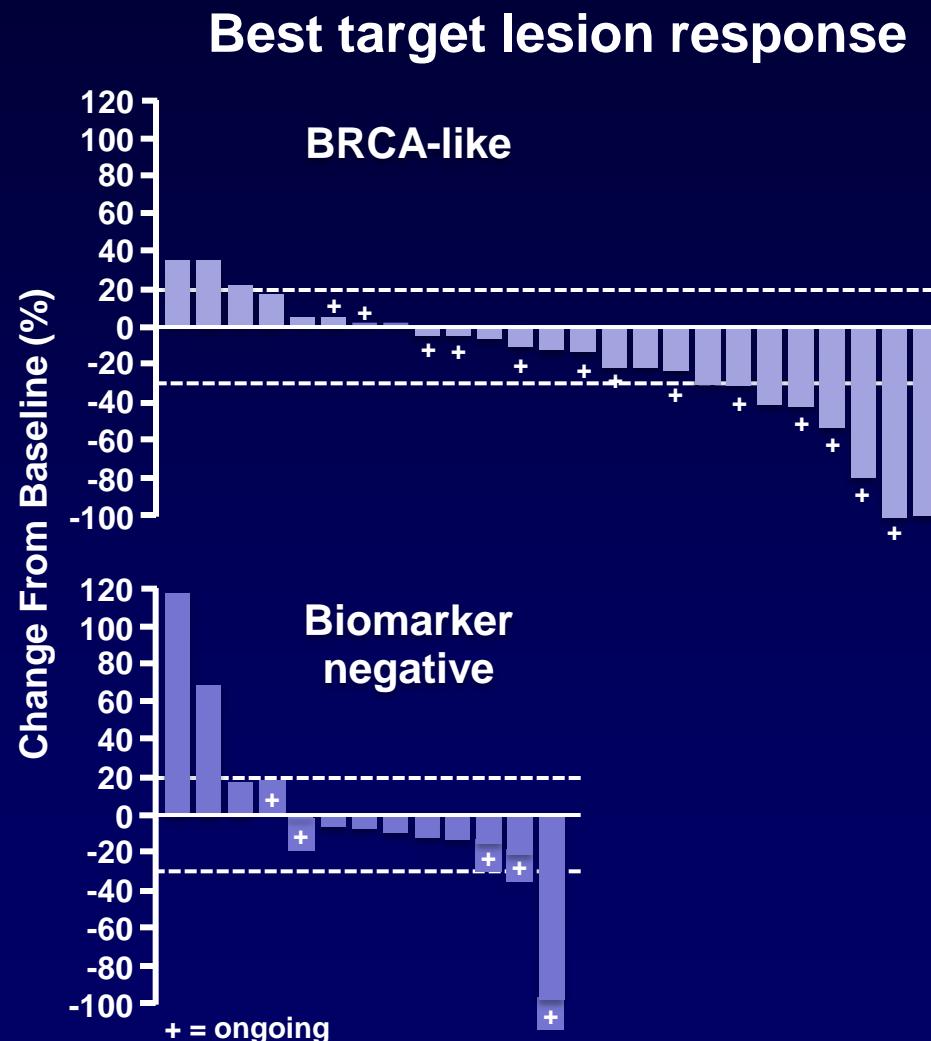
- Robust clinical activity observed in BRCA^{mut} patients (n = 23)
 - 61% ORR (RECIST)
 - 70% ORR (RECIST & CA-125)
 - 83% of patients continuing on treatment (+)
- Responses observed in germline and somatic BRCA^{mut} tumors

Best target lesion response



...and Differential Rucaparib Activity Seen in Patients With/Without BRCA-Like Signature

- Clinical activity observed in BRCA^{wt} patients with BRCA-like signature (n = 25)
 - 32% ORR (RECIST)
 - 40% ORR (RECIST & CA-125)
 - 52% of patients continuing on treatment (+)
- Few responses observed in BRCA^{wt} patients without BRCA-like signature (n = 13)
 - 8% ORR (RECIST)
 - 8% ORR (RECIST & CA-125)
 - 38% of patients continuing on treatment (+)



Genomic Assays

- Multiple different companies
- Multiple genomic platforms
 - Sequencing
 - Expression profiling
 - IHC
- Accurate assessments but clinical correlations not validated
- Could be used to identify appropriate clinical trial

Conclusions

- Molecular analysis has demonstrated that ovarian cancer is a heterogeneous disease
- Genomic abnormalities can be targeted for clear cell and low grade serous ovarian cancers
- High grade serous cancers have extensive genomic instability
- Genomic signature for survival, debulking, and anti-angiogenesis response under development
- Predictors of response to PARP inhibitors under development
- Genomic analysis of tumors (outside of fanconi pathway) is of little clinical value
- Personalized medicine is coming

2015

Progress and Controversies in Gynecologic Oncology Conference

