

Breast cancers

Pathology and predictive criteria

Molecular biology aspects

P de Cremoux, J Lehmann-Che,
H de Thé

*Unité d'Oncologie Moléculaire, Service de Biochimie
Université Paris-Diderot, Inserm U944, UMR 7212
Hôpital Saint Louis, Paris, France*

2nd International Congress of Breast Disease Centers 9-10 /02/ 2012

Rationale

Breast cancer is a heterogeneous disease

Predictive markers are crucial for patients management



**At present: only ER, PR and HER2 are applied to predict
specific response to a therapy in breast cancer
management**

The present

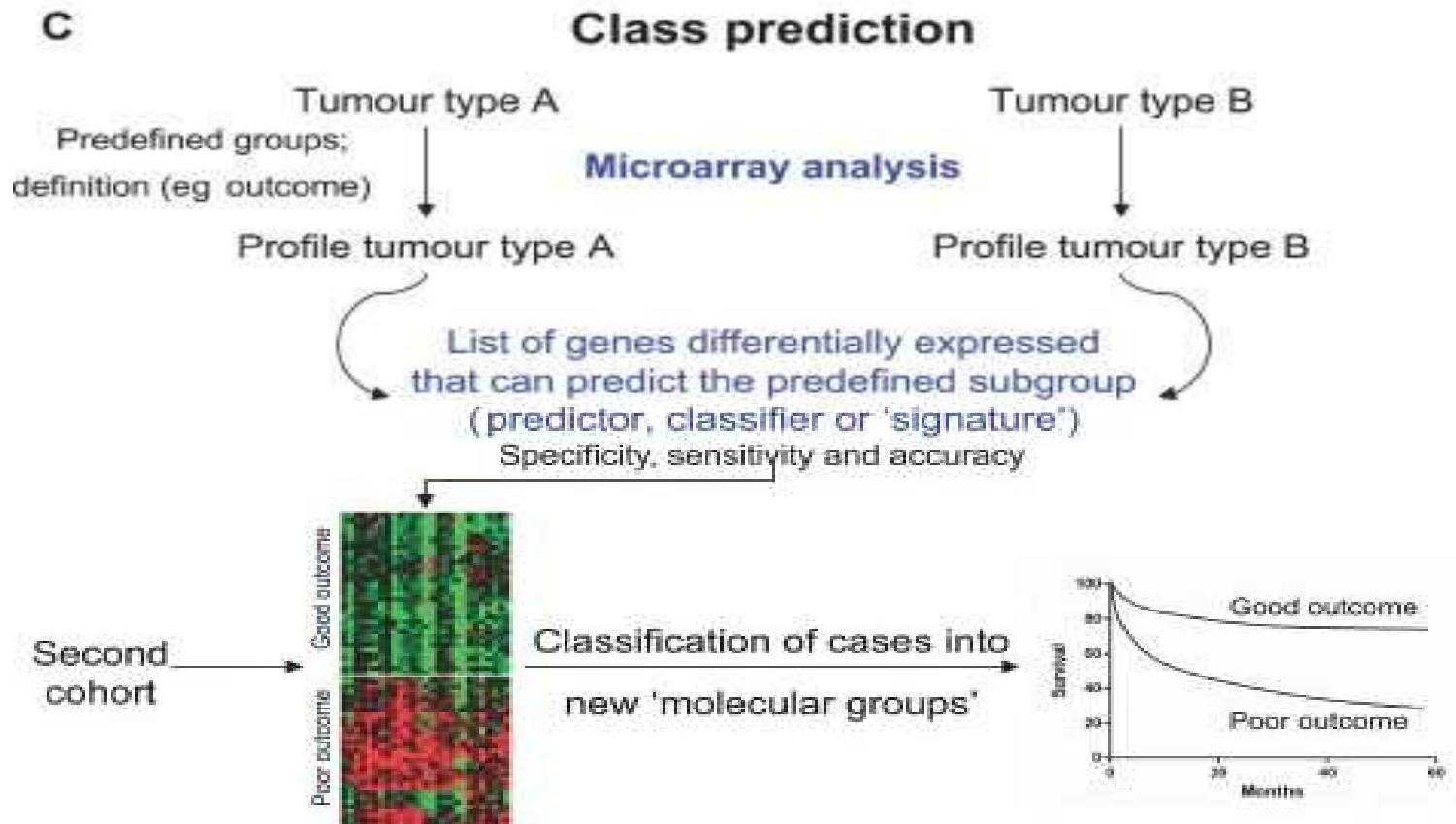
1. **Several treatment options**
2. **Several gene expression profiling studies**
3. **Availability of the Human Genome Project**



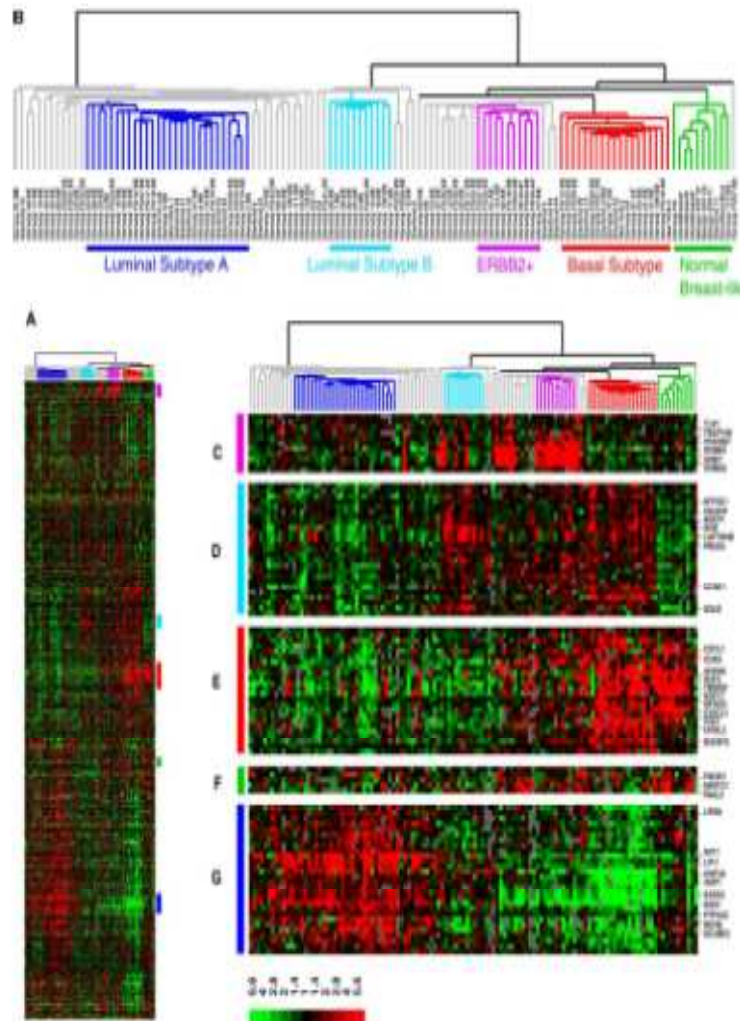
Molecular complexity of breast carcinoma

Potential new molecular targets for drug development

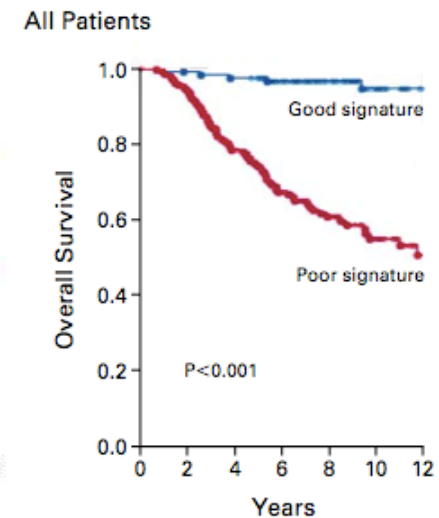
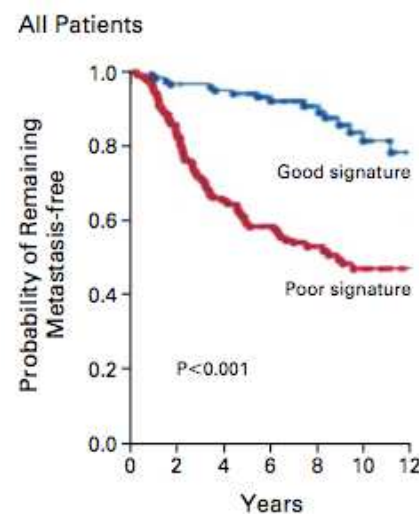
High throughput analysis



Breast cancer molecular classification (1)



- 70 genes signature
- Five molecular subgroups
 - Luminal A
 - Luminal B
 - Basal-like (TN/Claudin-Low)
 - HER2-like
 - Normal like
- Prognosis and therapeutical consequences



(Perou, 1999, 2000; Sorlié, 2001, 2003;
van't Veer, 2003; van de Vijer, 2002)

Breast cancer molecular classification (2)

Molecular apocrine tumours (ER-, AR+, FOXA1+, HER2+/-)

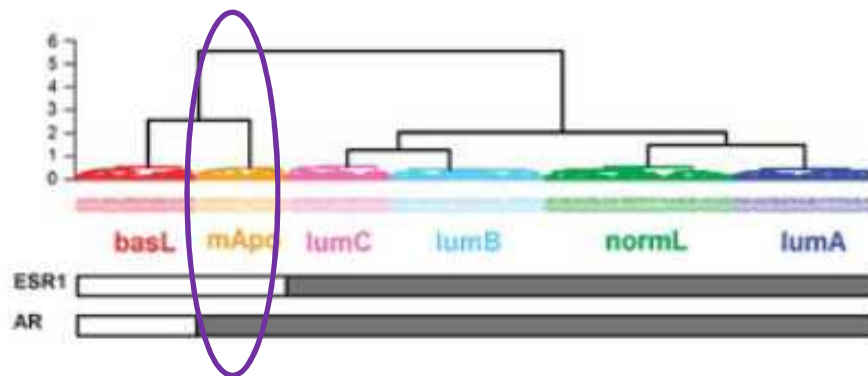
Open

Oncogene (2011) 1–11
 © 2011 Macmillan Publishers Limited All rights reserved 0950-9232/11
 www.nature.com/onc

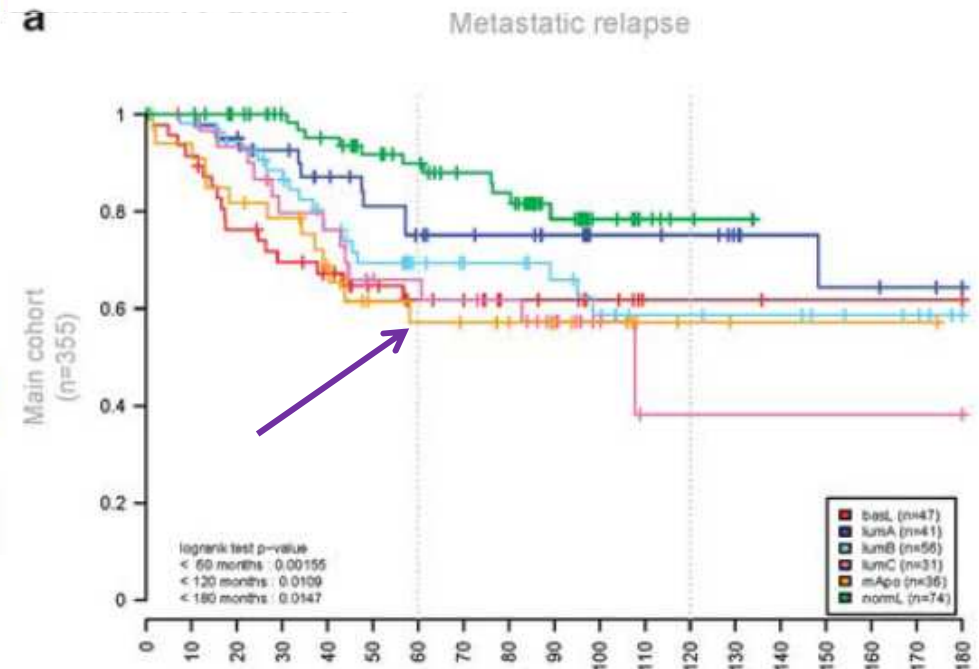
ONCOGENOMICS

A refined molecular taxonomy of breast cancer

M Guedj^{1,15}, L Marisa^{1,15}, A de Reynies^{1,15}, B Orsetti^{2,3}, R Schiappa¹, F Bibeau⁴, G MacGrogan⁵,
 F Lerebours⁶, P Finetti⁷, M Longy⁵, P Bertheau⁸, F Bertrand⁶, F Bonnet⁵, AL Martin⁹,
 JP Feugas^{10,11,12}, I Bièche⁶, J Lehmann-Che^{10,11,12}, R Lidereau⁶,
 H de Thé^{6,10,11,12,15} and C Theillet^{2,13,14,15}




a



Predictive markers

1. **Definition**: prediction generic or specific sensitivity to treatment; prediction resistance to treatment
2. **Neoadjuvant setting**: direct assessment of response to treatment
 - Monitoring tumour size during treatment
 - Surrogate marker for long term treatment : pCR

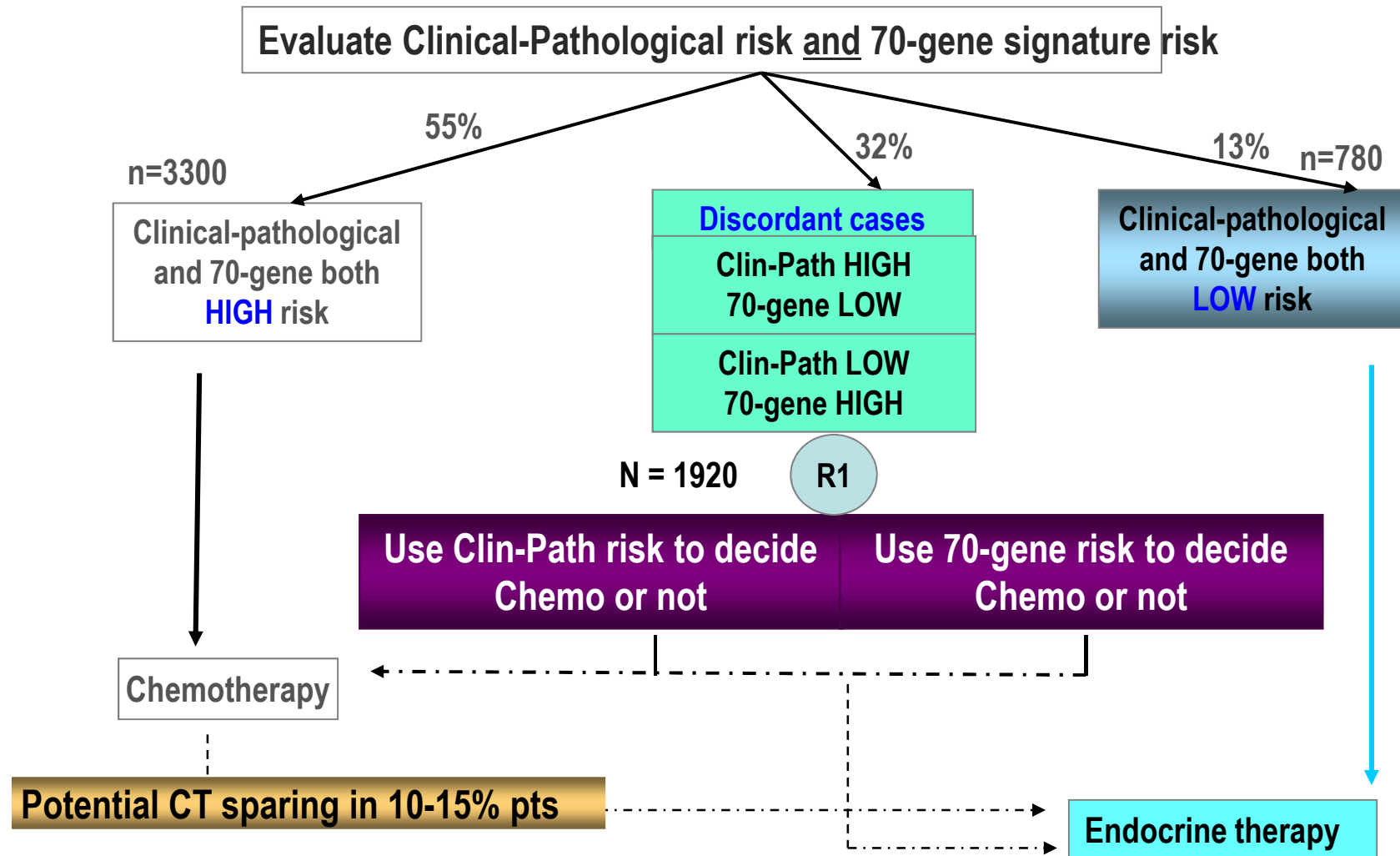
Predictive signatures

- **Some prognosis signatures**  **prediction of response to chemotherapy?**
 - ✓ **Recurrent score-RS (Oncotype DX™, Health care)**
 - ✓ **70 - gènes signature (MammaPrint™)**
 - ✓ **Genomic Grade index (GGI, MapQuant)**
 - ✓ **DLD30 (MD Anderson Cancer center)**
 - ✓ **.....**

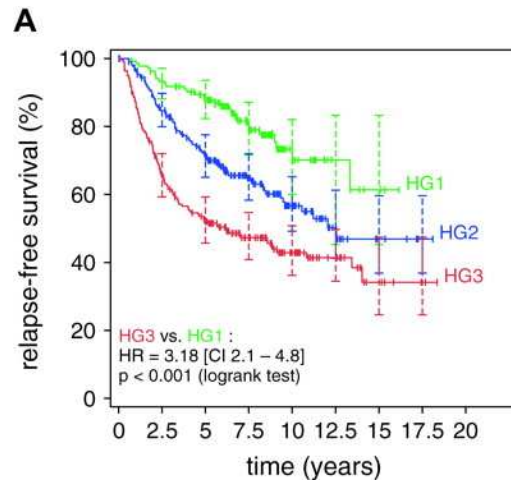
70- gènes signature (MammaPrint™)

Essai EORTC-BIG MINDACT

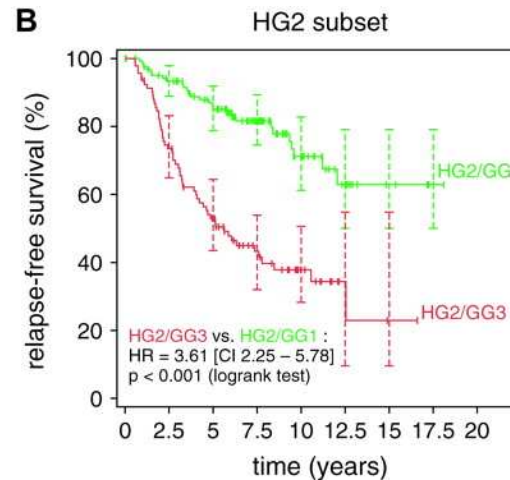
(6000 patients with NO breast cancer)



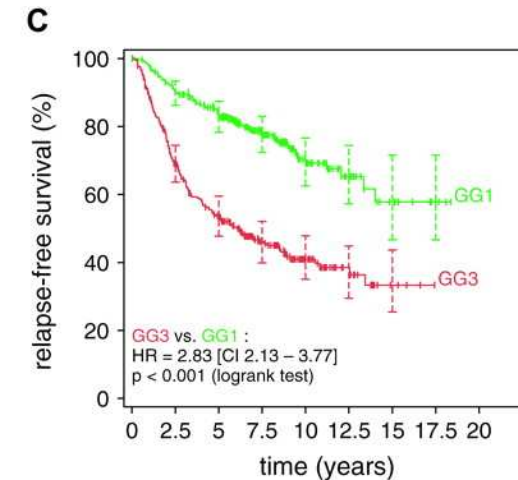
Genomic grade index (GGI).



number at risk	
HG1	134 123 107 59 23 8 4
HG2	216 174 136 80 40 16 6 1
HG3	220 137 102 67 35 20 6 2
total	570 434 345 206 98 44 16 3



number at risk	
HG2/GG1	124 108 91 55 28 13 5 1
HG2/GG3	92 66 45 25 12 3 1
total	216 174 136 80 40 16 6 1

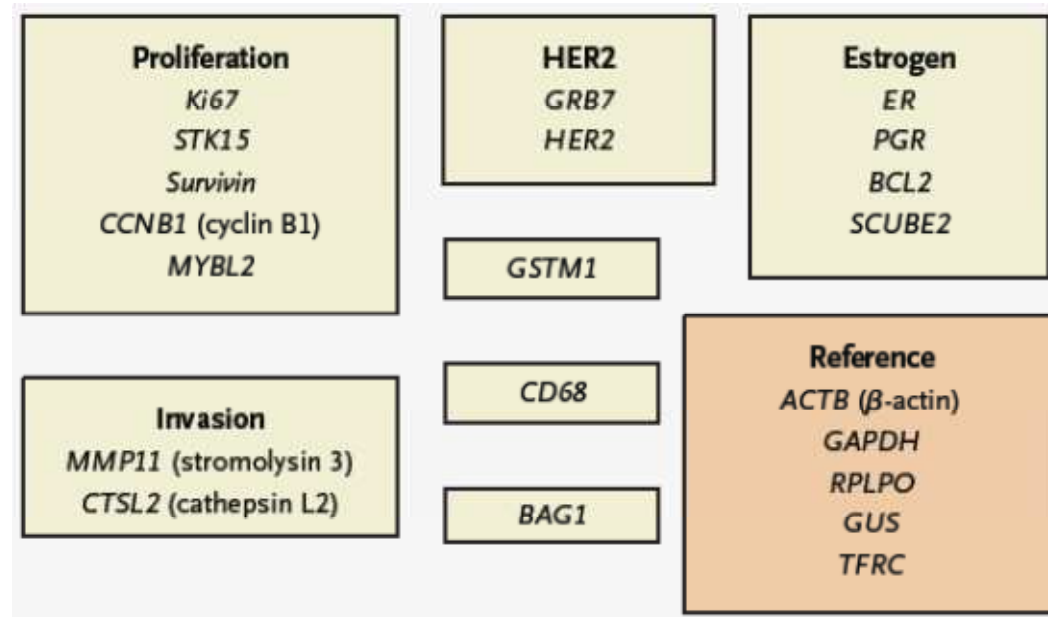


number at risk	
GG1	279 243 206 123 59 26 12 3
GG3	291 191 139 83 39 18 4
total	570 434 345 206 98 44 16 3

GGI ,

- score based on 97 genes expression (proliferation and differentiation)
- Differential expression in grade 1 and 3 breast tumours
- Reclassification of intermediate grade tumours (grade 2)

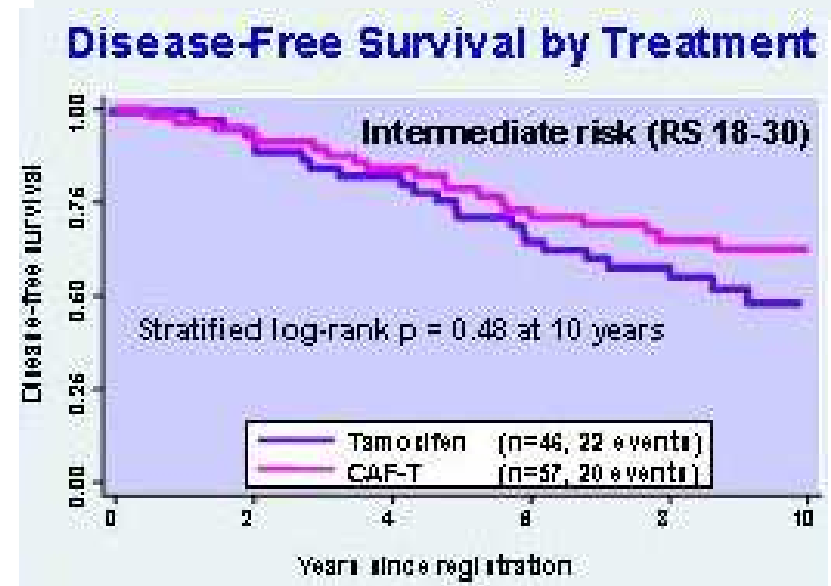
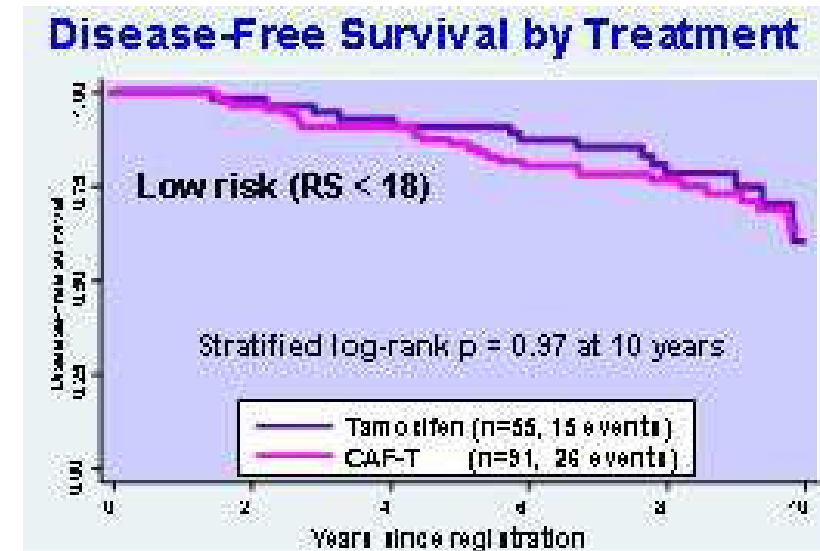
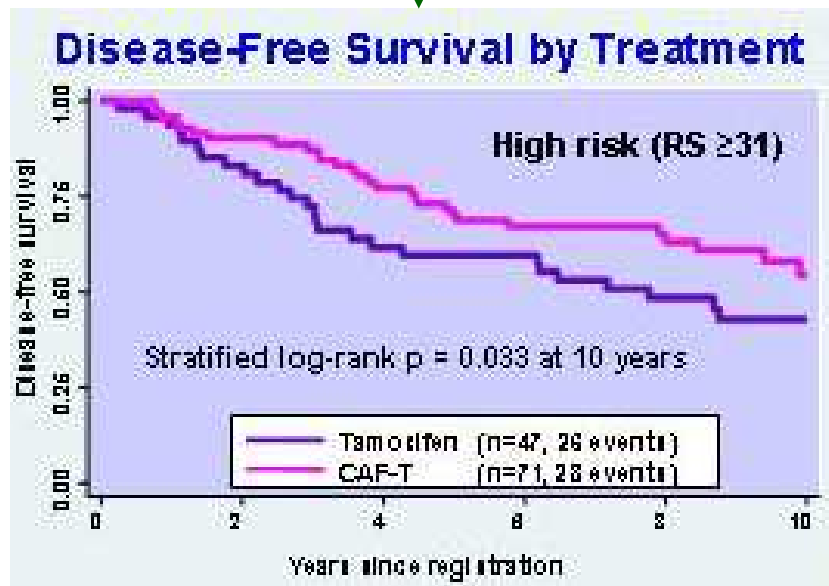
Panel of 21 (16+5) genes and the recurrence-score algorithm (Oncotype DX, Genomic Health)



- **GRB7 group score** = $0.9 \times \text{GRB7} + 0.1 \times \text{HER2}$
- **ER group score** = $(0.8 \times \text{ER} + 1.2 \times \text{PGR} + \text{BCL2} + \text{SCUBE2}) \div 4$
- **Proliferation group score** = $(\text{Survivin} + \text{Ki67} + \text{MYBL2} + \text{CCNB1} + \text{STK15}) \div 5$
- **Invasion group score** = $\text{CTSL2} \div 2$
- **RSu** = $+ 0.47 \times \text{GRB7 group score} - 0.34 \times \text{ER group score} + 1.04 \times \text{proliferation group score} + 0.10 \times \text{invasion group score} + 0.05 \times \text{CD68} - 0.08 \times \text{GSTM1} - 0.07 \times \text{BAG1}$

Prediction

Benefit CAF for the group of patients BK N+ with high RS



Prospective validation

MINDACT (Mammaprint)

- 6000 ptes
- N0 ER+, PR+, HER2-, Stages I & II
- Frozen samples
- DNA microarrays
- Randomisation : Patients with discordant risk (clin/ biol, 32%)
- MFI

TAILORx (Oncotype DX)

- 10500 patientes
- N0 ER+, PR+, HER2-, Stages I & II
- Fixed samples
- RT-qPCR (16 targets genes)
- Randomisation : Patients with RS de 19 à 25 (44%)
- DFI

TP53 mutations and breast cancer response to high dose chemotherapy

OPEN ACCESS Freely available online

2007 PLOS MEDICINE

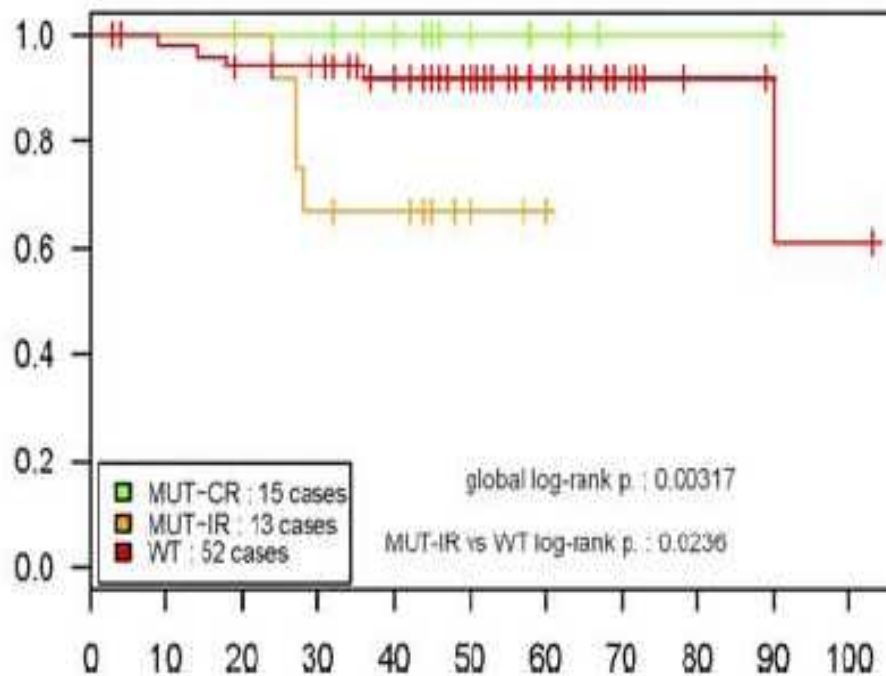
Exquisite Sensitivity of *TP53* Mutant and Basal Breast Cancers to a Dose-Dense Epirubicin–Cyclophosphamide Regimen

Philippe Bertheau^{1,2}, Elisabeth Turpin^{3,4}, David S. Rickman⁵, Marc Espie⁶, Aurélien de Reyniès⁵, Jean-Paul Feugeas³, Louis-François Plassa³, Hany Soliman³, Mariana Varna^{1,2}, Anne de Roquancourt¹, Jacqueline Lehmann-Che^{3,4}, Yves Beuzard³, Michel Marty⁶, Jean-Louis Misset⁶, Anne Janin^{1,2}, Hugues de Thé^{3,4*}

TP53	Mutated	Wild type
pCR	15	0
Non pCR	13	52


Fischer exact test: $<10^{-8}$

OS



Pathological complete response only in mutated TP53 tumours

Conclusions

- Ten years of high throughput analysis in breast cancers
 Molecular classification of breast carcinoma
- Today, in order to cover the main fields in breast cancer clinical research and daily practice, breast cancer centers should be associated with translational research platforms.
- Performances of these platforms can be optimized by their interaction with many centers at a national or international level.