



# **“Genes and signatures” associati a pCR: i dati derivanti dagli studi clinici**

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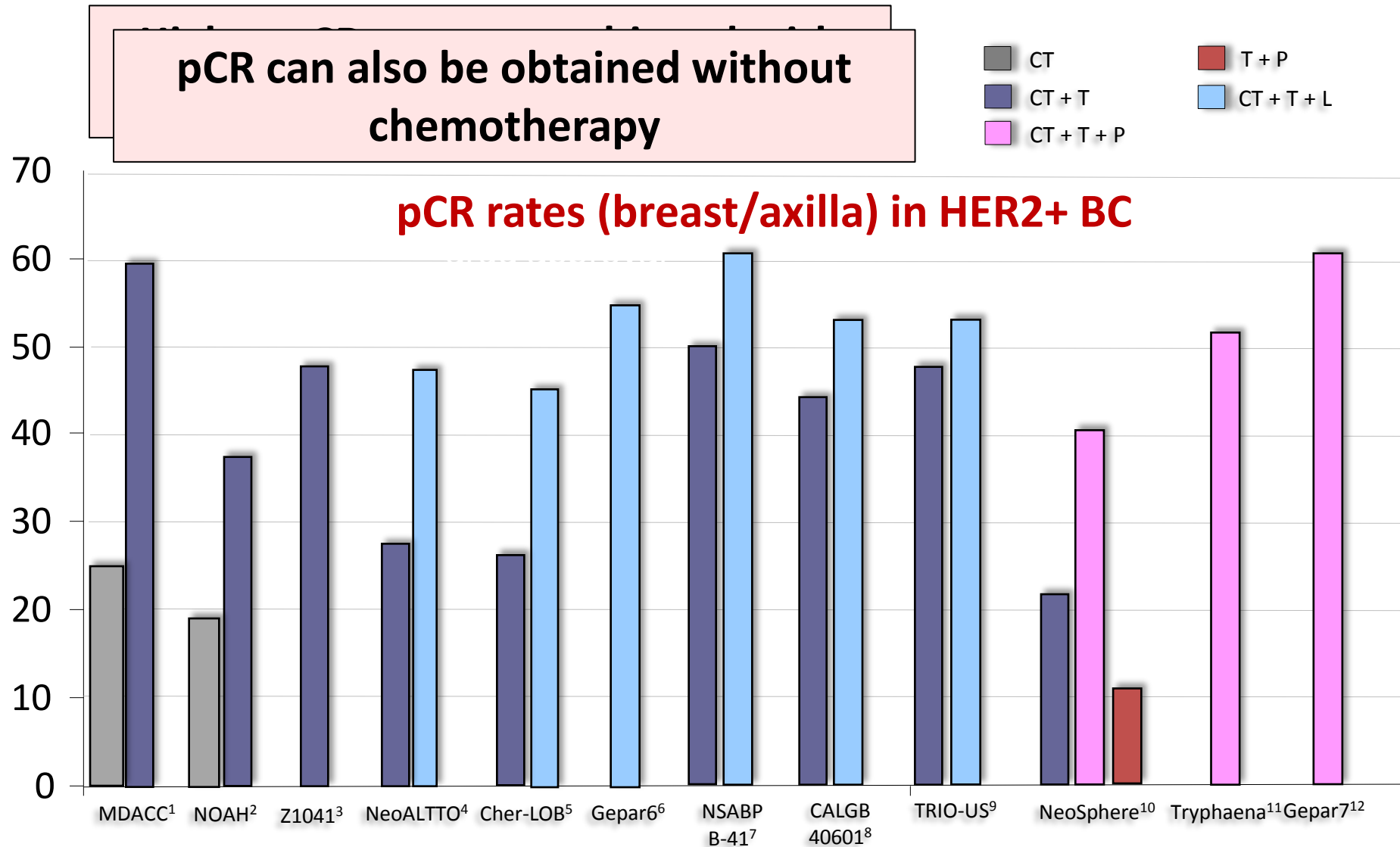
# Optimizing patients selection

- **HER2+ BC:** predicting response to HER2-targeted agents
  - Gene-expression and intrinsic subtypes
  - PIK3CA mutational status
- **HR+ BC:** chemo vs endocrine neoadjuvant treatment
  - Gene-expression profiling

can we predict sensitivity to additional agents?

  - PIK3CA mutational status
- **TNBC:** Tackling tumor heterogeneity

# Neoadjuvant therapy in HER2+ BC



1. Buzdar AU, J Clin Oncol 2005, CCR 2007; 2. Gianni L, Lancet 2010. 3. Buzdar AU, Lancet Oncol 2013. 4. Baselga J. Lancet 2012; 5. Guarneri V. J Clin Oncol 2012; 6. von Minckwitz. Lancet Oncol 2014; 7. Robidoux A. Lancet Oncol 2013; 8. Carey L. ASCO 2013; 9. Hurvitz S. SABCS 2013. 10. Gianni L. Lancet Oncol 2012; 11. Schneeweiss A. Ann Oncol 2013; 12. Untch M. SABCS 2014;

# pCR rates are lower in HR+ HER2+ BC

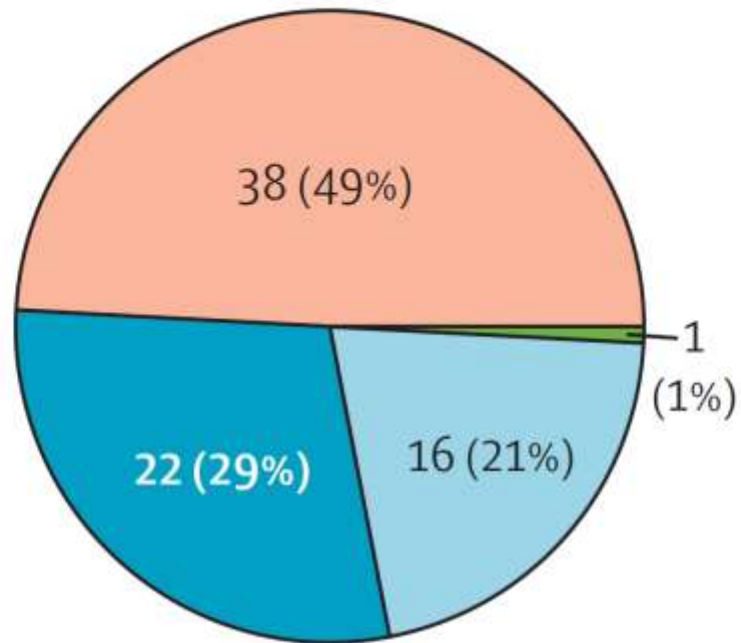
Trial	HER2 targeted agents	pCR in HR+	pCR in HR-
NeoSphere <sup>1</sup>	<b>Pertuzumab</b> + Trastuzumab	26%	63%
NeoALTTO <sup>2</sup>	<b>Lapatinib</b> + Trastuzumab	42%	61%
CALGB 40601 <sup>3</sup>	<b>Lapatinib</b> + Trastuzumab	42%	77%
TRYPHAENA <sup>4</sup>	<b>Pertuzumab</b> + Trastuzumab	46-50%	65-84%
NeoSphere <sup>1</sup> (chemofree arm)	<b>Pertuzumab</b> + Trastuzumab	5.9%*	27.3%*
TBCRC-006 <sup>5</sup>	<b>Lapatinib</b> + Trastuzumab (+ endocrine if HR+)	21%*	36%*
PAMELA <sup>6</sup>	<b>Lapatinib</b> + Trastuzumab (+ endocrine if HR+)	18.2%*	43.2%*
CherLOB <sup>7</sup>	<b>Lapatinib</b> + Trastuzumab	27%	44%

\*pCR in breast only

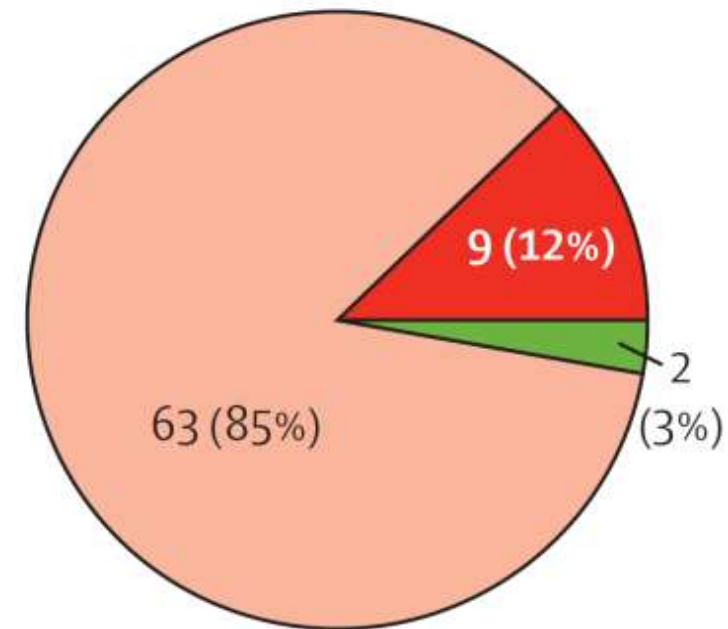
1. Gianni L, et al. Lancet Oncol 2012. 2. Baselga J, et al. Lancet 2012 and de Azambuja E, et al. Lancet Oncol 2014. 3. Carey LA, et al. J Clin Oncol 2016. 4. Schneeweiss A, et al. Ann Oncol 2013. 5. Rimawi MF, et al. J Clin Oncol 2013. 6. Llombart-Cussac A, et al. Lancet Oncol 2017. 7. Dieci et al, The Oncologist 2015

# Intrinsic subtypes and heterogeneity in HER2+ BC

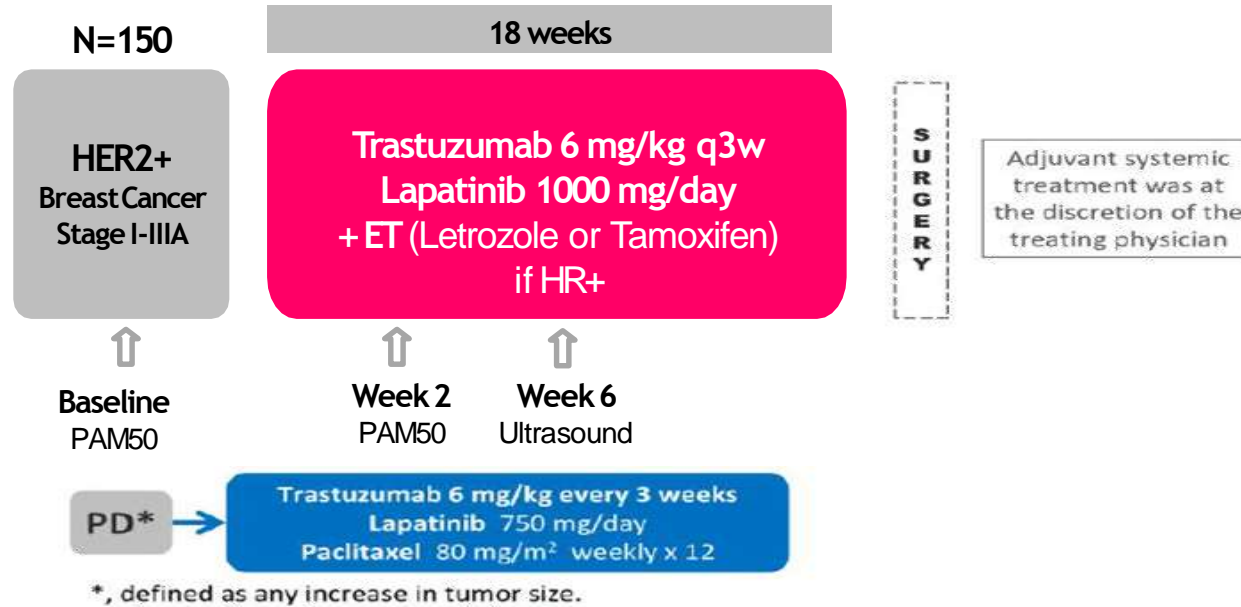
**HR+/HER2+**



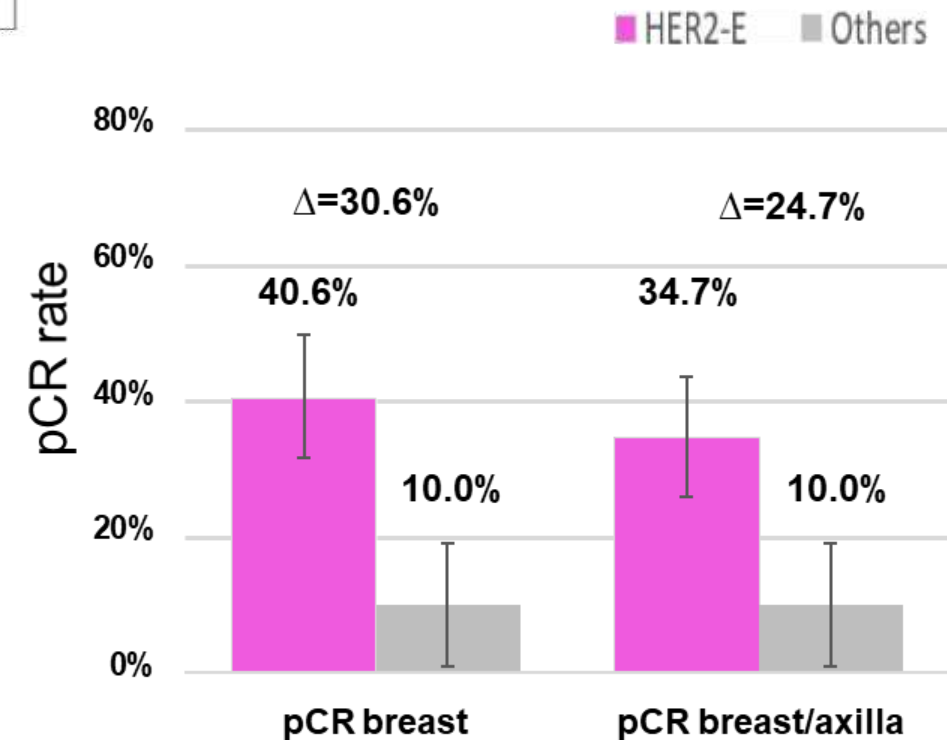
**HR-/HER2+**



# PAMELA: Intrinsic Subtype as a predictor of response to a neoadjuvant anti-HER2-based chemo-free regimen

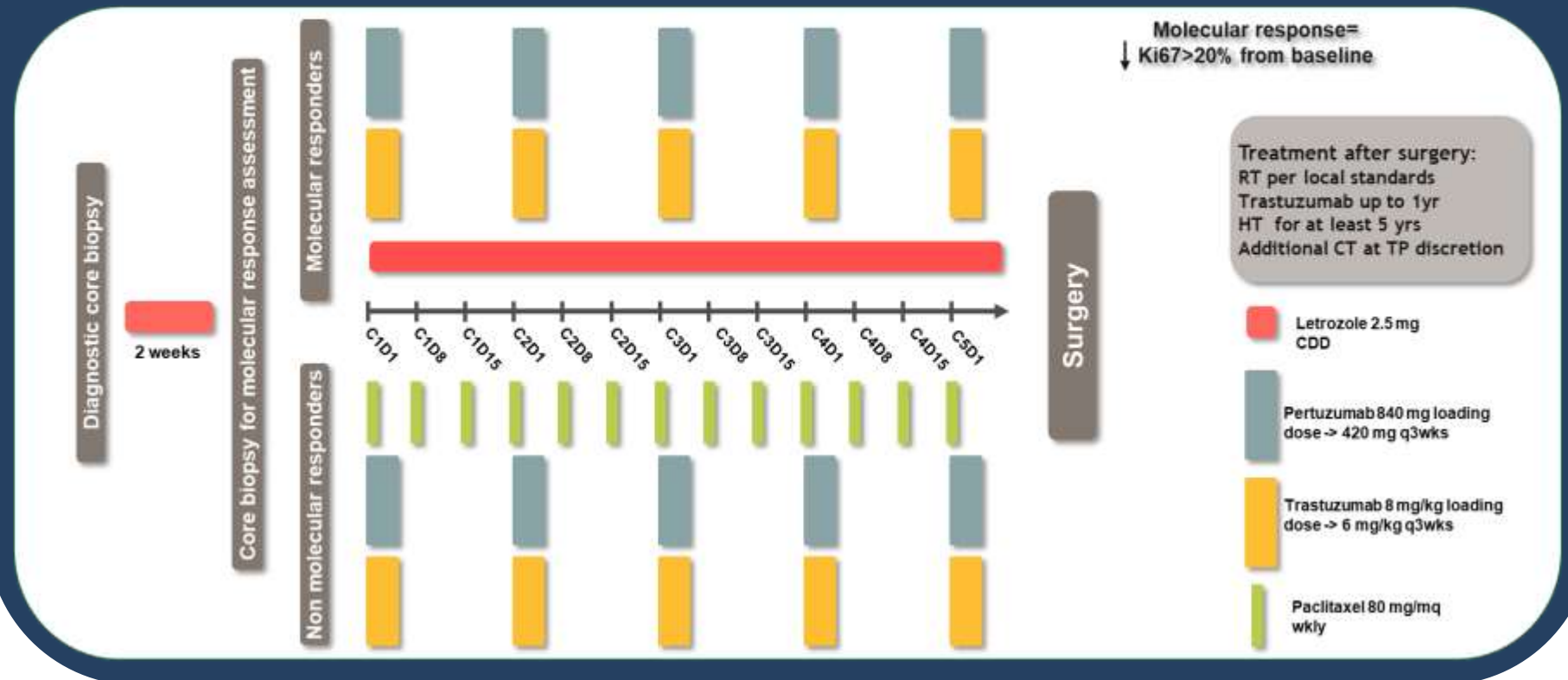


HER2-enriched tumors presented significantly higher pCR rates



# PerElisa

## Preoperative Study With Trastuzumab, Pertuzumab and Letrozole in Patients With Breast Cancer Sensitive to Hormonal Therapy



### Main inclusion criteria:

- Stage II-IIIa breast cancer
- HR positivity (ER $\geq$ 10%)
- HER2 positivity (IHC 3+ or ISH +)
- Postmenopausal status

### Primary endpoint:

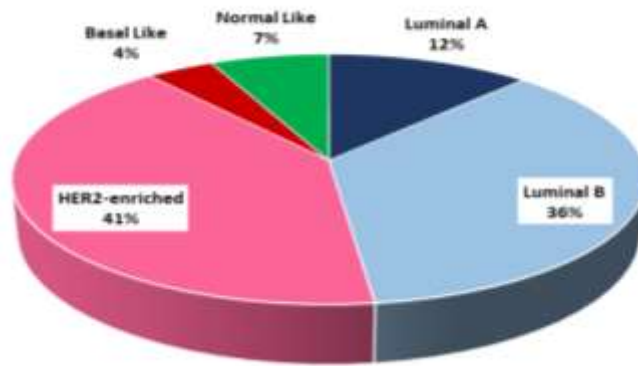
- pathologic complete response (pCR) rate in breast and axilla (8pCR/43 responder pts)

### Investigator-driven, non profit study.

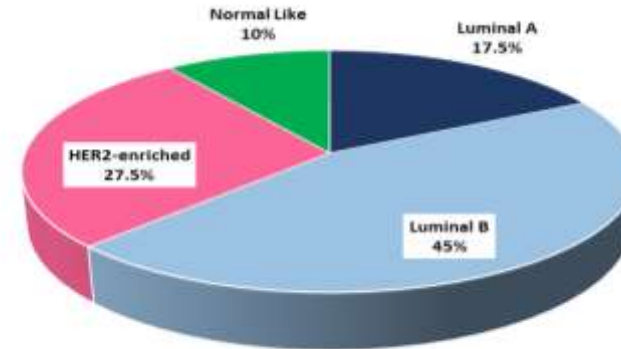
EUDRACT 2013-0022662-40



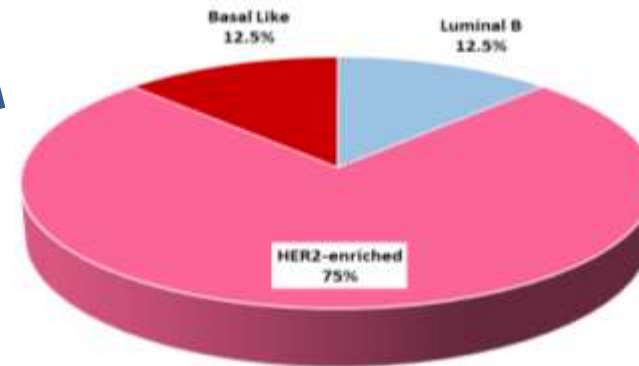
# PAM50 subtype according to molecular response



**Overall**



**Molecular responder**

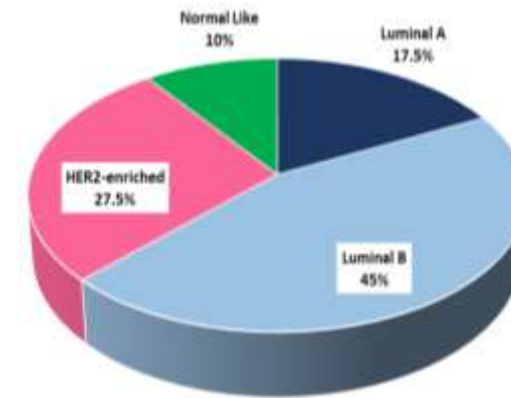
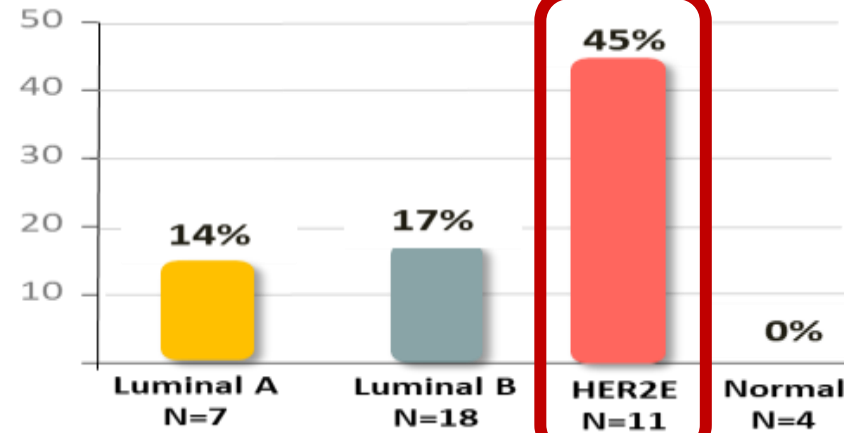


**Molecular non responder**

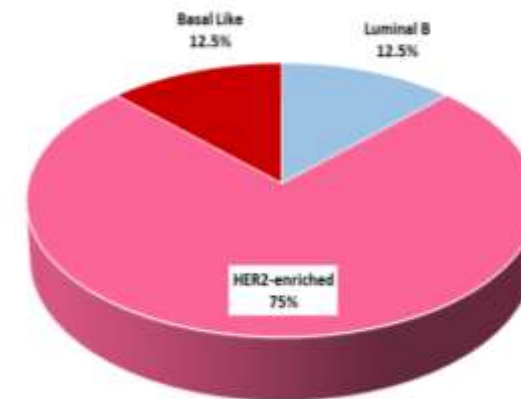
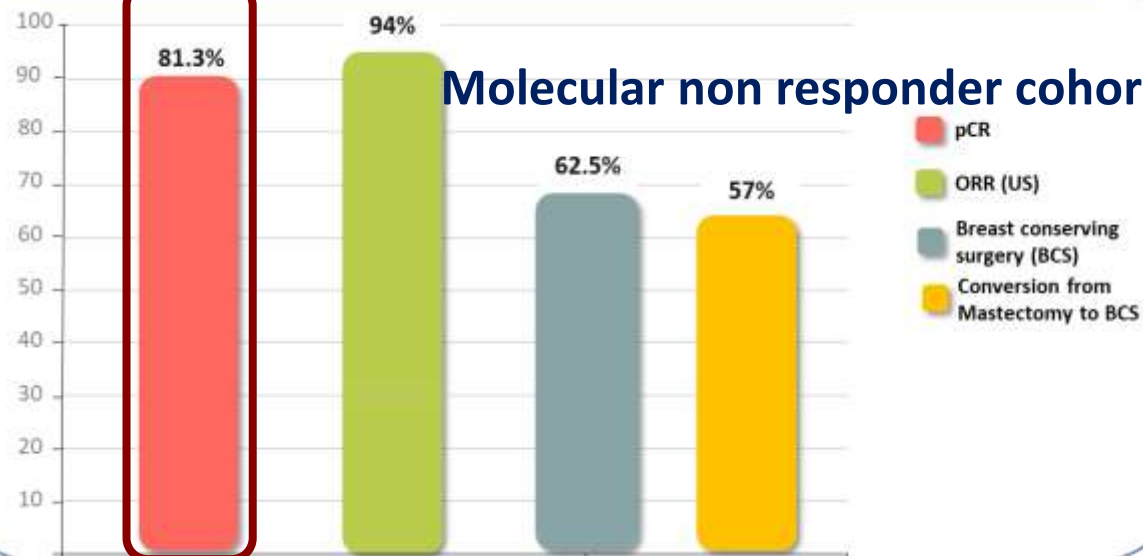


# Efficacy outcomes

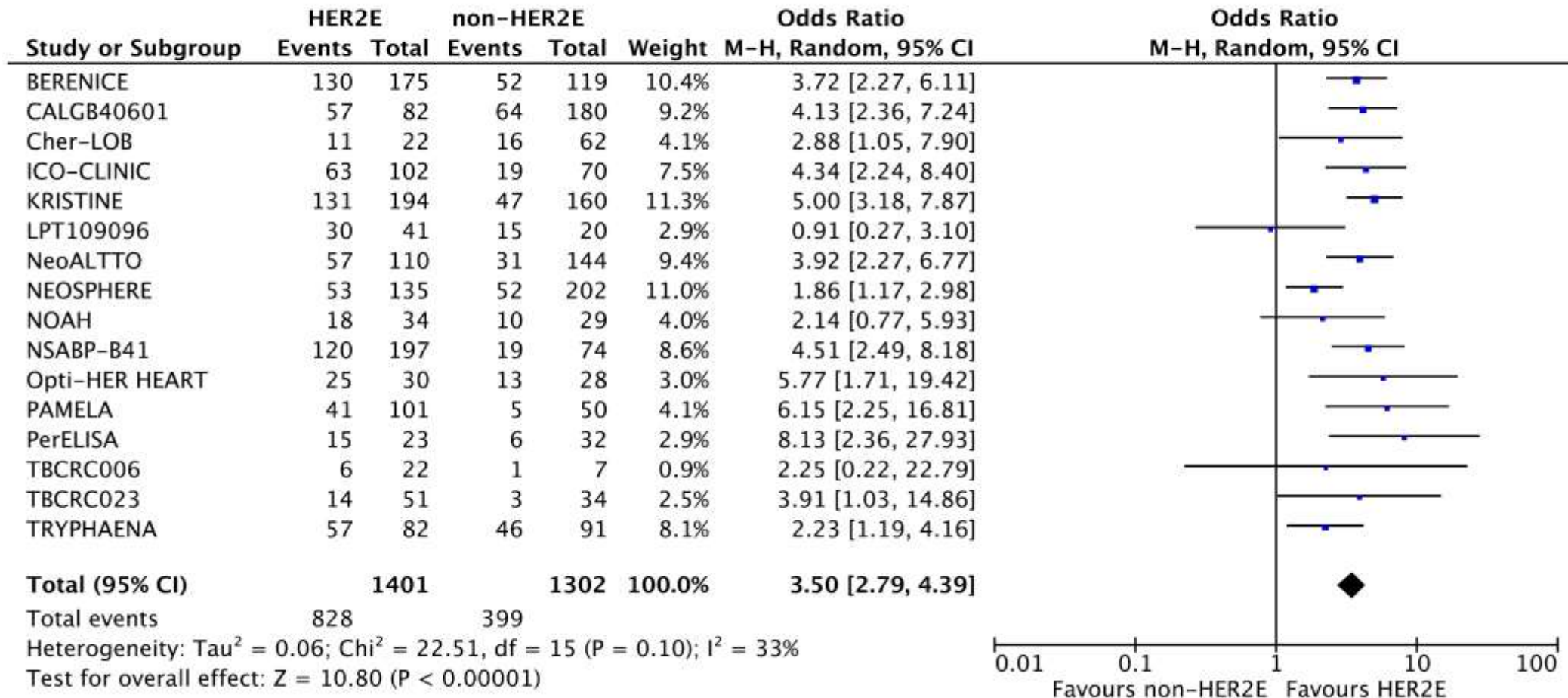
pCR according to PAM50 in molecular responders



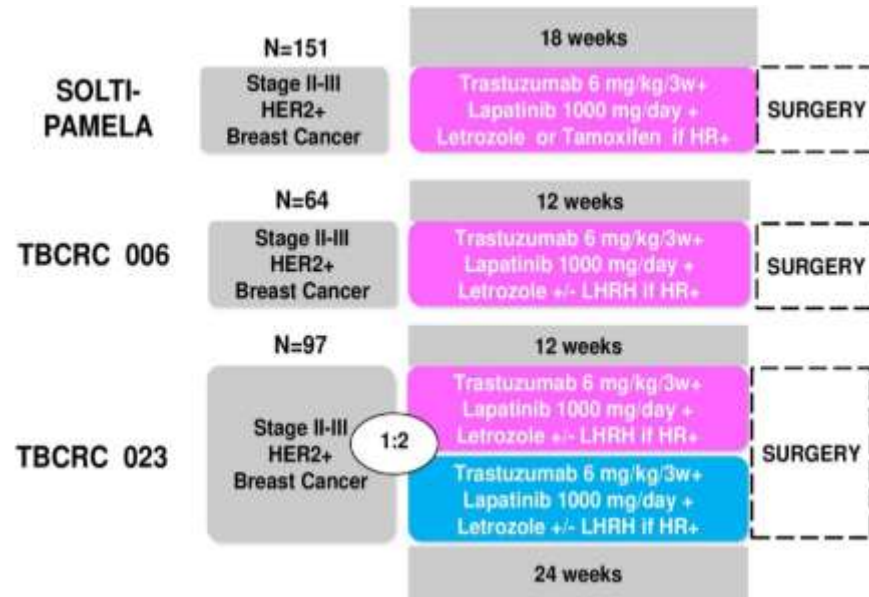
Molecular non responder cohort



# HER2-enriched subtype and pCR following anti-HER2-based neoadjuvant treatment (16 studies – 2,703 patients)

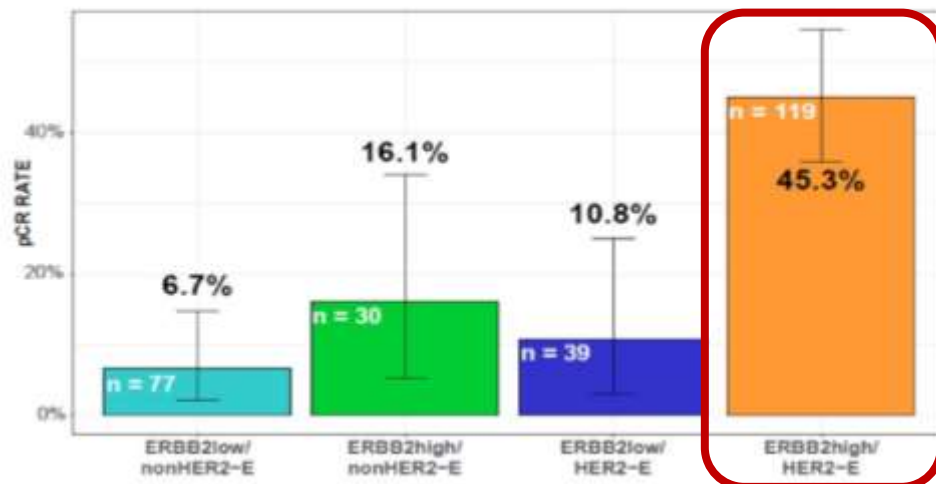


# Refining biomarkers to predict pCR in early HER2+ BC treated with dual HER2-blockade (w/o chemo)



A cutoff for ERBB2 expression (high vs low) was determined on samples from the PAMELA trial

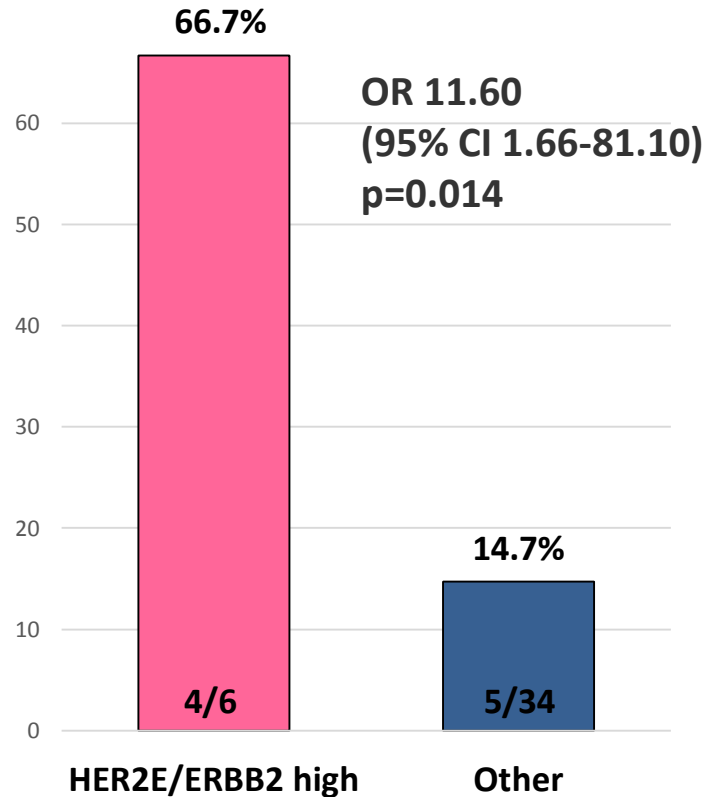
and was then applied on the combined three study cohort



Combining HER2-E and ERBB2 mRNA levels better identifies anti-HER2 sensitivity than each variable alone

# Combined biomarker to predict pCR in early HER2+ BC treated with dual HER2-blockade (w/o chemo)

pCR rates according to combined biomarker in responder cohort



The combined biomarker (HER2E/ERBB2 high) confirmed its association with pCR in the molecular responder cohort of the PerElisa trial

# Refining biomarkers to predict pCR in early HER2+ BC: 41-gene classifier TRAR

Association of TRAR with pCR in the NeoALTTO trial (N=226)

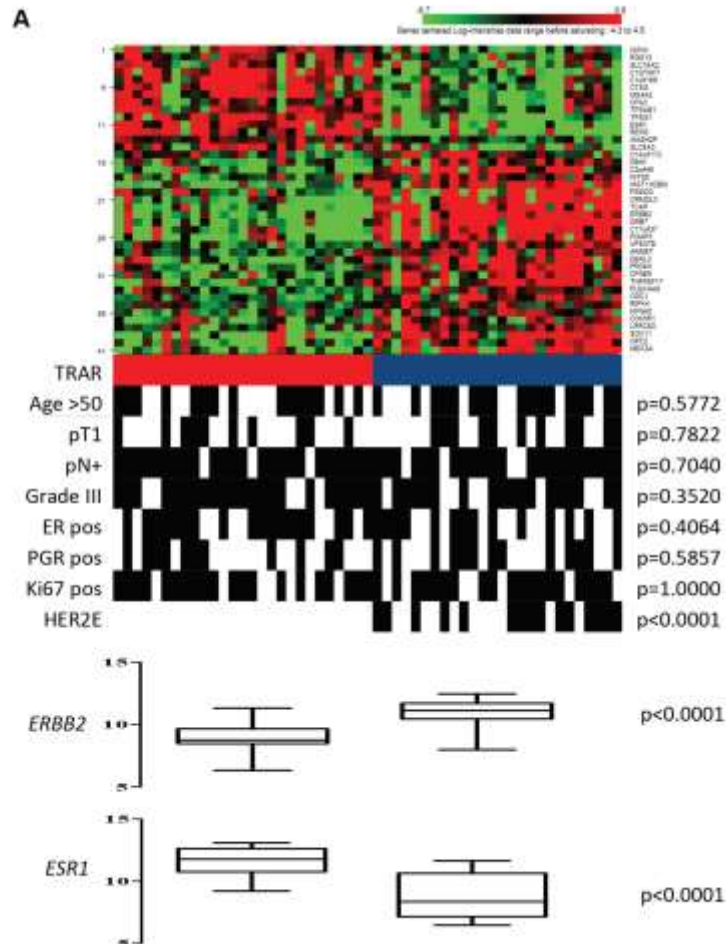
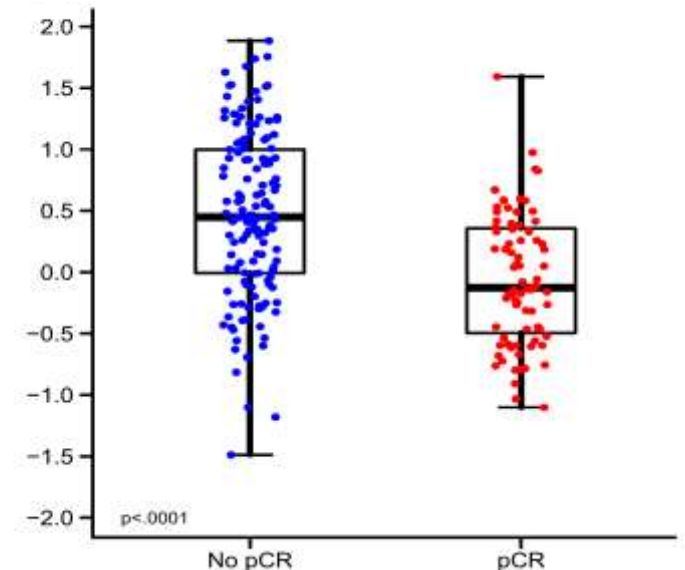


Table 1

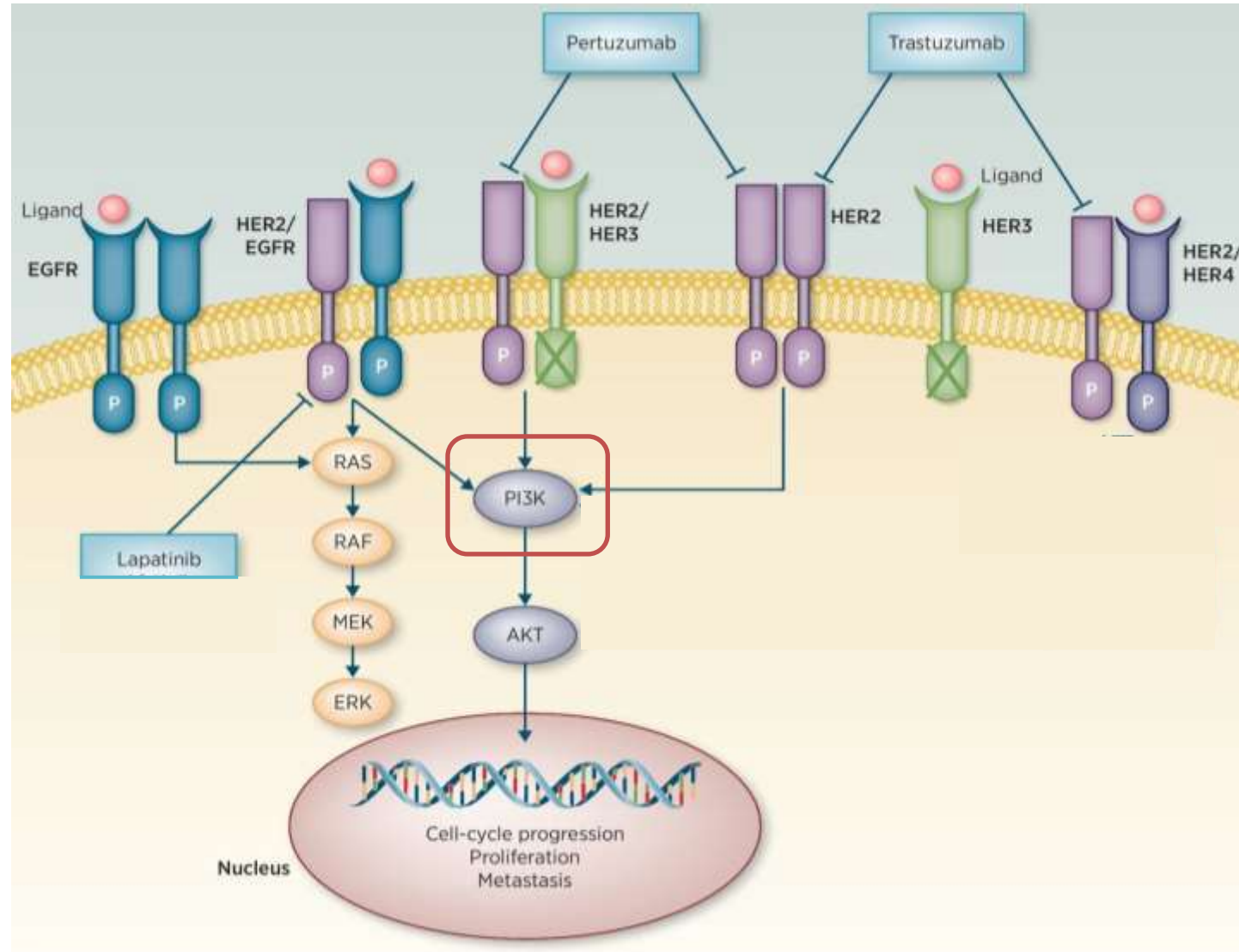
Association of TRAR and clinicopathological variables with pathological complete response (pCR): Univariate and multivariate logistic regression model.

Variables	Univariate OR (95% CI)	Multivariate OR (95% CI)
<b>TRAR score</b>	<b>0.25 (0.15–0.42)</b>	<b>0.26 (0.14–0.47)</b>
<b>Treatment</b>		
L versus T	0.95 (0.46–1.97)	0.95 (0.43–2.09)
L+T versus T	<b>2.77 (1.39–5.52)</b>	<b>3.08 (1.45–6.58)</b>
<b>ER status</b>		
Neg versus Pos	<b>2.62 (1.46–4.69)</b>	1.25 (0.61–2.57)
<b>Age</b>		
≤5 versus > 5	0.91 (0.52–1.59)	
<b>Nodal status</b>		
N0/1 versus ≥ N2	0.62 (0.31–1.26)	



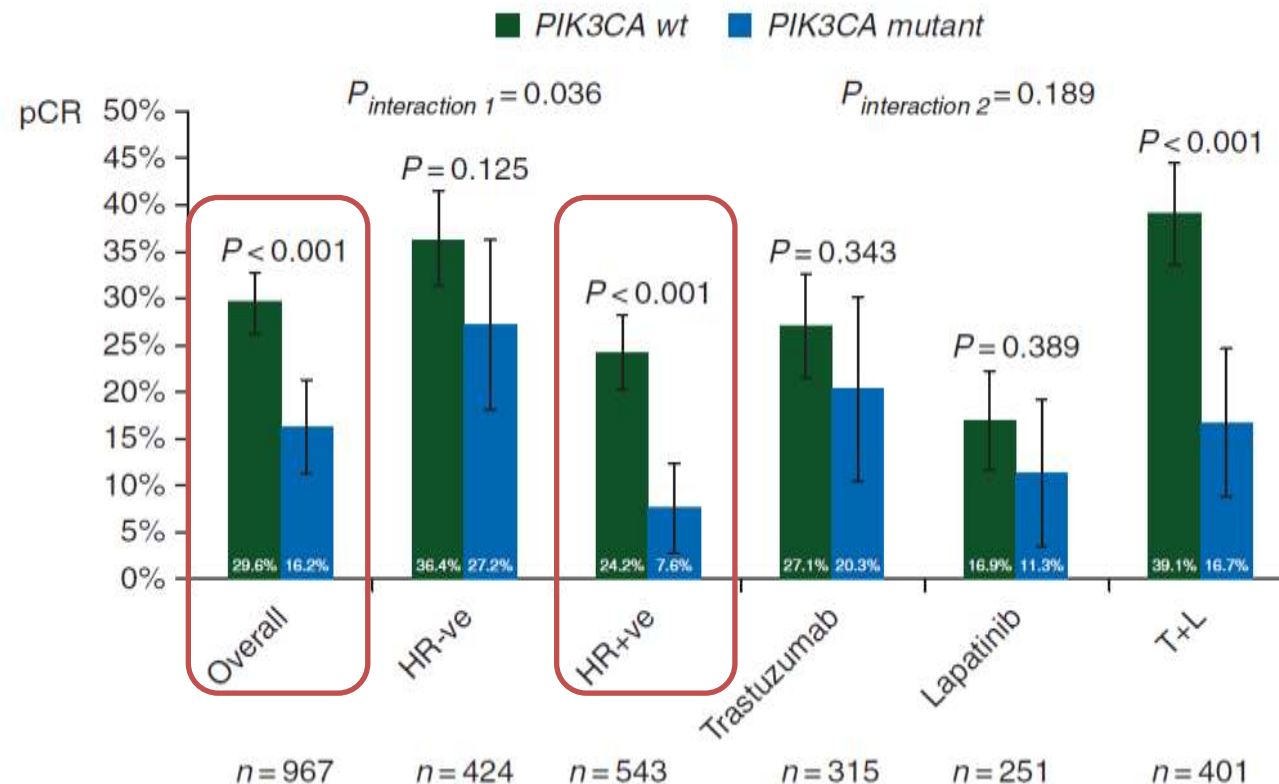


# HER2 Signaling and PI3K pathway



# **PIK3CA mutations are associated with reduced pathological complete response rates in primary HER2-positive breast cancer: pooled analysis of 967 patients from five prospective trials investigating lapatinib and trastuzumab<sup>†</sup>**

S. Loibl<sup>1\*</sup>, I. Majewski<sup>2</sup>, V. Guameri<sup>3</sup>, V. Nekljudova<sup>1</sup>, E. Holmes<sup>4</sup>, E. Bria<sup>5</sup>, C. Denkert<sup>6</sup>, C. Schem<sup>7</sup>, C. Sotiriou<sup>8</sup>, S. Lo<sup>9</sup>, M. Untch<sup>10</sup>, P. Conte<sup>3</sup>, R. Bernards<sup>2</sup>, M. Piccart<sup>8</sup>, G. von Minckwitz<sup>1</sup> & J. Baselga<sup>11</sup>



N=967 (GeparQuattro, GeparQuinto, GeparSixto, NeoALTTO, CHERLOB)  
Chemotherapy + antiHER2 (single vs. dual)

**pCR rate was lower for PIK3CA mut compared with wt (16.2% vs 29.6%;  $P < 0.001$ )**

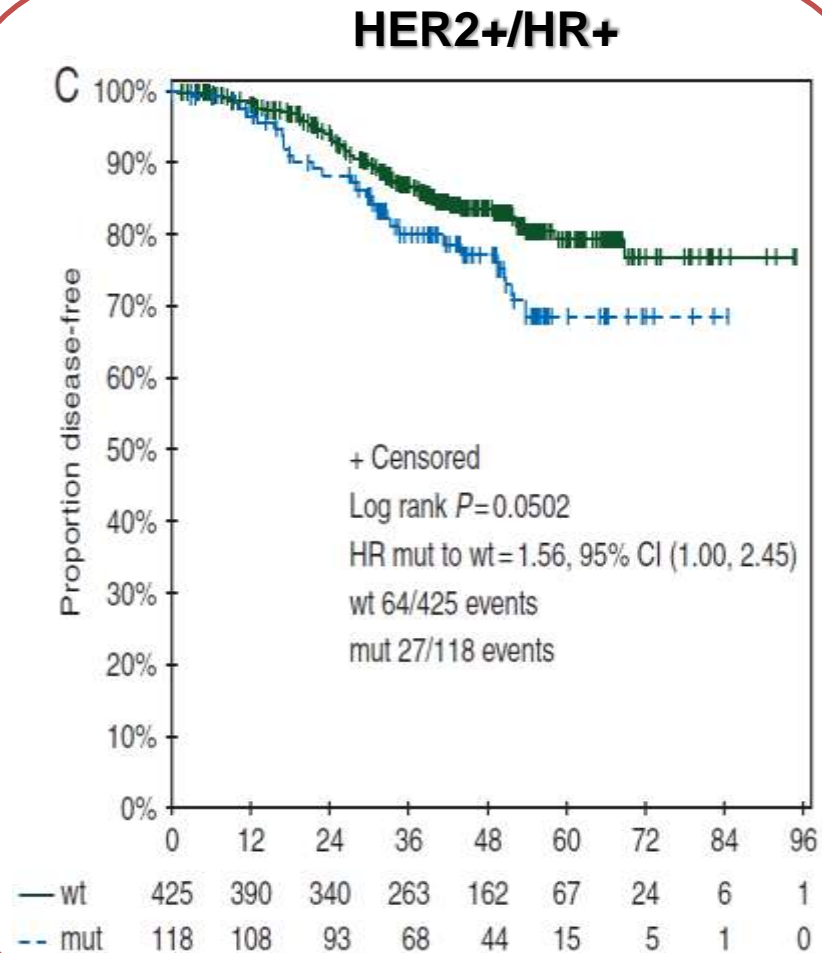
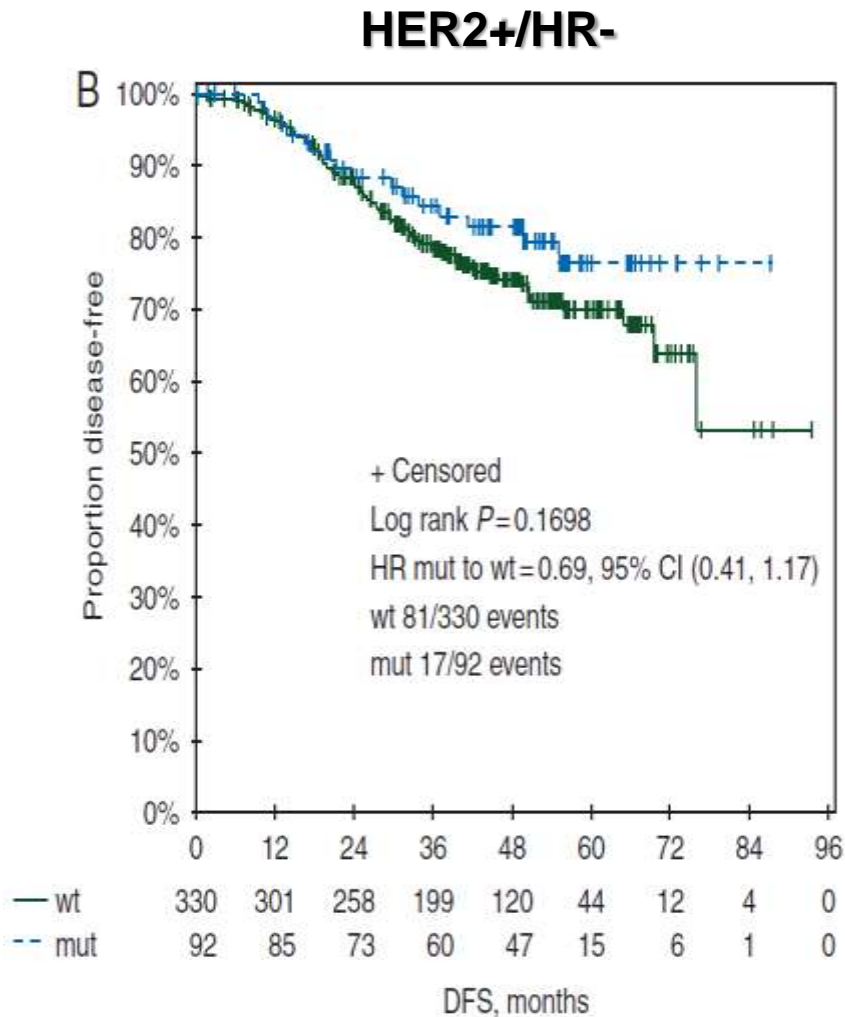
**In HR+HER2+ BC, PIK3CA mut had a pCR rate of only 7.6% (vs 24.2% of wt;  $p < 0.001$ )**



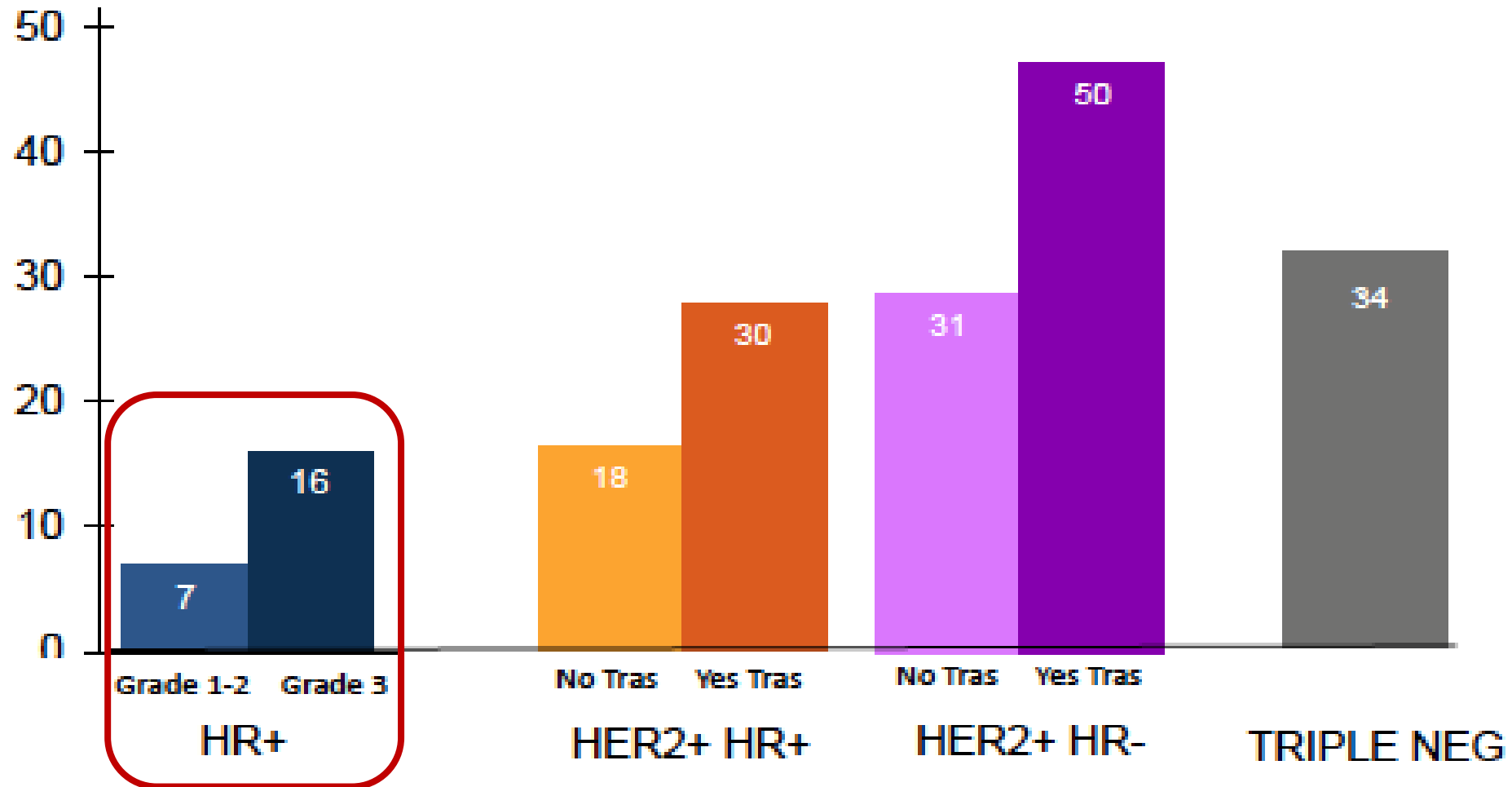
# PIK3CA mut tumors have worse survival in HER2+/HR+ BC

N=967 (GeparQuattro, GeparQuinto, GeparSixto, NeoALTTO, CHERLOB)

Chemotherapy + antiHER2 (single vs. dual)



# pCR rates by tumor subtypes



# Strategies in the neoadjuvant therapy of HR+ BC

- Tumor biology, rather than stage, is the driver of treatment selection
- Many patients with HR+/HER2- disease can be offered adjuvant hormonal therapy alone, even in case of N+ disease
- Aromatase inhibitors have opened the possibility of using HT as neoadj treatment

	NET	N	Duration	Clinical Response
Thomas (2007)	Letrozole	103	3 months	89% vs 85%
Semiglazov (2007)	Anastrozole or Exemestane	239	3 months	65% vs 64%
Generali (2011)	Letrozole	114	6 months	73% vs 88%
Alba (2011)	Exemestane +/- goserelin	95	6 months	48% vs 66%
Palmieri (2014)	Letrozole	44	18-23 weeks	59% vs 55%

Patient selection remains a problem

# Goals of neoadjuvant therapy in HR+ BC

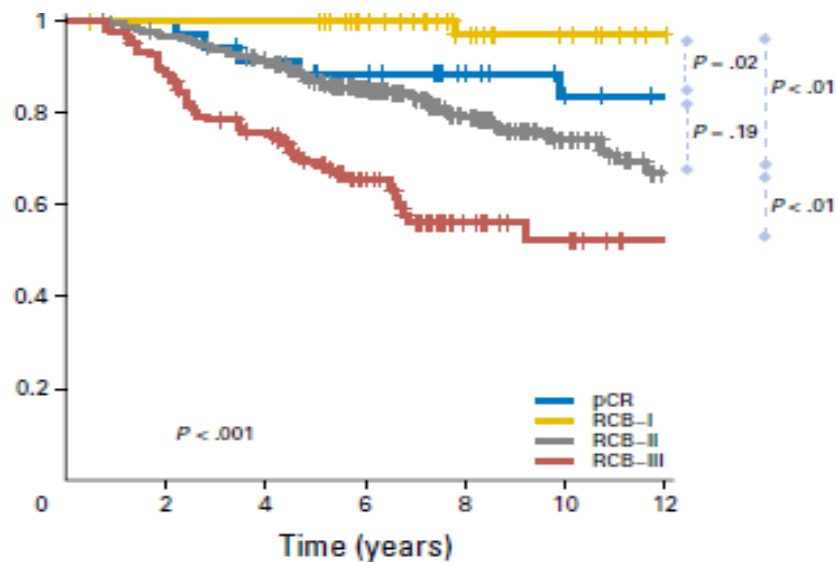
- Improve surgical options and reduce the extent of surgery (ORR and BCS)
- Refine prognosis based on response to neoadjuvant treatment



Which response predicts for long term prognosis?

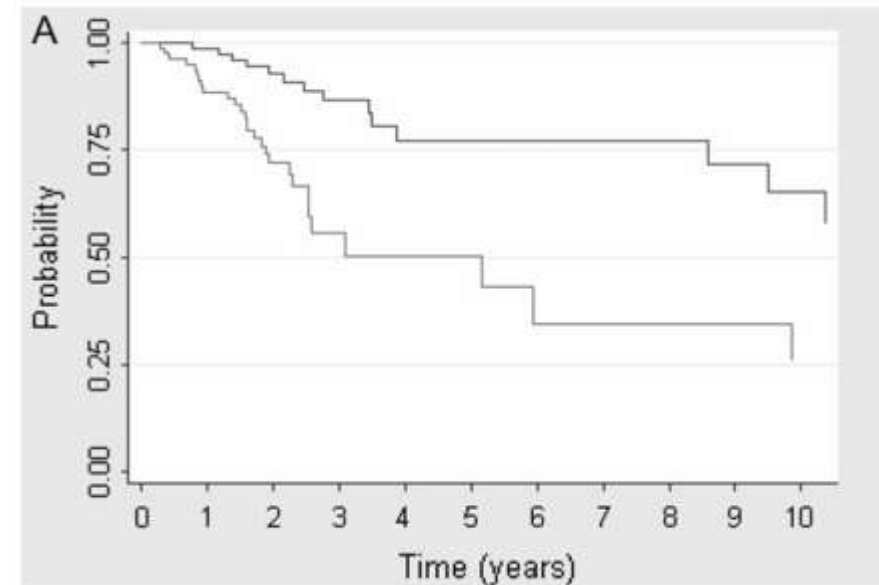
## Residual Cancer Burden (RCB)<sup>1</sup>

standardized method to assess pathological response after NACT



## Biological Response<sup>2</sup>

DFS according to post-treatment Ki67  $\geq 15\%$  vs  $< 15\%$

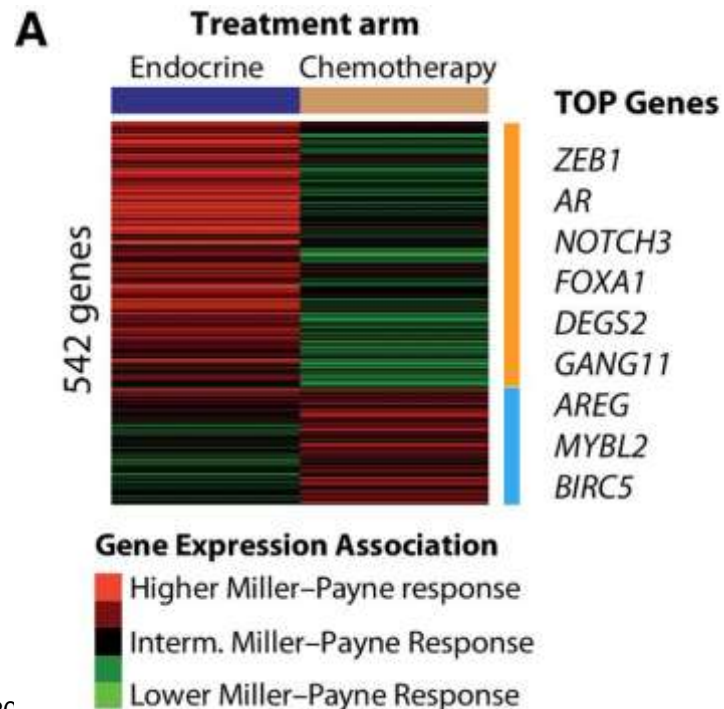


<sup>1</sup>Symmans et al, JCO 2017; <sup>2</sup> Guarneri V et al, Ann Oncol 2009

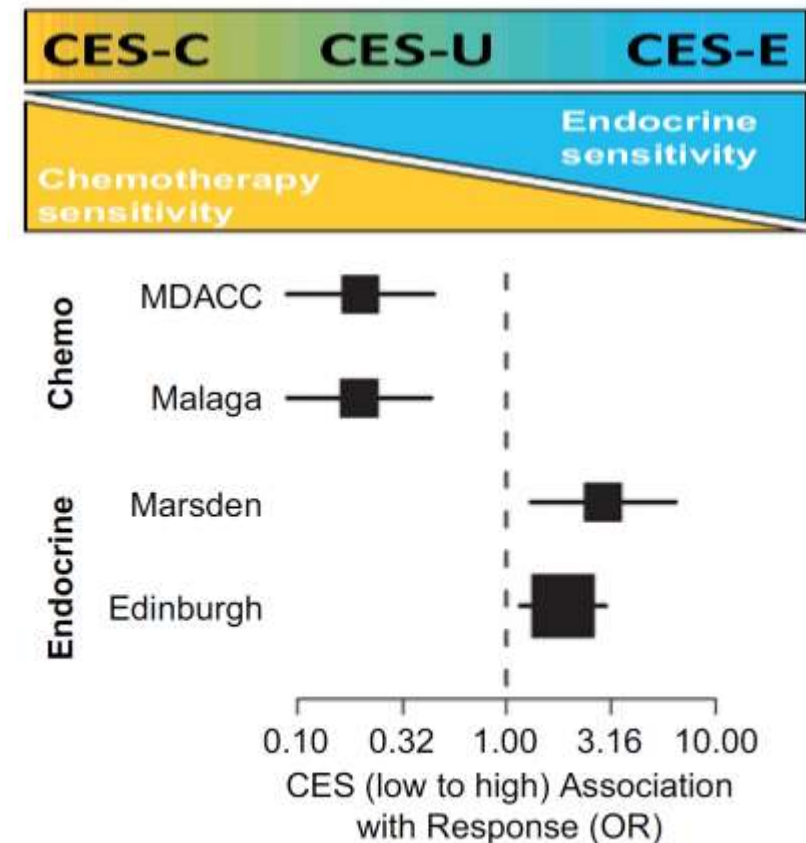
# Endocrine sensitivity vs Chemosenstivity

**In BC endocrine sensitivity and sensitivity to chemotherapy are biologically opposite phenomena**

Genes whose expression is associated with endocrine sensitivity are usually associated, at the same time, with chemotherapy resistance, and vice versa.

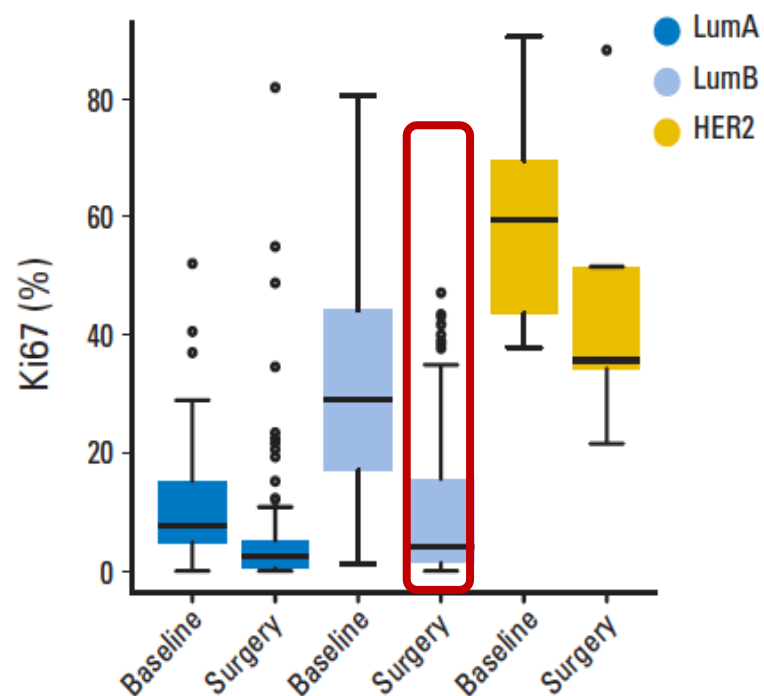


**CES = CC to Luminal A –CC to Basal-like**

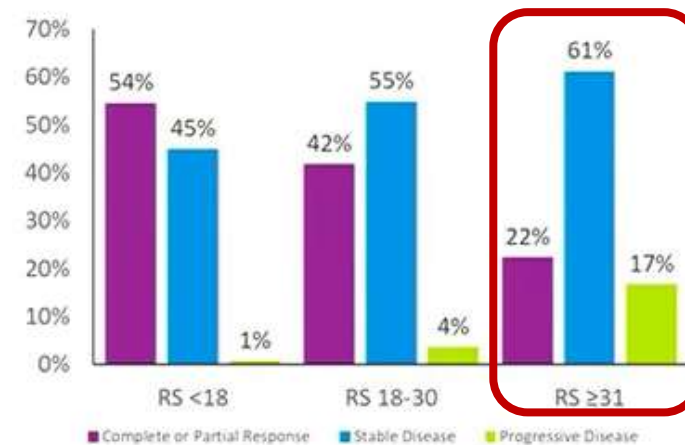


# Biology predicts response to neoadjuvant HT

**Ki67 suppression by PAM50 subtype in patients receiving neoadjuvant AIs**



**Clinical response by OncotypeDX RS in patients receiving neoadjuvant AIs**



Clinical response, n	RS <18	RS 18-30	RS ≥31	Total
CR + PR	85	35	12	132
SD	70	46	33	149
PD	1	3	9	13
Total	156	84	54	294

But none of these methods are validated for use in clinical practice as tests to decide if a patient should receive neoadjuvant CT or HT

# Biology predicts response to neoadjuvant HT

**989 patients** identified from the National Cancer Database:

- available RS
- underwent neoadjuvant CT

**TABLE 1** Study cohort characteristics according to pCR subgroup

Characteristic	No pCR <i>n</i> = 947 (95.8%) %	PCR <i>n</i> = 42 (4.3%) %	<i>p</i> value
<i>Age (years)</i>			
Mean (SD)	54.6 (11.0)	51.4 (12.3)	
<i>Ethnicity</i>			
Non-hispanic white	97.0	3.0	< 0.001
Other	91.6	8.4	
<i>Clinical T stage</i>			
T1	98.6	1.4	< 0.001
T2/T3	93.6	6.5	
<i>Node status</i>			
Negative	95.2	4.8	0.152
Positive	97.4	2.6	
<i>Tumor grade</i>			
1	99.2	0.8	< 0.001
2	97.3	2.7	
3	92.3	7.7	
<i>Oncotype score</i>			
Low	97.8	2.2	< 0.001
Intermediate	98.4	1.6	
High	90.4	9.6	

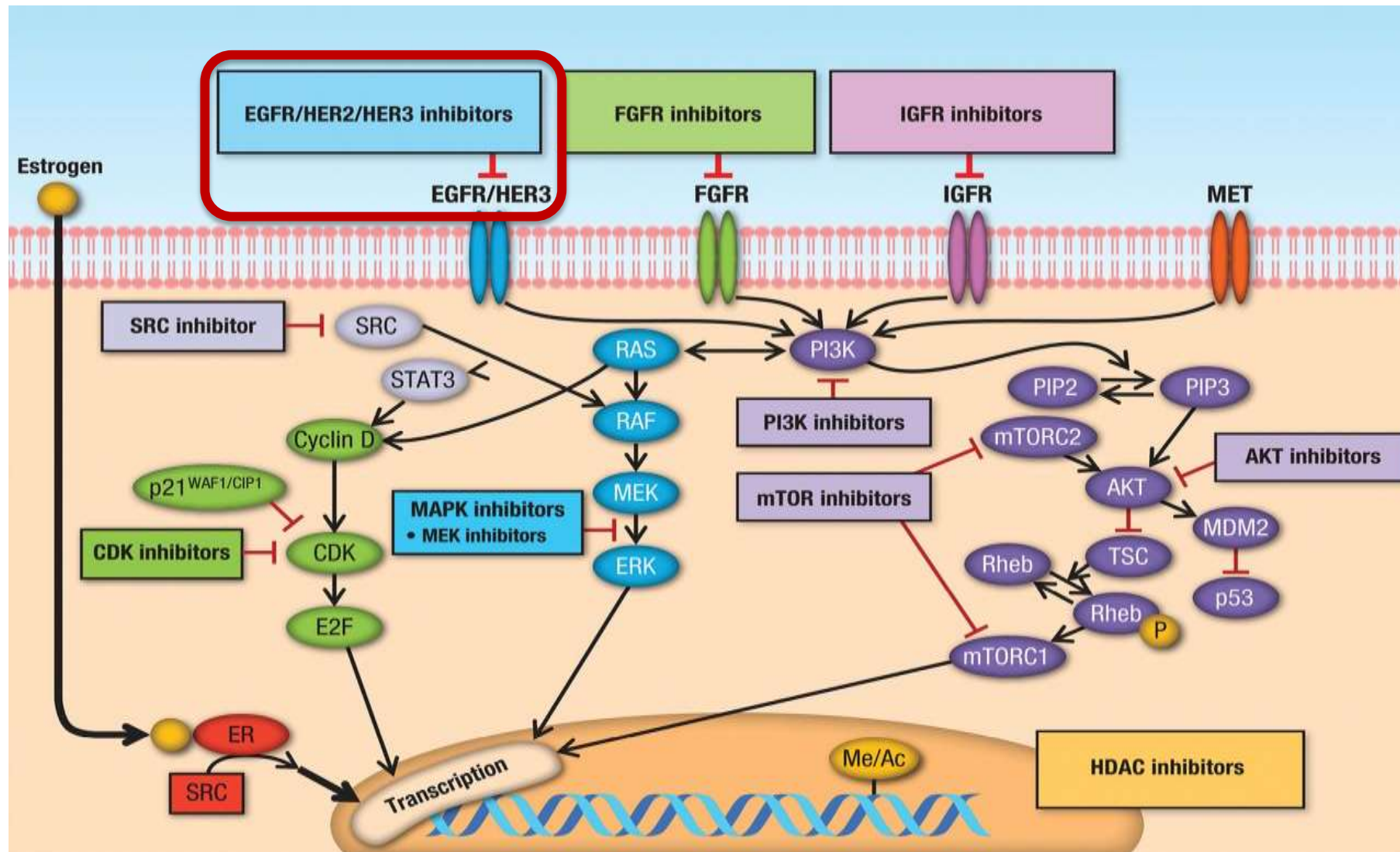
**High RS** was positively associated with **pCR** (compared to intermediate RS): **OR 6.73; 95% CI 2.92–15.54**

**Multivariable** logistic regression analysis confirmed association between **pCR** and **high RS: OR 4.87; 95% CI 2.01–11.82**

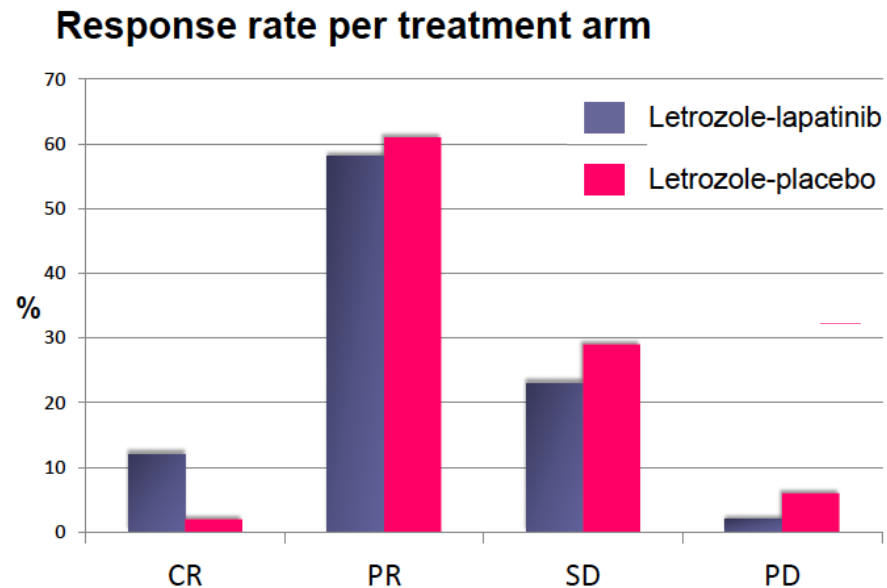
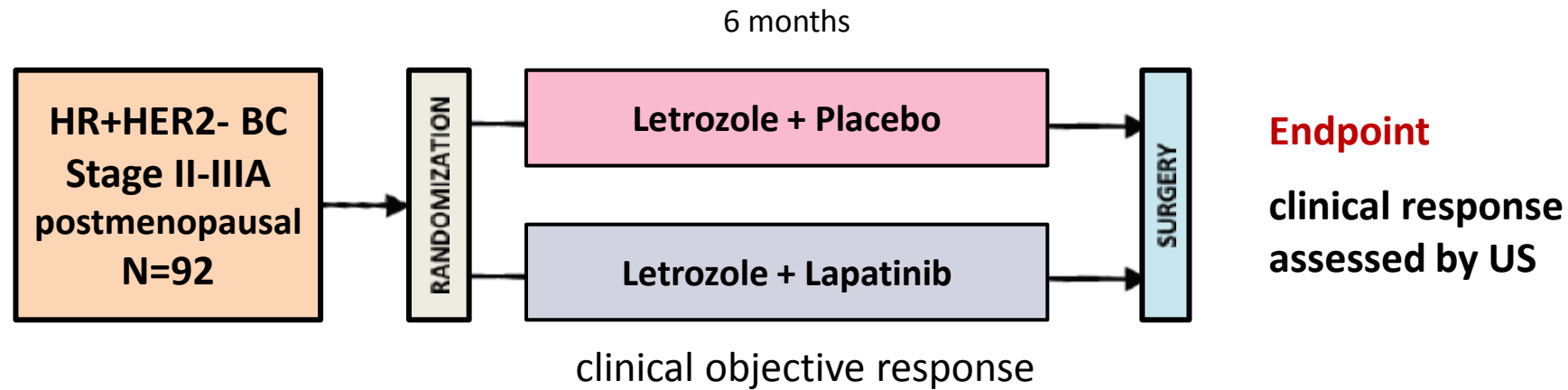
<18  
18-30  
>30



# Can novel agents address resistance to HT in a biologically driven way?



# LET-LOB trial: preoperative letrozole +/- lapatinib for HR+HER2- operable BC



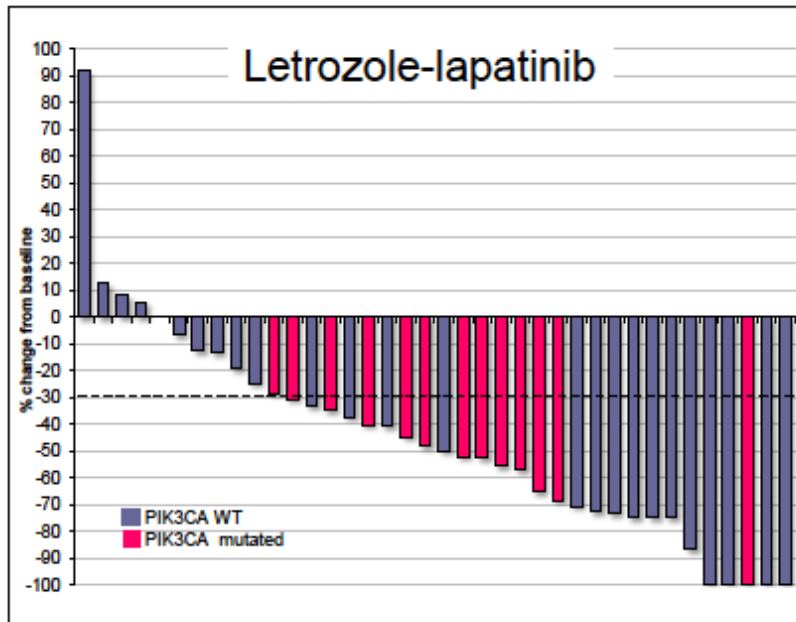
Numerically similar clinical response rates (CR+PR) were observed:

- 70% for letrozole-lapatinib
- 63% for letrozole-placebo

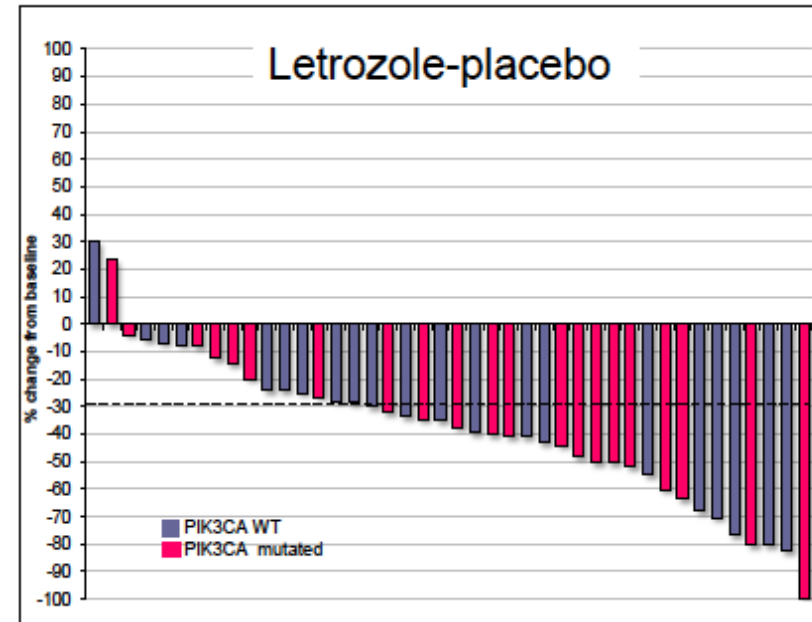
# LET-LOB trial: preoperative letrozole +/- lapatinib for HR+HER2- operable BC

## Responses (ORR) according to PIK3CA status

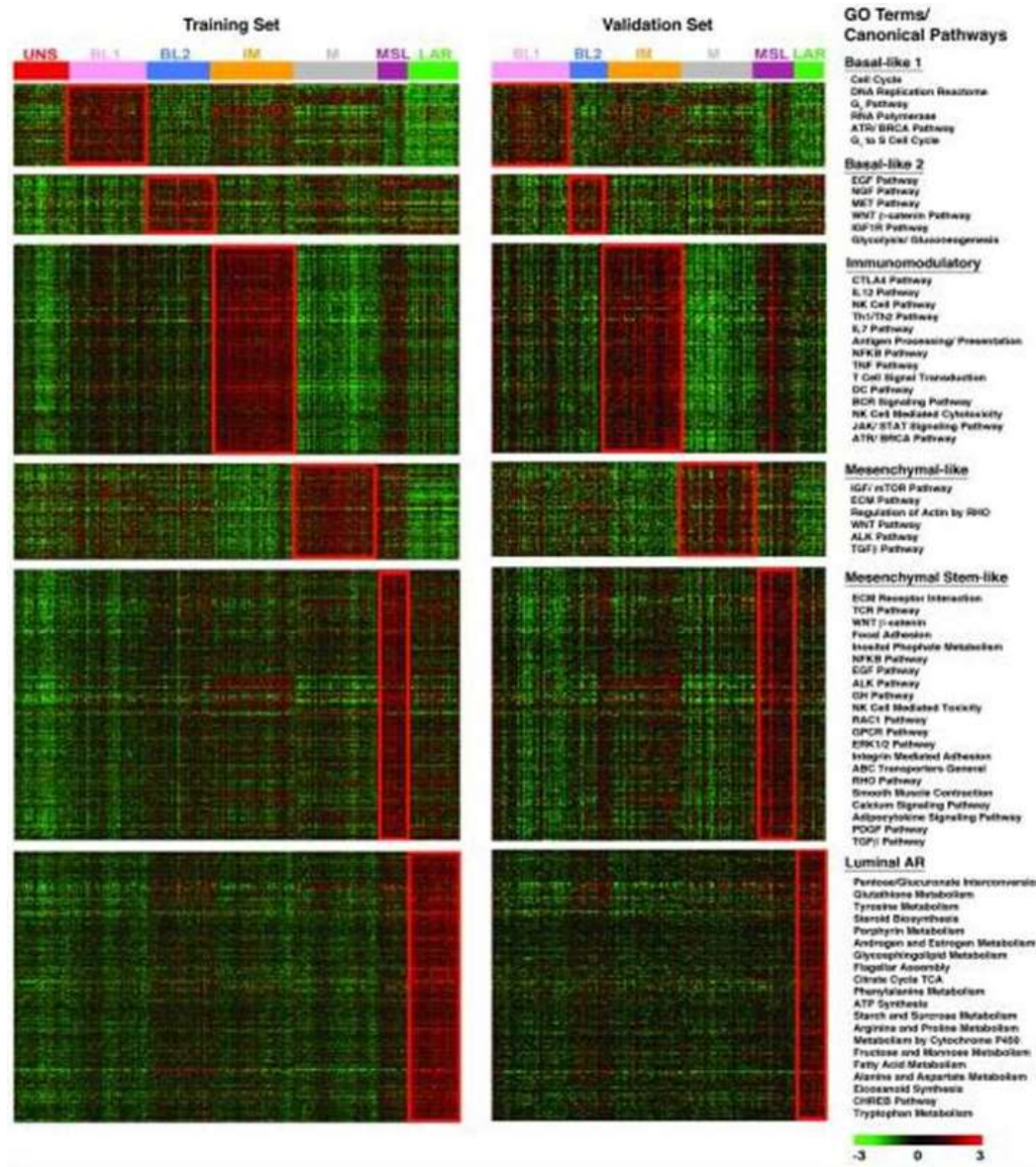
63% in WT tumors  
vs 93% in PIK3CA mutated tumors  
p=0.037



66% in WT tumors  
vs 63% in PIK3CA mutated tumors  
p=0.79



# Tackling TNBC heterogeneity



**Basal-like 1:** cell cycle, DNA repair and proliferation genes

**Basal-like 2:** growth factors (EGFR, MET, Wnt, IGF1R)

**Immunomodulatory:** Immune signalling

**Mesenchymal-like and Mesenchymal stem-like:** EMT, motility and growth-factor pathways

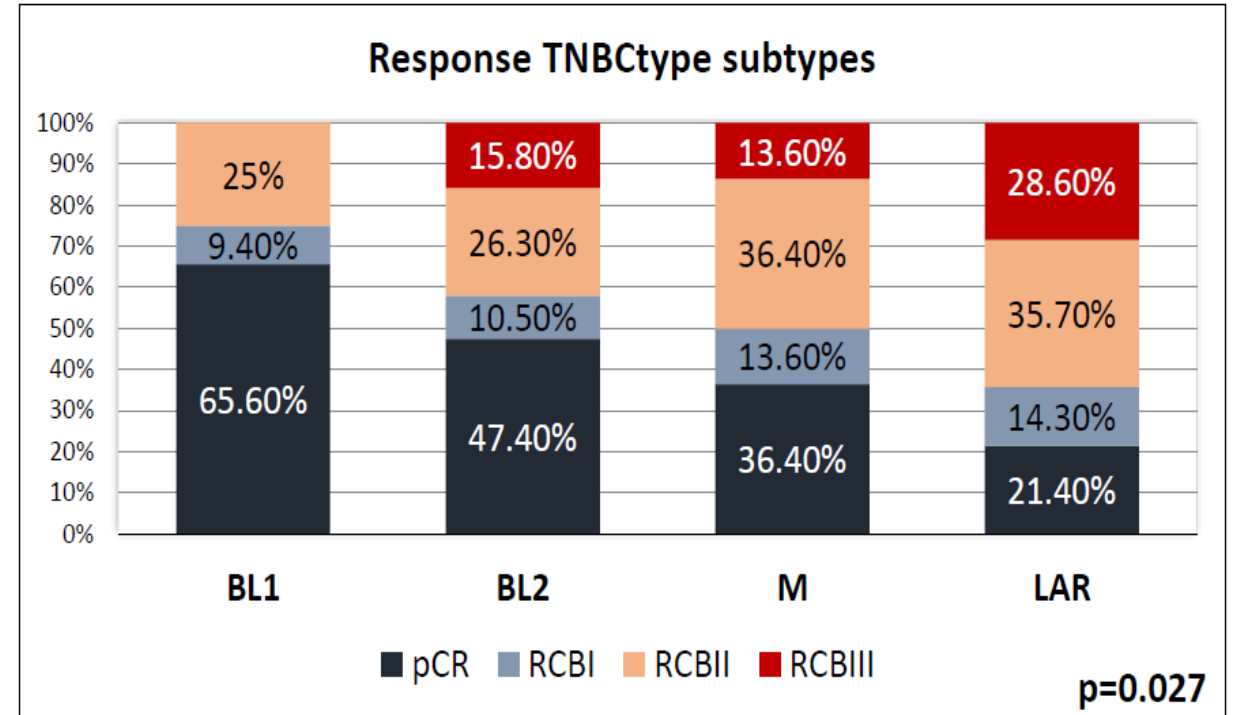
**Luminal AR:** Androgen receptor signaling



# TNBC subtypes predict for response to CT

	BL1	BL2	M	LAR	P
N	32	19	22	14	
Age median	41	51	50.5	67.5	<0.001
T size (median)	48	40	40	58.5	0.40
N + (%)	78.1%	52.6%	63.6%	85.7%	0.13
Median Ki67	80%	60%	70%	40%	<0.001
G3 (%)	84.4%	63.2%	72.7%	64.3%	0.17

- BL1 was associated with a significant younger age at diagnosis and higher ki67 values.



# Conclusions

- Neoadjuvant treatment gives the opportunity to **test tumor biology** and **refine prediction of prognosis** based on response
- Evaluation of gene expression profiling and mutational status can help predict response to neoadjuvant treatment, but are **not** currently **validated in the clinic**
- More and more trials are selecting patients based on GEP and mutational status, so this will probably change in the near future