



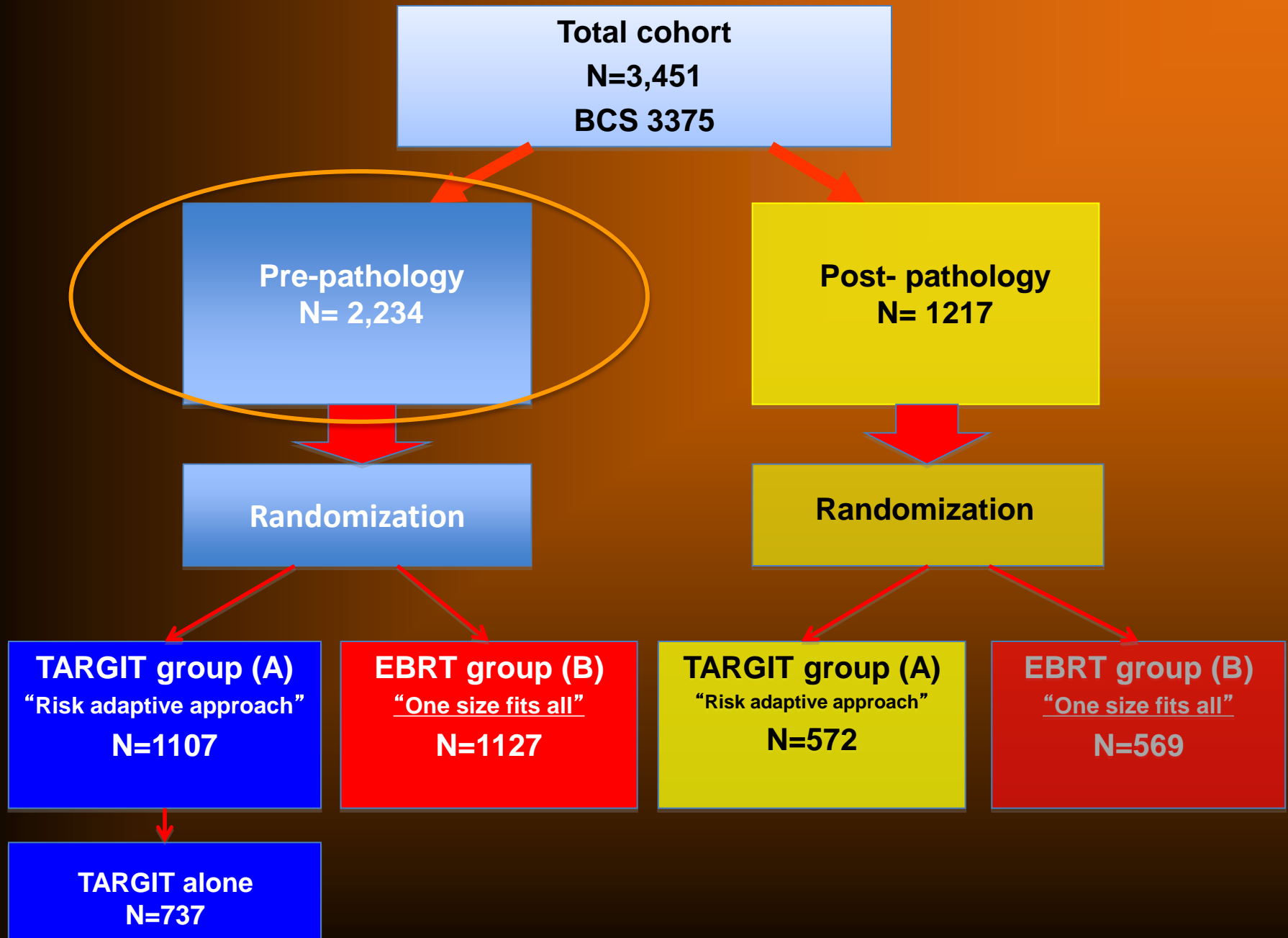
# ***PROFFERED PAPERS EARLY BREAST CANCER***

## ***Abstracts 2450, 2460, LBA10***

**Fatima Cardoso, MD**  
**ESO Breast Cancer Program Coordinator**  
**EORTC Secretary General**  
**Director Breast Cancer Unit**  
**Champalimaud Cancer Center**  
**Lisbon, Portugal**

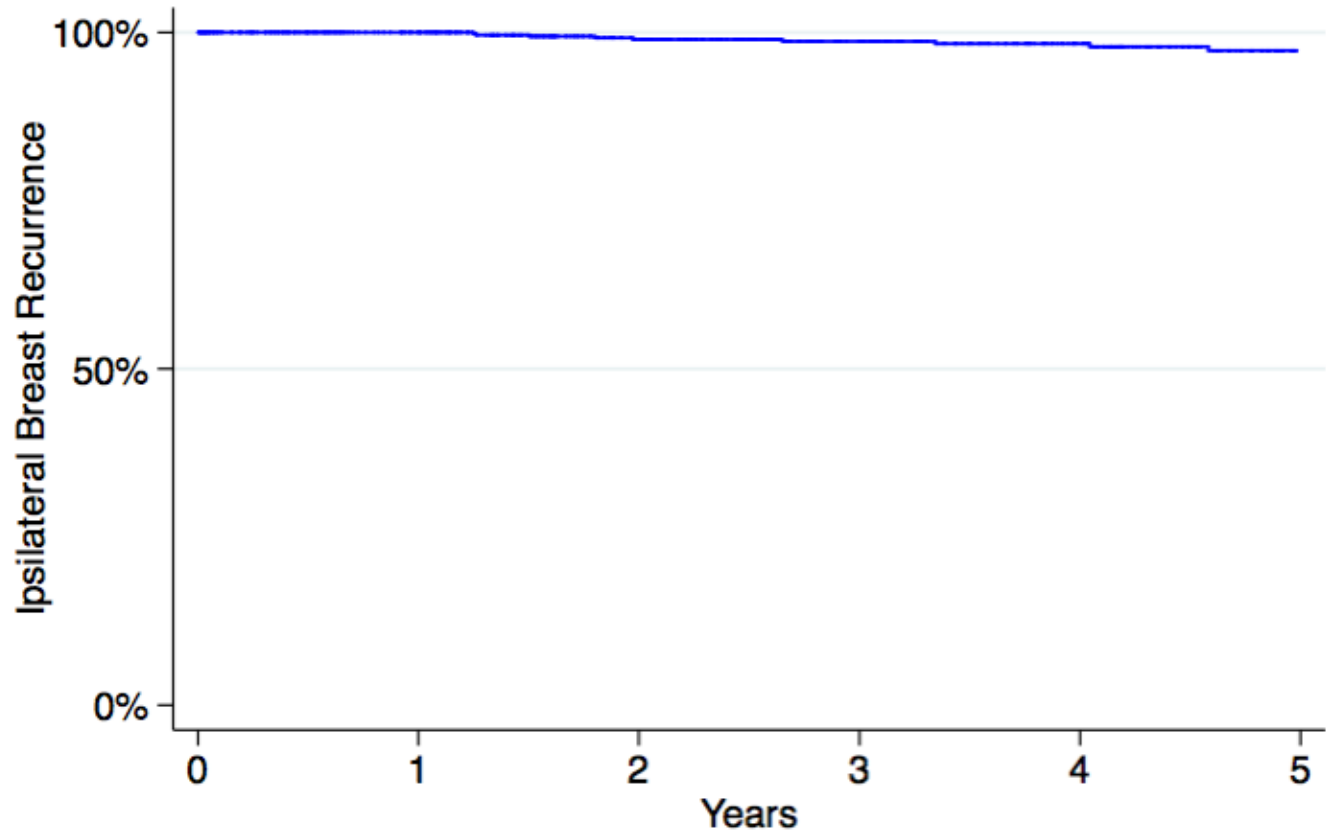


# Breast cancer being treated with Breast Conserving Surgery



## Ipsilateral Breast Recurrence

Prepathology TARGIT alone



Number at risk

TARGIT 737

560

424

314

231

135

## Relevant findings

- The BC mortality in this low risk group is low
- Contralateral disease is more common than ILR outside IQ

## Limitations

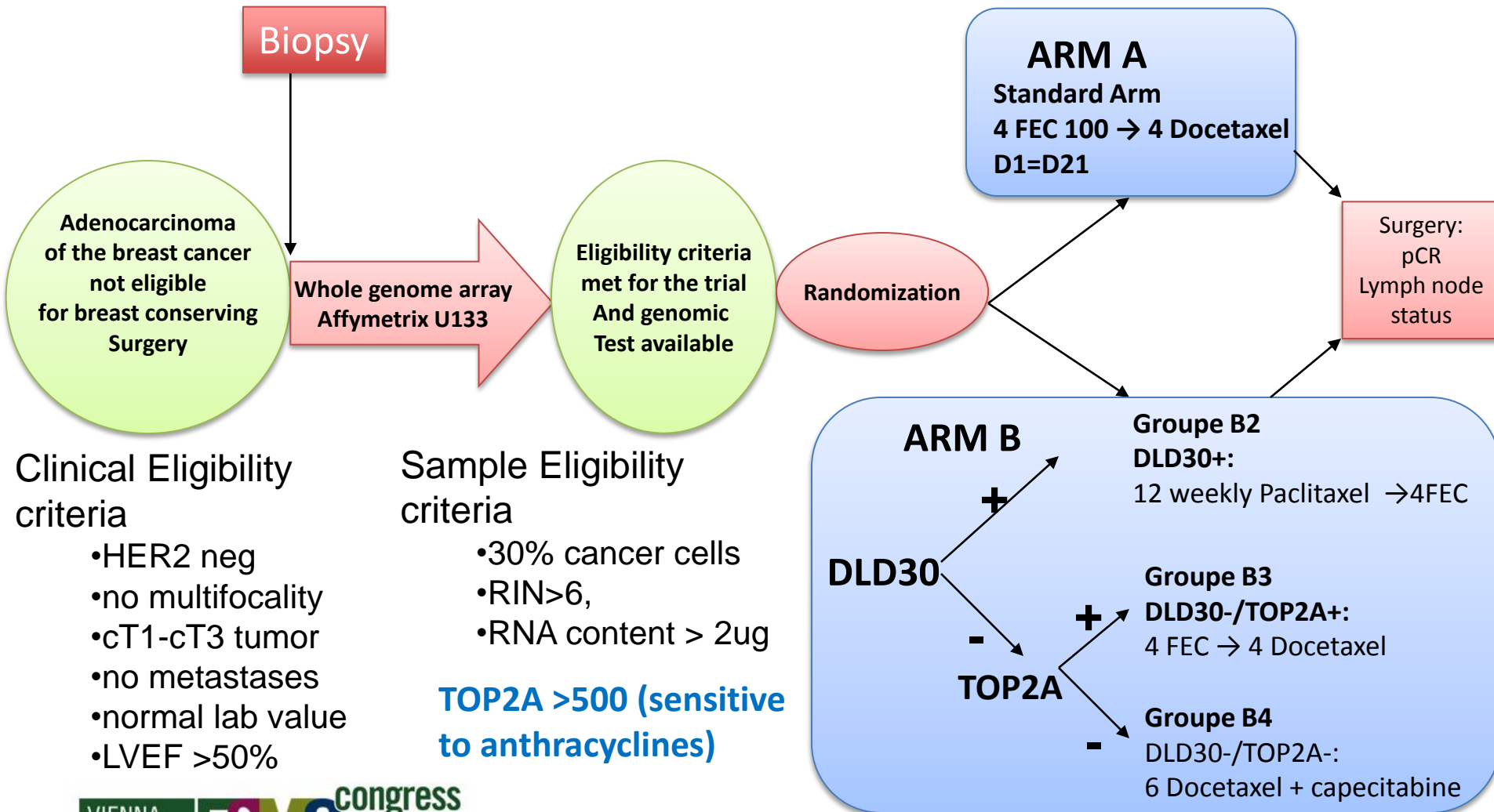
- It's a highly selected low risk population
- Does not address the role of “slightly larger” surgery
- Need to wait for final comparison with whole breast RT
- Need (much) longer FU

# Comments

- **64% were screen-detected**
  - **If not screen-detected, most probably more advanced & not amenable to this much less invasive loco-regional treatments**
  - **One can not and should not infer from this trial the benefits of breast cancer screening**
- **Importance of **all cause mortality** outcomes in trials of screening: **agree!****

# REMAGUS 04 Trial design

Phase III randomized trial : standard neoadjuvant chemotherapy  
vs a genomic-driven neoadjuvant chemotherapy



# OBJECTIVES

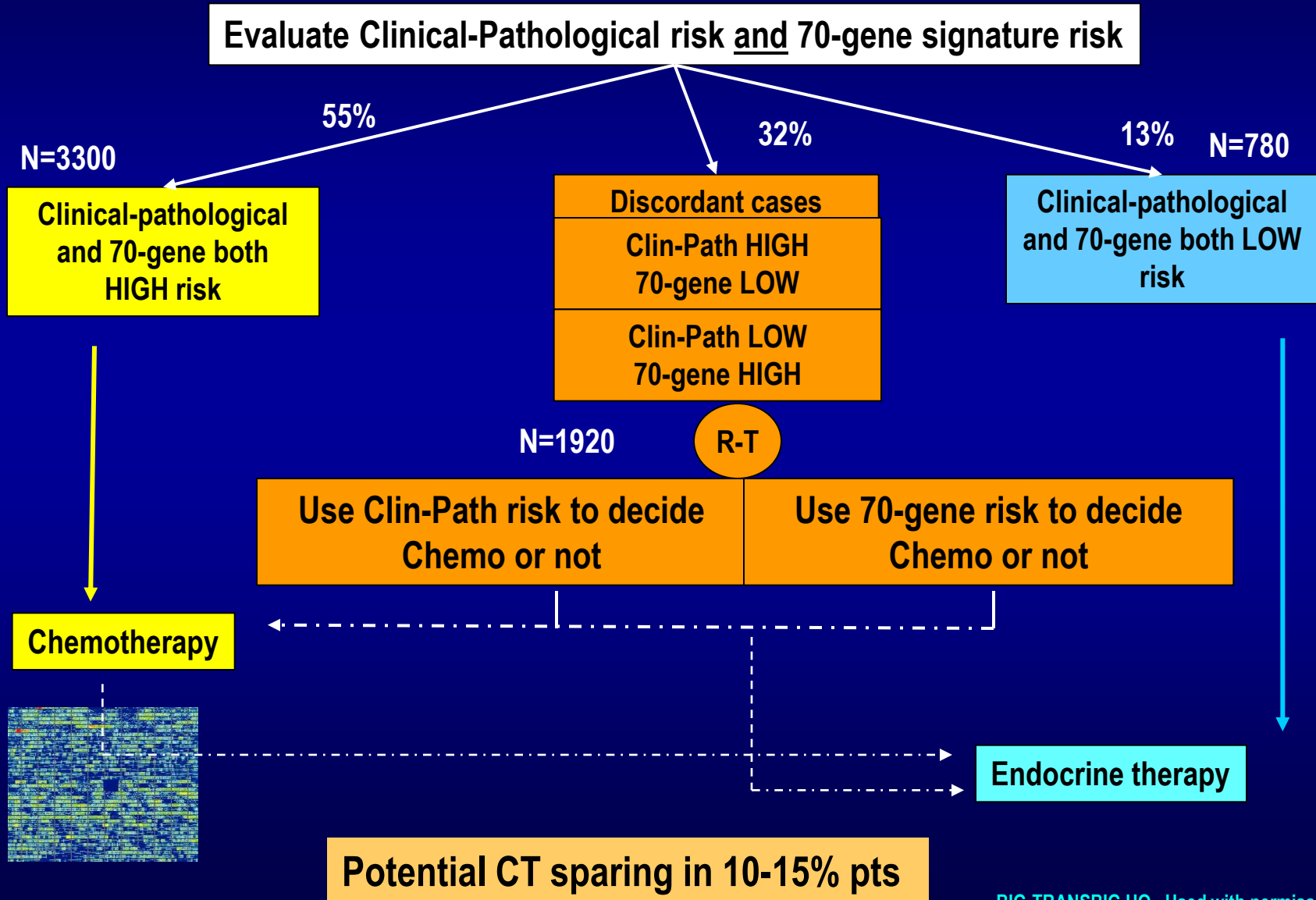
- Evaluate whether whole genome array approach is feasible in the context of daily practice
- Evaluate Diagonal Linear Discriminant Analysis–30 (DLDA-30) probe set model as predictor of resistance to neoadjuvant CT with a better sensitivity than standard parameters<sup>1</sup>
- Evaluate TOP2A amplification as a predictor for the efficacy of anthracyclines-based CT<sup>2</sup>
- Evaluate whether the use of a genomic score (DLD30) combined with TOP2A level could improve neoadjuvant chemotherapy efficacy.

- Evaluate whether whole genome array approach is feasible in the context of daily practice
- Whole genome array is feasible within 15 days in a multicentric setting
- The success rate for genomic analysis was 61% (142/232) for the eligible patients and 67% for the screened population.
- Main sources of loss of samples are low % tumor cell in biopsy and RNA quality

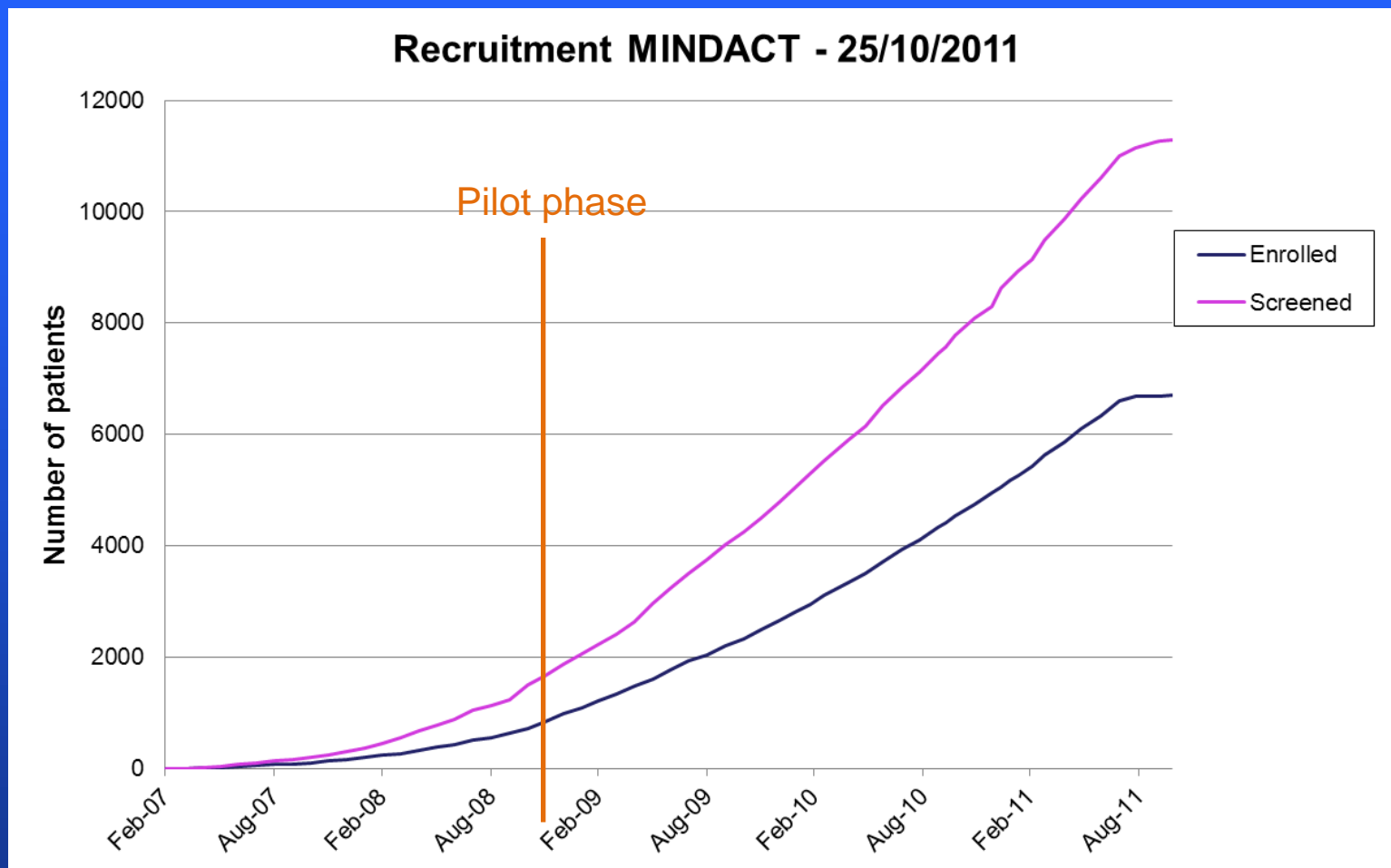


# EORTC 10041 BIG 3-04 trial MINDACT TRIAL DESIGN

## 6,000 Node - & 1-3 N+ women



# MINDACT – final accrual curve



	Registered	Screened	Enrolled
Number of patients	11291	11291	6694 (59.3%)

# Reasons for non enrollment (4200 pts registered but not enrolled)

## Eligibility criteria

Criteria	Number of patients
<b>Sample damaged or defrosted</b>	<b>1</b>
<b>&lt;30% (&lt;50% pre amend.) tumor cells</b> <b>Bad RNA quality and quantity</b>	<b>976</b>
<b>Unsuccessful genomic test</b>	<b>11</b>
<b>“Clinical-related” reasons</b>	<b>3212</b>

Cut-off date for all included data: 02/03/2011

- Evaluate whether whole genome array approach is feasible in the context of daily practice

## TAKE-HOME MESSAGES

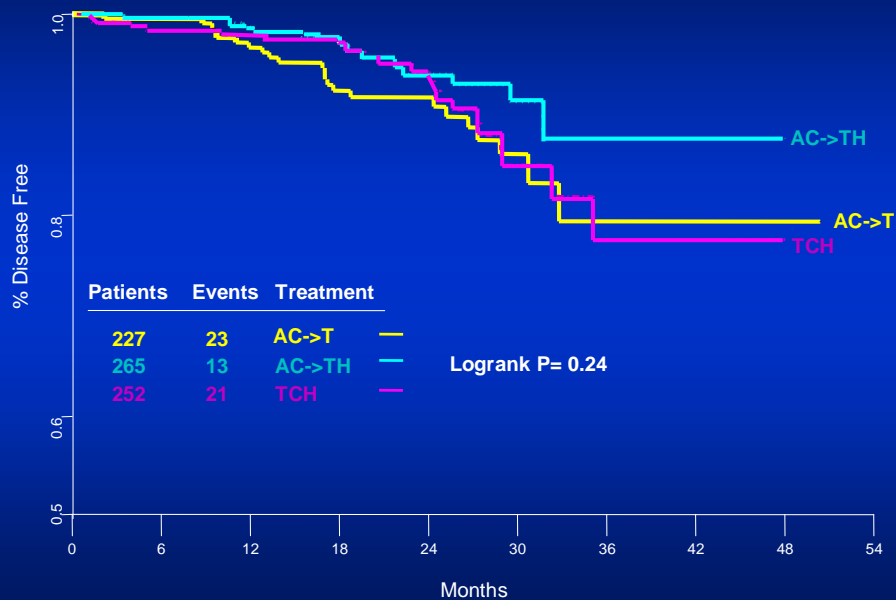
- Genome arrays are **feasible in a real-time basis and in a multicentric and multinational setting**
- The success rate is linked to **quality of samples making logistics set-up, pathologists training/learning curve crucial**

- **Evaluate TOP2A amplification as a predictor for the efficacy of anthracyclines-based CT**

## **TAKE-HOME MESSAGES**

- **Non-anthracyclines-based regimen with very low pCR rate (4%)**
- **Role of Topo-II-A as a predictive marker for anthracyclines: still not ready for clinical practice**

## DFS CO-AMPLIFIED TOPO II BY ARM



Slamon D., SABCS 2005



AC → TH

>>

AC → T or TCH

Anthracyclines &  
trastuzumab are imp

AC → TH & TCH

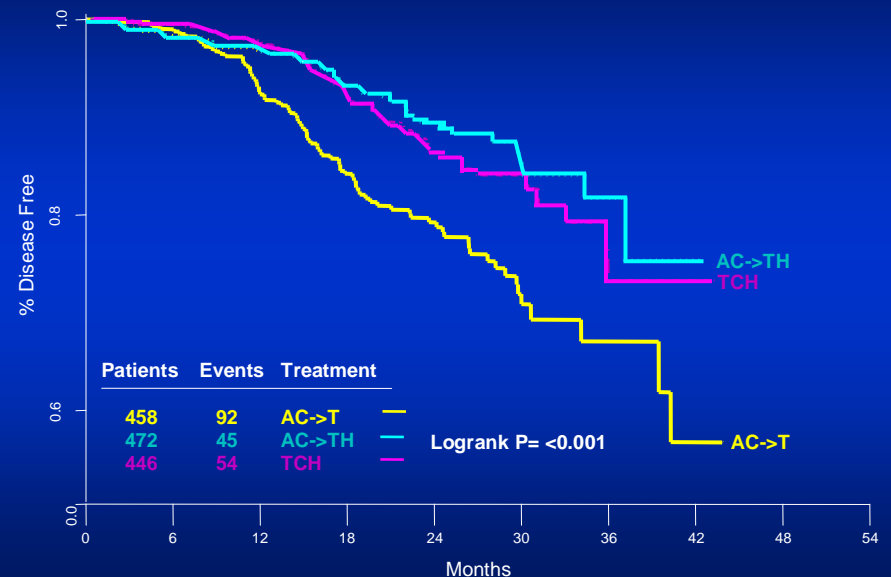
>>

AC → T

Only trastuzumab is imp

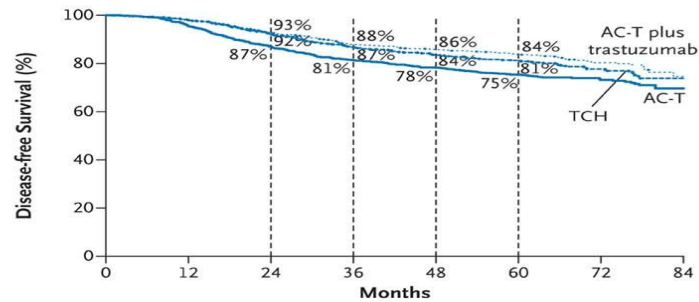


## DFS NON CO-AMPLIFIED TOPO II BY ARM



Slamon D., SABCS 2005

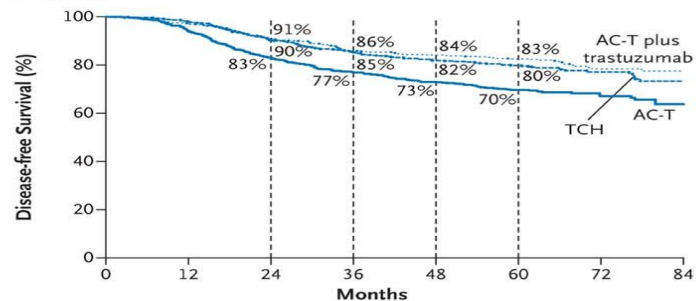
**A All Patients**



**No. at Risk**

AC-T	1073	977	861	774	695	555	202	29
AC-T plus tras- tuzumab	1074	1028	951	861	774	620	226	37
TCH	1075	1021	939	848	770	606	208	33

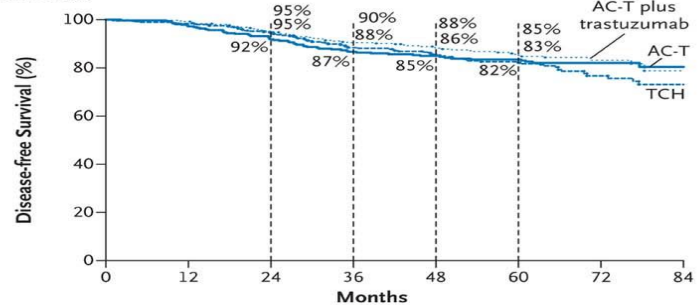
**B Without TOP2A**



**No. at Risk**

AC-T	643	586	502	450	397	315	116	18
AC-T plus tras- tuzumab	643	615	565	509	462	365	137	22
TCH	618	594	537	487	444	345	120	14

**C With TOP2A**



**No. at Risk**

AC-T	328	312	288	261	236	189	71	7
AC-T plus tras- tuzumab	357	343	317	290	256	209	69	12
TCH	359	347	325	291	262	207	72	14

**DFS in all patients**  
(TCH numerically not statistically  
inferior to A-based;  
trial hypothesis (superiority)  
**NOT proven!**)

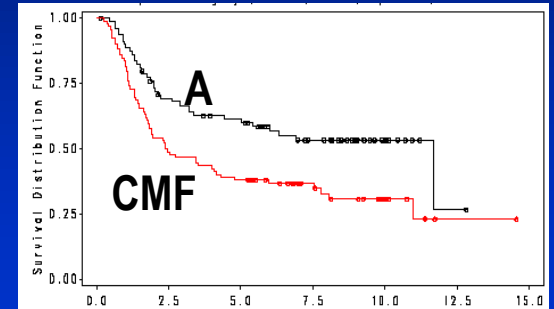
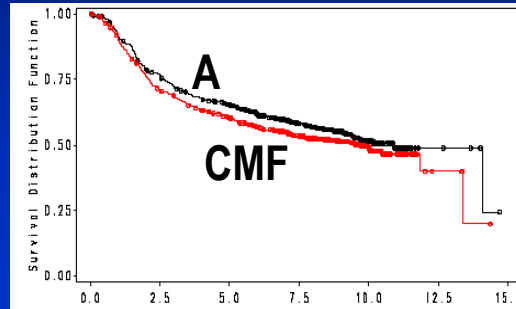
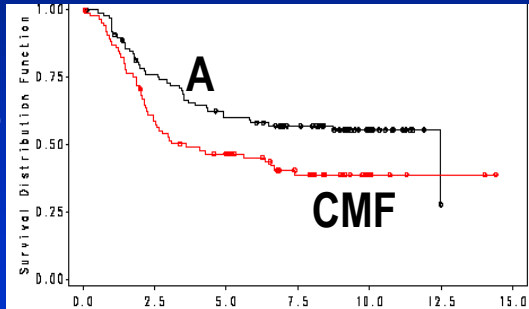
**DFS in patients without  
TOP2A co-amplification**  
(TCH “less” inferior to A-based)

**DFS in patients with  
TOP2A co-amplification**  
(A-based clearly superior)

# DFS AND OS BY TOPO IIA STATUS

## KAPLAN-MEIER CURVES

DFS

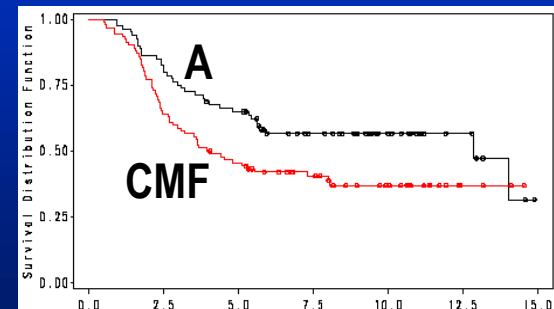
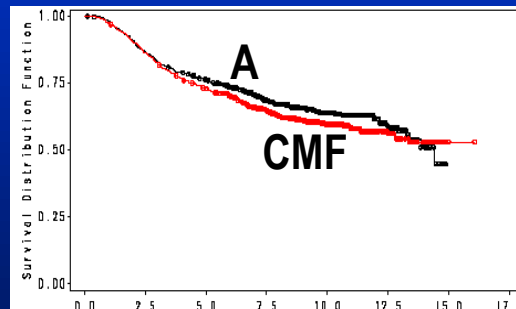
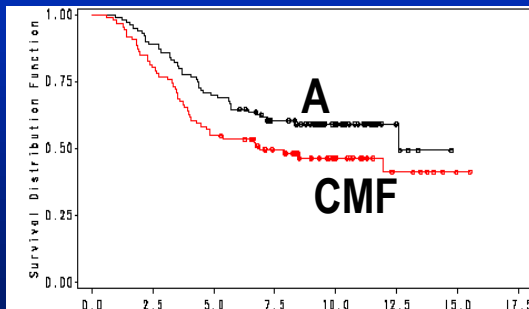


Amplified

Normal

Deleted

OS

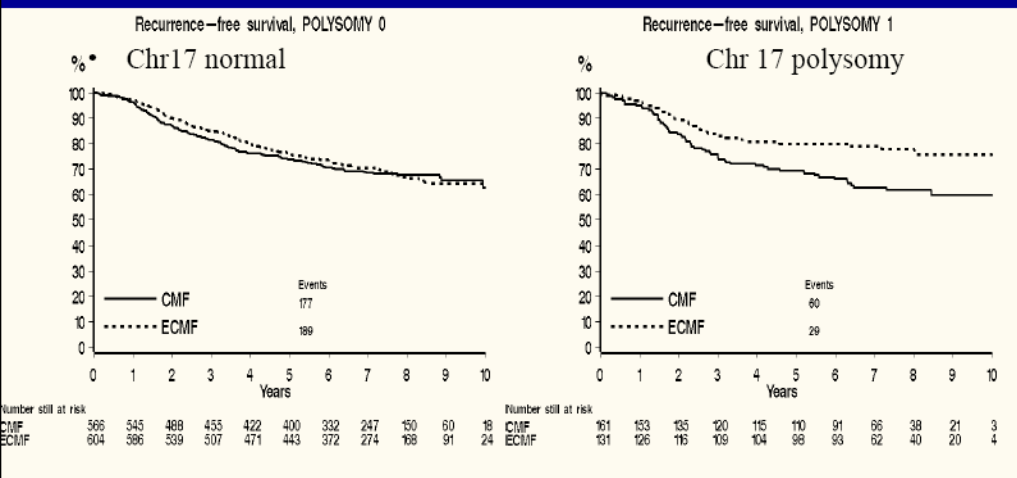




# CONCLUSIONS

- The results of this planned interim analysis show that HER-2 and topo II $\alpha$  genes have a **clinically modest and a statistically borderline value** in predicting sensitivity to anthracyclines in early breast cancer patients
- **Caveats:** 1) lack of reproducibility in topo II $\alpha$  scores by FISH in 30.8% (38/123) of cases submitted to the central lab; 2) trials heterogeneity
- **Exploratory analysis:**
  - 1) In HER-2+ patients benefit from anthracyclines seems to be independent of topo II $\alpha$  gene status
  - 2) Anthracyclines benefit does not seem to be confined to HER-2 positive patients
  - 3) Topo II $\alpha$  protein levels might be a relevant predictive marker independently of gene status

# Polysomy 17 predicts anthracycline benefit in the NEAT study (RFS)



• Test for interaction: HR 0.59 (0.35-0.98)  $p = 0.04$

$N = 1462$

Endocrine  
Cancer Group

## CHOMOSOME 17 POLYSOMY:

the true predictor of  
anthracycline benefit?

HER-2 & Topo-II maybe surrogates for ch17 polysomy

### Polysomy: duplication of Ch17

- Duplication of genes without amplification
- Associated with chromosomal instability

Polysomy (N = 1462)		
	Ch 17 Norm	Ch 17 Poly
HER2 -ve	968 (84%)	190 (16%)
HER2 Amp	202 (66%)	<b>102 (34%)**</b>
TOP2A -ve	1069 (85%)	250 (19%)
TOP2A amp	101 (71%)	<b>42 (29%)*</b>
TOP2A -ve	1121 (85%)	200 (15%)
TOP2A Del	49 (35%)	<b>92 (65%)**</b>

\*  $p = 0.004$ , \*\*  $p < 0.0001$

Courtesy J Bartlett, SABCS08

Endocrine  
Cancer Group

- Evaluate Diagonal Linear Discriminant Analysis–30 (DLDA-30) probe set model as predictor of resistance to neoadjuvant CT with a better sensitivity than standard parameters

## TAKE-HOME MESSAGES

- DLD30+ score seems a good new predictive marker of response to CT: associated with an increased likelihood of pCR (36% versus 3% for DLD30-) but not a discriminator between different CT regimens
- Factors associated with pCR: DLD30+, ER and tumor grade

- Evaluate whether the use of a genomic score (DLD30) combined with TOP2A level could improve neoadjuvant chemotherapy efficacy

## TAKE-HOME MESSAGES

- The overall pCR rate was 22%. No difference between genomic driven arm and standard CT arm (pCR rates: 22 % and 21% respectively).

- Evaluate whether the use of a genomic score (DLD30) combined with TOP2A level could improve neoadjuvant chemotherapy efficacy

## TAKE-HOME MESSAGES

- There is still **NO factor available for clinical use allowing for a tailoring of the type of neoadjuvant CT to the individual patient!**
- Therefore: **neoadjuvant CT regimens should be the standard ones** (as in adjuvant) i.e. Anthracyclines and Taxanes, no other cytotoxic agents, no extra number of cycles.

# HE 10/05

(ACTRN 12610000151033)

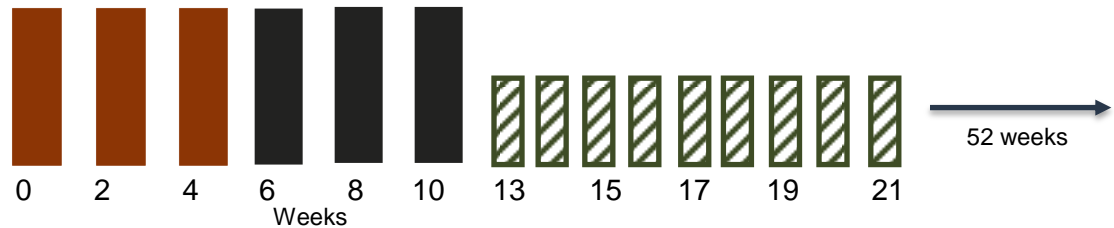
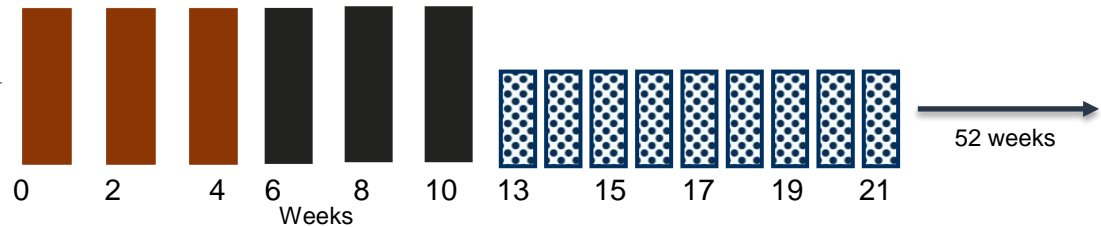
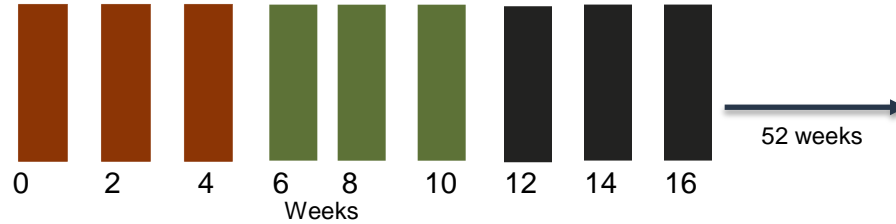
- Stratification by:
- Center
  - Menopausal status (Pre- vs Post-)
  - N of involved nodes (0 vs 1-3 vs  $\geq 4$ )

R  
A  
N  
D  
O  
M  
I  
Z  
A  
T  
I  
O  
N

Arm A

Arm B

Arm C



990 eligible pts



Epirubicin 110 mg/m<sup>2</sup> with G-CSF



Docetaxel 35 mg/m<sup>2</sup>



Paclitaxel 200 mg/m<sup>2</sup> with G-CSF



Paclitaxel 80 mg/m<sup>2</sup>



Cyclophosphamide 840 mg/m<sup>2</sup>  
Methotrexate 57 mg/m<sup>2</sup>  
Fluorouracil 840 mg/m<sup>2</sup>



Trastuzumab

# Limitations

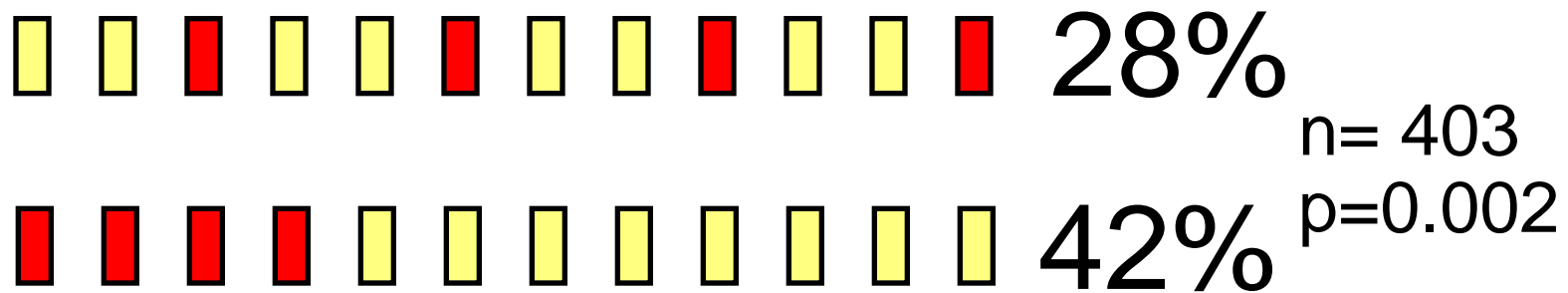
- Acceptable **control arm**?
- **Relatively small** adjuvant trial (~1000 pts) and too many variables
- **Dose dense** but also **dose intense** regimens
- **All BC subtypes** included (about 75% ER+ & about 28% HER-2+)

# Relevant findings


- **Low rate of recurrence** with all 3 regimens
  - **Taxanes** matter
  - **Dose** matters
  - **Interval** (dose dense) matters
  - **Sequential** regimens matters
- **Toxicity acceptable** in all 3 regimens but ARM A overall better tolerated (less discontinuations: 5.8% vs. 13.2% vs. 14.9%)



# Sequential or alternating Rx 10 year disease-free survival

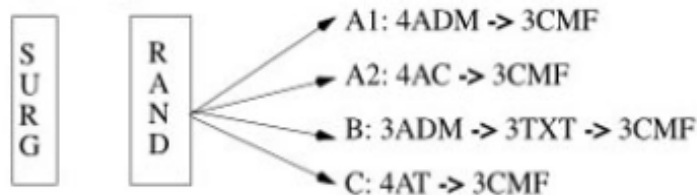


 Dox, 75 mg/m<sup>2</sup>

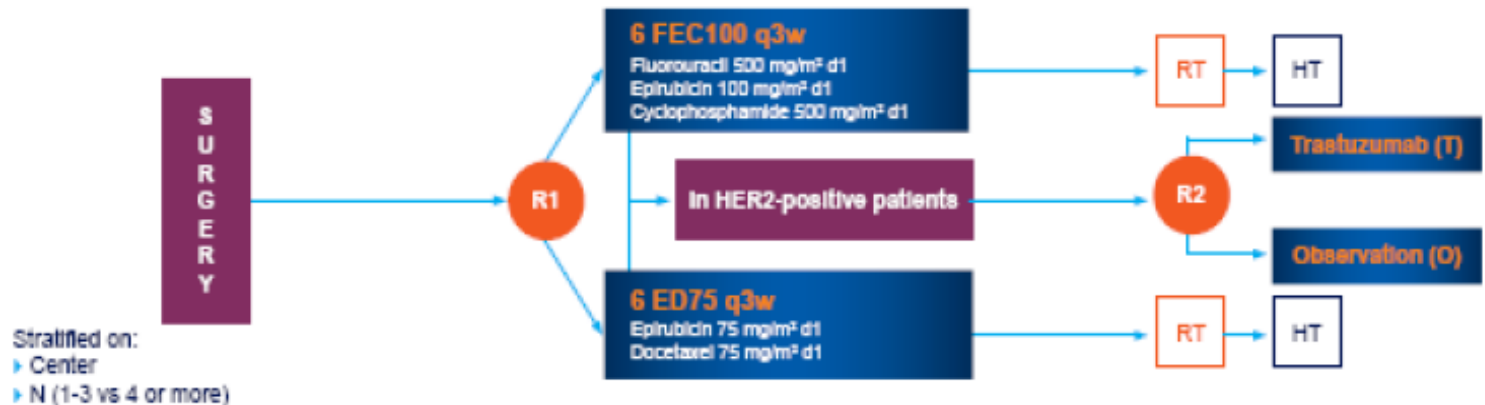
 CMF, 600/40/600 mg/m<sup>2</sup>

# Sequential taxanes > combination in EBC

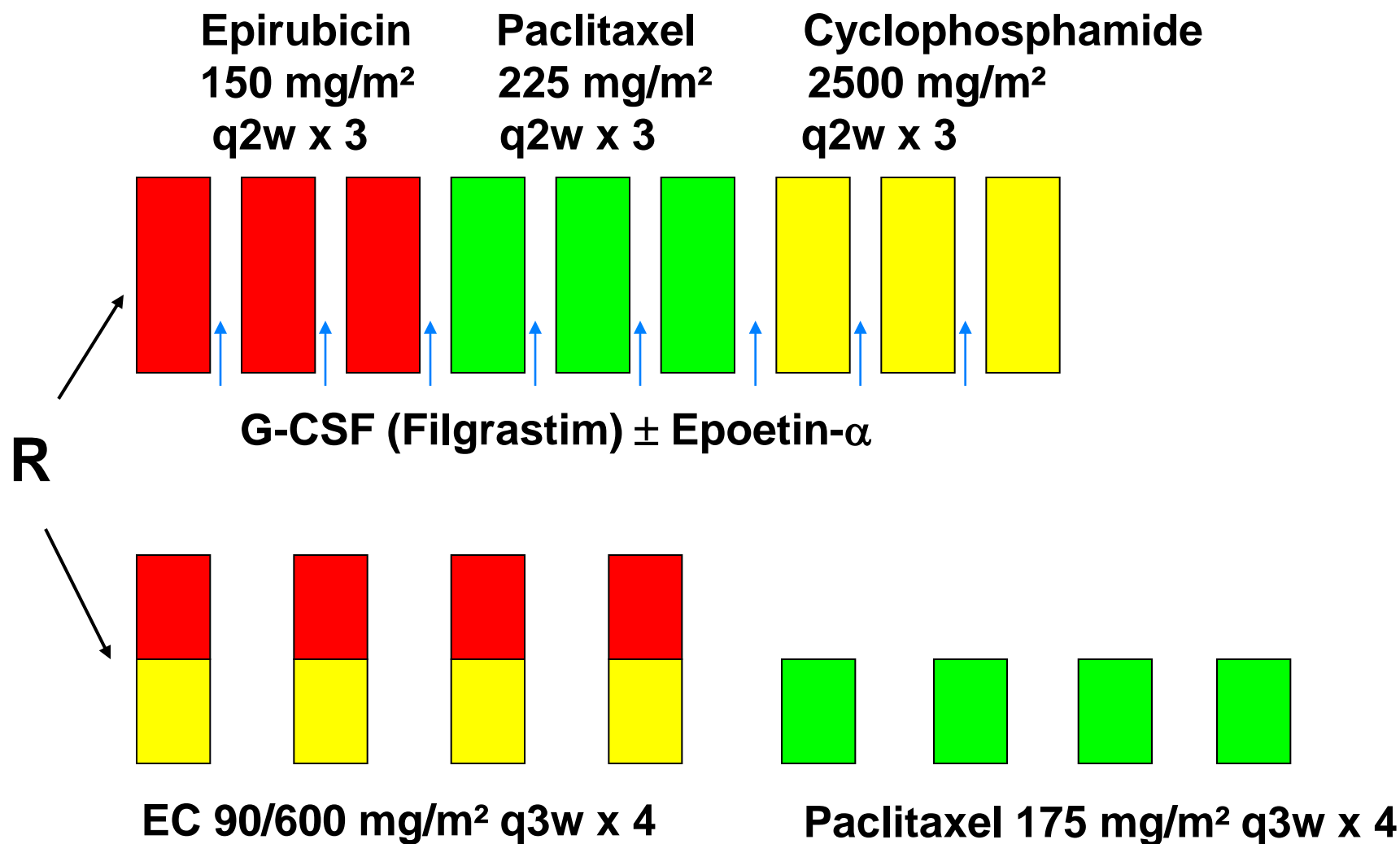
- BIG 2-98: DFS (HR 0.84) and OS (HR 0.79) better for arm B (A -> T) vs C (A+T)
  - Exploratory: no benefit of taxanes in triple negative



- PACS04: DFS and OS similar

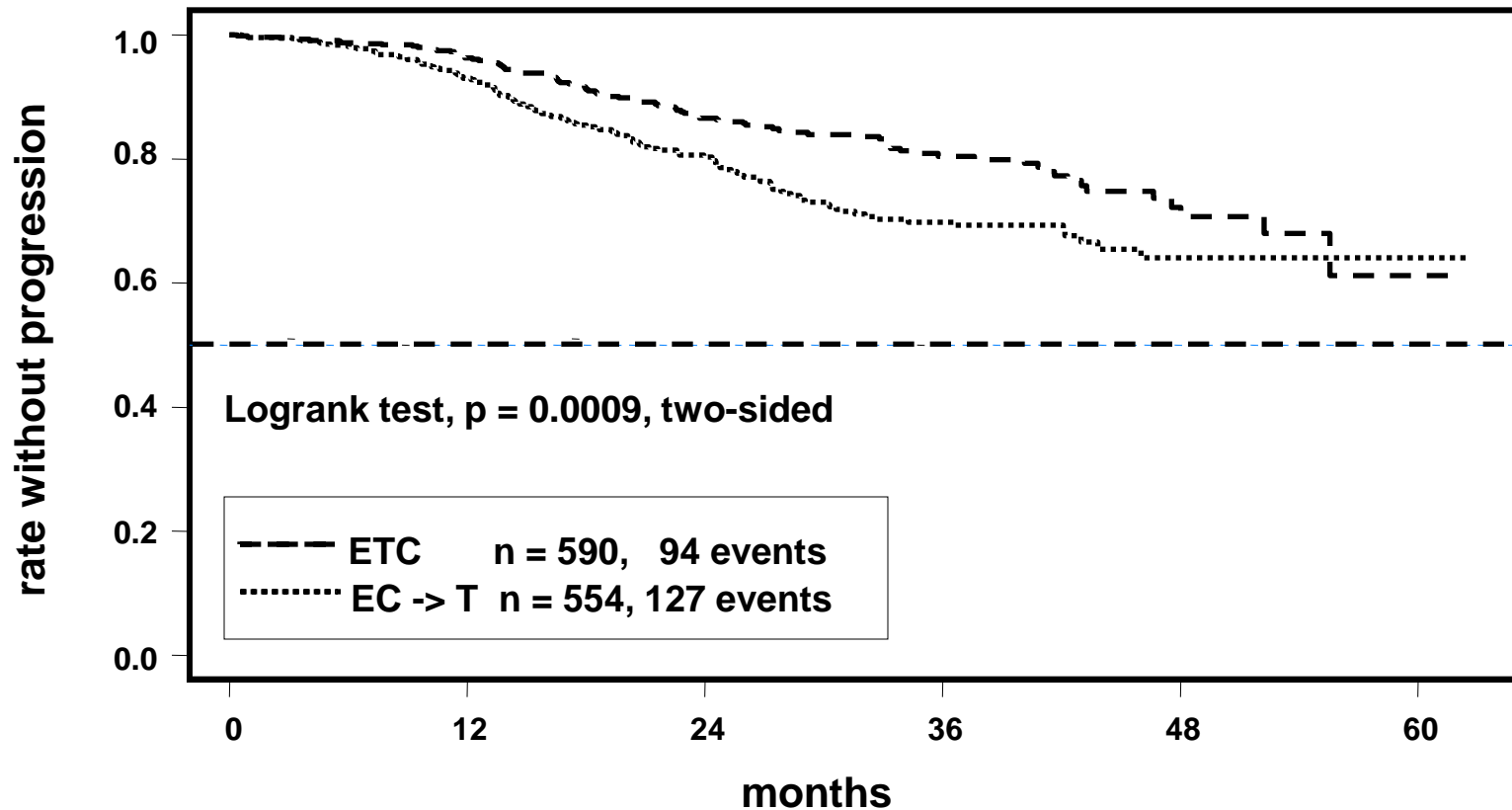


# AGO-Trial ETC vs. EC→T in patients with $\geq 4+$ lymph nodes



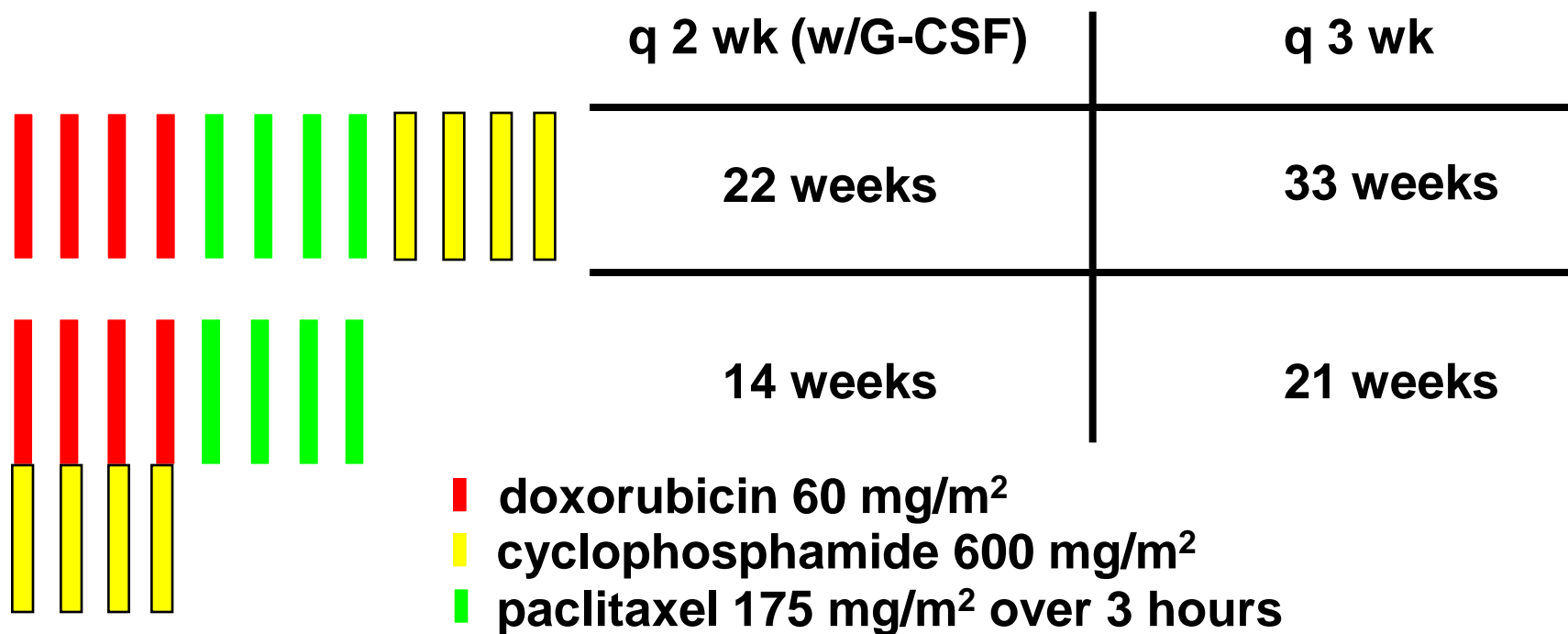
# AGO-Trial ETC vs EC→T

## Time to relapse by therapy



# Intergroup Node (+) Trial

## CALGB 9741 – 2 x 2 Factorial Design

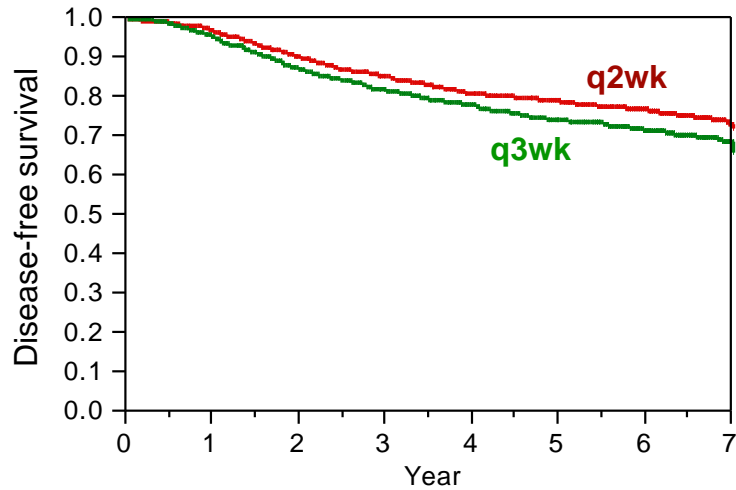


Radiation therapy and tamoxifen follow as appropriate

Accrued 9/97-3/99 with n=2005

## DFS by Dose Density (Q2 vs Q3)

11/30/2005



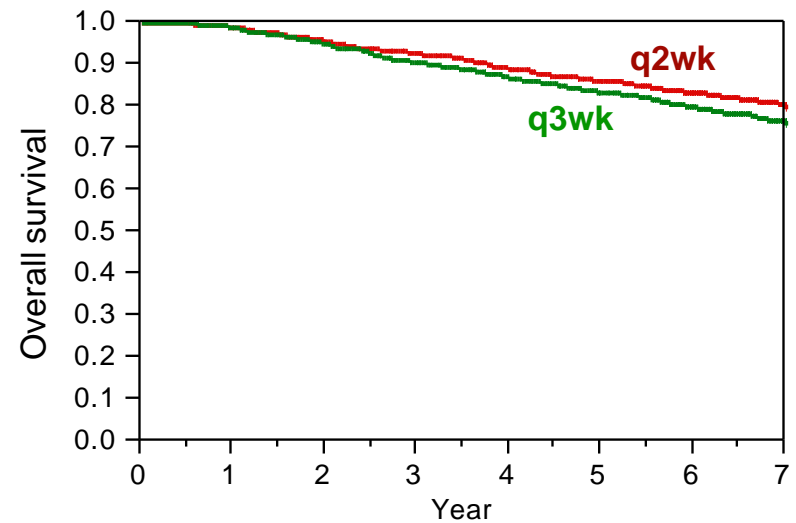
**Q2 n = 988 Events = 230**

**Q3 n = 984 Events = 278**

**p = 0.012**

## OS by Dose Density (Q2 vs Q3)

11/30/2005



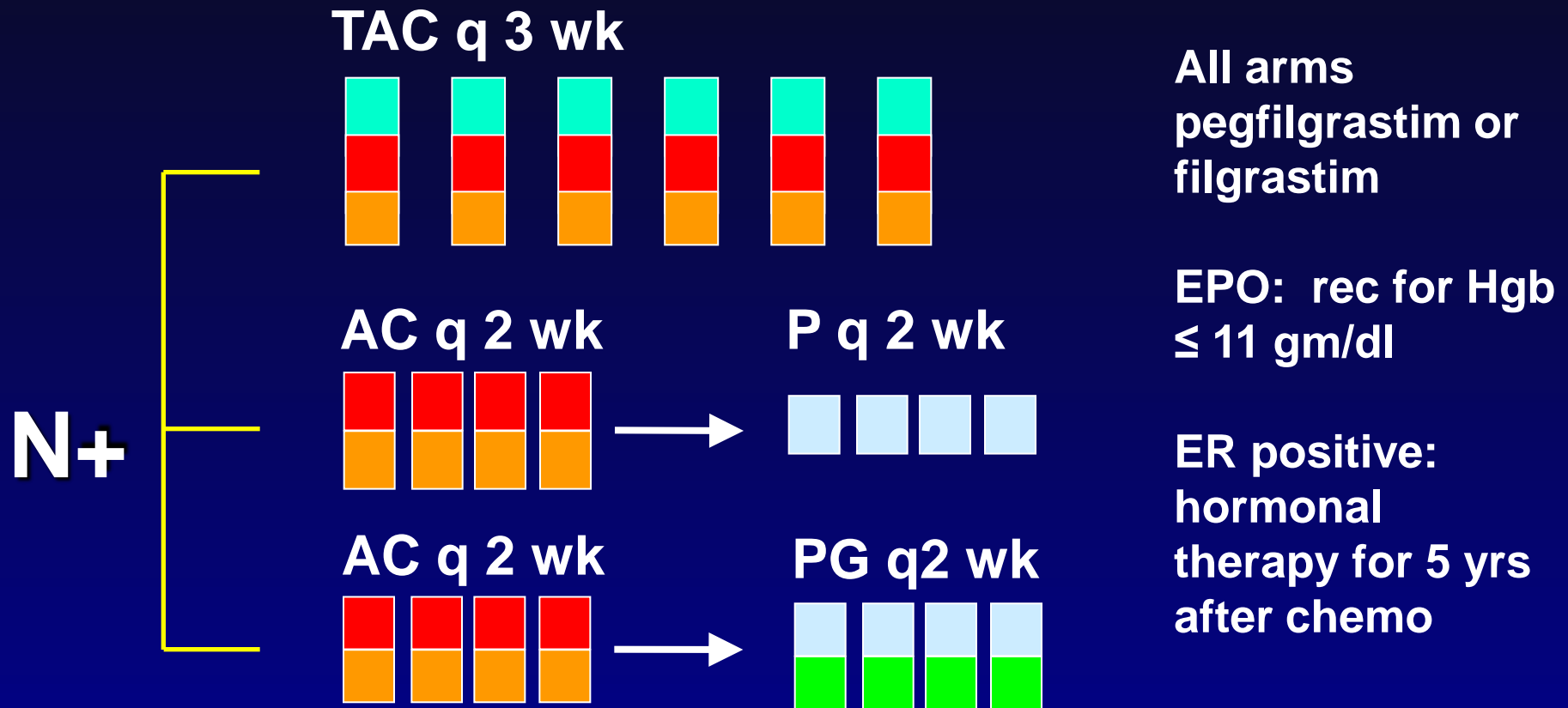
**Q2 n = 988 Events = 168**

**Q3 n = 984 Events = 202**

**p = 0.049**

# NSABP B-38 Schema

**Stratification:** # nodes, Hormone receptor, Surgery and RT



# NSABP B-38

## Disease-Free Survival (DFS)

- **Five-year DFS:**

- TAC: 80.1% (95% CI = 78, 82)
- DD AC→P: 82.2% (95% CI = 80.2, 84)
- DD AC→PG: 80.6% (95% CI = 78.5, 82.5)

- **Pairwise comparisons:**

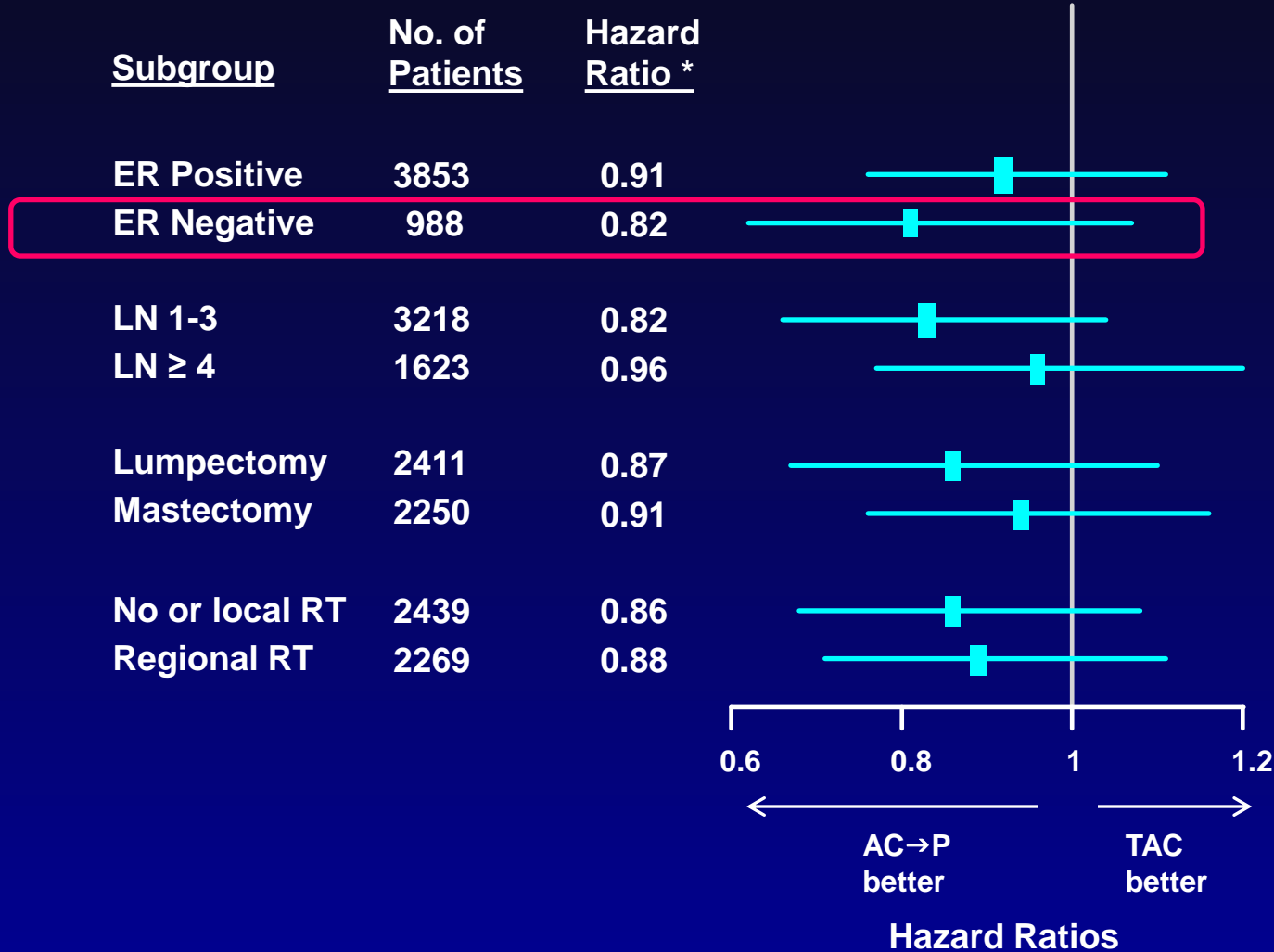
- DD AC→PG vs. TAC: HR=0.93 (p=0.39)
- DD AC→PG vs. DD AC→P: HR=1.07 (p=0.41)
- DD AC→P vs. TAC: HR=0.87 (p=0.074)



# NSABP B-38

## Hazard Ratios for DFS

AC→P vs TAC



\* Adjusted for randomization factors

# NSABP B-38

## Deaths on Treatment (N)

Grade	TAC (1612)	AC→P (1623)	AC→PG (1612)
5	13	5	7

**P=0.2**