

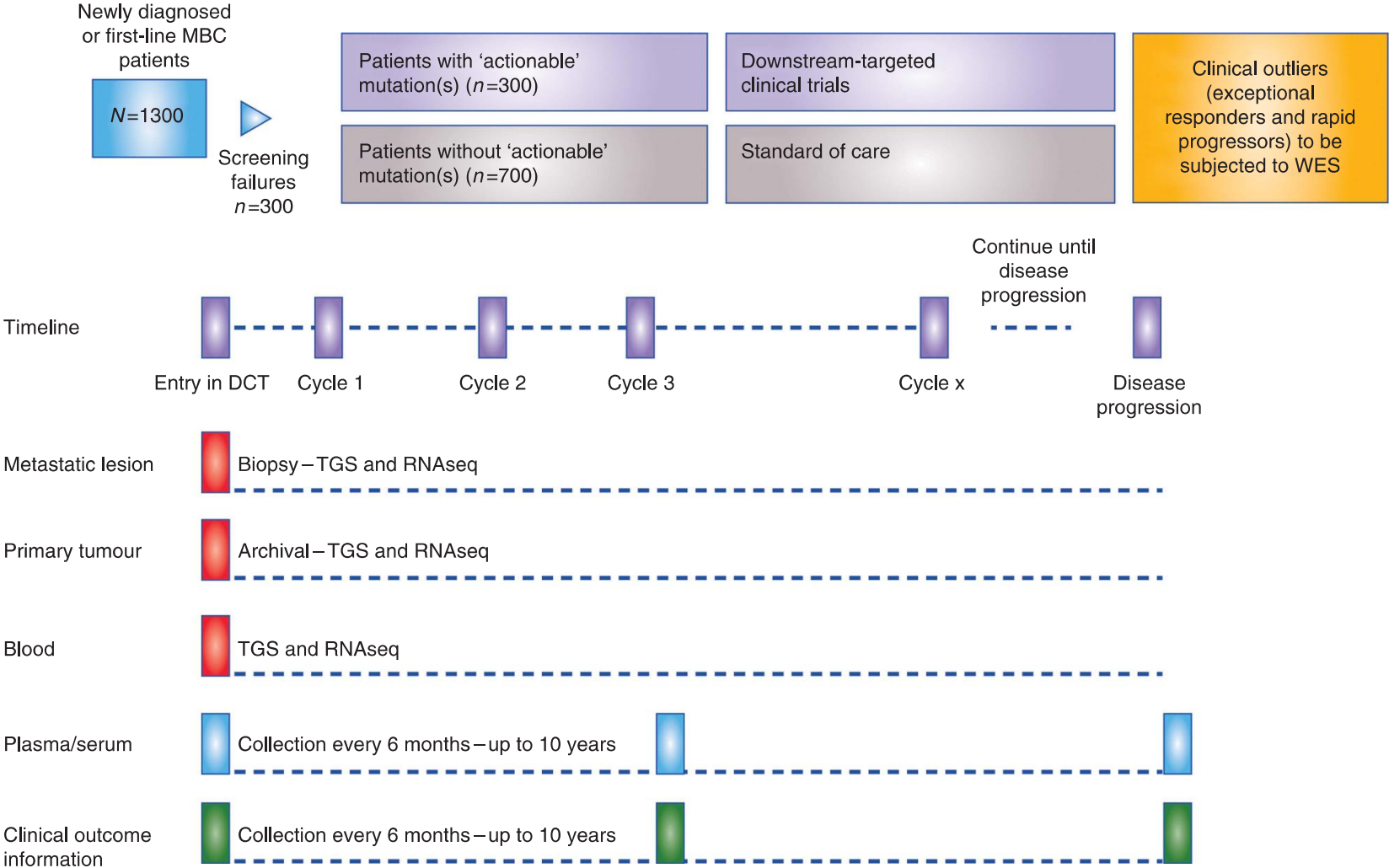
# **Should I order sequencing for my ER+ metastatic breast cancer patients?**

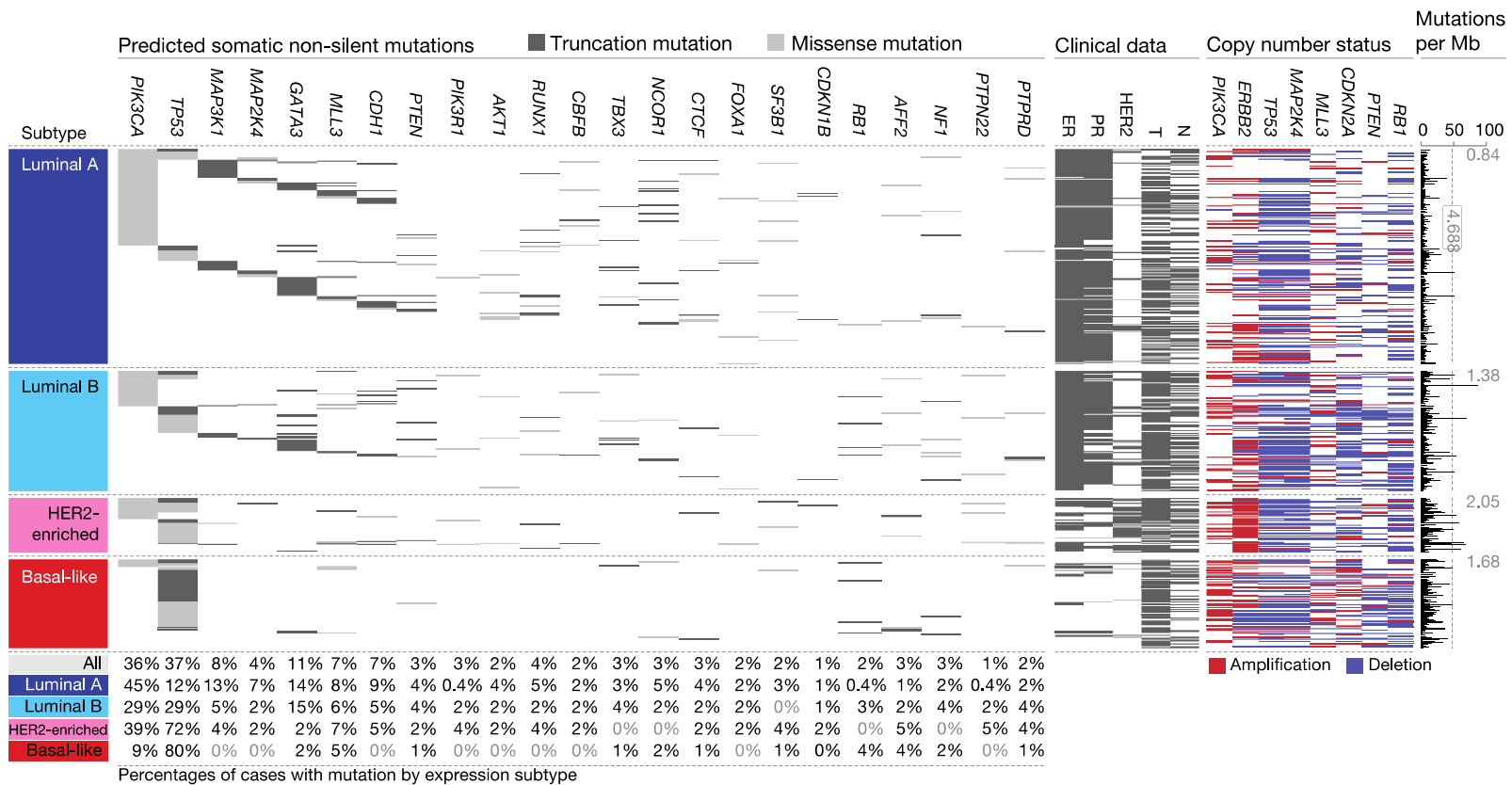
Soonmyung Paik, MD

Division of Pathology, NSABP Foundation/NRG Oncology

Breast Center and Institute for Personalized Cancer Therapy, Yonsei Cancer Center

Yonsei Genome Center, Severance Biomedical Science Institute



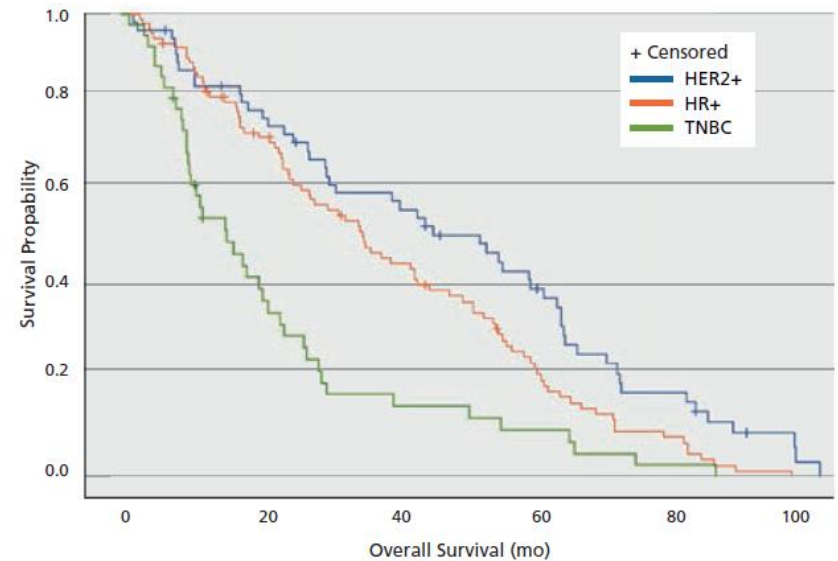
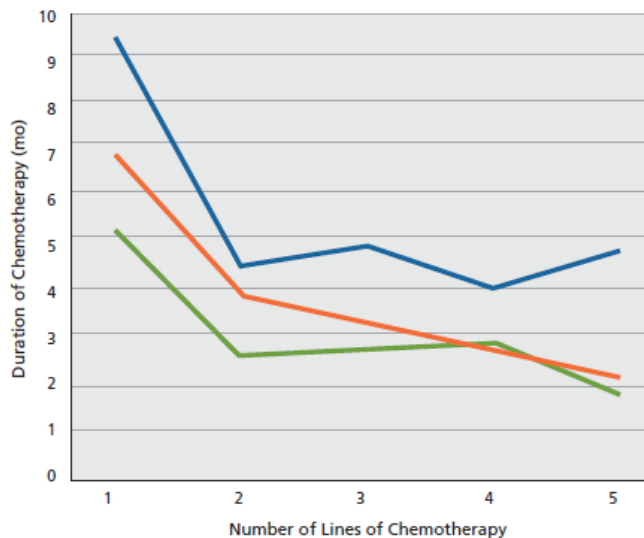
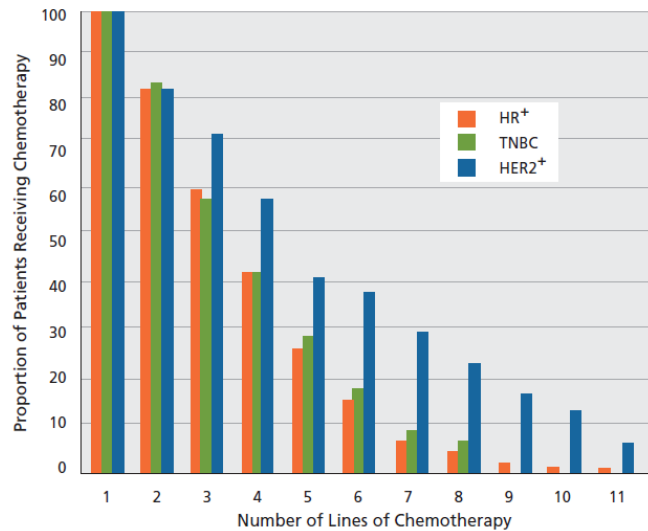


# **Intrinsic subtype change during progression**

**Should Rx based on subtyping of the metastatic site?**

# Duration of chemotherapy in metastatic pts according to subtype and line of therapy at Dana Farber Cancer Institute (N=199, between 2004 and 2007)

Seah D et al, J Natl Comprehensive Cancer Network 2014



## Can chemotherapy be safely delayed to later lines of Rx?

Meta-analysis of chemotherapy vs endocrine therapy for metastatic ER+ BC for mortality  
(Wilcken et al, Cochrane database)

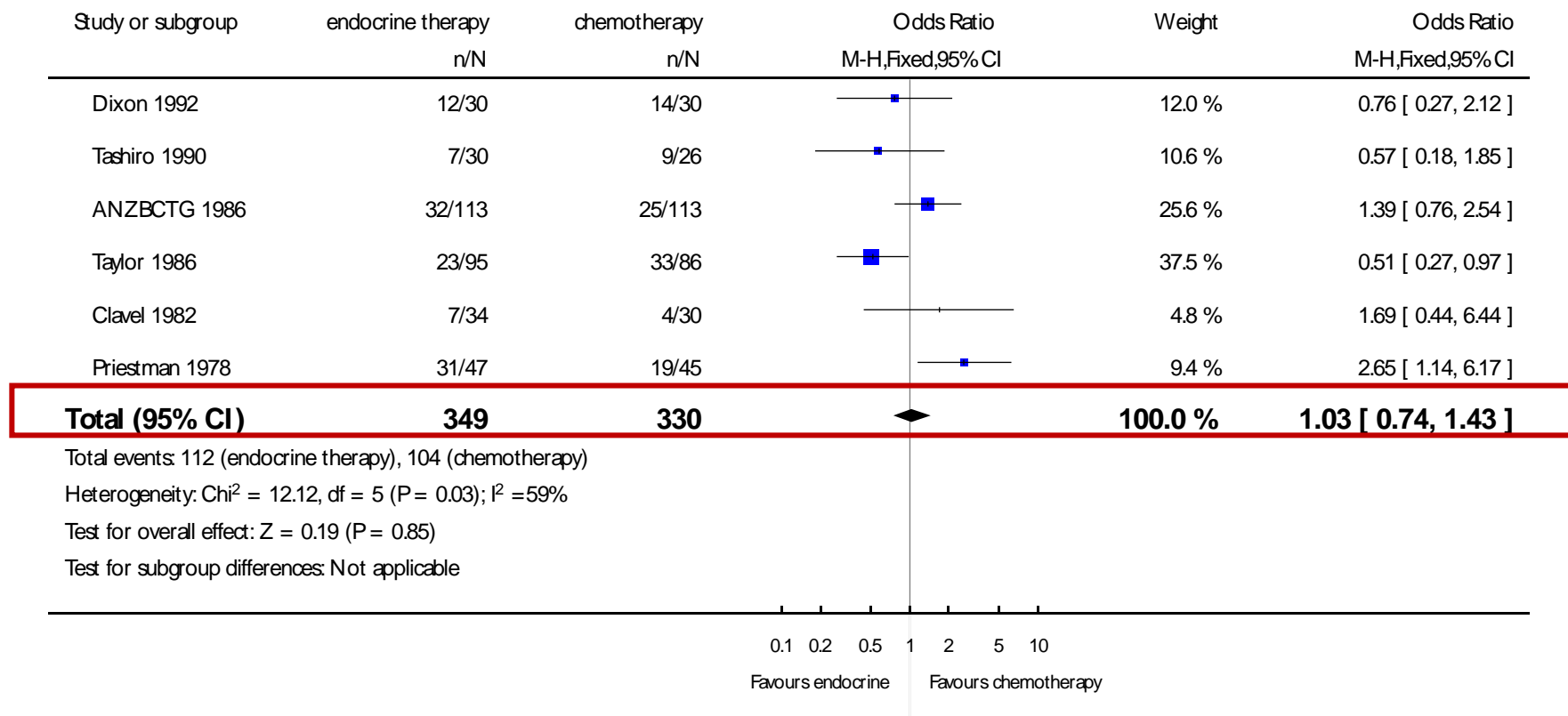


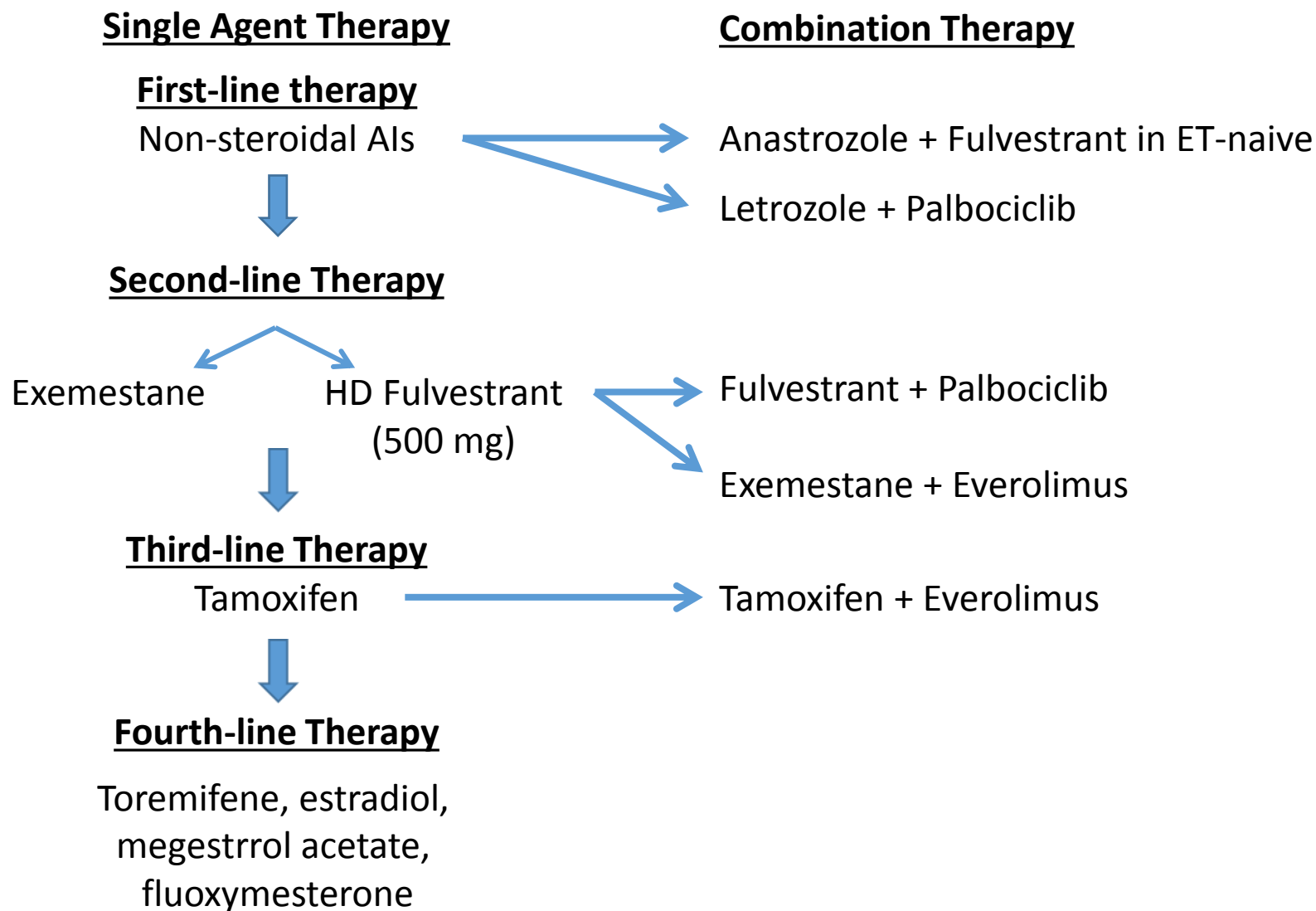
Table 1 | Criteria to support first-line choices in ER+, HER2– advanced disease<sup>13,44</sup>

Criteria	In favour of chemotherapy	Uncertain*	In favour of endocrine therapy
DFI <sup>‡</sup>	<1 year	1–2 years	>2 years
Visceral metastases	High burden, impending organ dysfunction (visceral crisis)	Moderate burden	Minimal burden or absent
Symptoms	Prominent	Moderate	Minimal or asymptomatic

\* The 'uncertain' column represents a grey area where either treatment might be justifiable, and tailoring to patient expectations would be of particular benefit. <sup>‡</sup>DFI accounts for disease tempo (rapidity of progression), as well as type of resistance; visceral metastases and symptoms relate to disease tempo and the rapidity of the response required. Abbreviations: DFI, disease-free interval; ER+, oestrogen receptor positive; HER2–, HER2 negative.

# Sequencing of endocrine therapy for 2016

(Courtesy of Dr. Maura Dickler, MSKCC)





# Prospective evaluation of the conversion rate in the receptor status between primary breast cancer and metastasis: results from the GEICAM 2009-03 ConvertHER study

Eduardo Martínez de Dueñas · Ana Lluch Hernández · Ángel Guerrero Zotano · Ramón María Pérez Carrión · José Ignacio Chacón López-Muñiz · Silvia Antolín Novoa · Ángela López Rodríguez · José Alejandro Pérez Fidalgo · Jaime Ferrer Lozano · Octavio Burgués Gasión · Eva Carrasco Carrascal · Andrés Hernando Capilla · Isabel Blancas López-Barajas · Montserrat Muñoz Mateu · María Helena López de Ceballos Reyna · Amparo Oltra Ferrando · Noelia Martínez Jañez · Vicente Carañana Ballerini · Antonio Antón Torres · Gustavo Catalán · José Ángel García Sáenz · Salomón Menjón · Ana María González-Angulo

Breast Cancer Res Treat 143:507-515, 2014

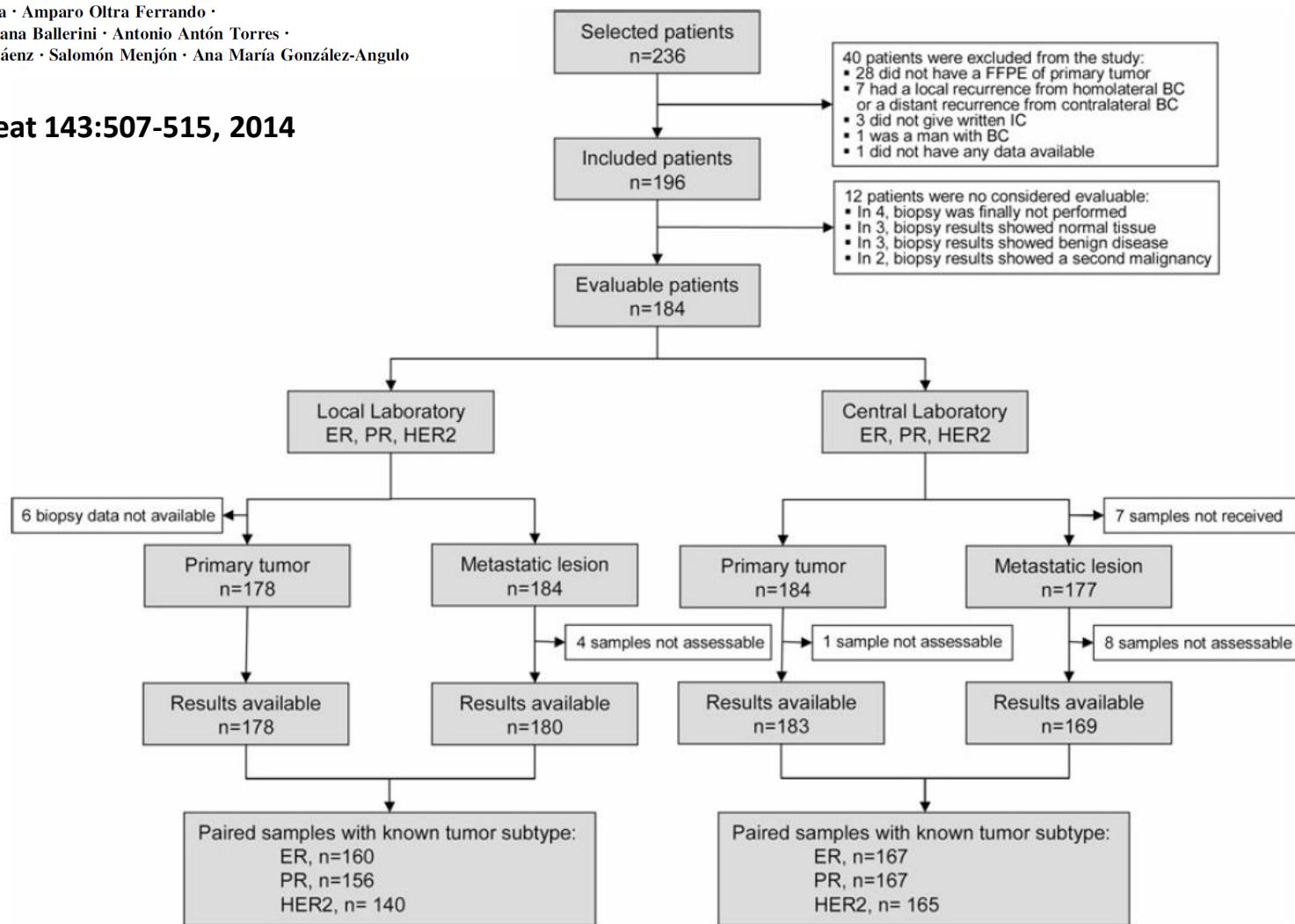


Fig. 1 CONSORT diagram of the ConvertHER study

# Prospective evaluation of the conversion rate in the receptor status between primary breast cancer and metastasis: results from the GEICAM 2009-03 ConvertHER study

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Primary tumor	Metastatic lesion					
	HR positive/HER2 negative <i>n</i> = 69		HER2 amplified <i>n</i> = 43		Triple negative <i>n</i> = 27	
	<i>n</i>	%	<i>n</i>	%	<i>n</i>	%
At local laboratory, <i>n</i> = 139						
HR positive/HER2 negative, <i>n</i> = 74	55	74	12	16	7	10
HER2 amplified, <i>n</i> = 38	8	21	29	76	1	3
Triple negative, <i>n</i> = 27	6	22	2	7	19	71
	HR positive/HER2 negative <i>n</i> = 108		HER2 amplified <i>n</i> = 36		Triple negative <i>n</i> = 21	
	<i>n</i>	%	<i>n</i>	%	<i>n</i>	%
	<i>n</i>	%	<i>n</i>	%	<i>n</i>	%
At central laboratory, <i>n</i> = 165						
HR positive/HER2 negative, <i>n</i> = 117	105	90	4	3	8	7
HER2 amplified, <i>n</i> = 31	0	0	31	100	0	0
Triple negative, <i>n</i> = 17	3	18	1	6	13	76

Of 54 pts with discordance, treatment was modified in 24 (46%)

# Intrinsic subtype and gene expression changes between primary and metastatic breast cancer

Alex Prat<sup>1,2</sup>, Eduardo Martínez de Dueñas<sup>3</sup>, Patricia Galván<sup>1</sup>, Susana Garcia<sup>4</sup>, Octavio Burgués<sup>4</sup>, Laia Paré<sup>2</sup>, Silvia Antolin<sup>5</sup>, Rossella Martinello<sup>6</sup>, Isabel Blancas<sup>6</sup>, Barbara Adamo<sup>7</sup>, Ángel Guerrero<sup>7</sup>, Montserrat Muñoz<sup>7</sup>, Paolo Nuciforo<sup>7</sup>, Maria Vidal<sup>7</sup>, Ramón M Pérez<sup>8</sup>, José I Chacón<sup>8</sup>, Rosalia Caballero<sup>10</sup>, Pere Gascón<sup>9</sup>, Eva Carrasco<sup>10</sup>, Federico Rojo<sup>11</sup>, Charles M Perou<sup>12</sup>, Javier Cortés<sup>1</sup>, Vincenzo Adamo<sup>13</sup>, Joan Albanell<sup>14</sup> and Ana Lluch<sup>1</sup>

<sup>1</sup> Vall d'Hebron Institute of Oncology (VHIO), Barcelona, Barcelona, Spain, 08035; <sup>2</sup> Hospital Clínic IDIBAPS, Barcelona, Barcelona, Spain, 08036; <sup>3</sup> Hospital Provincial de Castellón, Castellón, Spain, 12005; <sup>4</sup> Hospital Clínico Universitario de Valencia, Valencia, Spain, 46100; <sup>5</sup> Complejo Hospitalario Universitario A Coruña, A Coruña, Spain, 15006; <sup>6</sup> Hospital Clínico San Cecilio de Granada, Granada, Spain, 18012; <sup>7</sup> Instituto Valenciano de Oncología, Valencia, Spain, 46100; <sup>8</sup> Hospital Universitario Quirón de Madrid, Madrid, Spain, 28022; <sup>9</sup> Hospital Virgen de la Salud, Toledo, Spain, 45004; <sup>10</sup> GEICAM, Spanish Breast Cancer Group, Madrid, Spain, 28070; <sup>11</sup> Fundación Jiménez Díaz, Madrid, Spain, 28040; <sup>12</sup> University of North Carolina, Chapel Hill, NC, United States, 27519; <sup>13</sup> University of Messina, Messina, Italy and <sup>14</sup> Hospital del Mar, Barcelona, Spain, 08003



Prat et al, SABCS 2015

	Metastasis				
Primary	Basal	HER2E	LumA	LumB	Genes diff expressed
Basal	12 (100%)	0	0	0	0
HER2E	2 (15.4%)	10 (76.9%)	1 (7.7%)	0	7
LumA	0	7 (14.9%)	21 (44.7%)	19 (40.4%)	24
LumB	0	4 (13.3%)	5 (16.7%)	21 (70%)	8

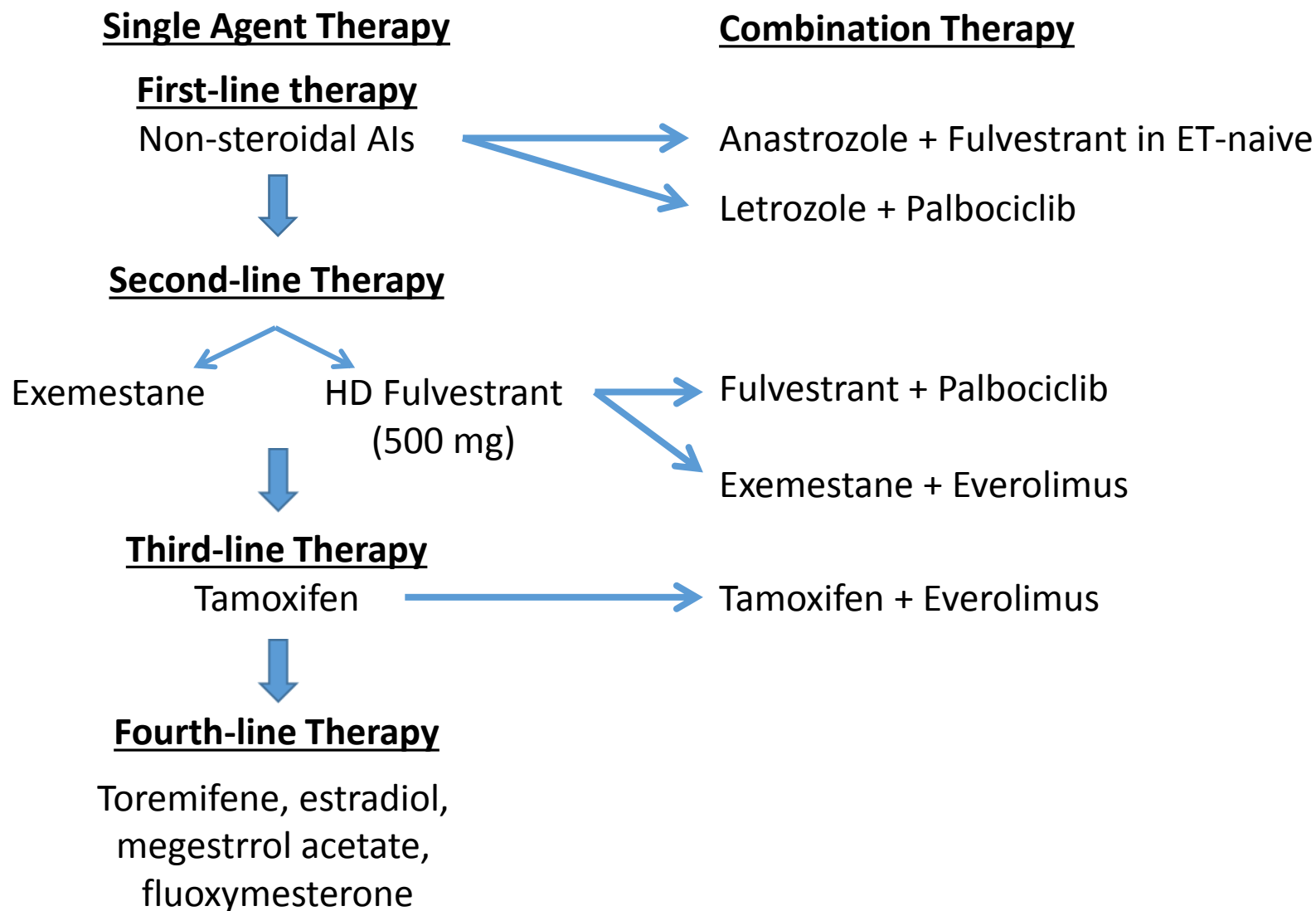
# Clinical implication of subtype switching?

- The ESMO ABC2 consensus guidelines recommend using targeted therapy if there has ever been receptor positivity
- No evidence yet for better OS when Rx changed by metastatic biopsy
  - But if we use intrinsic subtype for adjuvant chemo decision, why not in metastatic setting to decide chemo?
- Biopsy of originally TNBC is justified

**Can we use genome sequencing of metastatic ER+ BC  
to guide endocrine (+ targeted) therapy?**

# Sequencing of endocrine therapy for 2016

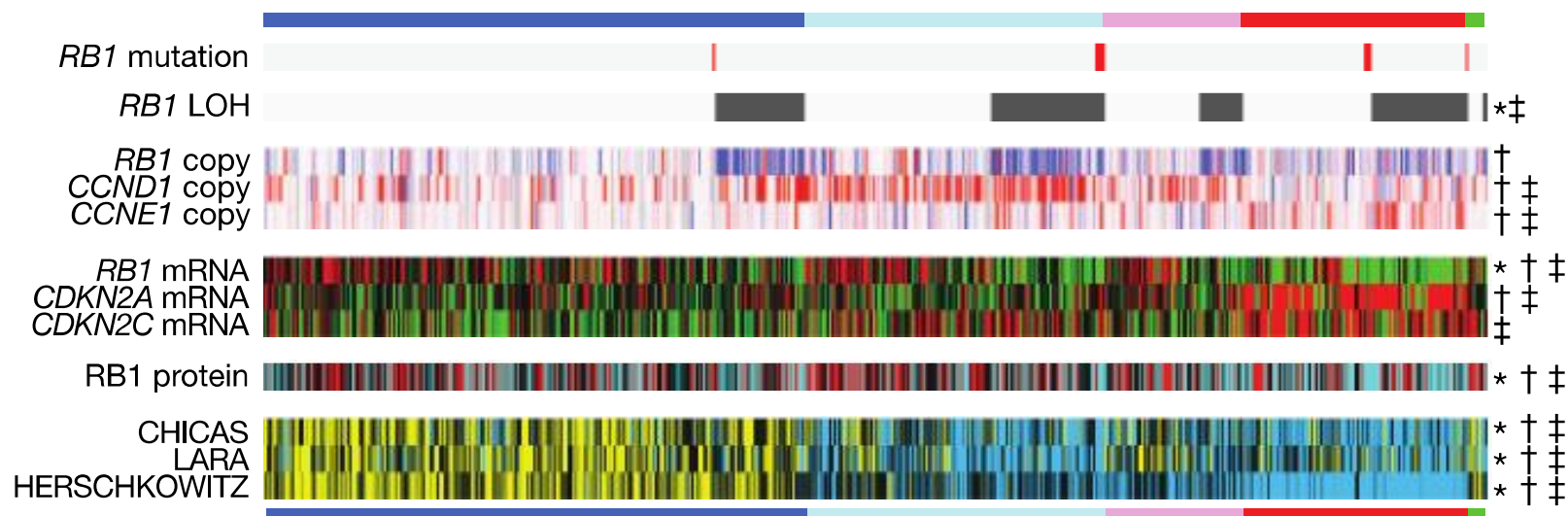
(Courtesy of Dr. Maura Dickler, MSKCC)



# RB is intact in most of ER+ tumors

(TCGA, Nature 2012)

RB pathway (506 tumours with mRNA/mutation data)



\* Differences by RB1 mutation ( $P < 0.003$ )

† Differences by RB1 LOH ( $P < 0.005$ )

‡ Differences by luminal A subtype vs others ( $P < 0.0001$ )

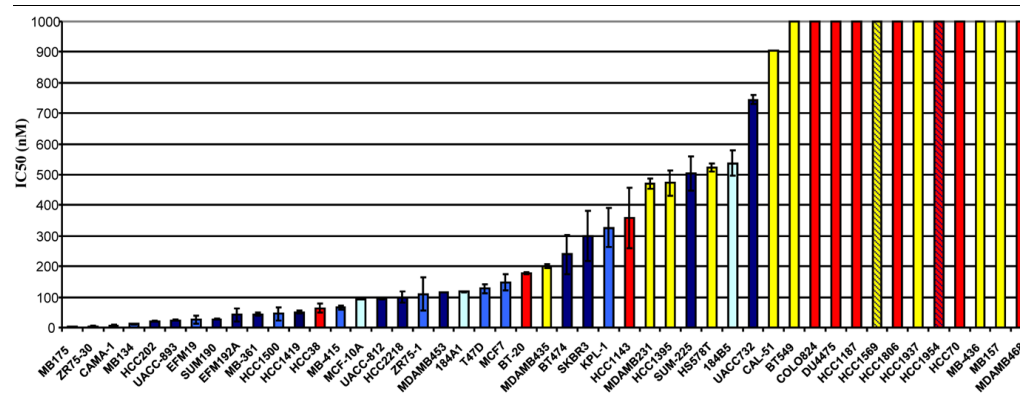
Copy change      mRNA expression      Protein expression      Gene signature activity

Loss ■ ■ ■ ■ Gain Low ■ ■ ■ ■ ■ High Low ■ ■ ■ ■ ■ ■ High Less ■ ■ ■ ■ ■ More

mRNA subtype: Luminal A ■ Luminal B ■ HER2-enriched ■ Basal-like ■ Normal-like ■

# Palbociclib (CDK4/6 inhibitor) inhibits growth of ER+ breast cancer (Fin RS et al, Breast Cancer Res, 2009 and SABCS abstract, 2012)

Figure 1



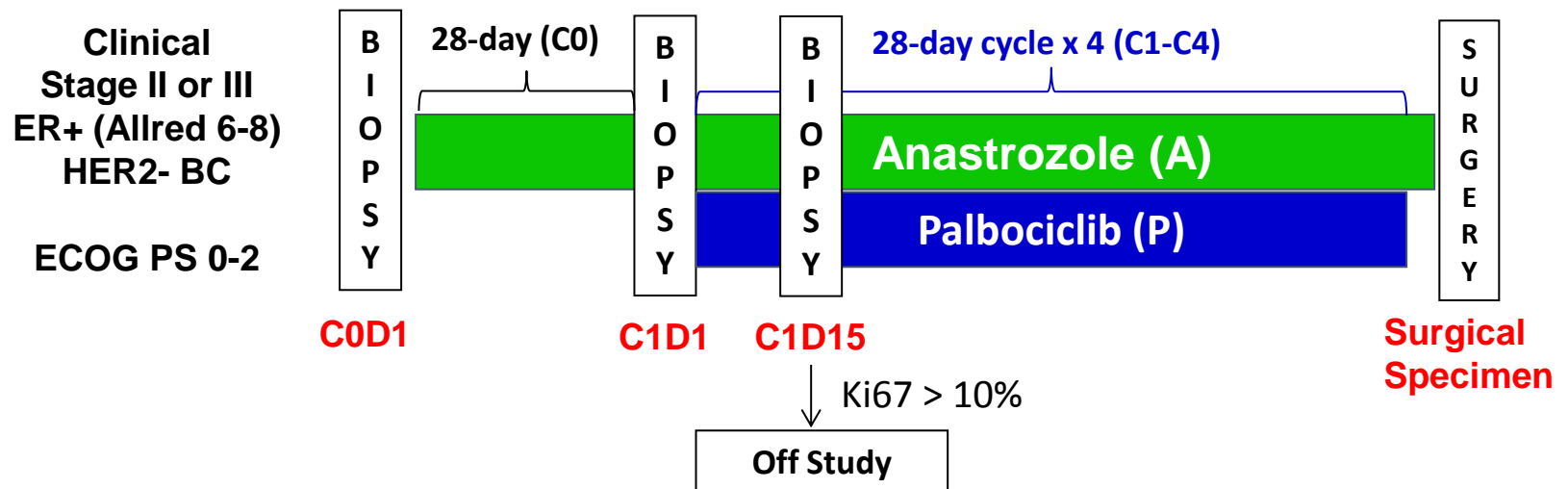


# Intrinsic subtypes as a predictor of response to Palbociclib?

- Phase 2 neoadjuvant trial - Cynthia Ma et al, SABCS 2015)

## Single Arm Phase II

## Schema

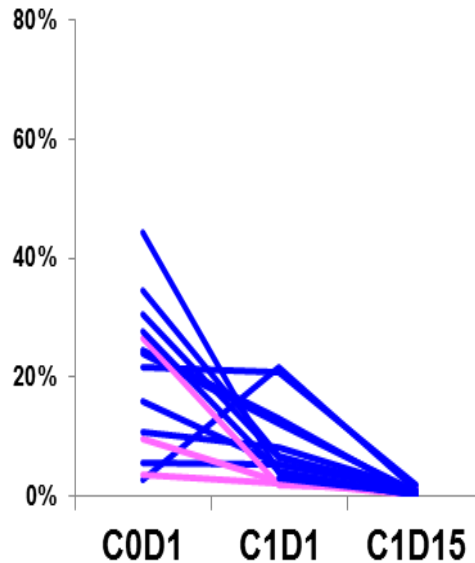
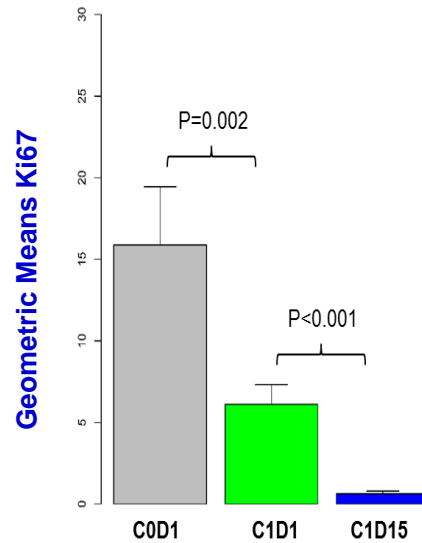


# Ki67 Response by *PIK3CA* Status

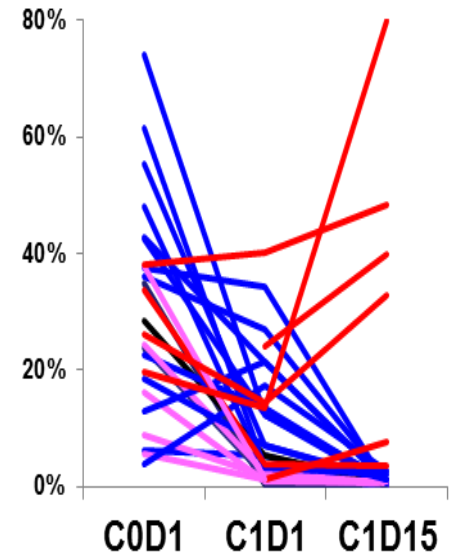
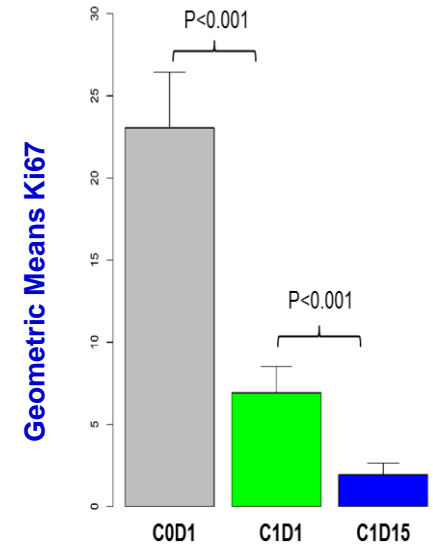


- H1047L/R
- E545K or E542K or Q546K
- C420R
- Insufficient tumor

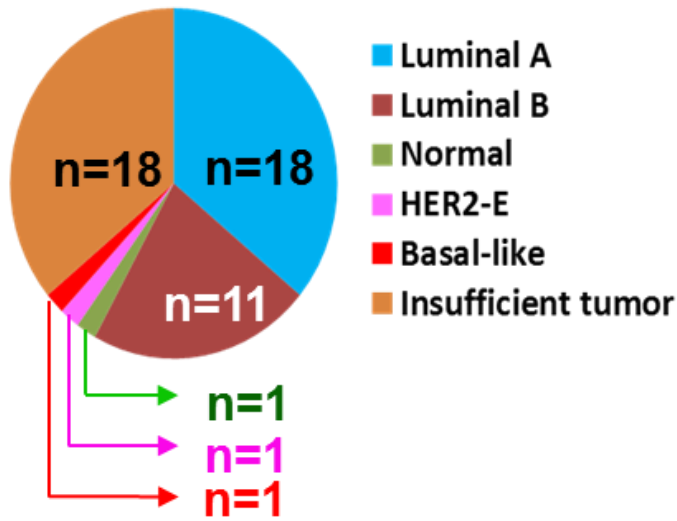
***PIK3CA* Mut. (n=15)**



***PIK3CA* WT (n=28)**

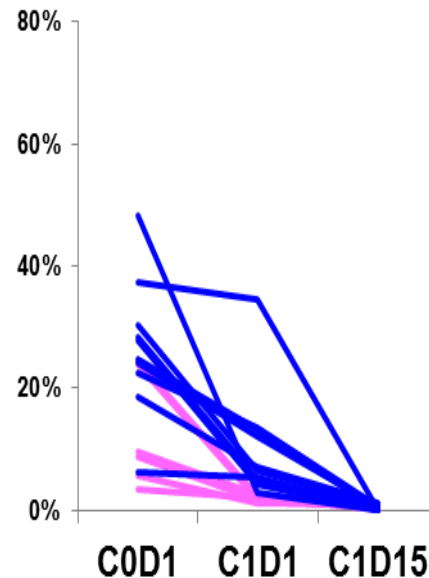
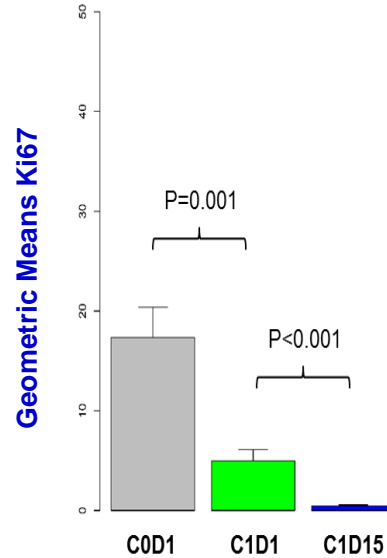


# Ki67 Response by Intrinsic Subtype

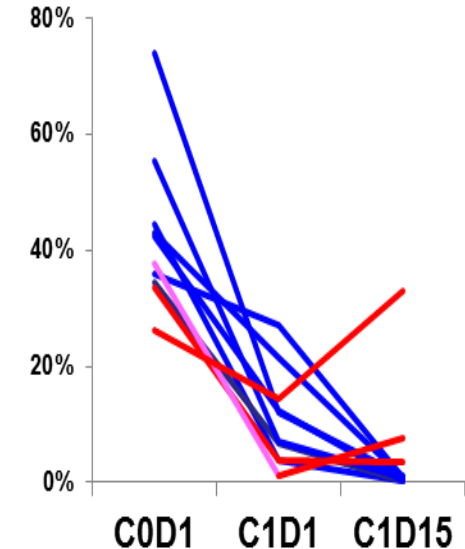
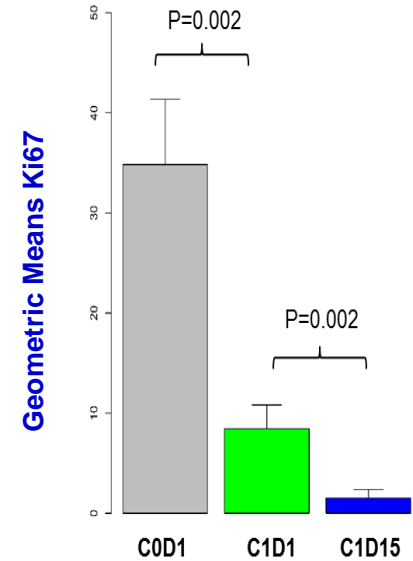


Agilent 4x44K array  
platform and Research Use  
Only PAM50 algorithm

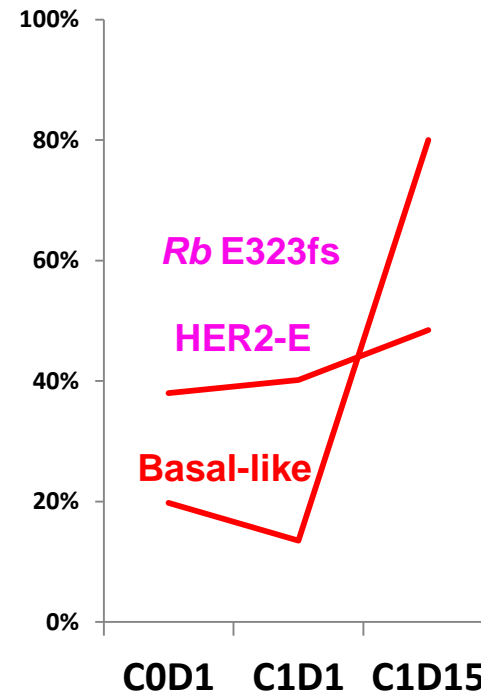
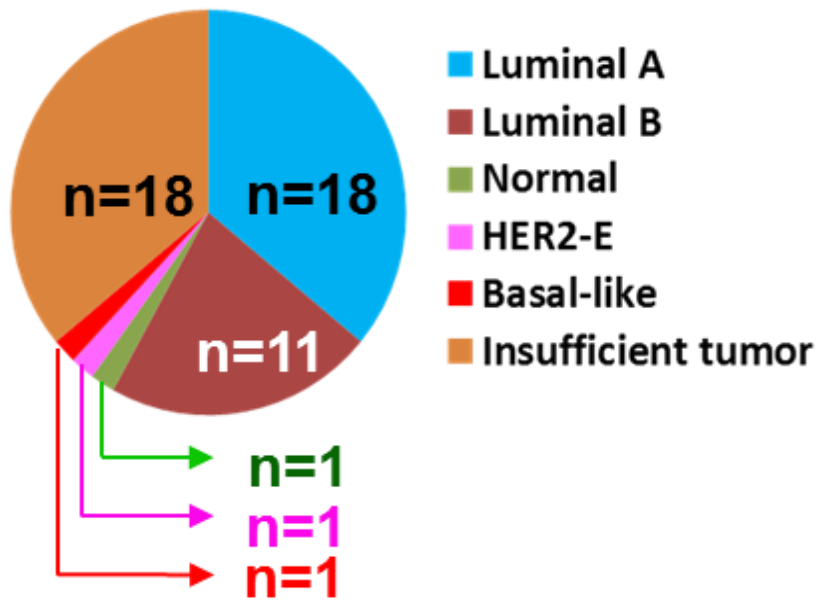
## Luminal A (n=18)



## Luminal B (n=11)



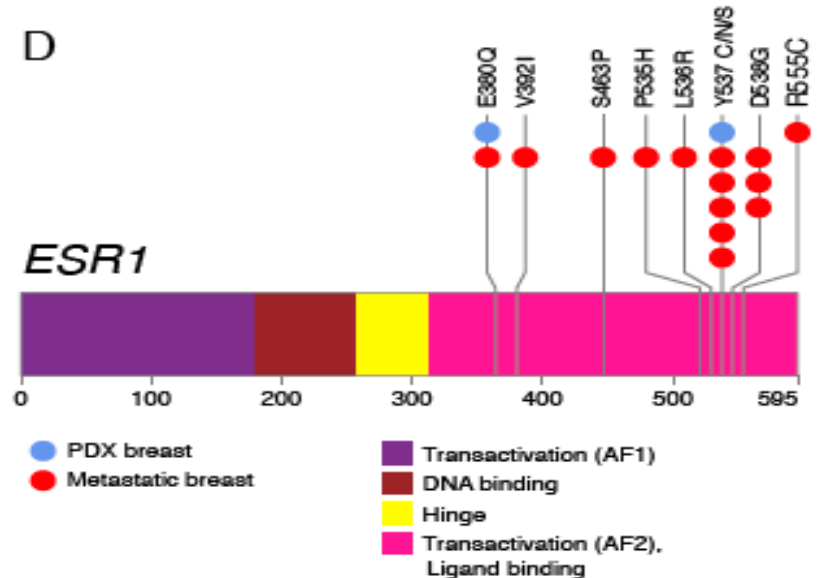
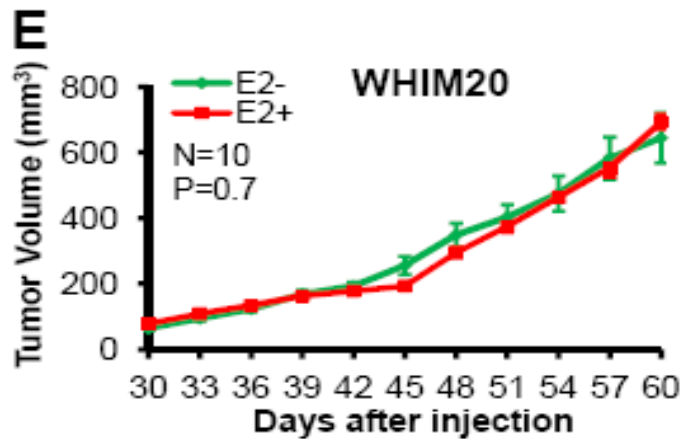
## Ki67 Response in Non-luminal BC



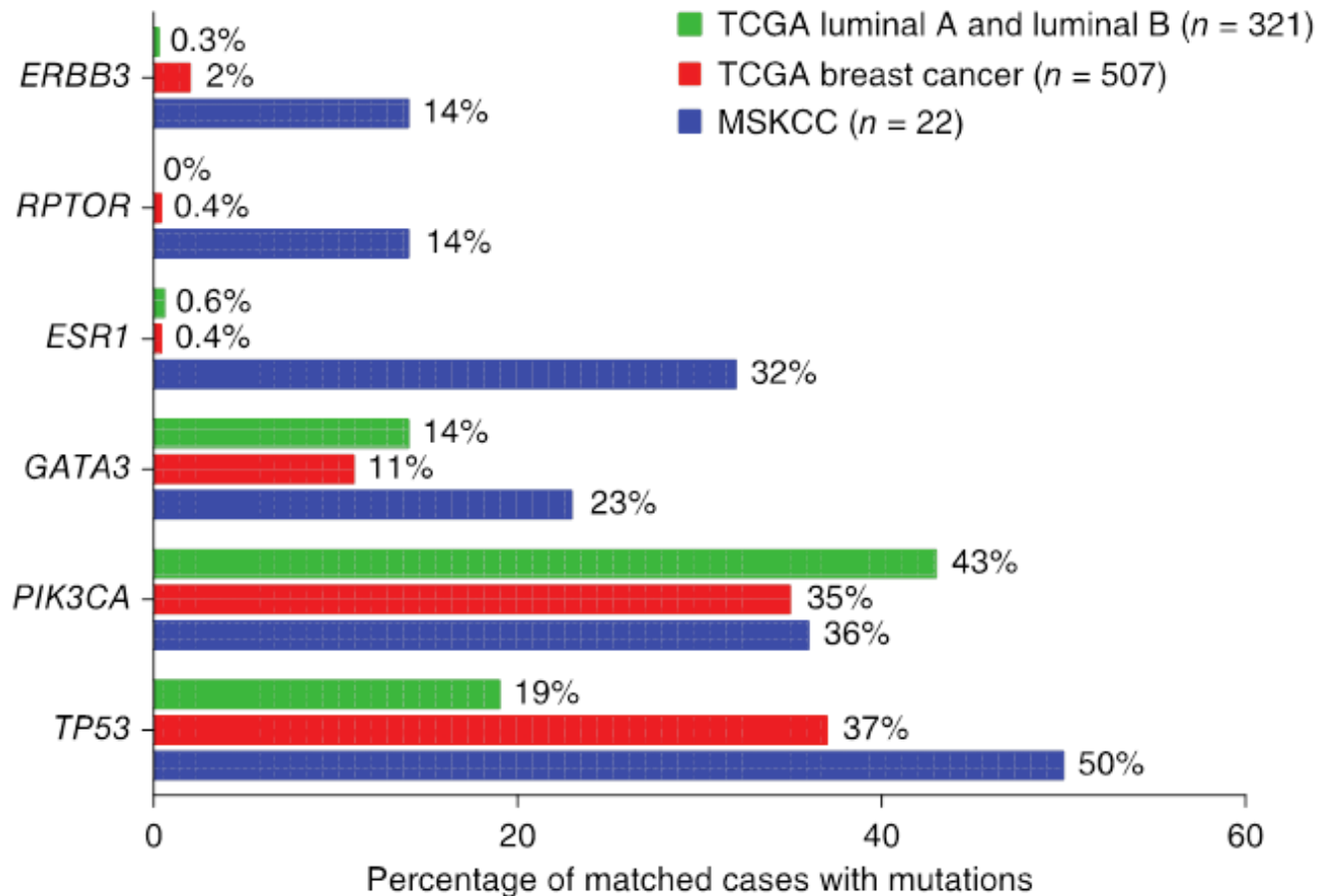
# ESR1 mutation as a mechanism of acquired resistance of ER positive tumors to estrogen deprivation therapy

- Li et al, Cell Reports 2013
- Toy et al, Nature Genetics 2013
- Robinson et al, Nature Genetics 2013

## Mutations in the ligand binding domain of ESR1 are an under-recognized cause of endocrine therapy resistance



## ESR1 mutation is rare in primary breast cancer but frequently found in metastatic breast cancer



# Emergence of Constitutively Active Estrogen Receptor- $\alpha$ Mutations in Pretreated Advanced Estrogen Receptor Positive Breast Cancer

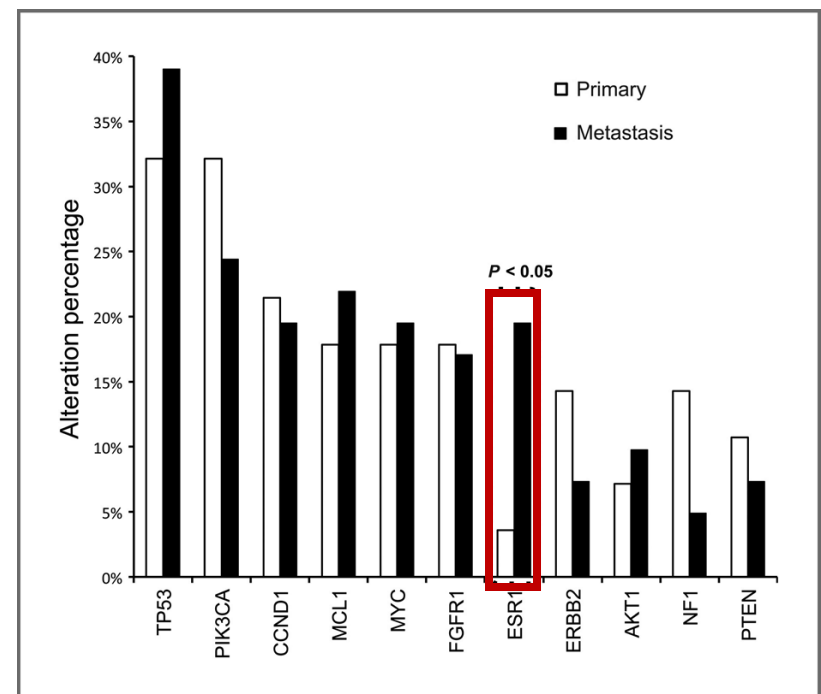
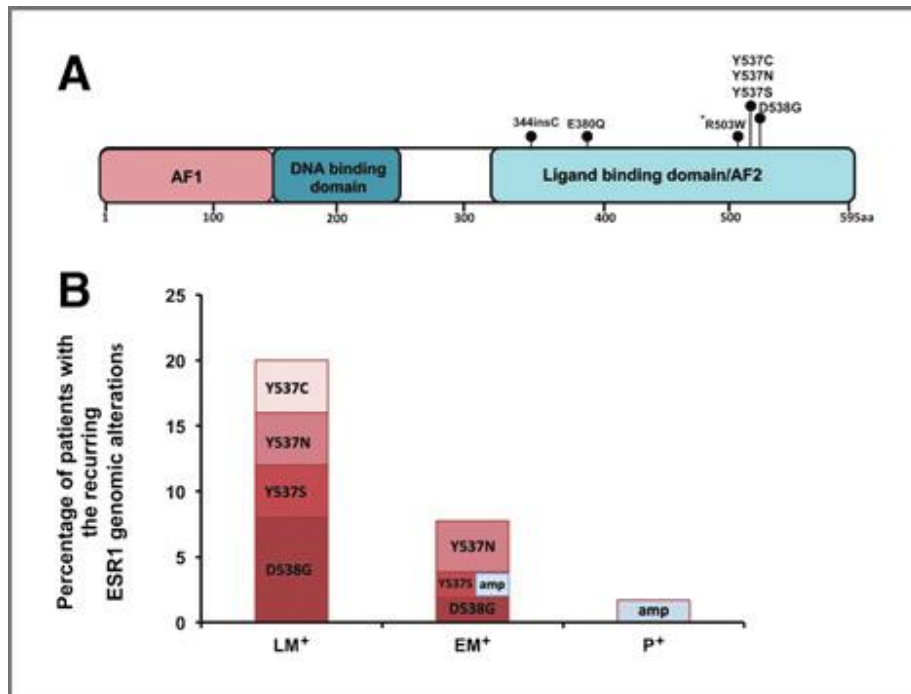
Jeselson et al, Clin Cancer Res 20(7):1757-67, 2014

**Table 1.** Patient cohorts

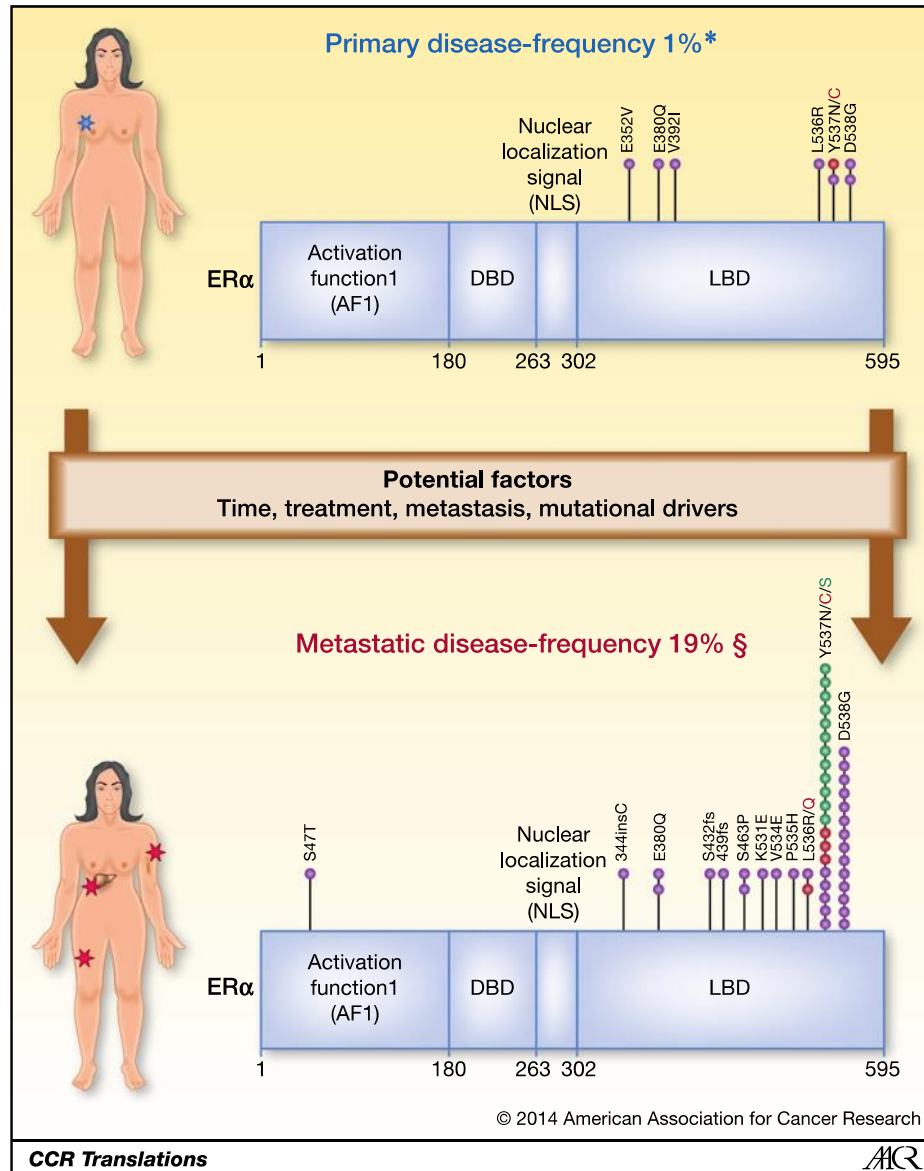
Patient cohort	No. of specimens	Average number of treatments <sup>a</sup> before biopsy
LM <sup>+</sup> Metastases from patients with advanced ER <sup>+</sup> disease that were heavily pretreated before biopsy (participants in "Personalized Treatment Selection for Metastatic Breast Cancer" trial NCT00780676)	25	7
EM <sup>+</sup> Metastases from patients with early metastatic ER <sup>+</sup> disease	51	1–2
P <sup>+</sup> Primary ER <sup>+</sup> tumors	58	NA
M <sup>-</sup> Metastases from patients with ER <sup>-</sup> disease	11	NA
P <sup>-</sup> Primary ER <sup>-</sup> primary breast cancer disease	104	NA

Abbreviations: EM<sup>+</sup>, early metastatic ER<sup>+</sup> disease; LM<sup>+</sup>, late metastatic ER<sup>+</sup> breast cancer; M<sup>-</sup>, ER<sup>-</sup> metastatic disease; P<sup>+</sup>, ER<sup>+</sup> primary breast cancer; and P<sup>-</sup>, ER<sup>-</sup> primary breast cancer.

<sup>a</sup>Including endocrine treatments and chemotherapy regimens.







## If ESR1 sequencing, what to sequence and with which method?

- Primary index tumor
- Biopsy of metastatic site
- Liquid biopsy

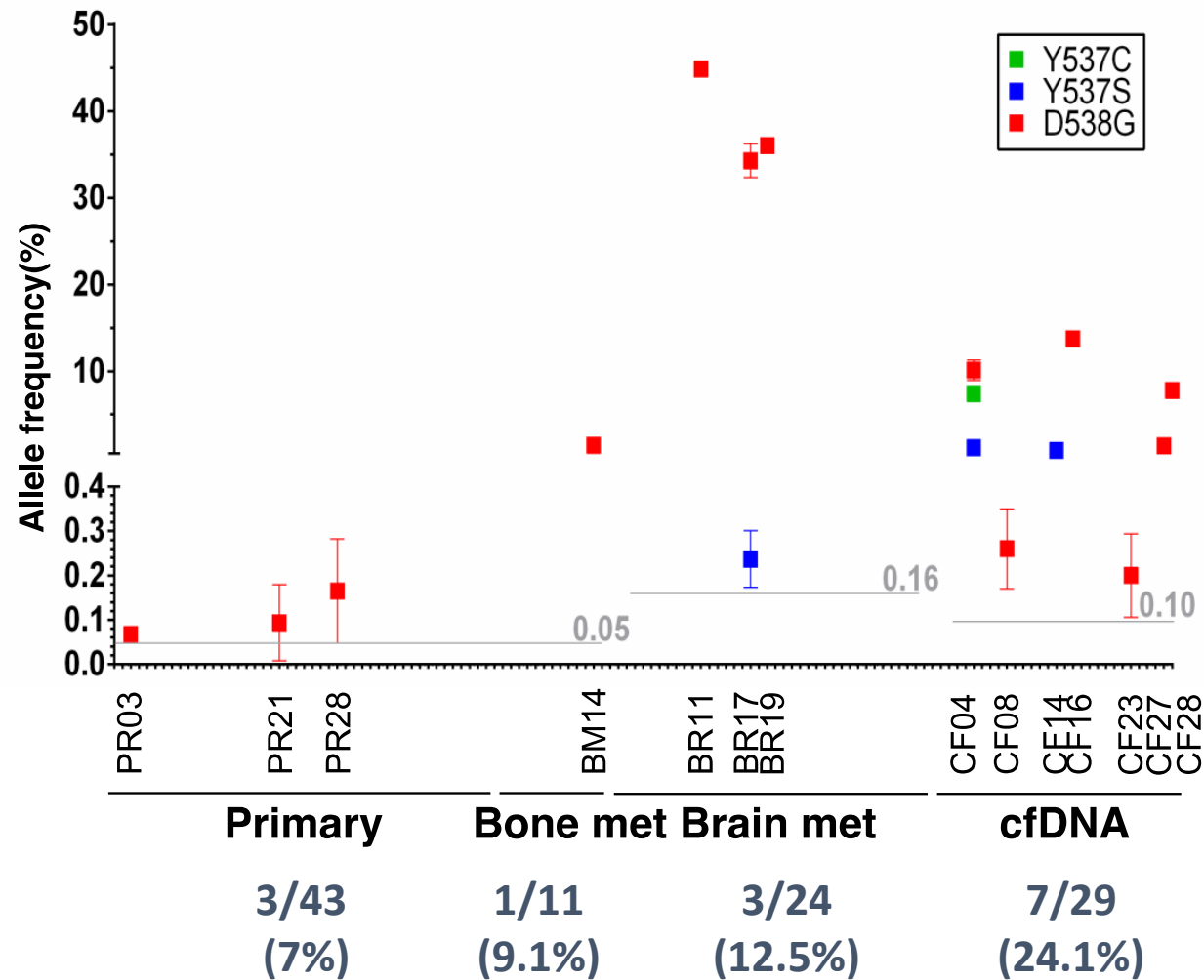
# ESR1 allele frequency is usually below the detection limit of usual NGS

Austin et al, SABCS poster

patient	cf DNA date	mutations: gene	mutation (AA)	percent mutant allele	lines of therapy	lines of ET	bone vs visceral metastases	ET duration
1	2/10/2015	ESR1	L536R	17.24%	5	3	both	7
		ESR1	D538G	7.74%				
	3/31/2015	NF1	D1237V	0.16%				
	6/2/2015	AR	E323K	0.10%				
		NF1	D1237V	0.10%				
	7/20/2015	ND						
	9/29/2015	ND						
2	9/9/2014	ND			3	2	bone	3
	11/4/2014	ND						
	2/10/2015	ESR1	D538G	0.28%				
3	2/4/2015	ESR1	D538G	0.44%	6	3	both	6
		ESR1	Y537N	4.52%				
		ESR1	C530Y	0.83%				
		ESR1	Y537S	23.76%				
4	2/4/2015	ESR1	Y537N	12.53%	9	3	both	5.5
		ESR1	D538G	3.76%				
5	2/11/2015	ESR1	Y537S	0.94%	6	4	bone	4
		ESR1	D538G	0.40%				
6	2/24/2015	ESR1	Y537S	2.73%	6	2	both	2
7	5/22/2015	ESR1	D538G	0.72%	10	4	both	3
	3/9/2015	ESR1	D538G	1.13%				
8	3/13/2015	ESR1	Y537C	0.38%	3	3	both	3.5
9	3/27/2015	ESR1	Y537S	1.06%	5	4	bone	4.5

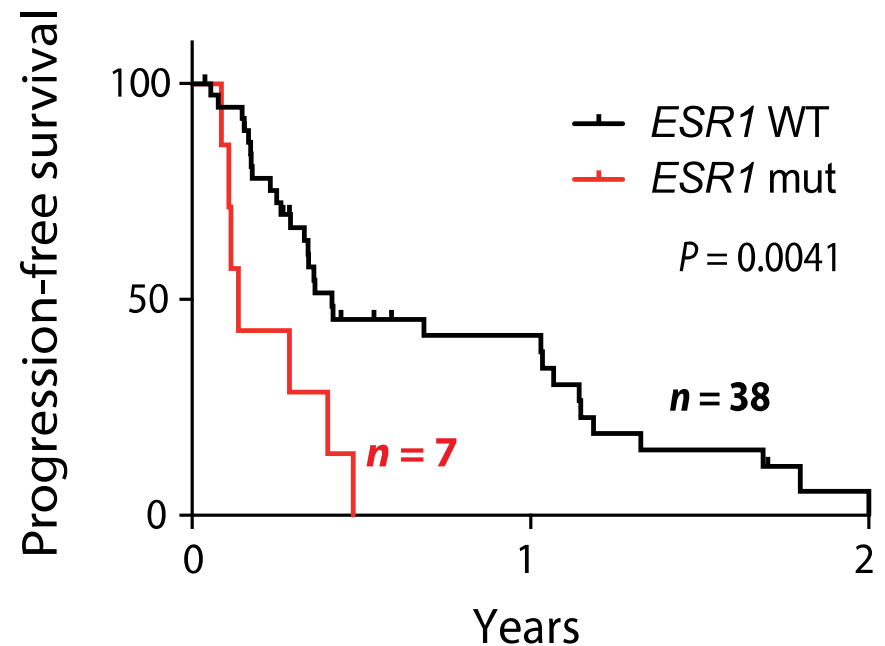
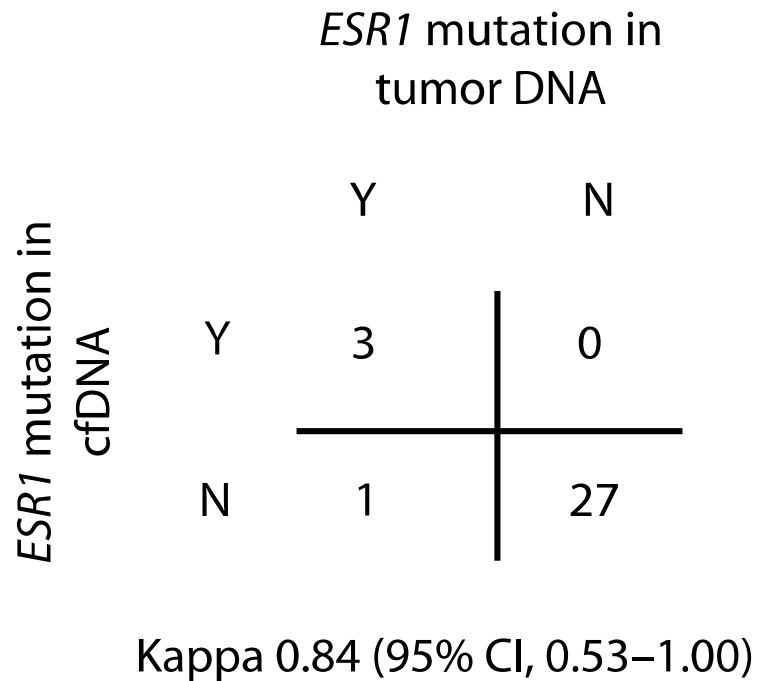
# In brain mets, ESR1 mutant clones are dominant

Wang P et al, CCR 2015



# Analysis of ESR1 mutation in circulating tumor DNA demonstrates evolution during therapy for metastatic breast cancer

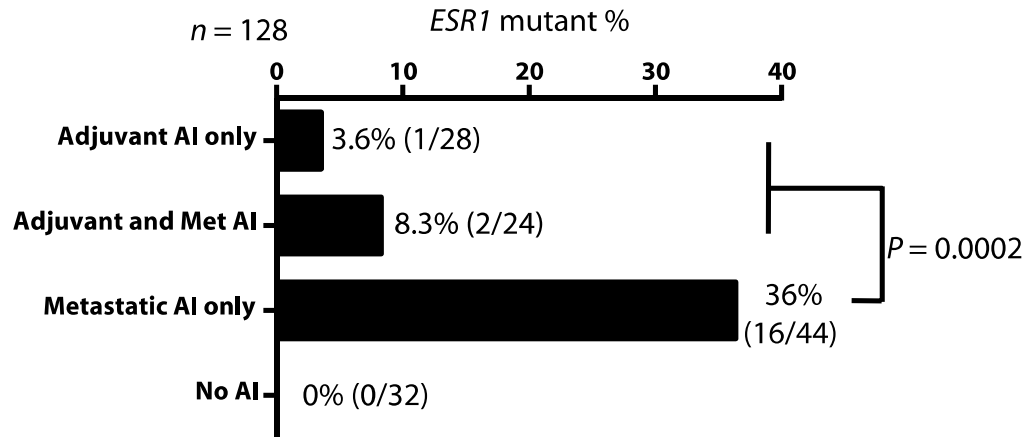
Schiavon et al, Science Trans Med 2015



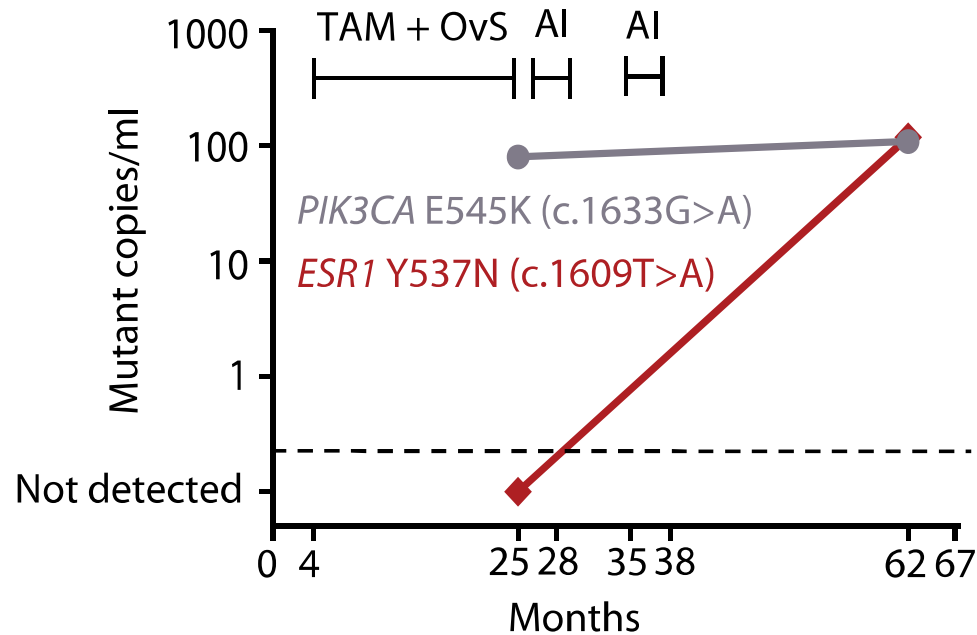
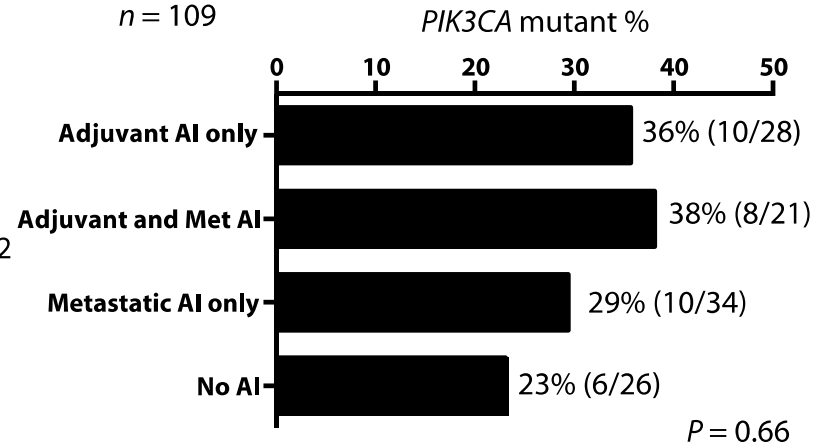
# ESR1 mutation emerged when metastatic disease is treated with AI

Schiavon et al, Science Trans Med 2015

**A**

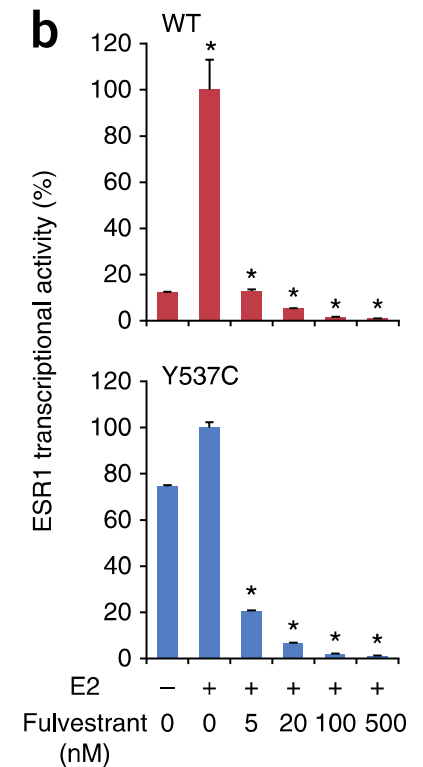
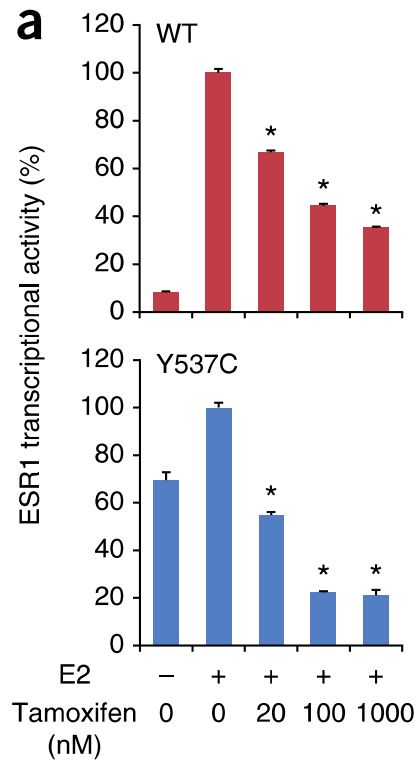
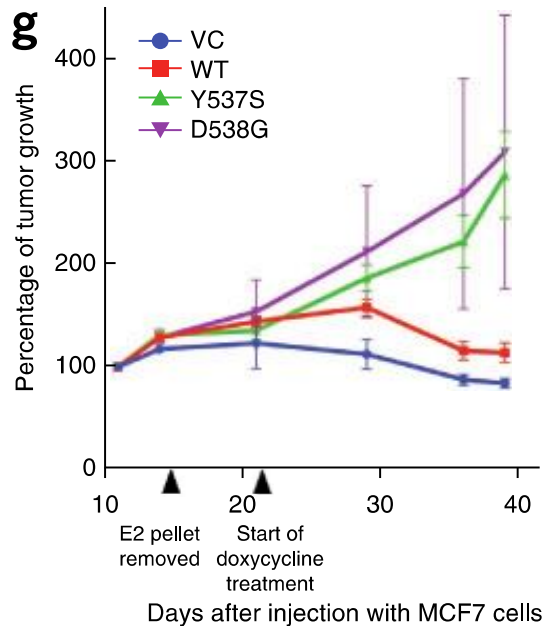


**B**



## **Therapeutic implication of ESR1 mutation**

# ESR1 mutants are resistant to estrogen deprivation but may be sensitive to high dose fulvestrant





# BOLERO-2 ctDNA analysis

Chandarlapaty et al, SABCS S2-07

- 541 of 724 pts analyzed
- Found ESR1 hotspot mutations in 156 (28.8%)
- ESR1 mutation associated with shorter OS (20.7 m vs 32.1 m)

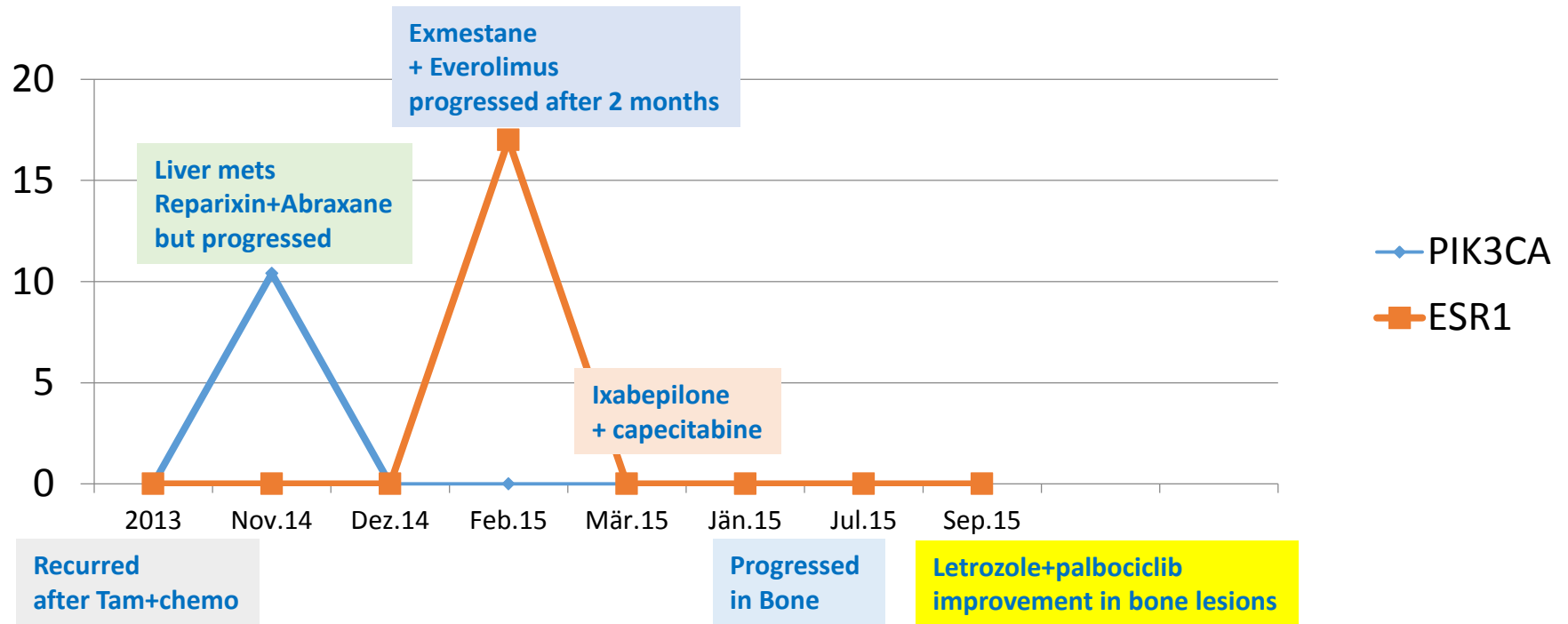
## DFS according to mutation and treatment regimen

	frequency	exemestane	everolimus plus exemestane
D538G	83 (15.3%)	2.7m	5.8m
Y537S	42 (7.8%)	4.1m	4.2m
D538G + Y537S	30 (5.5%)	2.78m	5.42m
All pts	541	3.2m	7.8m

## **Serial monitoring of ESR1 mutation in cfDNA**

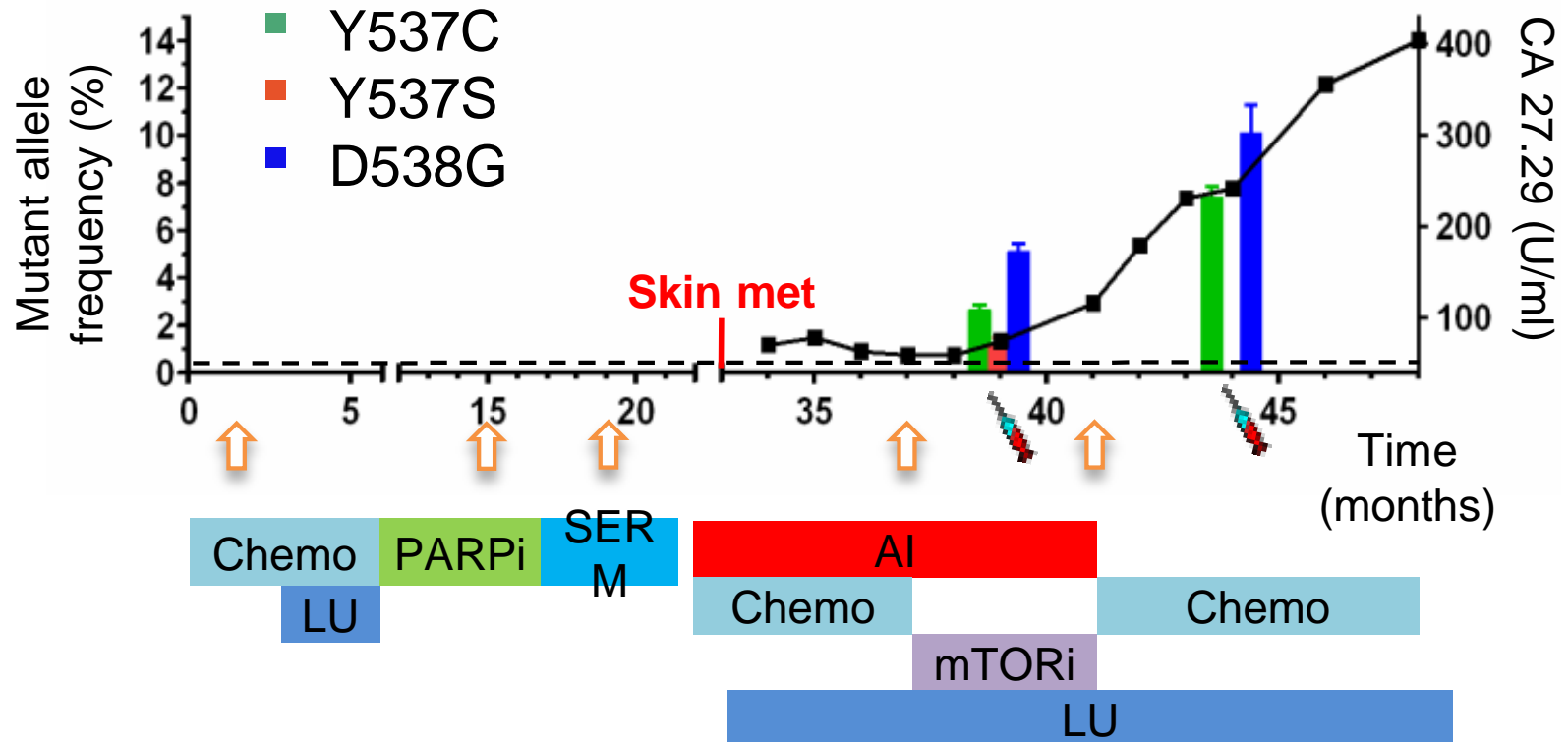
## ctDNA mutatiuon profiling (using Guardant360 Panel)

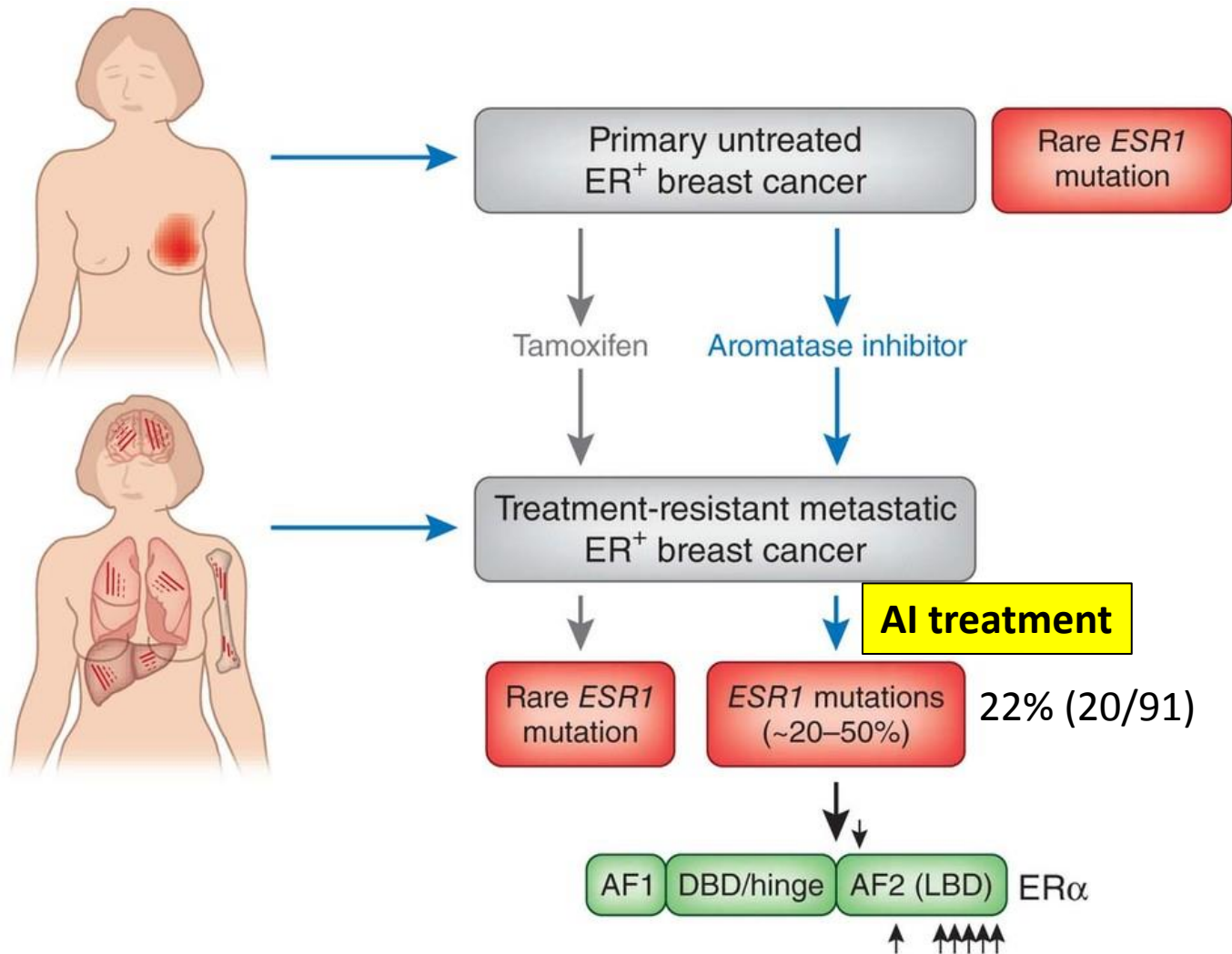
Austin et al, SABCS poster



# Rising ESR1 mutant allele frequency is associated with rise in CA27.29

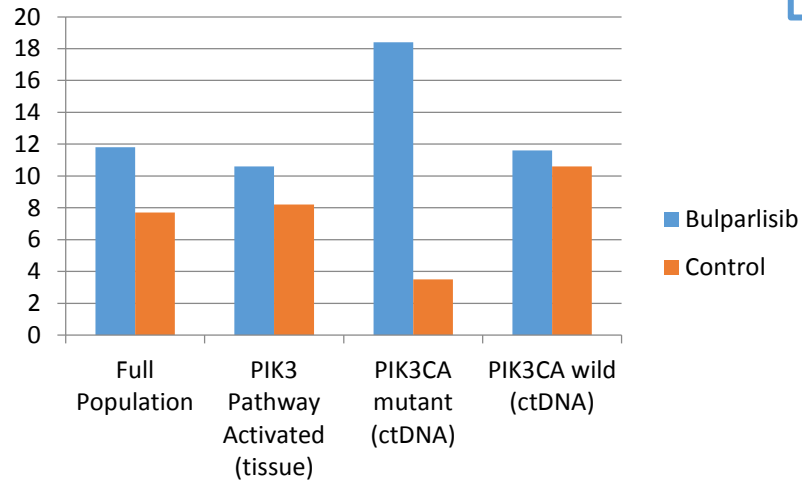
Wang P et al, CCR 2015





## **PIK3CA mutation as a predictive marker for PIK3CA inhibitors**

# PIK3CA inhibitor (Bulparlisib)



BELLE-2

AI failure  
(N=1147)

Fulvestrant 500mg + placebo

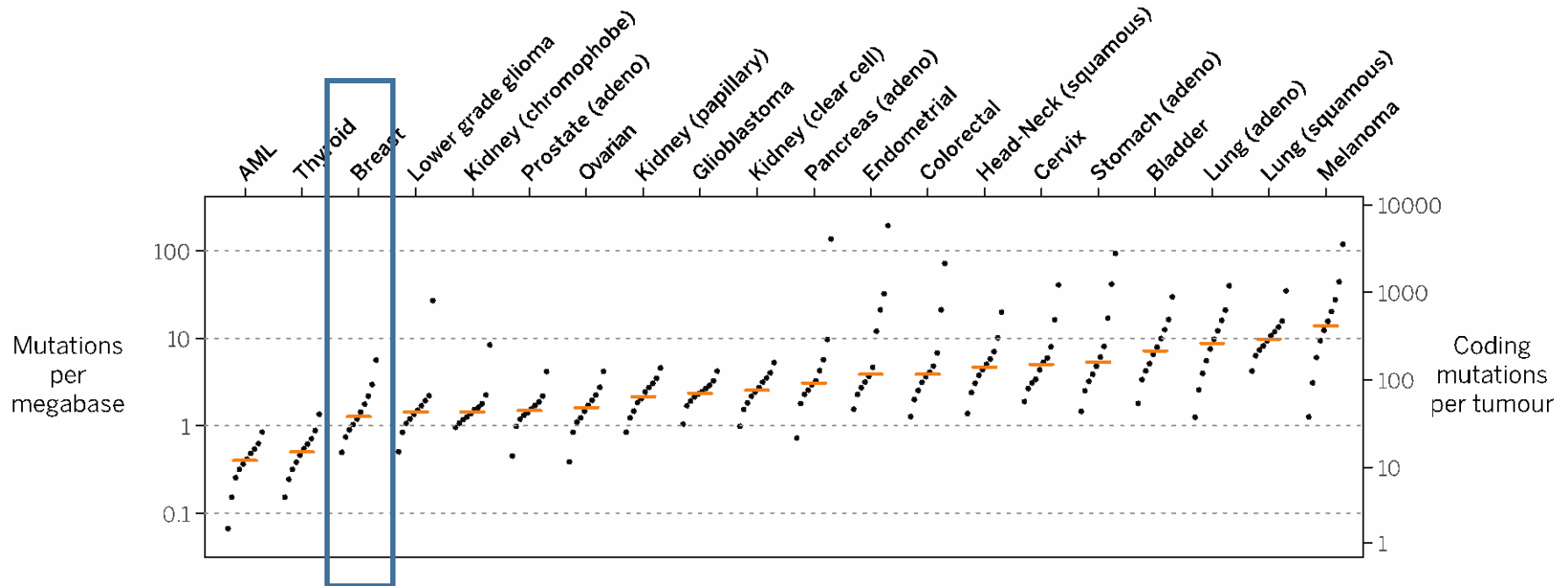
Fulvestrant 500mg + bulparlisib

Median PFS, Mos (95% CI)	Buparlisib + Fulvestrant	Placebo + Fulvestrant	HR (95% CI)	P Value
Overall population (n=1147)	6.9 (6.8-7.8)	5.0 (4.0-5.2)	0.78 (0.67-0.89)	< .001
PI3K-activated pts (n=372)	6.8 (4.9-7.1)	4.0 (3.1-5.2)	0.76 (0.60-0.97)	.014 <sup>†</sup>
ctDNA <i>PIK3CA</i> mutant (n = 200)	7.0 (5.0-10.0)	3.2 (2.0-5.1)	0.56 (0.39-0.80)	< .001
ctDNA <i>PIK3CA</i> non mutant (n = 387)	6.8 (4.7-8.5)	6.8 (4.7-8.6)	1.05 (0.82-1.34)	.642

**Is there a role for immune check point therapy  
for ER+ metastatic BC?**



# Overall mutation burden (TCGA)



But a subset of ER+ mets have higher mutation burden similar to TNBC

# Genome sequencing for ER+ metastatic BC

- Most of the KOL surveyed do not order sequencing for ER+ metastatic breast cancer in clinical practice
  - The ESMO ABC2 consensus guidelines recommend using targeted therapy if there has ever been receptor positivity
  - Sequencing based targeted approaches low yield
    - SAFIR01 – 43/423 pts received targeted Tx – 4 objective response
- Focused assays for ctDNA - potential utility as a predictive markers for
  - CDK4/6 inhibitors (Palbociclib)
  - SERDs
  - PIK3CA inhibitors
- Exome/RNAseq - potential utility as a predictive marker for
  - Immune Checkpoint therapy