

Supplemental Online Content

Bueno-Muiño C, Echavarría I, López-Tarruella S, et al. Assessment of a genomic assay in patients with *ERBB2*-positive breast cancer following neoadjuvant trastuzumab-based chemotherapy with or without pertuzumab. *JAMA Oncol*. Published online April 27, 2023. doi:10.1001/jamaoncol.2023.0187

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This supplemental material has been provided by the authors to give readers additional information about their work.

	TCH		TCHP	
	N	%	N	%
N	67	-	88	-
Age (mean and range)	52.2 (22-74)		48.8 (27-72)	
Ki67 IHC (mean and range)	36.3 (10-80)		36.9 (1-90)	
Menopausal*				
Pre-menopausal	32	47.8%	53	60.9%
Post-menopausal	35	52.2%	34	39.1%
Clinical tumor stage				
cT1-2	38	56.7%	61	69.3%
cT3-4	29	43.3%	27	30.7%
Clinical nodal stage				
cN0	29	43.3%	27	30.7%
cN1-3	38	56.7%	61	69.3%
Pathological response (breast and axilla)				
pCR	35	52.2%	54	61.4%
Residual disease	32	47.8%	34	38.6%
Hormone receptor status				
Positive	43	64.2%	62	70.5%
Negative	24	35.8%	26	29.5%
Intrinsic subtype				
Luminal A	18	26.9%	20	22.7%
Luminal B	9	13.4%	17	19.3%
HER2-enriched	37	55.2%	43	48.9%
Basal-like	2	3.0%	6	6.8%
Normal-like	1	1.5%	2	2.3%

eTable 1. Patient characteristics of the GOM neoadjuvant cohort according to treatment (TCH versus TCHP)

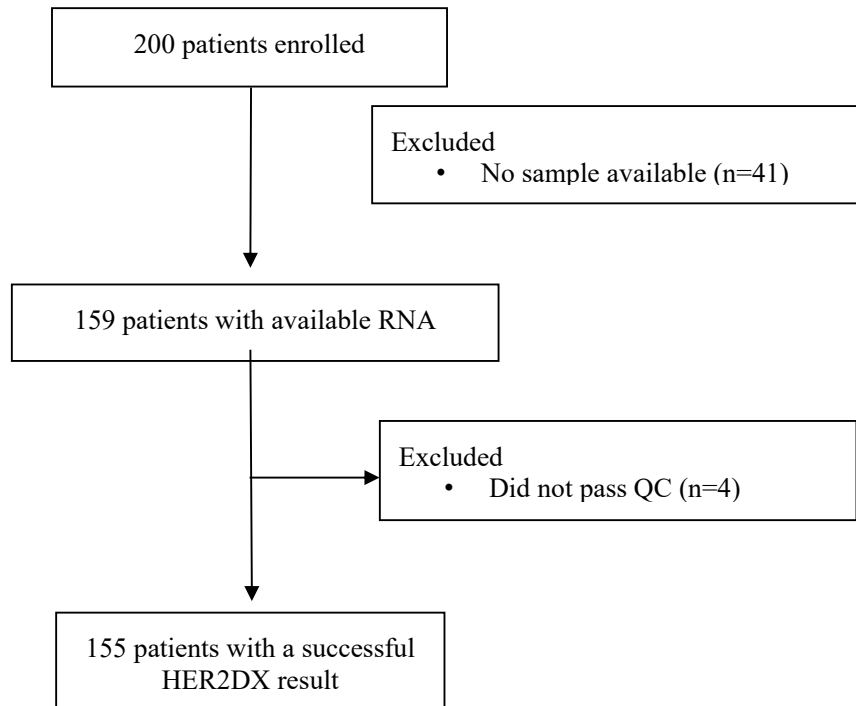
	HER2DX sub-population		Original trial population	
	N	%	N	%
N	80	-	98	-
Age (mean and range)	50.3 (26-78)		49.5 (24-78)	
Clinical tumor stage				
cT1	15	18.7%	18	18.4%
cT2-3	65	81.3%	80	81.6%
Clinical nodal stage				
cN0	52	65.0%	65	66.3%
cN1-3	28	35.0%	33	36.7%
Pathological response (breast and axilla)				
pCR	48	60.0%	55	56.7%
Residual disease	32	40.0%	42	43.3%
Hormone receptor status				
Positive	56	70.0%	65	66.3%
Negative	24	30.0%	33	33.7%

Abbreviations: pCR, pathologic complete response.

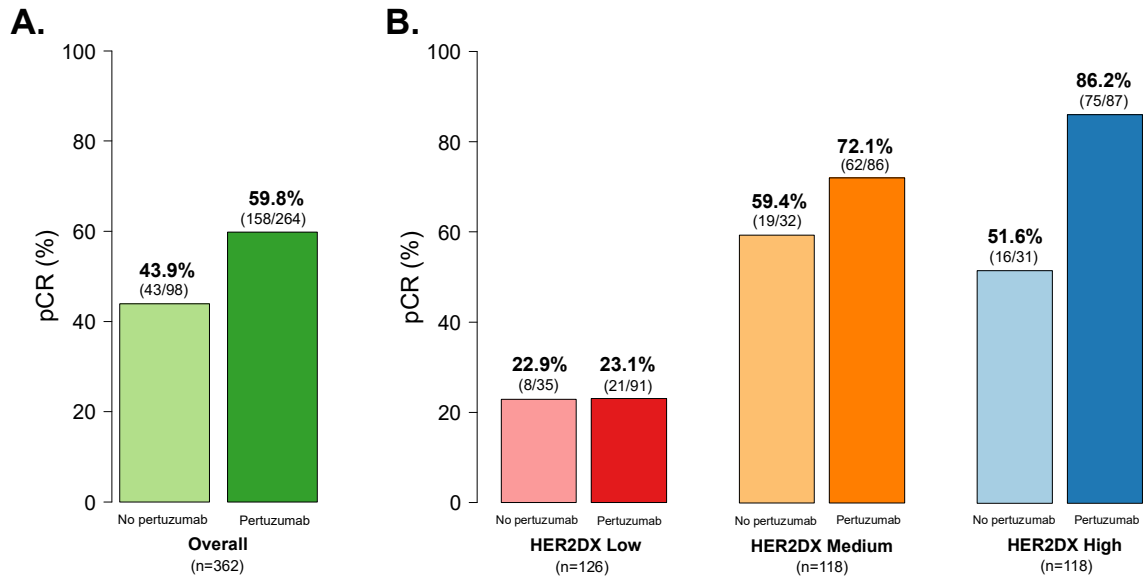
eTable 2. Main patient population of the DAPHNe trial cohort and HER2DX sub-population

Characteristic	T-DM1/P (n = 52)	THP (n = 45)	CONTROL (n = 31)
Median age, yr (range)	48 (33–72)	47 (29–70)	50 (29–71)
Ethnicity, n (%)			
White	42 (81%)	37 (82%)	25 (81%)
African American	4 (8%)	4 (9%)	2 (6%)
Asian	5 (10%)	2 (4%)	4 (13%)
Other/mixed	1 (2%)	2 (4%)	0 (0%)
HR Status, n (%)			
Positive	35 (67%)	29 (64%)	19 (61%)
Negative	17 (33%)	16 (36%)	12 (39%)
Median tumor size, cm (range)	3.3 (1.5–12)	3.4 (1.8–9)	3.5 (1.3–11.7)
Baseline node status, n (%)			
Palpable	18 (35%)	17 (38%)	10 (32%)
Non-palpable	24 (46%)	22 (49%)	21 (68%)
N/A	10 (19%)	6 (13%)	0 (0%)
HER2 qualifying test, n (%)			
IHC	35 (67%)	30 (67%)	18 (58%)
FISH	17 (33%)	15 (33%)	13 (42%)
HER2 IHC, n (%)			
IHC 3+	35 (67%)	30 (67%)	17 (55%)
IHC 2+	10 (19%)	8 (18%)	6 (19%)
IHC 1+	2 (4%)	1 (2%)	1 (3%)
Not reported	5 (10%)	6 (13%)	7 (23%)
HER2 FISH, n (%)			
Positive	29 (56%)	25 (56%)	15 (48%)
Equivocal	0 (0%)	0 (0%)	1 (3%)
Negative	1 (2%)	0 (0%)	1 (3%)
Not reported	22 (42%)	20 (44%)	14 (45%)

eTable 3. Main patient population of the ISPY-2 trial cohort with HER2DX data
The table has been obtained from Clark et al.



eFigure 1. CONSORT diagram of the GOM cohort



eFigure 2. Association of HER2DX pCR score with response to pertuzumab in a combined patient-level analysis from GOM, DAPHNe and ISPY-2 neoadjuvant cohorts (n=362)
(A) pCR rates according to pertuzumab use in the combined cohort. **(B)** pCR rates according to HER2DX pCR score groups and pertuzumab use.

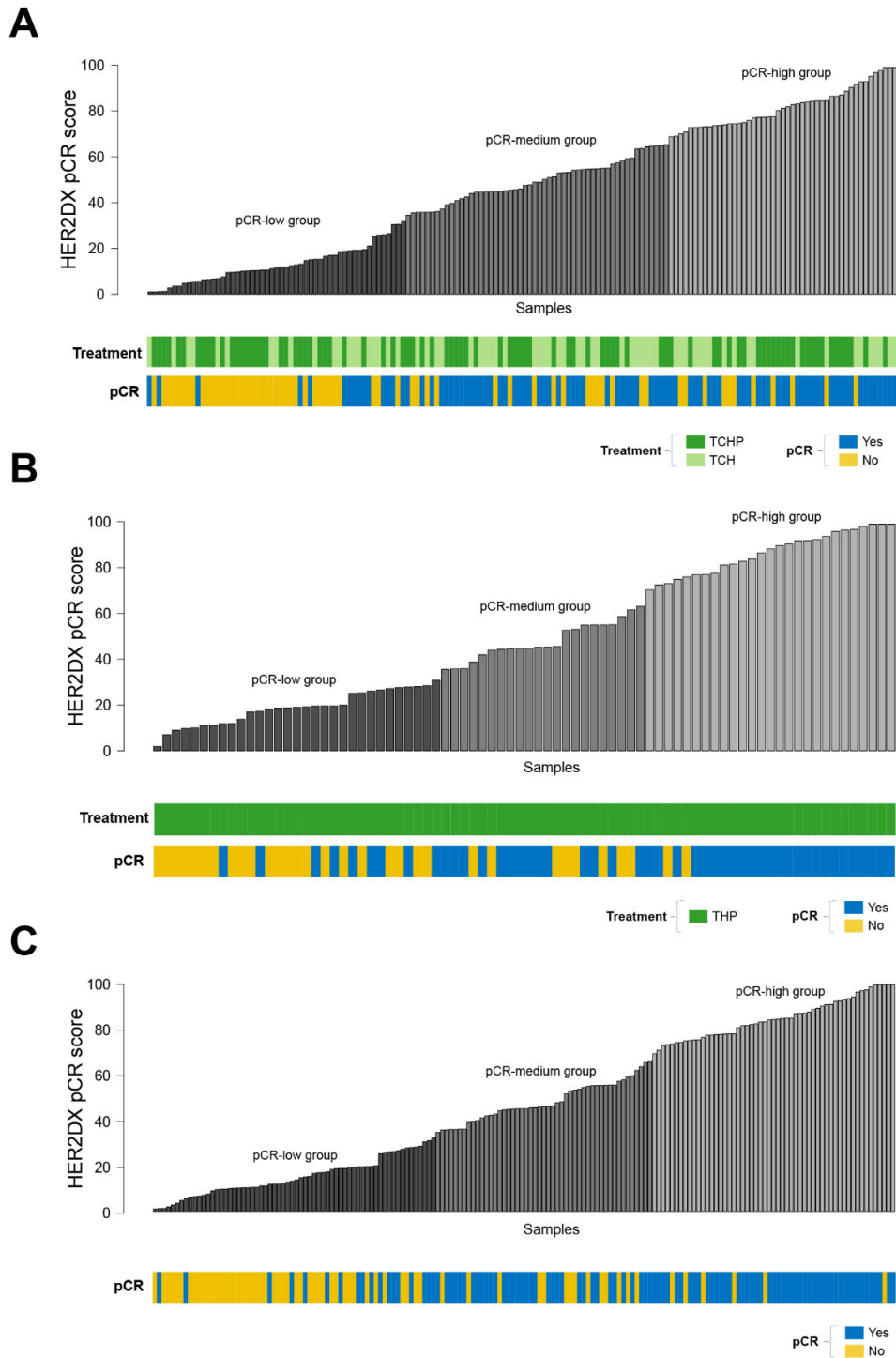


Figure 3. Relationship between HER2DX pCR score, treatment and pCR (A) GOM cohort; (B) DAPHNe cohort; (C) combined cohort.