Histopathology

Histopathology 2022, **81**, 511–519. DOI: 10.1111/his.14728

The frequency and clinical significance of *centromere enumeration probe 17* alterations in human epidermal growth factor receptor 2 immunohistochemistry-equivocal invasive breast cancer

Ayaka Katayama,[1,2] Jane Starczynski,[3] Michael S Toss,[1] Abeer M Shaaban,[3,4] Elena Provenzano,[5] Cecily M Quinn,[6] Grace Callagy,[7] Colin A Purdie,[8] Rebecca Millican-Slater,[9] David Purnell,[10] Leena Chagla,[11] Tetsunari Oyama,[2] Sarah E Pinder,[12] Steve Chan,[13] Ian Ellis,[1,14] Andrew H S Lee[14] & Emad A Rakha[1,14]

[1]*Translational Medical Sciences Unit, School of Medicine, University of Nottingham,* [13]*Department of Oncology, Nottingham University Hospitals NHS Trust, Nottingham,* [3]*Department of Cellular Pathology, University Hospitals Birmingham NHS Foundation Trust,* [4]*Institute of Cancer and Genomic Sciences, The University of Birmingham, Edgebaston, Birmingham,* [5]*Department of Histopathology, Cambridge University NHS Foundation Trust, Cambridge,* [8]*Department of Breast Pathology, Ninewells Hospital and Medical School, Dundee,* [9]*Department of Histopathology, St James's University Hospital, Leeds,* [10]*Histopathology Department, University Hospitals of Leicester, Leicester,* [11]*Burney Breast Unit, St Helens and Knowsley Teaching Hospital NHS Trust, Prescot,* [12]*Division of Cancer Studies, King's College London, Guy's Hospital, London, UK,* [2]*Diagnostic Pathology, Gunma University Graduate School of Medicine, Maebashi, Japan,* [6]*Department of Histopathology, St. Vincent's University Hospital, Dublin, and School of Medicine, University College Dublin, Dublin,* [7]*Discipline of Pathology, School of Medicine, Lambe Institute for Translational Research, NUI, Galway, Ireland,* [14]*Department of Histopathology, Nottingham University Hospitals NHS Trust, Nottingham, UK*

Date of submission 7 April 2022
Accepted for publication 21 July 2022
Published online *Article Accepted* 25 July 2022

Katayama A, Starczynski J, Toss M S, Shaaban A M, Provenzano E, Quinn C M, Callagy G, Purdie C A, Millican-Slater R, Purnell D, Chagla L, Oyama T, Pinder S E, Chan S, Ellis I, Lee A H S & Rakha E A (2022) *Histopathology* **81**, 511–519. https://doi.org/10.1111/his.14728

The frequency and clinical significance of *centromere enumeration probe 17* alterations in human epidermal growth factor receptor 2 immunohistochemistry-equivocal invasive breast cancer

Background and aims: Chromosome 17 alterations affect the assessment of *HER2* gene amplification in breast cancer (BC), but its clinical significance remains unclear. This study aimed to identify the prevalence of centromere enumeration probe 17 (CEP17) alterations, and its correlation with response to neoadjuvant therapy (NAT) in BC patients with human epidermal growth factor receptor 2 (HER2) immunohistochemistry-equivocal score.

Methods and results: A large BC cohort (n = 6049) with HER2 immunohistochemistry score 2+ and florescent *in-situ* hybridisation (FISH) results was included to assess the prevalence of CEP17 alterations. Another cohort (n = 885) with available clinicopathological data was used to evaluate the effect of CEP17 in the setting of NAT. *HER2*-amplified tumours with monosomy 17 (CEP17 copy number < 1.5 per nucleus), normal 17 (CEP17 1.5–< 3.0) and polysomy 17 (CEP17 ≥ 3.0) were observed in 16, 59 and 25%, respectively, compared with 3, 74 and 23%, respectively, in *HER2*-non-amplified tumours. There was no significant relationship between CEP17 alterations and pathological complete response (pCR) rate in both *HER2*-amplified and *HER2*-non-amplified tumours. The independent predictors of pCR were

Address for correspondence: Professor Emad A Rakha, Department of Histopathology, Nottingham University Hospital NHS Trust, City Hospital Campus, Hucknall Road, Nottingham NG5 1PB, UK. e-mail: emad.rakha@nottingham.ac.uk, emad.rakha@nuh.nhs.uk

oestrogen (ER) negativity in *HER2*-amplified tumours [ER negative versus positive; odds ratio (OR) = 11.80; 95% confidence interval (CI) = 1.37–102.00; P = 0.02], and histological grade 3 in *HER2* non-amplified tumours (3 versus 1, 2; OR = 5.54; 95% CI = 1.61–19.00; P = 0.007).

Conclusion: The impacts of CEP17 alterations are not as strong as those of *HER2*/CEP17 ratio and *HER2* copy number. The hormonal receptors status and tumour histological grade are more useful to identify BC patients with a HER2 immunohistochemistry-equivocal score who would benefit from NAT.

Keywords: alterations, breast cancer, *CEP17*, *chromosome 17*, HER2

Introduction

Human epidermal growth factor receptor 2 (HER2) protein overexpression and/or gene amplification occurs in approximately 15% of invasive breast cancer (BC).[1,2] Patients with HER2-positive BC are often treated with a combination of sequential chemotherapy and HER2-targeted therapy in the neoadjuvant and/or adjuvant setting.[3] HER2 status is determined by immunohistochemistry (IHC) and *in-situ* hybridisation (ISH). The current American Society of Clinical Oncology/College of American Pathologists (ASCO/CAP) guidelines and United Kingdom (UK) recommendations for HER2 testing recommend a two-tiered system using IHC and ISH testing if required. BC with HER2 IHC score 2+ are considered equivocal and require the assessment of *HER2* gene amplification status using dual-probe ISH.[4–6] In the dual-probe ISH assay, *HER2* gene copy number is reported relative to the centromere enumeration probe 17 (CEP17) nuclear signal as an internal control, and hence the *HER2*/CEP17 ratio is influenced not only by average *HER2* copy number but also by CEP17 alterations.

Previous studies have shown that the *HER2*/CEP17 ratio and *HER2* gene copy number are predictive for neoadjuvant trastuzumab and chemotherapy response in HER2-positive BC.[7–10] Our previous study demonstrated that the maximum benefit of neoadjuvant anti-HER2 therapy is observed in the subgroup of patients with tumours that are HER2 IHC score 3+, histological grade 3 or HER2 IHC score 2+/*HER2*-amplified co-existing with oestrogen receptor (ER) negativity in HER2-positive BC patients.[11] Although CEP17 alterations are common, their significance has received less attention in clinical practice.

Chromosome 17 (Ch17) alterations include whole chromosome gains or losses, gene copy number anomalies, allelic losses and structural rearrangements.[12,13] Whether the number of CEP17 signals by ISH reflects true polysomy or monosomy of Ch17 has been examined, and recent data have shown that an increased CEP17 copy number is usually related to focal peri-centromeric gains rather than to true polysomy.[12,14] However, most previous studies have interpreted CEP17 copy number by ISH as whole Ch17 alterations.[13,15] CEP17 copy number was reported to affect HER2 status assessment, and is associated with the clinical outcome and tumour grade.[15] However, the definition of CEP17 alterations (monosomy, duplication or polysomy), BC cohorts (early BC, metastatic BC, HER2-positive BC or *HER2*-amplified/non-amplified BC) and type of chemotherapy and anti-HER2 therapy have varied among studies, leading to conflicting results. Some earlier reports observed that CEP17 copy number gains correlated with poor prognosis, whereas other studies did not demonstrate any prognostic significance.[15,16] Based on the retrospectively assessed clinical trials, the N9831 adjuvant trastuzumab trial suggests a treatment benefit independent of CEP17 alterations in patients with HER2-positive tumours,[17] while the NEAT/ER9601 adjuvant epirubicin trial suggests that CEP17 duplication predicts benefit from anthracyclines in early stage BC.[18]

In clinical practice, ISH testing is performed in IHC HER2 equivocal tumours. As this subgroup of tumours comprises a relatively low proportion of BCs and includes both HER2-positive (*HER2*-amplified) and HER2-negative (*HER2*-non-amplified) BCs, a large cohort of HER2 tested BCs is required to analyse the clinical significance of centromere alterations adequately. Herein, we hypothesise that patients with IHC HER2-equivocal BC with different CEP17 alterations show variable responses to therapy. This study included two large cohorts of BCs with IHC HER2-equivocal for which *HER2* florescent *in-situ* hybridisation (FISH) data were available and aimed to identify the prevalence of CEP17 alterations and to assess their clinical impacts in the setting of neoadjuvant treatment (NAT).

Materials and methods

STUDY COHORT

The initial cohort included 6049 BCs with HER2 IHC 2+ and available *HER2* FISH data from a single

Table 1. HER2 status and CEP17 alterations

Term		Definition
HER2-amplified		*HER2*/CEP17 ratio ≥ 2.0 or HER2 CN ≥ 6.0
HER2-non-amplified		*HER2*/CEP17 ratio < 2.0 and HER2 CN < 6.0
CEP17 alternations	CEP17 monosomy (monosomy 17)	CEP17 signal number < 1.5 per nucleus
	CEP17 normal (normal 17)	CEP17 signal number 1.5–3.0 per nucleus
	CEP17 polysomy (polysomy 17)	CEP17 signal number ≥ 3.0 per nucleus

CEP17, centromere enumeration probe 17; *HER2*, human epidermal growth factor receptor 2; FISH, fluorescent *in situ* hybridisation; CN, copy number.

centre, the University Hospitals Birmingham NHS Foundation Trust, as a large, unselected patient cohort. This cohort was mainly used to assess the prevalence of CEP17 alteration in BC. Detailed clinicopathological and treatment data were available in the second multicentre cohort (n = 885). The majority of patients were treated at Nottingham University Hospitals NHS Trust, Nottingham (n = 395), with additional patients from Addenbrookes Hospital, Cambridge; University Hospitals of Leicester NHS Trust; St Vincent's University Hospital, Dublin; University Hospital Galway, Galway; Burney Breast Unit, St Helens and Knowsley Teaching Hospital NHS Trust, Liverpool; Guy's and St Thomas' NHS Foundation Trust, London; Ninewells Hospital, Dundee; and University of Turin, Turin Italy.

Patients were considered eligible for anti-HER2 therapies if their tumours showed a *HER2*/CEP17 ratio ≥ 2.0 regardless of the *HER2* gene copy number or if the *HER2* gene copy number was ≥ 6.[6] Patients were divided into three groups: NAT received including chemotherapy alone; chemotherapy with trastuzumab; and chemotherapy with dual anti-HER2 agents (i.e. trastuzumab with either pertuzumab or lapatinib). The type of chemotherapy included anthracycline and taxane, anthracycline without taxane and non-anthracycline regimens. Pathological complete response (pCR) was defined as no residual invasive carcinoma in both breast and axillary lymph nodes regardless of the presence of residual ductal carcinoma *in situ* (DCIS) (ypT0/Tis ypN0).[19] All data used in the analysis were derived from the original pathology reports.

IMMUNOHISTOCHEMISTRY AND FISH ASSAY

IHC for ER and progesterone receptor (PR) and both IHC and FISH for HER2 on biopsy specimens were assessed according to UK guidelines.[6,20] For ER and PR, tumours were classified as positive when there was ≥ 1% nuclear staining in invasive tumour cells.[20] HER2 IHC was scored as positive (3+), equivocal (2+) or negative (1+/0). IHC score 2+ tumours were tested for *HER2* gene amplification by FISH.[6] As defined by the current ASCO/CAP guidelines, *HER2* ISH status was assigned to one of five groups (Table 1).[4,5] HER2 amplification was defined as *HER2*/CEP17 ratio ≥ 2.0 or *HER2* copy number ≥ 6.0.[6] As there is no optimal cut-off value of CEP17 copy number for classifying centromere alterations, we selected the commonly adopted threshold: monosomy (CEP17 copy number < 1.5 per nucleus), normal (CEP17 1.5–3.0) and polysomy (CEP17 ≥ 3.0) by FISH (Table 1 and Figure 1).[13,16,18,21]

STATISTICAL ANALYSIS

Statistical analysis was performed using EZR software (Saitama Medical Center Jichi Medical University; http://www.jichi.ac.jp/saitama-sct/SaitamaHP.files/statmed.html), which is a graphical user interface for R (the R Foundation for Statistical Computing, Vienna, Austria, version 2.13.0).[22] Associations between CEP17 alterations and clinicopathological variables or pCR were examined with Fisher's exact tests or Pearson's χ^2 test, as appropriate. A logistic regression model was applied to evaluate the effect of covariates on pCR. If a variable remained at a level of P value ≤ 0.15, it was incorporated into the final multivariable model.[23] A P-value < 0.05 was considered statistically significant.

Ethical approval and consent to participate

This study was approved by the Nottingham Research Tissue Bank Access Committee under the IRAS Project ID: 184265. All patients included were consented to participate in research. Data collected were fully anonymised. The study was performed in accordance with the Declaration of Helsinki.

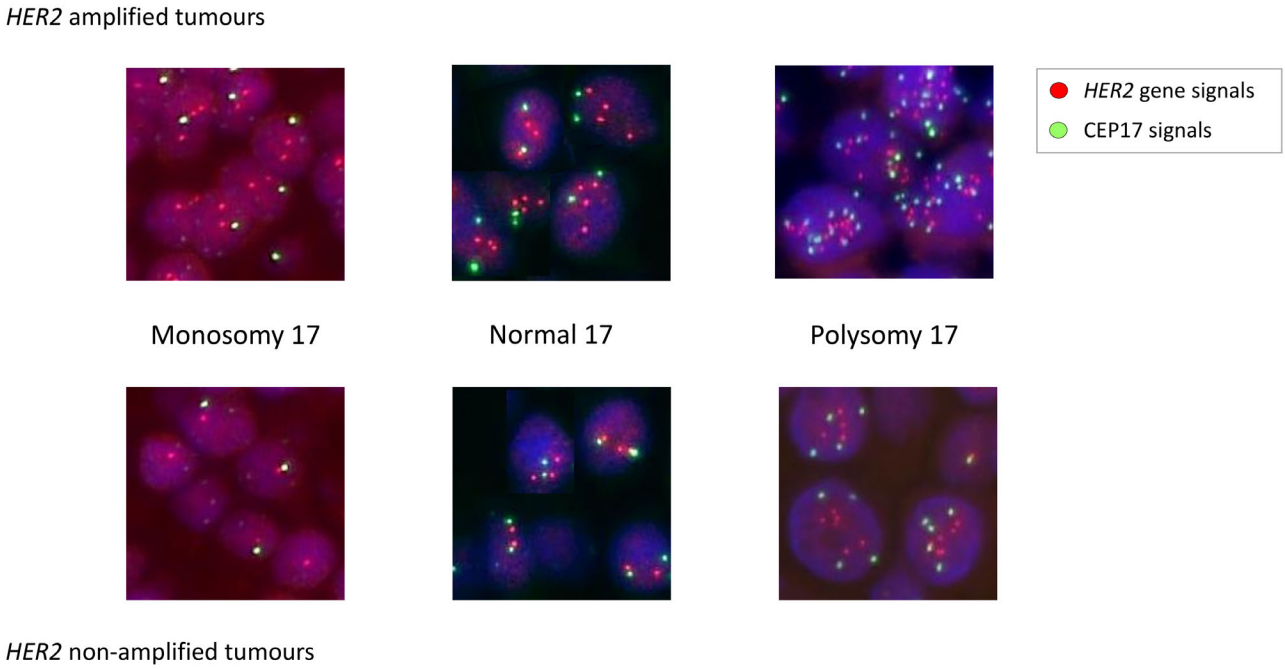

Figure 1. The examples of human epidermal growth factor receptor 2 (HER2) fluorescent *in-situ* hybridisation (FISH) result categories focusing on centromere enumeration probe 17 (CEP17) alterations.

Results

THE PREVALENCE OF CEP17 ALTERATIONS

Fourteen per cent of tumours with IHC score 2+ were *HER2*-amplified (HER2-positive) and 86% were non-amplified (HER2-negative). Of the amplified group, 87% of cases were defined based on a *HER2*/CEP17 ratio of ≥ 2.0, while 13% of cases were defined based on the mean *HER2* copy number alone (≥ 6.0). Figure 2 shows the distribution of CEP17 alterations (cut-off of 1.5 CEP17 copy number for monosomy and 3.0 CEP17 copy number for polysomy). *HER2*-amplified

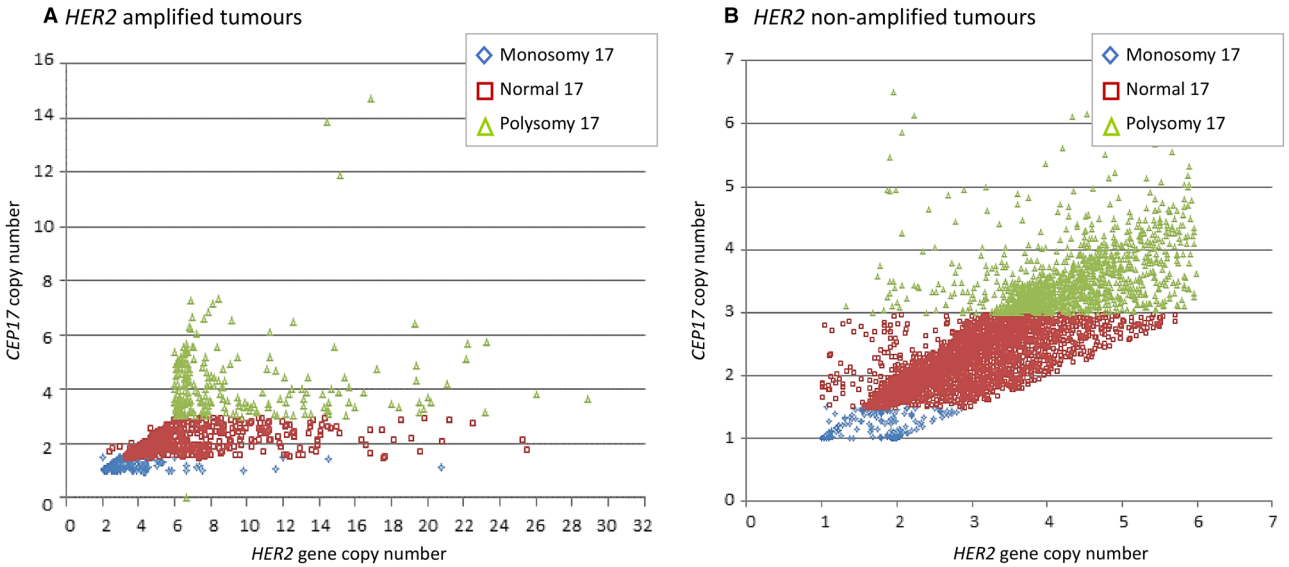

Figure 2. Scatter plot showing the prevalence of centromere enumeration probe 17 (CEP17) alterations in the initial cohort (n = 6049). **A**, HER2-amplified tumours (n = 877); **B**, HER2-non-amplified tumours (n = 5172).

tumours with monosomy, normal and polysomy of CEP17 were observed in 16, 59 and 25% of cases, respectively, and in *HER2*-non-amplified tumours in 3, 74 and 23%, respectively ($P < 0.05$).

THE RELATIONSHIP BETWEEN CEP17 ALTERATIONS AND CLINICOPATHOLOGICAL FEATURES

In the second cohort ($n = 885$), 369 cases showed *HER2* gene amplification while 516 tumours did not show evidence of *HER2* gene amplification. The median CEP17 signal number was 2.1 (range = 1.0–12.6) and *HER2* gene copy numbers was 4.1 (range = 1.4–42.4). *HER2*-amplified tumours with monosomy, normal and polysomy of CEP17 were observed in 20, 62 and 18% of cases, respectively, while *HER2*-non-amplified tumours with monosomy, normal and polysomy of CEP17 were observed in 7, 66 and 27%, respectively (Table 2). In *HER2*-non-amplified tumours, polysomy 17 was associated with higher tumour grade ($P < 0.001$). There was no significant relationship between CEP17 alterations and histological type or hormone receptor status.

THE RELATIONSHIP BETWEEN CEP17 ALTERATIONS AND PCR

Full data on NAT were available in 39% of patients ($n = 345$ of 885), including 165 with *HER2*-amplified and 180 with *HER2*-non-amplified tumours. pCR rate was calculated in tumours classified according to HER2 status and CEP17 alterations, taking account of treatment regimens (Table 3). There was no significant relationship between CEP17 alterations and pCR rate in patients with *HER2*-amplified tumours and *HER2*-non-amplified tumours. The association between clinicopathological parameters and the attainment of a pCR was examined in both *HER2*-amplified tumours and *HER2*-non-amplified tumours by univariate and multivariate stepwise regression models (Table 4). In *HER2*-amplified tumours, ER negativity was identified as an independent predictor of pCR [ER negative versus positive; odds ratio (OR) = 11.80; 95% confidence interval (CI) = 1.37–102.00; $P = 0.02$]. In *HER2*-non-amplified tumours, histological grade 3 was an independent predictor of pCR (3 versus 1, 2; OR = 5.54; 95% CI = 1.61–19.00; $P = 0.007$).

Discussion

Focusing on BC patients with a HER2 immunohistochemistry-equivocal score, we revealed the prevalence of CEP17 alterations and their association with response to NAT. Our results showed that polysomy 17, defined by increased CEP17 copy number by ISH, was observed in 24% of HER2 IHC-equivocal BC and was associated with an increasing *HER2* copy number. In addition, we observed that polysomy 17 was little more frequent in *HER2*-non-amplified tumours than *HER2*-amplified, as shown in a previous study.[24] Although Ch17 alterations have been estimated by counting CEP17 copy number by ISH in most previous studies, the definition of CEP17 alterations and the patient cohorts vary among studies, leading to conflicting results.[13,15] Our cut-off for polysomy 17 (mean of ≥ 3 CEP17 signals per nucleus) is a commonly adopted threshold.[13,15] Merola *et al.*[25] reported a 46% prevalence of polysomy 17 in HER2 IHC-equivocal BC using a similar definition. Although a higher rate of polysomy 17 in HER2 IHC-equivocal BC was reported by Merola *et al.*,[25] their cohort was smaller than our current series and the clinicopathological parameters were not clearly defined. Moreover, we emphasise that ISH analysis is routinely evaluated in HER2 IHC-equivocal BC, so the clinical significance of CEP17 alterations needs to be analysed in a large cohort of HER2 IHC-equivocal BC patients.

Others have reported monosomy 17 in 4% of HER2-positive cases.[17] In our cohort, which comprised HER2 IHC-equivocal BC only, monosomy 17 was present in 16% of *HER2*-amplified tumours compared to 3% of *HER2*-non-amplified tumours. These findings indicate that some cases with a low *HER2* copy number were classified as *HER2*-amplified because of low CEP17 when positivity is defined using *HER2*/CEP17 ratio alone.[6] Mathematically, the lower the value of denominator (as in cases of Ch17 monosomy), the higher value of the overall ratio, even with a fixed numerator. Biologically, in cells with normal genetic content (2 N), there is usually one active allele for each gene while the other copy is dormant. In monosomy 17, the single CEP17 signal binding would result in a higher *HER2*/CEP17 ratio (> = 2.0) even with lower levels of amplification of the active *HER2* allele. Although the response rate of these HER2 IHC 2+ cases with monosomy 17 and low levels of *HER2* gene amplification classified as HER2 positive based on *HER2*/CEP17 ratio to anti-HER2 therapy is uncertain, there is no evidence that their response is significantly lower than other HER2 IHC 2+ with *HER2* gene copy number > 6.0.[11] Emerging new anti-HER2 antibody drug conjugates (ADC) for 'HER2-low expression groups' would also help to refine the definition of HER2 positivity for therapeutic purposes.[26]

Table 2. Clinicopathological characteristics according to CEP17 alternations in both *HER2*-amplified and *HER2*-non-amplified tumours

Characteristics	Total number (%)	*HER2*-amplified				*HER2*-non-amplified			
		Monosomy 17, no. (%)	Normal 17, no. (%)	Polysomy 17, no. (%)	*P*-value	Monosomy 17. no. (%)	Normal 17, no. (%)	Polysomy 17, no. (%)	*P*-value
Total number	885 (100)	75 (20.3)	227 (61.5)	67 (18.2)		36 (7.0)	339 (65.7)	141 (27.3)	
CEP17 copy number (median [range])	2.1 [1.0–12.6]	1.3 [1.0–1.5]	1.9 [1.5–2.9]	4.2 [3.0–6.7]		1.4 [1.2–1.5]	2.1 [1.5–3.0]	3.60 [3.00–12.60]	
HER2 copy number (median [range])	4.1 [1.4–42.4]	3.0 [2.1–42.4]	4.6 [3.0–38.4]	6.8 [1.7–31.2]		2.0 [1.4–2.8]	3.2 [1.6–5.4]	4.5 [1.4–5.9]	
Age (median [range])	59 [23–96]	54 [31–84]	56 [26–96]	59 [36–80]		54 [26–76]	60 [23–95]	62 [28–92]	
Histology type									
No special type	804 (91.0)	70 (94.6)	208 (91.6)	66 (98.5)	0.36	31 (86.1)	298 (87.9)	131 (93.6)	0.08
Lobular	50 (5.7)	3 (4.1)	13 (5.7)	1 (1.5)		1 (2.8)	26 (7.7)	6 (4.3)	
Mixed (no special type and lobular)	29 (3.3)	1 (1.3)	6 (2.7)	0		4 (11.1)	15 (4.4)	3 (2.1)	
Tumour grade									
1	82 (9.4)	5 (6.8)	13 (5.8)	2 (3.0)	0.34	9 (25.7)	42 (12.5)	11 (7.9)	< **0.001**
2	577 (65.9)	54 (74.0)	142 (63.7)	45 (67.2)		19 (54.3)	240 (71.2)	77 (55.0)	
3	216 (24.7)	14 (19.2)	68 (30.5)	20 (29.8)		7 (20.0)	55 (16.3)	52 (37.1)	
ER									
Negative	121 (14.8)	8 (13.8)	36 (18.1)	8 (17.4)	0.75	7 (19.4)	47 (13.9)	15 (10.6)	0.35
Positive	698 (85.2)	50 (86.2)	163 (81.9)	38 (82.6)		29 (80.6)	292 (86.1)	126 (89.4)	
PR									
Negative	209 (27.5)	17 (32.7)	55 (32.5)	11 (24.4)	0.56	9 (26.5)	87 (26.9)	30 (21.9)	0.52
Positive	551 (72.5)	35 (67.3)	114 (67.5)	34 (75.6)		25 (73.5)	236 (73.1)	107 (78.1)	

CEP17, centromere enumeration probe 17; *HER2*, human epidermal growth factor receptor 2; ER, oestrogen receptor; PR, progesterone receptor.
Significant *P*-values are shown in bold type.

There are limited studies showing the relationship between CEP17 alterations and treatment response in the neoadjuvant setting, but multiple studies have investigated pathological biomarkers predicting response or resistance to NAT. *HER2* amplification level determined by FISH was associated with pCR, and the pCR rate was significantly higher in highly amplified tumours.[27] Hormone receptor status, especially ER negativity, and high histological grade have been shown to predict response to neoadjuvant chemotherapy alone, and combined chemotherapy and anti-HER2 therapy in BC.[11,28–30] In our current cohort of

Table 3. Correlation between CEP17 alterations and pCR

Treatment	Total number	Monosomy 17 pCR/non-pCR, no. (%)	Normal 17 pCR/non-pCR, no. (%)	Polysomy 17 pCR/non-pCR, no. (%)	*P*-value
HER2-amplified tumours					
Chemotherapy and anti-HER2 therapy	165	5/20 (20.0)	25/98 (20.3)	2/15 (11.8)	0.70
Anti-HER2 therapy given (single)	146	5/18 (21.7)	22/86 (20.4)	1/14 (6.7)	0.43
Anti-HER2 therapy given (dual)	19	0/2 (0)	3/12 (20.0)	1/1 (50.0)	0.46
Chemotherapy containing anthracycline given	110	2/18 (10.0)	16/64 (20.0)	1/9 (10.0)	0.47
HER2-non-amplified tumours					
Chemotherapy	180	1/15 (6.3)	13/105 (11.0)	7/39 (15.2)	0.59
Chemotherapy containing anthracycline given	165	0/15 (0)	11/102 (9.7)	5/32 (13.5)	0.33

CEP17, centromere enumeration probe 17; pCR, pathological complete response; HER2, human epidermal growth factor receptor 2.

Table 4. Univariate and multivariate logistic regression model for pCR in both *HER2*-amplified and *HER2*-non-amplified tumours

		Univariant analysis					Multivariant analysis		
Parameters	Risk/reference	pCR/non-pCR, no. (%)	pCR/non-pCR, no. (%)	OR	95% CI	*P*-value	OR	95% CI	*P*-value
HER2-amplified tumour									
CEP17	Mono, poly/normal	7/35 (16.7)	25/98 (20.3)	0.78	0.31–1.97	0.61	–	–	–
ER	Negative/positive	14/22 (38.9)	18/111 (14.0)	3.92	1.70–9.04	**0.001**	11.80	1.37–102.00	**0.02**
PR	Negative/positive	14/36 (28.0)	13/65 (16.7)	1.94	0.83–4.58	0.13	0.26	0.03–2.10	0.20
Histological grade	3/1, 2	22/54 (28.9)	10/74 (11.9)	3.01	1.32–6.88	**0.009**	2.04	0.79–5.25	0.14
HER2-non-amplified tumour									
CEP17	Mono, poly/normal	8/54 (12.9)	13/105 (11.0)	1.20	0.47–3.06	0.71	–	–	–
ER	Negative/positive	10/31 (24.4)	11/128 (7.9)	3.75	1.46–9.63	**0.006**	1.46	0.29–7.32	0.64
PR	Negative/positive	12/48 (20.0)	6/92 (6.1)	3.83	1.35–10.80	**0.01**	2.67	0.53–13.50	0.24
Histological grade	3/1, 2	16/54 (22.9)	4/103 (3.7)	7.63	2.43–24.00	< **0.001**	5.54	1.61–19.00	**0.007**

CEP17, centromere enumeration probe 17; CI, confidence interval; ER, oestrogen receptor; HER2, human epidermal growth factor receptor 2; OR, odds ratio; pCR, pathological complete response; PR, progesterone receptor.
Significant *P*-values are shown in bold type.

HER2 IHC-equivocal BC within both *HER2*-amplified and *HER2*-non-amplified tumours, there was no significant relationship between CEP17 alterations and pCR rate. Similar to previous studies, hormone receptor status and histological grade highlighted subgroups showing higher pCR rates. Page *et al.*[16] provided evidence that patients with *HER2*-amplified monosomy 17 in early-stage BC benefited from

trastuzumab, supporting that pCR is not related to CEP17 alterations.

The NEAT/ER9601 adjuvant epirubicin trial[18] showed CEP17 duplication, determined as CEP17 signal number > 1.86, predicted benefit from anthracyclines in early BC, and Tibau *et al.*[21] reported that CEP17 duplication predicted pCR to primary anthracycline-based chemotherapy in BC. However, our cohort showed no difference in the rate of pCR among the different CEP17 in patients who received anthracycline-based NAT.

The strengths of the study include the large sample size of the cohort, including more uncommon FISH patterns (ASCO/CAP FISH group 2, 3 and 4), reliable well-validated FISH assessment in regional testing centres and the inclusion of a large single-centre cohort consisting of unselected patients. However, our study has some limitations. This was a retrospective non-randomised study and our samples were collected from multiple institutions, which may have some selection bias effect. Also, we have not technically determined if the cases in our series have true monosomy or loss of a portion of the chromosome and true polysomy or gain of a portion of the chromosome.

In conclusion, our findings suggest that the clinicopathological significance of CEP17 alterations is not as strong as that of the *HER2*/CEP17 ratio and *HER2* gene copy number. The hormonal receptor status and tumour histological grade are more useful to identify patients who will benefit from NAT in HER2 IHC-equivocal BC.

Acknowledgments

We acknowledge all those who contributed to the collection of patients in this study. E.R., M.S.T. and I.O.E. are part of the PathLAKE digital pathology consortium. These new centres are supported by a £50 m investment from the Data to Early Diagnosis and Precision Medicine strand of the government's Industrial Strategy Challenge Fund, managed and delivered by UK Research and Innovation (UKRI). We thank Dr Michael Neat (Division of Cancer Studies, King's College London, Guy's Hospital, London, UK) for excellent technical assistance. We also thank the Japanese Breast Cancer Society for supporting A.K. through the International Fellowship Grant, the NIHR Cambridge Biomedical Research Centre for supporting E.P. and the Birmingham CR–UK Centre (C17422/A25154) for supporting A.M.S.

Conflicts of interest

The authors have no conflicts of interest to declare.

Data availability statement

The authors confirm the data that has been used is available on reasonable request.

References

1. Dodson A, Parry S, Ibrahim M *et al.* Breast cancer biomarkers in clinical testing: analysis of a UK national external quality assessment scheme for immunocytochemistry and *in situ* hybridisation database containing results from 199 300 patients. *J. Pathol. Clin. Res.* 2018; **4**; 262–273.
2. Giordano SH, Temin S, Kirshner JJ *et al.* Systemic therapy for patients with advanced human epidermal growth factor receptor 2-positive breast cancer: American Society of Clinical Oncology clinical practice guideline. *J. Clin. Oncol.* 2014; **32**; 2078–2099.
3. Burstein HJ, Curigliano G, Loibl S *et al.* Estimating the benefits of therapy for early-stage breast cancer: the St. Gallen International Consensus Guidelines for the primary therapy of early breast cancer 2019. *Ann. Oncol.* 2019; **30**; 1541–1557.
4. Wolff AC, Hammond MEH, Allison KH *et al.* Human epidermal growth factor receptor 2 testing in breast cancer: American Society of Clinical Oncology/College of American Pathologists Clinical Practice Guideline Focused Update. *J. Clin. Oncol.* 2018; **36**; 2105–2122.
5. Wolff AC, Hammond ME, Hicks DG *et al.* Recommendations for human epidermal growth factor receptor 2 testing in breast cancer: American Society of Clinical Oncology/College of American Pathologists clinical practice guideline update. *J. Clin. Oncol.* 2013; **31**; 3997–4013.
6. Rakha EA, Pinder SE, Bartlett JM *et al.* Updated UKRecommendations for HER2 assessment in breast cancer. *J. Clin. Pathol.* 2015; **68**; 93–99.
7. Wu Z, Xu S, Zhou L *et al.* Clinical significance of quantitative. *Onco. Targets. Ther.* 2018; **11**; 801–808.
8. Veeraraghavan J, De Angelis C, Mao R *et al.* A combinatorial biomarker predicts pathologic complete response to neoadjuvant lapatinib and trastuzumab without chemotherapy in patients with HER2+ breast cancer. *Ann. Oncol.* 2019; **30**; 927–933.
9. Kogawa T, Fouad TM, Liu DD *et al.* High HER2/centromeric probe for chromosome 17 fluorescence *in situ* hybridization ratio predicts pathologic complete response and survival outcome in patients receiving neoadjuvant systemic therapy with trastuzumab for HER2-overexpressing locally advanced breast cancer. *Oncologist* 2016;**21**:21–27.
10. Singer CF, Tan YY, Fitzal F *et al.* Pathological complete response to neoadjuvant trastuzumab is dependent on HER2/CEP17 ratio in HER2-amplified early breast cancer. *Clin. Cancer Res.* 2017; **23**; 3676–3683.
11. Katayama A, Miligy IM, Shiino S *et al.* Predictors of pathological complete response to neoadjuvant treatment and changes to post-neoadjuvant HER2 status in HER2-positive invasive breast cancer. *Mod. Pathol.* 2021; **34**; 1271–1281.
12. Halilovic A, Verweij DI, Simons A *et al.* HER2, chromosome 17 polysomy and DNA ploidy status in breast cancer; a translational study. *Sci. Rep.* 2019; **9**; 11679.
13. Reinholz MM, Bruzek AK, Visscher DW *et al.* Breast cancer and aneusomy 17: implications for carcinogenesis and therapeutic response. *Lancet Oncol.* 2009; **10**; 267–277.
14. Yeh IT, Martin MA, Robetorye RS *et al.* Clinical validation of an array CGH test for HER2 status in breast cancer reveals

that polysomy 17 is a rare event. *Mod. Pathol.* 2009; **22**; 1169–1175.
15. Hanna WM, Rüschoff J, Bilous M *et al.* HER2 *in situ* hybridization in breast cancer: clinical implications of polysomy 17 and genetic heterogeneity. *Mod. Pathol.* 2014; **27**; 4–18.
16. Page DB, Wen H, Brogi E *et al.* Monosomy 17 in potentially curable HER2-amplified breast cancer: prognostic and predictive impact. *Breast Cancer Res. Treat.* 2018; **167**; 547–554.
17. Perez EA, Reinholz MM, Hillman DW *et al.* HER2 and chromosome 17 effect on patient outcome in the N9831 adjuvant trastuzumab trial. *J. Clin. Oncol.* 2010; **28**; 4307–4315.
18. Bartlett JM, Munro AF, Dunn JA *et al.* Predictive markers of anthracycline benefit: a prospectively planned analysis of the UKNational Epirubicin Adjuvant Trial (NEAT/BR9601). *Lancet Oncol.* 2010; **11**; 266–274.
19. Cortazar P, Zhang L, Untch M *et al.* Pathological complete response and long-term clinical benefit in breast cancer: the CTNeoBC pooled analysis. *Lancet* 2014; **384**; 164–172.
20. Hammond ME, Hayes DF, Dowsett M *et al.* American Society of Clinical Oncology/College of American Pathologists guideline recommendations for immunohistochemical testing of estrogen and progesterone receptors in breast cancer. *J. Clin. Oncol.* 2010; **28**; 2784–2795.
21. Tibau A, López-Vilaró L, Pérez-Olabarria M *et al.* Chromosome 17 centromere duplication and responsiveness to anthracycline-based neoadjuvant chemotherapy in breast cancer. *Neoplasia* 2014; **16**; 861–867.
22. Kanda Y. Investigation of the freely available easy-to-use software 'EZR' for medical statistics. *Bone Marrow Transplant.* 2013; **48**; 452–458.
23. Bursac Z, Gauss CH, Williams DK, Hosmer DW. Purposeful selection of variables in logistic regression. *Source Code Biol. Med.* 2008; **3**; 17.
24. Salido M, Tusquets I, Corominas JM *et al.* Polysomy of chromosome 17 in breast cancer tumors showing an overexpression of ERBB2: a study of 175 cases using fluorescence *in situ* hybridization and immunohistochemistry. *Breast Cancer Res.* 2005; **7**; R267–R273.
25. Merola R, Mottolese M, Orlandi G *et al.* Analysis of aneusomy level and HER-2 gene copy number and their effect on amplification rate in breast cancer specimens read as 2+ in immunohistochemical analysis. *Eur. J. Cancer* 2006; **42**; 1501–1506.
26. Kurozumi S, Katayama A, Shirabe K, Horiguchi J, Rakha EA. Clinicopathological utility of human epidermal growth factor receptor 2 (HER2)-heterogeneity for next-generation treatments of triple-negative breast cancer. *Oncotarget* 2021; **12**; 2302–2304.
27. Arnould L, Arveux P, Couturier J *et al.* Pathologic complete response to trastuzumab-based neoadjuvant therapy is related to the level of HER-2 amplification. *Clin. Cancer Res.* 2007; **13**; 6404–6409.
28. Krystel-Whittemore M, Xu J, Brogi E *et al.* Pathologic complete response rate according to HER2 detection methods in HER2-positive breast cancer treated with neoadjuvant systemic therapy. *Breast Cancer Res. Treat.* 2019; **177**; 61–66.
29. Hurvitz SA, Martin M, Symmans WF *et al.* Neoadjuvant trastuzumab, pertuzumab, and chemotherapy versus trastuzumab emtansine plus pertuzumab in patients with HER2-positive breast cancer (KRISTINE): a randomised, open-label, multicentre, phase 3 trial. *Lancet Oncol.* 2018; **19**; 115–126.
30. Huober J, von Minckwitz G, Denkert C *et al.* Effect of neoadjuvant anthracycline-taxane-based chemotherapy in different biological breast cancer phenotypes: overall results from the GeparTrio study. *Breast Cancer Res. Treat.* 2010; **124**; 133–140.

