



## Review

# Understanding the role of primary tumour localisation in colorectal cancer treatment and outcomes



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**Abstract** Metastatic colorectal carcinoma (mCRC) is a heterogeneous disease with differing outcomes and clinical responses and poor prognosis. CRCs can be characterised by their primary tumour location within the colon. The left-sided colon, derived from the hindgut, includes the distal third of the transverse colon, splenic flexure, descending colon, sigmoid colon and rectum. The right-sided colon, derived from the midgut, includes the proximal two-thirds of the transverse colon, ascending colon and caecum. Sometimes, the rectum is described separately, despite originating from the hindgut, and in many clinical series, the left-sided colon includes only tumours within and distal to the splenic flexure. Differences in the microbiome, clinical characteristics and chromosomal and molecular characteristics have been reported between the right and left side of the colon, regardless of how this is defined. There is now strong evidence from clinical studies in patients with mCRC for the prognostic effect of primary tumour location. The impact of primary colonic tumour location on response to treatment is now under investigation in a large number of clinical studies in patients with mCRC.

In this review, we summarise the microbiome, clinical, chromosomal and molecular differences associated with the primary location of CRC. We present an overview of the proven

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prognostic impact of primary tumour location for patients with mCRC and discuss emerging data for the predictive impact of primary tumour location on clinical outcome.

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## 1. Introduction

In Europe, colorectal carcinoma (CRC) is the second most commonly diagnosed cancer and a leading cause of death [1,2]. Metastatic CRC (mCRC) is a heterogeneous disease with differing outcomes and clinical responses. Over the past 20 years, the clinical outcome for these patients has greatly improved because of the expansion in available systemic therapies and ablative techniques, in addition to improved diagnosis and referral for surgery [3]. However, prognosis for mCRC patients remains poor [3]. Clinical studies, to date, have reported a median overall survival (OS) of approximately 24–30 months, achieved with the aid of multiple lines of treatment followed by best supportive care (BSC) [3].

CRCs can be characterised by their primary tumour location within the colon and rectum [4]. Historically, publications have defined CRCs within three compartments of the gut: distal colon, proximal colon and rectum [4–6]. Right-sided colon carcinomas (RCCs) are located within the colon derived from the embryologic midgut, which encompasses the proximal two-thirds of the transverse colon, ascending colon and caecum (Fig. 1). Left-sided colon carcinomas (LCCs) lie within the colon derived from the embryologic hindgut, which includes the distal third of the transverse colon, splenic flexure, descending colon, sigmoid colon and rectum (Fig. 1). It should be noted that the rectum is sometimes described separately although it embryologically belongs to the hindgut. Most clinical series have used a slightly different definition, with any tumour proximal to the splenic flexure considered a right-sided primary and any tumour

from the splenic flexure and distally (including the rectum) considered a left-sided primary. With this definition, at least 63% of patients with CRC have LCC [7].

Prognostic biomarkers predict a likely disease outcome, independent of the treatment received. Strong evidence for the prognostic effect of primary tumour location is available from clinical studies in patients with mCRC [8–13]. Predictive biomarkers may identify patients who are most likely to benefit from a certain treatment. Clinical studies in patients with mCRC are now evaluating the impact of primary colonic tumour location on response to treatment, with a particular focus on biologics [12–17].

Here, we present an overview of the microbiome and molecular differences associated with the primary location of CRC, and we discuss the prognostic and predictive impact of primary tumour location on clinical outcome for these patients.

## 2. Embryology of the midgut and hindgut

During gastrulation, the right (midgut) and left (hindgut) side of the gut develop from the endoderm and extend along the length of the embryo from the buccopharyngeal membrane to the cloacal membrane [18]. The midgut gives rise to the duodenum distal to the ampulla, the entire small bowel, the caecum, appendix, ascending colon and the proximal two-thirds of the transverse colon [19].

The distal third of the transverse colon, splenic flexure, descending colon and sigmoid rectum and the upper part of the anal canal originate from the hindgut [19]. The most distal portion of the hindgut enters into the posterior region of the cloaca, called the primitive anorectal canal, from which the anal region is derived.

Because both the right and left side of the colon derive from the endoderm [18], embryology does not appear to be the major source of the differences observed in the prognosis of CRC. Distinct gene expression differences, reflecting the midgut and hindgut differences, have been reported between the right and left side of the normal colon, as described later in this article [11,20–22].

## 3. Microbiome differences between the normal gut and CRC

Limited data are available on the differences of the microbiome within healthy colon tissue, and there are currently no large analyses published on the distinct differences between the transverse and descending colon.

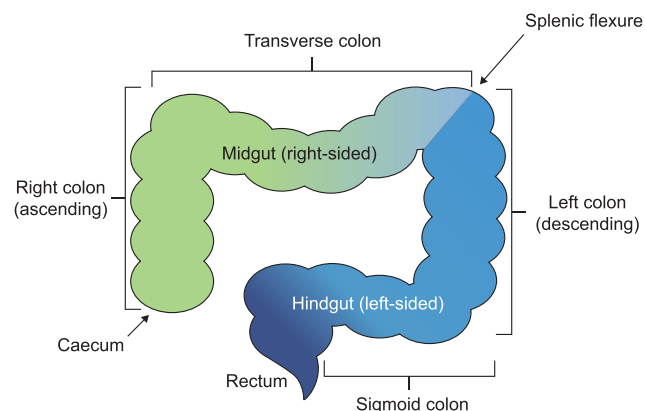


Fig. 1. Schematic diagram of the most commonly used definition of left- and right-sided regions of the colon and rectum.

However, an increasing microbial richness from the proximal colon to the rectum has been reported [23]. The microbiome is believed to play an important part in the formation of CRC. Bacterial phylotypes are known to vary depending on the primary tumour location (Table 1) [23–25]: RCCs have a relatively higher abundance of *Prevotella*, *Pyramido-bacterium*, *Selenomonas* and *Peptostreptococcus* than LCC, which have a higher prevalence of *Fusobacterium*, *Escherichia-Shigella* and *Leptotrichia* compared with RCC [23]. A significantly higher incidence of *Escherichia coli* phylogroup B2 has been detected in mucosal biopsies from patients with RCC compared to those with LCC [24], and a higher risk of *Helicobacter pylori* infection was reported in patients with LCC compared to those with RCC [25]. A lower abundance of Gram-positive, fibre-fermenting clostridia and an increased prevalence of Gram-negative, pro-inflammatory bacteria (i.e. *E. coli* phylogroup B2) has been reported in patients with CRC compared with controls [24,26].

Dense bacterial aggregates, or biofilms, are located within the normal gut and are associated with decreased E-cadherin, enhanced interleukin-6 (IL-6) and signal

transducer and activator of transcription 3 (STAT3) activation and increased epithelial cell proliferation [27]. Biofilms can invade the mucus layer of the colon and may be pathogenic when they make direct contact with the mucosal epithelial cells. Invasive poly-microbial bacterial biofilms have been detected on the majority of RCCs, but on only a small percentage of LCC [27].

It remains unclear whether the changed mucosa following the development of CRC attracts different bacteria or if different bacteria have an ability to destroy the mucosa, which then leads to CRC. Both mechanisms have been postulated. *Prevotella*, *Pyramido-bacterium*, *Selenomonas* and *Peptostreptococcus* were identified in relatively higher abundance in proximal tumours compared with distal tumours [23]. Conversely, *Fusobacterium*, *Escherichia-Shigella* and *Leptotrichia* were relatively abundant in distal colorectal tumours compared with proximal tumours [23]. Recently published data show that CRC-associated bacterial clusters are differentially correlated with mucosal gene expression profiles [28]. Some clusters are partly associated with the expression of pro-inflammatory genes in the mucosa, which may result in CRC in future [28].

Table 1

Microbiome differences between RCC and LCC.

RCC	LCC
<ul style="list-style-type: none"> <li>• Higher abundance of <i>Prevotella</i>, <i>Pyramido-bacterium</i>, <i>Selenomonas</i> and <i>Peptostreptococcus</i> [23]</li> <li>• Higher incidence of <i>Escherichia coli</i> phylogroup B2 [24]</li> </ul>	<ul style="list-style-type: none"> <li>• Higher prevalence of <i>Fusobacterium</i>, <i>Escherichia-Shigella</i> and <i>Leptotrichia</i> [23]</li> <li>• Higher risk of <i>Helicobacter pylori</i> infection [25]</li> </ul>

LCC, left-sided colon carcinoma; RCC, right-sided colon carcinoma.

Table 2

Chromosomal and molecular characteristics of RCC and LCC.

RCC	LCC
<ul style="list-style-type: none"> <li>• High MSI and CIMP [9,11]</li> <li>• Hypermethylation state</li> <li>• <i>KRAS</i> mutations [9,11]</li> <li>• <i>BRAF</i> mutations [9,11]</li> <li>• <i>TGFβR2</i> mutations [33]</li> <li>• <i>PI3KCA</i> mutations [33]</li> <li>• Distribution of CMS subtypes [20] <ul style="list-style-type: none"> <li>◦ CMS1 – 31%</li> <li>◦ CMS2 – 26%</li> <li>◦ CMS3 – 19%</li> <li>◦ CMS4 – 24%</li> </ul> </li> </ul>	<ul style="list-style-type: none"> <li>• Chromosomal aberrations <ul style="list-style-type: none"> <li>◦ Deletion of 8p, 17p (including <i>TP53</i>), 18p (including <i>SMAD4</i>), gain of chromosome 7, 8q (including <i>MYC</i>), 20q, loss of 18q [33]</li> </ul> </li> <li>• Aneuploidy [50]</li> <li>• Frequently mutated genes: [33] <ul style="list-style-type: none"> <li>◦ <i>TP53</i></li> <li>◦ <i>APC</i></li> <li>◦ <i>KRAS</i></li> </ul> </li> <li>• Overexpression: <ul style="list-style-type: none"> <li>◦ EGFR and HER2 gain [22,36]</li> <li>◦ High EGFR ligand expression (EREG and AREG expression) [22,35]</li> <li>◦ High VEGF-1 mRNA expression [38]</li> <li>◦ COX-2 [39]</li> </ul> </li> <li>• Distribution of CMS subtypes [20] <ul style="list-style-type: none"> <li>◦ CMS1 – 7%</li> <li>◦ CMS2 – 56%</li> <li>◦ CMS3 – 10%</li> <li>◦ CMS4 – 27%</li> </ul> </li> </ul>

AREG, amphiregulin; CIMP, CpG island methylator phenotype; CMS, consensus molecular subtype; EGFR, epidermal growth factor receptor; EREG, epiregulin; LCC, left-sided colon carcinoma; MSI, microsatellite instability; RCC, right-sided colon carcinoma; VEGF-1, vascular endothelial growth factor 1.

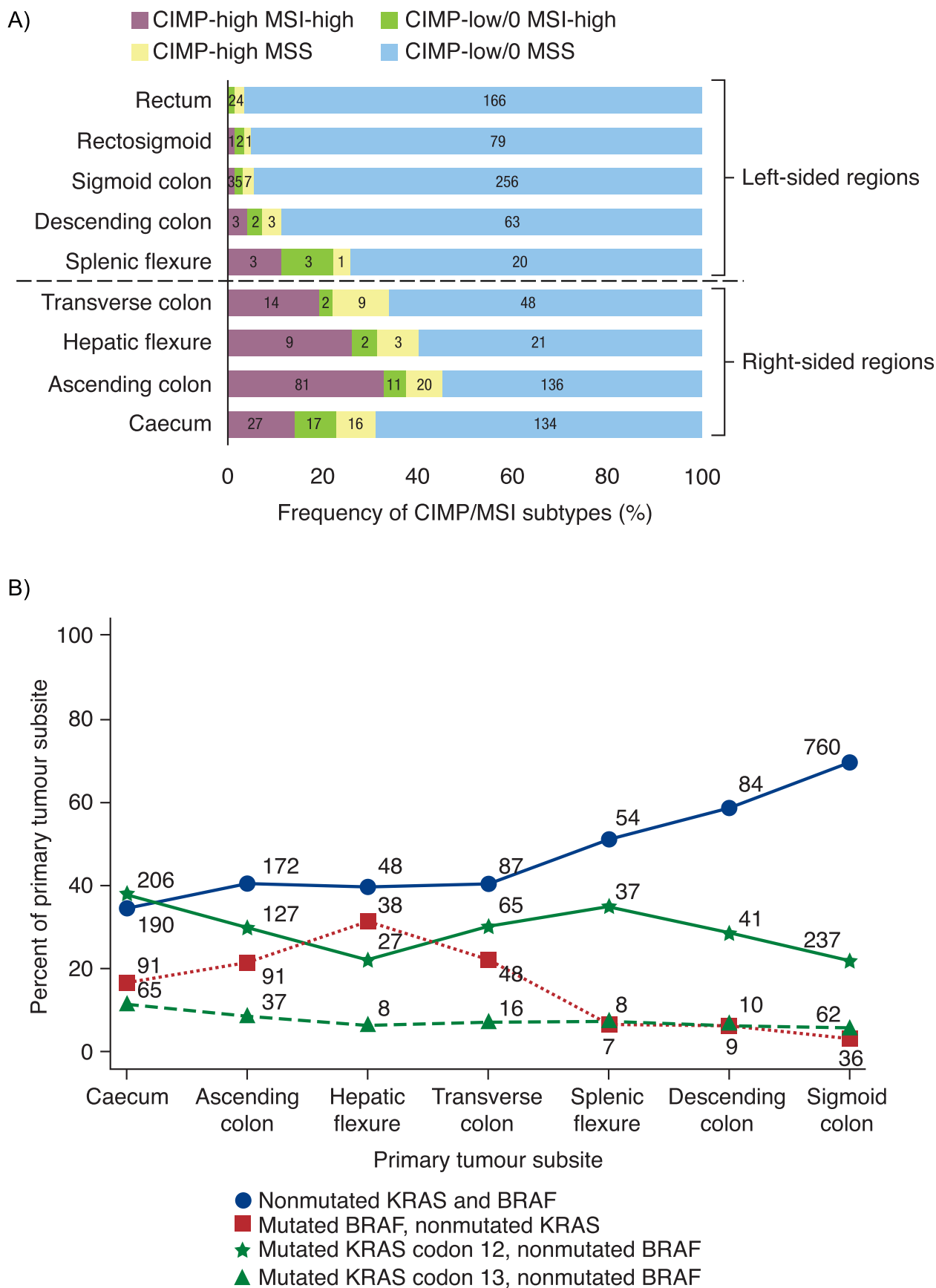


Fig. 2. A) Molecular characteristics of CRC [32] [Reproduced from *Gut* 2012, 'Assessment of colorectal cancer molecular features along bowel subsites challenges the conception of distinct dichotomy of proximal versus distal colorectum', Yamauchi M et al, 61, 847–54,

#### 4. Differences in clinical characteristics according to primary tumour location

A similar or greater proportion of patients with RCC are female, and the median age of patients with RCC at diagnosis is higher compared to patients with LCC [7,8,11]. RCCs are more likely to have high-grade histology and a more advanced tumour stage at initial presentation compared with LCC [7,11,29]. A low-fibre diet, smoking and alcohol excess tend to be associated with LCC [30].

Metastatic spread also differs depending on the primary location of the CRC. RCC more often metastasise to the peritoneum, and a greater proportion of LCC will metastasise to liver and lung [22].

#### 5. Chromosomal and molecular differences according to primary tumour location

A number of chromosomal and molecular differences have been reported between RCC and LCC (Table 2). Chromosomal instability has been detected in approximately 75% of LCC and 30% of RCC [30].

Hypermutation is more prevalent in RCC compared with LCC [22]. RCC have been shown to be associated with an increase in *RAS* and phosphoinositide 3-kinase pathway mutations [31], CpG island methylator phenotype (CIMP)—high and microsatellite instability—high subtypes (Fig. 2A) and *BRAF* mutations (Fig. 2B) [22,32]. The frequency of *KRAS/BRAF* mutations has been noted to progressively decrease from the caecum to sigmoid colon (Fig. 2B) [11]. A higher expression of *TGF $\beta$ 2* mutations also occurs within the RCC compared with the LCC [33].

Mutations in the *APC*, *KRAS*, *SMAD4* and *TP53* genes occur more often in LCC compared with RCC [34]. In addition to the increased chromosomal instability of LCC, these tumours have also been associated with more frequent overexpression of the epidermal growth factor receptor (EGFR) ligands, epiregulin (EREG) and amphiregulin (AREG) and amplification of EGFR and human epidermal growth factor receptor 2 (HER2) [22,35,36]. High AREG expression is inversely associated with *BRAF* mutation and CIMP-high status [35]. Hypermethylation and suppression of EREG and AREG expressions have been demonstrated to be strongly associated with RCC and CIMP-high status [37].

The predominant angiogenic factor, vascular endothelial growth factor (VEGF-1), plays a key role in the progression of CRC. The expression of VEGF-1 has

been reported to be significantly higher in LCC compared with RCC [38]. Similarly, a more frequent expression of cyclooxygenase-2 (COX-2), which also has a role in angiogenesis, was identified in LCC compared with RCC [39].

The CRC Subtyping Consortium has defined four molecular subtypes of CRC (consensus molecular subtypes [CMS] 1–4), based on six published gene expression-based CRC subtyping algorithms and the reported differences in clinical, chromosomal and molecular characteristics between the primary tumour locations [20]. RCC are predominantly CMS1 (microsatellite instability and strong immune activation) and LCC are mostly CMS2 (canonical) (Table 2) [37].

#### 6. Prognostic effects of primary tumour location on clinical outcome

The different clinical and biological profiles of RCC and LCC suggested that primary tumour location might have a potential impact on the prognosis of these patients and strong evidence is now available to confirm this (Table 3) [8–13]. Although tumour localisation is not included within the European Society for Medical Oncology consensus guidelines for the treatment of patients with mCRC, it is mentioned in the current National Comprehensive Cancer Network (NCCN) guidelines [3,40].

The prognostic effect of primary tumour localisation on clinical outcome was first reported in 1990 [4]. In a randomised phase III study (FIRE-1), patients with RCC had a significantly shorter progression-free survival (PFS) and OS compared with those who had LCC [15] (Table 3). This study was limited, however, by its small sample size. Further conclusive evidence was provided by multivariable analysis of a prospective pharmacogenetic study (PROVETTA) and two randomised phase III studies (AVF2107g and NO16966) of over 2000 patients with previously untreated mCRC: superior OS and PFS were observed in patients with LCC compared with RCC across all three studies [8]. RCC was therefore confirmed as a negative prognostic variable. A stepwise improvement in OS from the RCC to LCC has been demonstrated by subgroup analysis of OS and time-to-recurrence (TTR) by primary tumour location (Fig. 3) [11]. Caecal tumours had the lowest TTR and OS, and sigmoid colonic tumours had the highest TTR and OS.

Recently, a meta-analysis of 66 clinical studies has been published, comparing the OS of RCC versus LCC



Table 3

Summary of the prognostic impact of CRC location on clinical outcomes.

Study details	Regimens	Median PFS (RCC versus LCC, months) HR (95% CI), P value	Median OS (RCC versus LCC, months) HR (95% CI), P value
<b>Prospective, pharmacogenetics study</b>			
PROVETTA <sup>a</sup> [8] (n = 200)	FOLFIRI + BEV	9.9 versus 12.1 0.52 (0.36–0.75), <0.001 <sup>a</sup>	24.8 versus 42.0 0.44 (0.28–0.70), <0.001 <sup>a</sup>
PROVETTA <sup>a</sup> : non-mucinous/ <i>BRAF</i> WT subgroup [8] (n = 155)	FOLFIRI + BEV	10.0 versus 13.0 0.54 (0.34–0.84), 0.01 <sup>a</sup>	28.8 versus 47.6 0.52 (0.30–0.93), 0.02 <sup>a</sup>
<b>Retrospective studies</b>			
Chinese 2-center study [17] (n = 110)	CT + CET	5.6 versus 9.1 ND, 0.244	25.1 versus 28.9 ND, 0.512
Chinese 2-centre study [17] (n = 117)	CT	5.7 versus 6.2 ND, 0.160	19.8 versus 20.1 ND, 0.593
Taiwanese single-centre case–control study [51] (n = 121)	FOLFOX or FOLFIRI + CET or BEV	5.8 versus 11.8 ND, <0.001 <sup>a</sup>	15.7 versus 27.7 ND, 0.008 <sup>a</sup>
<b>Randomised, phase II studies</b>			
AIO KRK-0104 [42] (n = 146)	CET + CAPIRI or CET + CAPOX	5.2 versus 7.8 0.67 (0.47–0.95), 0.02	14.8 versus 26.3 0.63 (0.43–0.92), 0.016
AIO KRK-0104: <i>KRAS</i> codon 12/13 WT [42] (n = 95)	CET + CAPIRI or CET + CAPOX	4.6 versus 8.4 0.54 (0.34–0.85), 0.007 <sup>a</sup>	13.0 versus 29.0 0.42 (0.25–0.67), <0.001 <sup>a</sup>
AIO KRK-0104: <i>KRAS</i> codon 12/13 MT [42] (n = 51)	CET + CAPIRI or CET + CAPOX	7.5 versus 5.8 1.01 (0.56–1.82), 0.96	18.9 versus 19.7 1.3 (0.68–2.34), 0.46
PEAK <sup>b</sup> [14] (n = 65)	Pmab + FOLFOX	10.3 versus 14.6 ND	22.5 versus 43.4 ND
PEAK <sup>b</sup> [14] (n = 66)	BEV + FOLFOX	12.6 versus 11.5 ND	23.3 versus 32.0 ND
<b>Randomised, phase III studies</b>			
FIRE-1 [15] (n = 423)	FUFIRI or mIROX	6.0 versus 8.2 0.75 (0.59–0.87), 0.024 <sup>a</sup>	13.6 versus 21.8 0.65 (0.50–0.84), 0.001 <sup>a</sup>
FIRE-1 [15] (n = 209)	mIROX	6.0 versus 7.8 0.84 (0.59–1.21), 0.35	14.0 versus 20.4 0.74 (0.51–1.08), 0.12
FIRE-1 [15] (n = 214)	FUFIRI	6.0 versus 8.7 0.66 (0.46–0.94), 0.02 <sup>a</sup>	12.5 versus 25.0 0.55 (0.39–0.79), 0.001 <sup>a</sup>
AVF2017g <sup>c</sup> [8] (n = 559)	CT ± BEV	7.1 versus 8.5 0.68 (0.55–0.83), <0.001 <sup>a</sup>	14.6 versus 20.4 0.55 (0.43–0.70), <0.001 <sup>a</sup>
AVF2017g <sup>c</sup> [8] (n = 277)	CT + BEV	8.7 versus 11.1 0.62 (0.45–0.85), 0.01 <sup>a</sup>	15.9 versus 24.2 0.49 (0.34–0.70), <0.001 <sup>a</sup>
AVF2017g <sup>c</sup> [8] (n = 282)	CT	5.4 versus 8.0 0.72 (0.55–0.96), 0.02 <sup>a</sup>	13.6 versus 18.0 0.62 (0.44–0.86), 0.01 <sup>a</sup>
NCIC CO.17 <sup>d</sup> : re-analysis [48] (n = 199)	BSC	ND	ND
NO16966 <sup>e</sup> [8] (n = 1268)	FOLFOX4 or XELOX or FOLFOX4 + BEV or XELOX + BEV	1.07 (0.79–1.44), 0.67 7.6 versus 8.9 0.90 (0.79–1.03), 0.12	0.96 (0.70–1.31), 0.78 18.0 versus 23.0 0.71 (0.62–0.82), <0.001 <sup>a</sup>
NO16966 <sup>e</sup> [8] (n = 441)	FOLFOX4 + BEV or XELOX + BEV	8.6 versus 10.0 0.95 (0.76–1.19), 0.64	20.6 versus 24.7 0.78 (0.61–0.99), 0.04 <sup>a</sup>
NO16966 <sup>e</sup> [8] (n = 827)	FOLFOX4 or XELOX	7.0 versus 8.3 0.87 (0.74–1.03), 0.10	17.0 versus 22.0 0.67 (0.57–0.80), <0.001 <sup>a</sup>
CALGB/SWOG 80405 <sup>f</sup> : <i>KRAS</i> WT [12] (n = 1025)	CET + CT or BEV + CT	8.9 versus 11.5 1.25 (1.08–1.46), 0.002	19.4 versus 34.2 1.56 (1.32–1.84), <0.0001
CALGB/SWOG 80405 <sup>f</sup> : <i>KRAS</i> MT [12] (n = 213)	CET + CT or BEV + CT	ND	23.1 versus 30.3 1.28 (0.95–1.73), <0.0001
PRIME <sup>g</sup> [14] (n = 182)	Pmab + FOLFOX	8.9 versus 12.9	22.5 versus 32.5
PRIME <sup>g</sup> [14] (n = 180)	FOLFOX	7.3 versus 9.3	21.5 versus 23.6
FIRE-3 <sup>h</sup> : <i>RAS</i> exon 2 WT [16] (n = 195)	CET + FOLFIRI	7.6 versus 10.7 2.0 (1.36–2.93), <0.001 <sup>a</sup>	18.3 versus 38.3 2.84 (1.86–4.33), <0.001 <sup>a</sup>
FIRE-3 <sup>h</sup> : <i>RAS</i> exon 2 WT [16] (n = 199)	BEV + FOLFIRI	9.0 versus 10.7 1.38 (0.99–1.94), 0.06	23.0 versus 28.0 1.48 (1.02–2.16), 0.04
CRYSTAL <sup>i</sup> : <i>RAS</i> WT [16] (n = 175)	FOLFIRI + CET	8.1 versus 12.0 1.77 (1.08–2.91), 0.02	18.5 versus 28.7 1.93 (1.24–2.99), 0.003
CRYSTAL <sup>i</sup> : <i>RAS</i> WT [16] (n = 189)	FOLFIRI	7.1 versus 8.9 1.54 (0.96–2.46), 0.07	15.0 versus 21.7 1.35 (0.93–1.97), 0.11

Table 3 (continued)

Study details	Regimens	Median PFS (RCC versus LCC, months) HR (95% CI), P value	Median OS (RCC versus LCC, months) HR (95% CI), P value
<b>Registry</b>			
Australian TRACC registry [13] (n = 926)	CT ± BEV	7.6 versus 10.2 (rectum 10.3) ND, <0.0001 <sup>a</sup>	18.2 versus 23.6 (rectum 26.2) ND, 0.0007 <sup>a</sup>

Clinicaltrials.gov identifiers: <sup>a</sup>NCT01363739; <sup>b</sup>NCT00819780; <sup>c</sup>NCT00109070; <sup>d</sup>NCT00079066; <sup>e</sup>NCT00069095; <sup>f</sup>NCT00265850; <sup>g</sup>NCT00364013; <sup>h</sup>NCT00433927; <sup>i</sup>NCT00154102.

BEV, bevacizumab; BSC, best supportive care; CAPIRI, capecitabine, irinotecan; CAPOX, capecitabine, oxaliplatin; CET, cetuximab; CI, confidence interval; CT, chemotherapy; FOLFOX, bolus 5-fluorouracil/leucovorin/oxaliplatin; FOLFIRI, bolus 5-fluorouracil/leucovorin/irinotecan; FUFIRI, infusional 5-fluorouracil/leucovorin/irinotecan; HR, hazard ratio; LCC, left-sided colon carcinoma; mIROX, irinotecan, oxaliplatin; MT, mutated; ND, not determined (not published in primary source cited); OS, overall survival; PFS, progression-free survival; Pmab, panitumumab; RCC, right-sided colon carcinoma; WT, wild-type; XELOX, capecitabine, oxaliplatin.

<sup>a</sup> Statistically significantly different (P<0.05).

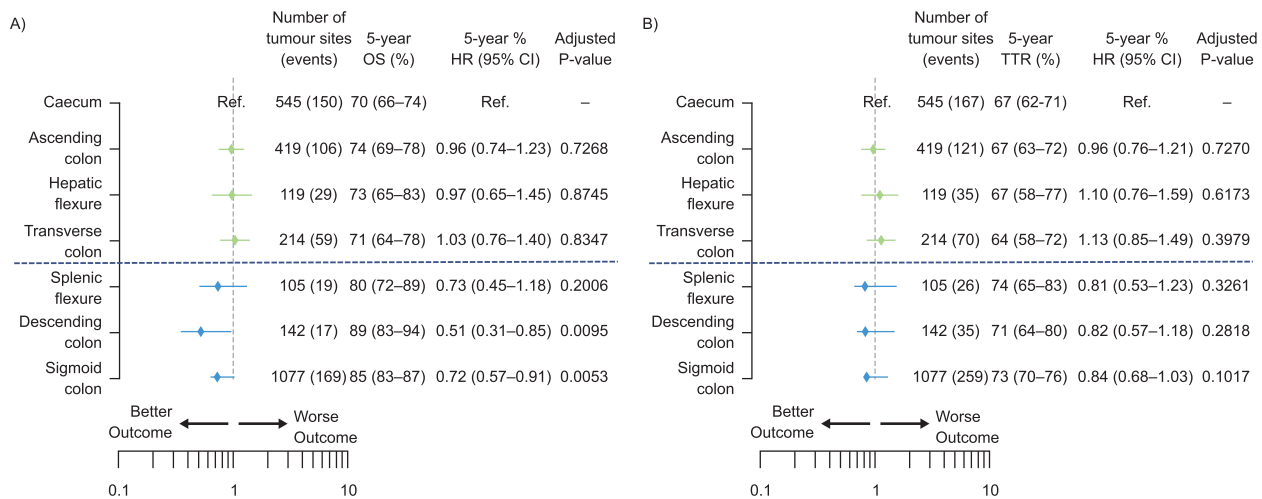


Fig. 3. Clinical outcome of patients with stage III CRC according to tumour localisation: A) overall survival and B) time-to-recurrence [11] [Reproduced from *Clin Cancer Res* 2015, ‘Analysis of molecular markers by anatomic tumor site in Stage III colon carcinomas from adjuvant chemotherapy trial NCCTG N0147 (Alliance)’ Sinicrope FA et al, 21(23), 5294-5304, copyright 2017 with permission from AACR]. CI, confidence intervals; CRC, colorectal carcinoma; HR, hazard ratio; OS, overall survival; Ref., reference group; TTR, time-to-response.

in over 1.4 million patients with early and advanced CRC [41]. A pooled hazard ratio of 0.82 (P<0.001) was reported in favour of LCC. Patients with LCC had a 20% reduction in the risk of death compared with RCC, independent of ethnicity, disease stage and type of study. This meta-analysis concluded that primary tumour location should be established as a key criterion for confirming OS outcomes in all stages of CRC.

Several studies have investigated the contribution of mutational status (i.e. *KRAS* and *BRAF*) and key marker expression (i.e. HER2 and EGFR) to the impact of primary tumour location on prognosis [11,12,35,42]. In patients with *KRAS* codon 12/13 wild-type (WT) CRC, LCC were associated with a significantly longer PFS and OS compared with RCC [42]. No impact of primary tumour location on clinical outcomes was observed in patients with *KRAS*-mutated (MT) mCRC in this study. In the North Central Cancer Treatment

Group (NCCTG) N0147 (Alliance) study, however, *KRAS*-MT LCC was associated with poorer OS compared with *KRAS*-MT RCC [11]. *BRAF* mutations have been shown to be associated with poorer outcomes for patients with mCRC than *BRAF* WT, and these are more prevalent in RCC than LCC [11]. The current international guidelines for the management of patients with mCRC recognise the prognostic impact of mutational status and recommend that patients are tested for *RAS* and *BRAF* mutation status before establishing a first-line treatment regimen [3,40].

However, *RAS* and *BRAF* mutational status are not the only prognostic factors for patients with mCRC. In a multivariate analysis of two randomised phase III studies (CRYSTAL and FIRE-3), LCC and RCC were highly prognostic for PFS and OS even when patients with *BRAF* mutation were excluded [16]. In subgroup analysis from two randomised phase III studies (FIRE-3

and TRIBE), *IL-6* genetic variants were identified as a prognostic factor for patients with mCRC treated with first-line bevacizumab-based chemotherapy, depending on primary tumour location [43].

To summarise, the primary tumour location is a known prognostic factor for patients with CRC [8–13]. A meta-analysis from prospective and retrospective clinical studies reporting OS data for LCC and RCC mCRC concluded that patients with RCC had poorer prognosis than those with LCC [41]. This appears to be independent of the mutational spectrum within these tumours [12,16].

## 7. Predictive effects of primary tumour location on clinical outcome

Given the differential expression of EGFR and of EGFR ligands, and the differing incidence of *KRAS* mutations between RCC and LCC, several studies have investigated the predictive effect of primary tumour location on clinical outcomes from treatment with EGFR and VEGF inhibitors in patients with CRC [12–17] (Table 4).

*Post-hoc* analysis of clinical studies suggests that although anti-EGFR therapy provides clinical benefit to patients with *RAS* WT mCRC, this benefit is not relevant for patients with RCC [12,16,44]. In a subgroup analysis by tumour location from the CALGB/SWOG 80405 study, prolonged OS and PFS were observed in patients with LCC treated with either cetuximab or bevacizumab plus 5-fluorouracil/leucovorin/irinotecan (FOLFIRI) or 5-fluorouracil/leucovorin/oxaliplatin (FOLFOX), however outcomes were poorer in patients with RCC who were treated with cetuximab plus FOLFIRI or FOLFOX [12]. In the FIRE-3 and CRYSTAL randomised phase III studies of patients with *RAS* WT CRC, differential treatment effects were observed between primary tumour locations [16]. Patients who received cetuximab plus FOLFIRI in the CRYSTAL study had significantly improved outcomes compared with those who received FOLFIRI alone. This benefit was greater in patients with LCC compared with those with RCC [16]. In FIRE-3, patients with LCC who received cetuximab plus FOLFIRI as first-line therapy had a significantly longer OS than those who received bevacizumab plus FOLFIRI [16]. No significant difference in clinical outcomes was observed between these treatment groups for patients with RCC. This may be driven by LCC having a higher EGFR expression than RCC, differences in EGFR ligand expression or other as yet unidentified factors [22]. The NCCN guidelines recommend the use of anti-EGFR substances for the treatment of *RAS* WT LCC only [40].

Similar data have been presented for the use of panitumumab in first-line mCRC [14]. A retrospective analysis of the PRIME study showed a significant

survival benefit for patients with LCC treated with FOLFOX plus panitumumab when compared with FOLFOX alone. In contrast, no benefit was associated with FOLFOX plus panitumumab in patients with RCC. Since this is in accordance with the cetuximab data, it appears to be a class effect. A meta-analysis comparing clinical outcome data from multiple clinical studies according to primary tumour location has already been published [45].

In the prospective PROVETTA clinical study of patients with CRC who received bevacizumab plus chemotherapy, VEGF expression was similar across primary tumour locations [8]. Efficacy results from the PROVETTA, AVF2107g and NO16966 studies confirmed that first-line bevacizumab in combination with chemotherapy improves clinical outcomes for patients with CRC, irrespective of primary tumour location [8]. Several other clinical studies have also provided evidence that tumour location does not appear to be predictive of benefit from bevacizumab treatment in patients with CRC [12,13,46,47].

Limited data are currently available on the predictive impact of primary tumour location on clinical outcome following second-line or later treatment (Table 5). In a re-analysis of the phase III NCIC CO-17 study of patients with *KRAS* WT mCRC who had failed standard chemotherapy, those with LCC who received cetuximab experienced a significantly improved PFS compared with those treated with BSC [48]. This clinical benefit was not observed in patients with RCC. Similarly, in preliminary efficacy data from another phase III study (Study 20050181), where patients with mCRC received second-line panitumumab plus FOLFIRI, improved clinical outcomes were observed in patients with LCC compared with RCC [14]. Although these findings suggest that tumour location may strongly predict clinical benefit with cetuximab or panitumumab, these studies were limited by their low sample size and a lack of stratification by *BRAF* status in some studies. Retrospective analysis from the phase III FIRE-3 study of patients with *KRAS* WT mCRC reported a significantly greater efficacy of second-line therapy in patients with LCC compared with RCC [44]. This difference was more evident for patients with LCC who received second-line cetuximab compared with those who received second-line bevacizumab. These observations indicate that efficacy of second-line therapy is associated with primary tumour location.

HER2/neu has been identified as a predictive biomarker in mCRC [36]. HER2/neu-amplifications have been shown to be more prevalent in LCC than in RCC. This suggests that patients with LCC may benefit more from a HER2-directed therapy, including agents such as trastuzumab [36]. A recent study has reported similar clinical outcomes for patients with HER2-amplified or HER2-non-amplified *RAS/BRAF* WT CRC on first-line therapy without anti-EGFR antibodies [49]. Patients with HER2-amplified *RAS/BRAF*



Table 4

Summary of the predictive impact of CRC location on clinical outcomes following first-line therapy.

Study details	PFS by treatment arm (months) HR (95% CI), P value		OS by treatment arm (months) HR (95% CI), P value	
	RCC	LCC	RCC	LCC
<b>Retrospective study</b>				
Chinese 2-centre study [17] (n = 227)	CT (5.7) versus CT + CET (5.6) ND, 0.904	CT (6.2) versus CT + CET (9.1) ND, 0.002 <sup>a</sup>	CT (19.8) versus CT + CET (25.1) ND, 0.553	CT (20.1) versus CT + CET (28.9) ND, 0.036 <sup>a</sup>
<b>Randomised, phase II study</b>				
PEAK <sup>a</sup> [14] (n = 133)	Pmab + FOLFOX (10.3) versus BEV + FOLFOX (12.6) 0.88 (0.39–2.02), ND	Pmab + FOLFOX (14.6) versus BEV + FOLFOX (11.5) 0.67 (0.44–1.02), ND	Pmab + FOLFOX (22.5) versus BEV + FOLFOX (23.3) 0.63 (0.26–1.54), ND	Pmab + FOLFOX (43.4) versus BEV + FOLFOX (32.0) 0.77 (0.46–1.28), ND
<b>Randomised, phase III studies</b>				
FIRE-1 [15] (n = 423)	FUFIRI (6.0) versus mIROX (6.0) 0.94 (0.60–1.489), 0.79	FUFIRI (8.7) versus mIROX (7.8) 1.17 (0.94–1.46), 0.17	FUFIRI (12.5) versus mIROX (14.5) 0.90 (0.57–1.43), 0.65	FUFIRI (25.0) versus mIROX (20.4) 1.17 (0.93–1.47), 0.19
CALGB/SWOG 8040 <sup>b</sup> : KRAS WT [12] (n = 1137)	CET (7.7) versus BEV (9.5) ND, ND ‘similar to OS’	CET (12.0) versus BEV (11.1) ND, ND ‘similar to OS’	CET (16.4) versus BEV (24.5) ND, 0.03 <sup>a</sup> (CET versus BEV superiority log rank)	CET (37.5) versus BEV (32.1) ND, 0.04 <sup>a</sup> (CET versus BEV superiority log rank)
PRIME <sup>c</sup> [14] (n = 362)	Pmab + FOLFOX (8.9) versus FOLFOX (7.3) 0.71 (0.4–1.27), ND	Pmab + FOLFOX (12.9) versus FOLFOX (9.3) 0.69 (0.54–0.88), ND	Pmab + FOLFOX (22.5) versus FOLFOX (21.5) 0.94 (0.53–1.67), ND	Pmab + FOLFOX (32.5) versus FOLFOX (23.6) 0.67 (0.56–0.86), ND
FIRE-3 <sup>d</sup> : RAS exon 2 WT [16] (n = 394)	FOLFIRI + CET (7.6) versus FOLFIRI + BEV (9.0) 1.44 (0.92–2.26), 0.11	FOLFIRI + CET (10.7) versus FOLFIRI + BEV (10.7) 0.90 (0.71–1.14), 0.38	FOLFIRI + CET (18.3) versus FOLFIRI + BEV (23.0) 1.31 (0.81–2.11), 0.28	FOLFIRI + CET (38.3) versus FOLFIRI + BEV (28.0) 0.63 (0.48–0.85), 0.002
CRYSTAL <sup>e</sup> : RAS WT [16] (n = 364)	FOLFIRI + CET (8.1) versus FOLFIRI (7.1) 0.87 (0.47–1.62), 0.66	FOLFIRI + CET (12.0) versus FOLFIRI (8.9) 0.50 (0.34–0.72), <0.001	FOLFIRI + CET (18.5) versus FOLFIRI (15.0) 1.08 (0.65–1.81), 0.76	FOLFIRI + CET (28.7) versus FOLFIRI (21.7) 0.65 (0.50–0.86), 0.002
<b>Registry</b>				
TRACC Australian Registry [13] (n = 926)	CT (4.9) versus CT + BEV (8.54) 0.46 (0.36–0.60), <0.001 <sup>a</sup>	CT (7.5; rectum: 7.1) versus CT + BEV (10.5; rectum 11.3) 0.71 (0.56–0.91) (rectum 0.64 [0.50–0.84]), 0.006 <sup>a</sup> (rectum 0.001 <sup>a</sup> )	ND ND	ND ND

Clinicaltrials.gov identifiers: <sup>a</sup>NCT00819780; <sup>b</sup>NCT00265850; <sup>c</sup>NCT00364013; <sup>d</sup>NCT00433927; <sup>e</sup>NCT00154102.

BEV, bevacizumab; CET, cetuximab; CI, confidence interval; CT, chemotherapy; FOLFOX, bolus 5-fluorouracil/leucovorin/oxaliplatin; FOLFIRI, bolus 5-fluorouracil/leucovorin/irinotecan; FUFIRI, infusional 5-fluorouracil/leucovorin/irinotecan; HR, hazard ratio; LCC, left-sided colon carcinoma; mIROX, irinotecan plus oxaliplatin; ND, not determined (not published in primary source cited); OS, overall survival; PFS, progression-free survival; Pmab, panitumumab; RCC, right-sided colon carcinoma.

<sup>a</sup> Statistically significantly different (P<0.05).

Table 5

Summary of the predictive impact of CRC location on clinical outcomes following second-line therapy.

Study details	PFS by treatment arm (months) HR (95% CI), P value		OS by treatment arm (months) HR (95% CI), P value	
	RCC	LCC	RCC	LCC
<b>Retrospective study</b>				
Chinese 2-centre study [17] (n = 189)	CT (4.2) versus CT + CET (3.3) ND, 0.761	CT (3.5) versus CT + CET (4.9) ND, 0.064	CT (13.0) versus CT + CET (13.4) ND, 0.652	CT (12.4) versus CT + CET (17.1) ND, 0.047 <sup>a</sup>
<b>Randomised, phase III studies</b>				
NCIC CO.17 <sup>a</sup> : re-analysis [48] (n = 399)	CET (1.8) versus BSC (1.8) 0.93 (0.66–1.29), 0.64	CET (3.6) versus BSC (1.8) 0.53 (0.41–0.69), <0.0001 <sup>a</sup>	CET (4.8) versus BSC (4.5) 1.00 (0.70–1.43), 1.00	CET (6.8) versus BSC (4.2) 0.60 (0.46–0.80), 0.0003 <sup>a</sup>
20050181 <sup>b</sup> [14] (n = 335)	Pmab + FOLFIRI (6.8) versus FOLFIRI (3.7) 0.62 (0.34–1.13), ND	Pmab + FOLFIRI (8.0) versus FOLFIRI (6.6) 0.89 (0.69–1.13), ND	Pmab + FOLFIRI (11.9) versus FOLFIRI (10.9) 0.84 (0.46–1.54), ND	Pmab + FOLFIRI (20.1) versus FOLFIRI (16.9) 0.97 (0.76–1.26), ND
FIRE-3 <sup>c</sup> : <i>RAS</i> exon 2 WT [44] (n = 411)	FOLFIRI + CET (4.0) versus FOLFIRI + BEV (3.3) 1.09 (0.62–1.90)	FOLFIRI + CET (7.3) versus FOLFIRI + BEV (5.3) 0.61 (0.44–0.84), 0.002		

Clinicaltrials.gov identifiers: <sup>a</sup>NCT00819780; <sup>b</sup>NCT00079066; <sup>c</sup>NCT00433927.

BSC, best supportive care; CET, cetuximab; CI, confidence interval; FOLFIRI, bolus 5-fluorouracil/leucovorin/irinotecan; HR, hazard ratio; LCC, left-sided colon carcinoma; ND, not determined (not published in primary source cited); OS, overall survival; PFS, progression-free survival; Pmab, panitumumab; RCC, right-sided colon carcinoma.

<sup>a</sup> Statistically significantly different (P<0.05).

WT CRC who received anti-EGFR antibodies after first-line therapy had a significantly shorter PFS compared to those with HER2-non-amplified CRC. HER2 amplification, therefore, appears to be a predictive biomarker for reduced benefit from anti-EGFR antibody therapy and potential benefit from HER2-targeted therapy (i.e. trastuzumab and lapatinib).

Primary tumour location appears, therefore, to have a predictive effect on first- [12,14,16] and second-line [14,44,48] anti-EGFR treatment and treatment in the chemo-refractory setting [48]. Primary tumour location does not appear to be predictive of clinical benefit from anti-VEGF treatment [8,12,13,46,47].

## 8. Conclusions

Distinct subsets of mCRC can be defined based on the location of the primary tumour. Patients with RCC and LCC differ in their microbiome, clinical characteristics, molecular profiling, clinical outcome and response to treatment. The driver(s) and reason(s) for these differences remain unknown.

Based on current knowledge, and until the use of anti-EGFR antibodies has been defined for each molecular subgroup of mCRC, we suggest that patients with *RAS* WT RCC may benefit more from initial treatment with bevacizumab in combination with chemotherapy and those with LCC should receive first-line treatment with anti-EGFR therapies and chemotherapy. Currently, data on *RAS*-MT LCC versus RCC are limited; therefore, the prognostic and predictive value of the primary tumour site within the *RAS* MT

population still requires evaluation. In addition, further investigations are required to determine if the primary tumour location and type of chemotherapy backbone used (i.e. oxaliplatin-based [XELOX or FOLFOX] or irinotecan-based [FOLFIRI or single-agent irinotecan]) are associated with different efficacies. Primary tumour location should not only be a critical stratification factor for clinical trials but should also be considered for the translational workup of clinical trials and the retrospective analyses of prognostic and predictive markers.

## Conflict of interest statement

SS has received honoraria and travel expenses and serves as an advisor for Amgen, Bayer, Lilly, Merck KGaA, Roche, Sanofi and Sirtex. ST has received honoraria from Amgen, Bayer, BMS, Eli Lilly, Merck Serono, MSD, Sanofi and Roche. PG has received research funding from Amgen, Bayer, Merck, Roche, Servier and Sirtex. LT is an employee of Roche Pharma AG. HJL has received honoraria and travel expenses and has served as an advisor for Bayer, Bristol-Myers Squibb, Boehringer-Ingelheim, Merck KGaA and Roche.

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