

1^ο Πανελλήνιο
Συνέδριο



Κολοπρωκτολογίας

Τεκμηριωμένη γνώση
εξατομικευμένη προσέγγιση

23-25

Ιανουαρίου 2020

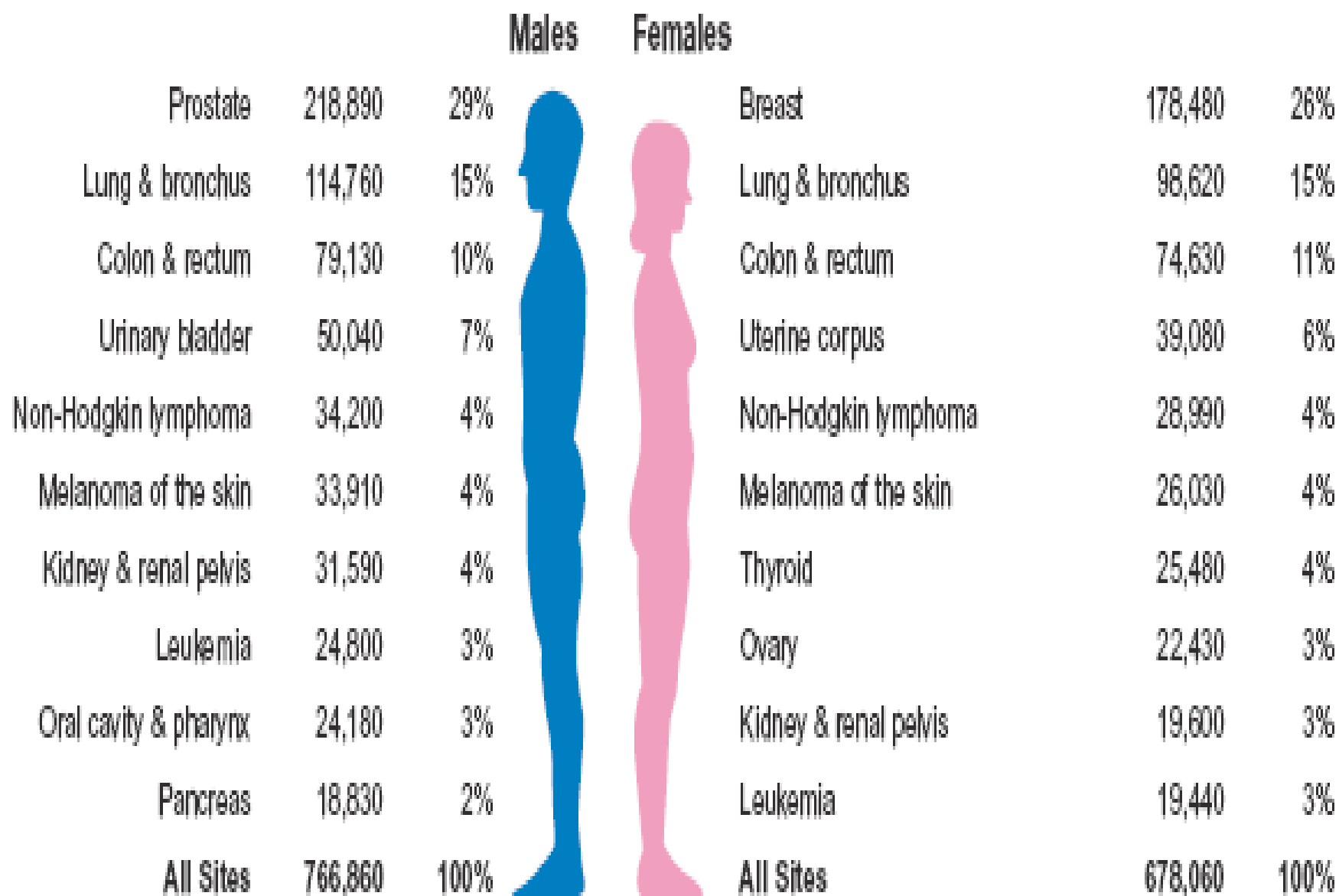
Εξατομικευμένη ογκολογική προσέγγιση ακριβείας στον Ορθοκολικό καρκίνο.

Αλέξανδρος Τζοβάρας, PhD
Παθολόγος Ογκολόγος

Disclosures (Conflicts of Interest)

▶ BMS, AMGEN, LEO

Estimated New Cases*



What Influences Treatment Choices in mCRC?

Patient characteristics

Comorbidities

Prior adjuvant treatment

Age

Performance status

Tumor characteristics

Tumor burden

Resectability

Tumor location

Molecular characteristics

RAS

BRAF

MSI-high

HER2

Patient preference

Quality of life

Toxicity profile



1L

2L

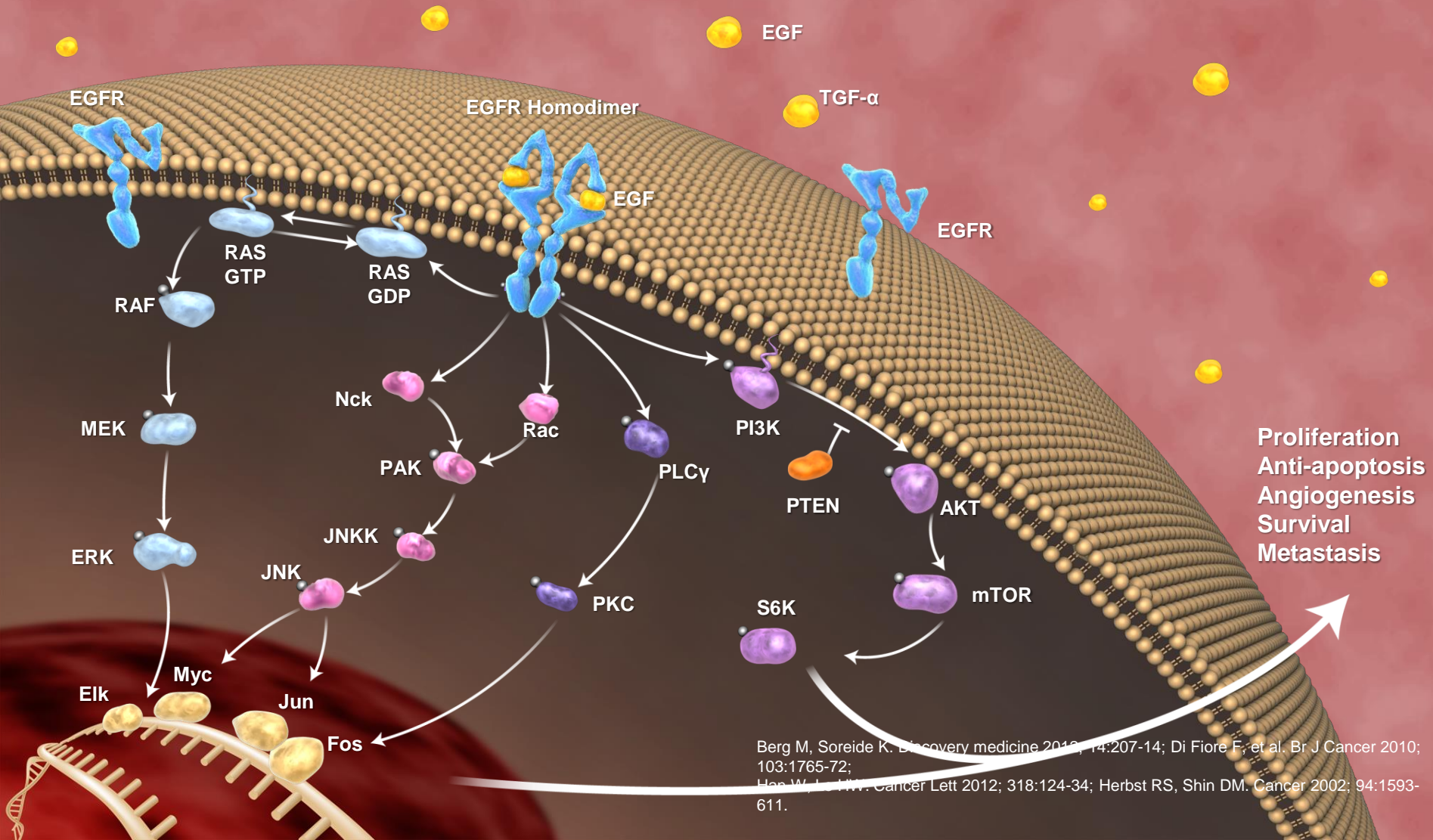
3L

4L

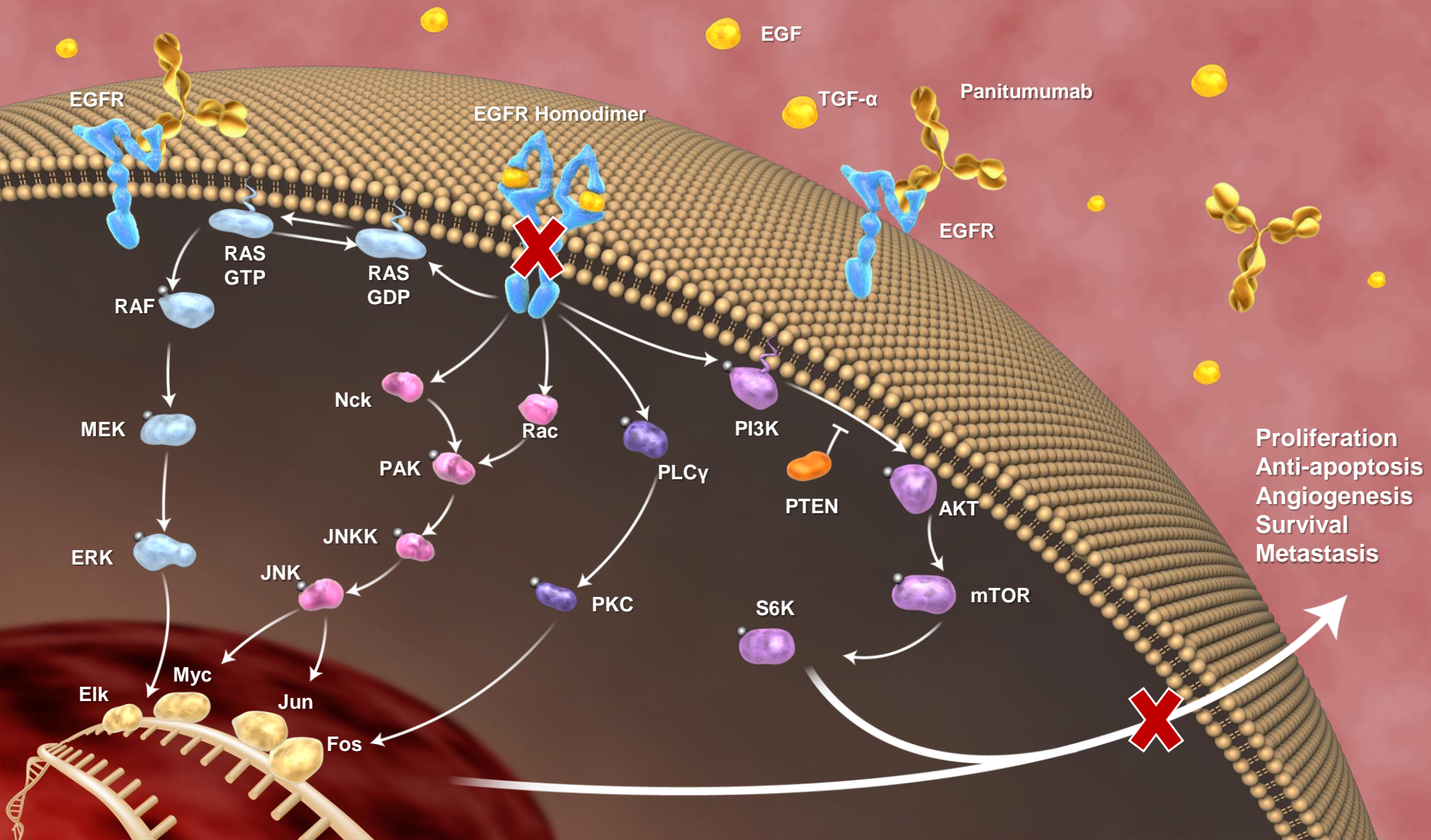


Therapy tailored according to individual patient needs

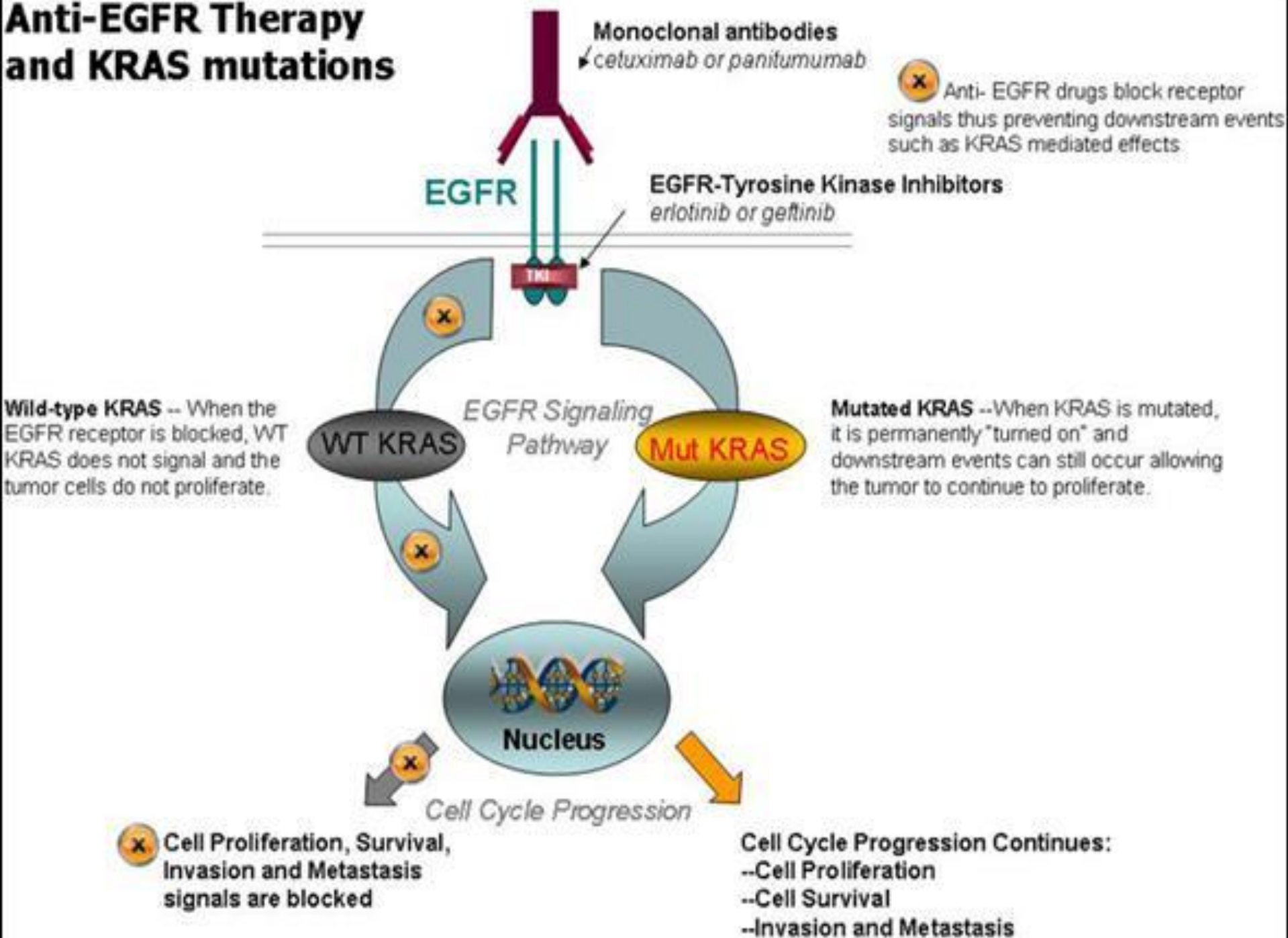
EGFR activation may involve downstream signalling pathways that include RAS proteins



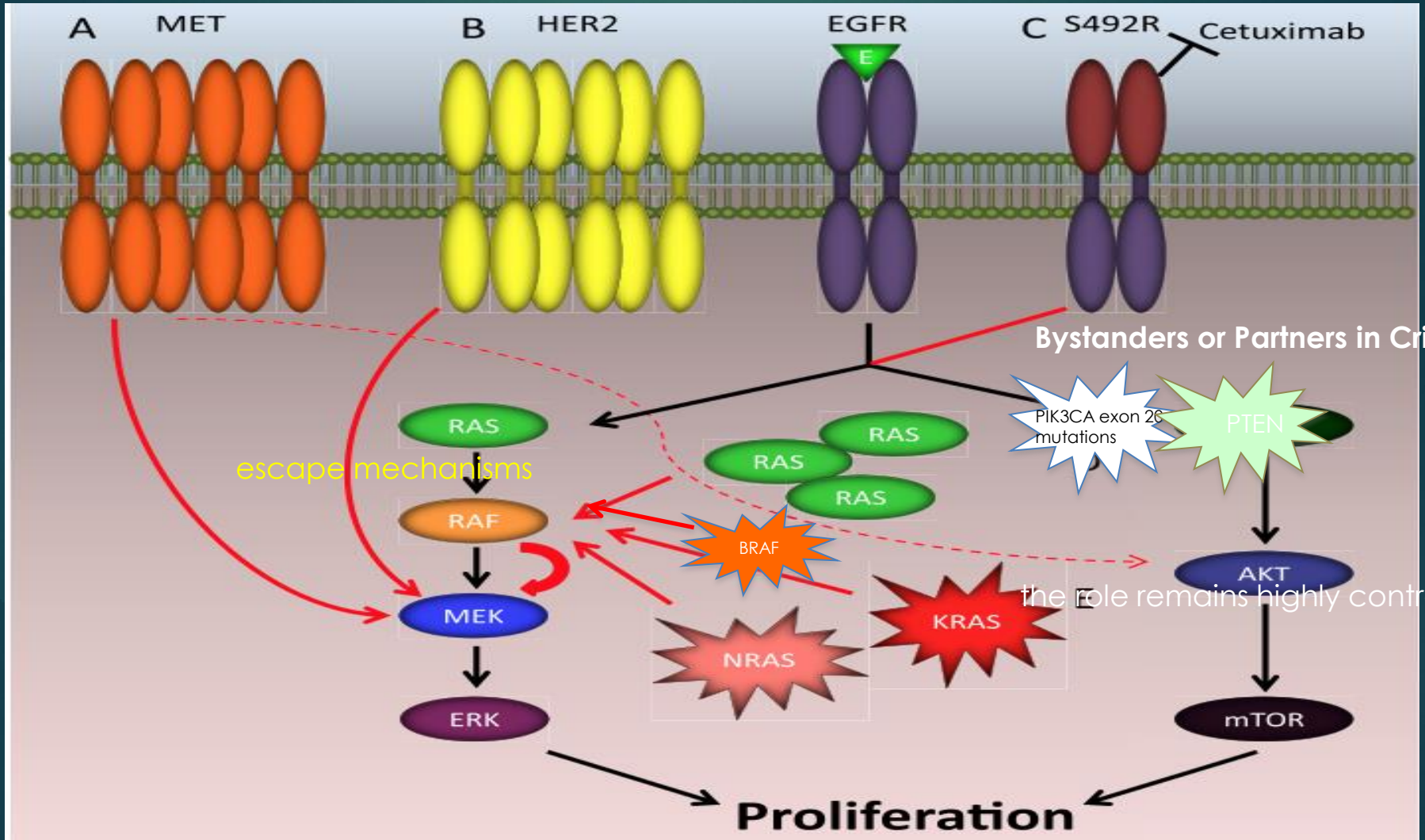
EGFR inhibitory Mabs inhibits EGFR dimerisation and subsequent downstream signalling



Anti-EGFR Therapy and KRAS mutations



Mechanisms of resistance are genetically heterogeneous but they biochemically converge on key signaling pathways



The RAS story

Major survival benefit in selected patients

Study	Comparison of targeted agents	OS HR (RAS wt)	Difference in median OS between treatment arms (months)
PRIME ¹	Panitumumab vs no	0.77	5.6 ↑
CRYSTAL ²	Cetuximab vs no	0.69	8.2 ↑
FIRE-3 ³	Cetuximab vs bev	0.70	8.1 ↑
PEAK ⁴	Panitumumab vs bev	0.63	12.4 ↑)

1. Douillard J-Y, et al. N Engl J Med 2013;369:1023–1034

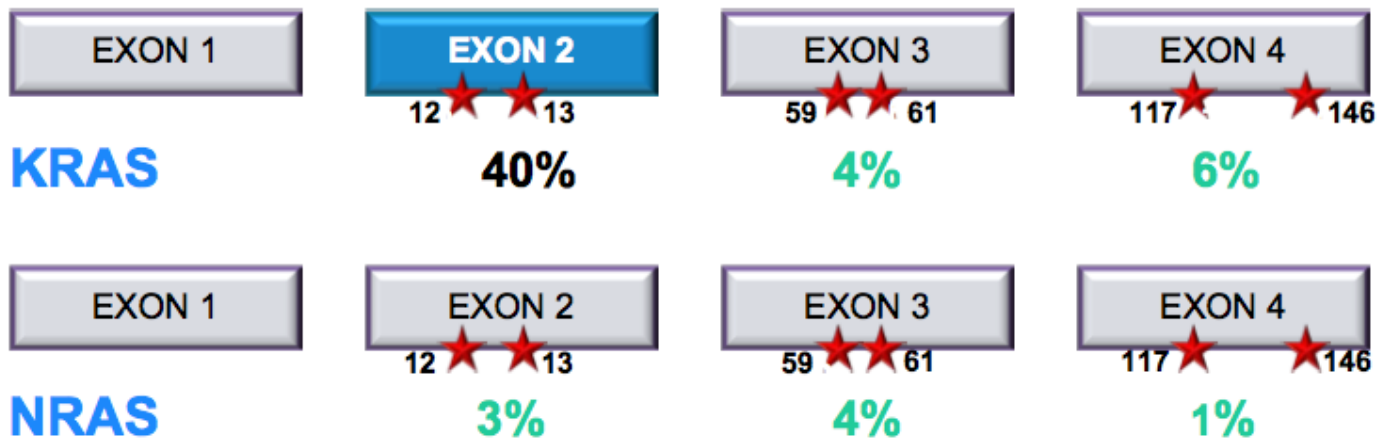
2. Ciardiello F, et al. J Clin Oncol 2014;32:5s (suppl) (Abstract No. 3506)

3. Stintzing S, et al. Ann Oncol 2014;25(suppl 4):v1–v41 (Abstract No. LBA11)

4. Karthaus M, et al. EJC 2013;49 (suppl 3) (Abstract No. 2262)

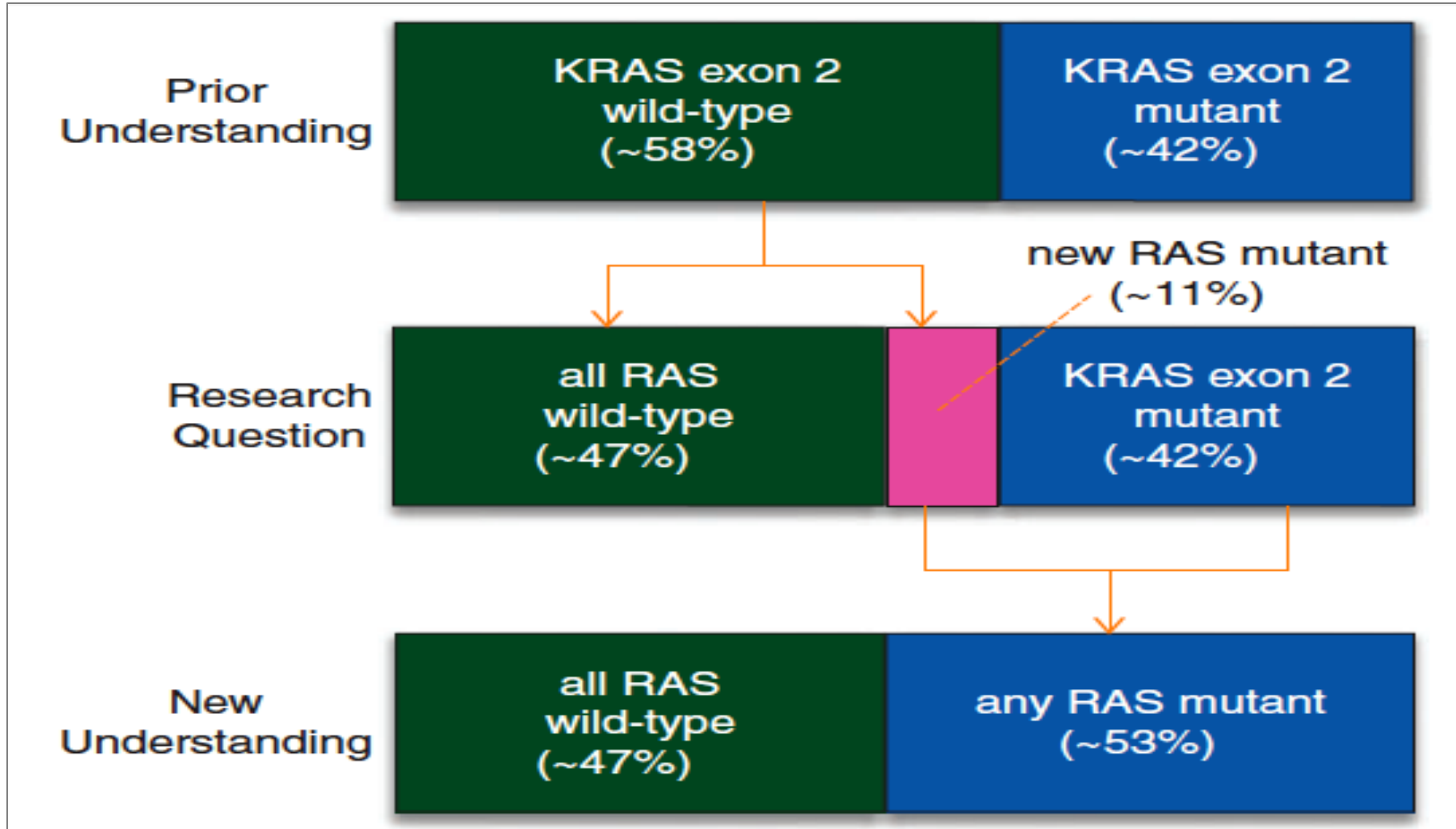
Primary resistance to anti-EGFR therapy

Mutations in KRAS and NRAS used in daily clinical practice



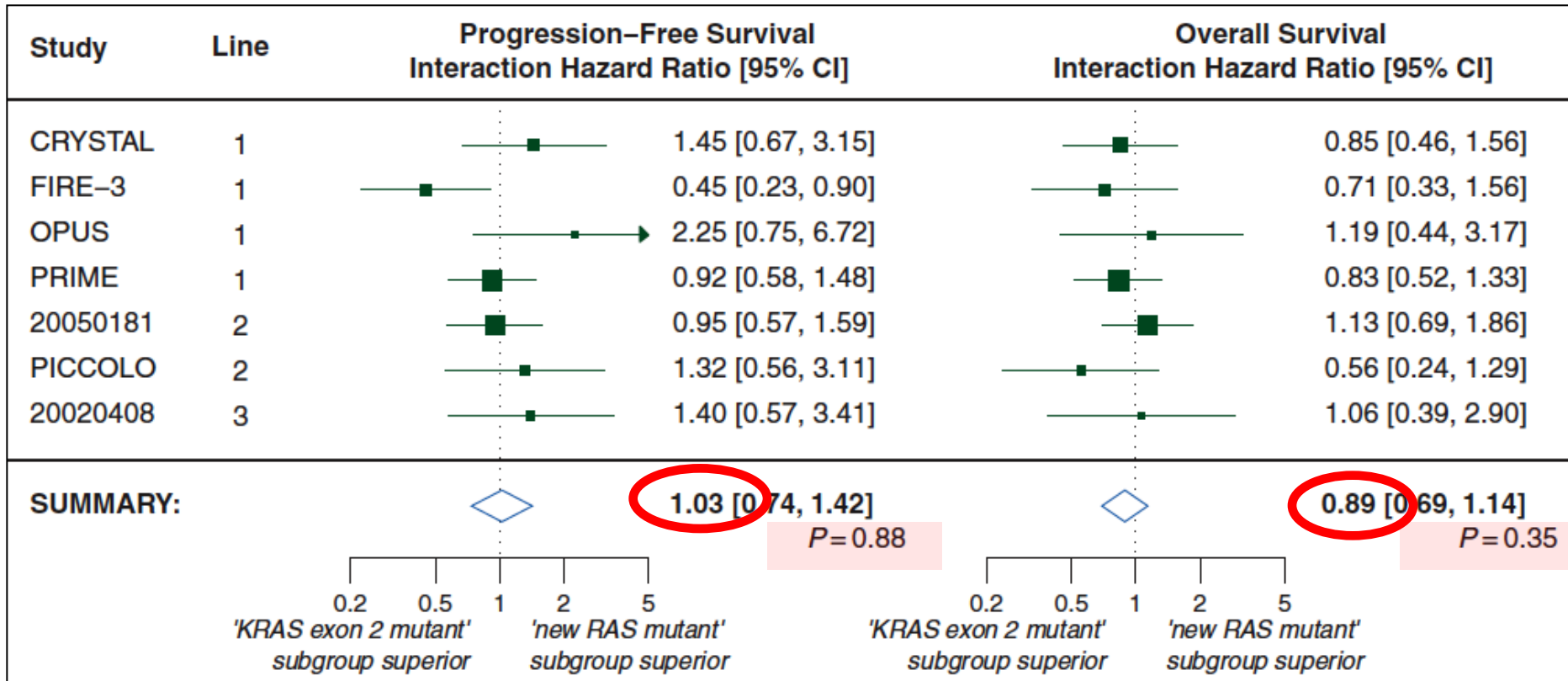
A meta-analysis of RCTs / 9 studies – 5948 pts

Extended RAS mutations



Extended RAS mutations: a meta-analysis

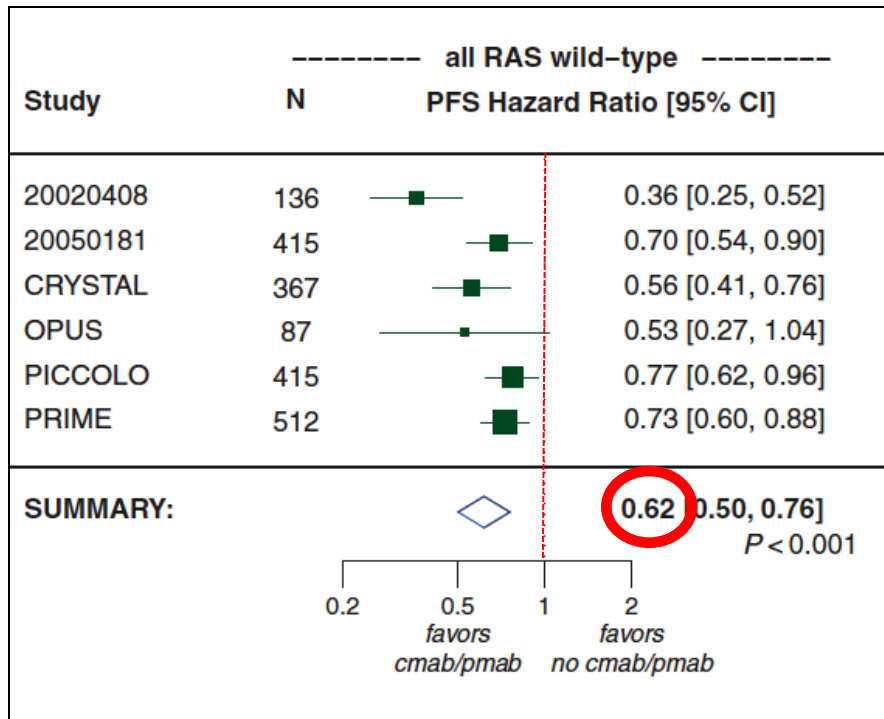
No difference in PFS or OS benefit between tumors with KRAS exon 2 mutations and tumors with the new RAS mutations



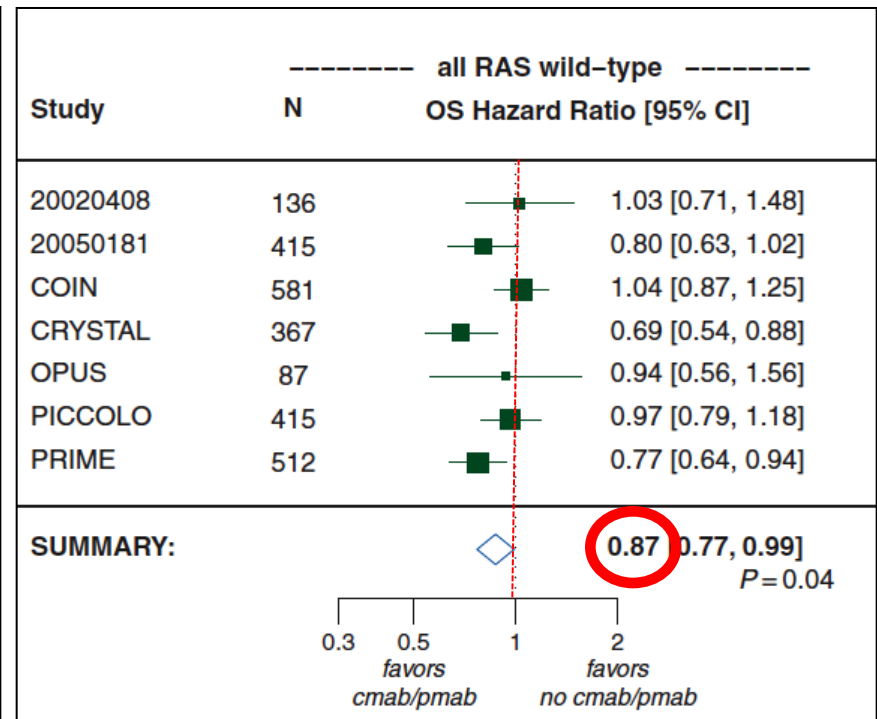
Extended RAS mutations: a meta-analysis

9 studies – 5948 pts

PFS



OS



MOLECULAR PROFILE MEANS...

ESMO consensus guidelines for the management of patients with metastatic colorectal cancer

recommendation 4: RAS testing.

- RAS mutational status is a negative predictive biomarker for therapeutic choices involving EGFR antibody therapies in the metastatic disease setting [I, A].
 - RAS testing should be carried out on all patients at the time of diagnosis of mCRC [I, A].
- RAS testing is mandatory before treatment with the EGFR-targeted monoclonal antibodies cetuximab and panitumumab [I, A].

recommendation 5: BRAF testing.

- Tumour BRAF mutation status should be assessed alongside the assessment of tumour RAS mutational status for prognostic assessment (and/or potential selection for clinical trials) [I, B].

recommendation 3: tissue selection.

- Tissue from either the primary tumour or a liver metastasis may be used for RAS mutation testing [III, A].
- Other metastatic sites such as lymph node or lung metastases may be used only if primary tumour or liver metastases samples are not available [II, B].

recommendation 9: emerging technologies.

- Although CTC number correlates with prognosis in patients with mCRC, the clinical utility of CTC assessments is not yet clear and therefore cannot be recommended [IV, D].
- The utility of liquid ctDNA biopsies to guide treatment decisions is currently under investigation in clinical trials, but cannot yet be recommended in routine practice [V, D].

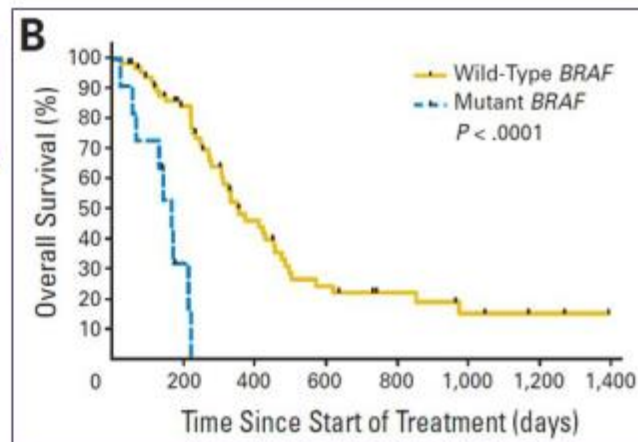
BRAF-Mutant Colorectal Cancer

BRAF V600 mutations occur in 5%-15% of CRC tumors

- Mutually exclusive of K- and N-*Ras* mutations
- Substantially worse prognosis than wild-type or *KRAS* mutant disease (OS for WT 34.7 months vs. BRAFm 10.4 months)
- *BRAF* testing is currently optional and not necessary for decision making around EGFR inhibitors, poor prognosis marker

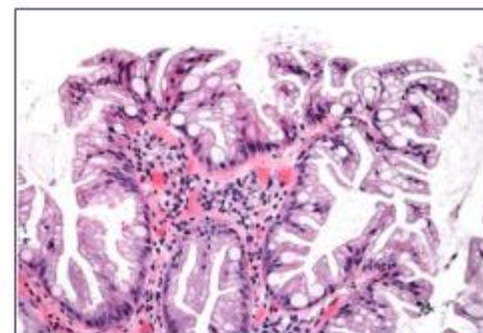
Distinct underlying biology of BRAFm metastatic CRC

- Female predominance, proximal colon lesions, poorly differentiated with increase peritoneal disease
- Unique pre-cancerous lesions (serrated adenoma)
- Hyper-mutated, MSI, and hyper-methylation in about half of the cases



Di Nicolantonio et al., JCO 2008

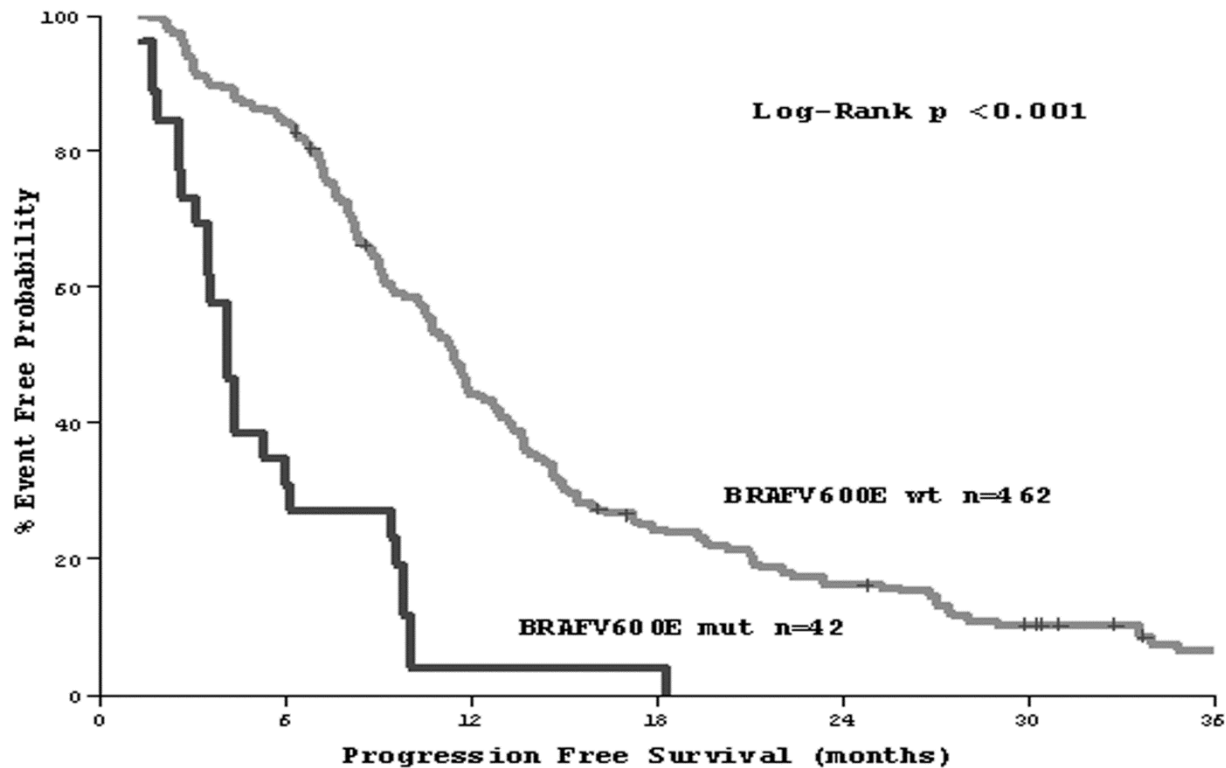
click to zoom



Serrated adenoma

Progression Free Survival according to the *BRAF*^{V600E} mutation (n=504)

Figure 1A

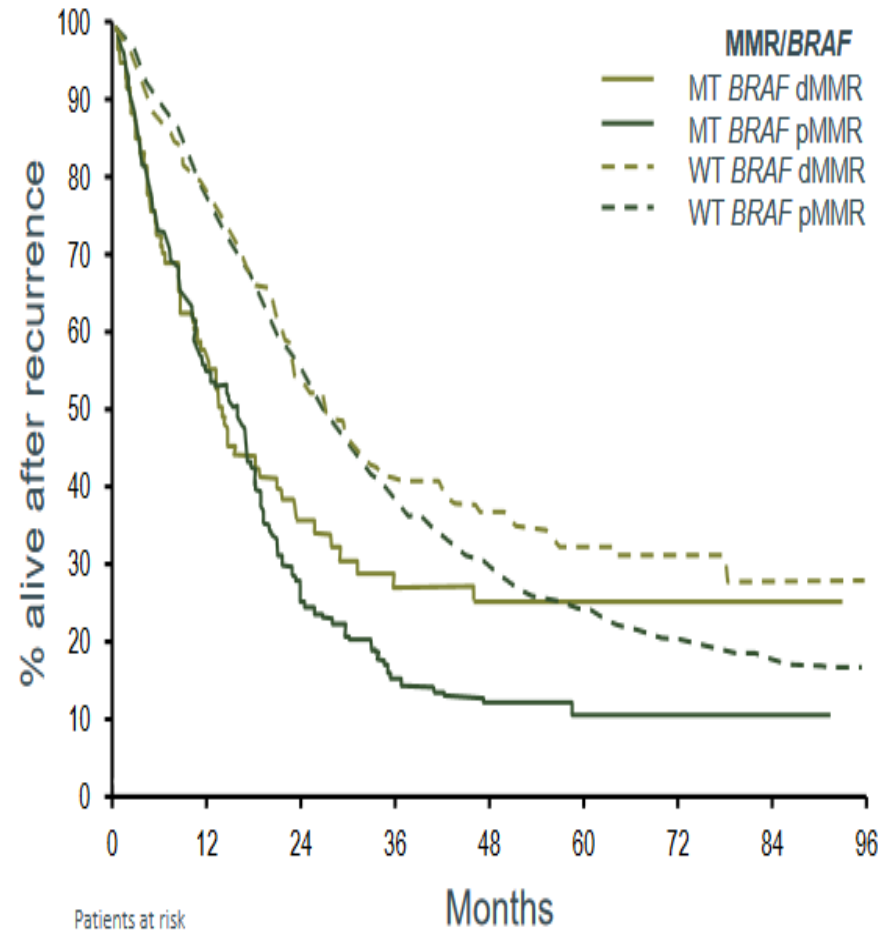


	Median (m)	95%ci
<i>BRAF</i> ^{V600E} mut (n=42)	4.1	
<i>BRAF</i> ^{V600E} wt	11.6	2.66-6.20

PROGNOSTIC ROLE OF *BRAF*V600E GUIDE DECISIONS

- Small population: 8 to 12% CRC¹
- Crossover of *BRAF* and sporadic MSI (promoter methylation) occurs in 30% of cases, with prognostic consequences²
- S III (ACCENT database): 2,600 patients with metastatic recurrence (7 adjuvant trials, 271 dMMR, 303 with *BRAF* mutation)

BRAF mutation is a poor prognostic factor in patients with MSS or MSI cancers



MT <i>BRAF</i> dMMR	77	33	17	11	10	6	4	2	0
MT <i>BRAF</i> pMMR	167	77	28	11	7	3	3	3	0
WT <i>BRAF</i> dMMR	143	102	60	40	30	16	12	5	1
WT <i>BRAF</i> pMMR	1600	1202	818	524	322	174	89	38	10

BRAF mutation

Anti-EGFR therapy / chemotherapy refractory disease

No objective responses have been reported for panitumumab or cetuximab monotherapy (NCI-CO17, ASPECCT)

J Clin Oncol 2008;26:5705–12

Anti-EGFR therapy / second line

PICCOLO trial (Subgroup of 131 pts)

A trend toward worse OS with the addition of panitumumab to irinotecan (HR, 1.4; 95% CI, 0.82 to 2.39)

Lancet Oncol 14:749-759, 2013

Update of the 20050181

Dismal outcomes in the BRAF-mut mCRC

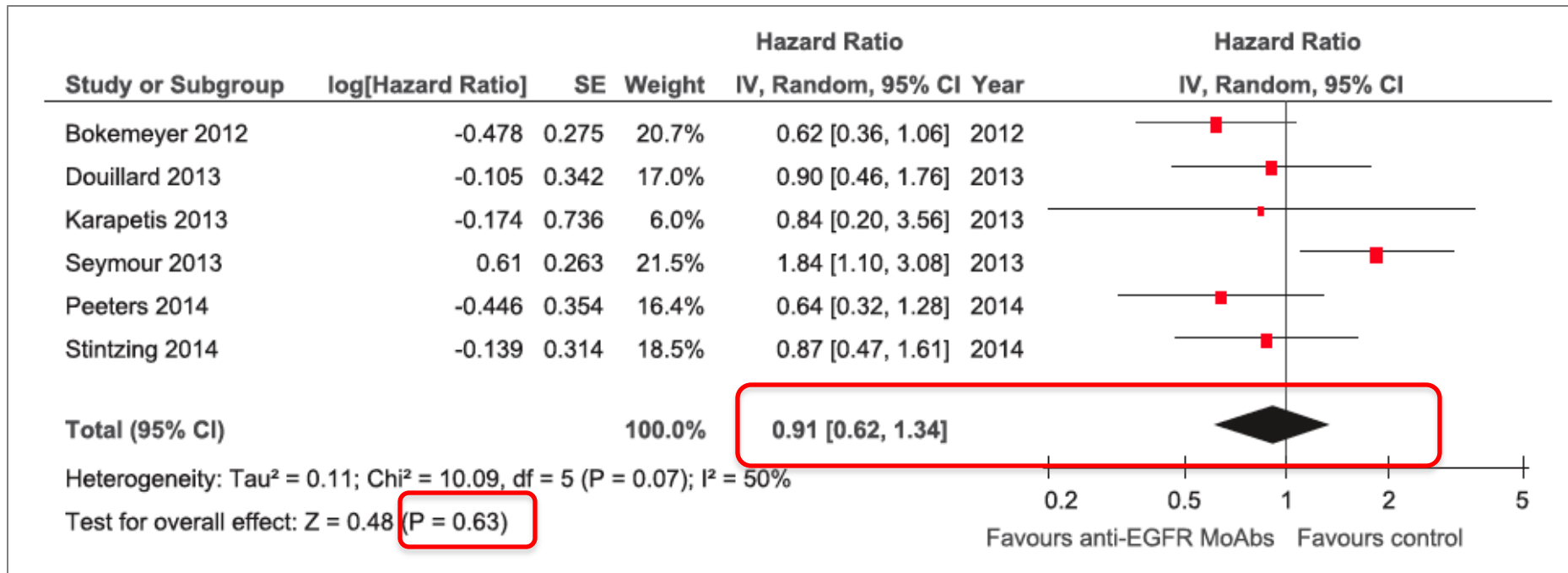
FOLFIRI-panitumumab vs FOLFIRI (median OS of 4.7 vs 5.7 months)

J Clin Oncol 32, 2014 (suppl 5s; abstr 3568)

Predictive role of BRAF mutations in patients with advanced CRC receiving cetuximab and panitumumab: A meta-analysis

- 9 phase III trials / 1 phase II trial / 463 RAS-wt/BRAF-mut
- 6 trials 1st-line and 2 second-line, 2 trials chemo-refractory patients

Forest plots showing HR for **overall survival** for anti-EGFR treatment in BRAF-mt colorectal cancer

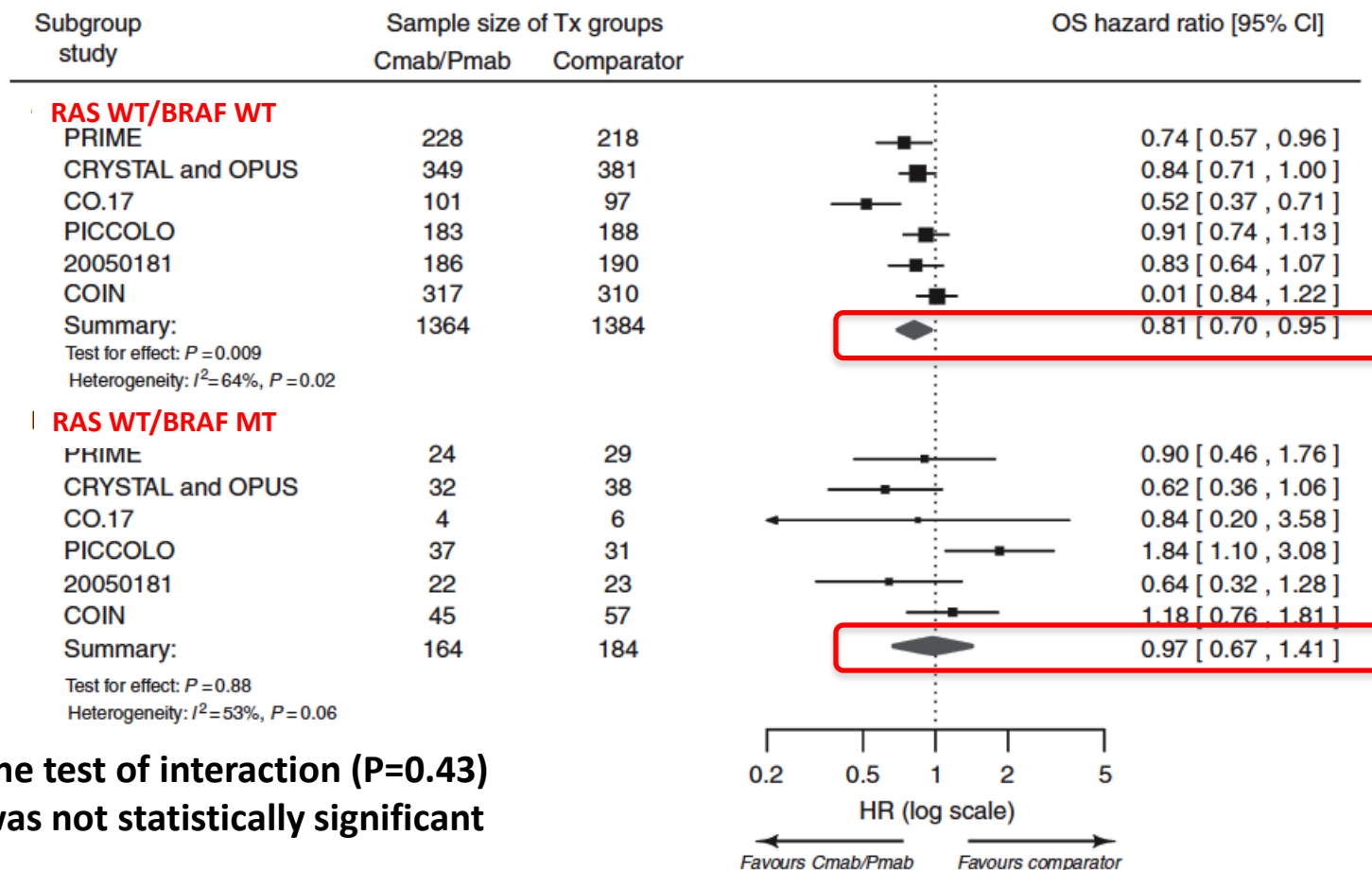


In a front-line, the effect was not significant in favour of anti-EGFR (HR, 0.76; 95% CI, 0.54–1.08; p= 0.13)

Meta-analysis of BRAF mutation as a predictive biomarker of benefit from anti-EGFR therapy

3168 participants with RAS WT tumours / 8 RCT
2817 BRAF WT / 351 (11.1%) BRAF MT tumours

Forest plot of the overall survival benefit with anti-EGFR mAb therapy



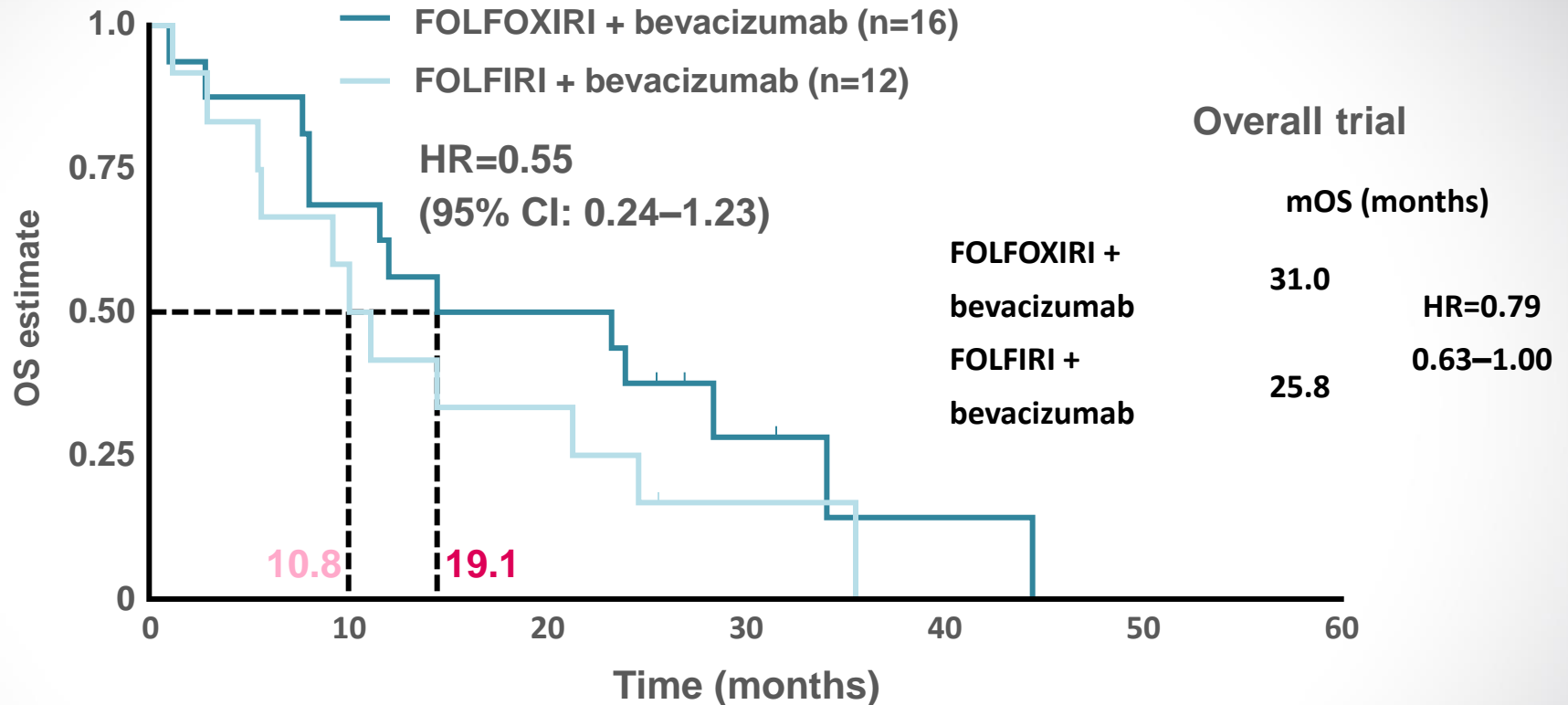
The test of interaction ($P=0.43$)
was not statistically significant

BRAF mt meta-analyses contrasting results

	<i>Pietrantonio F et al.</i>	<i>A Rowland et al</i>
Conclusion	Anti-EGFR therapy did not increase the benefit	Insufficient evidence to definitively consider BRAF MT a negative predictive biomarker
Statistical methods	Simply estimating anti-EGFR mAb efficacy in the BRAF MT subgroup	Assesed whether anti-EGFR mAb efficacy differs based on BRAF mutation status
Inclusion criteria	Included trials comparing anti-EGFR mAb therapy with bevacizumab	Excluded trials comparing anti-EGFR mAb therapy with bevacizumab

Pietrantonio F et al. Eur J Cancer 51: 587–594, 2015
A Rowland et al. B J Cancer 112, 1888–1894, 2015

TRIBE: benefit of more intensive treatment for patients with *BRAF*-mutated mCRC



TREATING BRAFV600E MUTATIONS IN mCRC

Basket trials include patients with a wide variety of histologies as long as they all harbor a cognate aberration. Often perceived as signal finding.

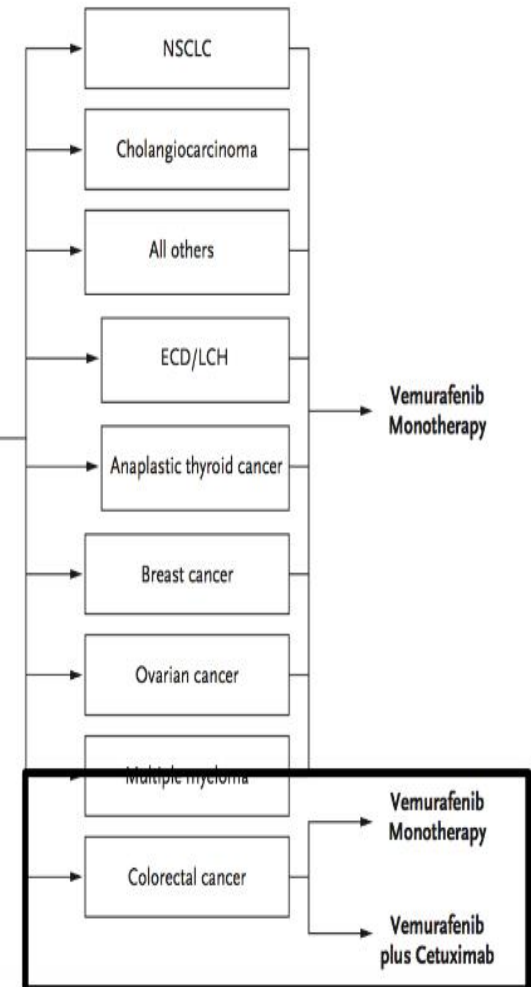
The NEW ENGLAND JOURNAL of MEDICINE

ORIGINAL ARTICLE

Vemurafenib in Multiple Nonmelanoma Cancers with BRAF V600 Mutations

David M. Hyman, M.D., Igor Puzanov, M.D., Vivek Subbiah, M.D., Jason E. Faris, M.D., Ian Chau, M.D., Jean-Yves Blay, M.D., Ph.D., Jürgen Wolf, M.D., Ph.D., Noopur S. Raje, M.D., Eli L. Diamond, M.D., Antoine Hollebecque, M.D., Radj Gervais, M.D., Maria Elena Elez-Fernandez, M.D., Antoine Italiano, M.D., Ph.D., Ralf-Dieter Hofheinz, M.D., Manuel Hidalgo, M.D., Ph.D., Emily Chan, M.D., Ph.D., Martin Schuler, M.D., Susan Frances Lasserre, M.Sc., Martina Makrutzki, M.D., Florin Sirzen, M.D., Ph.D., Maria Luisa Veronese, M.D., Josep Tabernero, M.D., Ph.D., and José Baselga, M.D., Ph.D.

BRAF V600–positive (testing per local methods)
Vemurafenib, 960 mg twice daily orally
Primary end point
Response rate at wk 8
Secondary end points
Progression-free survival
Time to progression
Best overall response
Time to response
Duration of response
Clinical benefit rate
Overall survival
Safety



The “Basket trial” is the paradigm of this approach

Targeting *BRAF*^{V600E}: studies to date

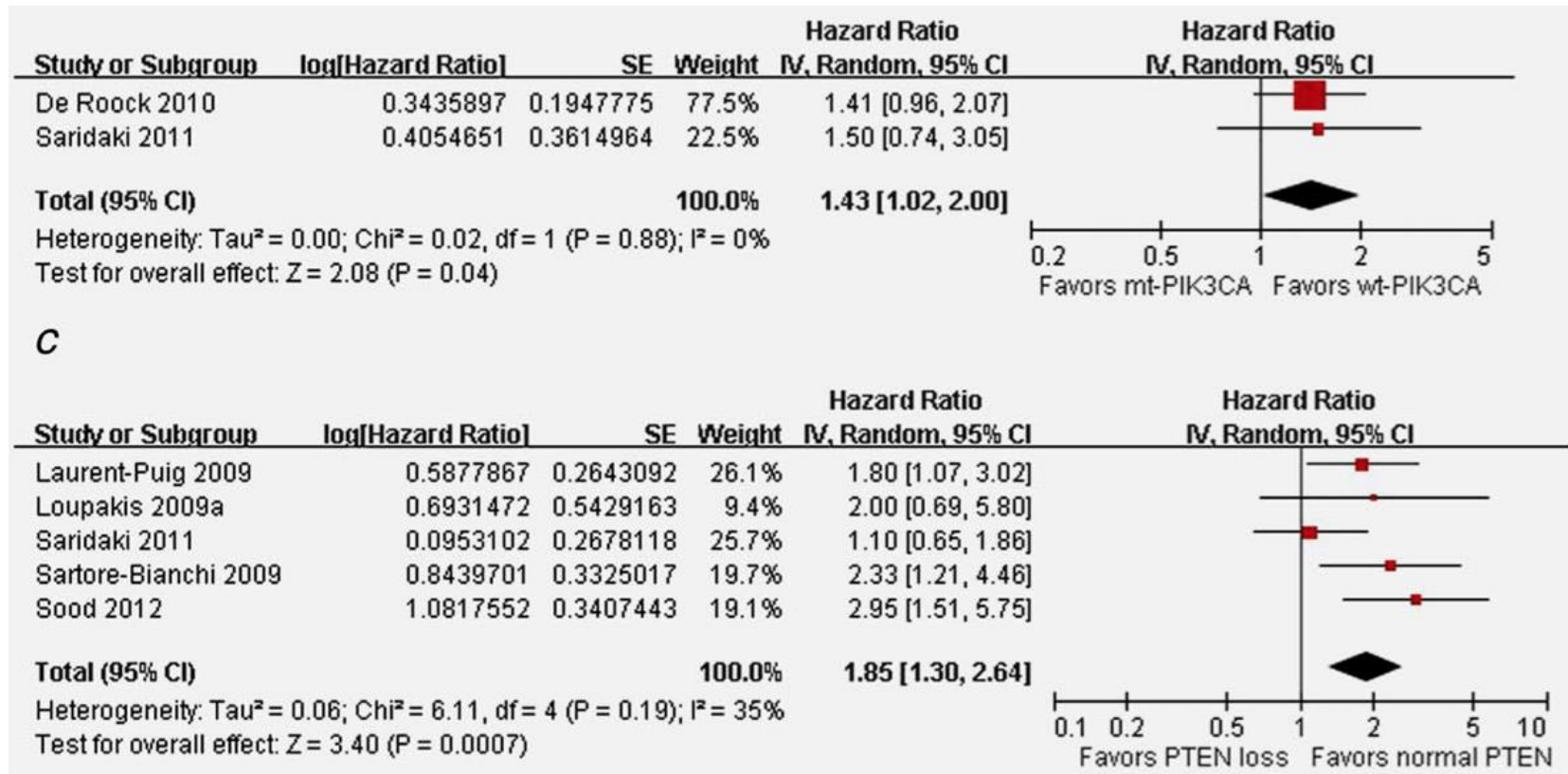


Regimen		Response rate*	PFS (months)	Citation
Single/doublet RAF/MEK	vemurafenib	5%	2.1	Kopetz, J Clin Oncol 2015
	dabrafenib	11%	NR	Falchook, Lancet 2008
	encorafenib	16%	NR	Gomez-Roca, ESMO 2014
	dabrafenib + trametinib	12%	3.5	Corcoran, J Clin Oncol 2015
Doublet with EGFR	vemurafenib + panitumumab	13%	3.2	Yeager et al., Clin Cancer Res 2015
	vemurafenib + cetuximab	4%	3.7	Hyman et al., New Engl J Med 2015
	encorafenib + cetuximab	19%	3.7	Van Geel et al., Cancer Discov 2017
	dabrafenib + panitumumab	10%	3.4	Atreya, ASCO 2015
Triplet with EGFR	vemurafenib + cetuximab + irinotecan	16%	4.4	Kopetz et al., ASCO 2017
	dabrafenib + trametinib + panitumumab	32%	4.2	Corcoran, ESMO 2016
	encorafenib + cetuximab + alpelisib	18%	4.2	van Geel et al., Can Disc 2017
	encorafenib + binimetinib + cetuximab	48%	8.0	Van Cutsem et al., GI ASCO 2018

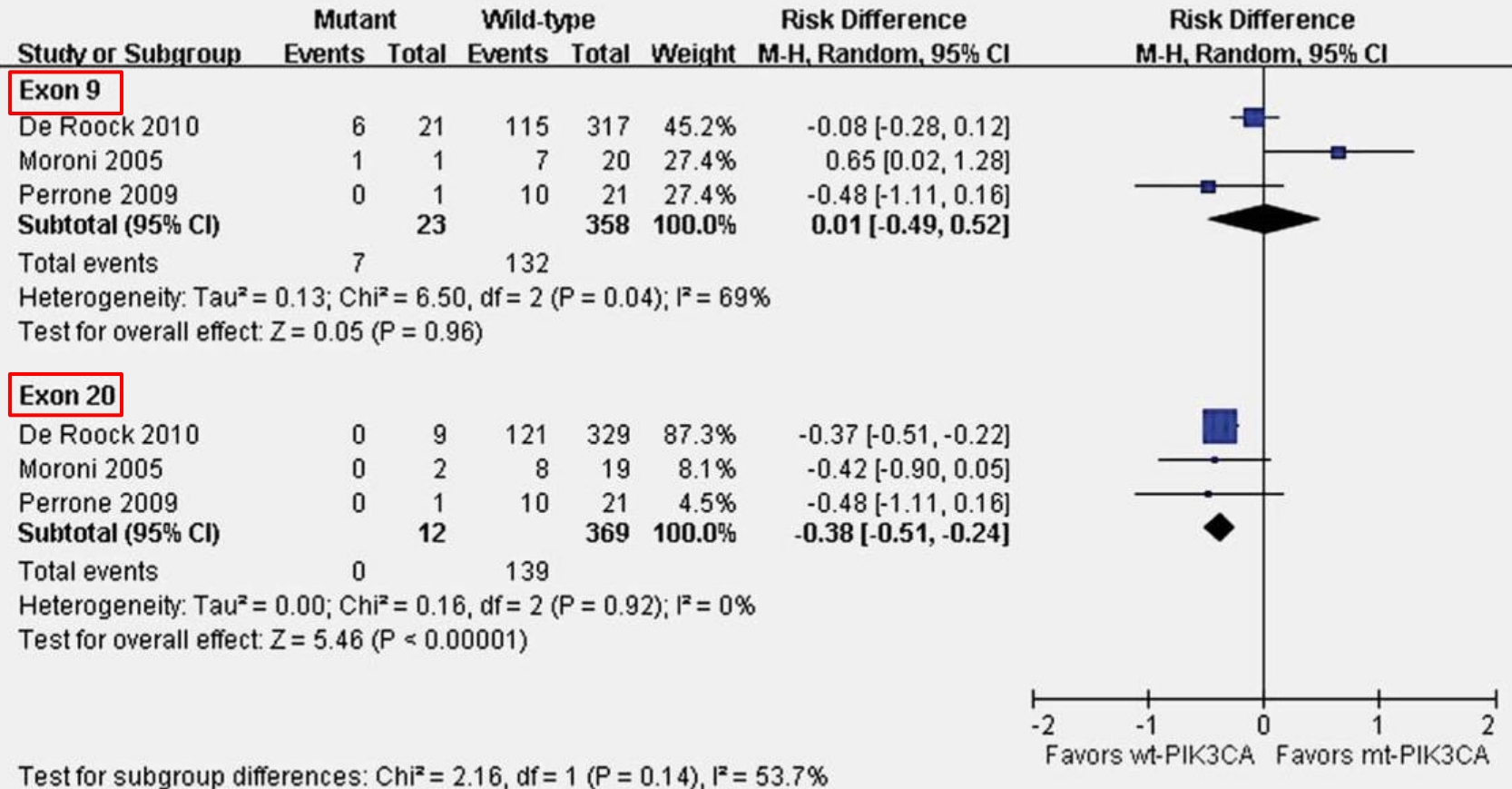
ADDITIONAL PERSPECTIVES

- ***PIK3CA*** is the gene that encodes for p100 α catalytic subunit of PI3K, a phosphoinositide kinase important in the PI3K/mTOR signalling pathway
 - Activation of this pathway leads to enhanced protein synthesis, cell cycle progression, cell growth and survival
 - Mutations in *PIK3CA* are found in about 20% of colorectal cancers (gene analysis included in most NGS panel investigations), with 48% of those occurring in the kinase domain and 43% occurring in the helical domain
- ***HER2*** amplification
 - Activation of human epidermal growth factor receptor 2 (HER2) is a rare event in colorectal cancers (3-5% of cases), leading to upregulation of RAS/RAF/MEK/ERK and PI3K/mTOR signaling pathways
 - Diagnostic: immunohistochemistry (as in gastric cancer), FISH

The associations of PIK3CA mutations and PTEN loss with the overall survival of wild-type-KRAS

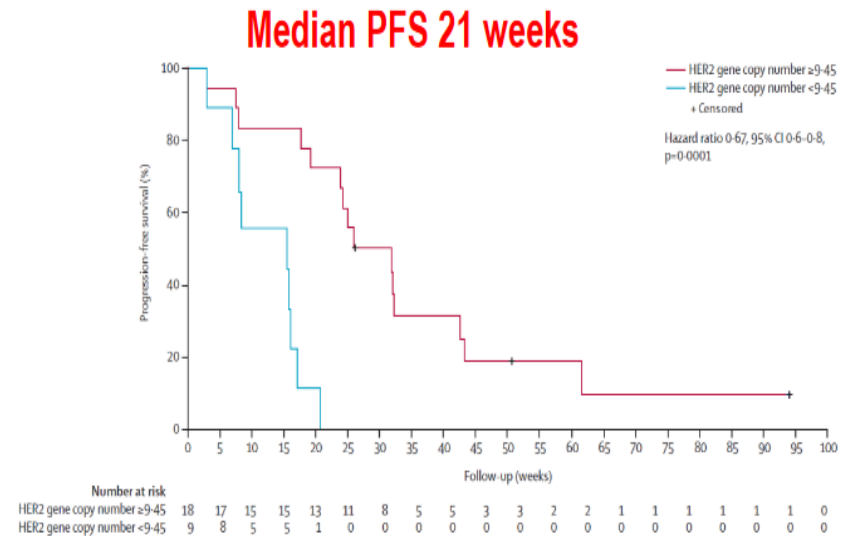
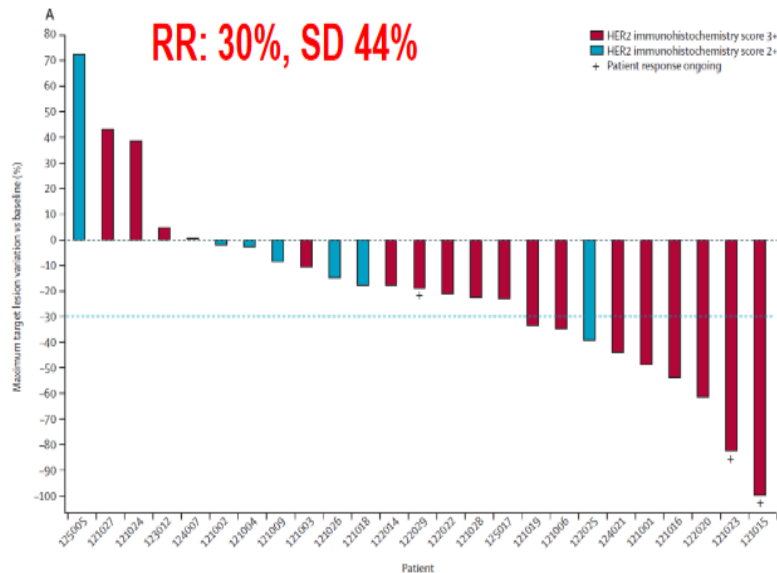


Comparison of PIK3CA exon 9 and exon 20 mutations with the objective response of wild-type-KRAS

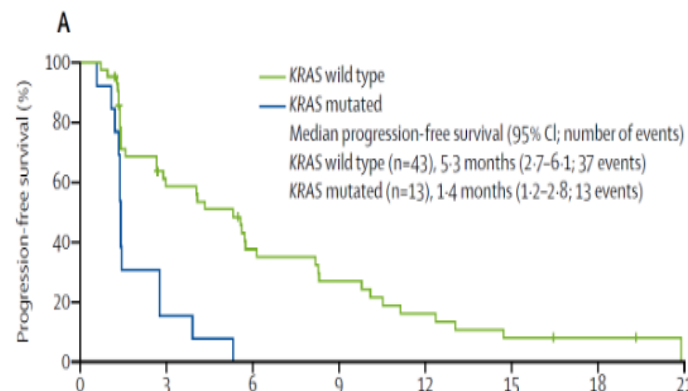
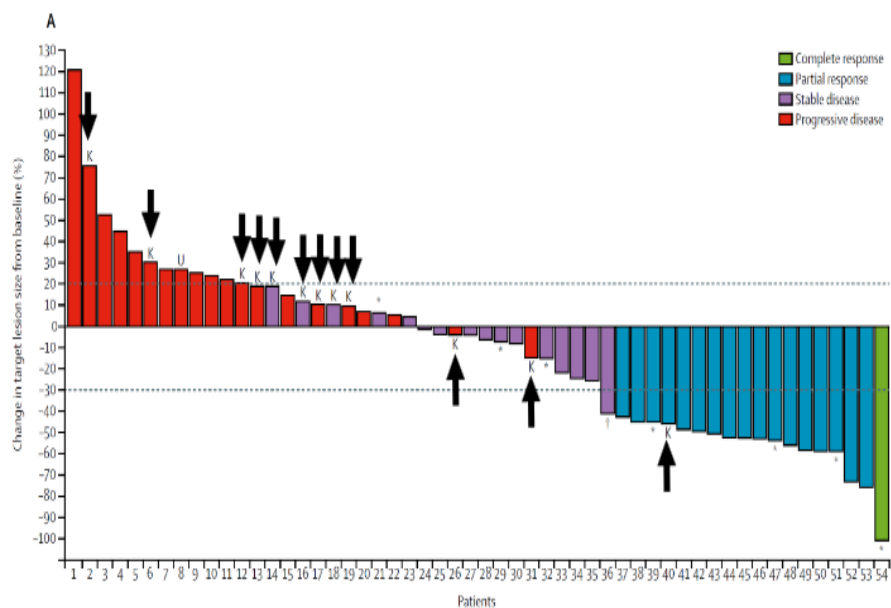


Trastuzumab plus lapatinib in HER2-positive mCRC (HERACLES)

- 914 patients with *KRAS* exon 2 (codons 12 and 13) wild-type mCRC were screened
- 48 (5%) had HER2-positive tumors

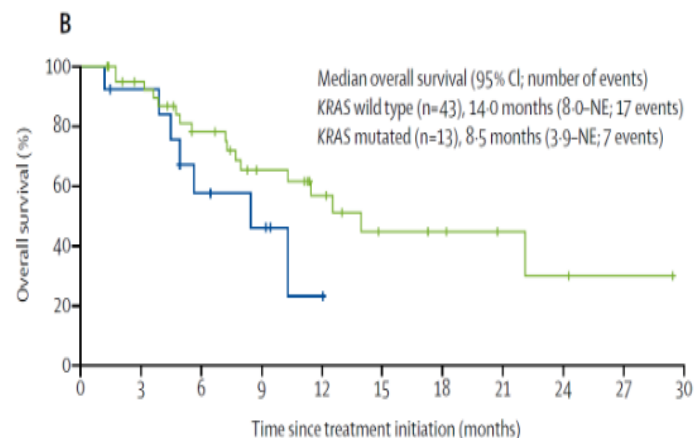


Pertuzumab plus trastuzumab for HER2-amplified mCRC (MyPathway)



Number at risk (number censored)

KRAS wild type	43 (0)	23 (3)	14 (4)	10 (4)	6 (4)	3 (4)	2 (5)	0 (6)
KRAS mutated	13 (0)	2 (0)	0 (0)

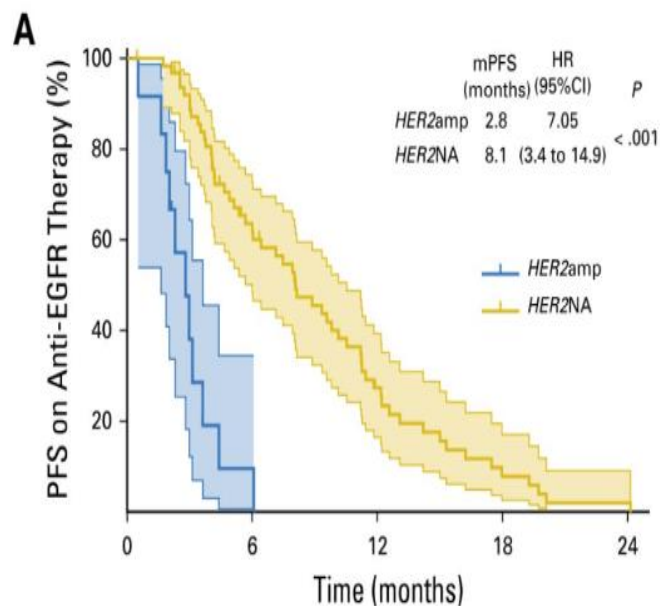


Number at risk (number censored)

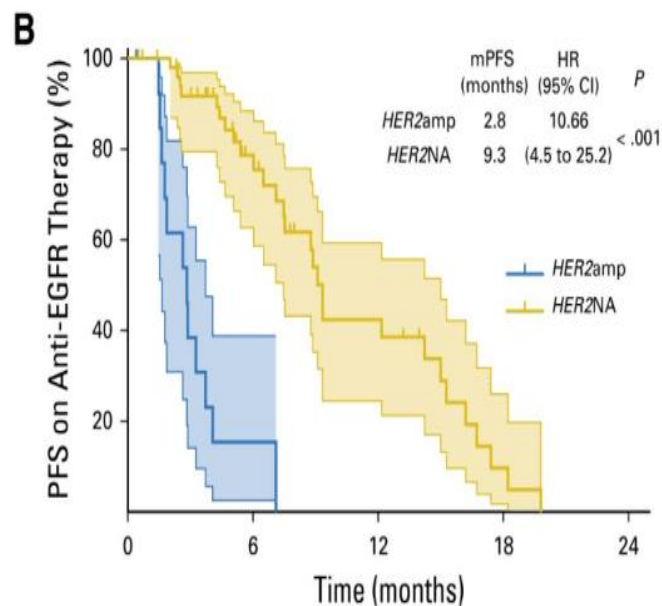
KRAS wild type	43 (0)	35 (6)	26 (9)	17 (14)	12 (17)	6 (21)	5 (22)	3 (24)	2 (24)	1 (25)	0 (26)
KRAS mutated	13 (0)	11 (1)	6 (2)	4 (3)	1 (5)	0 (6)

HER2 amplification in mCRC

- Found in about 2% of CRC
- More frequent in patients with KRAS/NRAS/BRAF wild type tumors (5%)
- Associated with resistance to anti-EGFR moAbs in retrospective analyses (2nd/3rd line treatment)

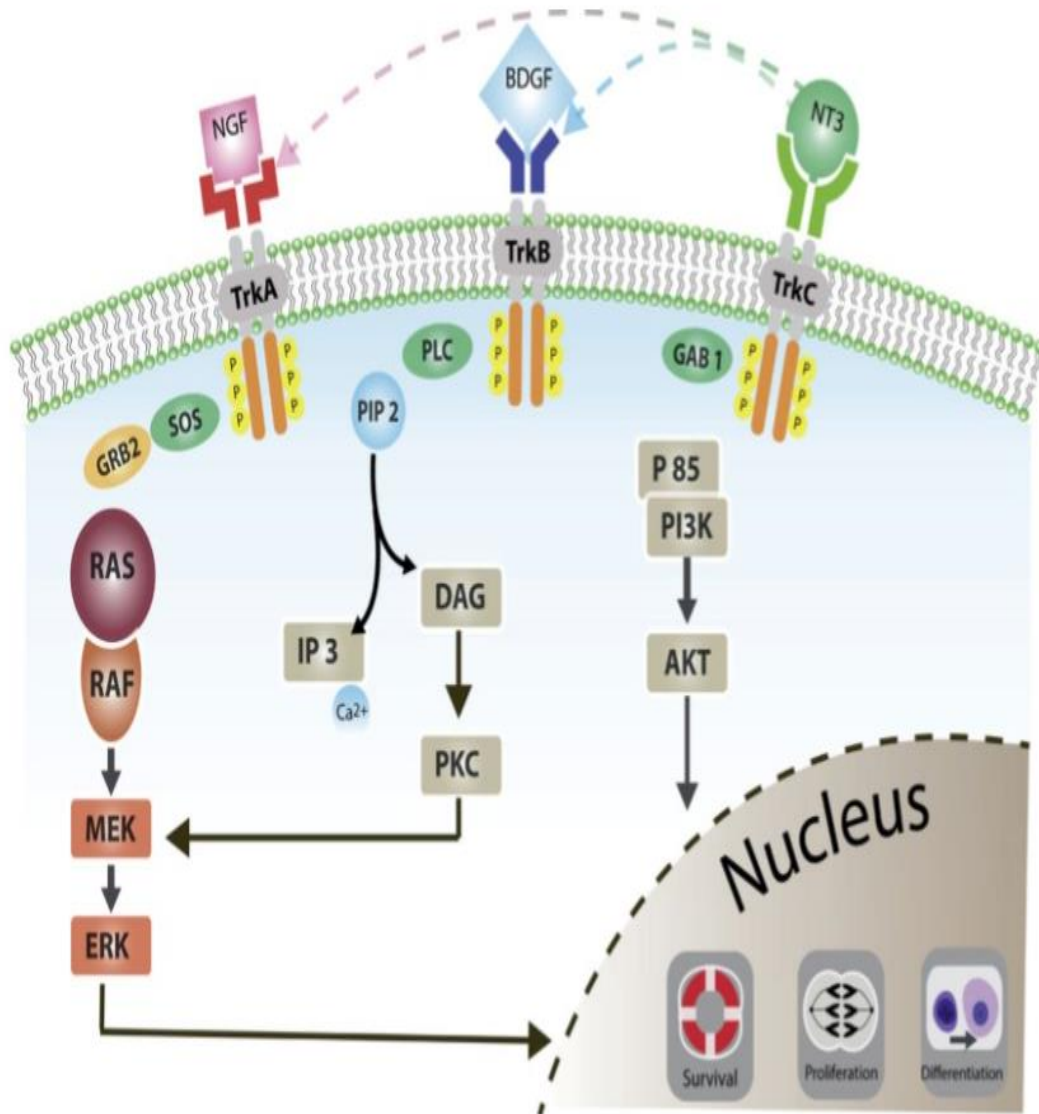


No. at risk	0	6	12	18	24
HER2amp	12	5	2	0	0
HER2NA	65	57	36	26	15



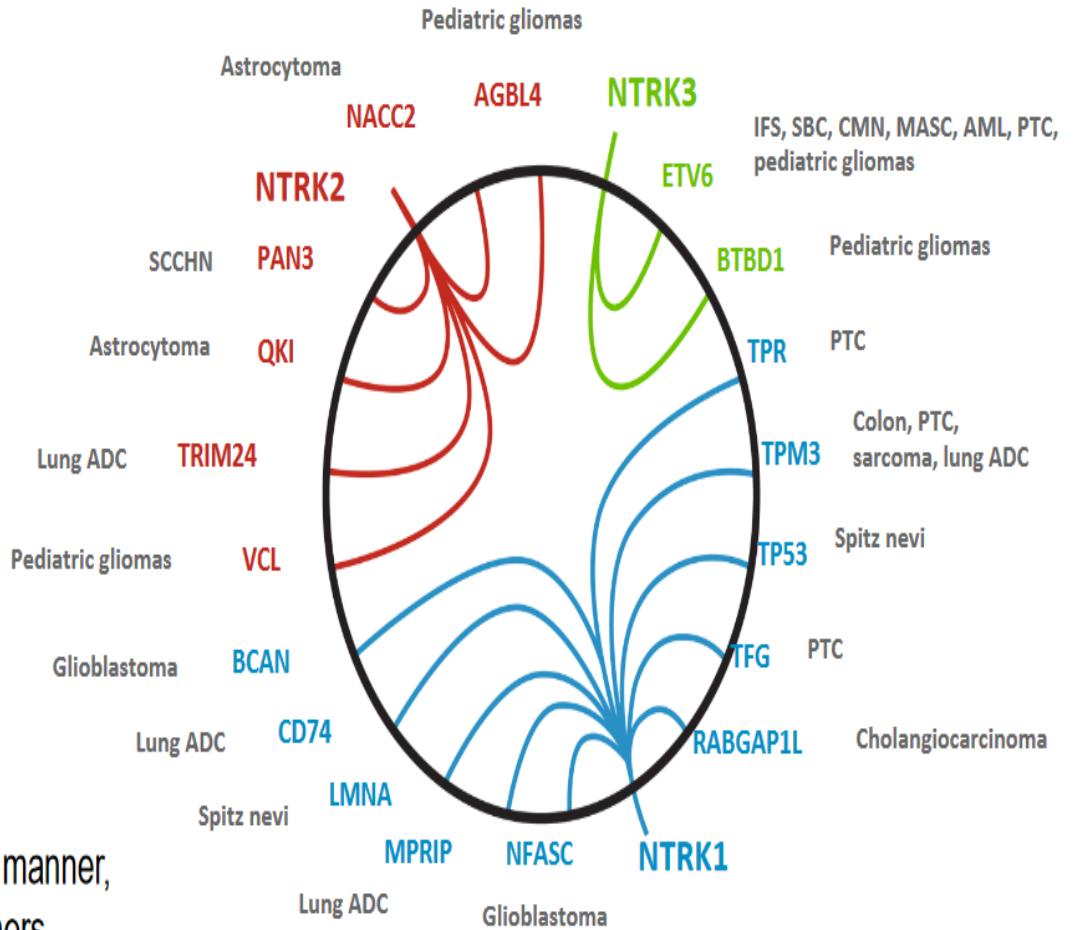
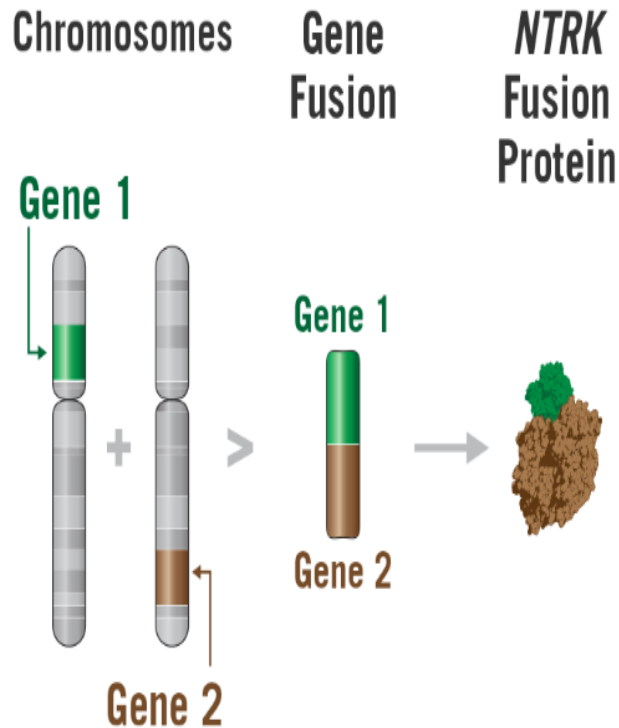
No. at risk	0	6	12	18	24
HER2amp	16	6	3	0	0
HER2NA	54	44	25	15	13

NTRK FUSIONS



- The tropomyosin receptor kinase family comprise three transmembrane proteins referred to as TrkA, B and C receptors that are encoded by the NTRK1, NTRK2 and NTRK3 genes
- Gene fusions (intra- / interchromosomal rearrangement) involving NTRK genes lead to transcription of chimeric Trk proteins with constitutively activated or overexpressed kinase function conferring oncogenic potential
- These genetic abnormalities have recently emerged as targets for cancer therapy (entrectinib, larotrectinib)

MULTIPLE BREAKPOINTS AND FUSION PARTNERS



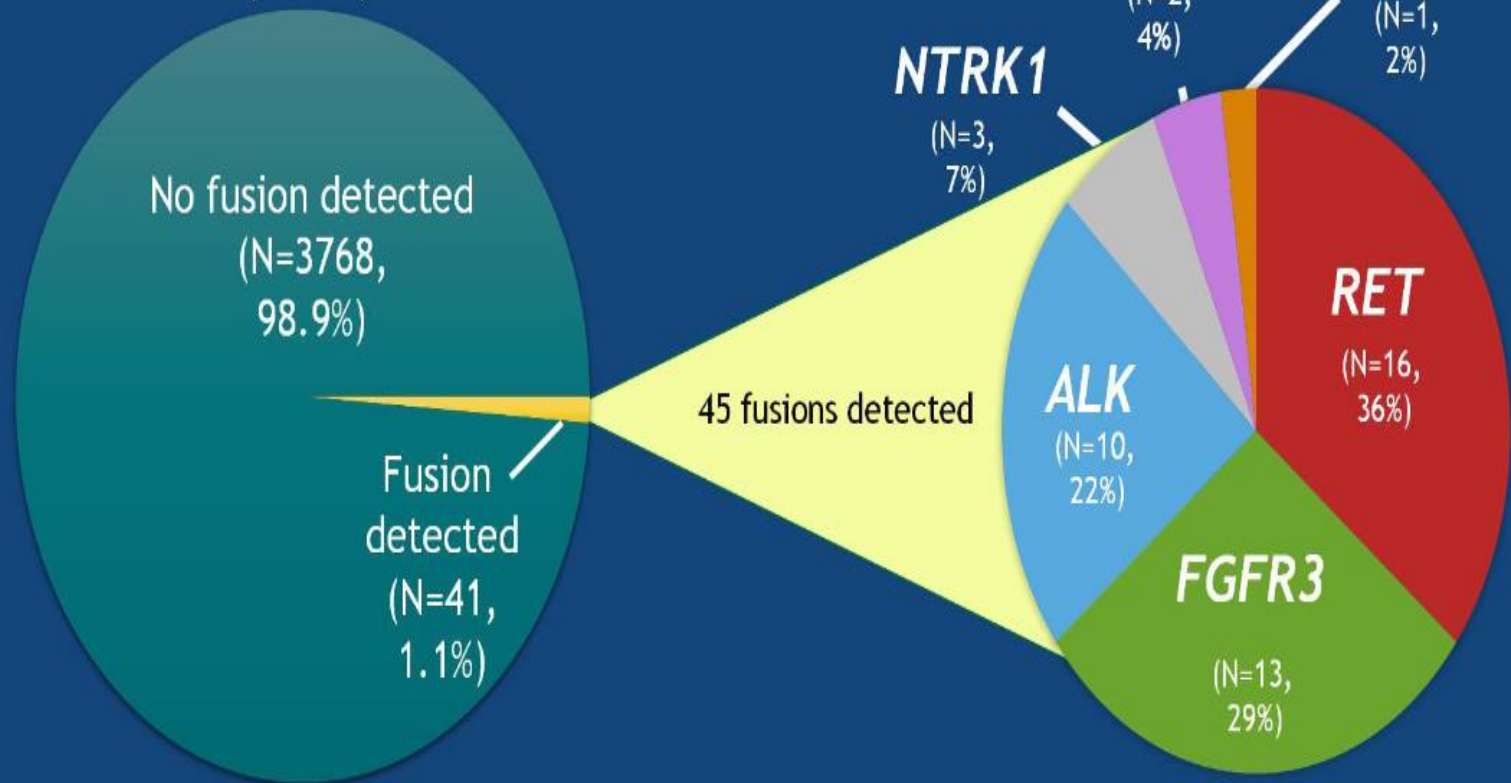
- NTRK gene fusions occur in a tumor-agnostic manner, with inconsistent break points and fusion partners
- The optimal detection method should not require knowledge of fusion break points and/or fusion partners

Gene fusions predictive value in metastatic CRC

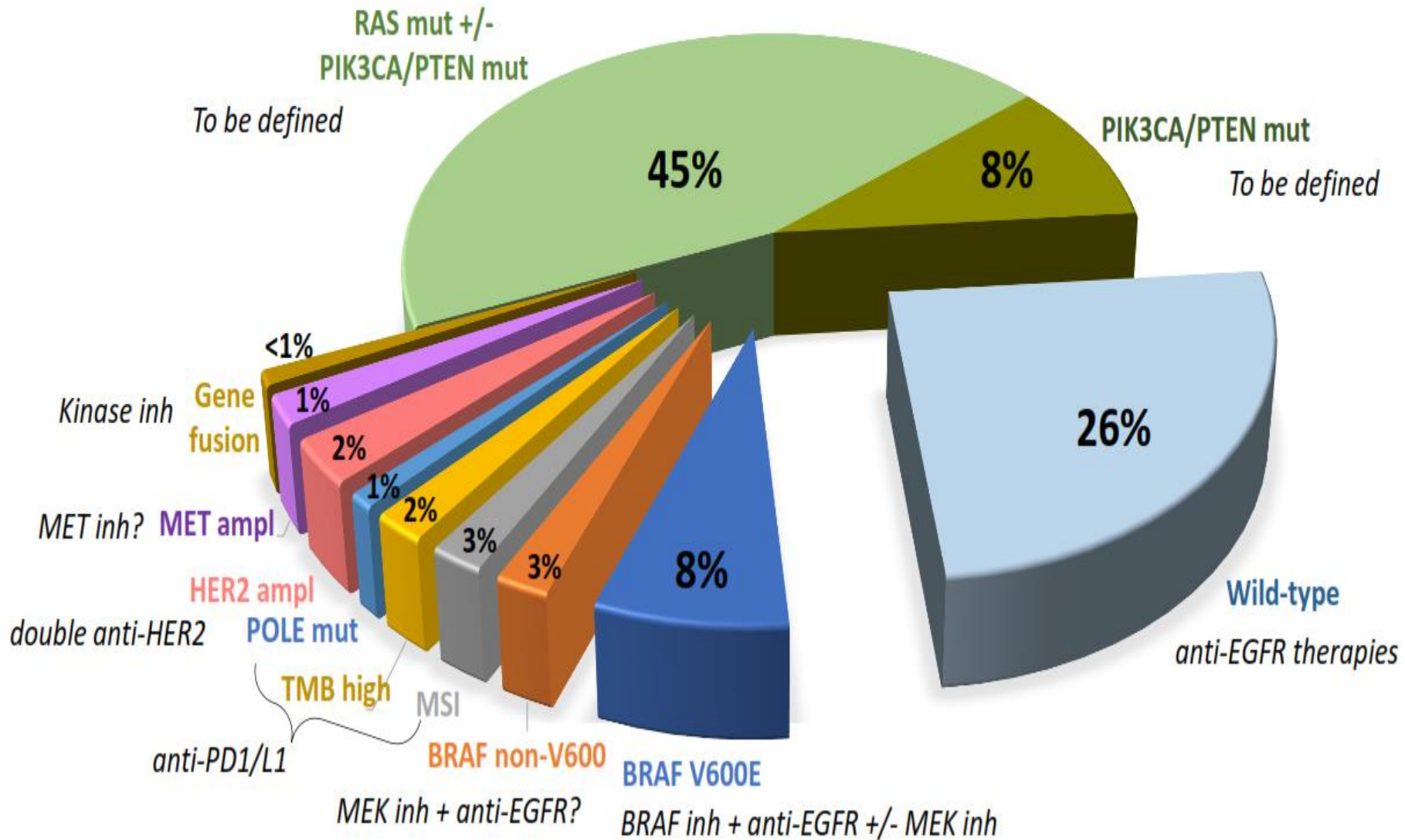
Alteration	Prevalence	Targetability evidence	Enrichment
<i>NTRK1-3</i> fusion	< 1%	Case reports	(> if right colon, <i>RAS/BRAF</i> wt, MSI) ¹
<i>ALK</i> fusion	< 1%	Case reports	(> if right colon, <i>RAS/BRAF</i> wt, MSI colitis-associated) ²
<i>ROS1</i> fusion	< 1%	Other tumors	(> if right colon, <i>RAS/BRAF</i> wt) ³
<i>RET</i> fusion	< 1%	Other tumors	(> if right colon, <i>RAS/BRAF</i> wt) ³
<i>FGFR2-3</i> fusion	<1%	Other tumors	(> if <i>RAS</i> mut) ⁴

Overall Fusion Prevalence in CRC with a ctDNA Assay

CRC patients with detectable alterations
(N=3809)

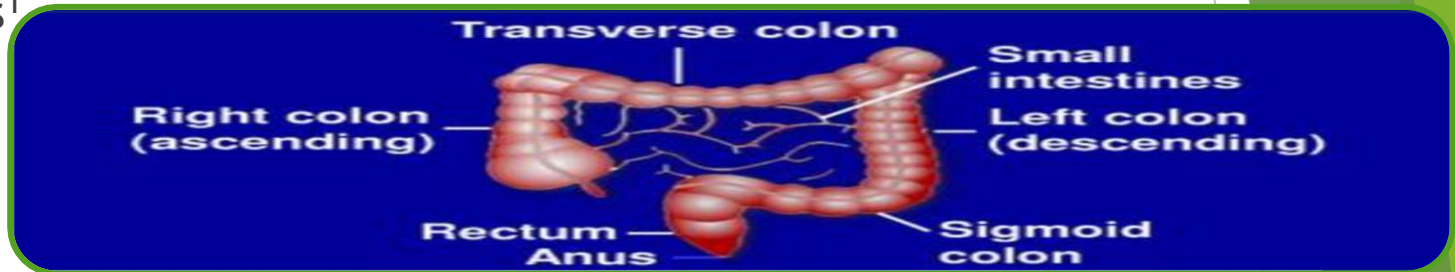


Genomic markers



The Colorectal Tract Is Highly Heterogeneous

- Developmental, genetic, and biologic differences in the proximal (right-side) and distal (left-side) segments of the colon have been documented for over 20 years, and may account for differences in left- vs right-side CRC tumours¹



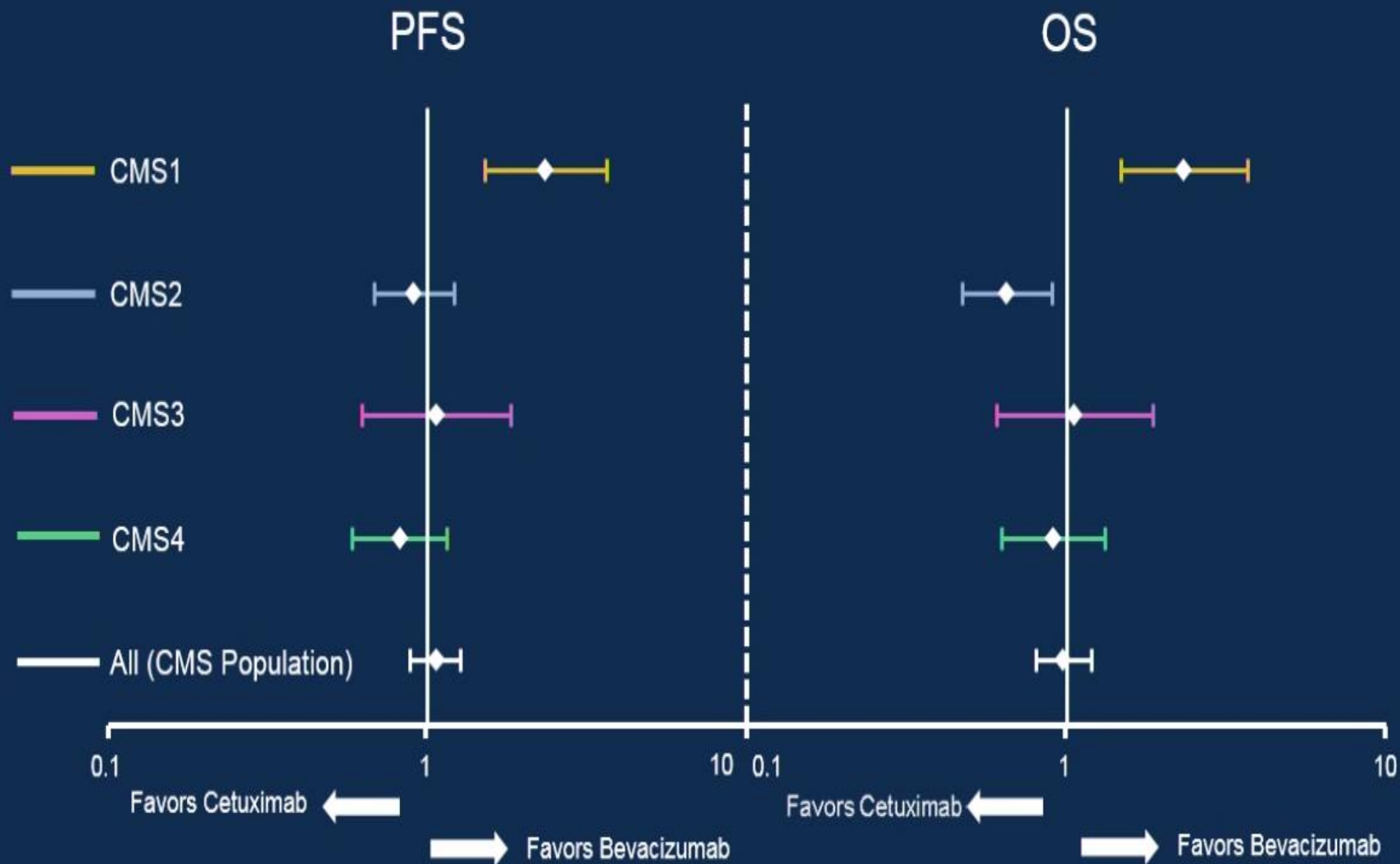
Right-side tumours	Left-side tumours
<ul style="list-style-type: none"> • Older patients • Higher incidence (40% increasing) • More common in female patients • Mucinous, signet ring histology • Poorly differentiated • Microsatellite instability • Hypermethylation, higher mutation rates • PI3KCA mutation • KRAS mutations • BRAF mutations • Carbs / Fat 	<ul style="list-style-type: none"> • Younger patients • Incidence 60% • Better prognosis • Predominately WT • Chromosomal aberrations; 18q loss and 20q gain • Aneuploidy • p53 mutation / COX2 expression • EGFR gain • HER2 gain • High EGFR ligand expression (EREG and AREG expression) - High VEGF-1 mRNA expression • Protein / Meat / lose Calcium

CMS1 MSI immune	CMS2 Canonical	CMS3 Metabolic	CMS4 Mesenchymal
14%	37%	13%	23%
MSI, CIMP high, hypermethylation	SCNA high	Mixed MSI status, SCNA low, CIMP low	SCNA high
<i>BRAF</i> mutations		<i>KRAS</i> mutations	
Immune infiltration and activation	WNT and MYC activation	Metabolic deregulation	Stromal infiltration, TGF- β activation, angiogenesis
Worse survival after relapse			Worse relapse-free and overall survival

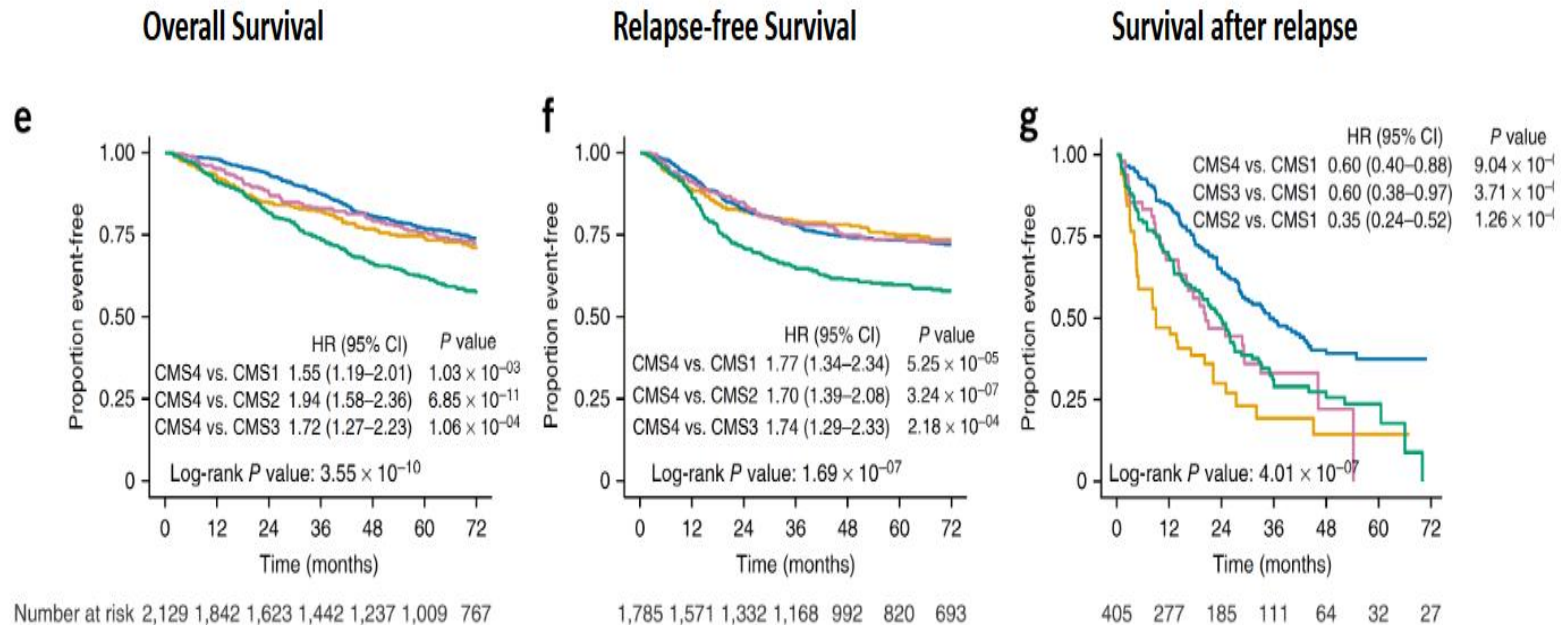
Mixed features samples (13%): possibly are a transition phenotype

the CMS groups the most robust classification system currently available for CRC—with clear biological interpretability—and the basis for future clinical stratification and subtype-based targeted interventions

Cetuximab vs Bevacizumab



Prognostic value of the CMS classification

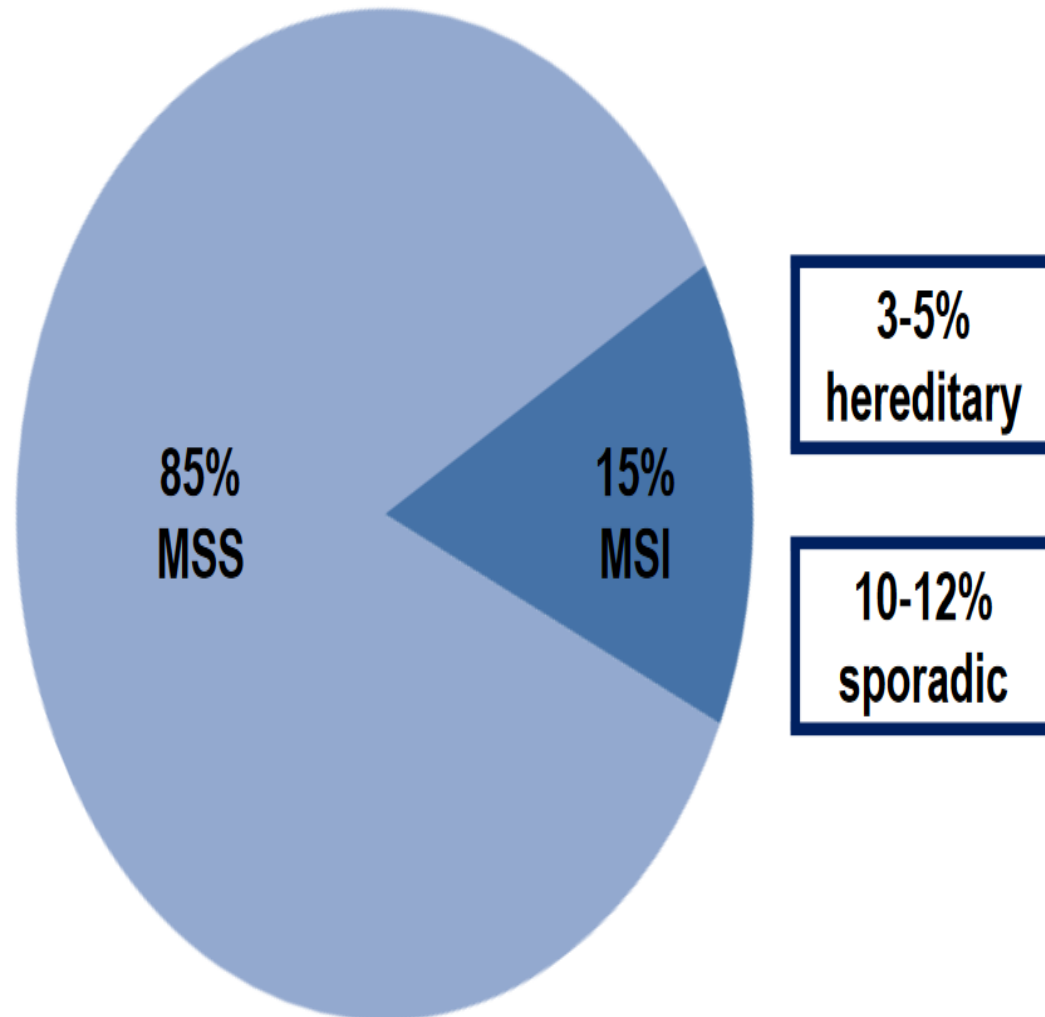


CMS1; CMS2; CMS3; CMS4

ESMO and NCCN Guidelines and Sidedness

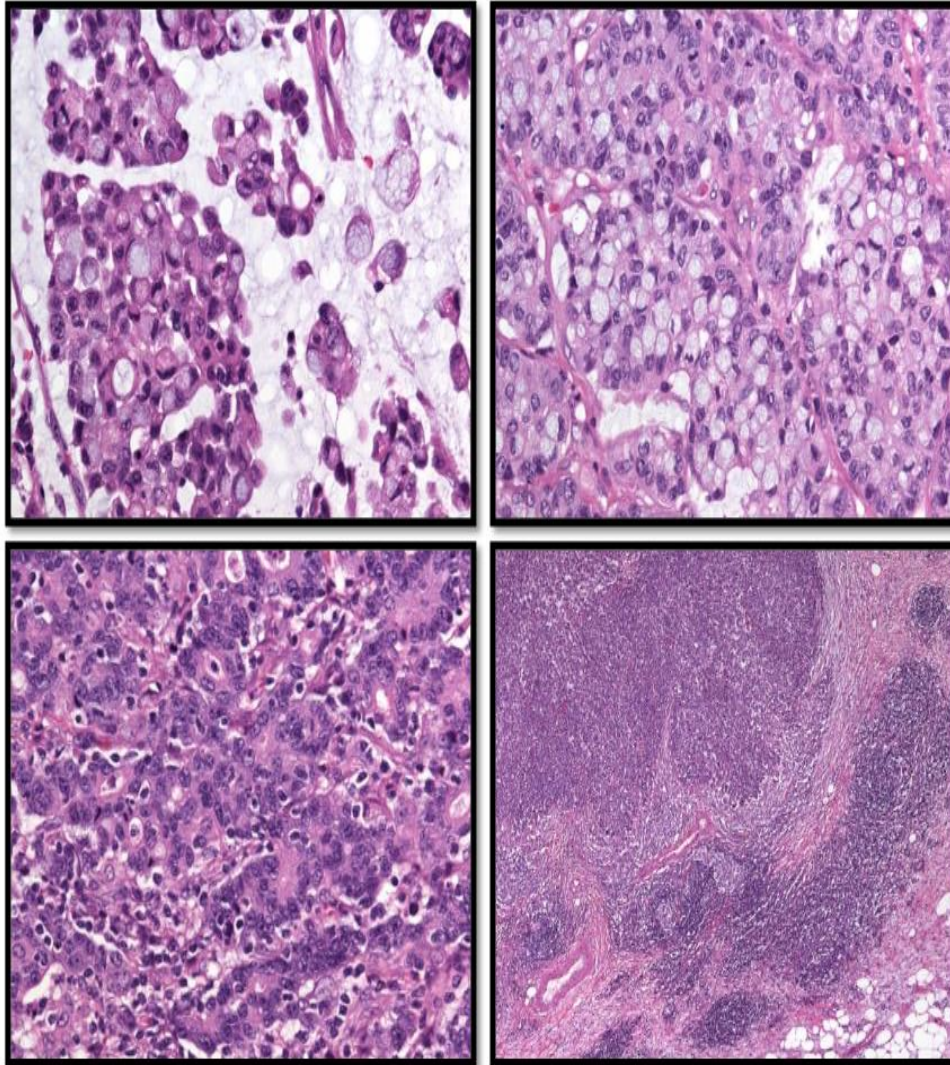
RAS/RAF WT	Treatment Recommendations	
Primary Location	ESMO	NCCN
Left	“Cytotoxic doublet plus an EGFR inhibitor is the treatment of choice”	No clear preference for EGFR mAbs or BEV in first-line
Right	Cytotoxic triplet plus BEV or a cytotoxic doublet plus an EGFR antibody	No EGFR mAbs in first-line and potentially not in any line

MICROSATELLITE INSTABILITY (MSI)



- Microsatellites are short repetitive sequences (e.g. tandem repeats) of DNA distributed throughout the genome that are commonly shortened (and display length variation, microsatellite instability, MSI) in the setting of deficient mismatch repair (dMMR) protein activity
- The most commonly altered DNA MMR genes are MLH1, MSH2, MSH6 and PMS2, with >90% having alterations in MLH1 and MSH2
- Secondary to dMMR status these tumours develop 100 to 1000s of mutations (→ enhanced neoantigen load) leading to the potential for enhanced immune recognition (→ candidates for immunotherapy)

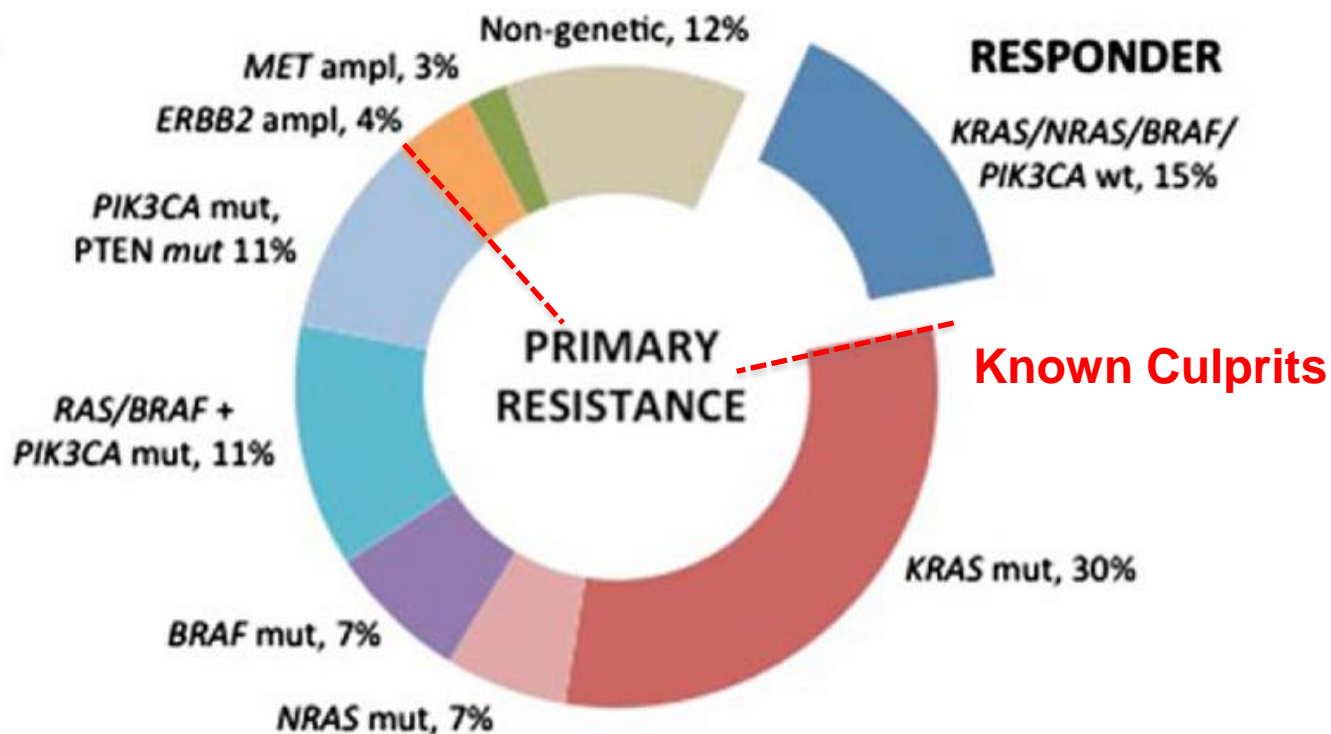
FEATURES THAT RAISE SUSPICION OF AN MSI TUMOUR



- **Clinical features**
 - Age < 60
 - Right-sided location
 - Multiple (synchronous or metachronous) CRCs
- **MSI-H histology**
 - Type: medullary, mucinous (“any mucin”), signet ring cell (“any signet ring cell”)
 - Inflammation: tumour-infiltrating lymphocytes (TILs), peritumoural lymphocytes, lymph follicles (“Crohn-like reaction”)
 - Histology: poor differentiation, expansive growth (“pushing border”), heterogeneity, no necrosis

Genes that, when mutated, drive primary resistance to anti-EGFR antibodies

Nearly 70% have heterogeneous genetic alterations in genes involved in EGFR signaling



CHALLENGES IN cfDNA ANALYSIS

- The absolute levels are low: few nanograms per ml of plasma
- The circulating cell-free DNA (cfDNA) contains both tumor-derived DNA (ctDNA) and normal DNA originating from dividing cells (blood cells, GI tract, skin)
- The ctDNA is only a fraction (<0.1% to 50%) of the cfDNA
- Levels are usually correlated with tumor burden and are higher in advanced cancer
- Highly fragmented, typically 50-200bp range (165bp peak)
- Short half-life (2 hours)

NGS assays: liquid biopsy

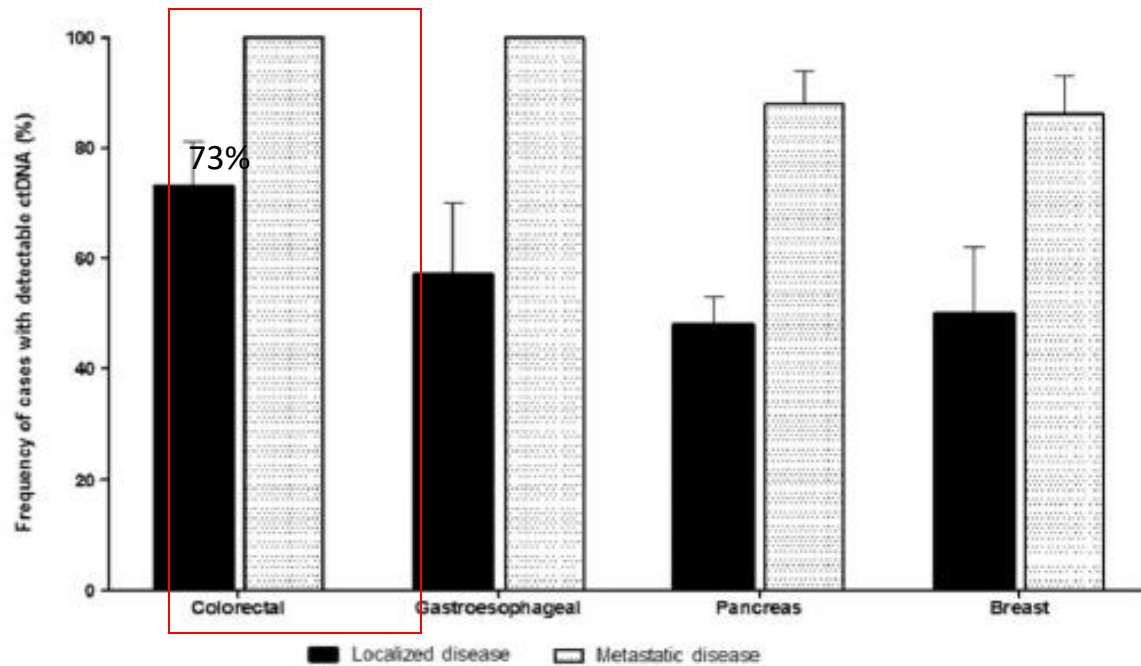


Test name*	FoundationOne® Liquid/bTMB	Guardant360/ GuardantOMNI™	MutatorDETECT	Unnamed	PredicineATLAS	Oncomine Pan- Cancer Cell-Free Assay	AVENIO ctDNA Kits
No. of genes measured	70/394	73/500+	64	508	600	52	17/77/197
Sequencing platform	Illumina HiSeq 4000	Guardant Health Digital Seq Platform	Illumina NGS†	Illumina NGS	Not reported	Ion GeneStudio S5 series	Illumina NextSeq
Types of alterations	SNVs	SNVs, indels, fusions, CNAs	SNVs, indels, fusions, CNVs	SNVs, indels, CNVs	SNV, CNV, rearrangements [§]	SNVs, indels, fusions, CNVs	SNVs, indels, fusions, CNVs
Sample requirement	(20 ng cfDNA)	1-2 mL plasma (5-30 ng cfDNA)	Two 10 mL tubes of peripheral whole blood or 6- 10 mL plasma†	Plasma (single blood draw)	Plasma (5 mL) [§]	20 ng cfNA	10-50 ng cfDNA

APPLICATIONS OF cfDNA ANALYSIS IN THE MANAGEMENT OF COLORECTAL CARCINOMA

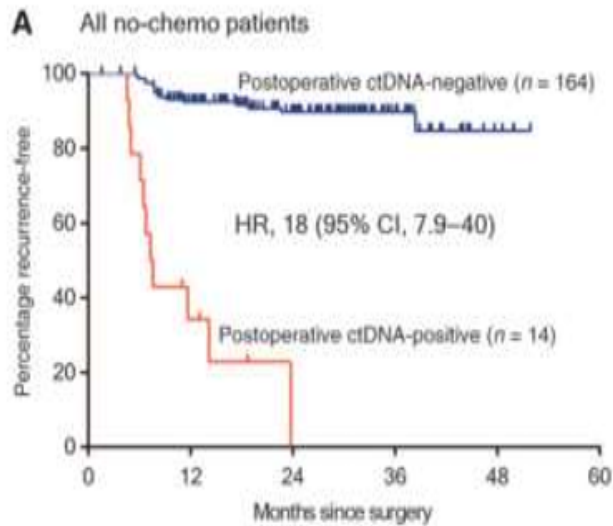
- Early diagnosis of cancer
- Detection of minimal residual disease
- Molecular profiling (identification of prognostic and predictive markers)
- Monitoring response to therapy and clonal evolution

Circulating tumor DNA (ctDNA) to detect tumors in 640 patients with various cancer types

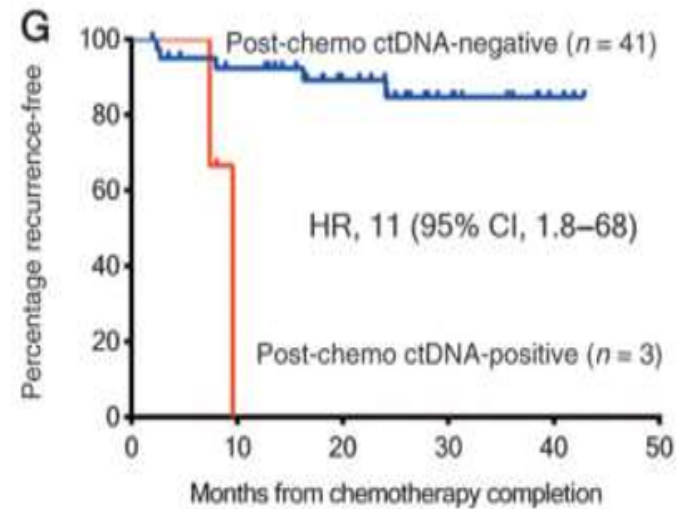


Fraction of patients with detectable ctDNA in localized (stages I to III) and metastatic colorectal, gastroesophageal, pancreatic, and breast cancers

ctDNA ANALYSIS PREDICTS RECURRENCE IN PATIENTS WITH STAGE II COLON CANCER



HR 28, CI 11-68, $p < 0.001$ at multivariate analysis



HR 14, CI 6.8-28, $p < 0.001$ at multivariate analysis

OncoBEAM RAS CRC ASSAY

OncoBEAM RAS CRC is the first liquid biopsy test to achieve CE-Mark status for RAS testing in metastatic colorectal cancer

Expanded RAS mutation analysis using BEAMing has been validated in anti-EGFR therapy clinical trials

- Over 1,200 patients have been tested using the BEAMing platform in the OPUS, CRYSTAL, and CALGN/SWOG 80405 clinical trials
- Expanded RAS testing was shown to improve the identification of mCRC patients eligible for anti-EGFR therapy

- Mutations Tested by OncoBEAM RAS CRC Kit:

Gene:	Exon 2	Exon 3	Exon 4
KRAS	G12S, G12R, G12C, G12D, G13D, G12A, G12V,	A59T, Q61L, Q61R, Q61H, Q61H	K117N, K117N, A146T, A146V
NRAS	G12S, G12R, G12C, G12D, G12A, G12V, G13R, G13D, G13V	A59T, Q61K, Q61R, Q61L, Q61H, Q61H	K117N, K117N, A146T

CONCORDANCE OF PLASMA AND TISSUE RAS MUTATION RESULTS

	Tumor tissue RAS result			PPA (95% CI)	NPA (95% CI)	OPA (95% CI)	
	RAS	Mutant	WT				Total
Plasma ctDNA RAS result	Mutant	47	3	50	$100 \times 47/52 = 90.4\%$ (79%, 96%)	$100 \times 43/46 = 93.5\%$ (82%, 98%)	$100 \times 90/98 = 91.8\%$ (85%, 96%)
	WT	5	43	48			
	Total	52	46	98			

Schmiegel Mol Oncol 2017

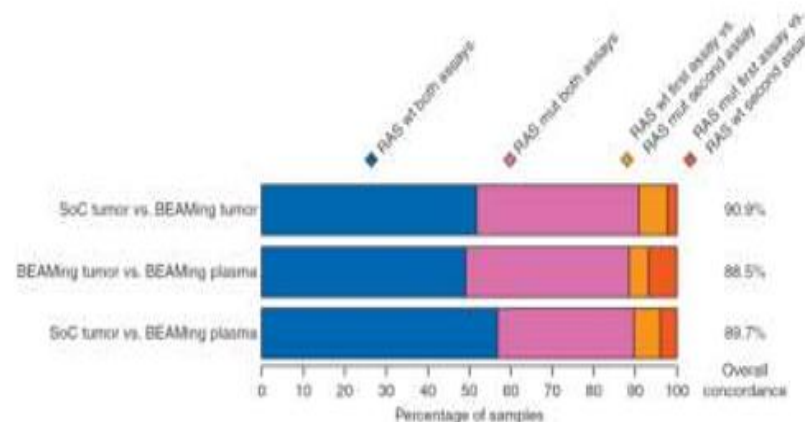
Plasma RAS result	Tissue RAS result			Total
	Mutated	No mutated		
Mutated	53	6		59
No mutated	2	54		56
Total	55	60		115

Positive agreement: 53/55: 96,4%

Negative agreement: 54/60: 90%

Overall agreement: 107/115: 93%

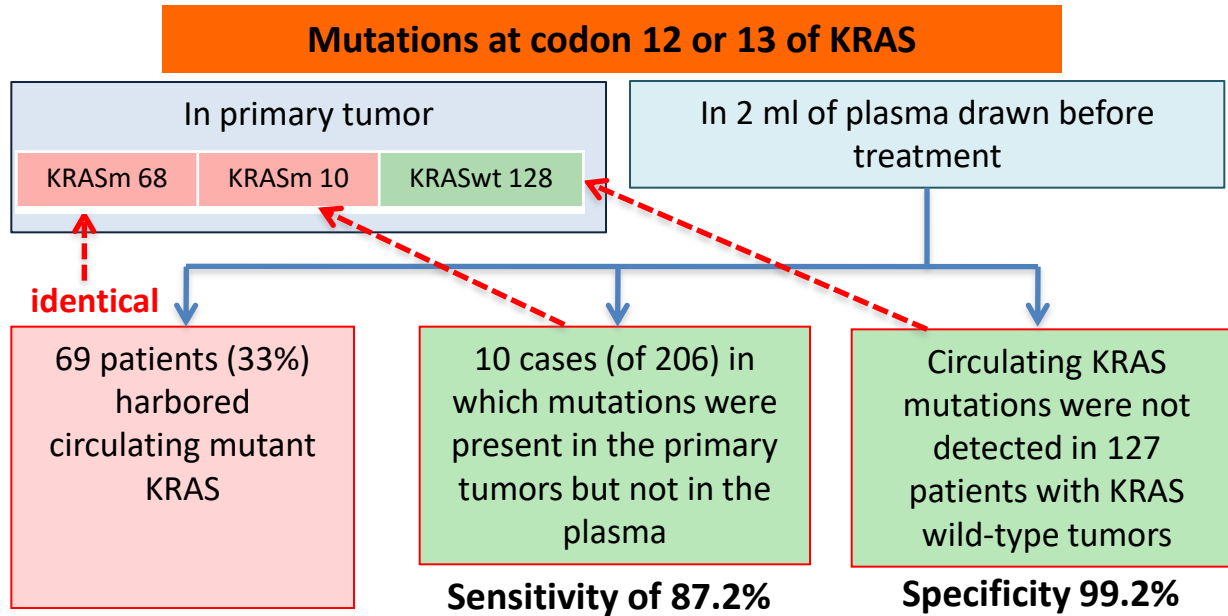
Vidal Ann Oncol 2017



Grasselli Ann Oncol 2017

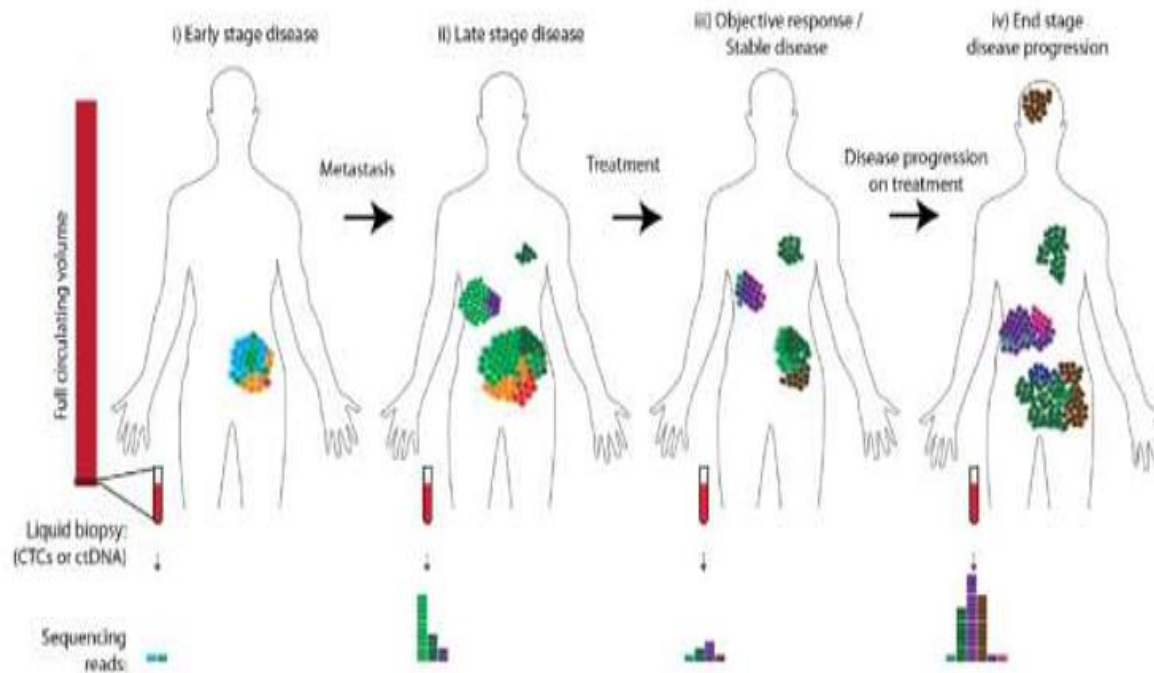
The sensitivity of the liquid biopsy

206 patients with metastatic CRC in a blinded fashion

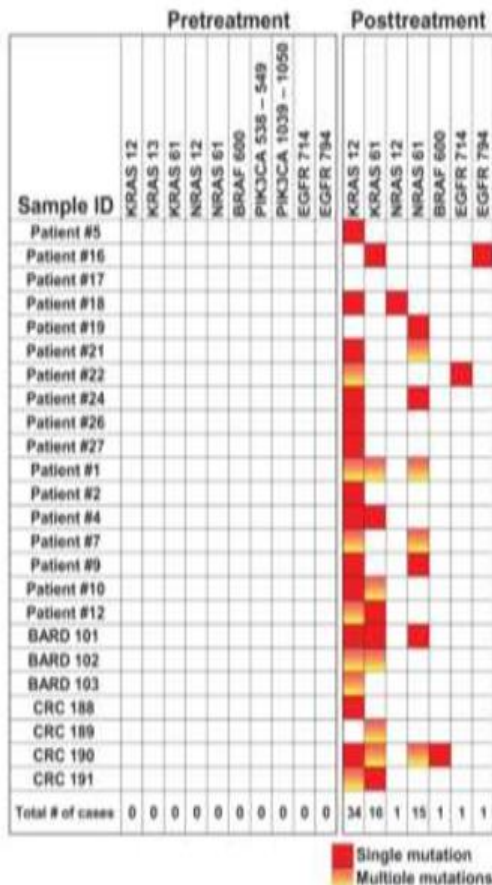


Concordance between KRAS mutation status in the plasma and tumor tissue 95%
Agreement highly significant (κ statistic = 0.88, $P < 0.0001$)

LIQUID BIOPSY CAN REPRESENT TEMPORAL AND SPATIAL HETEROGENEITY IN CANCER PROGRESSION



DETECTION OF DIFFERENT MECHANISMS OF RESISTANCE TO ANTI-EGFR MoAbs IN PLASMA OF CRC PATIENTS



Bettgowda Sci Transl Med 2014

Table 1 Identification of genetic alterations associated with resistance to anti-EGFR antibodies in plasma samples

Patient ID	Therapy	Resistance	Plausible genetic mechanism	Oncogenic alteration in COSMIC database
MOL1-CRC02	Cetux + Irino	Primary	<i>KRAS</i> p.Q61L	YES
ONCGH-CRC01	Cetux + Irino	Primary	<i>ERBB2</i> amplification*	YES
MOL1-CRC16	Cetux + Folfiri	Primary	<i>FLT3</i> amplification*	YES
MOL1-CRC07	Cetux + Folfiri	Primary	N.I.	-
ONCGH-CRC11	Cetux + Folfiri	Primary	<i>ERBB2</i> amplification*	YES
MOL1-CRC06	Panit	Primary	<i>KRAS</i> p.G12D	YES
MOL1-CRC15	Panit + Folfex4	Primary	<i>ERBB2</i> amplification*	YES
ONCG-CRC13	Panit	Primary	<i>MAP2K1</i> p.K57N*	YES
ONCG-CRC41	Panit	Primary	N.I.	-
ONCGH-CRC06	Cetux + Irino	Primary	<i>ERBB2</i> amplification* <i>FLT3</i> amplification*	YES
ONCG-CRC57	Panit	Acquired	<i>MET</i> amplification*	YES
ONCG-CRC57	Panit	Acquired	<i>KRAS</i> p.Q12A <i>KRAS</i> p.G12D <i>KRAS</i> p.G130	YES
AQJP-CRC04	Panit + Folfexri	Acquired	<i>KRAS</i> p.Q61H	YES
MOL1-CRC04	Cetux + Folfiri	Acquired	<i>KRAS</i> p.Q61H	YES
AQJP-CRC05	Panit + Folfexri	Acquired	<i>KRAS</i> p.G12D	YES
ONCG-CRC59	Cetux; then Panit	Acquired	<i>KRAS</i> p.G12Y <i>KRAS</i> p.G130	YES
AQJP-CRC01	Cetux + Folfexri	Acquired	<i>KRAS</i> p.Q61L	YES
MGH-CRC02	Cetux	Acquired	<i>KRAS</i> amplification*	YES
AQJP-CRC06	Cetux + Folfexri	Acquired	<i>KRAS</i> p.Q61L	YES
AQJP-CRC03	Panit + Folfexri	Acquired	<i>KRAS</i> p.Q61L	YES
AQJP-CRC02	Panit + Folfexri	Acquired	<i>KRAS</i> p.Q61H	YES
ONCG-CRC70	Panit + Irino	Acquired	<i>KRAS</i> p.Q61H <i>EGFR</i> p.S464L <i>EGFR</i> p.Q465R	YES
ONCG-CRC71	Panit	Acquired	<i>KRAS</i> p.Q61H	YES
ONCG-CRC72	Panit	Acquired	<i>MET</i> amplification* <i>EGFR</i> p.Q465R <i>EGFR</i> p.Q465E	YES
MOL1-CRC12	Cetux + Folfex4	Acquired	N.I.	-
ONCG-CRC73	Panit	Acquired	<i>MET</i> amplification*	YES

Siravegna Nat Med 2015

CONCLUSIONS 1

- *RAS* mutational status is a negative predictive biomarker for therapeutic choices involving EGFR antibody therapies in the metastatic disease setting [I, A].
 - *RAS* testing should be carried out on all patients at the time of diagnosis of mCRC [I, A].
- *RAS* testing is mandatory before treatment with the EGFR-targeted monoclonal antibodies cetuximab and panitumumab [I, A].
- Primary or metastatic colorectal tumour tissue can be used for *RAS* testing
RAS analysis should include at least *KRAS* exons 2, 3 and 4 (codons 12, 13, 59, 61, 117 and 146) and *NRAS* exons 2, 3 and 4 (codons 12, 13, 59, 61 and 117).
- Laboratories providing *RAS* testing of colorectal tumours should demonstrate their successful participation in a relevant external quality assessment scheme, and be appropriately accredited.

CONCLUSIONS 1

- ▶ BRAF mutation as a prognostic biomarker of poor prognosis
- ▶ Emerging biomarkers(PI3K,HER2,) not recommended for routine patient management outside of a clinical trial setting
- ▶ prevalence of MSI and *BRAF* mutations in the tumours of patients with mCRC is low.
- ▶ MSI testing has strong predictive value for the use of immune check-point inhibitors in the treatment of patients with mCRC

CONCLUSIONS

- Highly sensitive methods are required for the detection of biomarkers in the cfDNA
- NGS-based techniques can provide a comprehensive molecular portrait of the tumor starting from cfDNA
- Liquid biopsy might have a relevant role in the management of early and advanced CRC patients
- Analysis of cfDNA reveals high levels of tumor heterogeneity and clinical trials are needed to translate this information in therapeutic strategies
- The quality of liquid biopsy testing in the real life must be adequately monitored through EQA programs

