

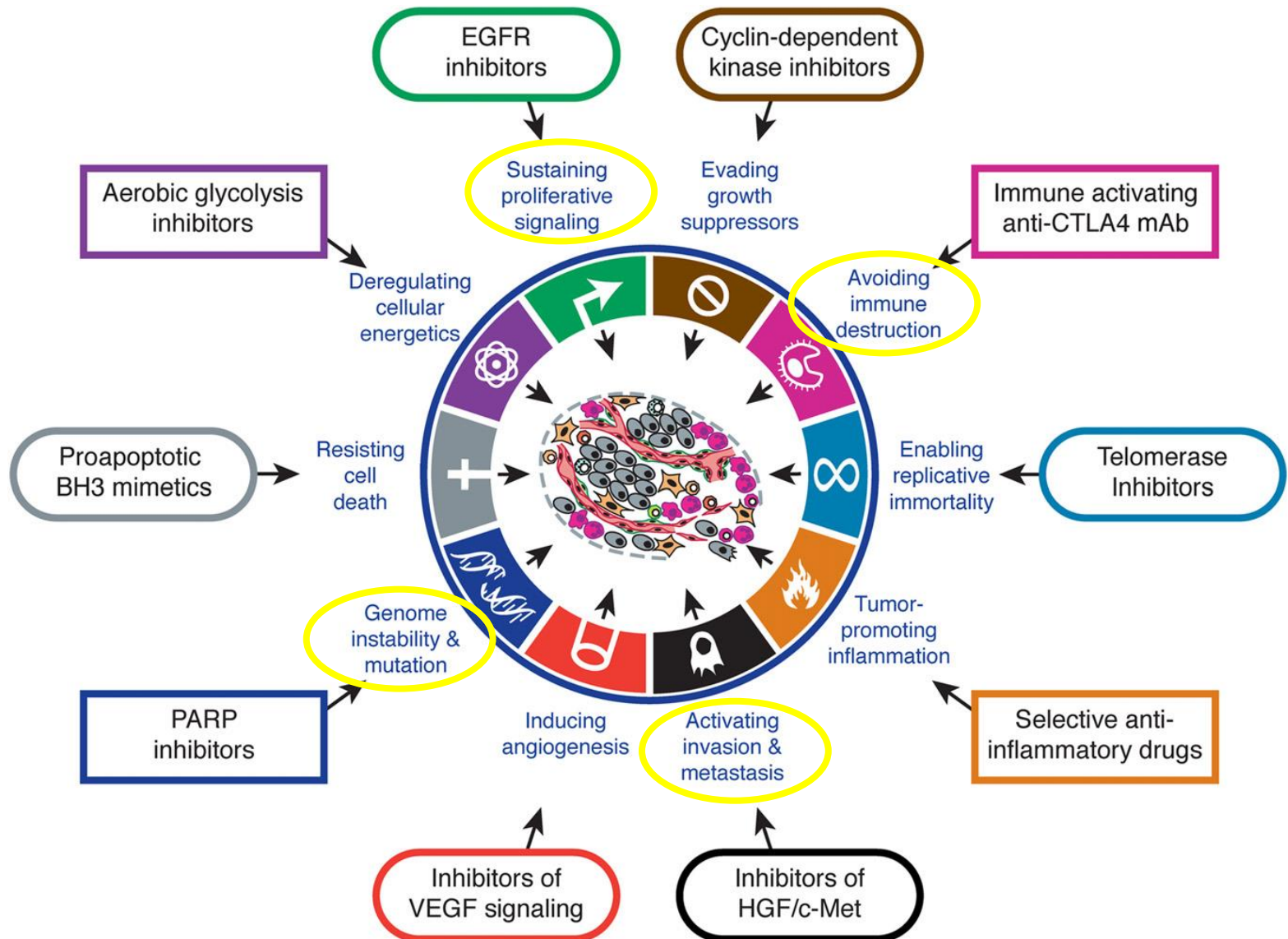


Signal transduction inhibitors and pipeline drugs

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Advances in precision medicine of metastatic colorectal cancer
ESMO 2014, Madrid, September 28th, 2014

Acquired capacities of cancer: phenotype



Beyond EGFR inhibition

- More efficient anti-EGFR MoAbs
- MoAbs directed to other members of the EGFR/HER family
- MoAbs directed to other receptors
- Combination with downstream effector inhibitors

New EGFR Inhibitors

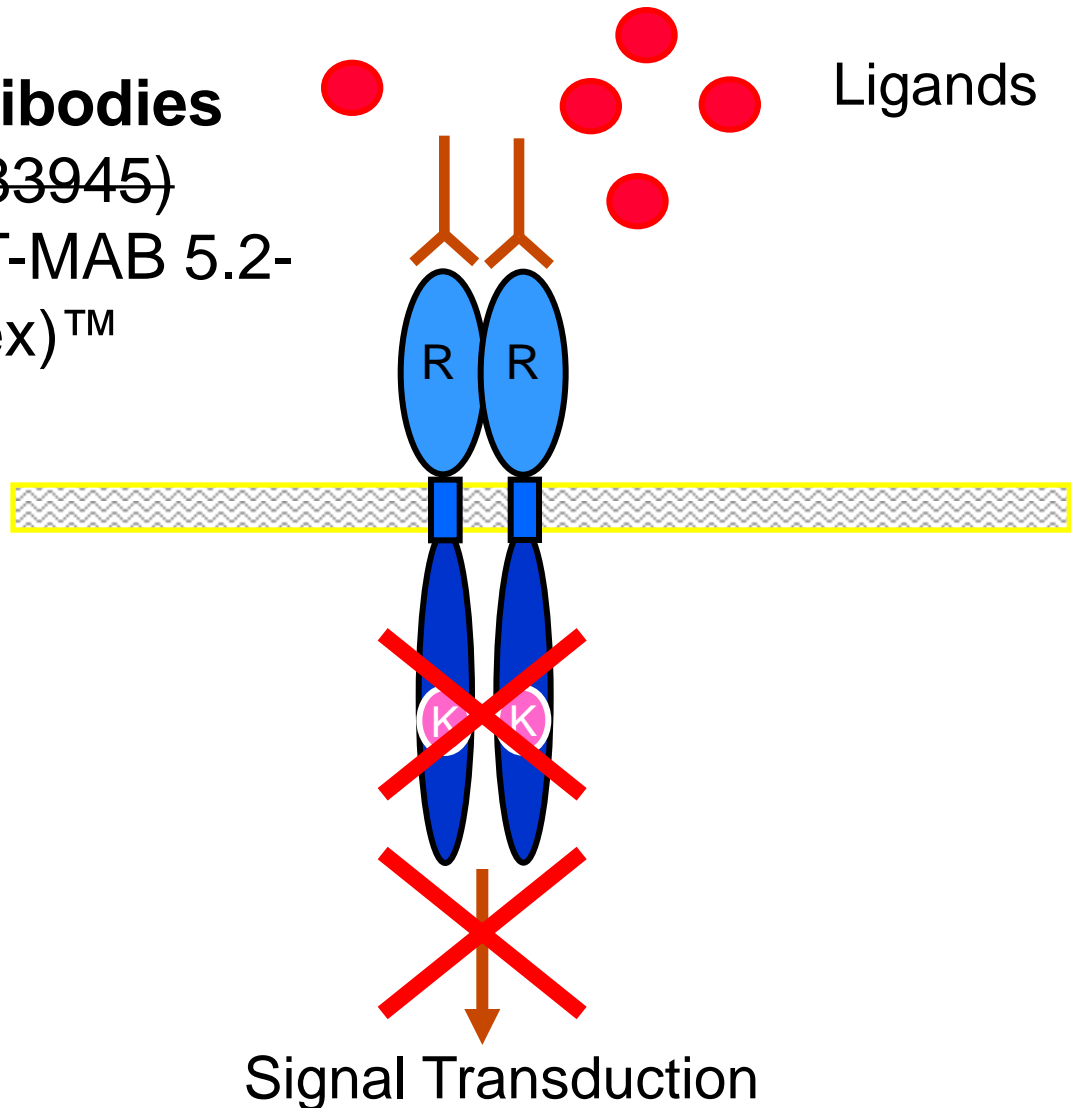
Monoclonal Antibodies

~~GA201 (RO5083945)~~

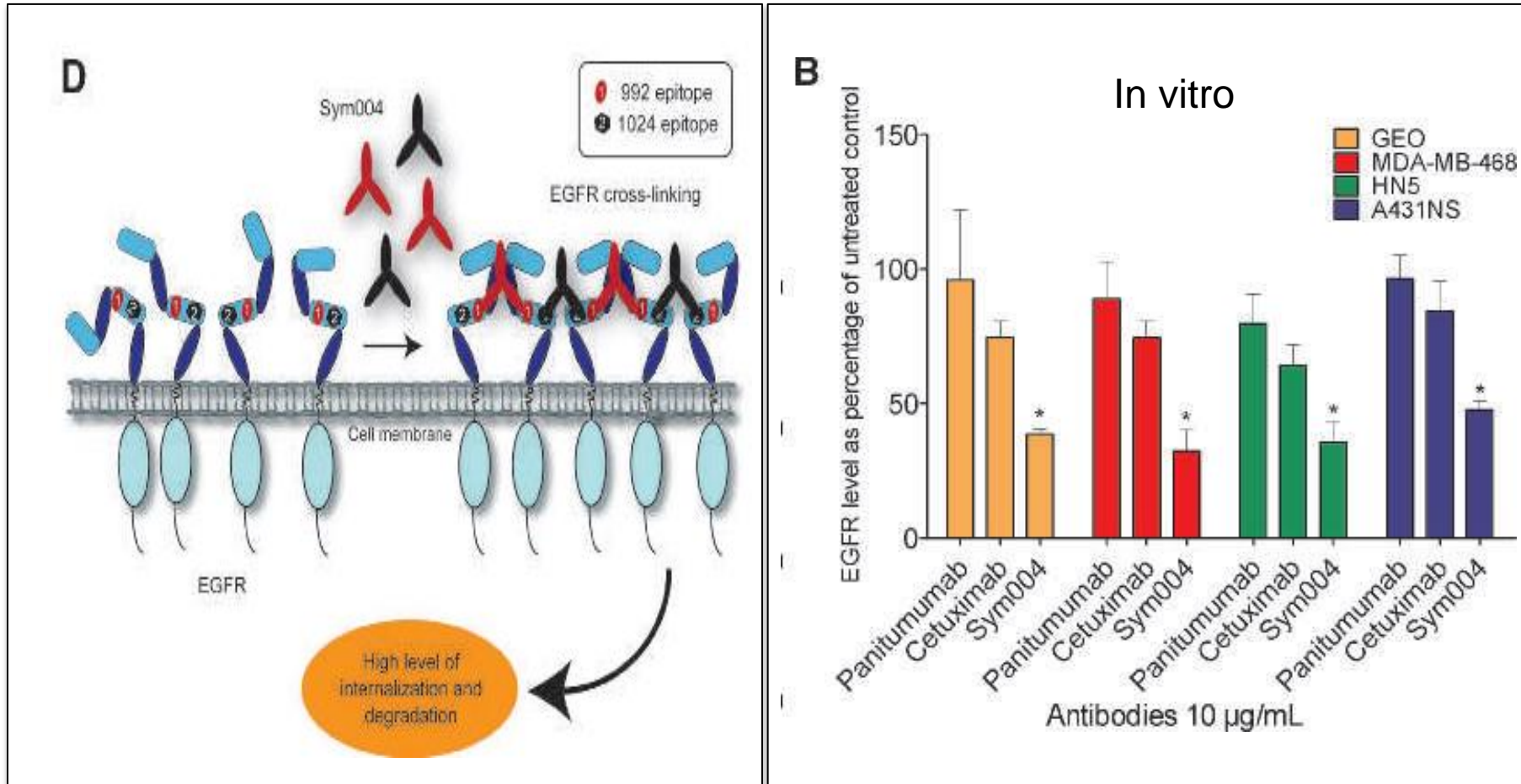
GlycoOptimized GT-MAB 5.2-

GEX (Cetugex)TM

Sym004



Sym004: A novel synergistic anti-EGFR Ab mixture



Sym004: A novel synergistic anti-EGFR Ab mixture

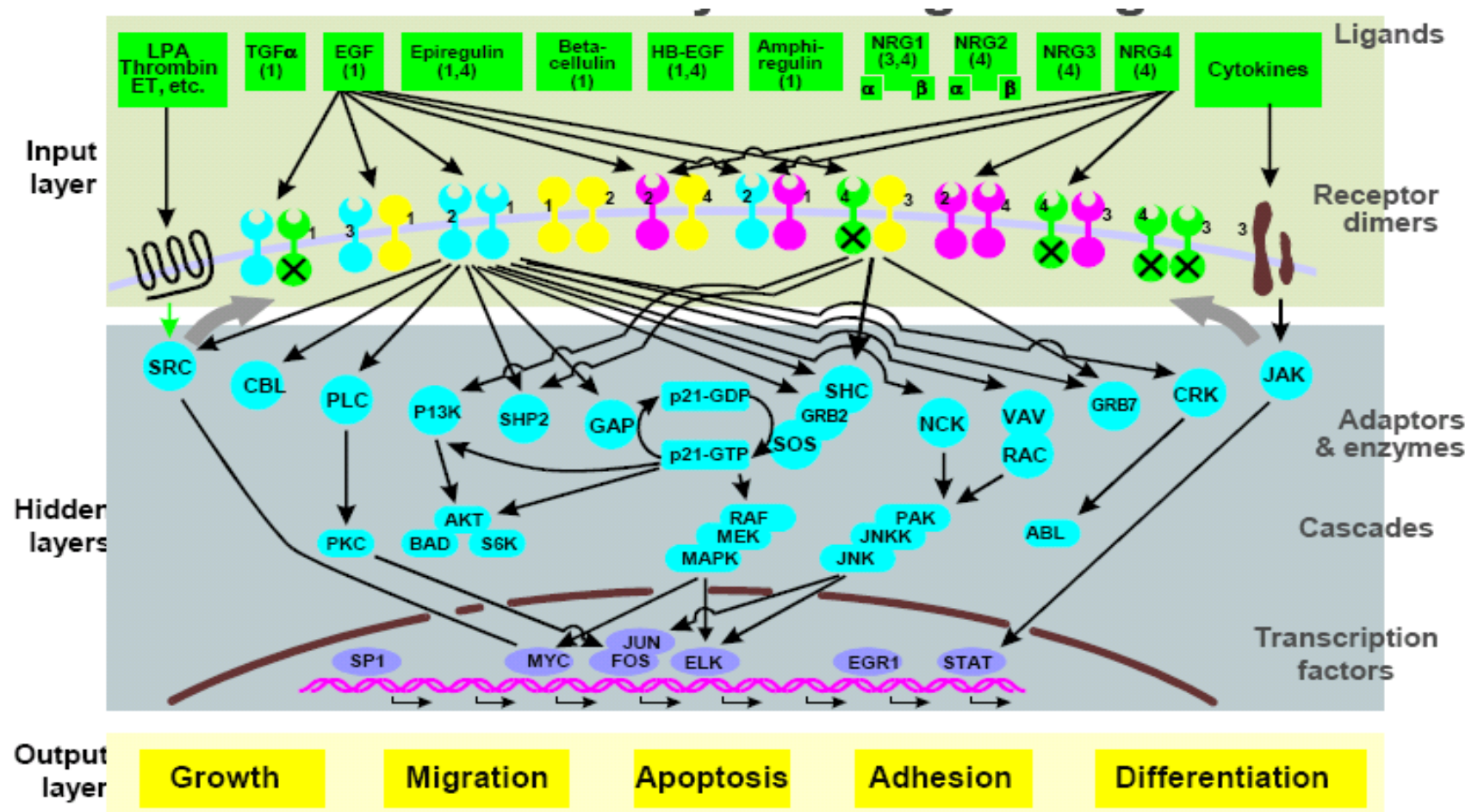
- Phase I study in advanced solid tumors (NCT01117428): ongoing
 - Enrichment with patients with colorectal cancer
 - Cohort of patients refractory to anti-EGFR MoAbs
- Randomized phase II study in refractory KRAS wt colorectal cancer launched (NCT02083653)

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EGFR & HER-3

EGFR & HER-2



HER-3 and colon cancer

- HER3 has been associated with tumor resistance to therapeutic agents targeting EGFR or HER2 in NSCLC and breast cancer¹
- HER3 is occasionally mutated in CCR, but increased HER3 mRNA or protein is commonly detected^{2,3}
- ERBB3 has been identified as a potential therapeutic target in breast cancer and NSCLC, and currently its potential role as a potential mechanism of resistance of EGFR inhibitors is being evaluated^{1,4}

¹Baselga & Swain, Nature Rev Cancer 2009

²Hu et al, J Biol Chem 2005

³Kountourakis Pet al, BMC Cancer 2006

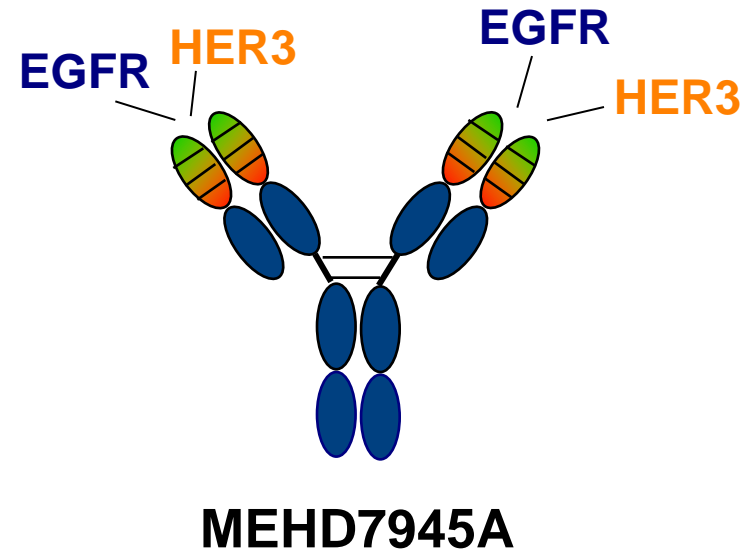
⁴Kruser et al, ExpCell Res 2010

MoAbs targeting HER-3

- U3-1287 - AMG888 (phase I NCT00730470)
- MM-121 (phase I NCT00734305)
- LJM716 (phase I NCT01598077)
- MEHD7945A, dual EGFR & HER3 MoAb (phase I NCT01207323, RP2 NCT01652482)

MEHD7945A (dual EGFR & HER-3 MoAb)

- IgG1 MoAb
- Blocks ligand binding to HER3 and EGFR and downstream signaling
 - K_d (hu HER3) = 0.39 nM
 - K_d (hu EGFR) = 1.9 nM
- Shows broader activity *in vitro* and *in vivo* compared to monospecific antibodies
- Shows significant activity in colon, lung, pancreatic, HNSCC, breast and ovarian xenograft models
- Clinical data reported at ASCO 2012
- 2nd-line mCRC: FOLFIRI + MEHD7945A vs FOLFIRI + Cetuximab (NCT01652482)

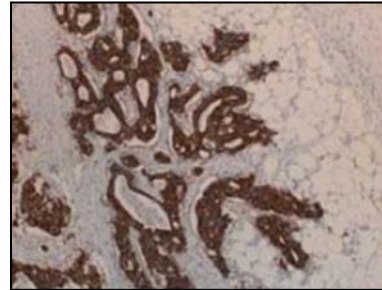
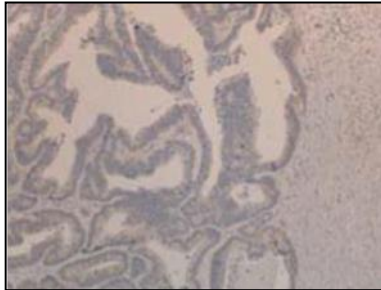


Correlation between HER2 amplification and therapeutic resistance to cetuximab in xenopatients

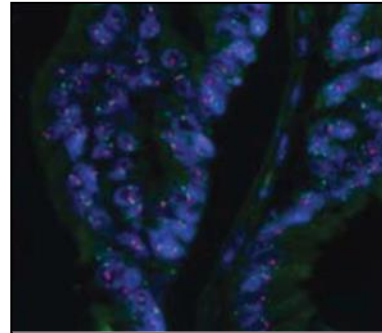
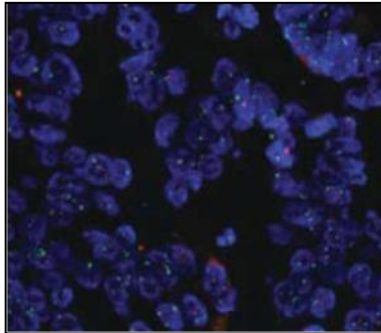
Normal

HER2 amplification

IHC - HER2

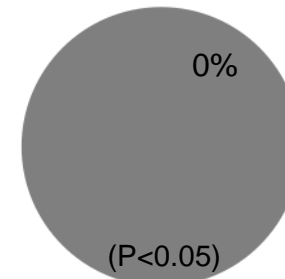


FISH - HER2

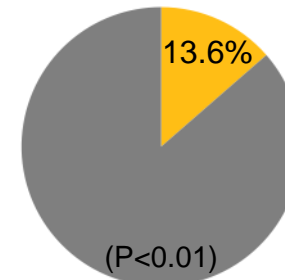


In mCRC patients there is a progressive enrichment of HER2 amplification along with refinement of genetic selection

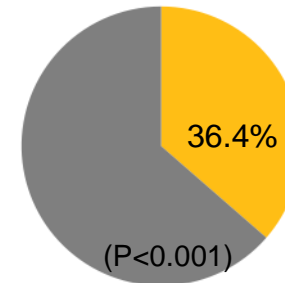
■ HER2 amplification



KRAS wt responders
(n=45 patients)



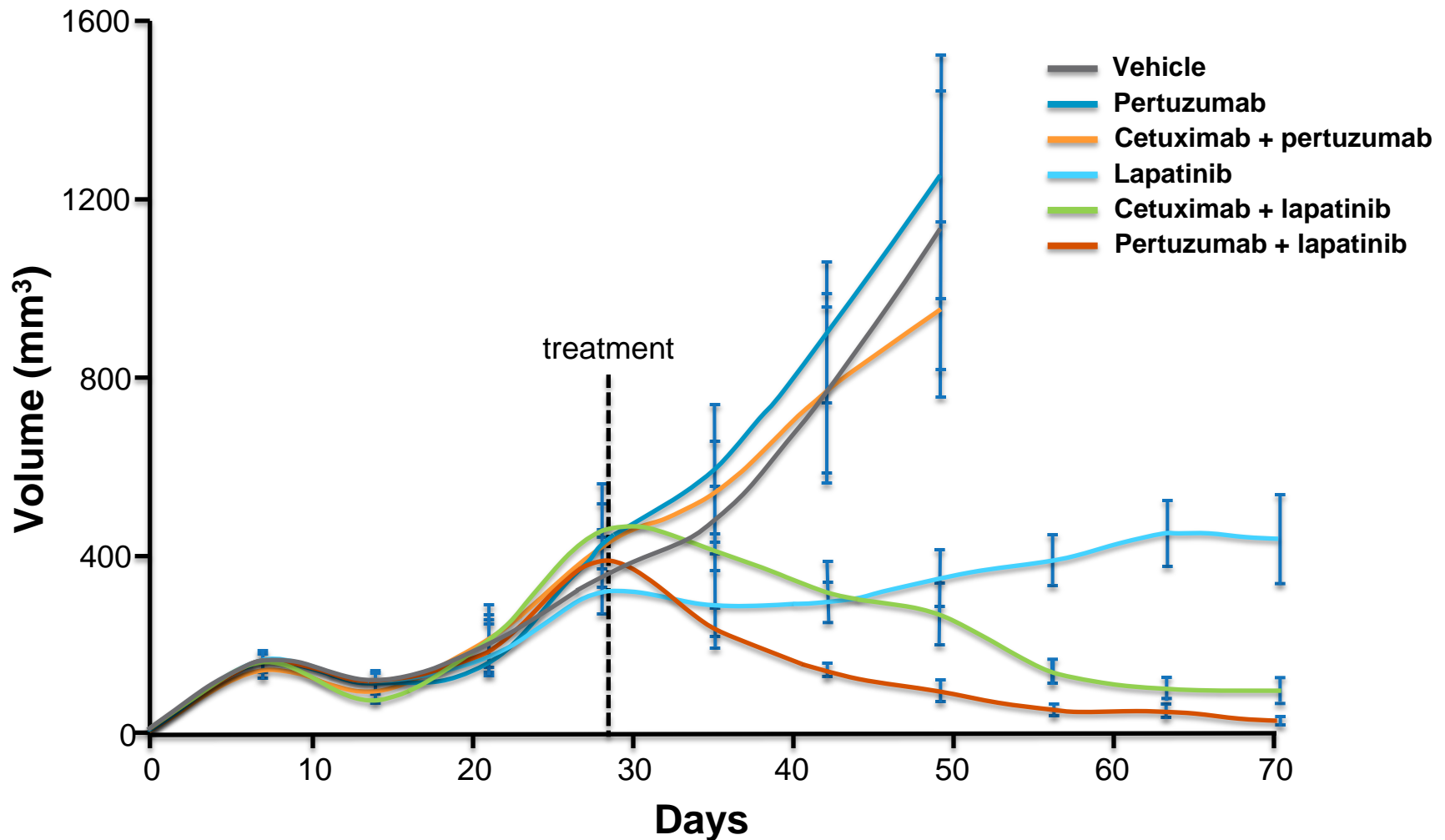
KRAS wt non-responders
(n=44 patients)



Quadruple* wt non-responders
(n=11 xenopatients)

* *KRAS/NRAS/BRAF/PIK3CA*

Anti-EGFR and anti-HER2 therapies in cetuximab-resistant HER2-amplified xenopatient with mCRC



Clinical anti-HER-2 strategies in mCRC

- Limited patient population: HER2 amplification (5%) was associated with resistance to cetuximab (Yonesaka et al, Sci Transl Med 2011)

HERACLES study

Single arm, Phase II, multi-center, sequential trial designed to assess the ORR in an HER2 amplification-enriched population of mCRC patients receiving, in two separate and consecutive cohorts:

- Cohort 1 trastuzumab + lapatinib
- Cohort 2 trastuzumab + pertuzumab

PI: S. Siena, Italy

MCLA-128

MCLA-128 is a human bispecific IgG1 antibody that simultaneously targets HER2 and HER3 receptors

- In phase I with expansion cohorts in mCRC Her-2 +

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c-Met and HGF

- Oncogene implicated in:
 - Tumor invasiveness, metastasis and proliferation
 - Angiogenesis
 - Resistance to treatment
- c-Met is a high affinity tyrosine kinase receptor for the HGF/SF
- Activation occurs through both autocrine and paracrine signaling (HGF)
- c-Met overexpression or mutation/amplification found in many tumors

Tumor Type	Primary Tumor		
	MET Expression (% patients)	MET Mutation (% patients)	MET Amplification (% patients)
Brain	54-88	0-9	9-20
Head & Neck	52-68	11-27	n/a
Mesothelioma	74-100	0	n/a
Lung	41-72	8-13	0
Thyroid	40-91	6-10	n/a
Breast	25-60	0	n/a
Renal Cell	54-87	13-100	(Trisomy 7)
Hepatoma	68-69	0-30	n/a
Colon	55-78	0	4-89
Cervical	30-72	0	n/a
Ovarian	64	0-4	0
Sarcoma	20-87	0-3	n/a
Melanoma	17-39	0	n/a
Multiple Myeloma	48-80	n/a	n/a
Gastric	75-90	n/a	10-20

c-Met and colon cancer

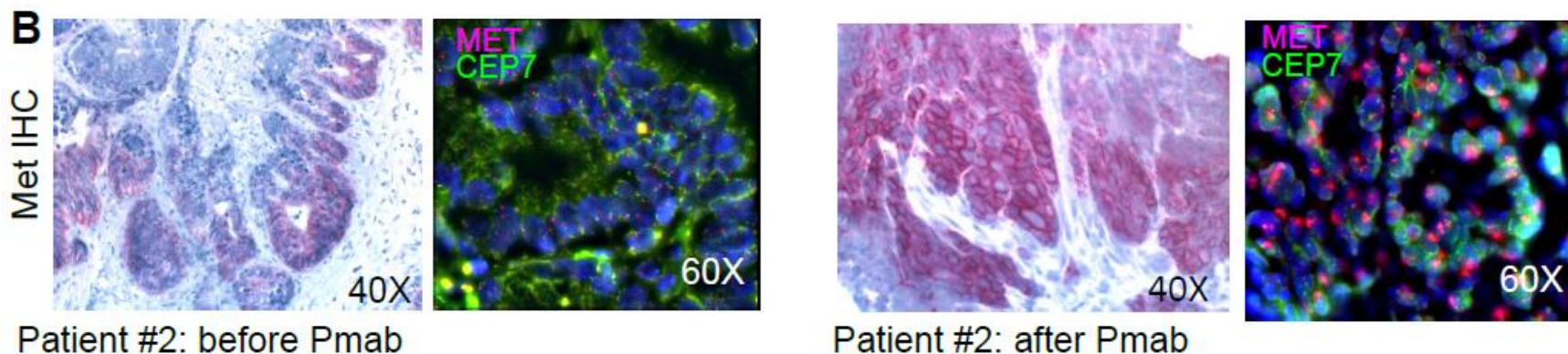
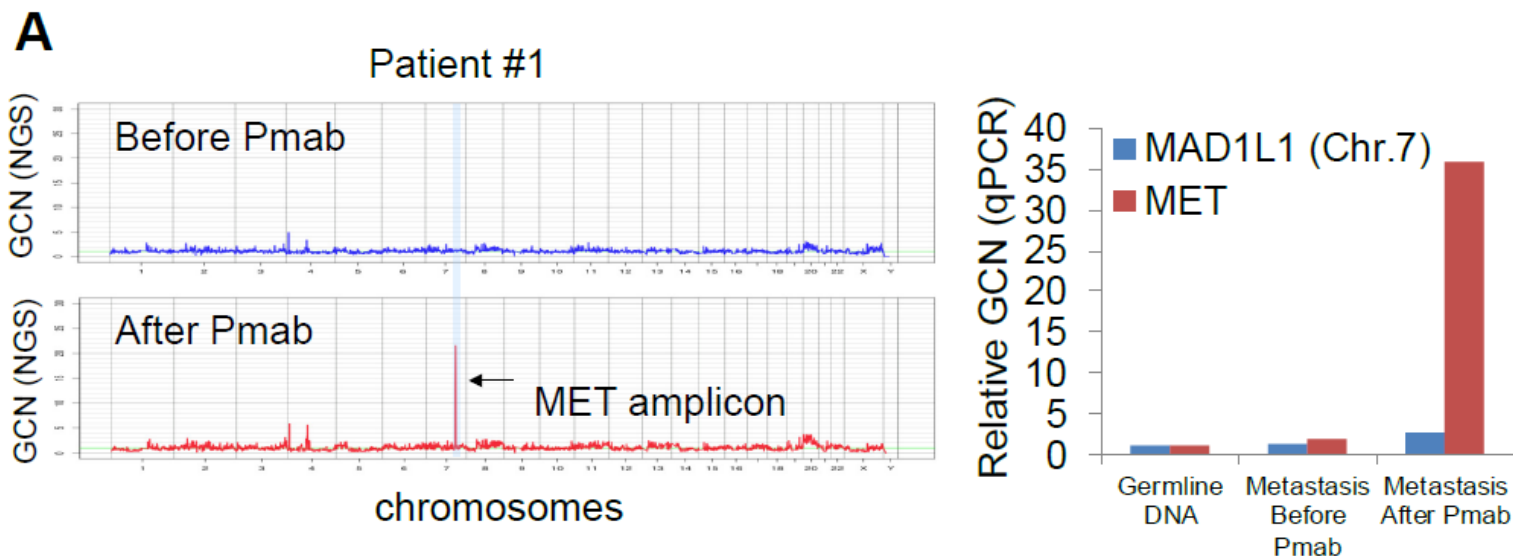
- c-Met activation by HGF plays an important role in metastatic growth of colon tumor cells in the liver and cooperates with *KRAS* mutation to enhance tumorigenicity of CRC cells¹
- The expression of the c-Met receptor and the ligand HGF has been correlated with advanced stage and poor survival in colon cancer²
- Amplification of c-Met receptor has been clinically demonstrated as one of the mechanisms of secondary resistance to EGFR inhibitors³
- Unselected population: inactive strategy
- Demonstration of dependency is cumbersome: amplification vs mutation vs (over)expression

¹Seiden-Long et al. Oncogene 2006

²Kammula et al. Cancer Lett 2007

³Bardelli et al. Cancer Discov 2013

c-Met amplification and secondary resistance to Anti-EGFR treatments



c-Met and colon cancer

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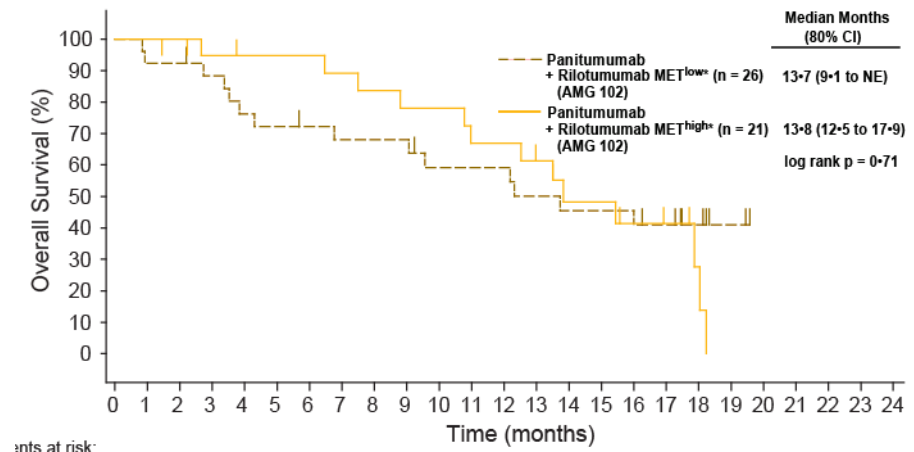
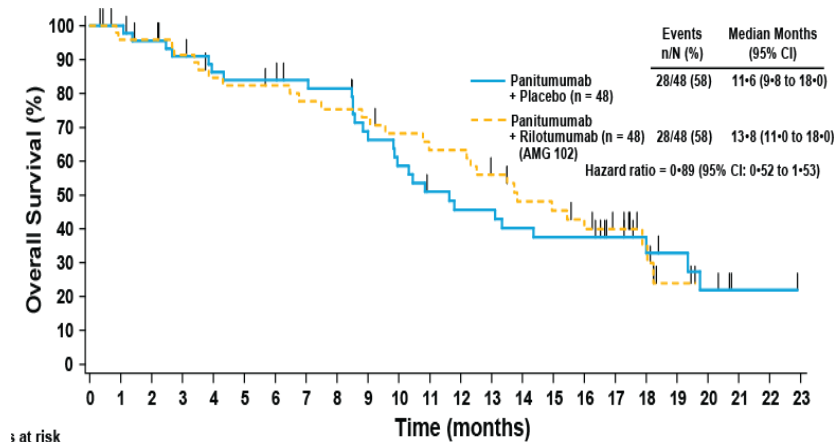
¹Seiden-Long et al. Oncogene 2006

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³Bardelli et al. Cancer Discov 2013

Panitumumab + Rilotumumab

- NCT00788957
- Phase Ib/randomized II study of Ganitumab or Rilotumumab in combination with panitumumab versus panitumumab alone in subjects with mCRC whose tumors are wt *KRAS*
- 142 patients refractory to Iri- and/or Oxl-based chemotherapy



Studies in EGFR RAS wild-type (naïve) mCRC

Genomic profile	Strategy	Trial
<i>KRAS</i> wt anti-EGFR naïve	• novel anti-EGFR/HER3 mAbs	Phase 2
	MEHD7945A + FOLFIRI vs. Cetuximab FOLFIRI	NCT01652482
	• anti-EGFR mAbs + irreversible ERBB TKIs	Phase 2
	Cetuximab + Afatinib vs. Cetuximab	NCT01919879
	• PI3K pathway inhibitors	Phase 2
	Cetuximab + Irinotecan vs. PF-05212384 + Irinotecan	NCT01925274

Studies in EGFR RAS wild-type (anti-EGFR pretreated) mCRC

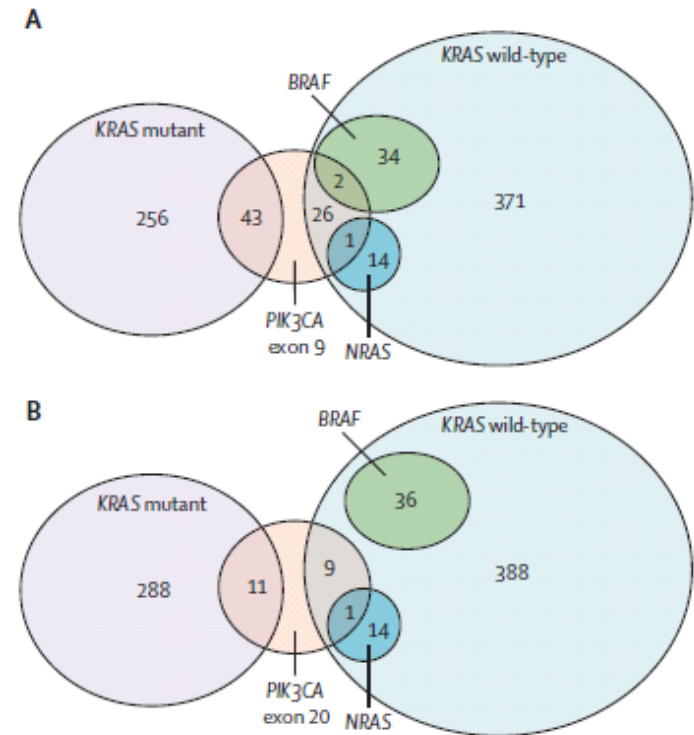
Genomic profile	Strategy	Trial
<i>KRAS</i> wt progressing to anti-EGFR mAbs	• novel anti-EGFR mAbs with potent ADCC SYM004	Phase 1/2 NCT01117428
		RP2 NCT02083653
	• anti-EGFR mAbs + MEK inhibitors Panitumumab + MEK162	Phase 2 NCT01927341
<i>KRAS</i> wt <i>HER2</i> amp progressing to anti-EGFR mAbs	• dual anti-HER2 therapy Trastuzumab + Pertuzumab or Lapatinib	Phase 2 Heracles trial
<i>KRAS</i> wt MET high progressing to anti-EGFR mAbs	• anti-EGFR mAbs + MET inhibitors Cetuximab + ARQ197	Phase 2 NCT01892527
Quadruple negative (<i>KRAS</i> , <i>NRAS</i> , <i>BRAF</i> , <i>PIK3CA</i>) progressing to anti-EGFR mAbs	• anti-EGFR mAbs + irreversible ERBB TKIs Cetuximab + Neratinib	Phase 2 NCT01960023

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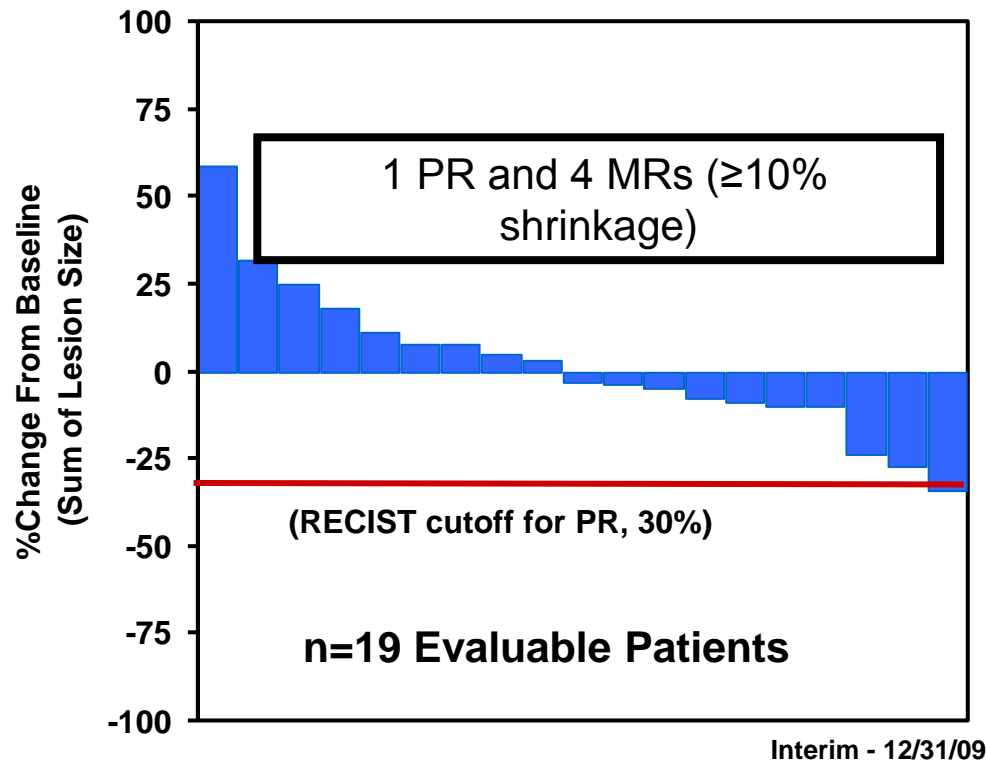
BRAF (V600E) mutated CRC

- Small population:
 - 8-10% early stage
 - 4-5% late stage
- BRAF V600E mutations as a biomarker?
 - very poor prognosis in late stage (mCRC)
 - no clear prognostic effect in early stage
 - predictive: negative predictive effect for anti-EGFR MoAbs in some studies:
 - Cetuximab: refractory (European cons.)^{1,2} & first-line setting (CRYSTAL study)³
 - Panitumumab: 2nd line setting (PICCOLO study)⁴
 - No change in the label by any regulatory authority predicted



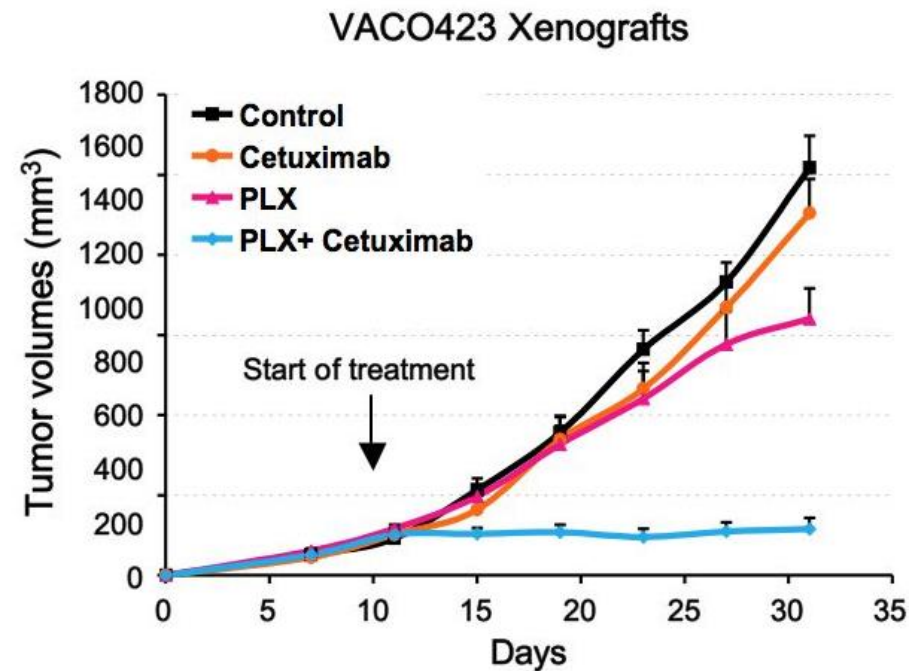
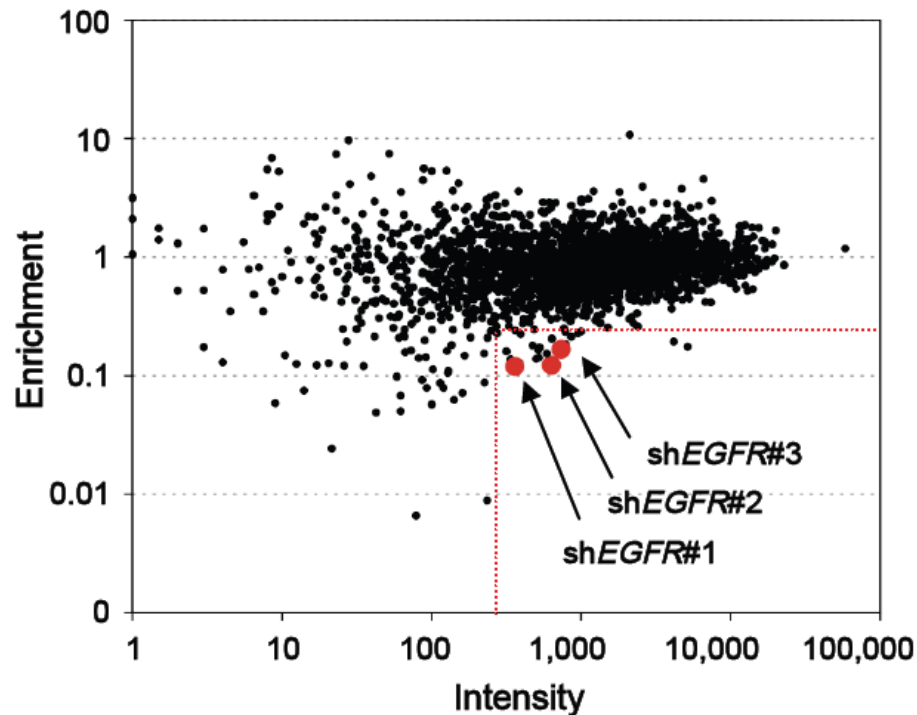
¹ Di Nicolantonio F, J Clin Oncol 2018; ² De Roock et al, Lancet Oncol 2010; ³ Van Cutsem et al, J Clin Oncol 2011; ⁴ Seymour MT et al, Lancet Oncol 2013

Vemurafenib in BRAF (V600E) mutant mCRC



- Outstanding activity of vemurafenib in metastatic melanoma with BRAF V600E mutations
- Preclinical activity shown in limited CRC BRAF V600 mutated cells¹
- Marginal activity in metastatic CRC with BRAF V600E mutations²

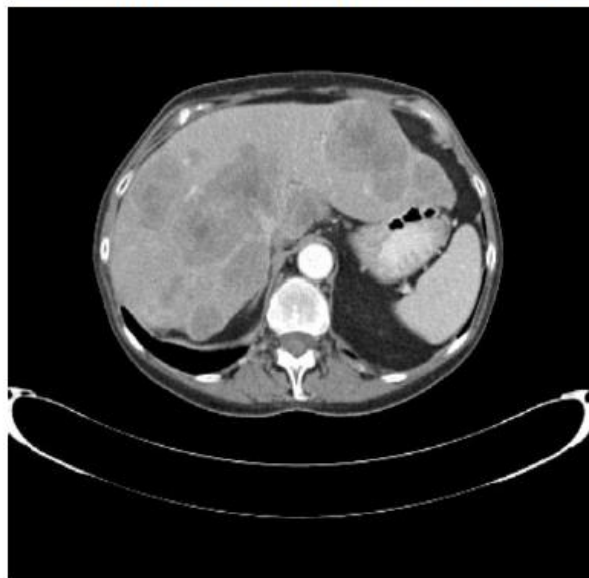
BRAF inhibitors + EGFR inhibitors have *in vivo* activity in BRAF^{V600E} mutated CRC xenografts



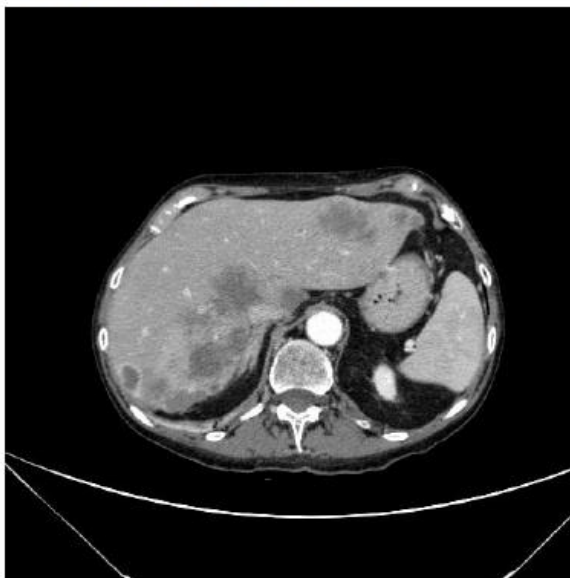
New studies in the BRAF^{V600E} mutant CRC population

- As examples of clinical trials evaluating the combination of BRAFV600E inhibitors plus anti-EGFR inhibitors in the BRAF mutant population in CRC:
 - NCT01524978: Vemurafenib + Cetuximab (BASKET) – Roche: Phase Ib
 - NCT01750918: BRAF/MEK Inhibitors (dabrafenib + trametinib) + Panitumumab – GSK: Phase Ib → RP2
 - NCT01719380: LGX818 and Cetuximab or LGX818, BYL719, and Cetuximab – Novartis: Phase Ib → RP2
 - NCT01787500 (MDACC): Vemurafenib + Cetuximab + Irinotecan

Baseline CT scan (11.07.2013)



CT scan 09.08.2013



Baseline CT scan (11.07.2013)



09.08.2013



Early efficacy comparison of BRAFi/EGFRi combos

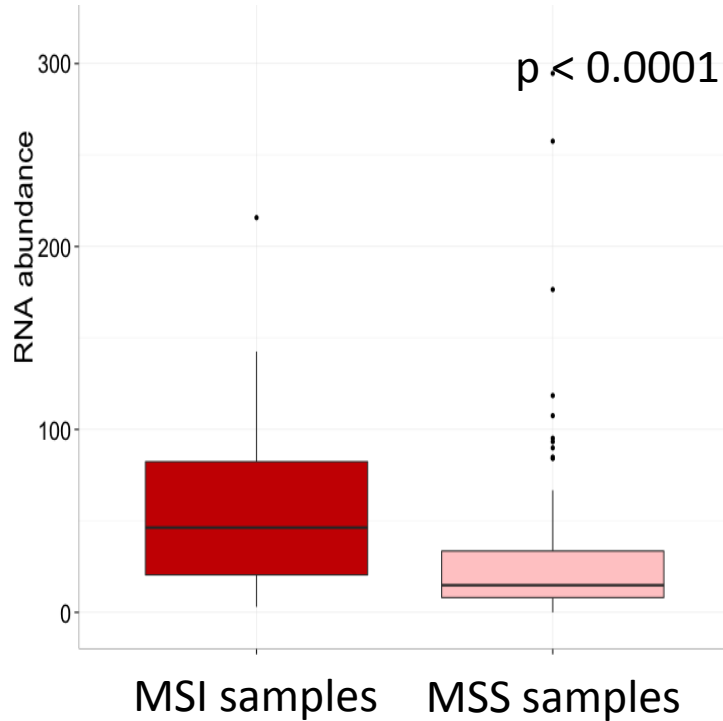
Regimen	N	PR/CR (%)	SD (%)	DCR (%)
Dabrafenib + Trabectinib	43	12	51	63
Dabrafenib + Panitumumab	15	13	73	87
Vemurafenib + Cetuximab*	11	-	36	36
Encorafenib + Cetuximab	24	29	50	79
Dabrafenib + Trabectinib + Panitumumab	15	40	40	80
Vemurafenib + Cetuximab + Irinotecan	8	50	50	100
Encorafenib + Cetuximab + BYL719	20	30	60	90

*No confirmation response assessment

Immune activating agents

Anti-PD1/PDL1 in mCRC

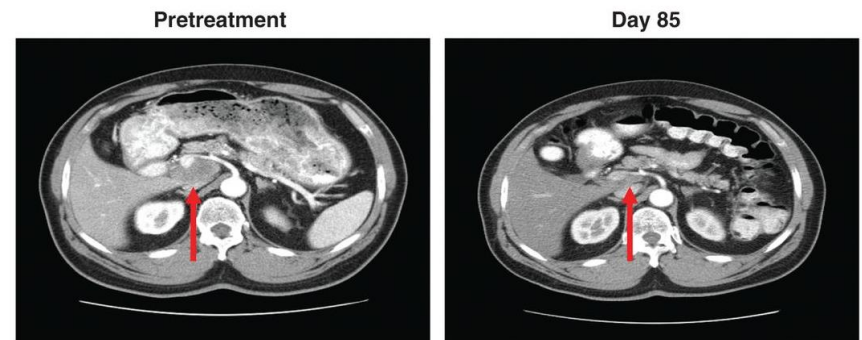
TCGA CRC - RNA seq (n=328)
CD274 (PDL1) gene expression



Dienstmann, Unpublished

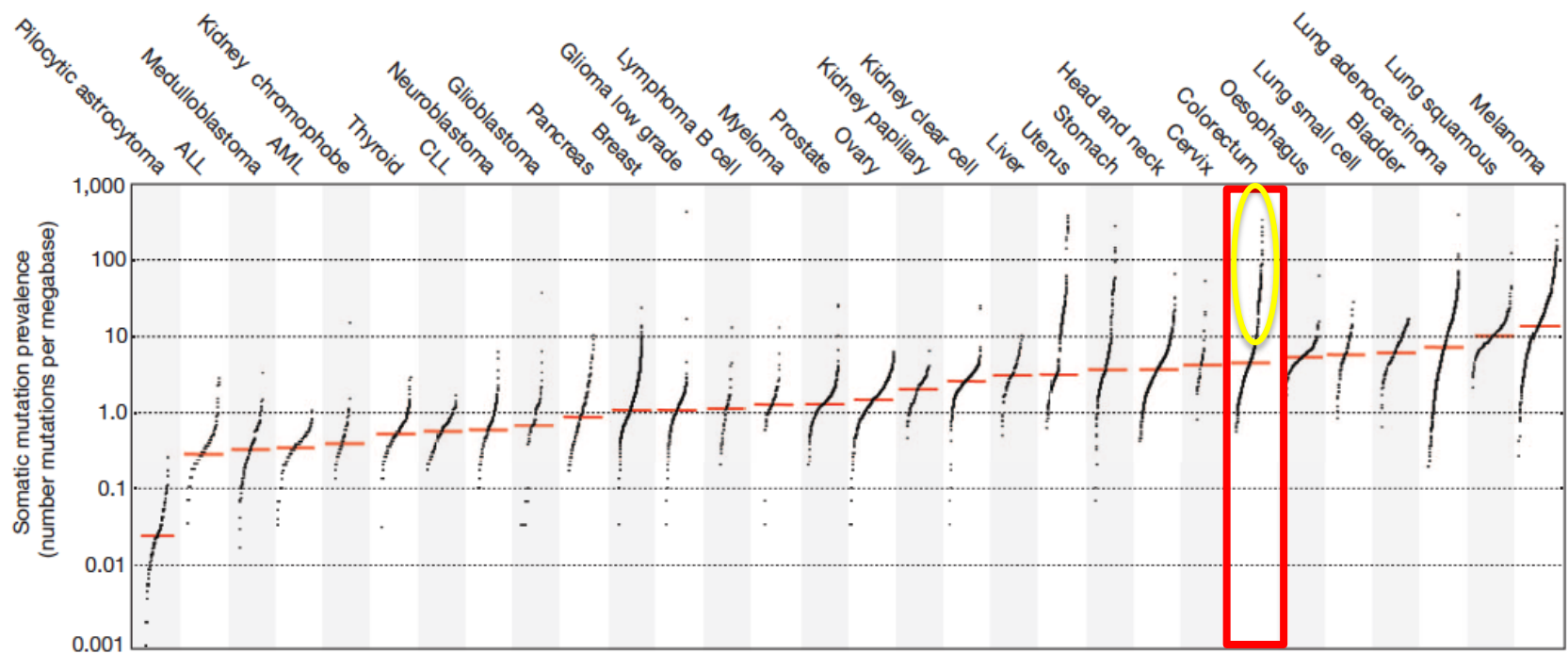
Case report of durable complete response

MSI CRC patient on anti-PD1 mAb



Molecular understanding of CRC

TCGA



CRCSC – clinical and molecular correlates

Epithelial A

High chromosomal instability
Microsatellite stable
CIMP negative
WNT and MYC activation

Epithelial B

Heterogeneous chromosomal/
microsatellite status
KRAS mutations
Metabolic reprogramming

Right colon



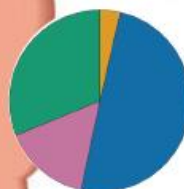
Left colon



Immune

Microsatellite instability
CIMP high
Hypermutation, *BRAF* mutations
Immune activation

Rectum



Mesenchymal

High chromosomal instability
TGF β activation
Invasion, matrix remodeling
Angiogenesis

Summary

- Target discovery has resulted in numerous novel drugs in clinical development but with very limited survival gain in mCRC
- Signal transduction inhibition does not guarantee tumor response:
 - Target presence and dependence
 - Redundancy, Cross-talk
- Need for molecular profile, characterization in multiple subtypes and selection
- Need for strong science-sound rationale for the combinations, these addressing mechanistic interactions: *BRAF* mutant
- Need to sequentially evaluate tumor cells (tumor tissue, CTCs, circulating DNA, ...) to have evolutive/dynamic information