

11. Jahrestagung der Berlin-Brandenburgischen Gesellschaft für Gastroenterologie und Hepatologie

Endlich Relevanz für molekulare Marker beim KRK?!

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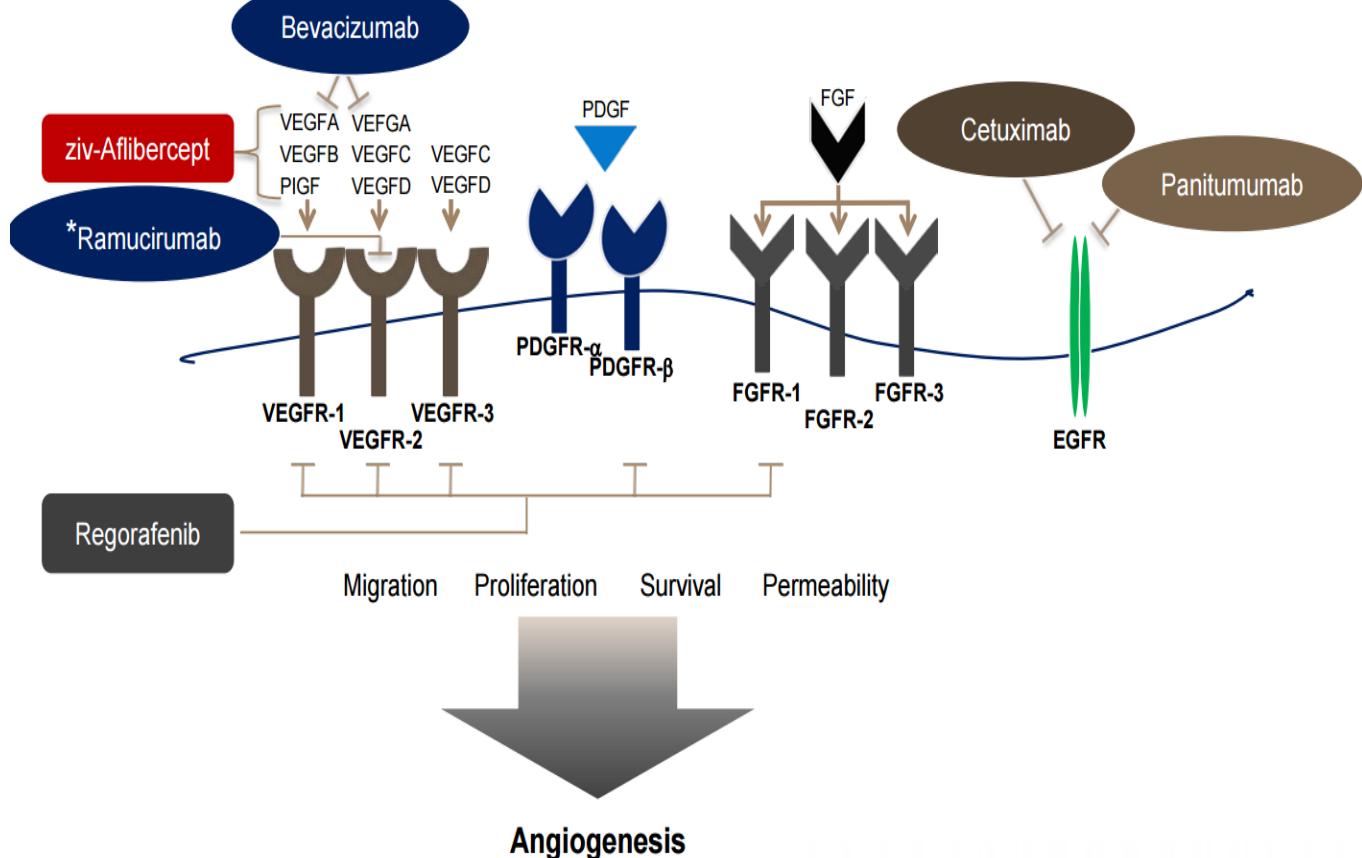


Therapiespektrum beim metastasierten KRK

Combination Chemo



Targeted Therapy



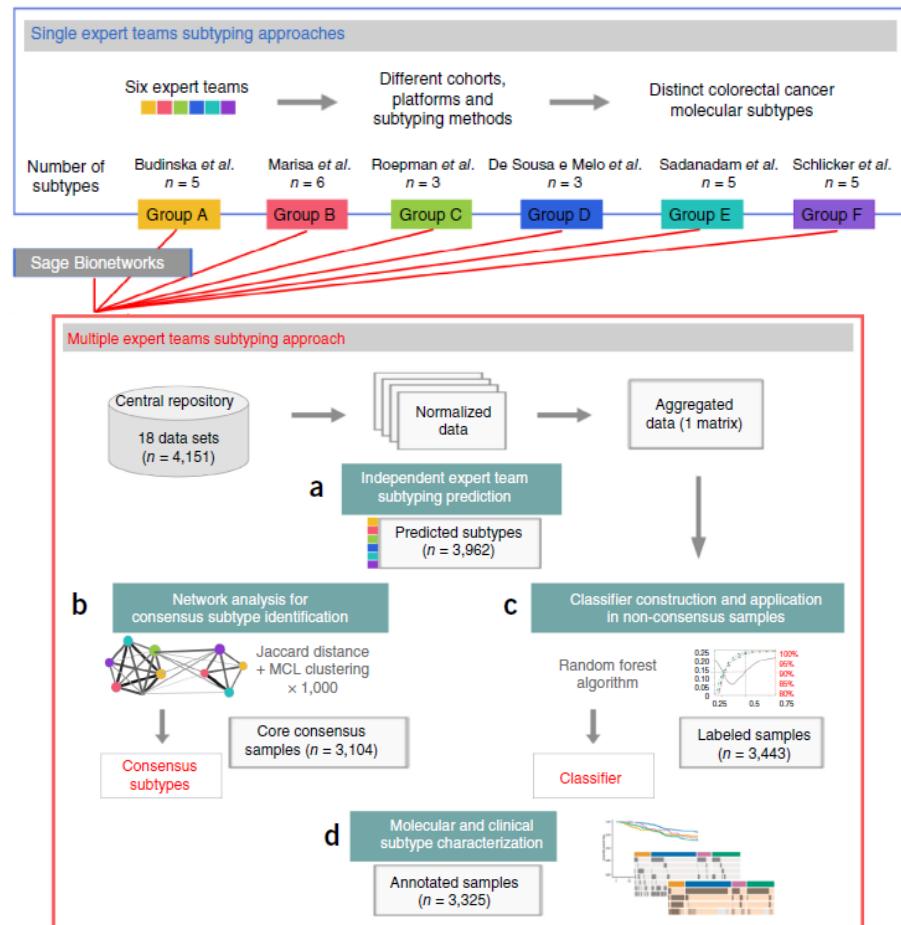
Molekulare Klassifizierung kolorektaler Karzinome

The consensus molecular subtypes of colorectal cancer

- 6 unabhängige Klassifikationssysteme



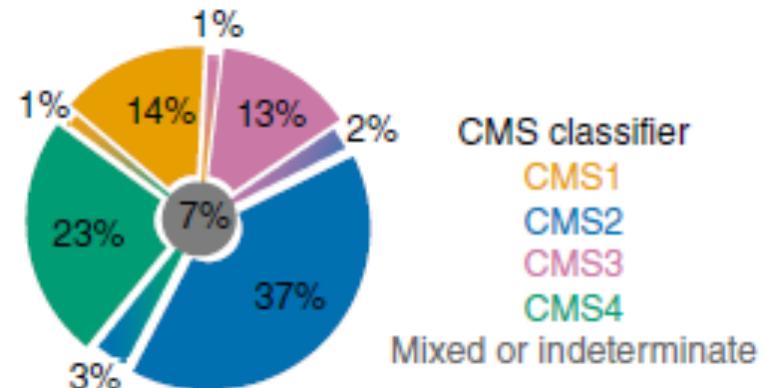
- 4 Consensus molecular subtypes (CMSs)
- Primärtumor



The consensus molecular subtypes of colorectal cancer

- **CMS1: Mikrosatellite instability, immune, 14%**

- Hypermutiert, hypermethyliert, MSI
- Starke Immunaktivierung
- Überexpression von Proteinen der DNA
Damage Repair



- **CMS2: Canonical, 37%**

- Epithelial: WNT und MYC Signalaktivierung

- **CMS3: Metabolic, 13%**

- Epithelial, metabolische Dysregulatioin

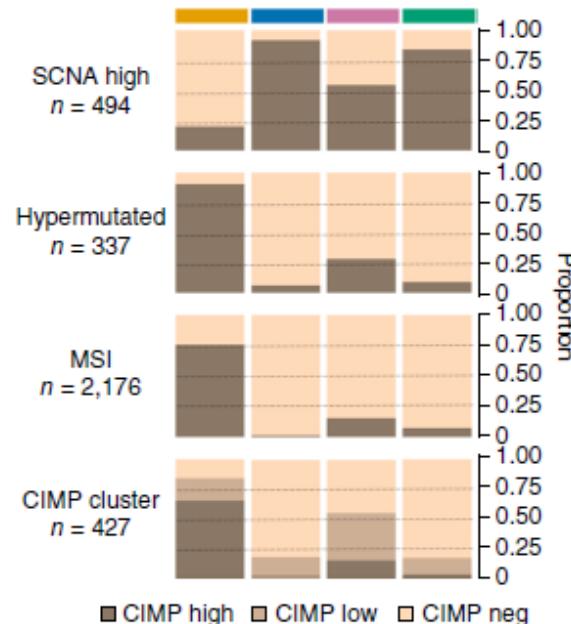
- **CMS4: Mesenchymal, 23%**

- TGFb-Aktivierung: Stromale Invasion

- Angiogenese

- **Mixed: 13%**

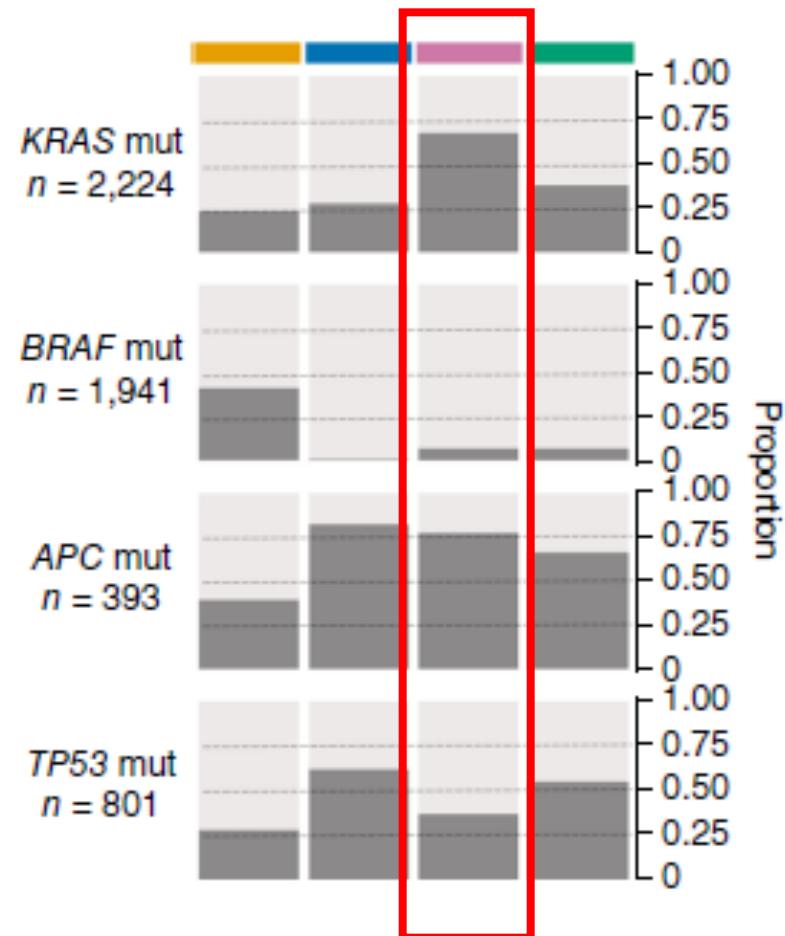
- Mischtyp oder intratumorale Heterogenität



Prognostische Relevanz der Subgruppen

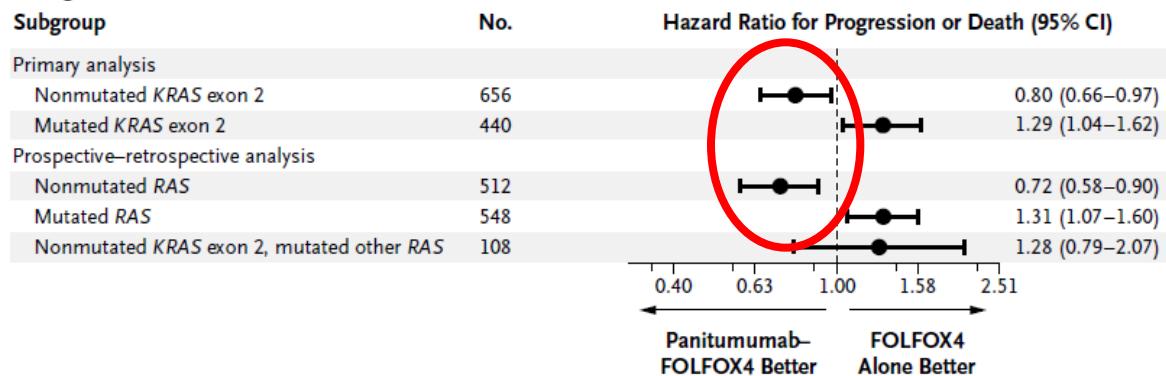
CMS1 MSI immune	CMS2 Canonical	CMS3 Metabolic	CMS4 Mesenchymal
14%	37%	13%	23%
MSI, CIMP high, hypermutation	SCNA high	Mixed MSI status, SCNA low, CIMP low	SCNA high
BRAF mutations		KRAS mutations	
Immune infiltration and activation	WNT and MYC activation	Metabolic deregulation	Stromal infiltration,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

Ras Mutationen in den Subgruppen

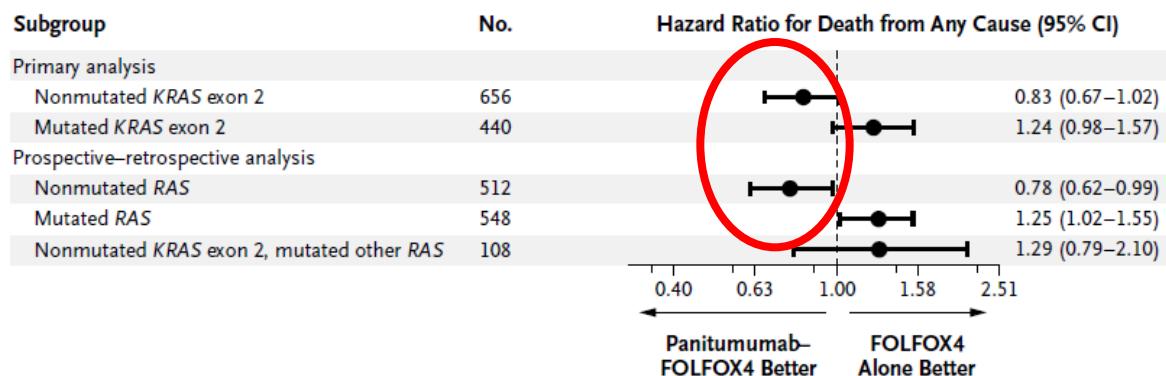


Nur Patienten mit Ras Wildtyp Status profitieren von einer anti-EGFR Therapie

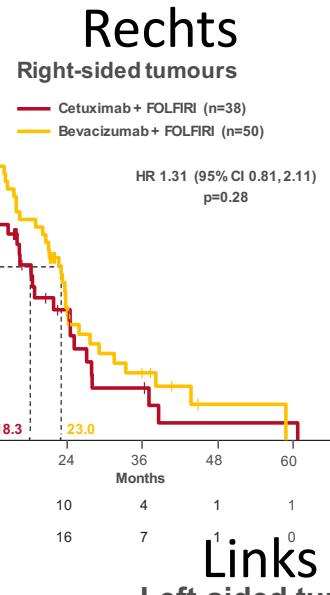
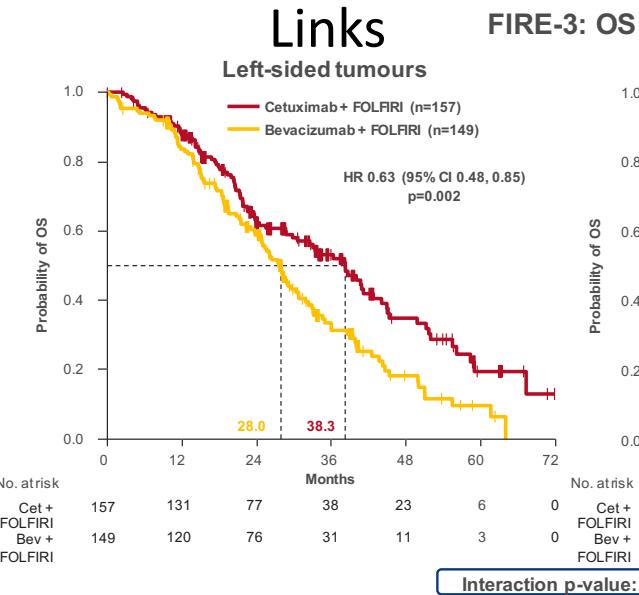
A Progression-free Survival



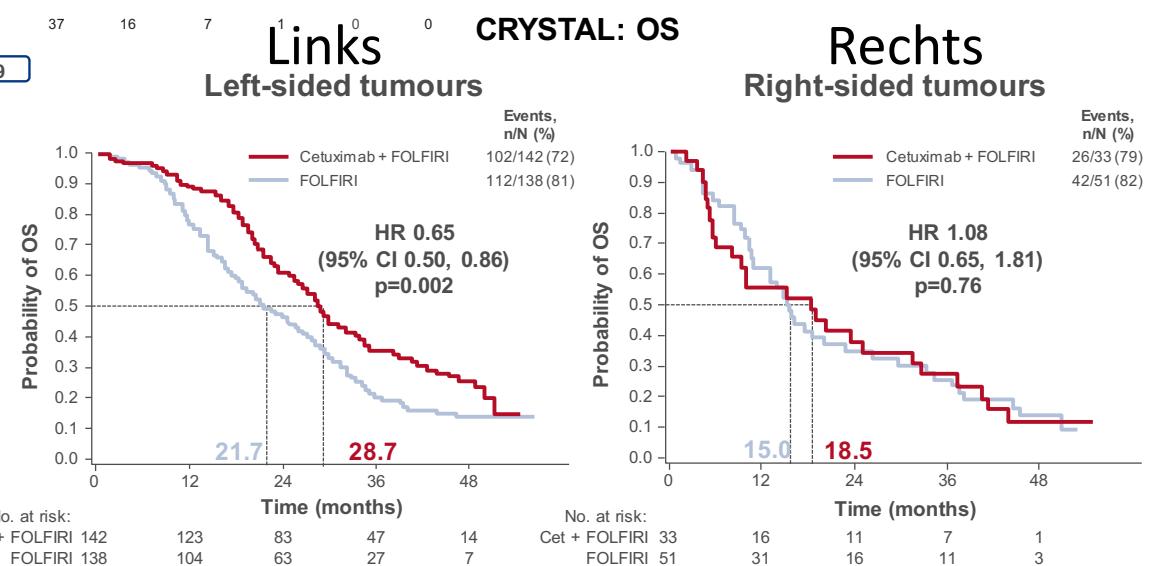
B Overall Survival



„Molekulare Anatomie“ des KRK



Alle Tumoren Ras Wildtyp!

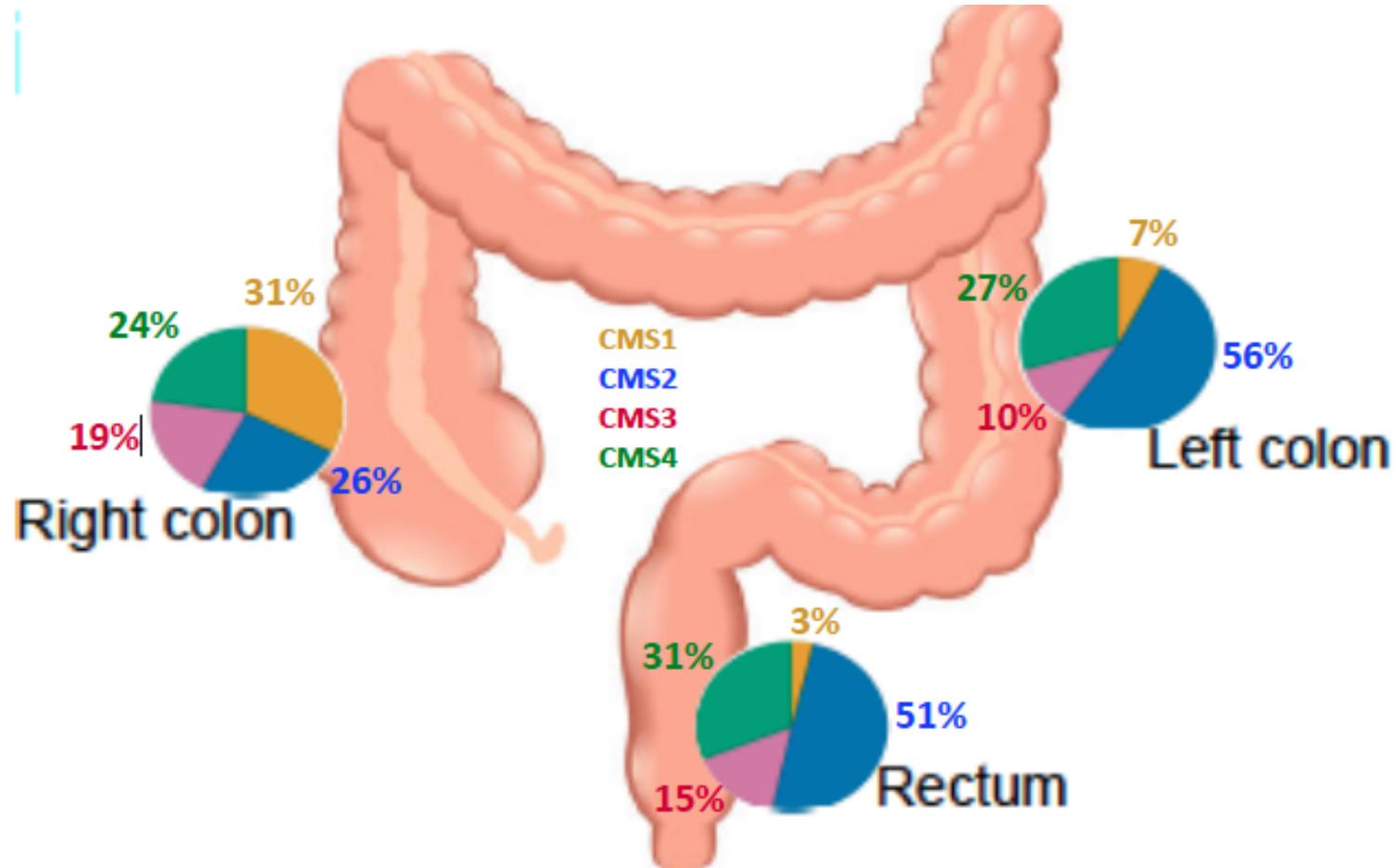


„Sideness“

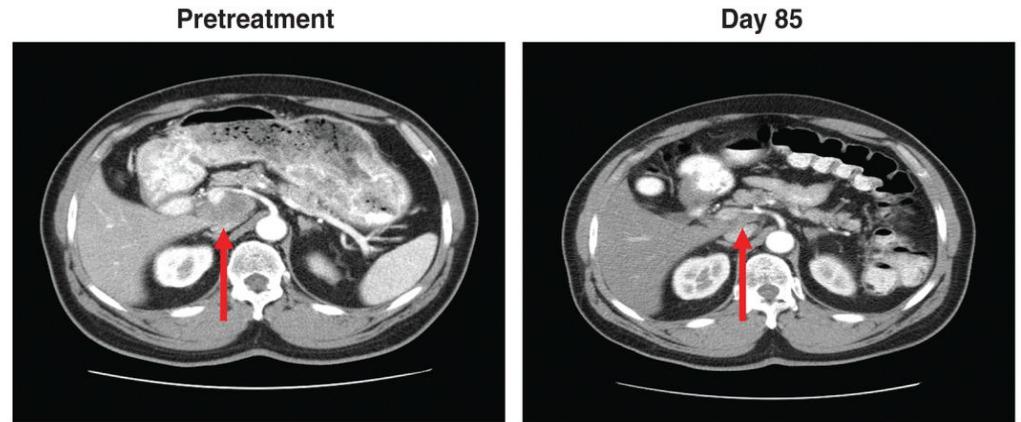
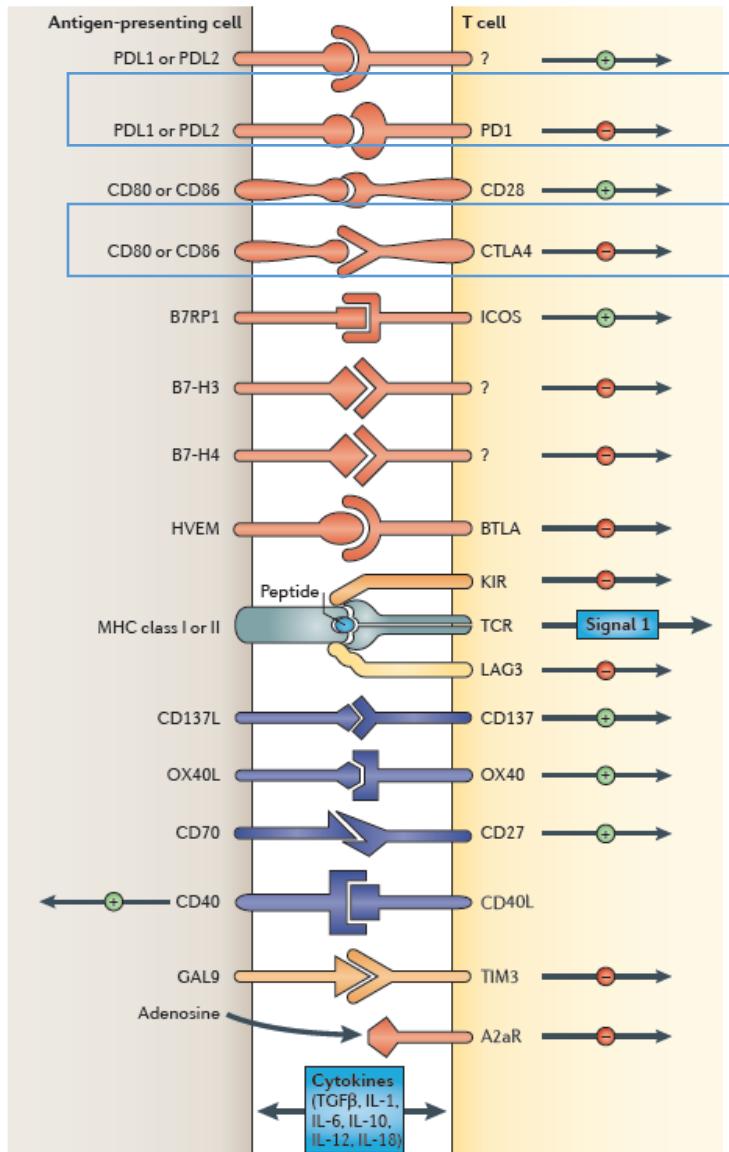
- Patienten mit linksseitigem Primärtumor und Ras Wildtyp Kombinationschemotherapie und anti-EGFR Antikörper
- Patienten mit rechtsseitigem Primärtumor und Ras Wildtyp profitieren nicht von einer anti-EGFR Therapie wie die obige Gruppe und sollten eine Kombinationschemotherapie mit anti-VEGF erhalten.



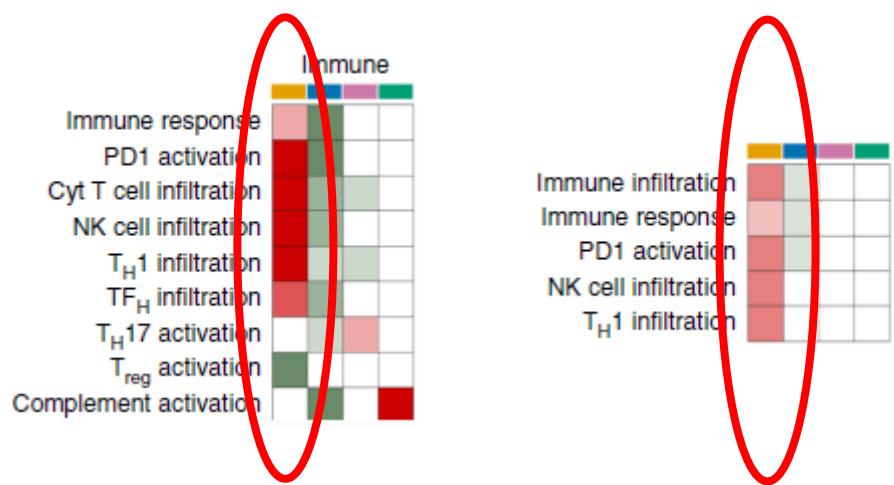
Tumorlokalisation und CMS



CMS I und Immunphänotyp



MSI CRC Patient mit anti-PD1 mAb behandelt



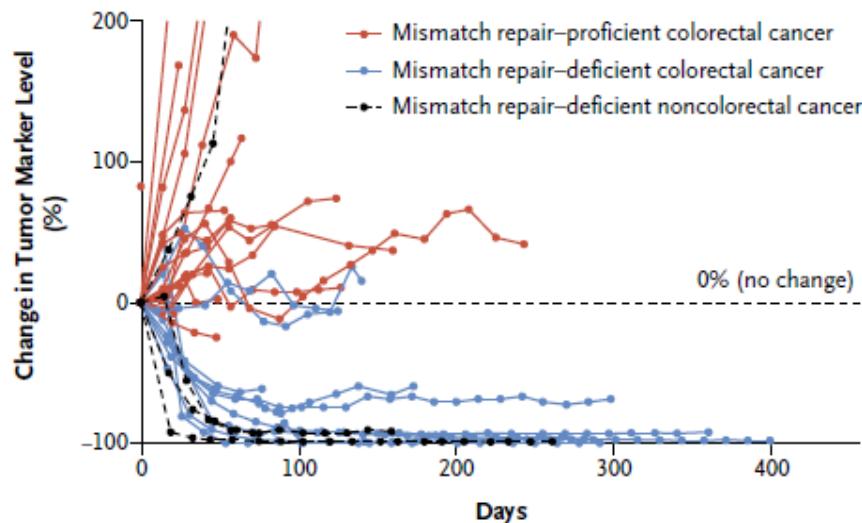
CMS1: Hypermutiert, MSI

Hypothese:

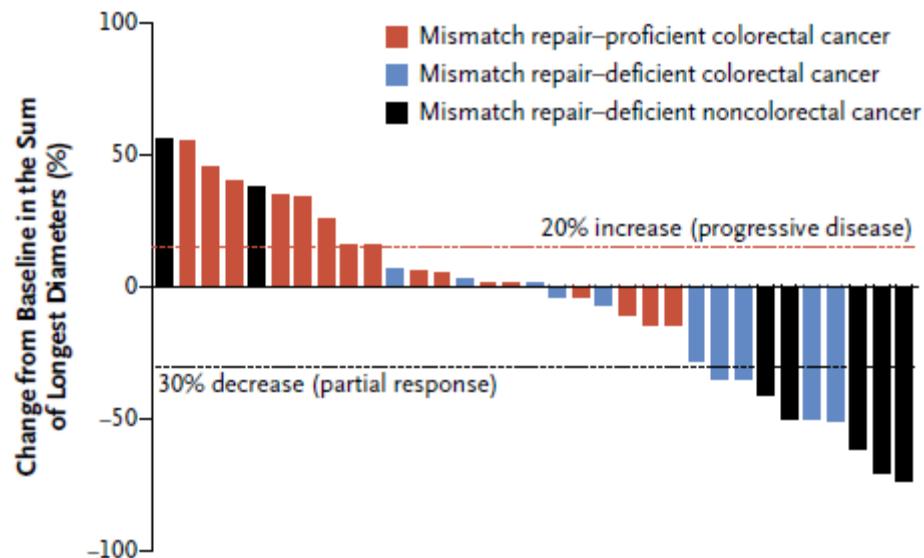
- Je „fremder“ ein Tumor für das körpereigene Immunsystem, desto höher die Effektivität einer Interferenz mit dem PD-1 Signalweg
- Konzept für hypermutierte/MSI Tumoren

PD-1 Blockade in Tumors with Mismatch-Repair Deficiency

A Biochemical Response

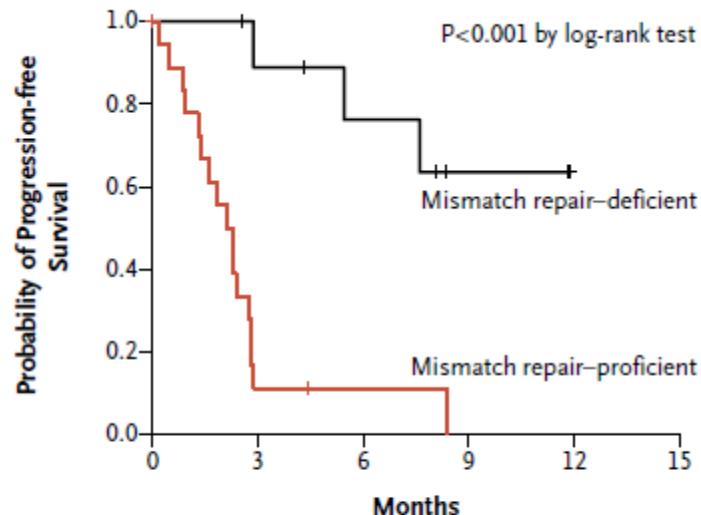


B Radiographic Response

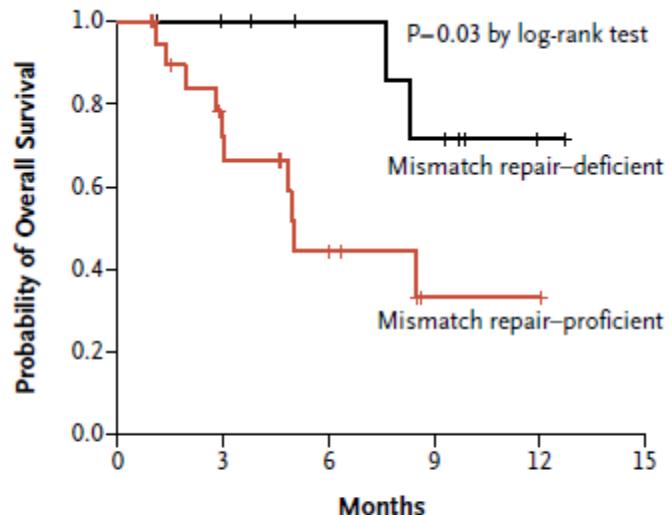


PD-1 Blockade in Tumors with Mismatch-Repair Deficiency

A Progression-free Survival in Cohorts with Colorectal Cancer



B Overall Survival in Cohorts with Colorectal Cancer



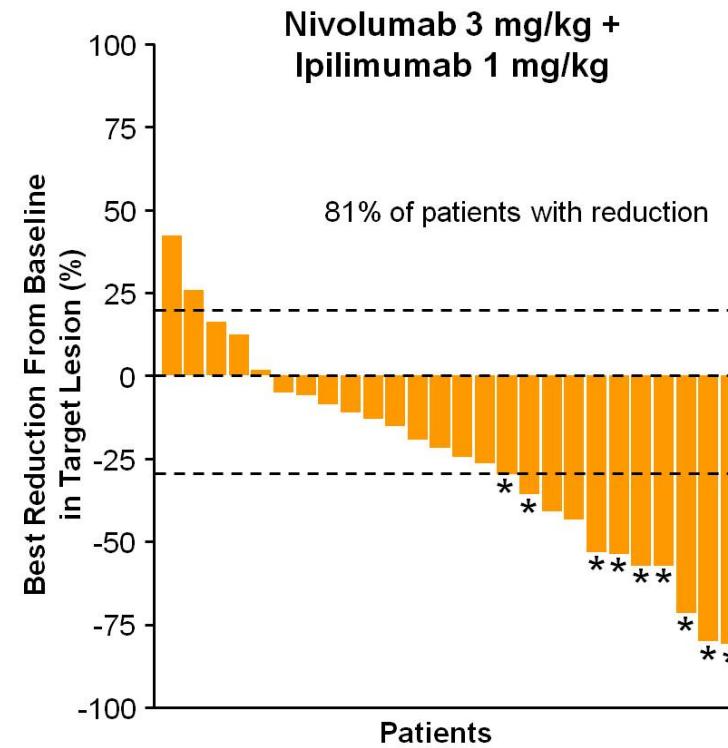
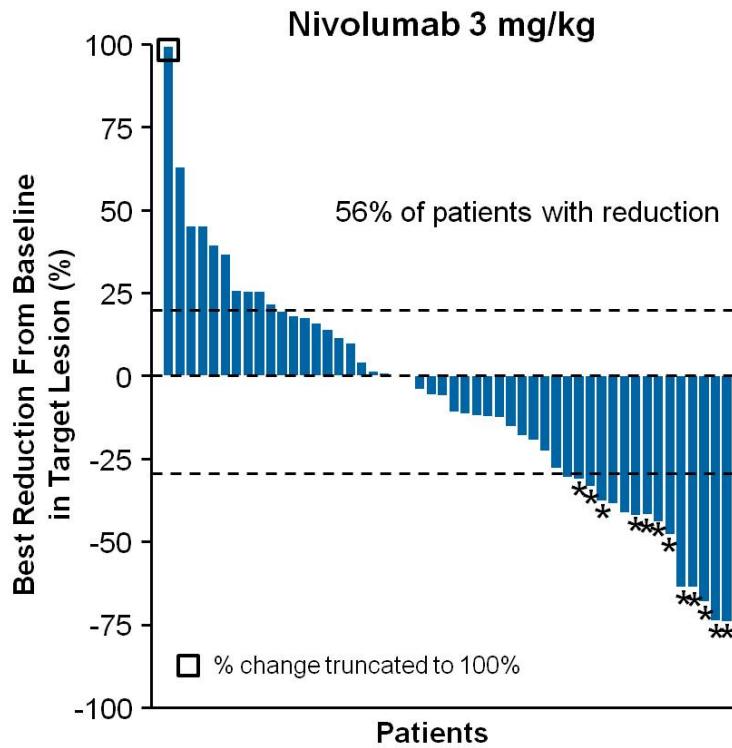
No. at Risk	
Mismatch repair-deficient	11
Mismatch repair-proficient	21

- Mehrzahl der Patienten hatte Lynch Syndrom
- Gesamtgruppe SIV: Nur geringerer Prozentsatz mit MSI-H
- Aber: Interessante Daten für die MSI-H /CMS I Subgruppe

9	7	5	1	0
12	5	1	1	0

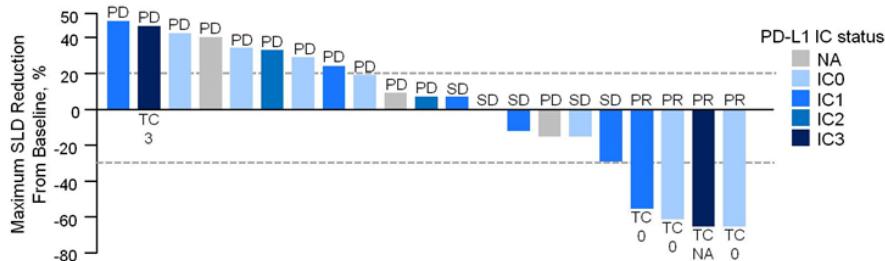
Checkpointinhibitoren bei MSI-H Tumoren

Best Reduction in Target Lesion Size in Patients With MSI-H



Checkpointinhibitoren bei MSI-H Tumoren: LBA-01: Safety and efficacy of cobimetinib (cobi) and atezolizumab (atezo) in a Phase 1b study of metastatic colorectal cancer (mCRC) – Bendell J, et al

Efficacy: Change in Tumor Burden



MEK-Inhibitor (soll TiL Zahl im Tumor erhöhen) plus PD1/PDL1 Blockade

- 4 patients had partial responses (confirmed per RECIST v1.1)
- MSI status of CRC patients was examined by NGS-based scoring: 3 of 4 responders were mismatch-repair proficient (not MSI-H); 1 responder had unknown MSI status and was nc* available
- Tumor volume reduction was not associated with PD-L1 status: TC3 (n =

PD-L1 IHC status on tumor cells (TC) and tumor-infiltrating immune cells (IC) defined as: TC3 = TC ≥ 50% PD-L1+ cells; IC3 cells; IC2 = IC ≥ 5% and < 10% PD-L1+ cells; TC1 = TC ≥ 1% and < 5% PD-L1+ cells; IC1 = IC ≥ 1% and < 5% PD-L1+ cells NA, not available; NGS, next generation sequencing. Efficacy-evaluable patients. 2 patients missing or unevaluable are not included.

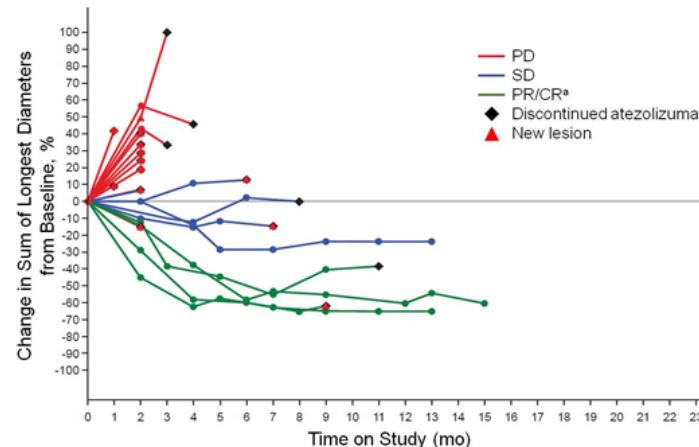
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Bendell J, et al

Eventuell Konzept für „kalte“, MSS-KRKs

Efficacy: Change in Tumor Burden Over Time



- Median duration of response was not reached (range: 5.4 to 11.1+ mo)
- Responses are ongoing in 2 of 4 responding patients

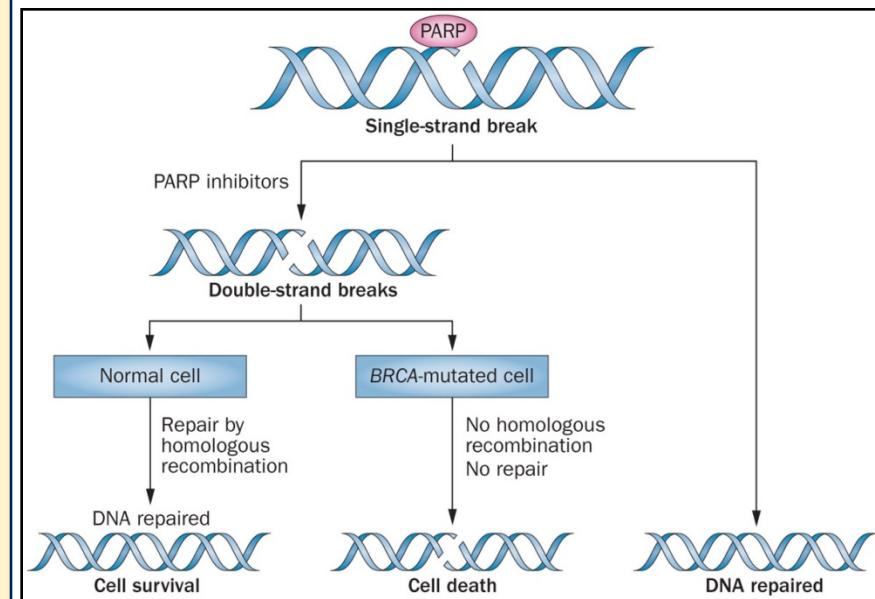
*Confirmed per RECIST v1.1. CR, complete response; PD, progressive disease; PR, partial response; SD, stable disease. Efficacy-evaluable patients. 2 patients missing or unevaluable are not included. Data cut-off February 12, 2016.

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CMS1: DNA Damage Response

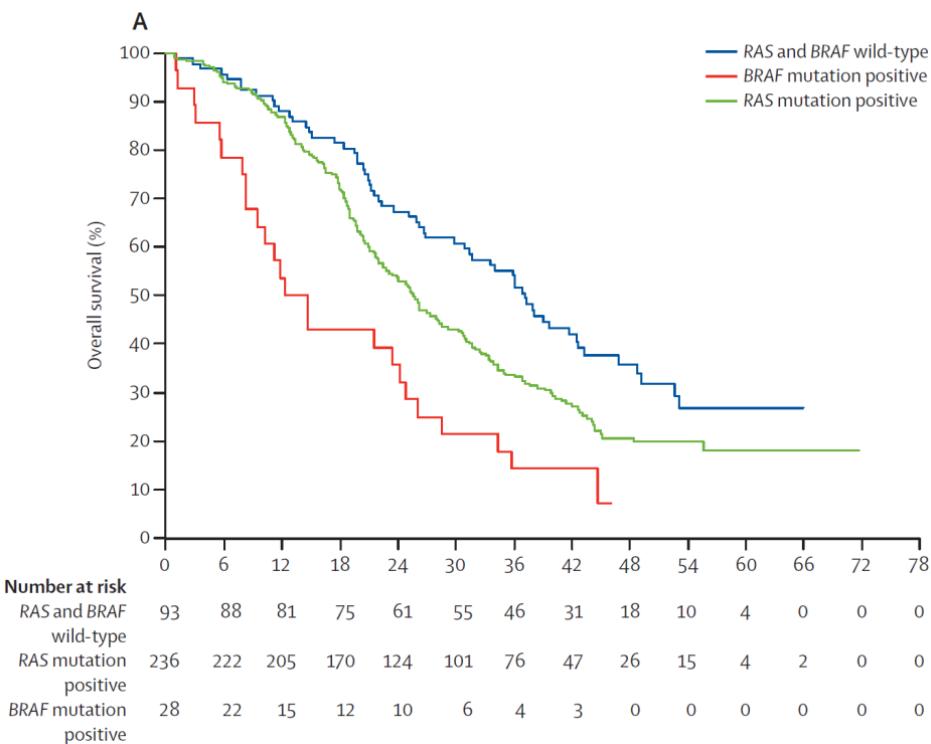
- BRCA, ATM, ATR
- BRCA mutierte Tumoren sensitiv gegen DNA-Repair-Inhibitoren und DNA-schädigende Agentien
 - Platin-basierte Therapien, PARP-Inhibitoren
- 5-fach gesteigertes Risiko für KRK bei BRCA1 Mutationsträgern jünger als 50 Jahren
- ATM inaktiviert in 37% der hypermutierten KRKs



BRCA/ATM Inhibitoren: Olaparib, Talazoparib, E7449, VX970 (ATR Kinase)

BRAF V600E Mutationen

- Nur in etwa 6% der KRKs
- Im SIV (negativ) prognostisch



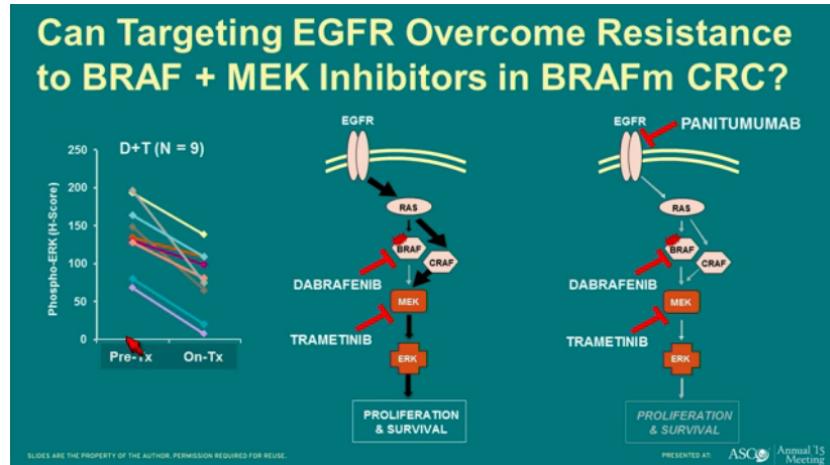
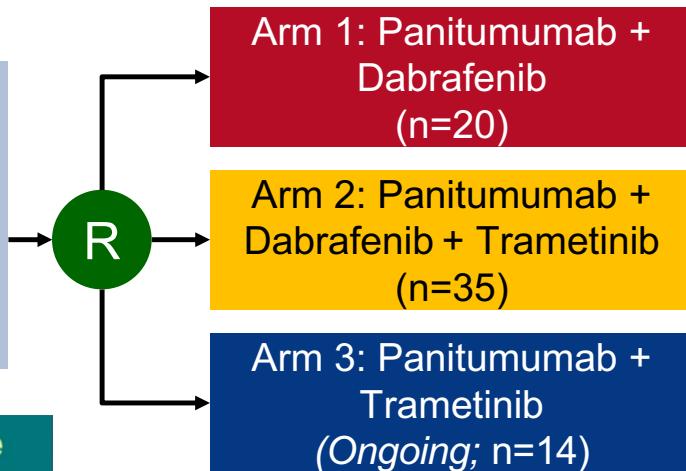
	Overall survival		
	Median (months)	Hazard ratio	p value
Intention-to-treat population			
FOLFIRI plus bevacizumab (n=256)	25.8 (22.5-29.1)	0.80 (0.65-0.98)	0.03
FOLFOXIRI plus bevacizumab (n=252)	29.8 (26.0-34.3)
Extended RAS and BRAF subgroup population			
FOLFIRI plus bevacizumab (n=176)	24.9 (21.1-29.1)	0.84 (0.66-1.07)	0.16
FOLFOXIRI plus bevacizumab (n=181)	28.6 (25.4-33.6)
RAS and BRAF wild-type subgroup			
FOLFIRI plus bevacizumab (n=45)	33.5 (22.3-39.7)	0.77 (0.46-1.27)	0.52*
FOLFOXIRI plus bevacizumab (n=48)	41.7 (30.1-53.1)
BRAF-mutation-positive subgroup			
FOLFIRI plus bevacizumab (n=12)	10.7 (3.1-24.8)	0.54 (0.24-1.20)	..
FOLFOXIRI plus bevacizumab (n=16)	19.0 (8.2-28.6)
RAS-mutation-positive subgroup			
FOLFIRI plus bevacizumab (n=119)	23.9 (20.5-27.9)	0.88 (0.65-1.18)	..
FOLFOXIRI plus bevacizumab (n=117)	27.3 (22.0-31.3)
RAS wild-type subgroup			
FOLFIRI plus bevacizumab (n=57)	26.8 (20.5-35.9)	0.78 (0.51-1.20)	0.66†
FOLFOXIRI plus bevacizumab (n=64)	37.1 (24.1-42.7)

Therapie bei BRAF Mutation

Braf-Inhibition alleine wegen redundanten Signaltransduktion nicht effektiv -> Doppel-/Triple Targeting

Einschlußkriterien

- $BRAF^{V600E}$ Mutation mCRC
- ECOG PS 0–1
- Meßbare Erkrankung (RECIST) (n=69)



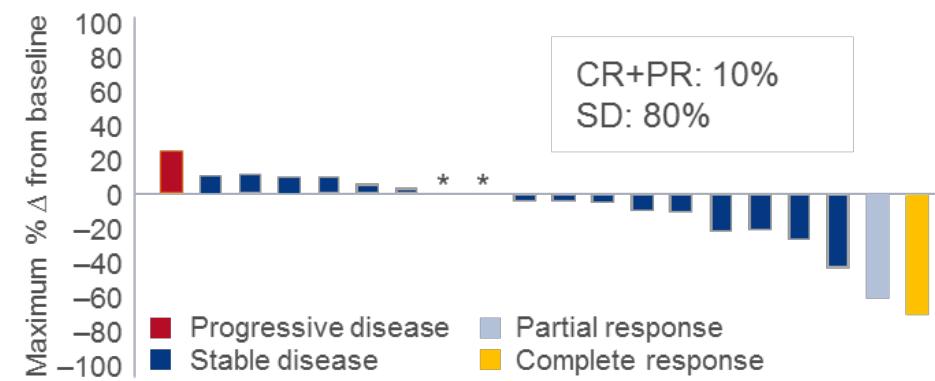
Primäre Endpunkte: Safety, Ansprechraten, PFS

Corcoran et al. J Clin Oncol 2015 (abstr.)

Therapie bei BRAF Mutation:

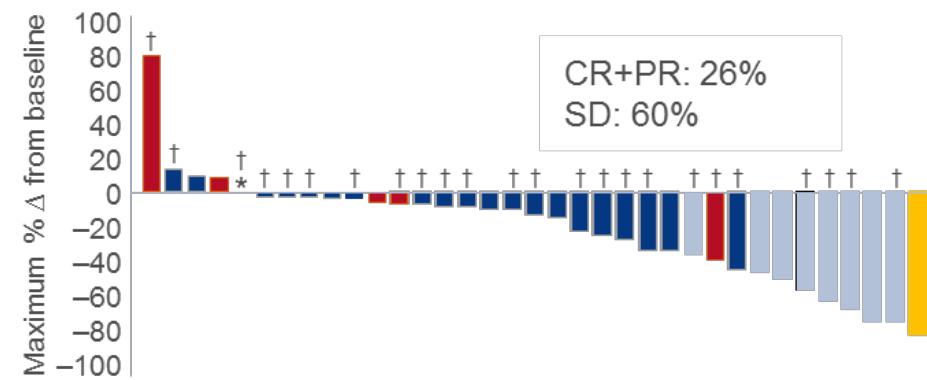
Zweifachtherapie

Best response (Arm 1)



Dreifachtherapie

Best response (Arm 2)

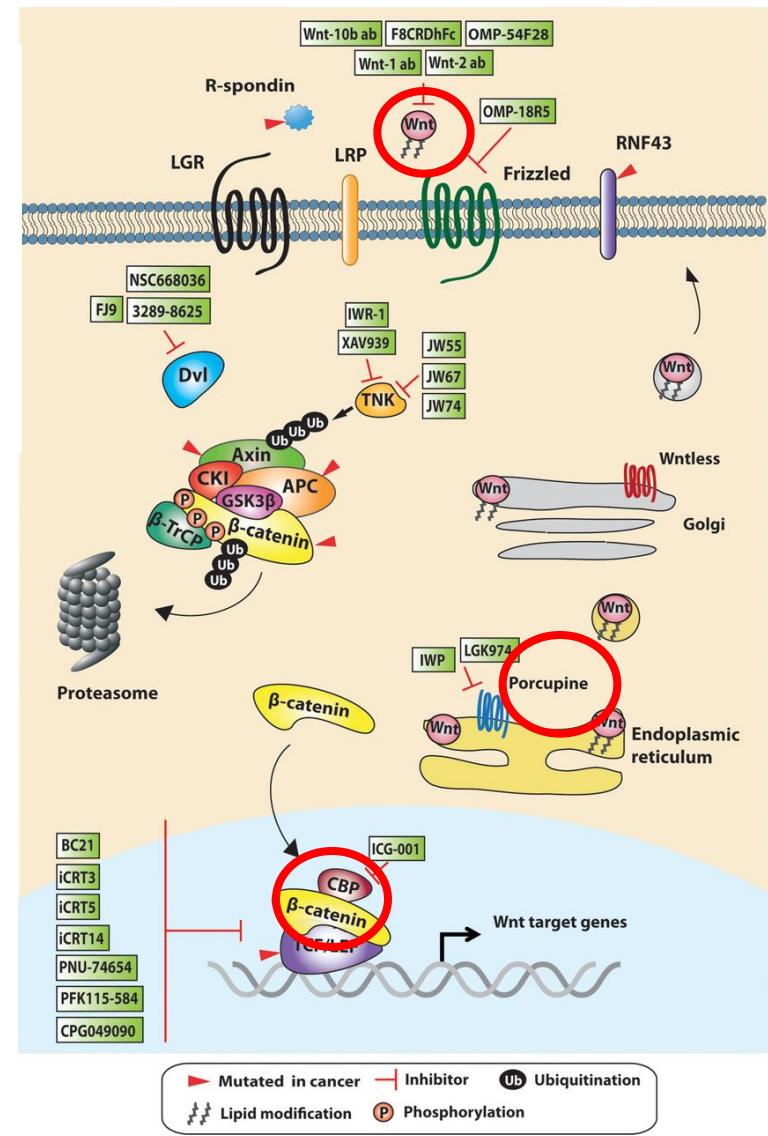
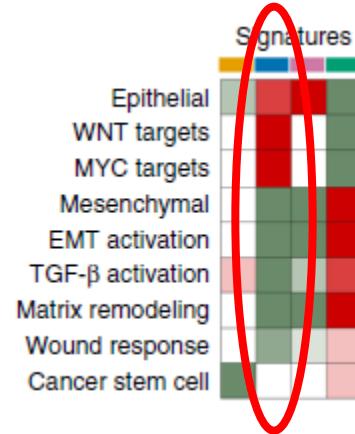


Corcoran et al. J Clin Oncol 2015 (abstr.)

CMS2

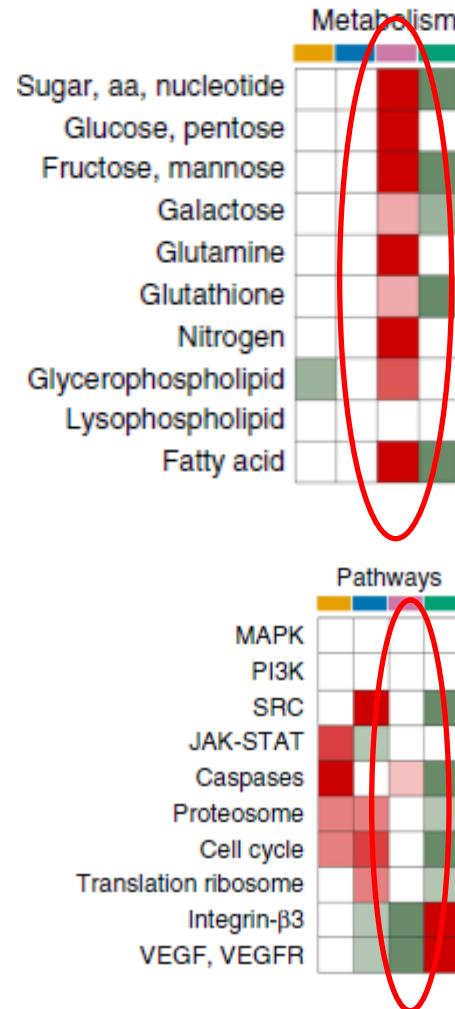
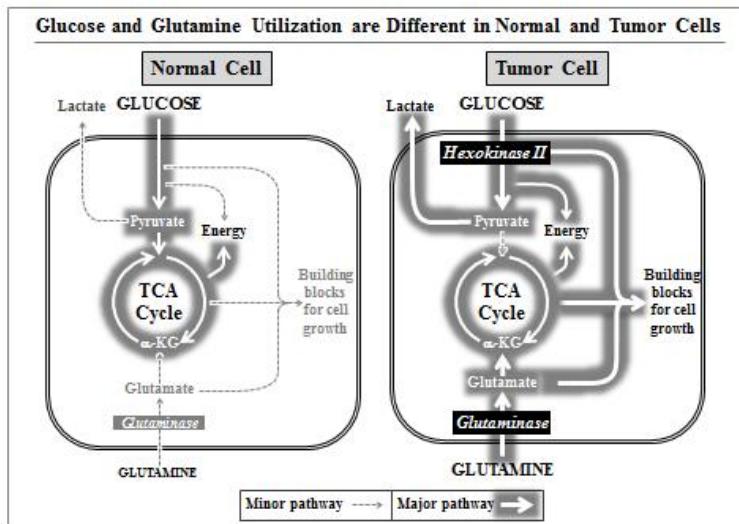
- CMS2

- WNT und MYC Signalaktivierung
- MYC schwer zu targeten, da essentiell
- WNT Inhibitoren in Phase I Studien
 - CGX1321
 - Small molecule
 - PRI-724
 - CBP/b-catenin Antagonist
 - ETC-1922159
 - Porcupine inhibitor



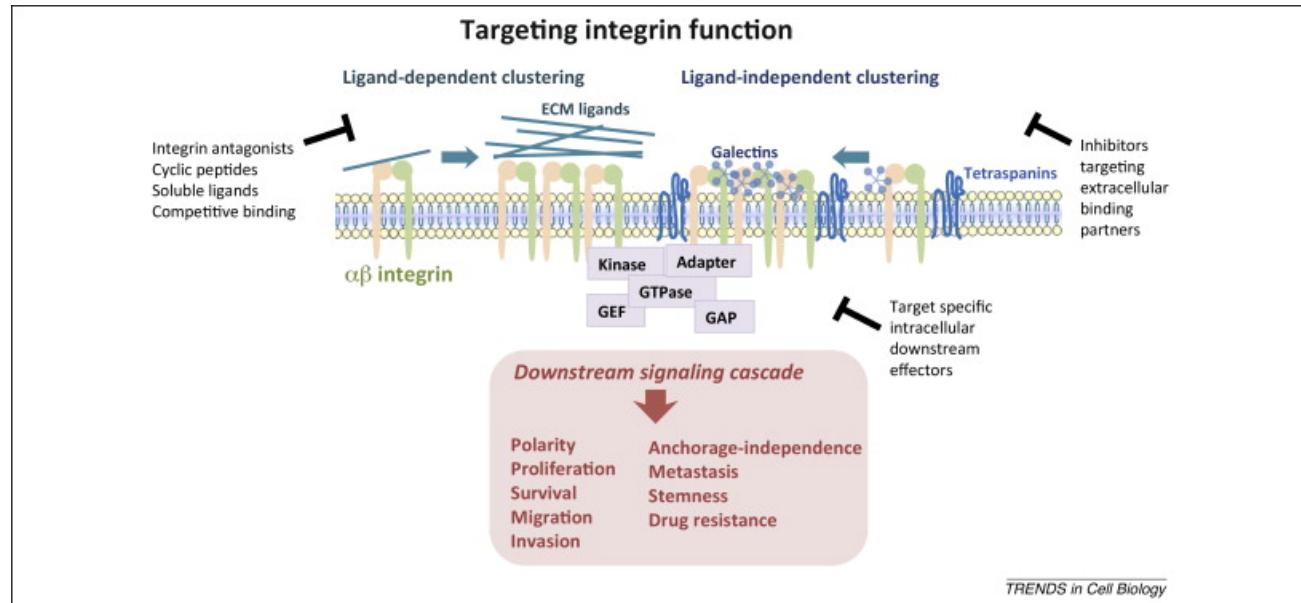
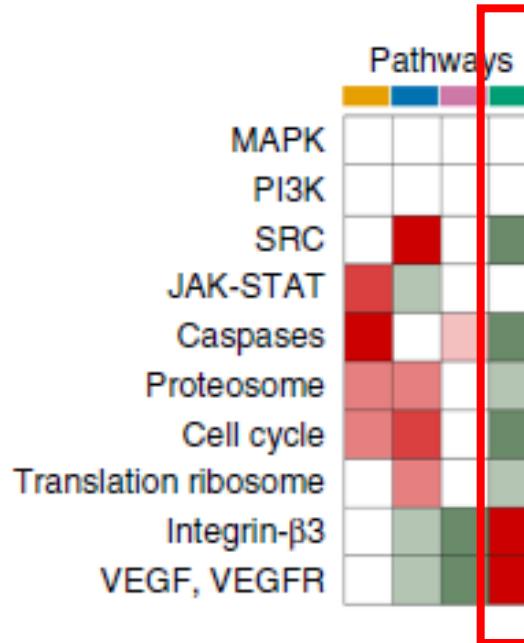
CMS 3 - metabolic

- Targeting des Tumormetabolismus
 - Pyruvatdehydrogenasekinase-inhibitoren
 - Glutaminaseinhibitoren
 - CB-839

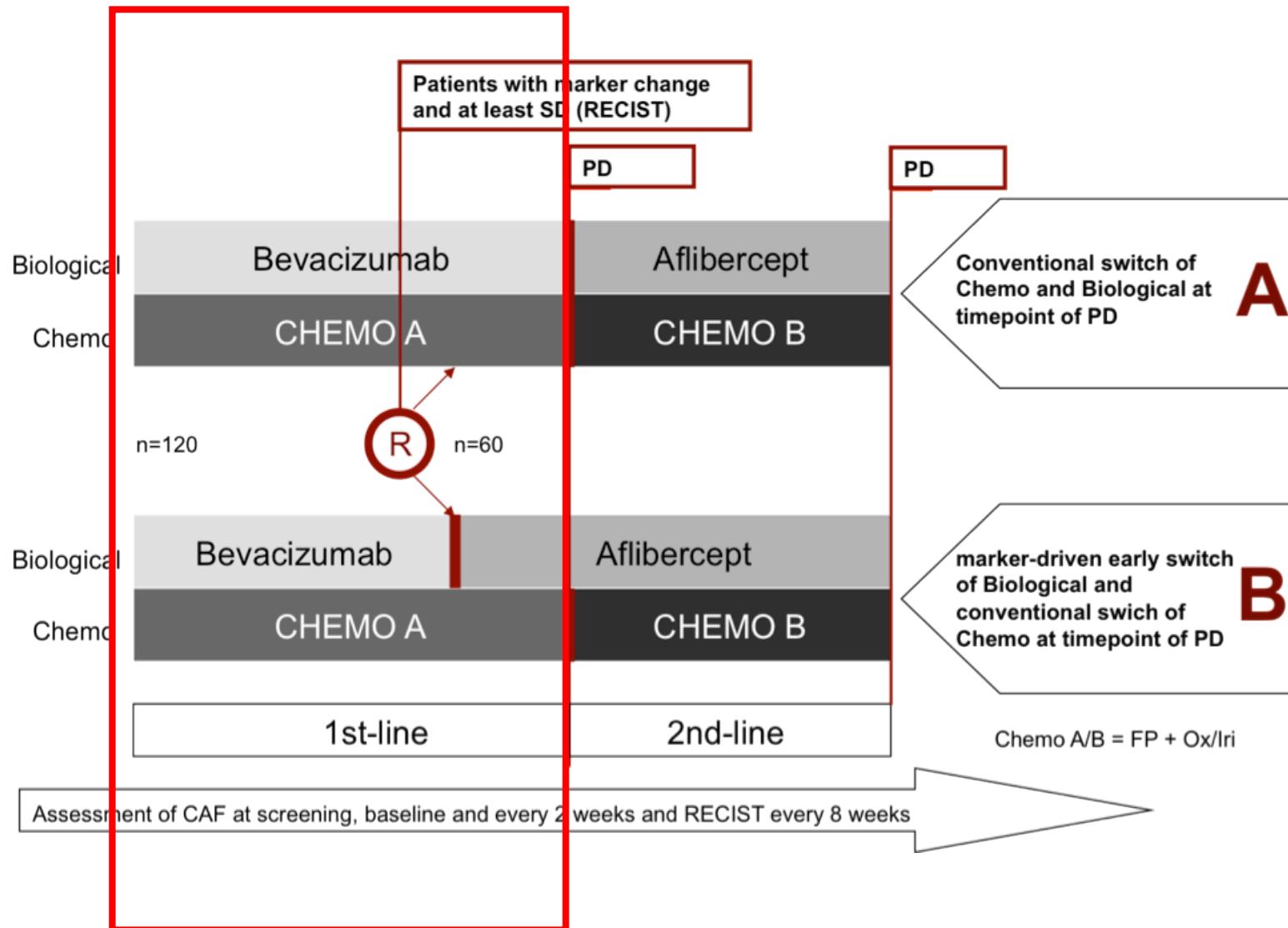


CMS4

- TGF β -Aktivierung
- Stromale Invasion
 - MEDI 522/Etaracizumab
 - mAb gegen avb3 Integrin
- Angiogenese
 - Bevacizumab
 - Aflibercept
 - Ramucirumab

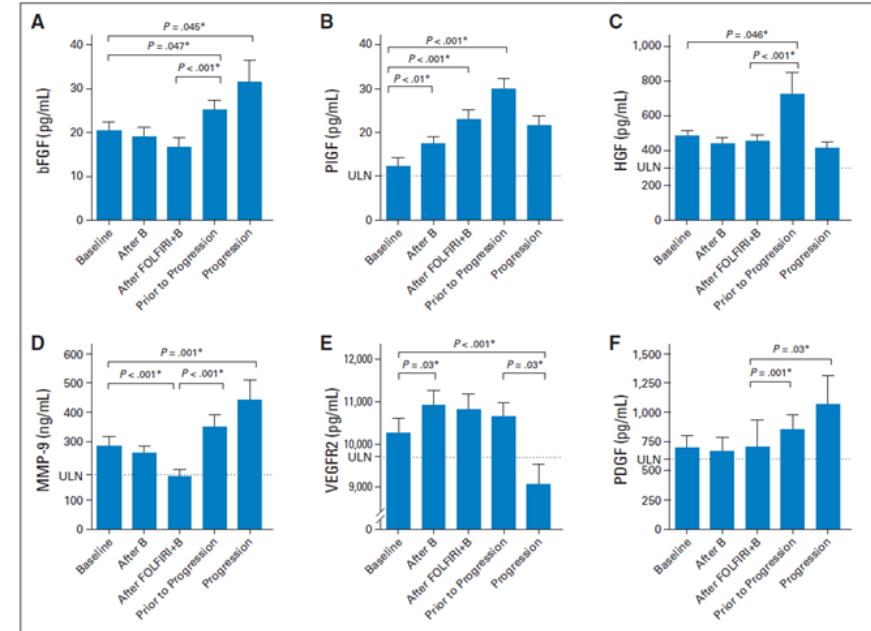


PERMAD Trial



PERMAD data evaluation

- no use of absolute values/ cut offs
- definition of a ***composite marker***, that integrates the course and kinetics of various cytokines by bioinformatics
- predictive value of such a marker for resistance to bevacizumab and switch to afibbercept?



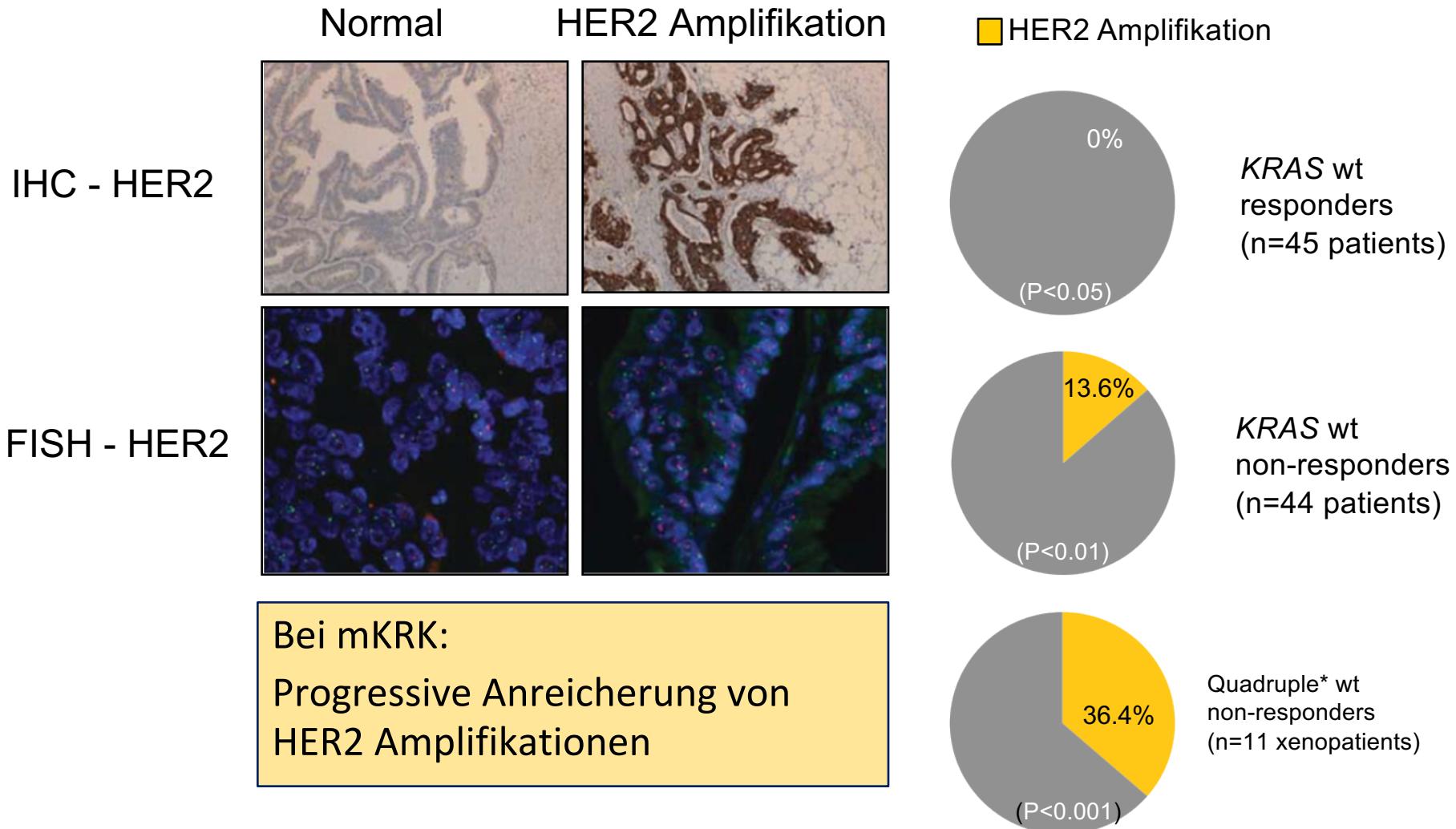
PERMAD: What is done?

- PIGF
- Ang 2
- VEGF
- G-CSF
- sVEGFR2
- HGF
- bFGF
- MMP-9

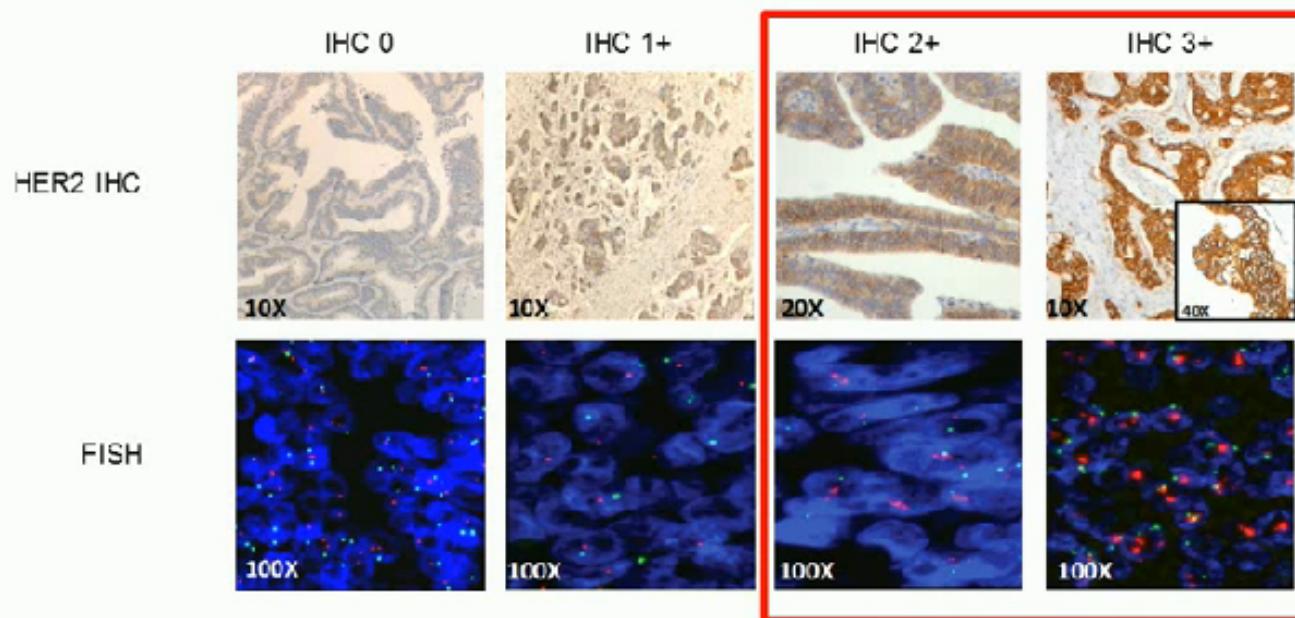


- screening (d -28 until -7),
- baseline (d1 prior to Tx)
- every 2 weeks (first phase)
- every 4 weeks in the randomized part

Tumorevolution: HER2 Amplifikation beim KRK unter Therapie



Heracles Studie



Valtorta E. et al, Modern Pathol 2015, in press

Positive tumor cells $\geq 50\%$



Eligible for HERACLES Trial

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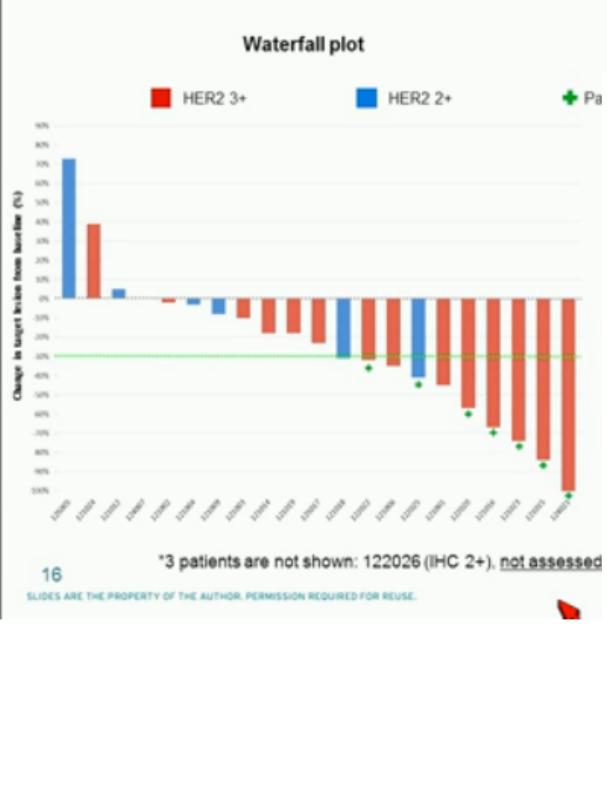
ASCO[®] Annual '15 Meeting

- Kras WT
- Vorbehandlung mit 5-FU, Iri, Ox, Cetuximab oder Panitumumab obligatorisch
- ECOG 0-1
- Primärer Endpunkt: ORR
- Therapie mit Trastuzumab plus Lapatinib

In der Studie:
5.4% der Ausgangspopulation

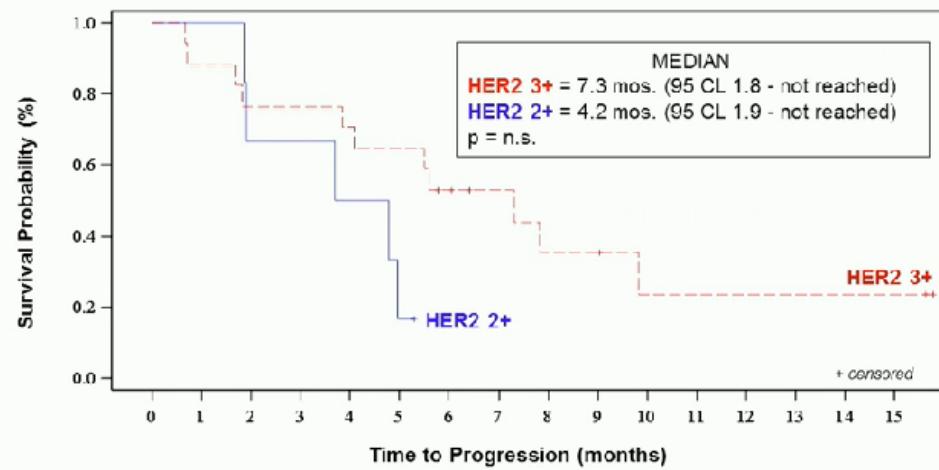
HERACLES-Studie

Responses by HER2 IHC Score



Spaghetti plot

Time to Progression by HER2 score



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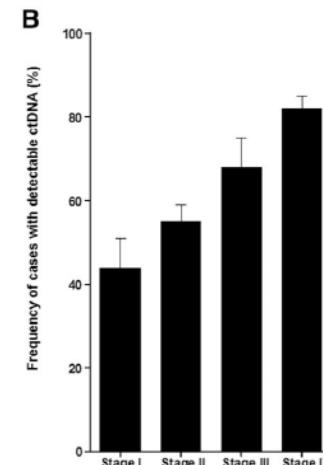
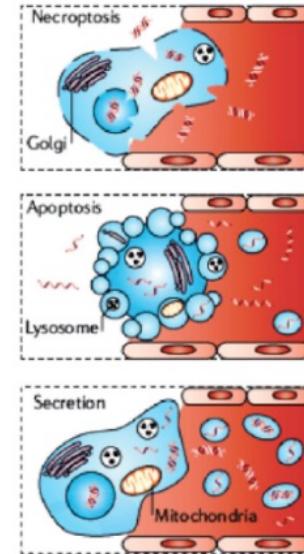
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ASCO | Annual 15 Meeting

Therapie gut toleriert (Haut-/GI-Toxizität)

Wie monitoren wir eine Tumorerkrankung? Wie finden wir neu aufgetretene Mutationen?

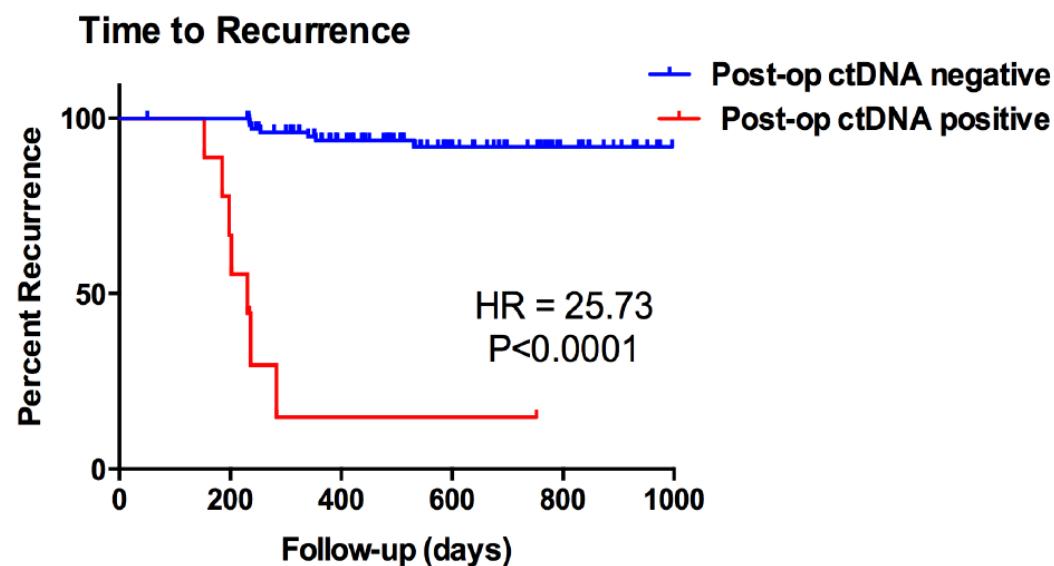
- Zirkulierende DNA
 - cfDNA, ctDNA
 - Freigesetzt durch Zellturnover oder via Exosomen
 - Kleine Fragmente (180-200 bp) im Plasma
- Fortgeschrittene Tumore: ctDNA in >75% detektierbar
 - 73% CRC



Detektion von MRD – KRK Stadium II/III

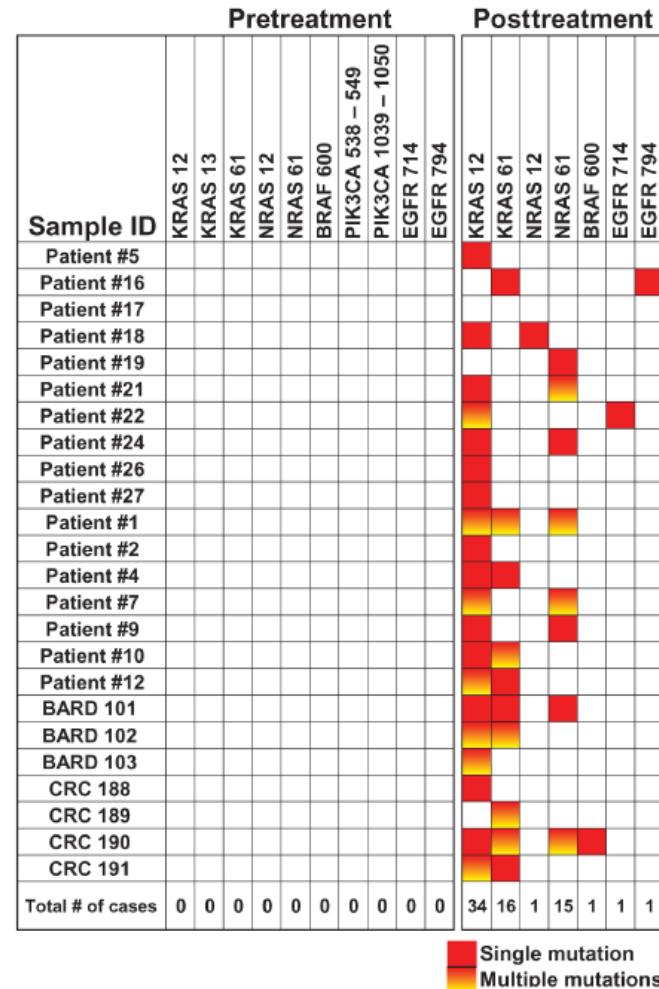
	Recurrence	No recurrence	Total
Post-op ctDNA - positive	7	2	9
Post-op ctDNA - negative	7	96	103
Total	14	98	112

Fisher's Exact P < 0.0001
RR = 11.44
(95% CI 5.16 – 25.37)

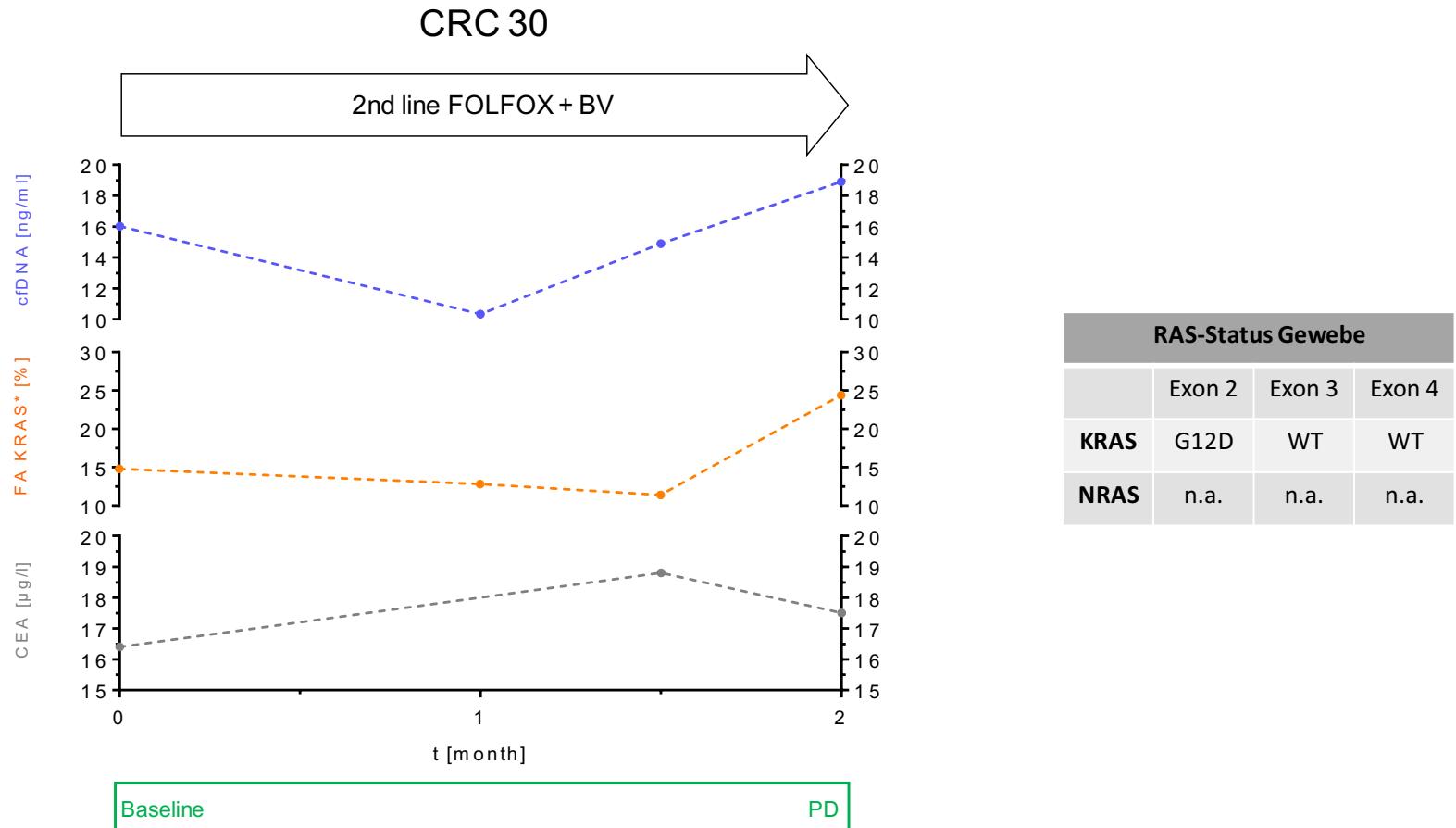


Monitoring von Tumorevolution unter einer anti-EGFR Therapie

- Tumortherapie triggert die Evolution multipler Subklone im Tumor
- Beispiel: CRC: Kras Codon 12 Mutationen analysiert mittels ctDNA
 - Sensitivität: 87.2%
 - Spezifität: 99.2%
 - Therapie-assoziierte Resistenz:
 - 96% eine oder mehrere Mutationen mim MEK-ERK Signalweg
 - 50% in Kras
 - Häufige Mutationen in Codon 61 von Kras



Monitoring von Therapieansprechen



* KRAS: G12A, G12C, G12D, G12R, G12S, G12V, G13D

Endlich Relevanz für molekulare Marker beim KRK?!

Ja, definitiv

	Ras-Status*	B-RAF V600E	HER2	MSI	(BRCA/ATM)
Erstdiagnose SIV	X	X		X	
SIV fortgeschrittene Erkrankung			X		X

*K-RAS exons 2, 3 und 4 (Codons 12, 13, 59, 61, 117 und 146) und n-RAS Exone 2, 3 und 4 (Codons 12, 13, 59, 61 und 117).

Endlich Relevanz für molekulare Marker beim KRK?!

- Molekulare Klassifizierung: Chance zur Anreicherung von Subgruppen zur Stratifizierung für klinische Studien, aber:
 - Nur für Primärtumor etabliert
 - Signaturen für Metastasen verwendbar?
- Therapeutische Konsequenzen wirklich klar?
 - CMS1: Immuntherapie
 - CMS2: WNT Inhibitoren
 - CMS3: Targeting metabolischer Pathways
 - CMS4: TGFb Inhibitoren
- Tumorevolution innovativ monitoren (ctDNA)
- Mögliche Konsequenzen:
 - Bessere Definition von Subgruppen
 - Effektivere Therapie über das „continuum of care“
 - schnellere Wirkstoffforschung



Vielen Dank für ihre Aufmerksamkeit!