



PRECIZNÍ ONKOLOGIE U CRC

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MOLEKULÁRNÍ TESTOVÁNÍ

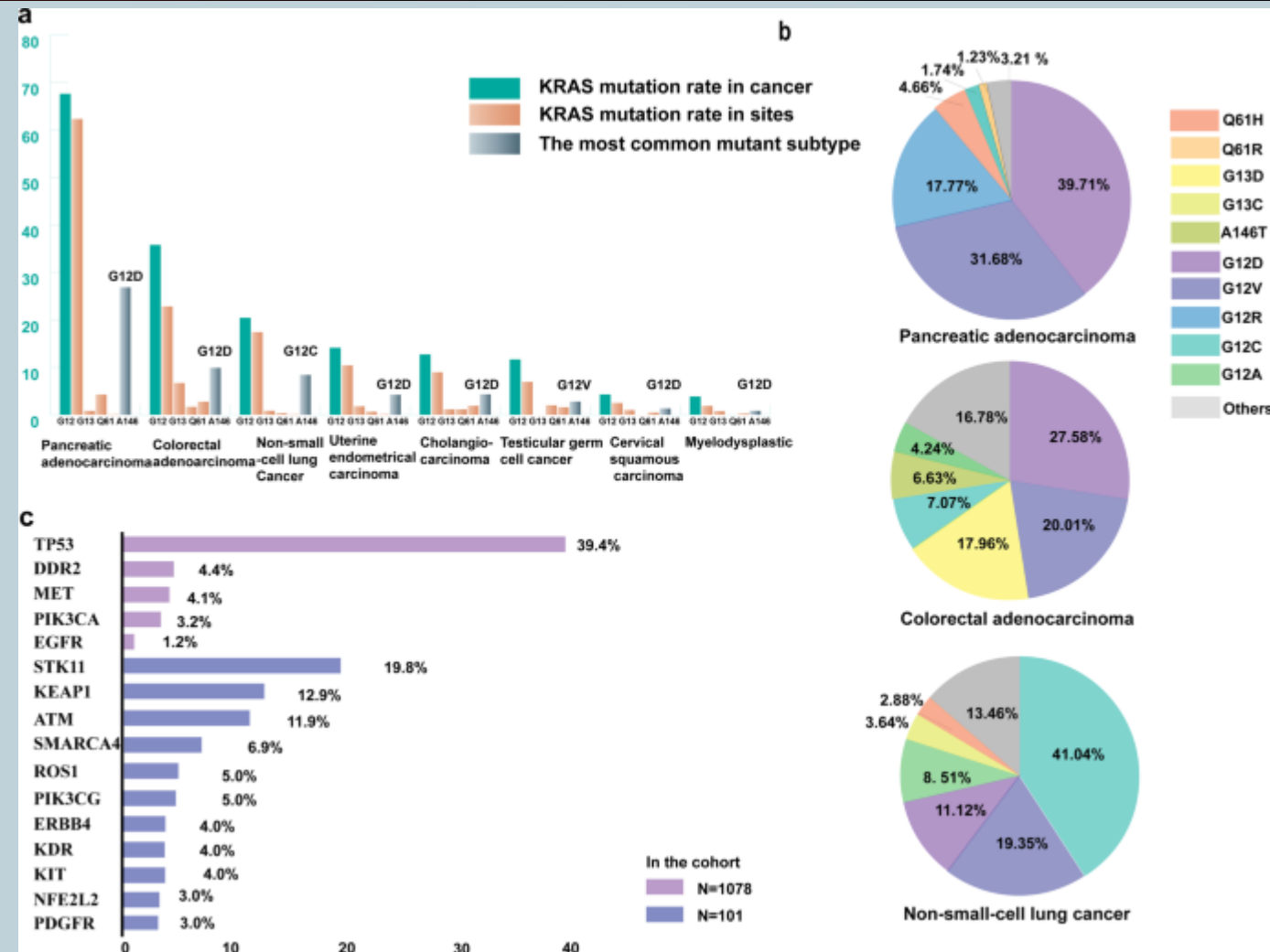
- Jak (co) testovat?
 - IHC (HER, BRAF)
 - qPCR, NGS DNA + RNA; jaký panel?
 - metylace
- Koho testovat?
 - arbitrárně všechny pacienty
 - mladé pacienty
 - vzácné diagnózy
- Kdy testovat?
 - před zahájením léčby
 - při progresi
 - při vyčerpaných možnostech

CRC STANDARD

- KRAS
- NRAS
- BRAF
- MMR
- MSI
- DPYD (UGT)

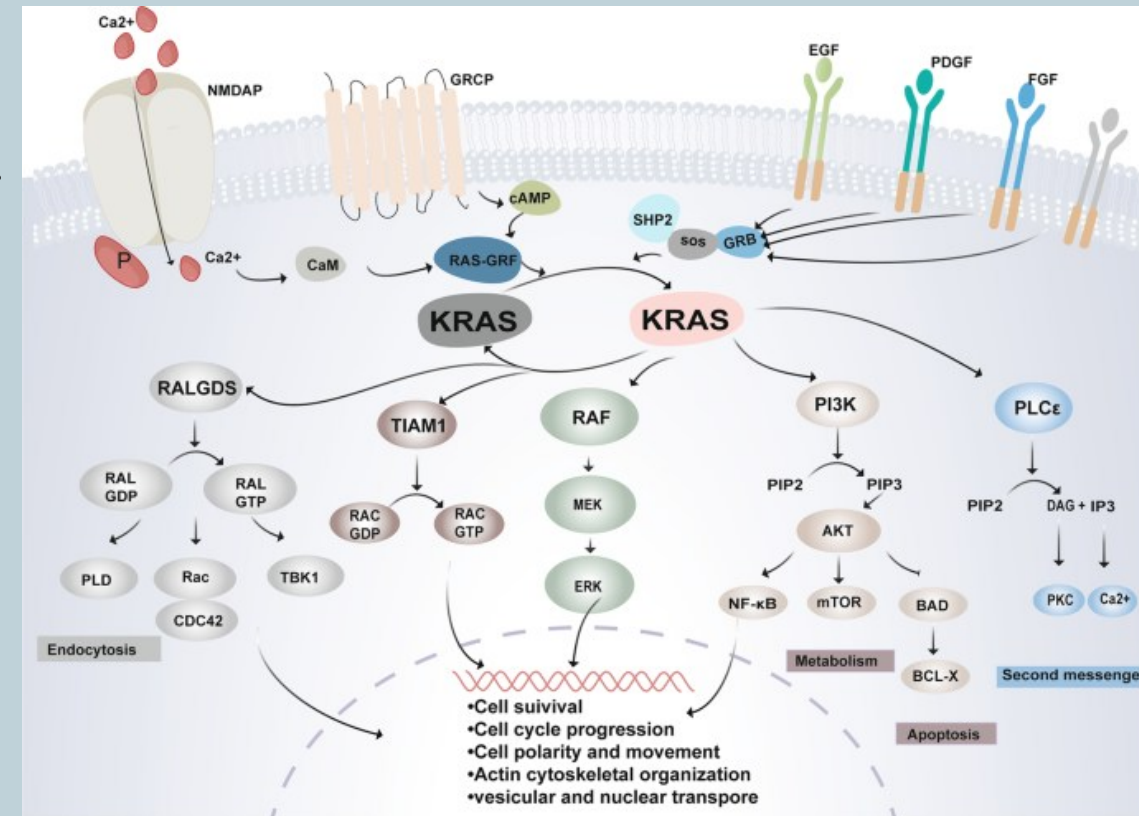
KRAS

- 45 % CRC
- První známý onkogen (1982)
- Rodina RAS (HRAS, NRAS)
- Různé biologické chování dle mutace



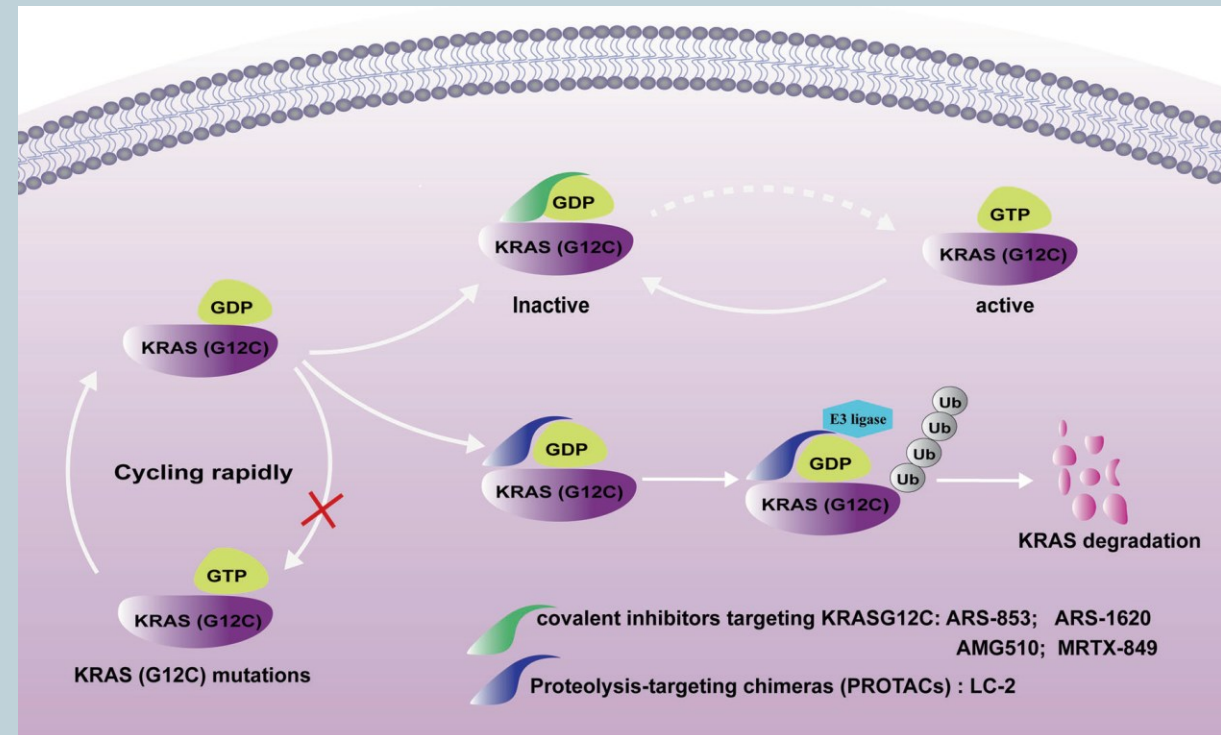
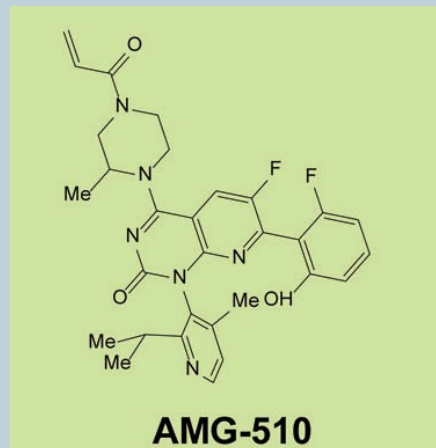
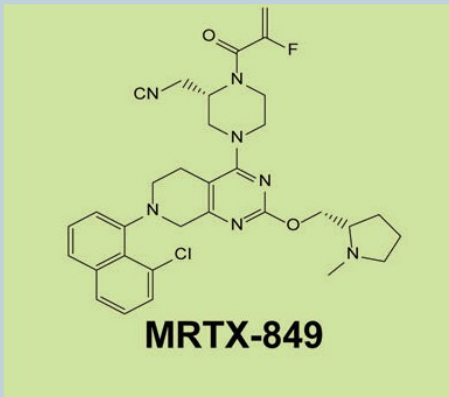
KRAS

- G-protein s vazbou na buněčnou membránu (farnesylace)
- Přenos signálu uvnitř buňky signálními cestami:
 - MAPK - proliferace
 - PI3K - přežívání
 - Alternativní aktivace (fúzní proteiny)
- Princip vypnuto/zapnuto - GDP/GTP



KRAS G12C

- 3-5 % CRC
- Cílení na disulfidický můstek Cys12 (blízko vazebnému místu pro GTP)
 - selektivita
 - větší aktivita (switch I, II region)
 - porušení interakce s efektorovými proteiny
 - degradace



INHIBICE:

sotorasib + panitumumab (CodeBreakK 300)

mPFS (95% CI)

soto 960 + pani 5.8 M (4.2–7.5)

soto 240 + pani 4.0 M (3.7–5.9)

SOC 2.0 M (1.9–3.9),

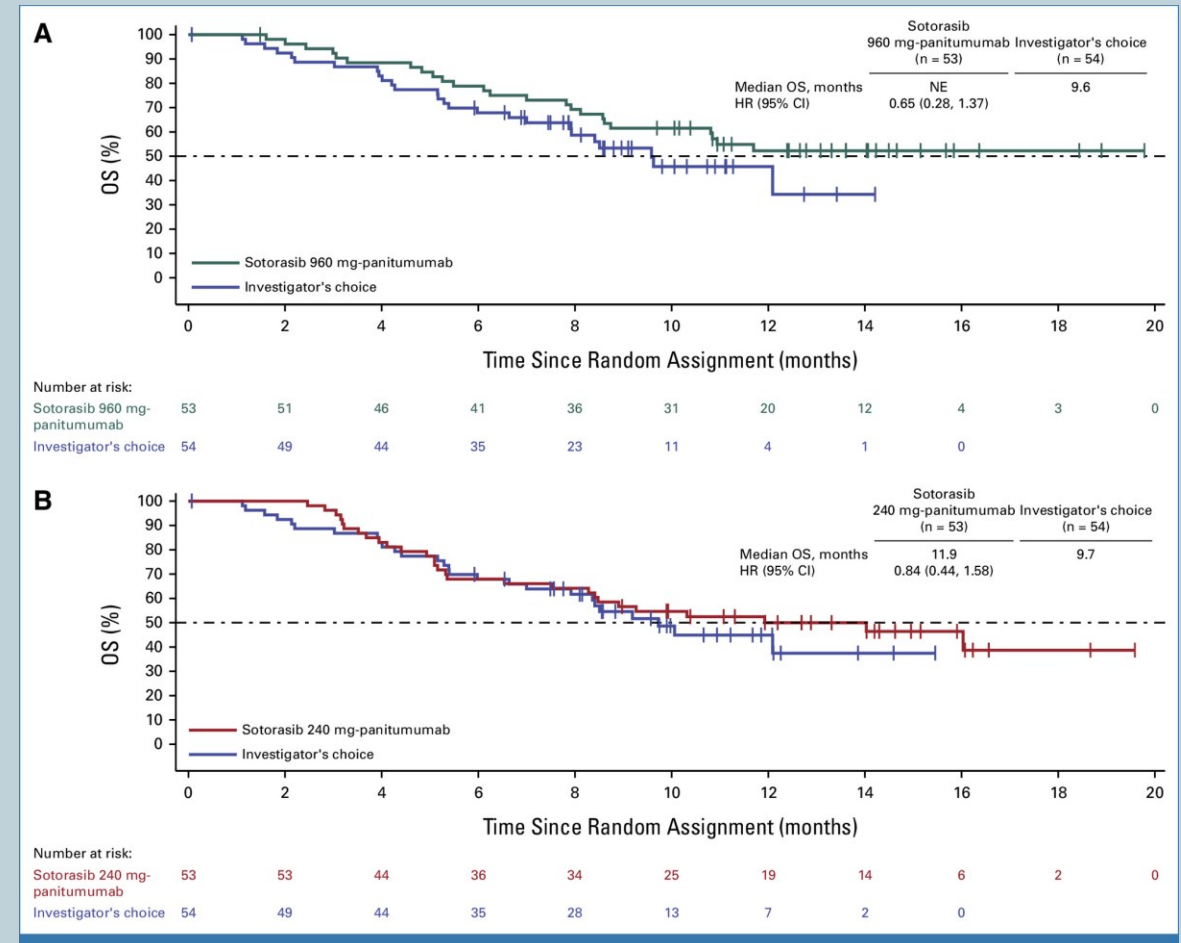
mOS

soto 960 + pani NE (95% CI, 8.61-NE)

soto 240 + pani 11.9 M (95% CI, 7.52 to NE)

SOC 10.3 M (95% CI, 7.00 to NE)

ORR 30 %



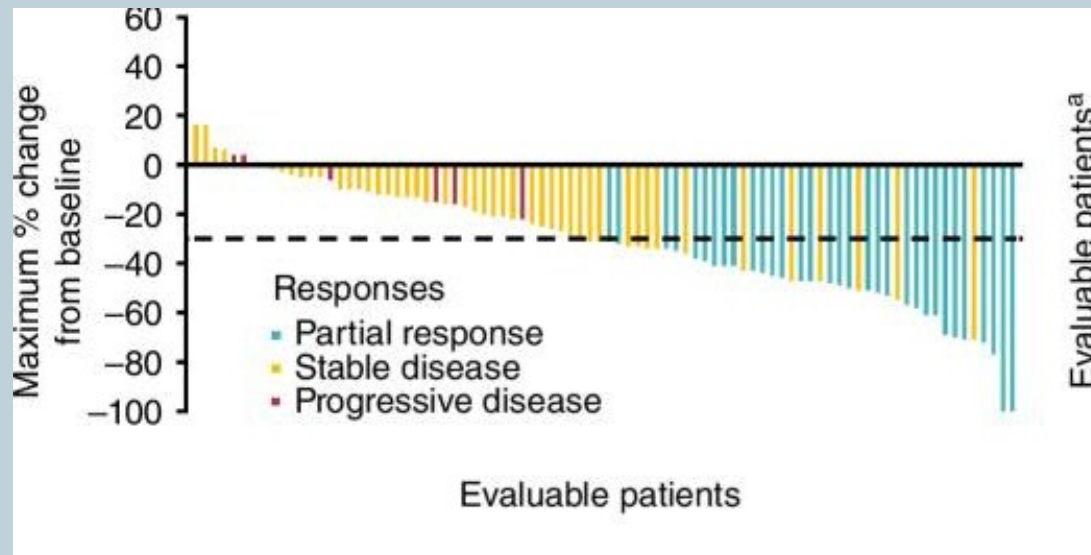
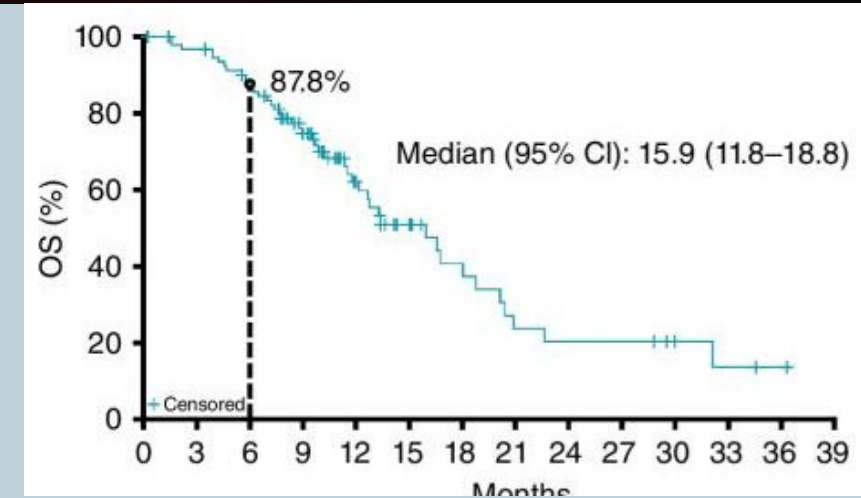
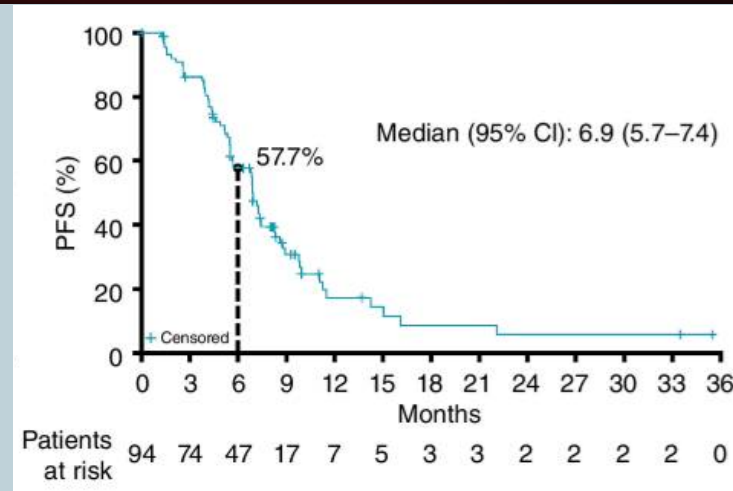
INHIBICE:

adagrasib + cetuximab (Krystal-1)

mPFS 6.9M (5.7–7.4)

mOS 15.9 M (11.8–18.8)

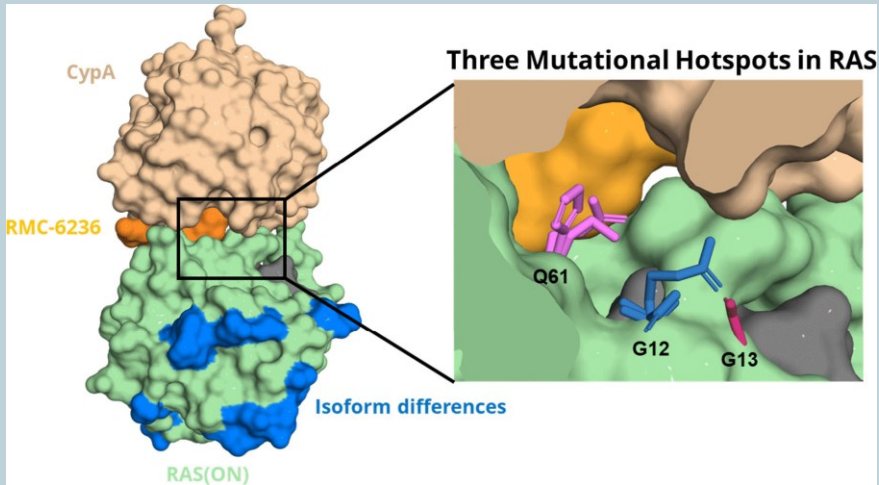
ORR 34.0 %



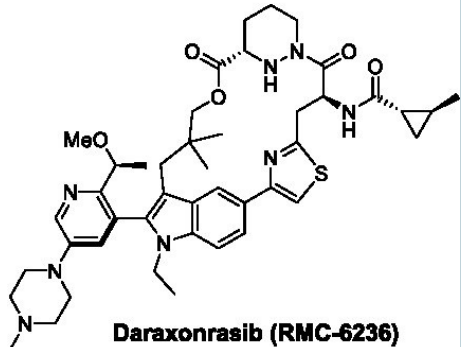
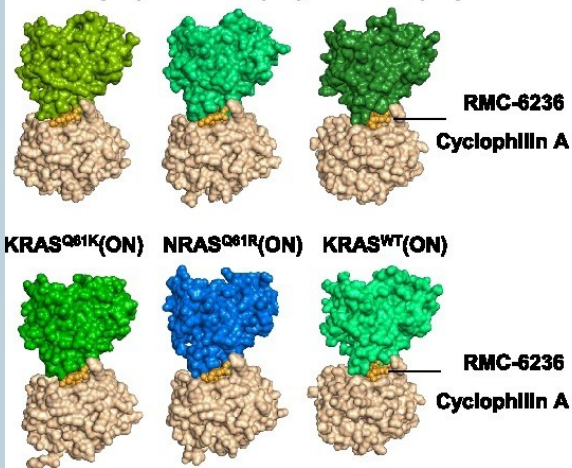
JINÉ non-G12C

- G12D
- panRAS (RMC-6236)

KRAS ^{G12D} Inhibitor	Mechanism of Drug action		Clinical stage
HRS-4642	KRAS ^{G12D} Inhibitor	HRS-4642 inhibits the binding of KRAS ^{G12D} to SOS1 or RAF1, thereby inhibiting the downstream MEK-ERK signaling pathway	Phase I/II clinical study
MRTX1133	Non-covalently bonded KRAS ^{G12D} selective inhibitor	MRTX1133 inhibits KRAS ^{G12D} inactive and active states	Phase I clinical study
GFH375(VS-7375)	KRAS ^{G12D} (ON/OFF) Inhibitor	GFH375 has a unique ON/OFF binding mechanism and can act on both activated (GTP-binding) and inactivated (GDP-binding) states of KRAS ^{G12D} mutant protein. GFH375 binds to KRAS G12D protein in a non-covalent form, thereby inhibiting its binding to downstream effector proteins and suppressing their pathway activation, and ultimately inhibiting tumor cell proliferation to achieve anti-tumor effects.	Phase I/II clinical study
AST2169	KRAS ^{G12D} Inhibitor (Liposome)	AST2169 liposome inhibits the function of KRAS G12D mutant protein, down-regulates the activity of related signaling pathways, effectively prevents cell cycle progression, induces apoptosis, and thus reduces the proliferation rate of tumor cells to achieve anti-tumor effects.	Phase I clinical study
RMC-9805	Covalent mutation-selective KRAS inhibitors	RMC-9805 selectively covalently modifies Asp-12 and interferes with RAS downstream signaling by forming a ternary complex with cyclophilin A (CypA) and the "ON" state of RASG12.	Phase I/II clinical study
ASP3082	KRAS ^{G12D} protein degrader	ASP3082 is a novel small-molecule targeted protein degradation chimera that binds to and selectively targets KRAS ^{G12D} mutant protein for degradation by recruiting an E3 ubiquitin ligase protein.	Phase I clinical study

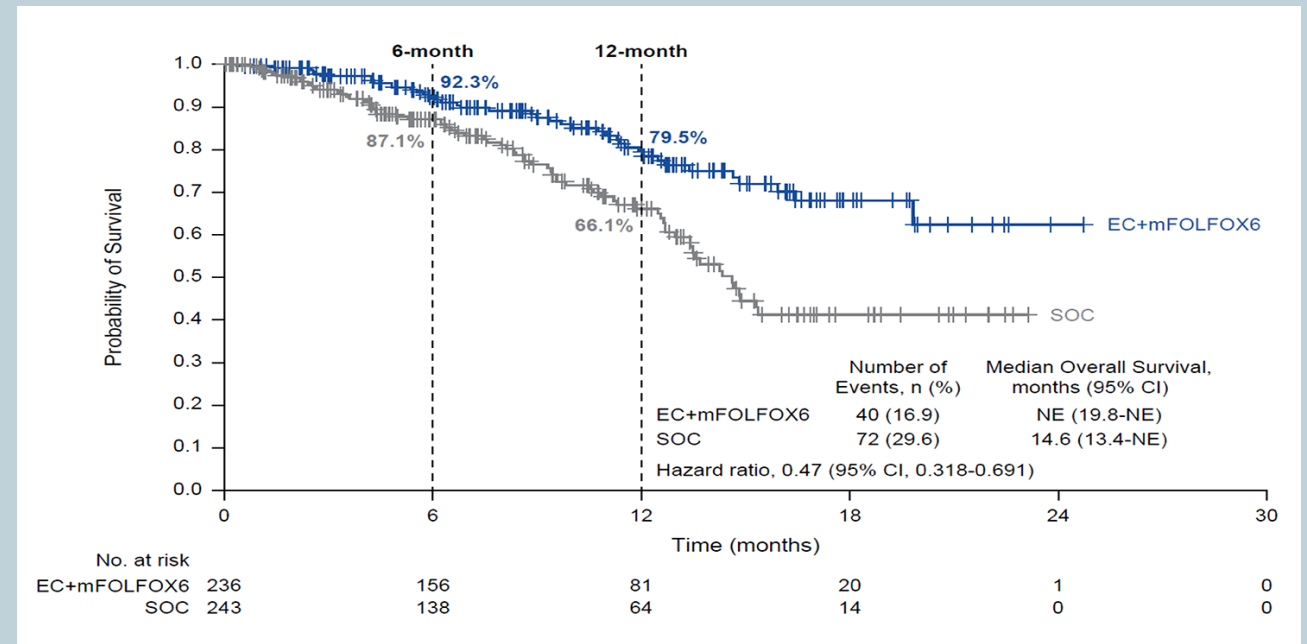
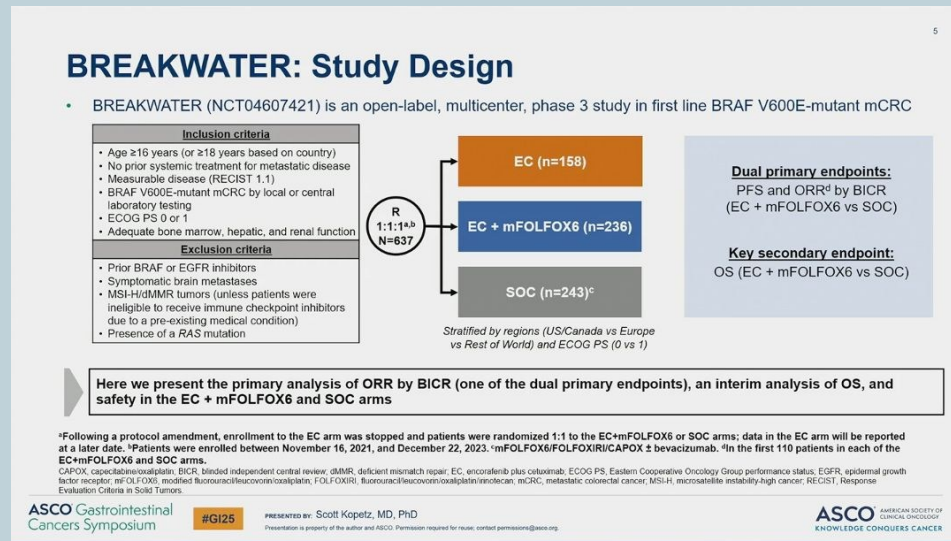


KRAS^{G12V}(ON) KRAS^{G12R}(ON) KRAS^{G12D}(ON)



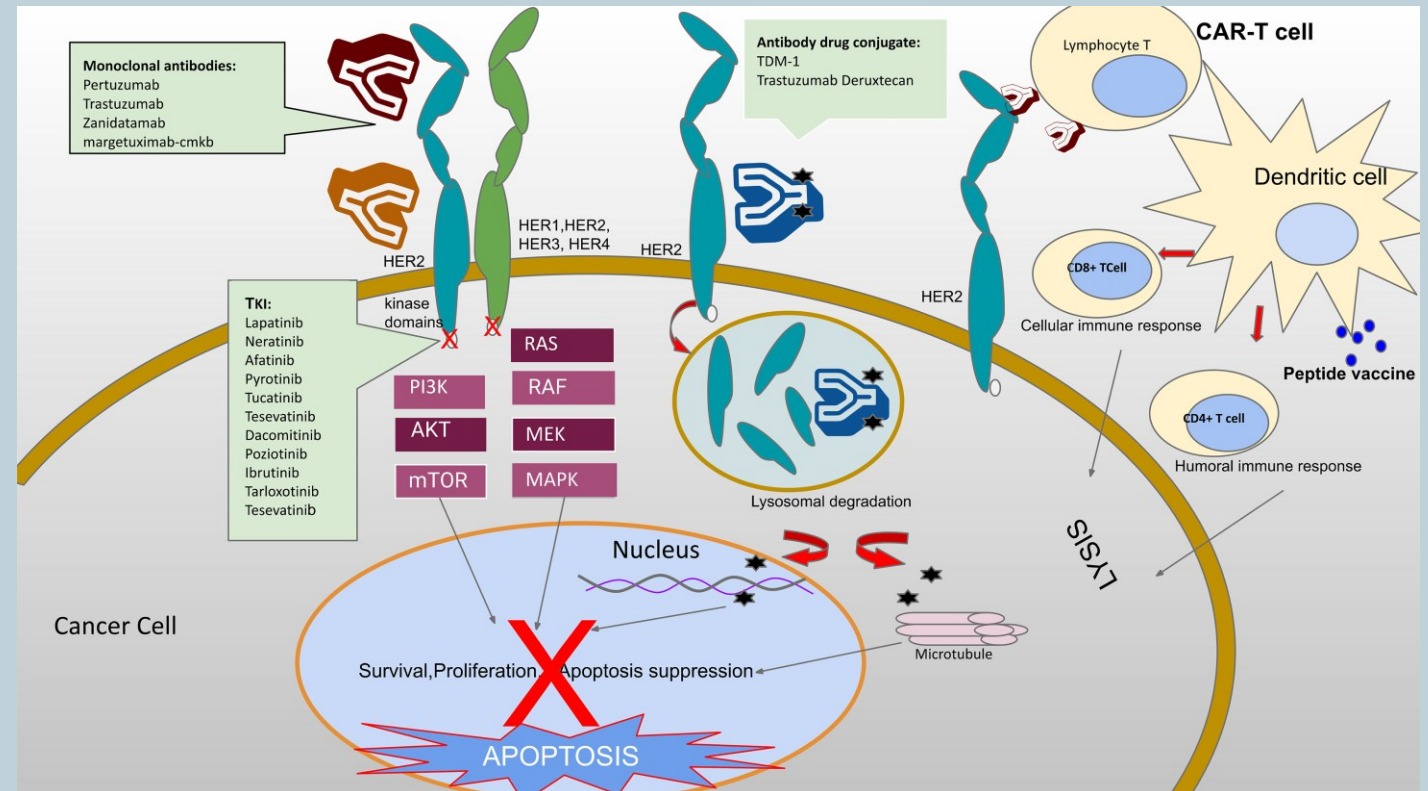
BRAF V600E

- 8-12 % CRC
- Breakwater:
encorafenib + cetuximab + mFOLFOX6
vs. CAPOX, FOLFOX, FOLFOXIRI +/- bevacizumab



HER2/neu

- amplifikace 3-5 % CRC
- častěji KRAS/BRAF-wt
- resistance k EGFRi
- častěji mozková meta
- mutace?
 - aktivační S310F, L755S, V777L, V842I



HER2/neu

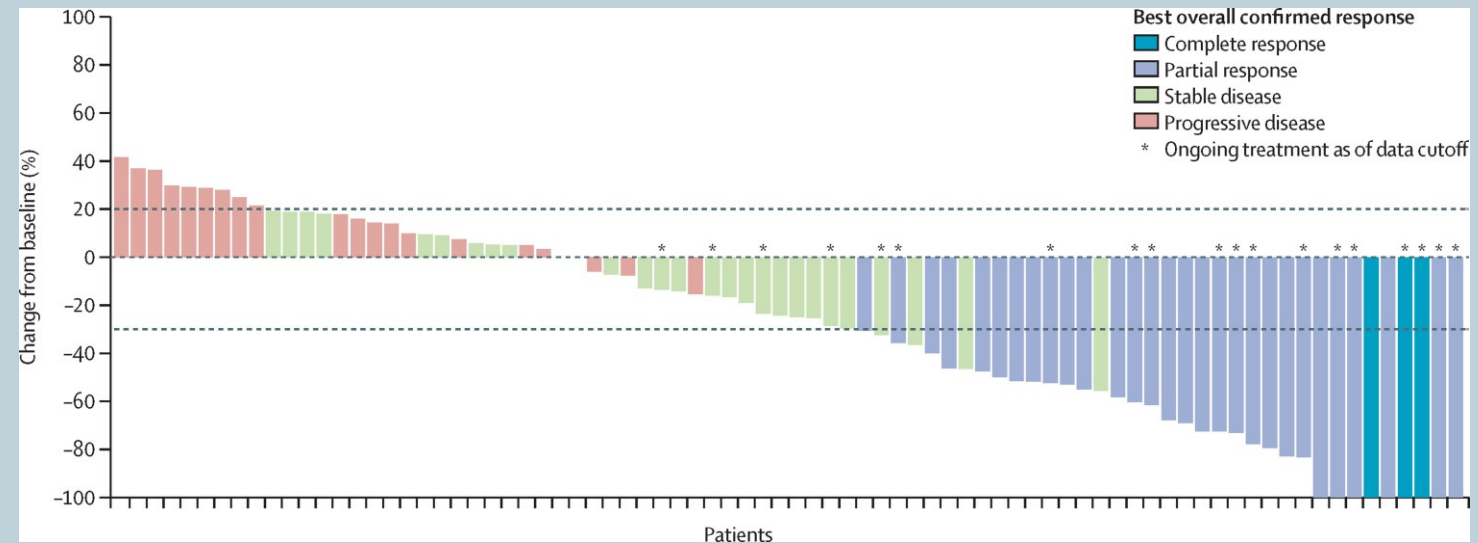
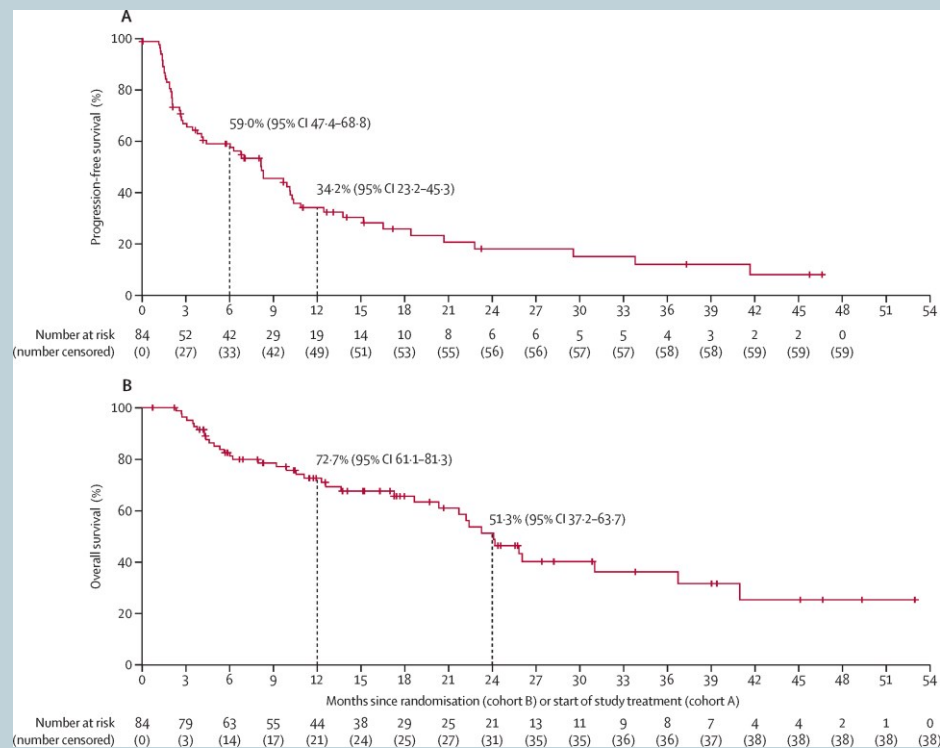
Trial name	Phase	Median number of prior therapy	Experimental regimen	Overall ORR, % (95% CI)	Overall DOR	Median OS (95% CI)	Subgroup analysis based on IHC score	Notable side effects
mAb								
MyPathway ²⁰	II	4	Trastuzumab plus pertuzumab	32% (20–45)	5.9 months	Not reported	Not reported	Ventricular dysfunction (2%)
TAPUR ³²	II	Not reported (77% received 1 to 2 prior lines of therapy)	Trastuzumab plus pertuzumab	25% (CI 11–45)	Not reported	60 weeks	Not reported	Ventricular dysfunction (1%)
Meric-Bernstam <i>et al.</i> ²⁶	I	4	Zanidatamab	38% (20–59)	6.3 months (in the dose escalation CRC group)	NA	NA	Diarrhea (all grades, 43–52%), arthralgia (2%), hypophosphatemia (2%)
TKI-containing regimens								
HERACLES-A ³³	II	5	Trastuzumab plus lapatinib	30% (CI 14–50)	4.7 months	46 weeks (33–68)	Not reported	Diarrhea (all grades, 78%)
MOUNTAINEER ^{11,34}	II	3 in doublet arm 2 in tucatinib alone arm	Tucatinib with or without trastuzumab	Tucatinib plus trastuzumab: 38.1% (95% CI not reported) Tucatinib alone: 3.3% (0.1–17.2) Tucatinib cross-over: 17.9% (6.1–36.9)	12.4 months	Not reported	ORR in HER2 IHC2+/FISH+ group: 20% ORR in IHC 3+ group: 41.1–46.7%.	Diarrhea (64% in the double arm, 33% in the tucatinib alone arm), acute kidney injury, elevated liver enzymes
HER2-FUSCC-G ³⁵	Ila	Not reported (inclusion criteria includes at least 2 prior lines of treatment)	Pyrotinib plus trastuzumab	57.1% (95% CI not reported)	Not reported	Not reached	Not reported	Diarrhea (grade 3, 25%), rash (grade 3, 6.3%)

HER2/neu

ADC								
DESTINY-CRC01 ¹⁰	II	4	Fam-trastuzumab deruxtecan	Cohort A (IHC3+ and 2+/FISH positive): 45.3% (31.6–59.6)	7 months	Cohort A: 5.4 months (95% CI not reported)	ORR in the ICH3+ group: 57.5% (40.9–73) ORR in ICH2+/FISH positive group: 7.7% (CI 0.2–36)	Pneumonitis (all grades, 6%, which included two cases of grade 2, one grade 3, and two grade 5)
DESTINY-CRC02 ³⁶	II	5.4 mg/kg T-DXd group: 3 6.4 mg/kg T-DXd group: 4	Fam-trastuzumab deruxtecan	5.4 mg/kg T-DXd group: 37.8% 6.4 mg/kg T-DXd group: 27.5%	5.5 months	NA	IHC3+ group that received 5.4 mg/kg T-DXd: 46.9% IHC2+/FISH+ group that received 5.4 mg/kg T-DXd: 5.6% IHC3+ group that received 6.4 mg/kg T-DXd: 29.4% IHC2+/FISH+ group that received 6.4 mg/kg T-DXd: 16.7%	Pneumonitis (8.4% with 5.4 mg/kg T-DXd, 12.8% with 6.4 mg/kg T-DXd)

HER2/neu

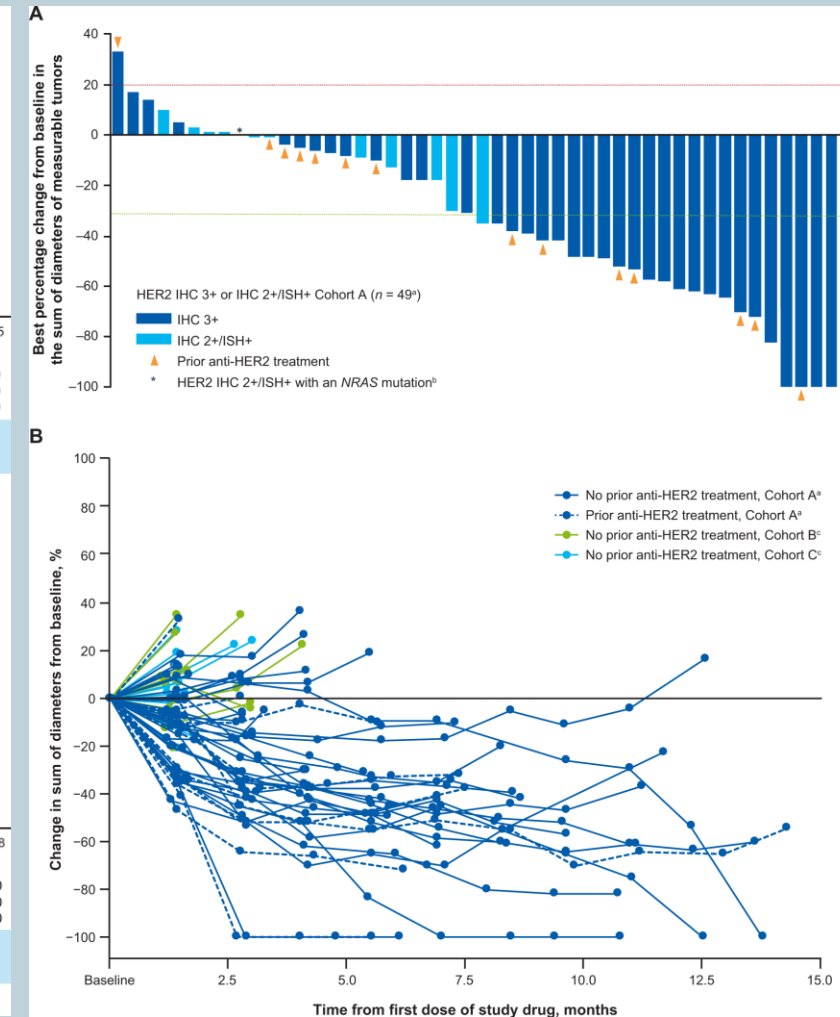
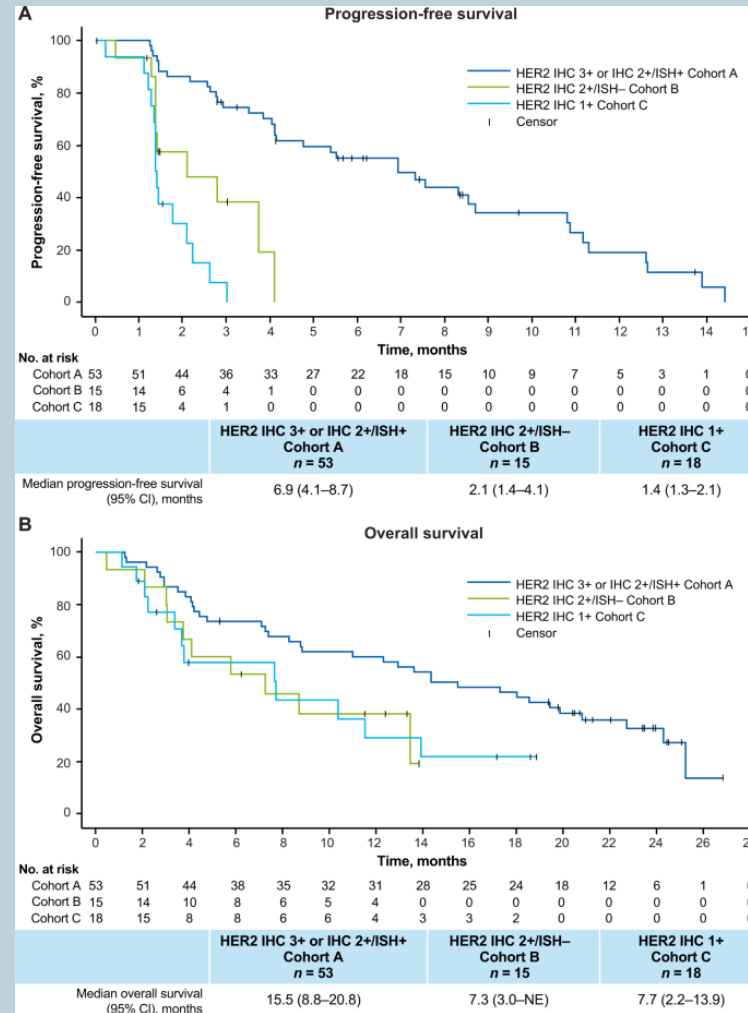
- Tucatinib + trastuzumab (Mountaineer)



HER2/neu

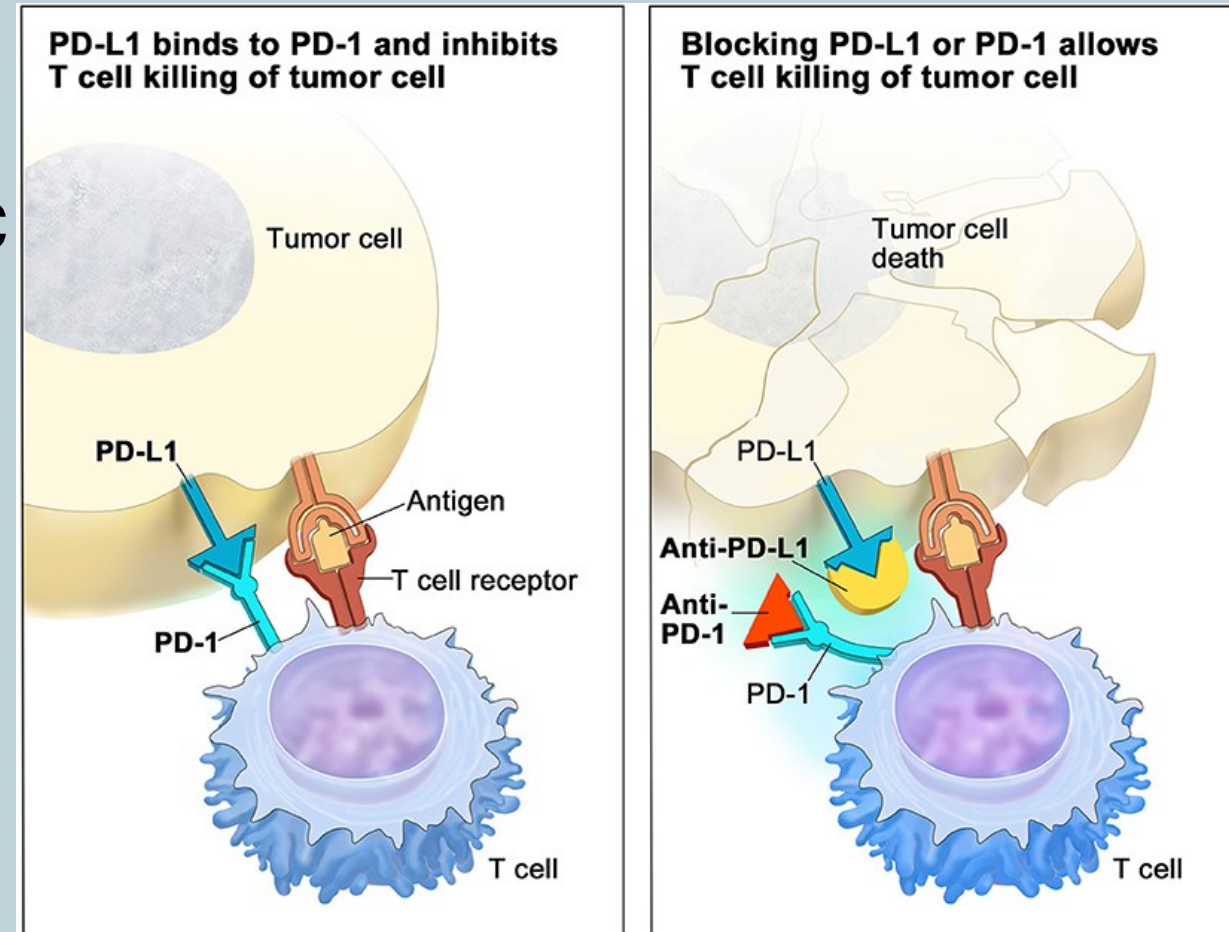
• Trastuzumab-deruxtecan (Destiny-CRC-01)

- amplifikace
- podskupina s mutací HER ORR <10 % (obdobně trastu/pertu ve studii MyPathway)



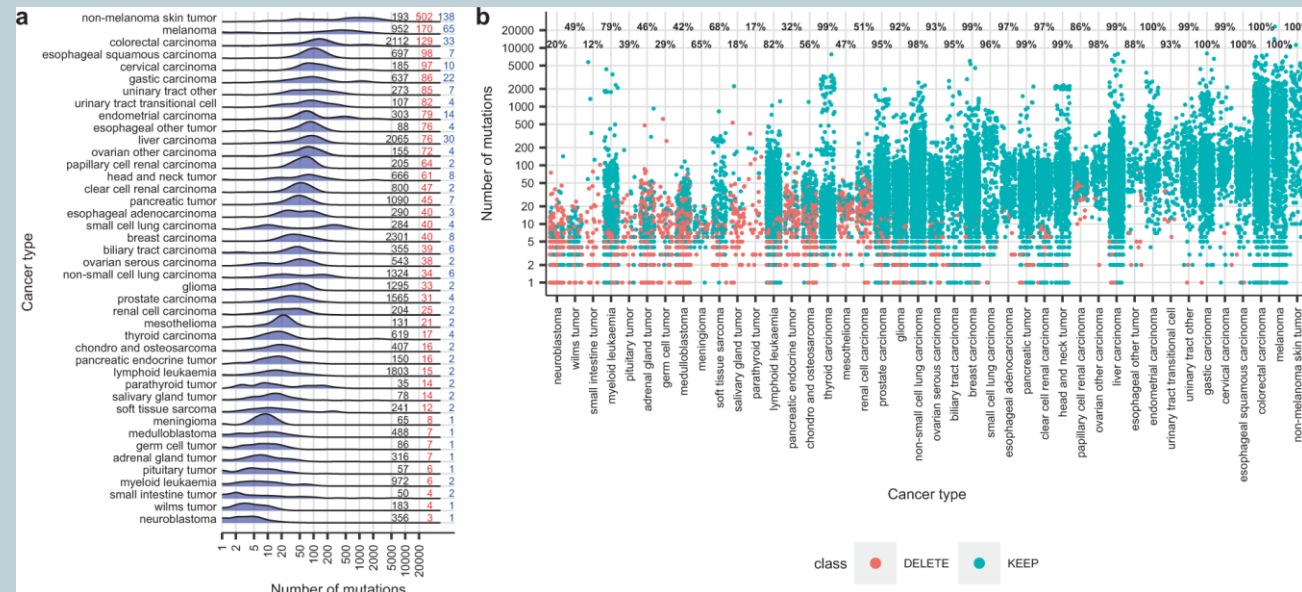
IMUNOTERAPIE - PDL-1

- velmi variabilní exprese
- ↑ exprese PD-L1 je spojena s horší prognózou v rámci MSI-H CRC
- potenciálně prognostický a prediktivní charakter
- standardní využití u CRC chybí



IMUNOTERAPIE - TMB

- potenciálně prediktivní marker imunoterapie
- počet somatických mutací v genomu (vyjádřeno megabázi gen. materiálu)
- různé hranice (10, 17, 20 mut/Mb), chybí standardizace (jaké mutace jsou počítány? z čeho? vzorky?)



Marques et al, Tumor mutational burden in colorectal cancer: Implications for treatment, Critical Reviews in Oncology / Hematology 197, 104342, 2024

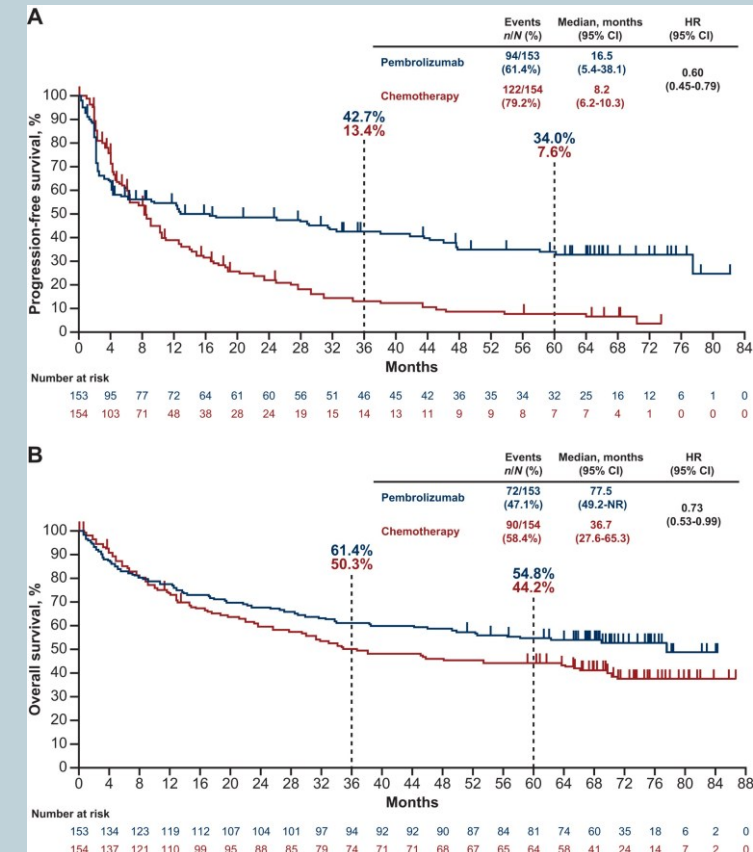
Martínez-Pérez et al, Panels and models for accurate prediction of tumor mutation burden in tumor samples, NPJ Prec Onc 5, Article number: 31, 2021

IMUNOTERAPIE - MSI/TMB/MMR

- bez hypermetylace promotoru MLH1, bez mutace EPCAM
- (15 %) pacientů s diskordantními výsledky
 - ztráta MMR bez mikrosatelitové nestability
 - zachovale MMR s MSI
- není korelace s TMB

IMUNOTERAPIE CRC

- PD(L)-1 inhibice, v kombinaci anti-CTLA-4
- pembrolizumab, nivolumab + nivolumab, dostarlimab
- zatím jediné prediktivní markery:
dMMR/MSI-H, POLE-mut (POL-D1)
- pembrolizumab (Keynote-177)



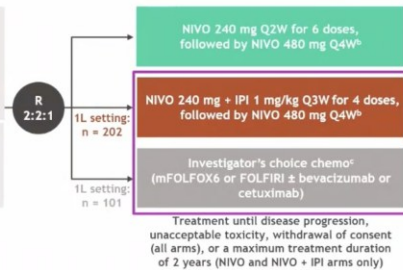
IMUNOTERAPIE CRC

- ipilimumab + nivolumab (Checkmate)

CheckMate 8HW study design

- CheckMate 8HW is a randomized, multicenter, open-label phase 3 study^a

- Key eligibility criteria:**
- Histologically confirmed unresectable or metastatic CRC
 - MSI-H/dMMR status by local testing
 - ECOG PS 0 or 1
- Stratification factors:**
- Prior lines of treatment (0 vs 1 vs ≥ 2)
 - Primary tumor location (right vs left)

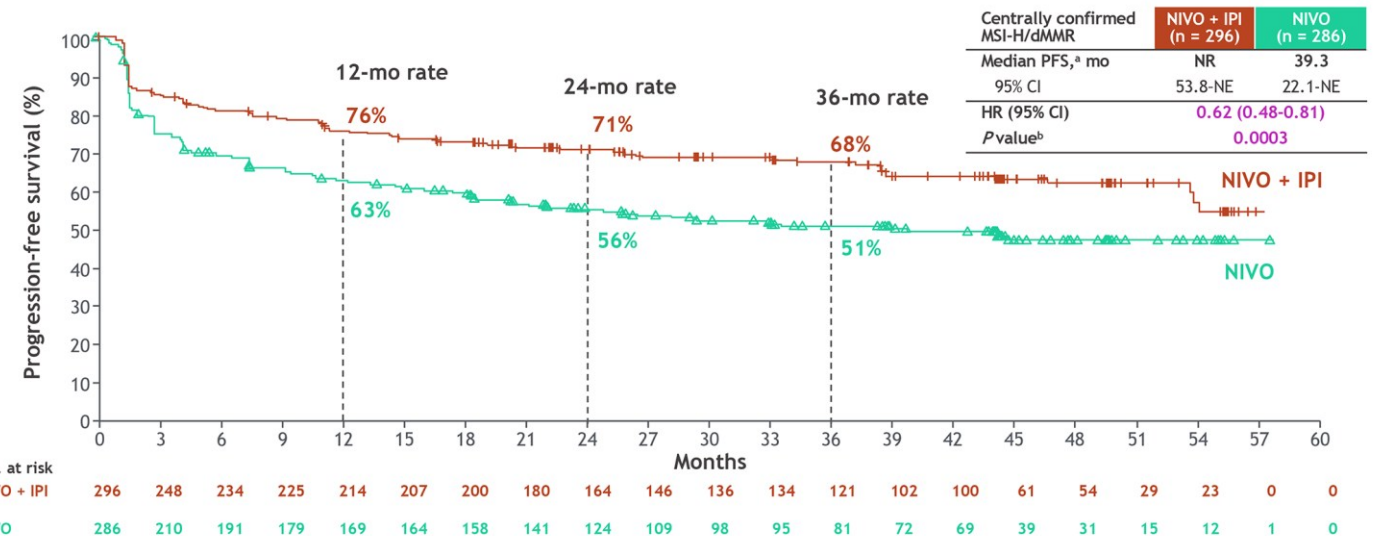


- Dual primary endpoints in patients with centrally confirmed MSI-H/dMMR status^d:**
- PFS by BICR^e (NIVO + IPI vs chemo in the 1L setting)
 - PFS by BICR^e (NIVO + IPI vs NIVO across all lines)
- Other select endpoints:**
- Safety
 - OS; ORR by BICR^e; HRQoL

- At data cutoff (October 12, 2023), the median follow-up^f was 31.5 (range, 6.1-48.4) months

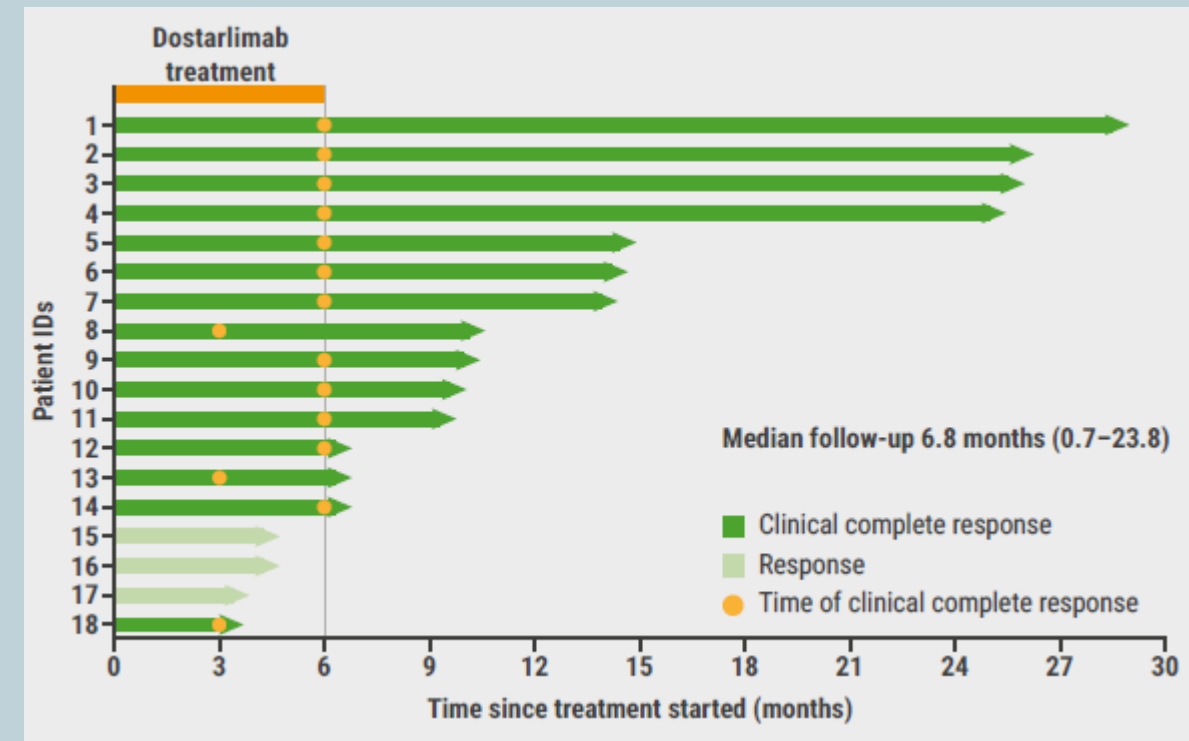
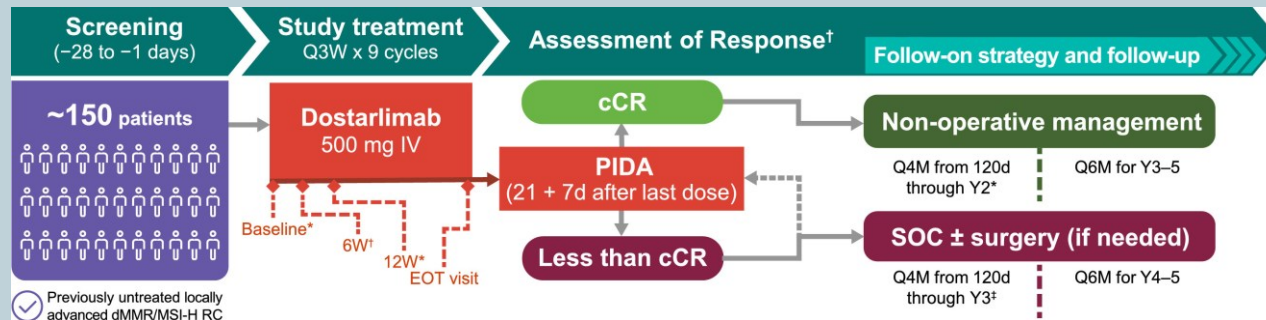
^aClinicalTrials.gov, NCT04008030. ^bPatients with ≥ 2 prior lines are randomized only to the NIVO or NIVO + IPI arms. ^cPatients receiving investigator's choice of chemotherapy are eligible to receive NIVO + IPI upon progression (crossover treatment). ^dConfirmed using either immunohistochemistry and/or polymerase chain reaction-based tests. ^eEvaluated using RECIST v1.1. ^fTime from randomization to data cutoff.

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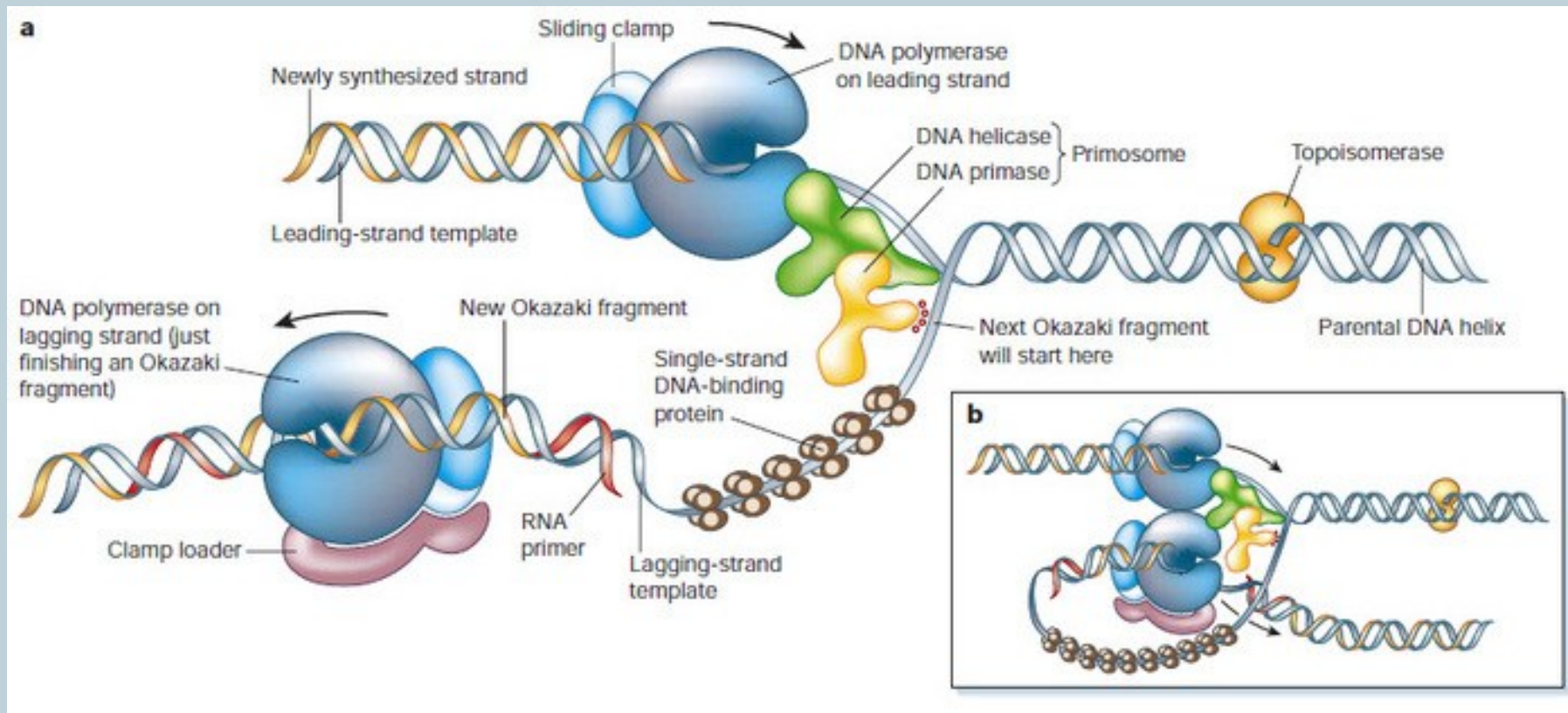
IMUNOTERAPIE

- dostarlimab (Azur-1,2)
 - dMMR
 - ORR 100 %,



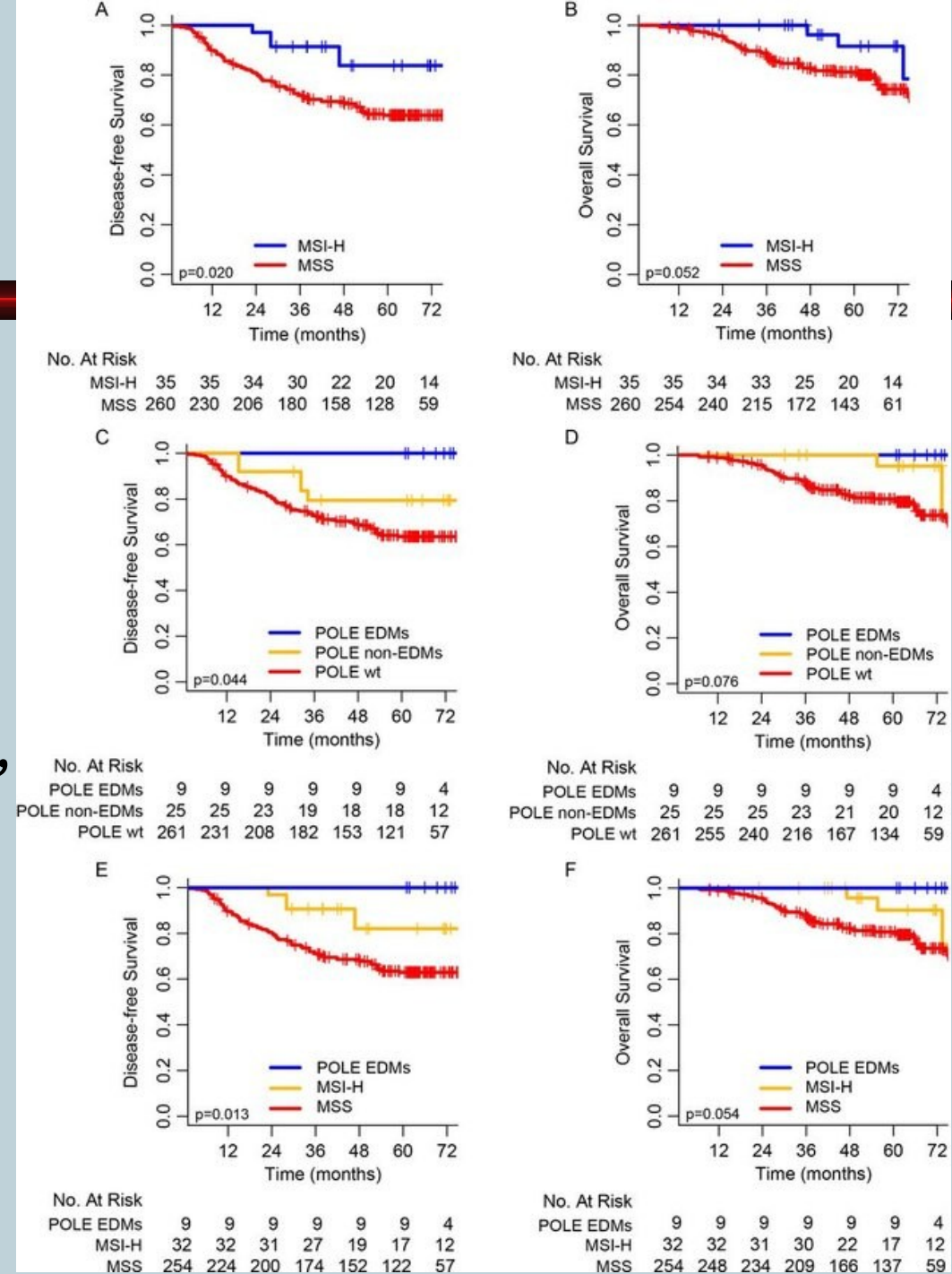
POLE

- u člověka 15 typů polymeráz (rodina A, B, X, Y)



POLE

- spojeno s tzv. hypermutovaný fenotypem (TMB 50 mut/Mb a více)
- ↑ přítomnost neoantigenů
- ↑ tumor-infiltrující lymfocyty
- častěji mladší muži, pravostranné tumory, zřídka KRAS-mut
- lepší prognóza (za podmínky mutace v exonukleázové doméně a TMB-high)

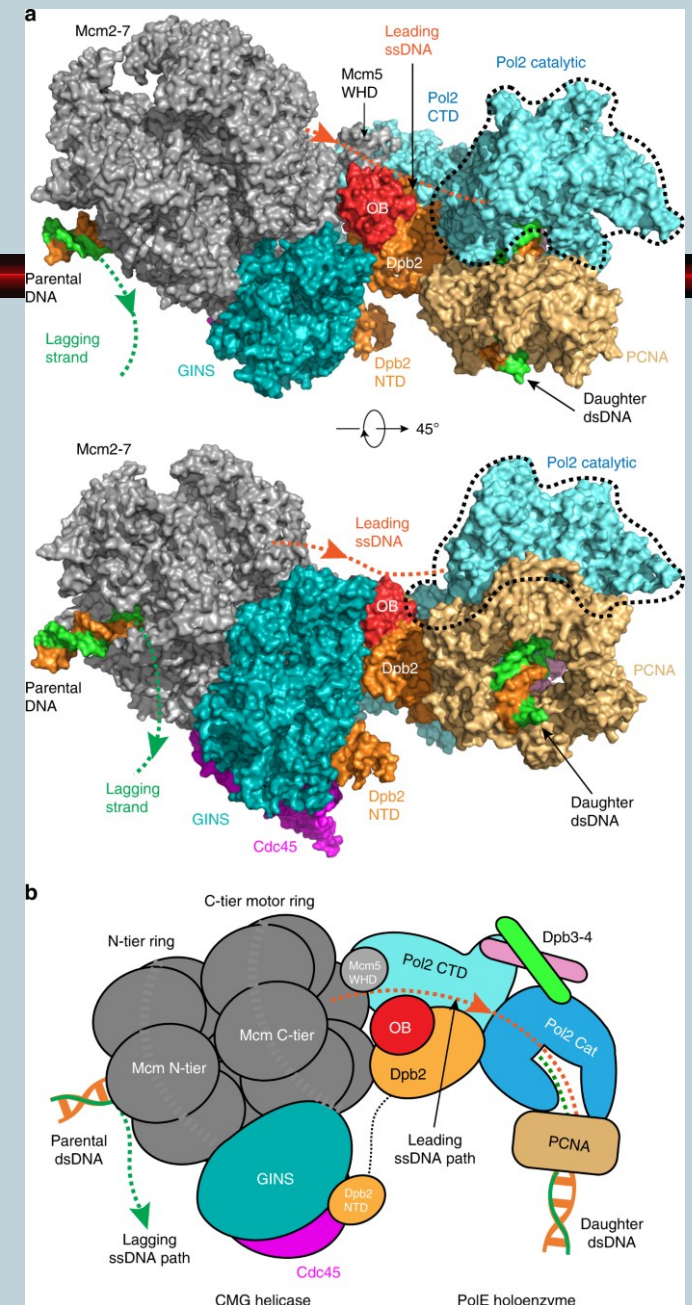
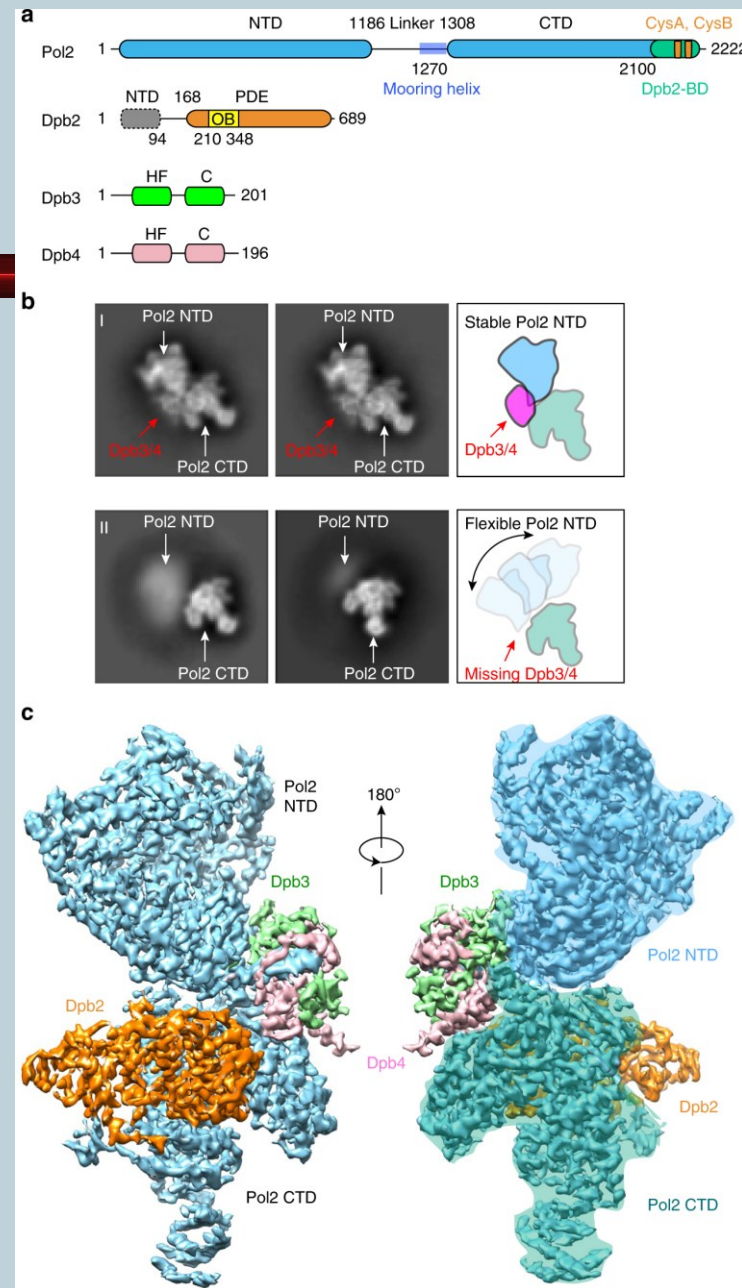


POLE

- rodina polymeráz B, multimerická (POLE 1-4)
 - replikace chromozomů (elongace vedoucího řetězce)
 - NER (nucleotide excision repair)
 - mismatch repair (proofreading)
- mutace v exonukleázové doméně vedou k poruše její funkce a zvýšení počtu SNV (single nucleotide variants)
- somatické mutace 2-8 % CRC (pMMR, MSS)
- zárodečné mutace POLE (polymerase proofreading-associated polyposis) spojeny s adenomy a adenokarcinomy tlustého střeva
- další souvislost s endometroidním karcinomem (vyšší frekvence)

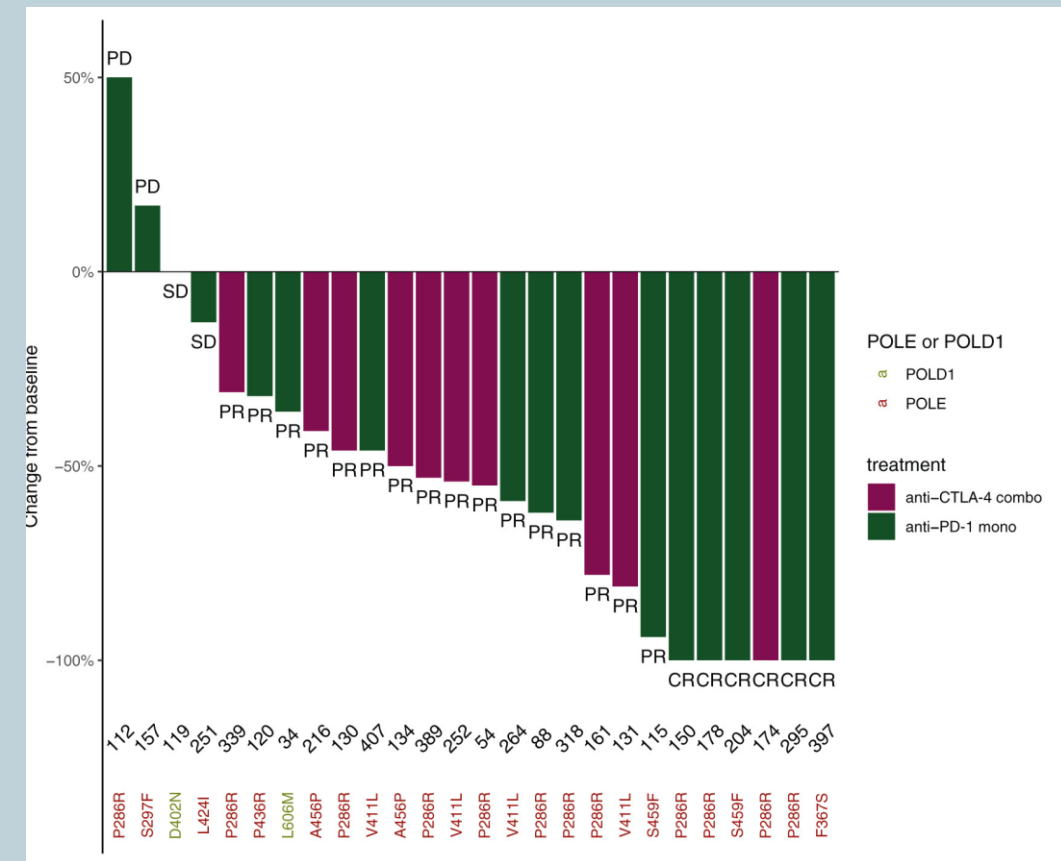
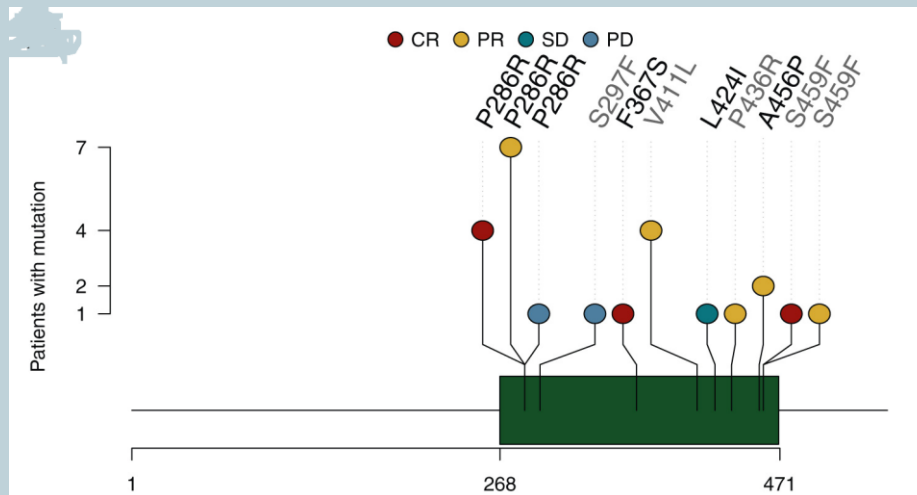
POLE

- 4 podjednotky
- úzké napojení na ostatní proteiny (PCNA, CMG helicáza, ...)
- opravy DNA



POLE

- lepší odpovídavost na imunoterapii i ve srovnání s dMMR/MSI-H CRC
- nejčastější mutace POLE
sporadické: P286R, V411L, P286H/S, F367S, S459F
germinální: V424L



POLE

- POLE je další z terapeutických cílů umožňující účinné podání imunoterapie
- nutnost detailního testování (napříč diagnosami);
- přetrvávají nežádoucí účinky spojené s imunoterapií

ZÁVĚR

- molekulární testování může přinést výsledky v každé fázi léčby CRC
- volba vhodného postupu by měla být závislá na rozhodnutí tumor-boardu