

Belgian Symposium on the Integration of Molecular Biology Advances  
into Oncology Clinical Practice

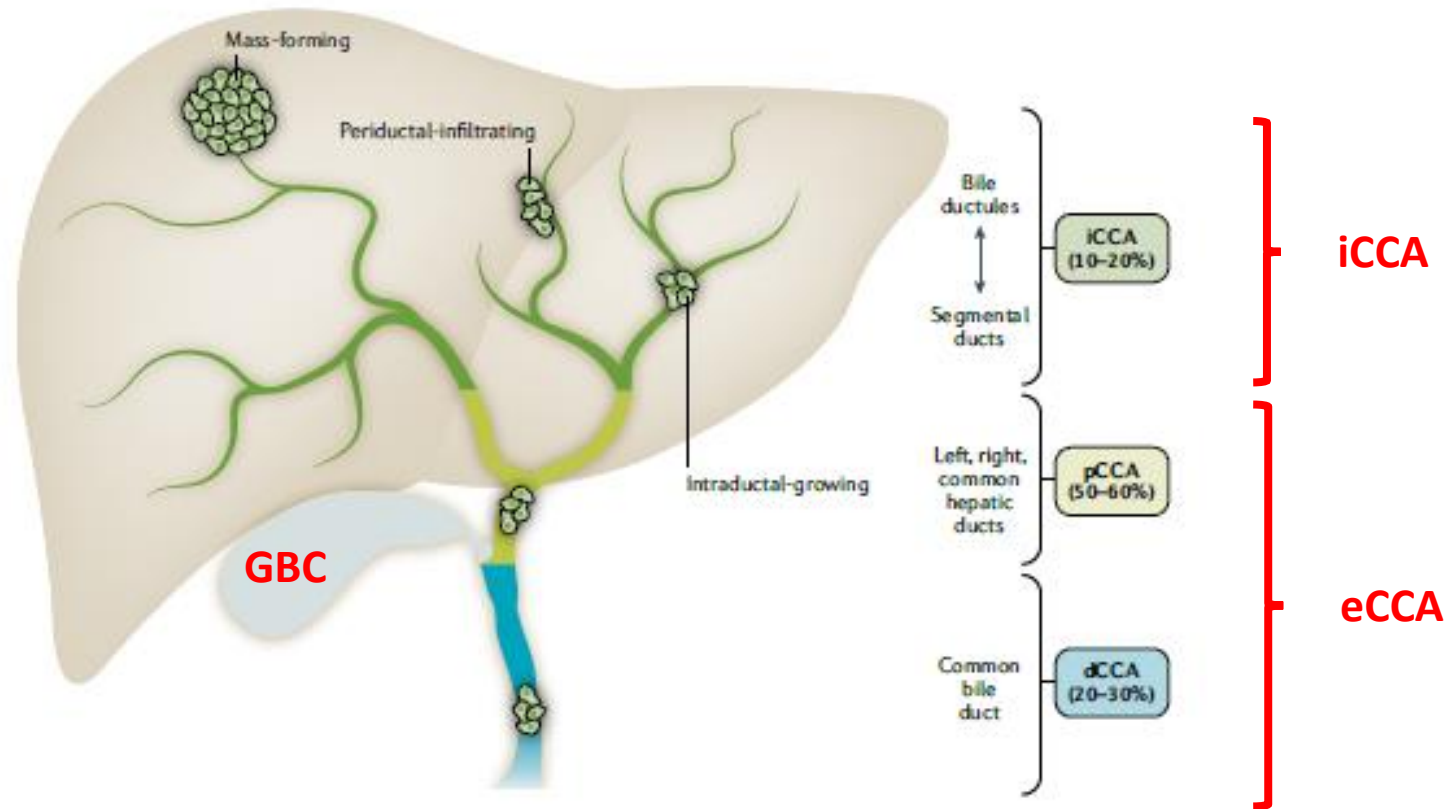
# Therapeutic strategies in molecular subtypes of biliary tract cancers and HCC

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# Disclosures C. Verslype

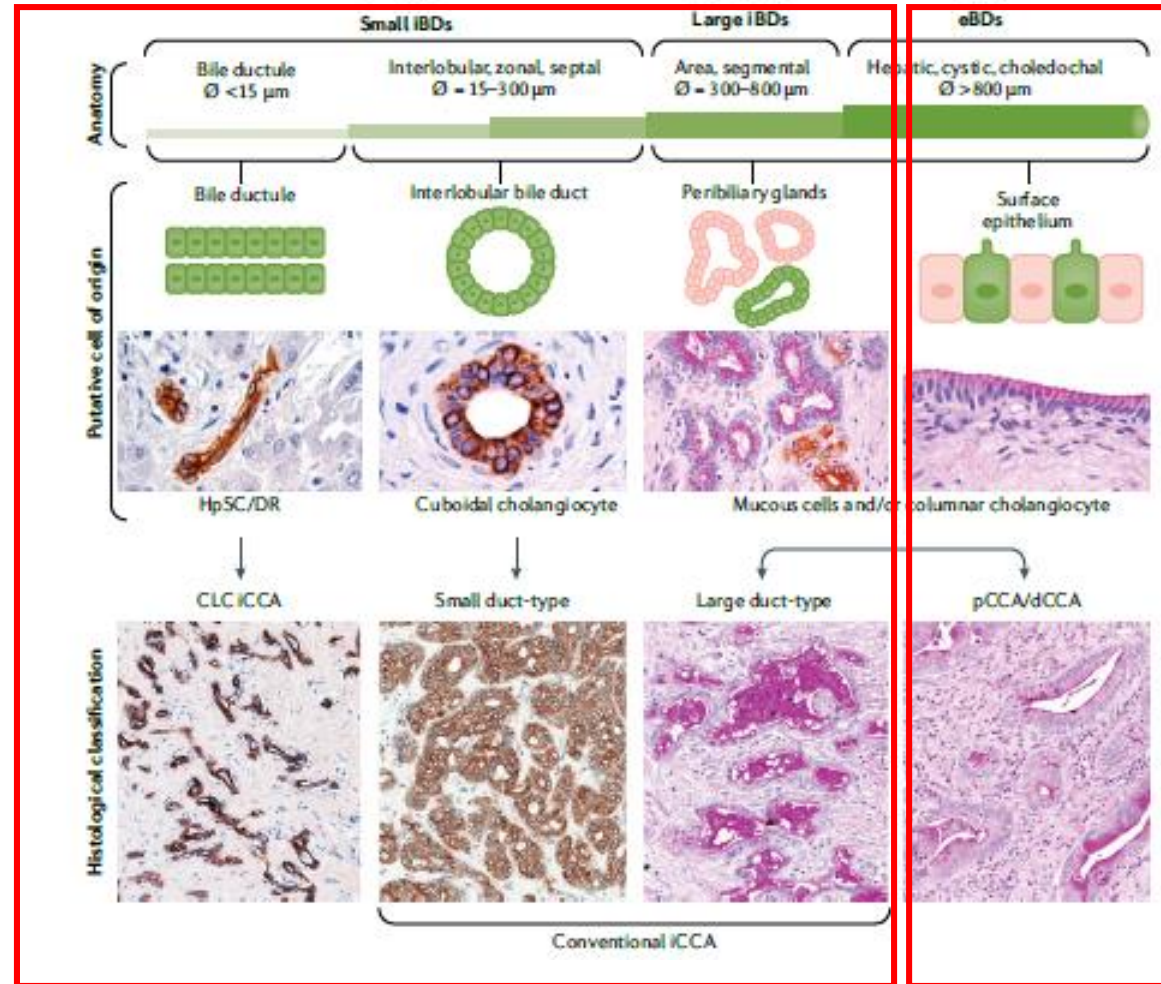
Consultancy and research grants:  
Bayer, Ipsen, Roche

# CCA: location



**Viral, cirrhosis**

**PSC, liver flukes**



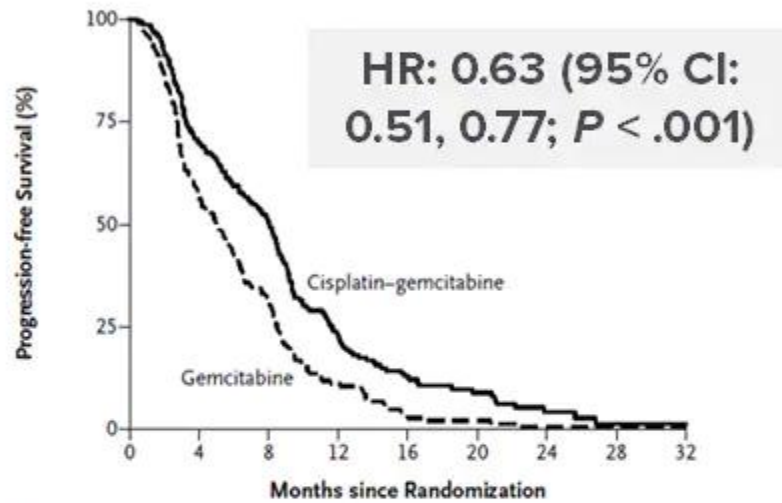
**iCCA**

**eCCA**

# Standard First-Line Treatment for Biliary Tract Cancer

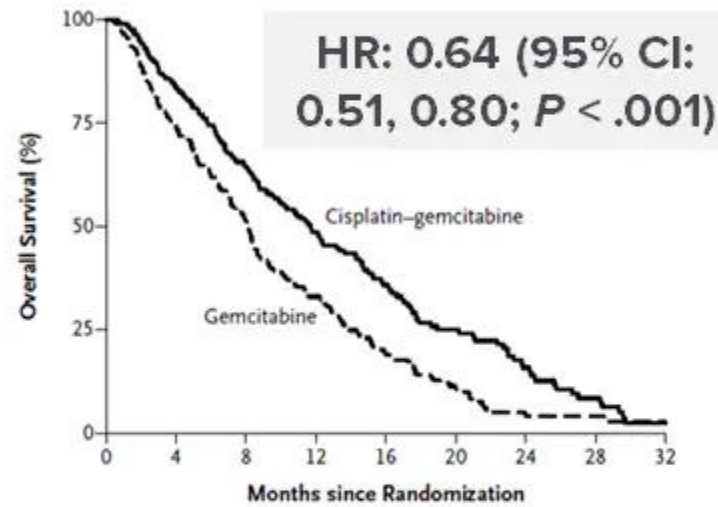
## Gemcitabine +/- Cisplatin

**ABC-02: PFS<sup>[a]</sup>**



No. at Risk		0	4	8	12	16	20	24	28	32
Gemcitabine	206	115	56	18	4	3	1	1	1	1
Cisplatin-gemcitabine	204	140	95	36	18	10	4	1	1	1

**ABC-02: OS<sup>[a]</sup>**



No. at Risk		0	4	8	12	16	20	24	28	32
Gemcitabine	206	151	97	53	28	15	4	3	2	2
Cisplatin-gemcitabine	204	167	120	76	51	28	17	8	2	2

### Patient selection criteria:<sup>[a,b]</sup>

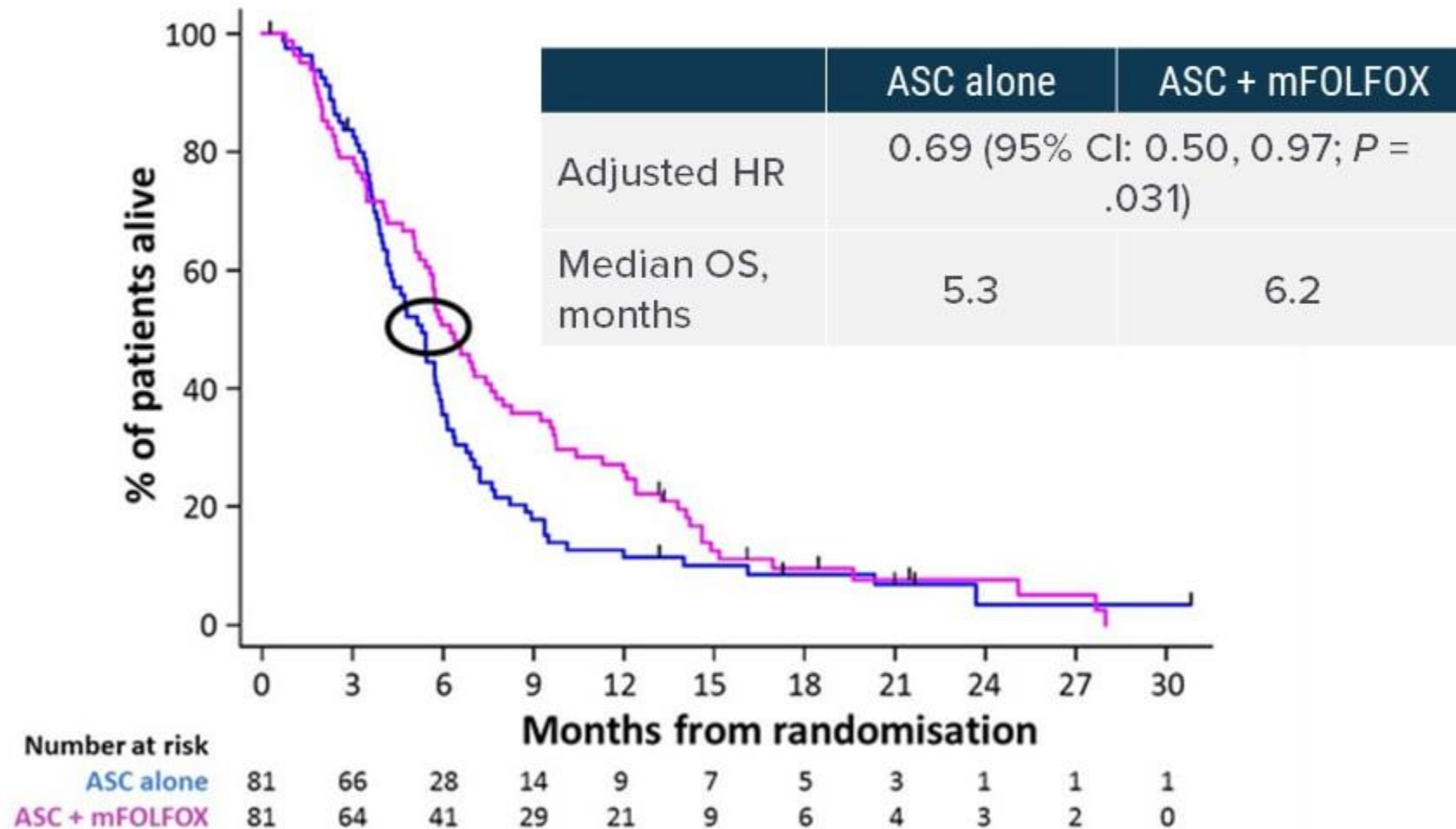
- Good ECOG PS
- Good liver function
- Clinical trial availability (preferable option)

Study	PFS (months)		OS (months)	
	Gemcitabine	Cisplatin Gemcitabine	Gemcitabine	Cisplatin Gemcitabine
ABC-02 <sup>[a]</sup>	5.0	8.0	8.1	11.7
BT-22 <sup>[b]</sup>	3.7	5.8	7.7	11.2

# Second-Line Treatment Option in CCA

## FOLFOX

### ABC-06: OS (ITT population)



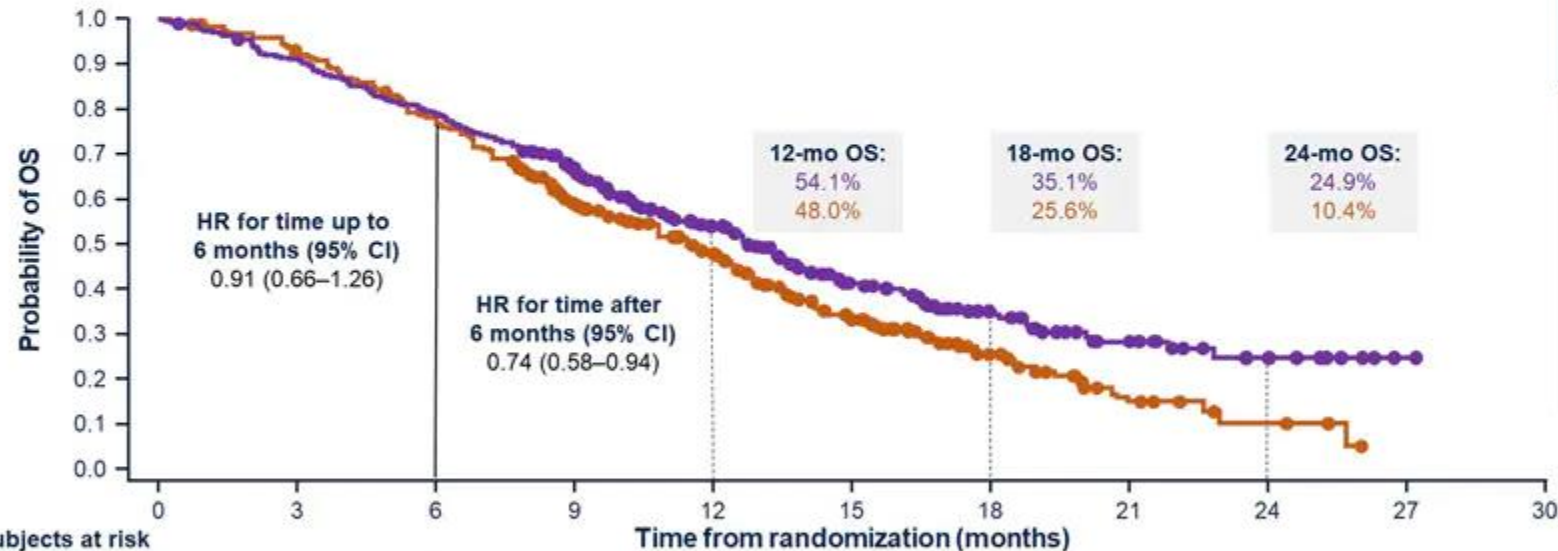
### Patient selection criteria:

- Good ECOG PS
- Good liver/renal function
- No targetable alterations
- No clinical trial availability

# Durvalumab in Untreated Advanced Biliary Tract Cancer *Topaz-1 Trial*

Randomized, double-blind, placebo-controlled phase 3 study of first-line durvalumab vs SOC

OS



	Median OS, Months (95% CI)	Hazard Ratio (95% CI)	P Value
Durvalumab + gemcitabine cisplatin (n = 341)	12.8 (11.1 to 14.0)	0.80 (0.66 to 0.97)	.021
Placebo + gemcitabine cisplatin (n = 344)	11.5 (10.1 to 12.5)		

Statistical significance cut-offs for OS: P = .03

Gemcis: max 8 cycles!

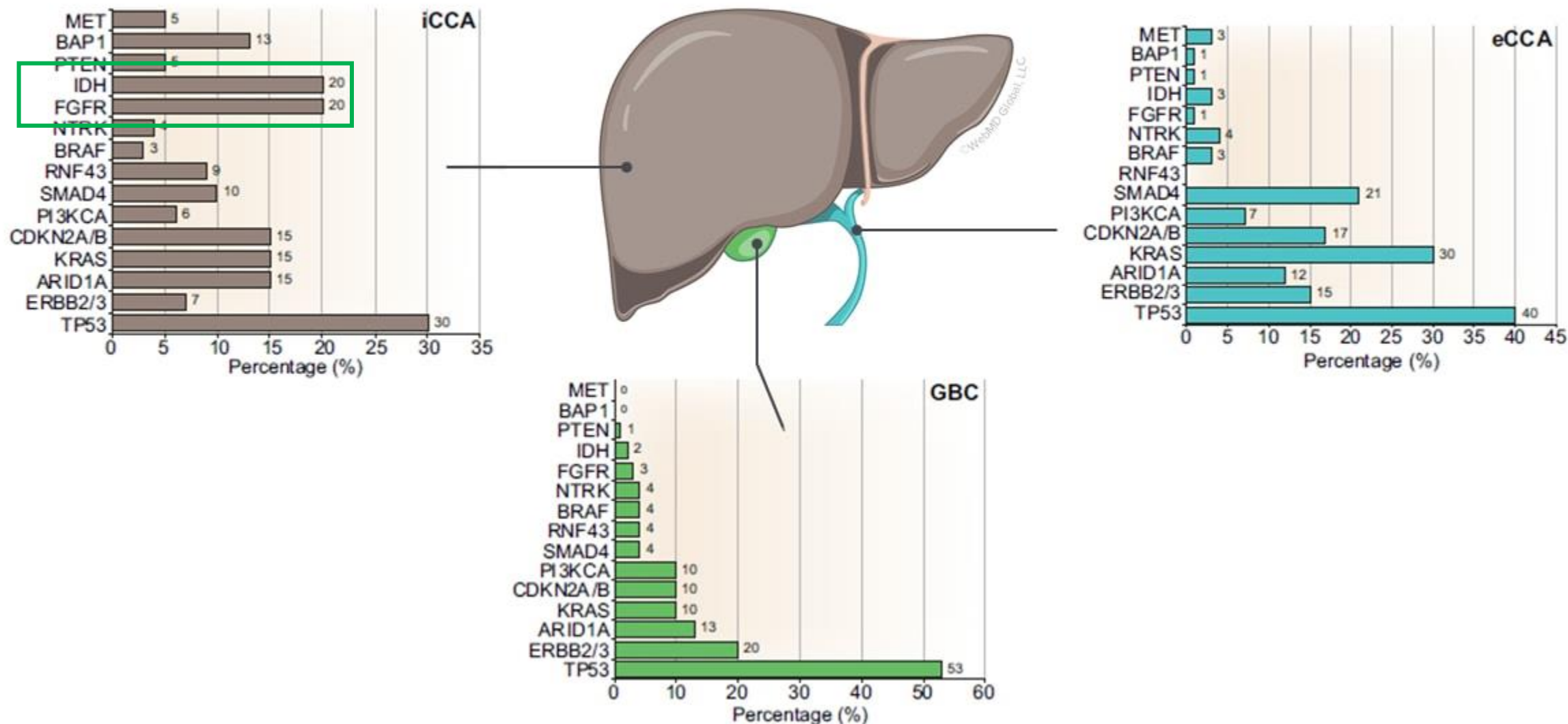
- Grade 3/4 TRAEs: 62.7% (n = 212/338) in durvalumab + SOC and 64.9% (n = 222/342) in SOC
- Most common 3/4 TRAEs: anemia (23.7% (n = 80/338) durvalumab + SOC vs 22.5% (n = 77/342 SOC) and decreased neutrophils (21.0% (n = 71/338) vs 25.7% (n = 88/342))

# Molecular profiling

- Methodology:
  - Targeted DNA sequencing: quest for actionable mutations
  - Whole-genome expression: transcriptome based classification (mostly done on resection specimens)
- Aim: to guide systemic treatments (for advanced disease)



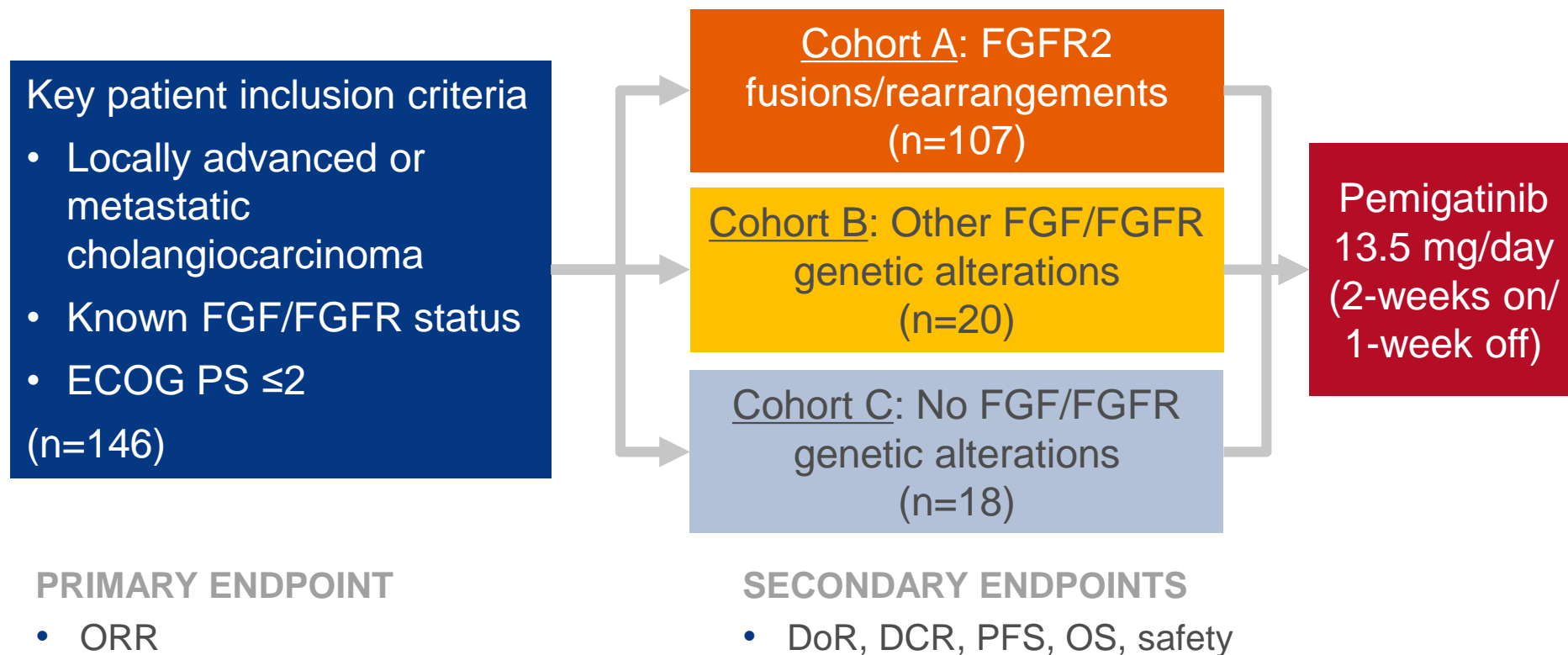
# Molecular Profiling of Biliary Tract Cancers



## FIGHT-202: A phase II study of pemigatinib in patients (pts) with previously treated locally advanced or metastatic cholangiocarcinoma (CCA)

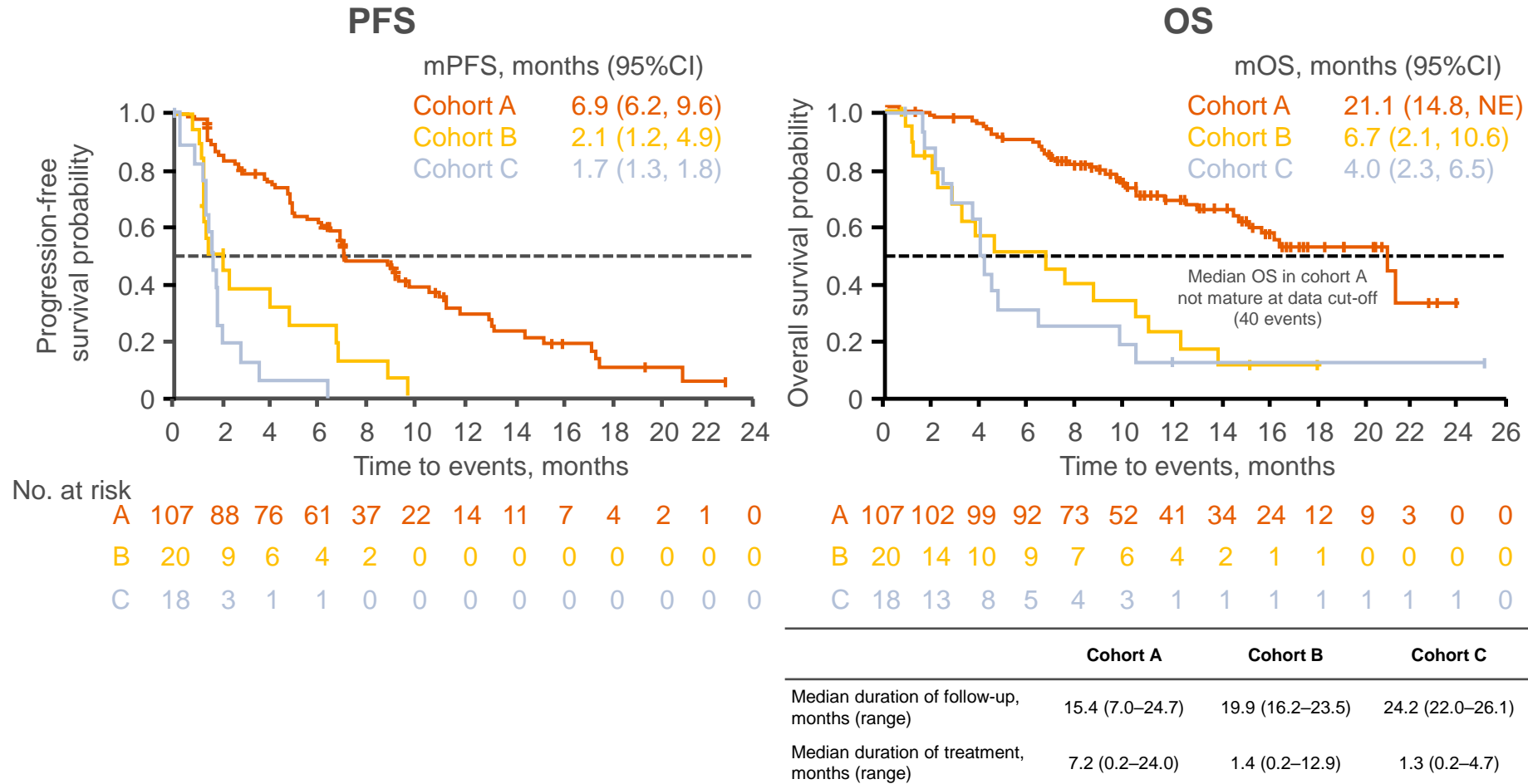
### Study objective

- To investigate the efficacy and safety of pemigatinib in patients with locally advanced or metastatic cholangiocarcinoma

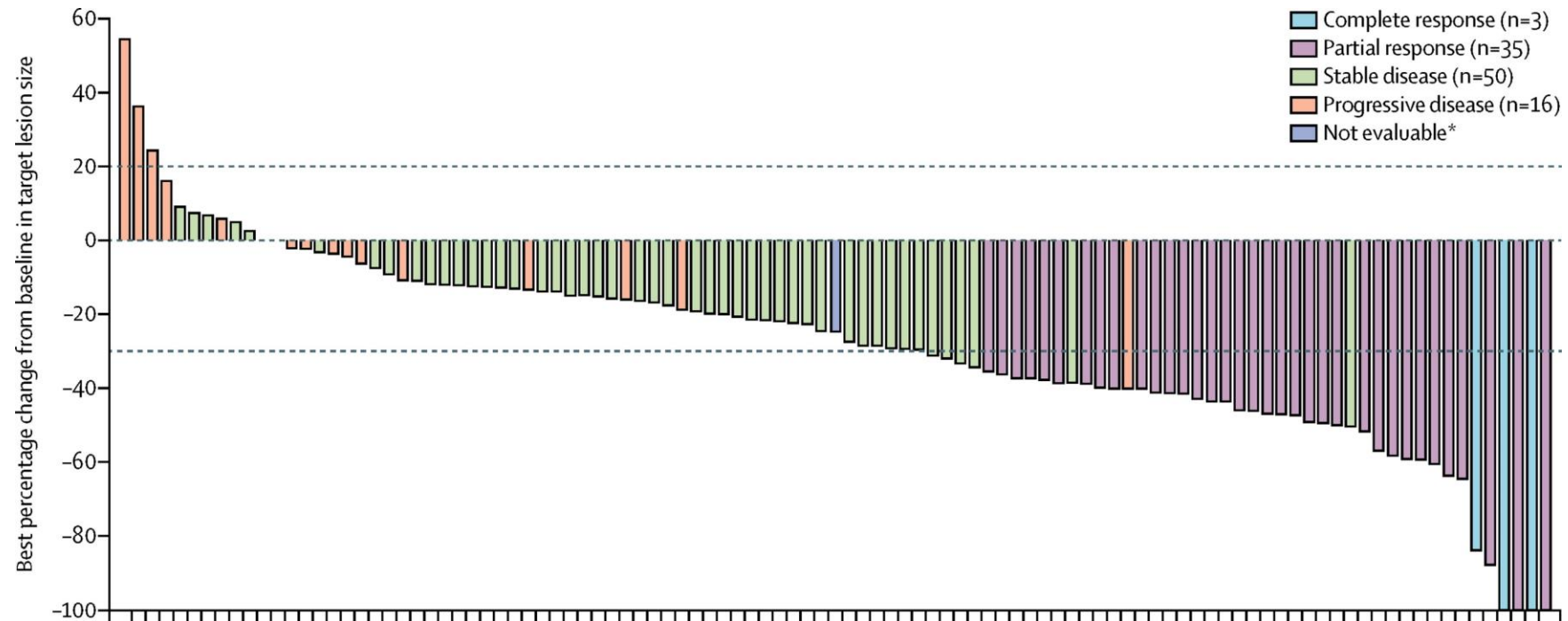


# FIGHT-202: A phase II study of pemigatinib in patients (pts) with previously treated locally advanced or metastatic cholangiocarcinoma (CCA)

## Key results (cont.)



## FIGHT-202: A phase II study of pemigatinib in patients (pts) with previously treated locally advanced or metastatic cholangiocarcinoma (CCA)



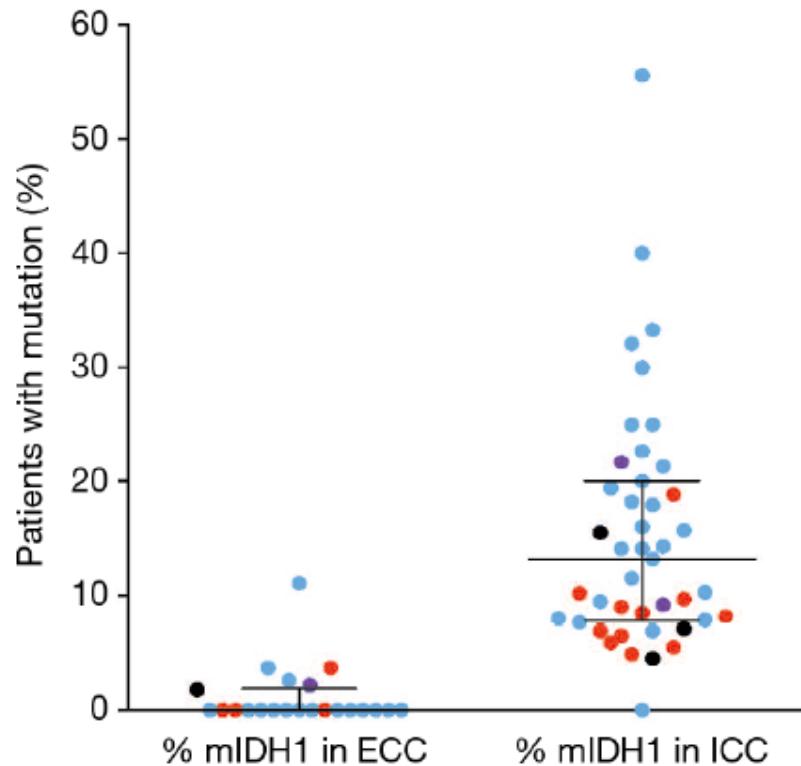
# FGFR2 Targeted Agents in Locally Advanced or Metastatic CCA Phase 2 Clinical Trials

Study	Drug	Key Inclusion Criteria	N	ORR	Median PFS	TRAEs	Most Frequent TRAEs
FIGHT-202 Abou-Alfa, ASCO® 2021 <sup>[a]</sup>	<b>Pemigatinib</b> (Selective FGFR1–3, reversible)	Cohort 1: <i>FGFR</i> fus/rea	108	37.0%	7.0	Grade 3 to 4: 64% <sup>[b]</sup>	Hyperphosphatemia (59%)
Javle, Lancet Gastro Hepatol 2021 <sup>[c]</sup>	<b>Infigratinib</b> (Selective FGFR1–3, reversible)	<i>FGFR</i> fus/rea	108	23.1%	7.3	Grade 3 to 4: 64%	Hyperphosphatemia (77%)
FOENIX-CCA2 Goyal, ASCO® 2020 <sup>[d]</sup>	<b>Futibatinib</b> (Selective FGFR1-4, irreversible)	<i>FGFR</i> fus/rea	103	41.7%	9	Grade ≥ 3: 57%	Hyperphosphatemia (85%)
FIDES-01 Droz Dit Busset, ESMO 2021 <sup>[e]</sup>	<b>Derazantinib</b> (TKI, reversible)	<i>FGFR</i> fus/rea	103	21.4%	8.0	Grade 3: 35%	Hyperphosphatemia (76%)

TRAE, treatment-related adverse event.

a. Abou-Alfa GK, et al. Presented at: ASCO® 2021; June 4-8, 2021. Presentation 4086; b. Abou-Alfa GK, et al. Lancet Oncol. 2020;21:671-684; c. Javle M, et al. Lancet Gastroenterol Hepatol. 2021;6:803-815; d. Goyal L, et al. Presented at: AACR 2021; April 9-14, 2021. Abstract CT010; e. Droz Dit Busset M, et al. ESMO 2021; September 16-21, 2021. Poster 47P.

# IDH1 mutations in cholangiocarcinoma: systematic review



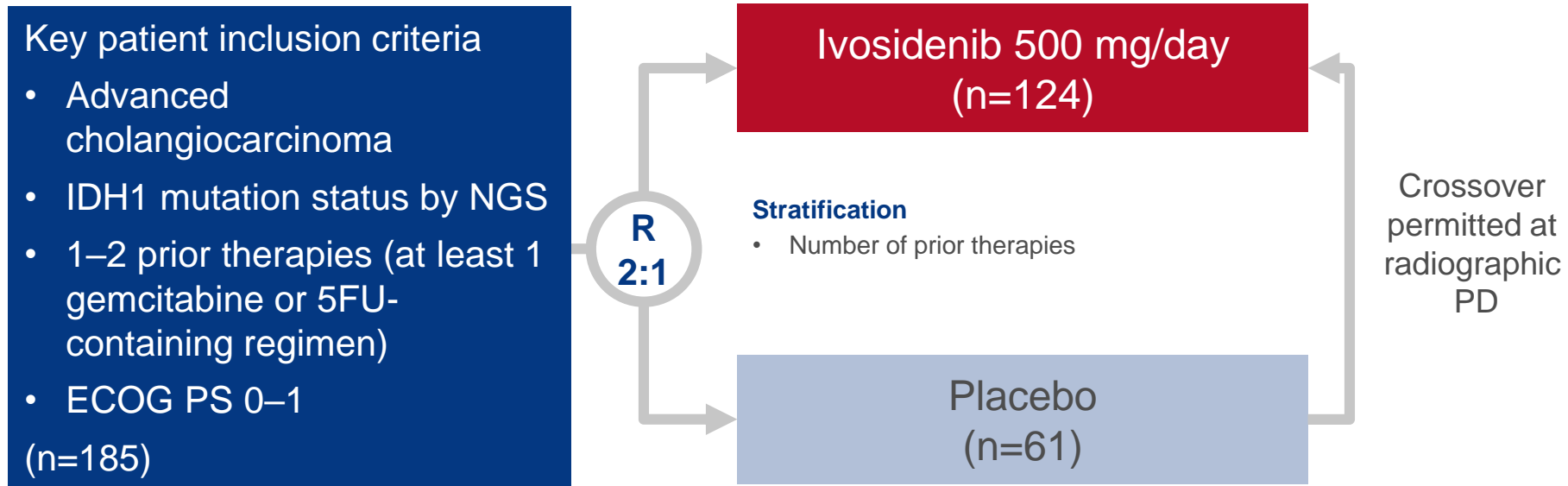
Isocitrate Dehydrogenase-1 (IDH1) mutations:

- 45 publications, n pts=5,393
- IDH1 mutation found in iCCA 13.1%; eHCC 0.8%
- Higher in non-Asian centres compared to Asian centres (16.5% vs. 8.8%; OR= 2.06)
- mIDH1 was not a prognostic factor (OS, PFS or TTP)

# ClarIDHy: A global, phase III, randomized, double-blind study of ivosidenib (IVO) vs placebo in patients with advanced cholangiocarcinoma (CC) with an isocitrate dehydrogenase 1 (IDH1) mutation

## Study objective

- To investigate the efficacy and safety of ivosidenib in patients with advanced cholangiocarcinoma and IDH1 mutation



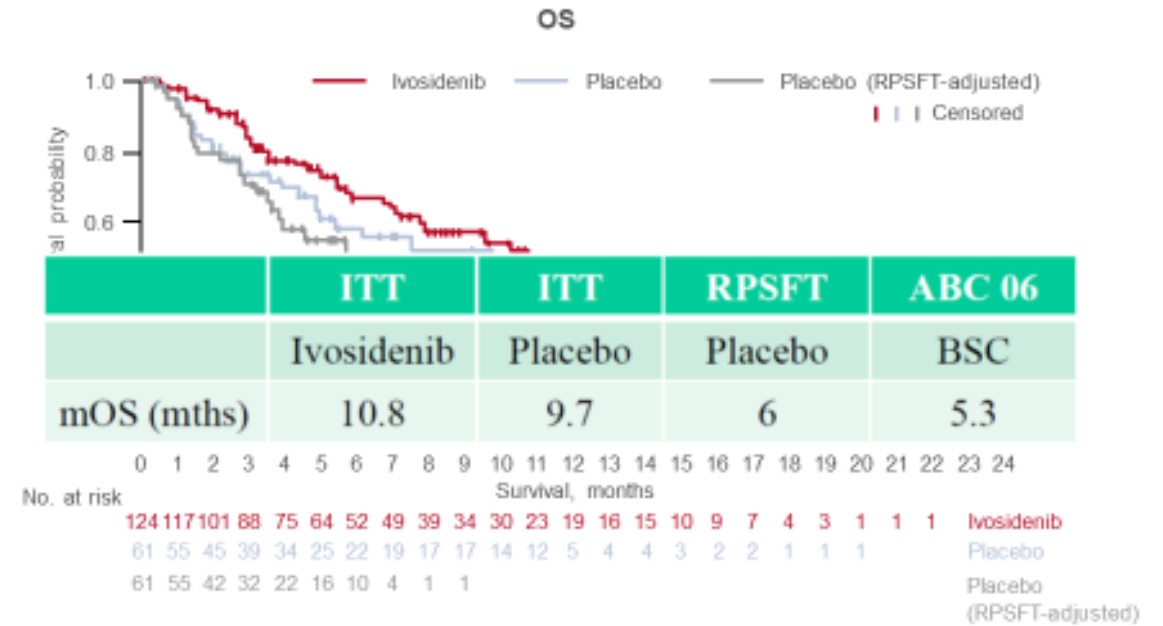
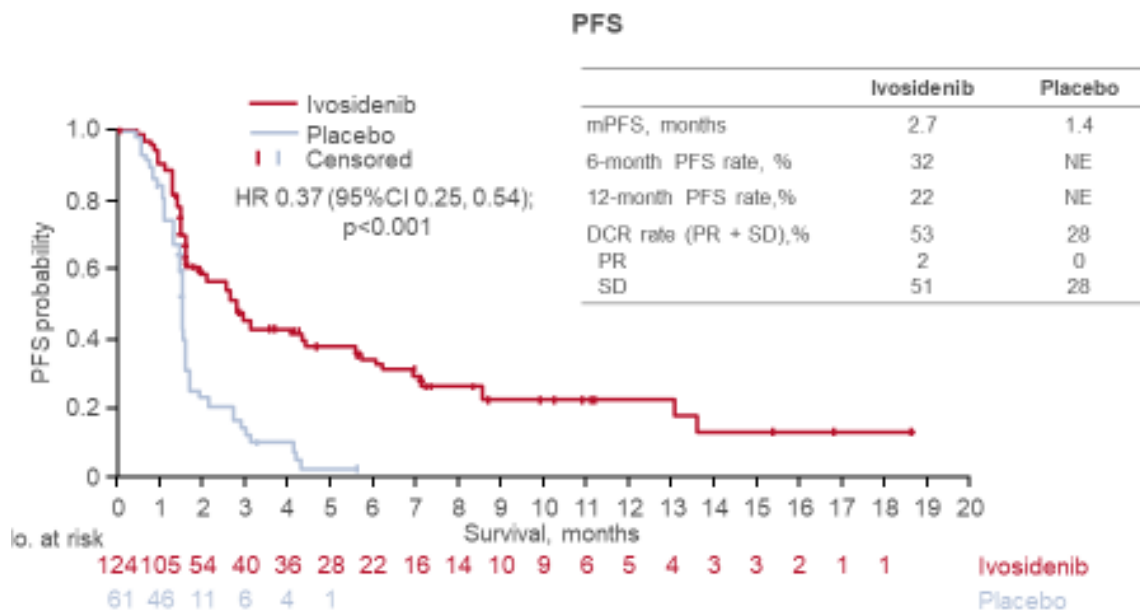
## PRIMARY ENDPOINT

- PFS

## SECONDARY ENDPOINTS

- OS, ORR, QoL, safety

# ClarIDHy: A global, phase III, randomized, double-blind study of ivosidenib (IVO) vs placebo in patients with advanced cholangiocarcinoma (CC) with an isocitrate dehydrogenase 1 (IDH1) mutation



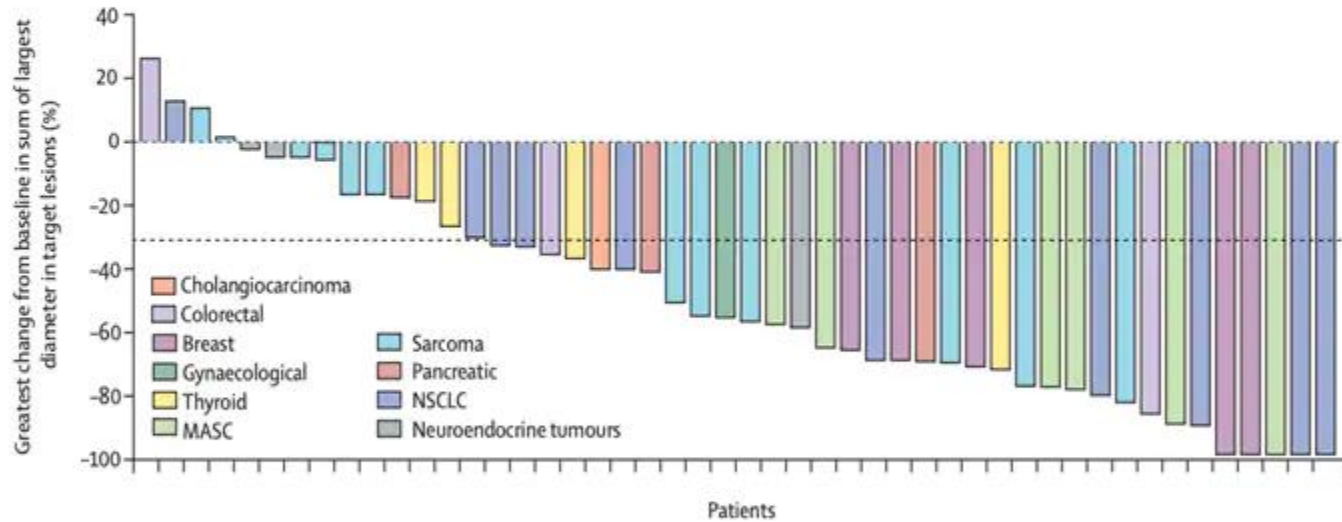


# NTRK Inhibitors in TRK Fusion Positive Solid Tumors

## Phase 1/2 Trials

NTRK fusions have been detected in ~ 3.5% of CCAs<sup>[a]</sup>

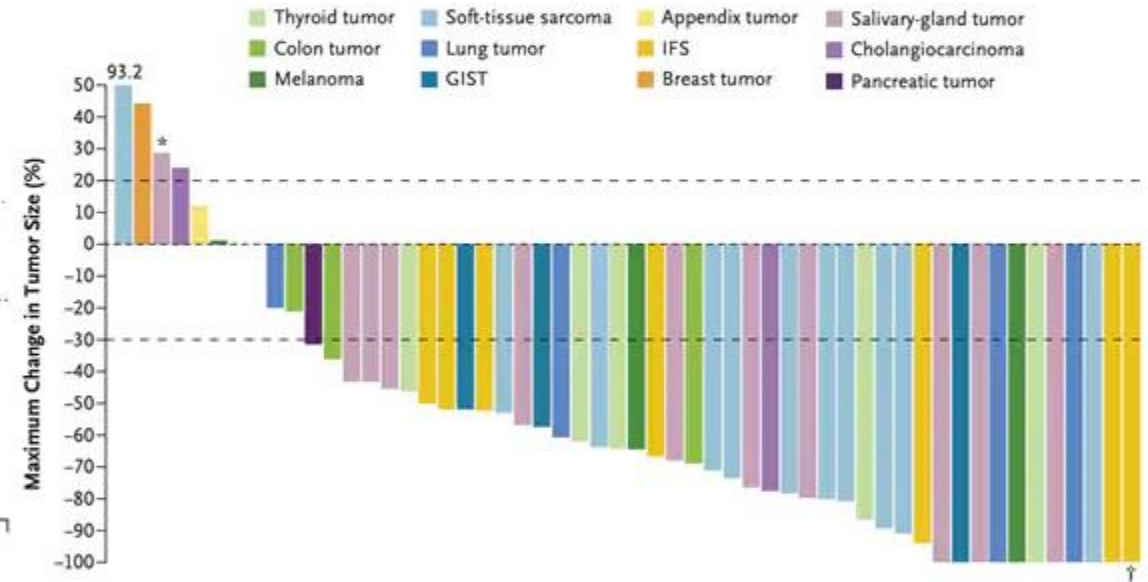
Maximum change in tumor size according to type with entrectinib<sup>[b]</sup>



### Adverse events:<sup>[b]</sup>

- Most common grade  $\geq 3$  AEs in the NTRK fusion-positive safety population: increased weight (10%; n = 7/68) and anemia (12%; n = 8/68)
- Most common serious TRAEs in the NTRK fusion-positive safety population: nervous system disorders (4%; n = 3/68)

Maximum change in tumor size according to type with larotrectinib<sup>[c]</sup>



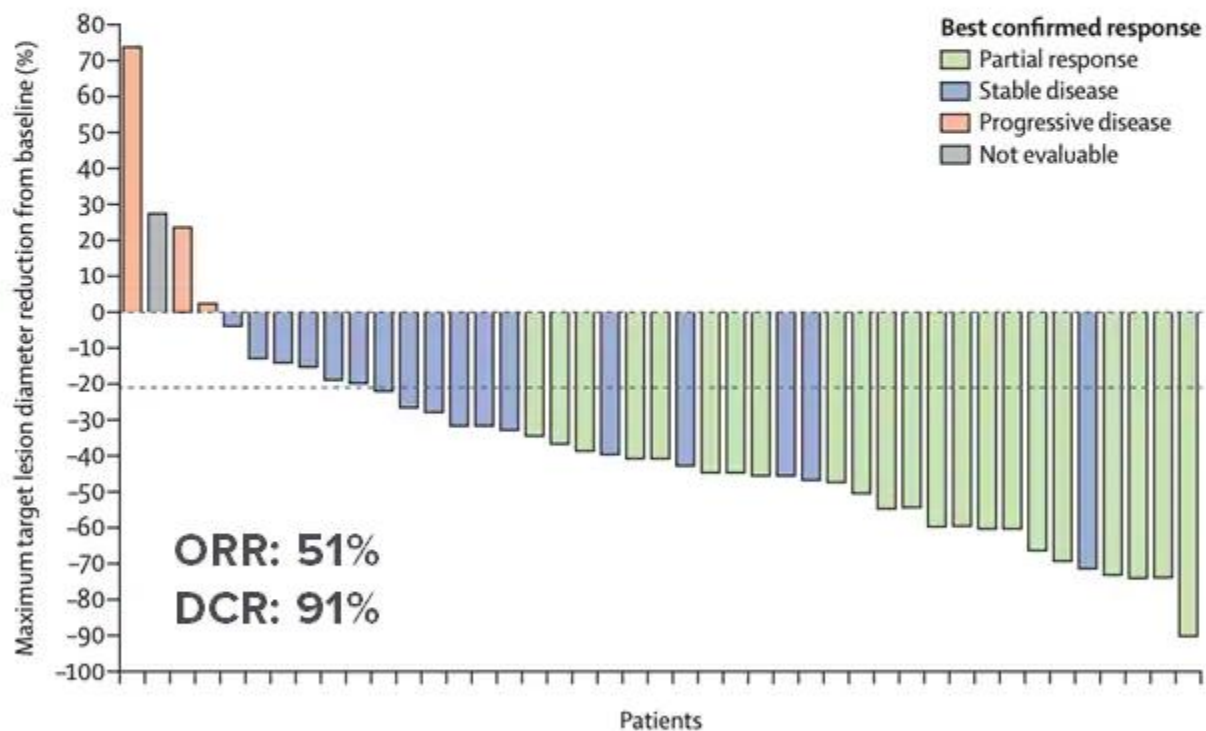
### Adverse events:<sup>[c]</sup>

- Most common AEs: anemia (11%), increase in alanine aminotransferase or aspartate aminotransferase level (7%), weight increase (7%), and decrease in neutrophil count (7%)
- No grade 4 or 5 events were considered by the investigators to be related to treatment

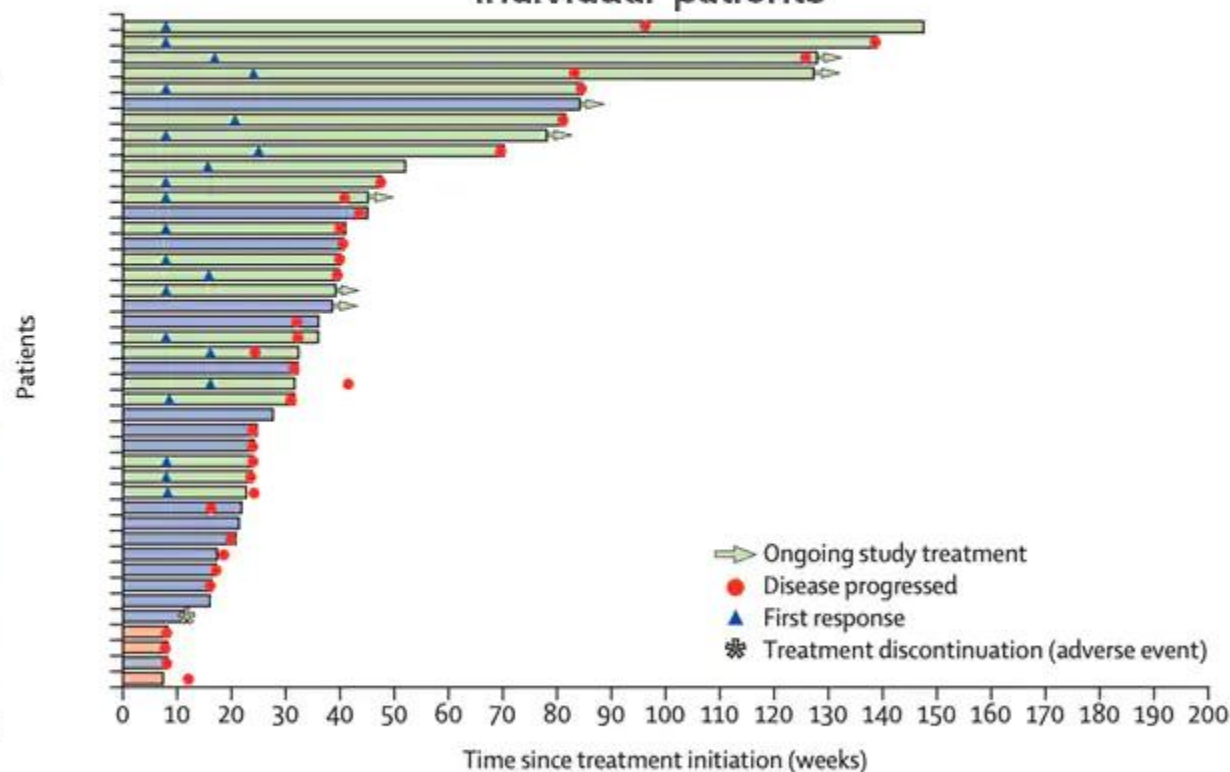
# Dabrafenib + Trametinib in *BRAF* V600E+ Biliary Tract Cancer *ROAR Trial*

Open-label, single-arm, multicenter phase 2 trial

Investigator-assessed maximum percent change from baseline in sum of the longest diameters of target lesion



Treatment duration and time to event for individual patients



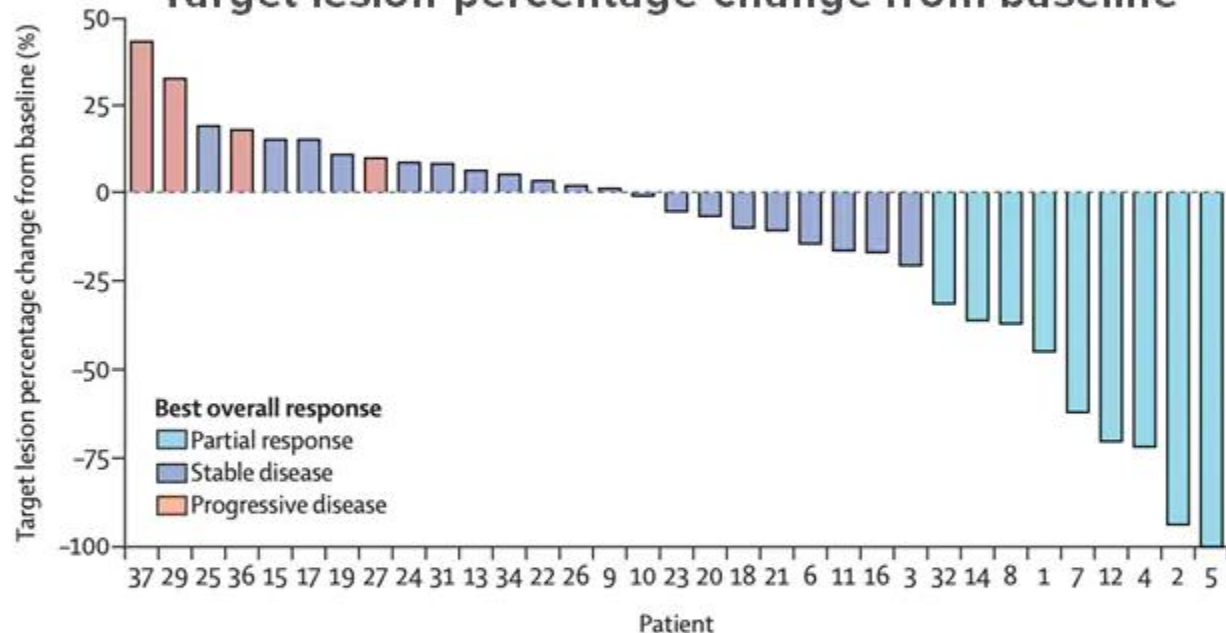
- Median PFS: 9 months (95% CI: 5, 10)
- Median OS: 14 months (95% CI: 10, 33)

- Most common any grade AE: pyrexia 67% (n = 29/43)
- Serious TRAEs: 19% (n = 8/43), the most frequent was pyrexia

# Trastuzumab + Pertuzumab in *HER2* Overexpressing Metastatic Biliary Tract Cancer: *MyPathway Trial*

Nonrandomized phase 2a multiple basket trial

Target lesion percentage change from baseline



## Adverse events:

- Grade 3 TRAEs: 8% (n = 3/39) including increased alanine aminotransferase, aspartate aminotransferase, blood alkaline phosphatase, and blood bilirubin
- Serious AEs: 26% (n = 10/39)

Clinical outcome summary

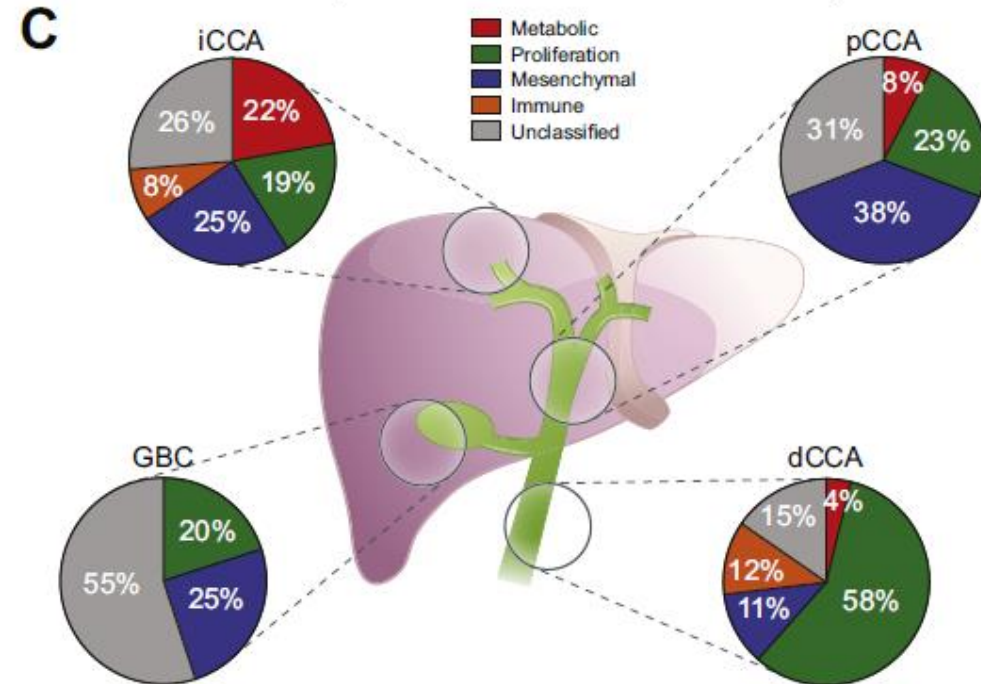
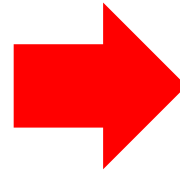
	Total (n = 39)
Best response	
Partial response	9 (23%)
Stable disease > 4 months	11 (28%)
Stable disease ≤ 4 months	9 (23%)
Progressive disease	10 (26%)
Objective response rate	9 (23%; 11 to 39)
Disease control rate	20 (51%; 35 to 68)
Duration of response, month	10.8 (0.7 to 25.4)
PFS, months	4 (1.8 to 5.7)
OS, months	10.9 (5.2 to 15.6)

# eCCA: transcriptome based classification

	Metabolic (18.7%)	Proliferation (22.5%)	Mesenchymal (47.3%)	Immune (11.5%)
Tumor and microenvironment molecular features	Bile-acid metabolism	<i>ERBB2</i> mutations /overexpression	EMT	High lymphocyte infiltration (CD8+)
	HDAC6 overexpression	mTOR signaling	Hedgehog signaling	PD1/PDL1 overexpression
	HNF4A upstream regulation	Cell cycle signaling	TNF- $\alpha$ signaling	IFN- $\gamma$ upstream regulation
	Hepatocyte-like phenotype	DNA repair signaling	TGF- $\beta$ 1 upstream regulation	
Clinical characteristics		MYC targets	High desmoplastic reaction	
		Papillary histology	Poor outcome (overall survival)	
		Precursor lesions (IPNB)		
Targeted therapies recommendation		dCCA		
		ERBB2 mAb/inhibitors		PD-1/PD-L1 inhibitors
Weak**	Nuclear receptor modulators and HDAC6 and SK2 inhibitors	mTOR, CDK4/6 and casein kinase II inhibitors	Hyaluronidase, hedgehog antagonists and TGF- $\beta$ inhibitors	

# eCCA molecular classifier

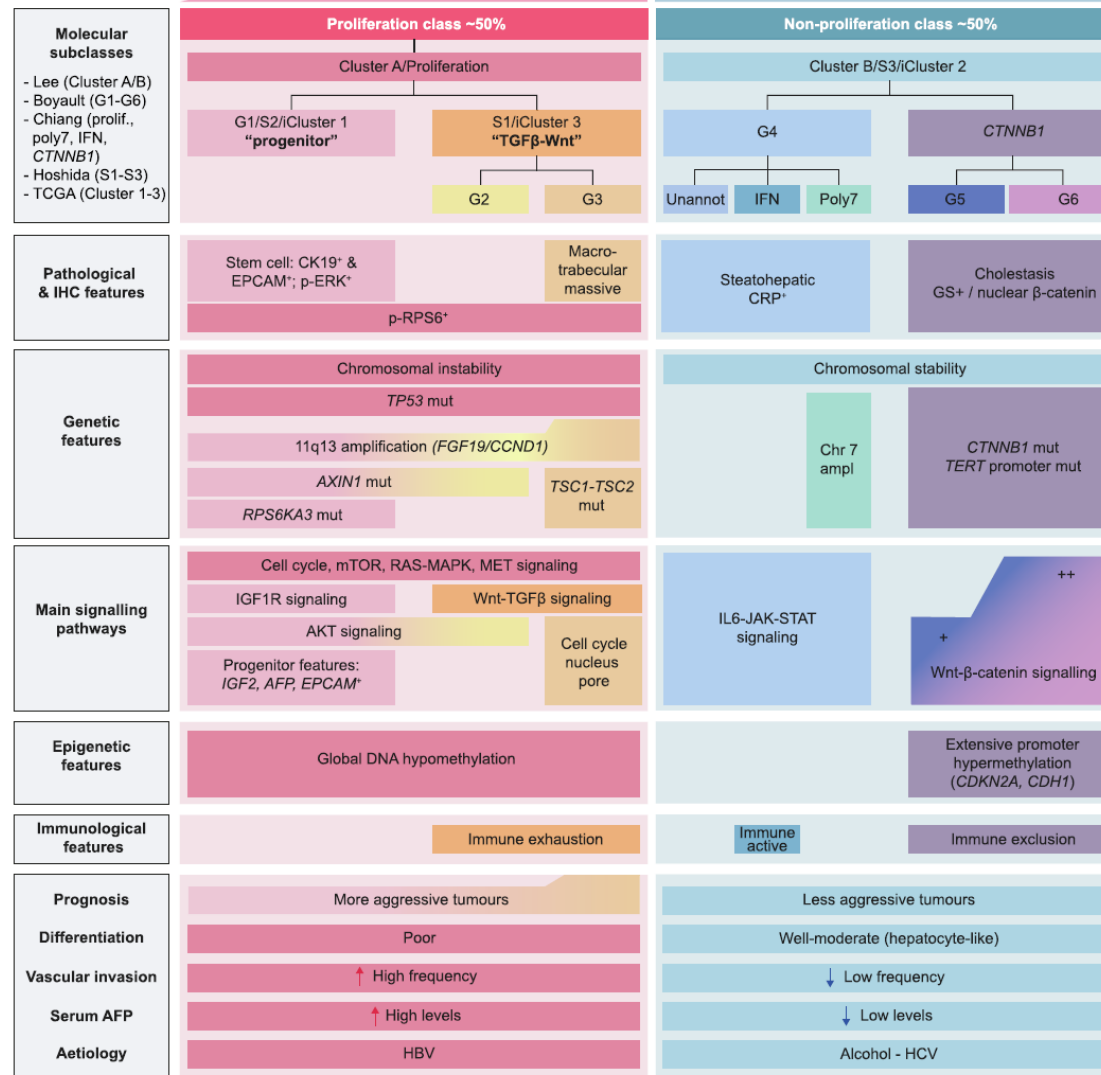
	Metabolic (18.7%)	Proliferation (22.5%)	Mesenchymal (47.3%)	Immune (11.5%)
Tumor and microenvironment molecular features	Bile-acid metabolism	<i>ERBB2</i> mutations /overexpression	EMT	High lymphocyte infiltration (CD8+)
	HDAC6 overexpression	mTOR signaling	Hedgehog signaling	PD1/PDL1 overexpression
	HNF4A upstream regulation	Cell cycle signaling	TNF- $\alpha$ signaling	IFN- $\gamma$ upstream regulation
	Hepatocyte-like phenotype	DNA repair signaling	TGF- $\beta$ 1 upstream regulation	
Clinical characteristics		MYC targets	High desmoplastic reaction	
		Papillary histology	Poor outcome (overall survival)	
		Precursor lesions (IPNB)		
Targeted therapies recommendation		dCCA		
		ERBB2 mAb/inhibitors		PD-1/PD-L1 inhibitors
	Strong* Weak**	Nuclear receptor modulators and HDAC6 and SK2 inhibitors	mTOR, CDK4/6 and casein kinase II inhibitors	Hyaluronidase, hedgehog antagonists and TGF- $\beta$ inhibitors



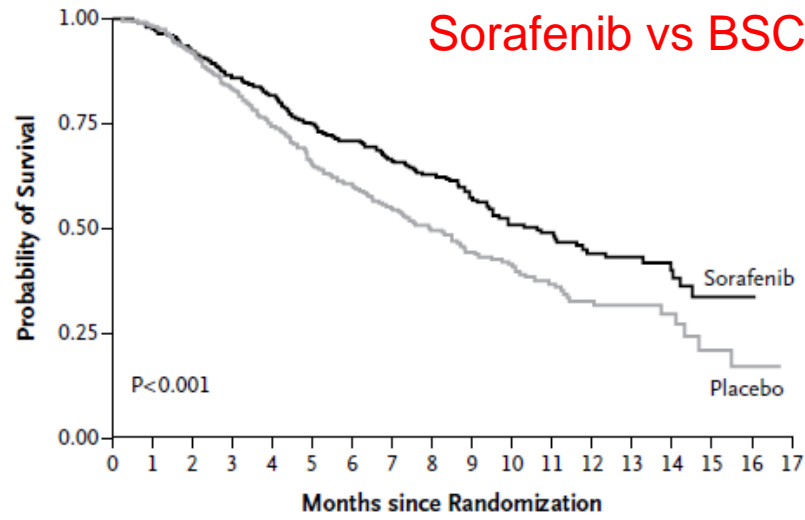
# Cholangiocarcinoma: conclusions

- CCA is heterogeneous according to location, histology, putative cell of origin and risk factors
- iCCA and eCCA are distinct molecular entities
- iCCA: molecular profiling may reveal actionable mutations in > 50% of patients, less in eCCA (FGFR2, IDH1/2, MMR, NTRK, BRAF, HER2)

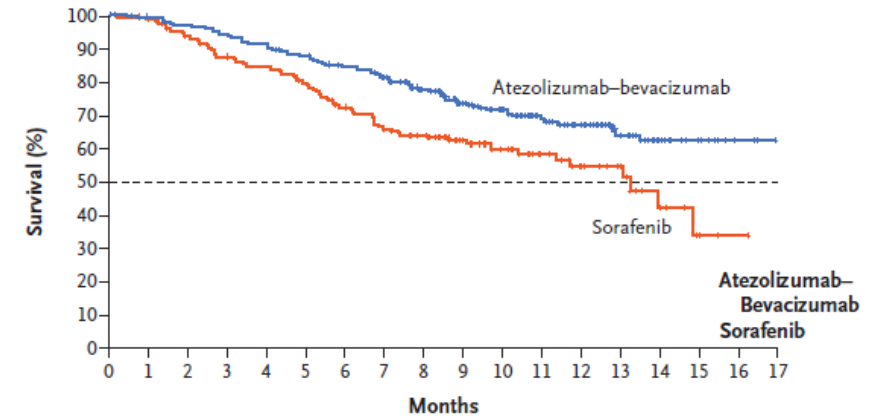
# HCC



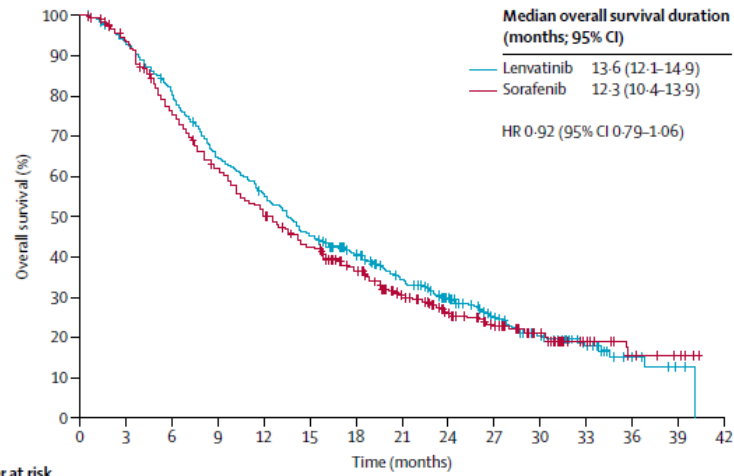
## Sorafenib vs BSC



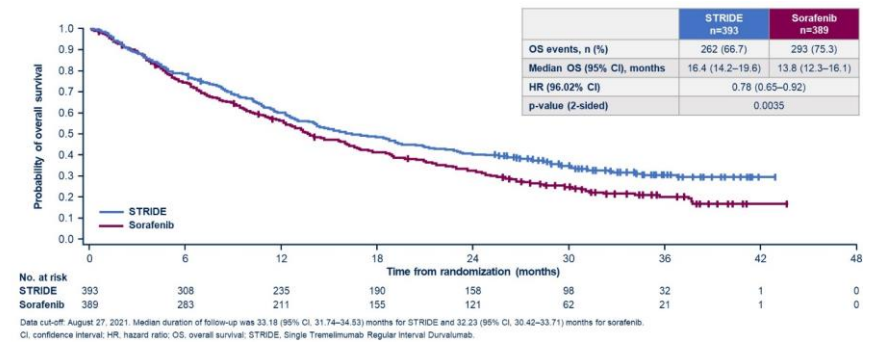
## Atezo-Beva vs Sorafenib



## Lenvatinib vs Sorafenib

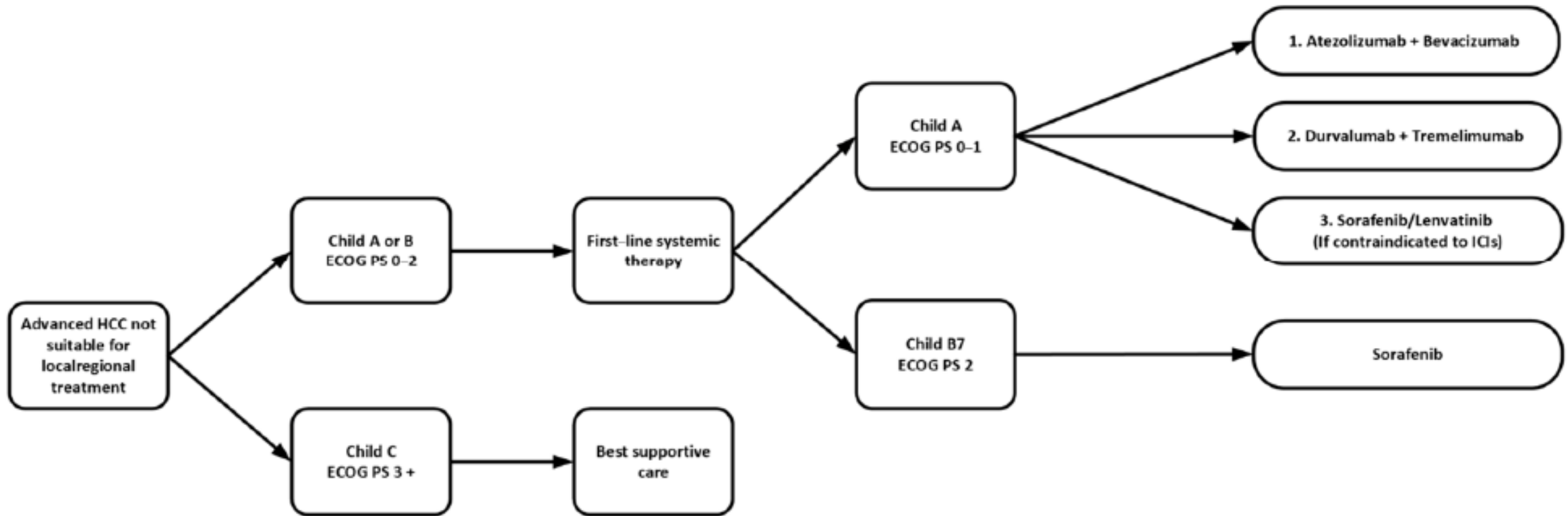


## STRIDE vs Sorafenib

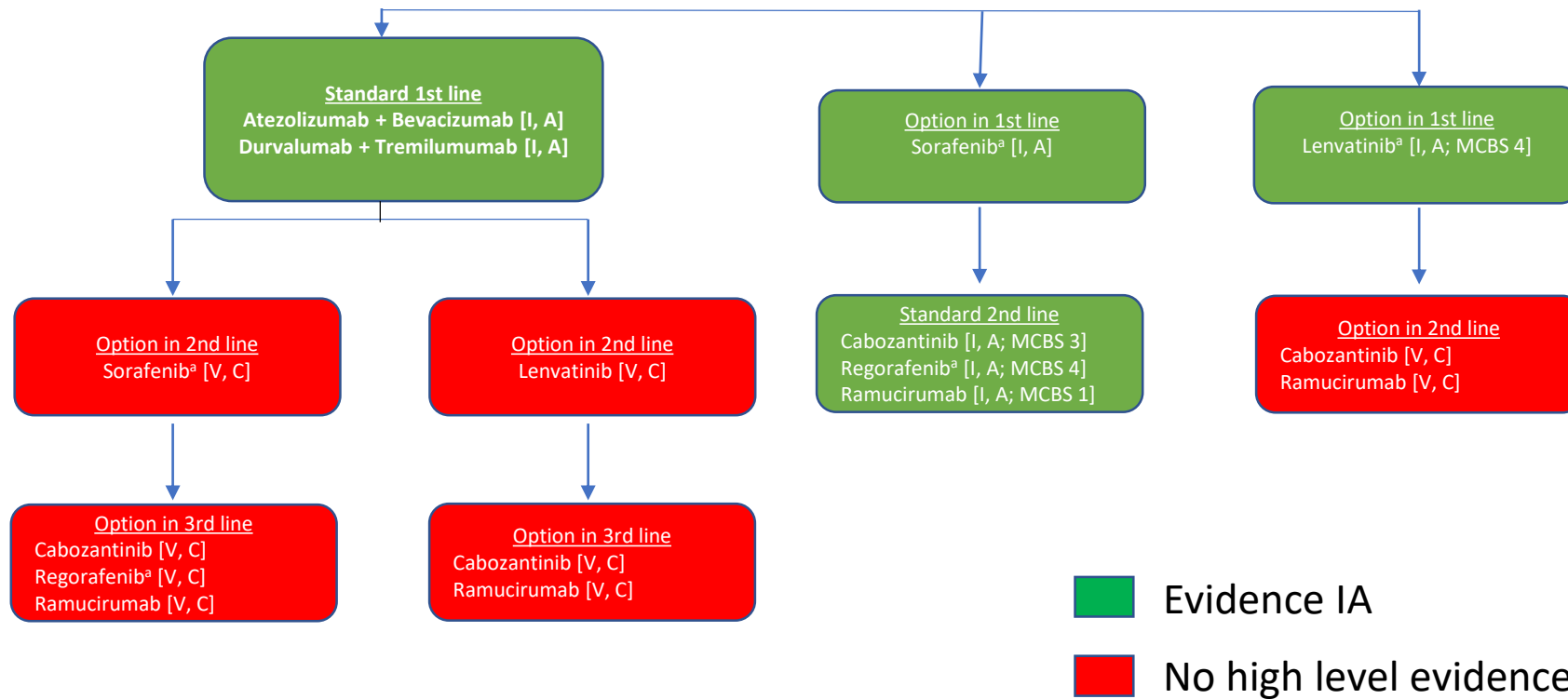




# HCC: therapeutic algorithm



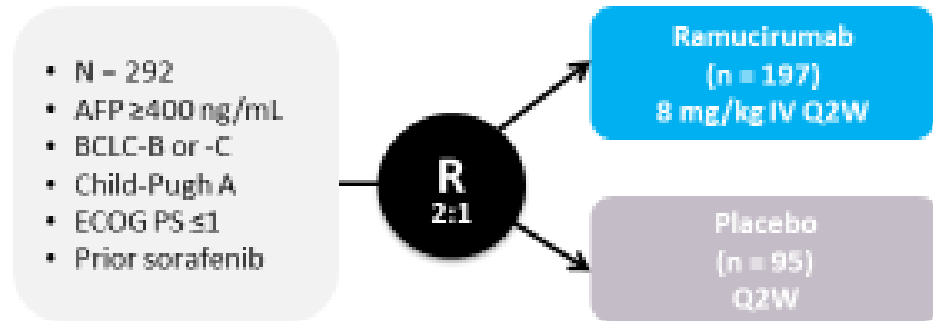
# HCC: therapeutic algorithm



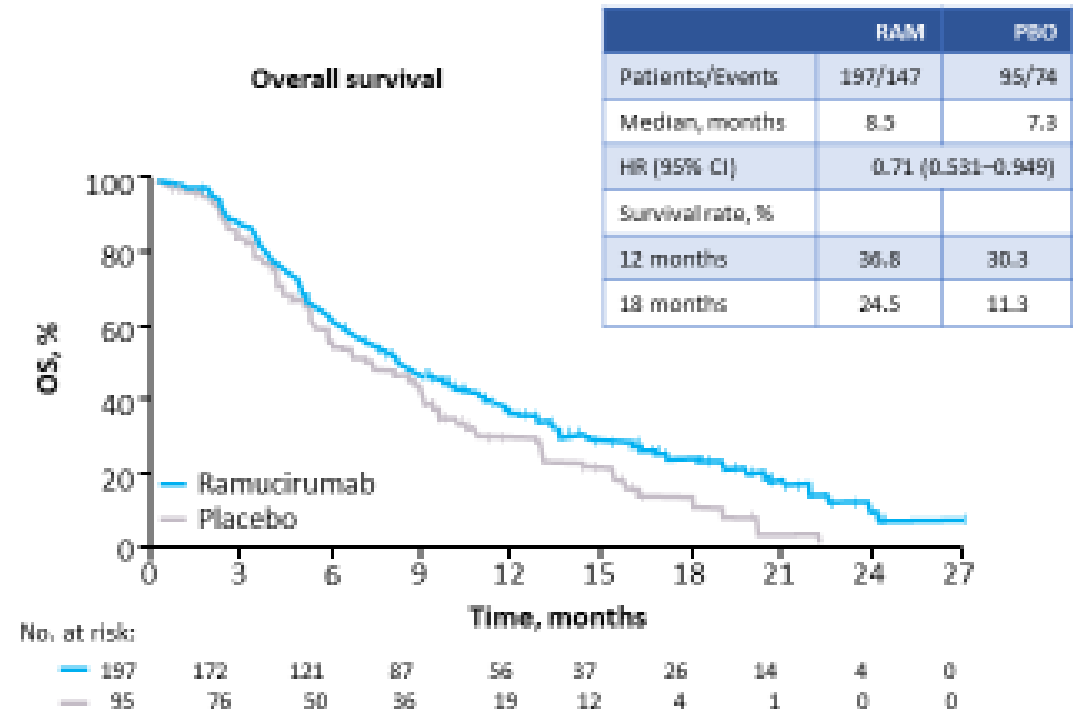
# Biomarkers for patient selection in HCC

- Immunostaining (PD1, PDL1, CD3, CD8): inconsistent results
- Genomic biomarker, TMB: more data needed
- *CTNNB1* mutations: associated with immune-excluded phenotype, but a subtype (enriched in CD8+ T cell and immune activation signatures) may respond to immune checkpoint blockade

# AFP as predictive biomarker for ramucirumab



- *Included patients with progression or intolerance to sorafenib*
- *Primary endpoint: OS*
- *Secondary endpoints: PFS, TTP, ORR*



# HCC: conclusions

- Several subclasses of HCC have been identified based on genetic alterations and transcriptomic dysregulation, that are closely related to risk factors, histology and prognosis
- No robust predictive biomarkers of response to targeted therapy and immunotherapy exist, except for AFP > 400 ng/ml for ramucirumab
- Active field of research



# Resistome

	MOC-1a	MOC-1b	MOC-2	MOC-3	MOC-4	MOC-5	MOC-6	MOC-7	MOC-8
MOC	↓ Drug uptake	↑ Drug export	↓ Intracellular proportion of active drug	Altered drug targets	↑ DNA repair	↓ Apoptosis	↑ Survival	Changes in tumour environment	↑ Epithelial to mesenchymal transition
Genes	SLC29A1 SLC28A1 SLC31A1 SLC22A1	ABCB1 ABCC1 ABCC3	UMPS TYMP UPP1 GSTP1	TYMS ESR1 ESR2 EGFR	ERCC1 RAD51 MSX2/3/6 MLH1 PMS2 RRM2B	MET FAS TP53 BAX BAK1	BCL2 ERK AKT1	LAM	HMGA1
Proteins	↓ ENT1 ↓ CNT1 ↓ CTR1 ↓ OCT1	↑ MDR1 ↑ MRP1 ↑ MRP3	↓ UMPS ↓ TYMP ↓ UPP1 ↑ GSTP1	↑ TYMS ↓ ERα ↓ ERβ ↓ EGFR	↑ ERCC1 ↑ RAD51 ↑ MutS ↑ MutLa ↑ p53R2	↓ HGFR ↓ FAS ↓ p53 ↓ BCL2L4 ↓ BCL2L7	↑ BCL-2 ↑ ERK ↑ AKT	↑ Laminin	↑ HMGA1
Drugs	Gemcitabine 5-FU Cisplatin TKIs	Many drugs	Gemcitabine 5-FU Cisplatin	5-FU Targeted drugs	Cisplatin Epirubicin Gemcitabine	Gemcitabine 5-FU	Cisplatin 5-FU Sorafenib	Doxorubicin Sorafenib	Gemcitabine