Deciphering the role of precision oncology in the treatment of UMOR biliary tract cancer in daily routine practice – retrospective FNTRUM analysis from the cancer centre Upper Austria Oberösterreich Doleschal B.¹, Piringer G.^{2,3,4}, Schreil G.⁵, Decker J.⁶, Aichberger K.⁶, Webersinke G.¹, Thaler J.⁴, Schmitt C.^{2,3},

¹Ordensklinikum Linz, Linz, Österreich, ²Kepler Universitätsklinikum, Linz, Österreich, ³Johannes Kepler Universität Linz, Medizinische Fakultät, Linz, Österreich, ⁴Klinikum Wels-Grieskirchen, Wels, Österreich, ⁵Klinikum Pyhrn-Eisenwurzen Klinikum, Steyr, Österreich, ⁶Klinikum Rohrbach, Rohrbach, Österreich

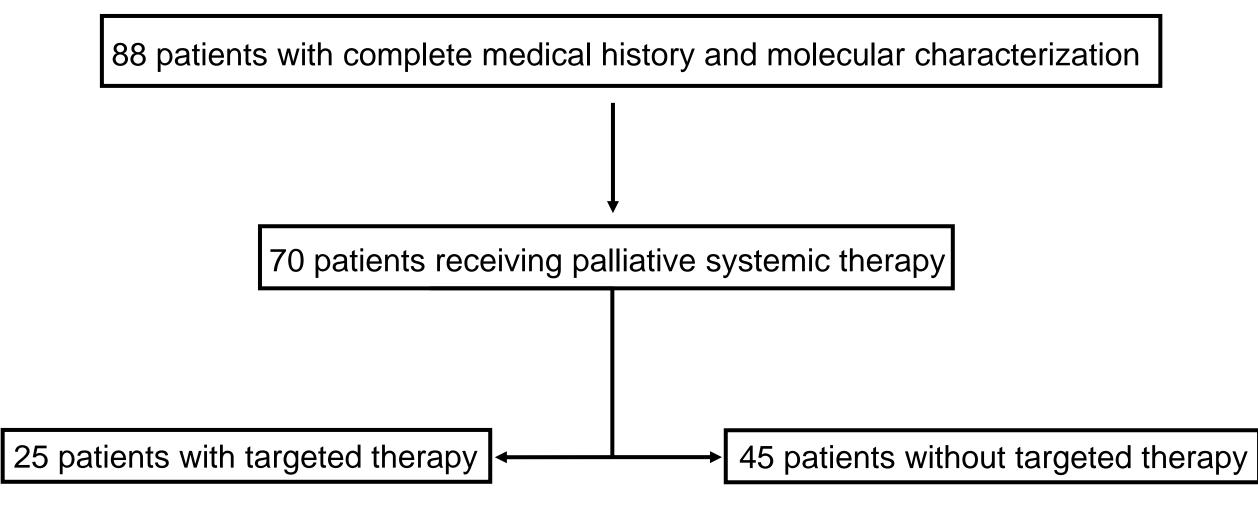
Introduction

The routine therapeutic landscape of metastatic CCC is still largely based on cytotoxic chemotherapy. This standard becomes increasingly challenged with the introduction of next generation sequencing (NGS) in routine practice and evolving trials of targeted therapies in CCC. However the value of comprehensive genetic profiling of CCC in actual routine clinical practice remains poorly characterized.

Methods

We performed a retrospective study at the clinical cancer centre of upper Austria (Tumorzentrum Oberösterreich, Kepler Uniklinikum Linz und Klinikum Wels-Grieskirchen) in 2018-2021. Tumor samples from 88 patients with CCC underwent comprehensive genetic profiling.TruSight Tumor 170 Assay (Illumina), Archer FusionPlex Panel (ArcherDX), Oncomine Focus Assay (Thermo Fisher Scientific) were used vor NGS analysis. Furthermore MSI status was determined by custom made Multiplex PCR-Based Methods. Immunhistochemistry (IHC) collected data on Her2neu and PDL-1expression.

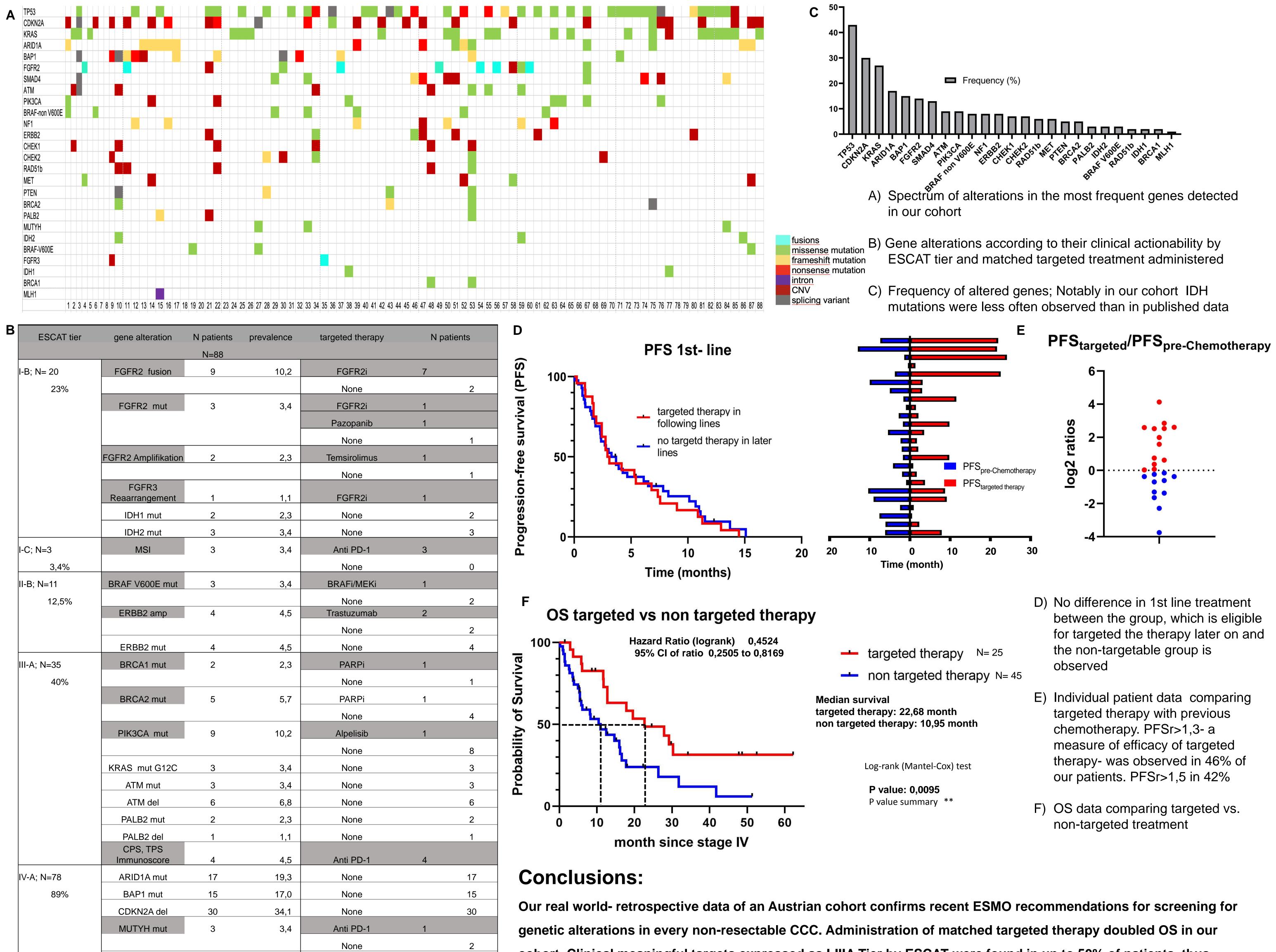
Trial flowchart



Patient characteristics & results

	Targeted therapy (n=25) N (%)	Non-Targeted therapy (n=45) N (%) 68y	
Age at diagnosis, median	60y		
Gender			
Male	16 (64%)	28 (62%)	
Female	9 (36%)	17 (38%)	
Localization			
eCC	11 (44%)	20 (44%)	
iCC	13 (52%)	22 (49%)	
GC	1 (4%)	3 (7%)	
Stage			
-	14 (56%)	23 (51%)	
IV	11 (44%)	22 (49%)	
Primary resection	9 (36%)	14 (31%)	
1st line platinum therapy	20 (80%)	39 (86%)	
Median lines of therapy	3	2	
Initiation of targeted therapy			
2nd line	14 (56%)		
3rd line	9 (36%)		
4th line	1 (4%)		
5th line	1 (4%)		

Petzer A.¹, Rumpold H.¹



ESCAT tier	gene alteration	N patients N=88	prevalence	targeted therapy	N
-B; N= 20	FGFR2 fusion	9	10,2	FGFR2i	7
23%				None	
	FGFR2 mut	3	3,4	FGFR2i	1
				Pazopanib	1
				None	
	FGFR2 Amplifikation	2	2,3	Temsirolimus	1
				None	
	FGFR3 Reaarrangement	1	1,1	FGFR2i	1
	IDH1 mut	2	2,3	None	•
	IDH2 mut	3	3,4	None	
-C; N=3	MSI	3	3,4	Anti PD-1	3
3,4%		C	0,1	None	Ū
II-B; N=11 12,5%	BRAF V600E mut	3	3,4	BRAFi/MEKi	1
				None	
	ERBB2 amp	4	4,5	Trastuzumab	2
				None	
	ERBB2 mut	4	4,5	None	
III-A; N=35	BRCA1 mut	2	2,3	PARPi	1
40%				None	
	BRCA2 mut	5	5,7	PARPi	1
				None	
	PIK3CA mut	9	10,2	Alpelisib	1
				None	
	KRAS mut G12C	3	3,4	None	
	ATM mut	3	3,4	None	
	ATM del	6	6,8	None	
	PALB2 mut	2	2,3	None	
	PALB2 del CPS, TPS	1	1,1	None	
	Immunoscore	4	4,5	Anti PD-1	4
V-A; N=78	ARID1A mut	17	19,3	None	
89%	BAP1 mut	15	17,0	None	
	CDKN2A del	30	34,1	None	
	MUTYH mut	3	3,4	Anti PD-1	1
				None	
	RAD51b del	6	6,8	None	
	CHEK1 del	7	8,0	None	

reinforcing the routine application of molecular tumor boards.

- D) No difference in 1st line treatment between the group, which is eligible for targeted the therapy later on and the non-targetable group is
- E) Individual patient data comparing targeted therapy with previous chemotherapy. PFSr>1,3-a measure of efficacy of targeted therapy- was observed in 46% of our patients. PFSr>1,5 in 42%
- F) OS data comparing targeted vs.

cohort. Clinical meaningful targets expressed as I-IIIA Tier by ESCAT were found in up to 50% of patients, thus