CHOL - Cholangiocarcinoma

Subtype		Genomic/Pathway	
	Biology & Expression	Alterations	Clinical Features
Mesenchymal &	Strong EMT and Wnt/	• Enrichment of	Poorer prognosis
Immunosuppressive	β-catenin activation	immune-evasion programs;	(median OS ~376 days)
(C1)	(tSNAI1, IL1B)	overexpression of	<ul> <li>High T-cell exclusion</li> </ul>
	<ul> <li>High infiltration of</li> </ul>	checkpoint ligands and	score
	M2-like TAMs and	co-inhibitors	<ul> <li>Candidate for</li> </ul>
	Tregs; upregulation of		checkpoint blockade
	immune-checkpoint		
	genes (e.g. CTLA-4,		
	PD-L1)		
Metabolic &	Upregulated	Activation of	Better prognosis
Proliferative (C2)	fatty-acid, bile-acid and	PI3K-AKT-mTOR and	(median OS ~565 days)
	xenobiotic metabolism	mTORC1 pathways; high	• Higher CD8 <sup>+</sup> T-cell
	(peroxisome genes,	proliferation signature	abundance
	ADH1A, CYP3A4)		<ul> <li>May benefit from</li> </ul>
	<ul> <li>Elevated MYC/E2F</li> </ul>		chemo-/radiotherapy
	targets and G2M		
	checkpoint activity;		
	ferroptosis-resistant		
	profile		