

## **Supplementary Figures**

**Establishment and characterization of 38 novel patient-derived primary cancer cell lines using multi-region sampling revealing intra-tumor heterogeneity of gallbladder carcinoma**

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**Supplementary Figure 1. The morphology of 38 PDPCs derived from 7 GBC patients**

**Supplementary Figure 2. Sample clustering with SNPs**

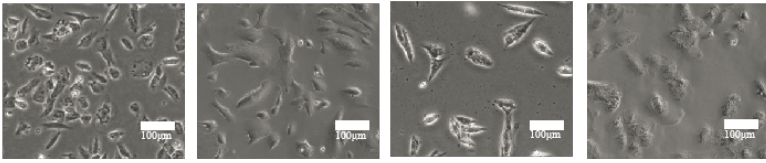
**Supplementary Figure 3. Gene Ontology (GO) enrichment analysis with DEGs.**

**Supplementary Figure 4. Scatterplot of three MHC class I genes against CIITA.**

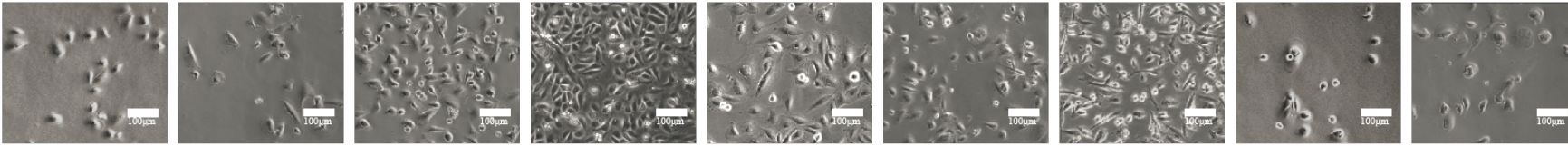
**Supplementary Figure 5. ITH of mutations in three patients with cholangiocarcinoma.**

## Supplementary Figure 1

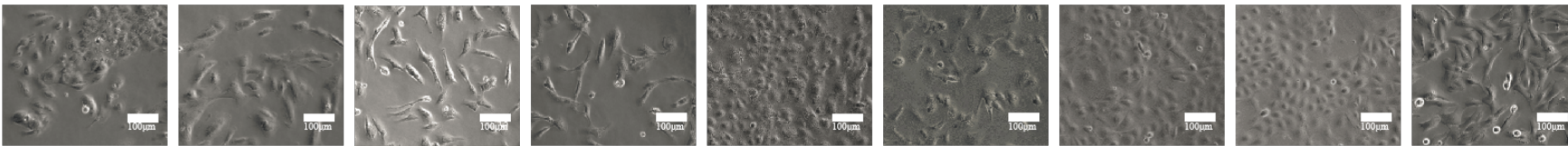
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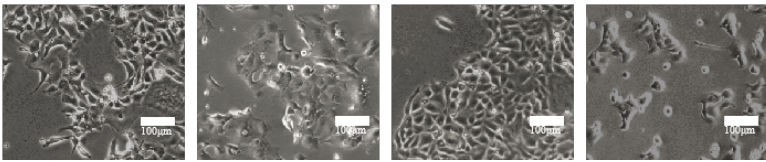
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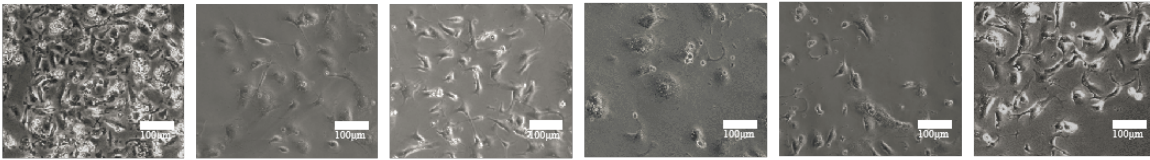
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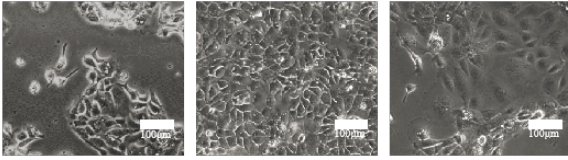
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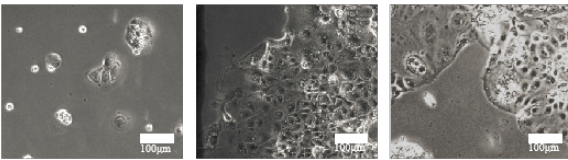
JXQ-3D-1436R1 JXQ-3D-1436R2 JXQ-3D-1436R3 JXQ-3D-1436R4 JXQ-3D-1436R5 JXQ-3D-1436R6



JXQ-3D-4160R1 JXQ-3D-4160R2 JXQ-3D-4160R3

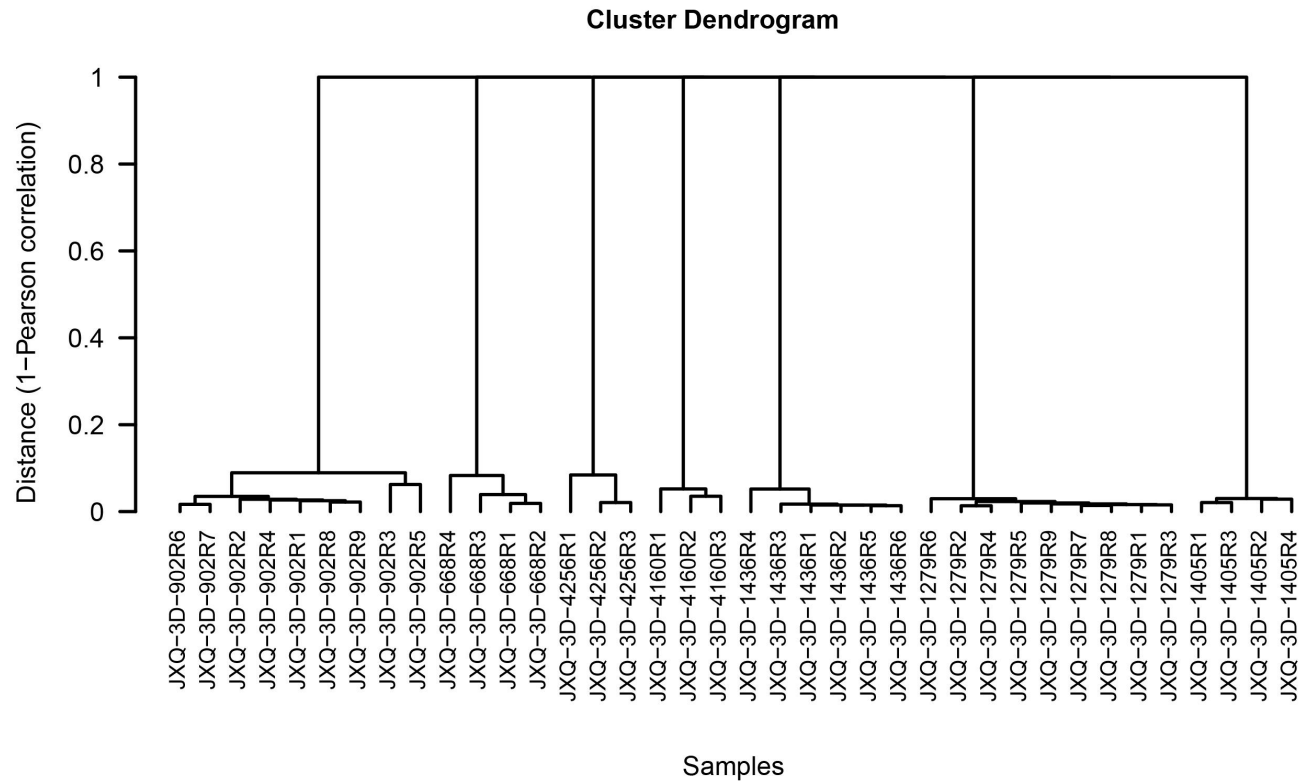


JXQ-3D-4256R1 JXQ-3D-4256R2 JXQ-3D-4256R3



**Supplementary Figure 1. The morphology of 38 PDPCs derived from 7 GBC patients**

## Supplementary Figure 2

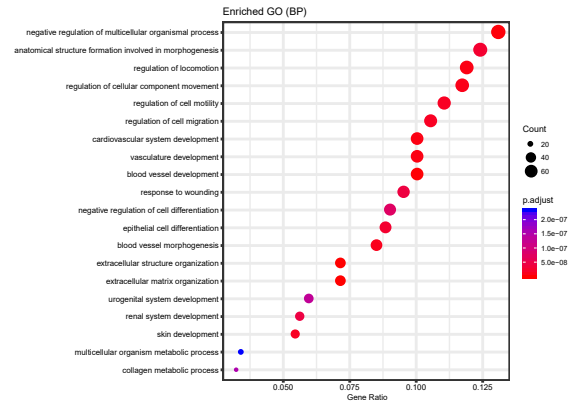


### Supplementary Figure 2 . Sample clustering with SNPs

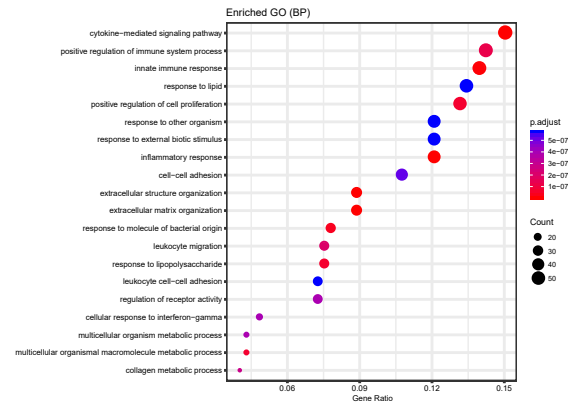
Samples were clustered based on the presence/absence of given SNPs. Samples from the same patient were clustered together which confirmed the origin of these PDC samples.

# Supplementary Figure 3

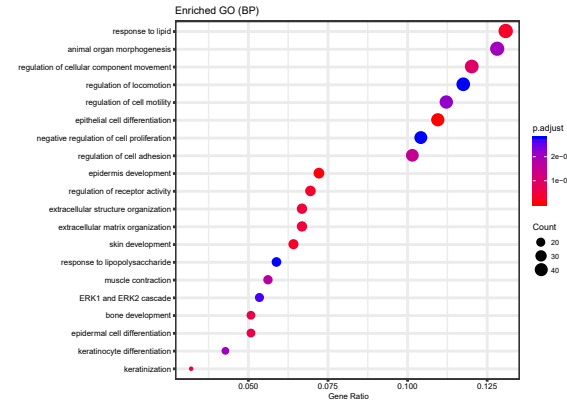
Patient 668



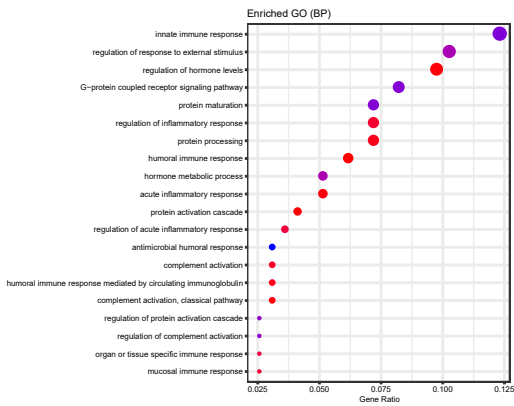
Patient 902



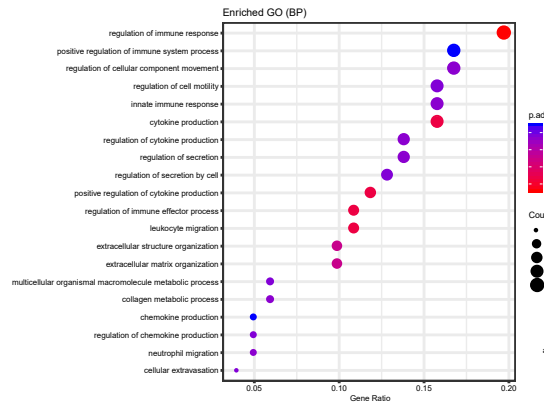
Patient 1279



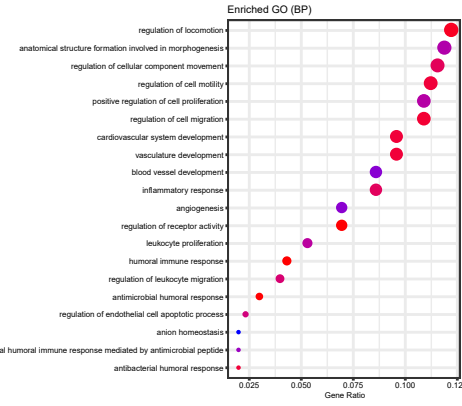
Patient 1405



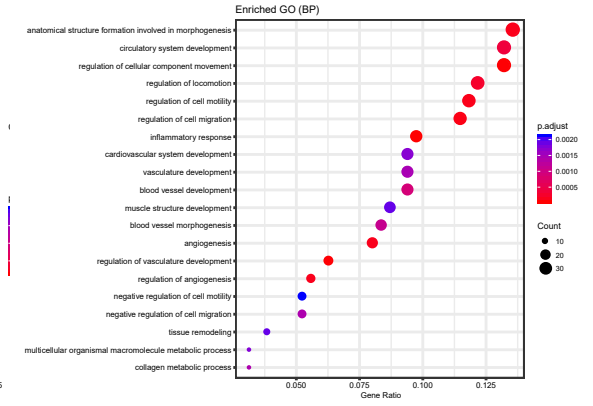
Patient 1436



Patient 4160

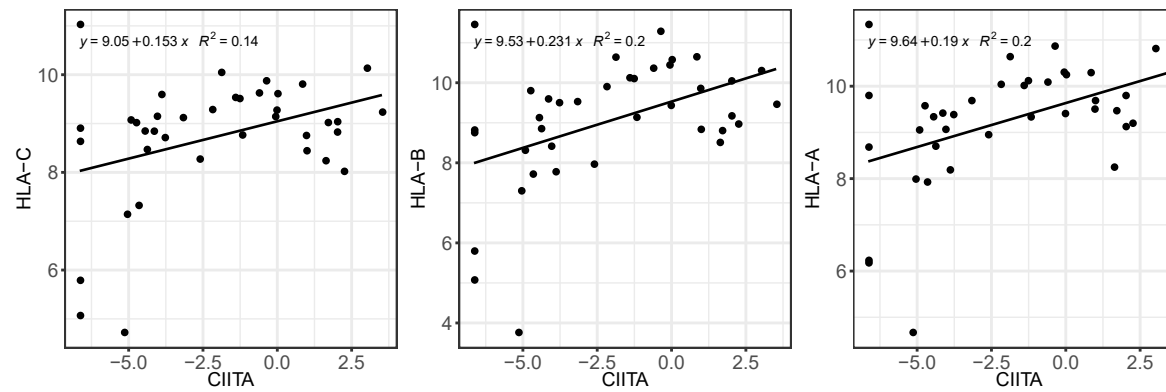


Patient 4256



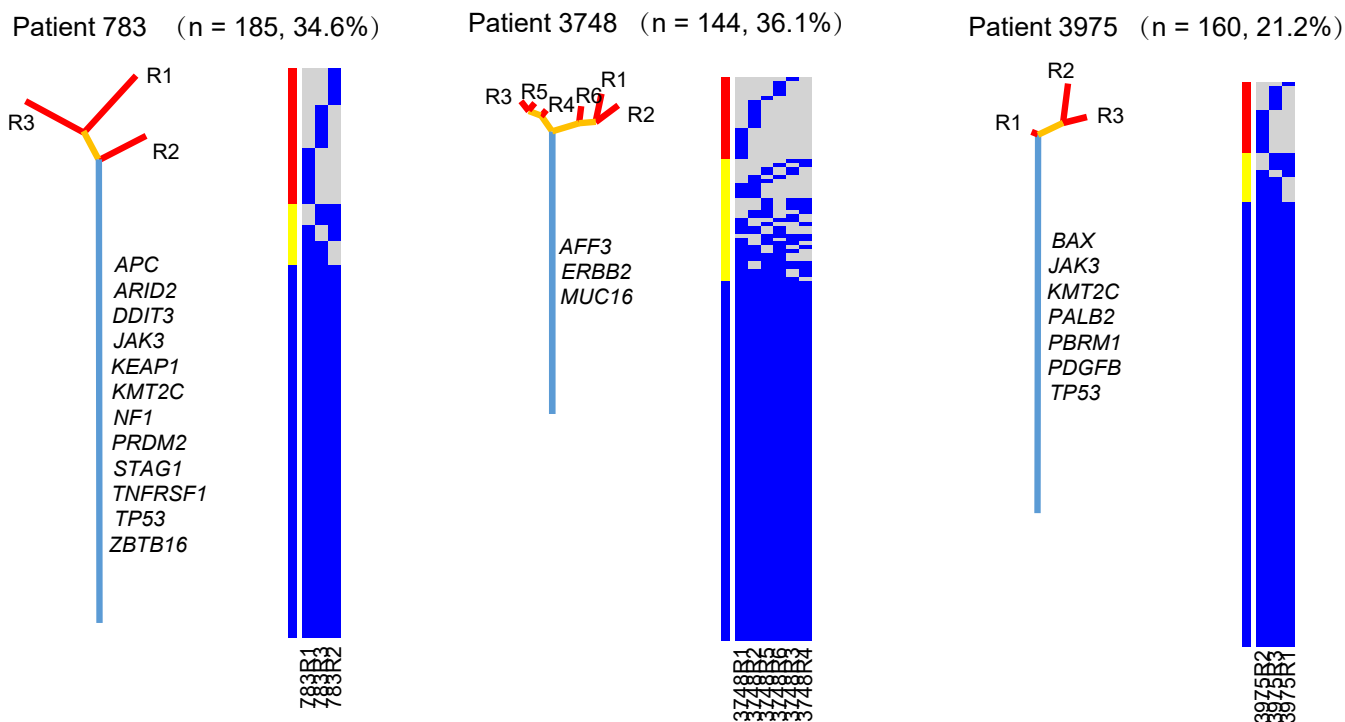
**Supplementary Figure 3. Gene Ontology (GO) enrichment analysis with DEGs.**  
Each panel showed the enriched GO terms of biological processes for each GBC patient.

## Supplementary Figure 4



**Supplementary Figure 4. Scatterplot of three MHC class I genes against CIITA.**  
A linear regression formula and pearson correlation were listed on the top left of each panel.

## Supplementary Figure 5



### Supplementary Figure 5. ITH of mutations in three patients with cholangiocarcinoma.

Phylogenetic trees were generated from somatic mutations using the parsimony ratchet method, and the branch lengths were scaled in proportion to the number of variants (see Methods). Heat map nearby each tree showed the occurrence (presence in blue and absence in grey) of each mutation in each PDC. Genes with putative driver mutations were displayed beside the trunk branch of each individual. The number of mutations and the ITH score were listed on the top of each individual panel. Blue: trunk mutations, yellow: shared mutations, red: private mutations.