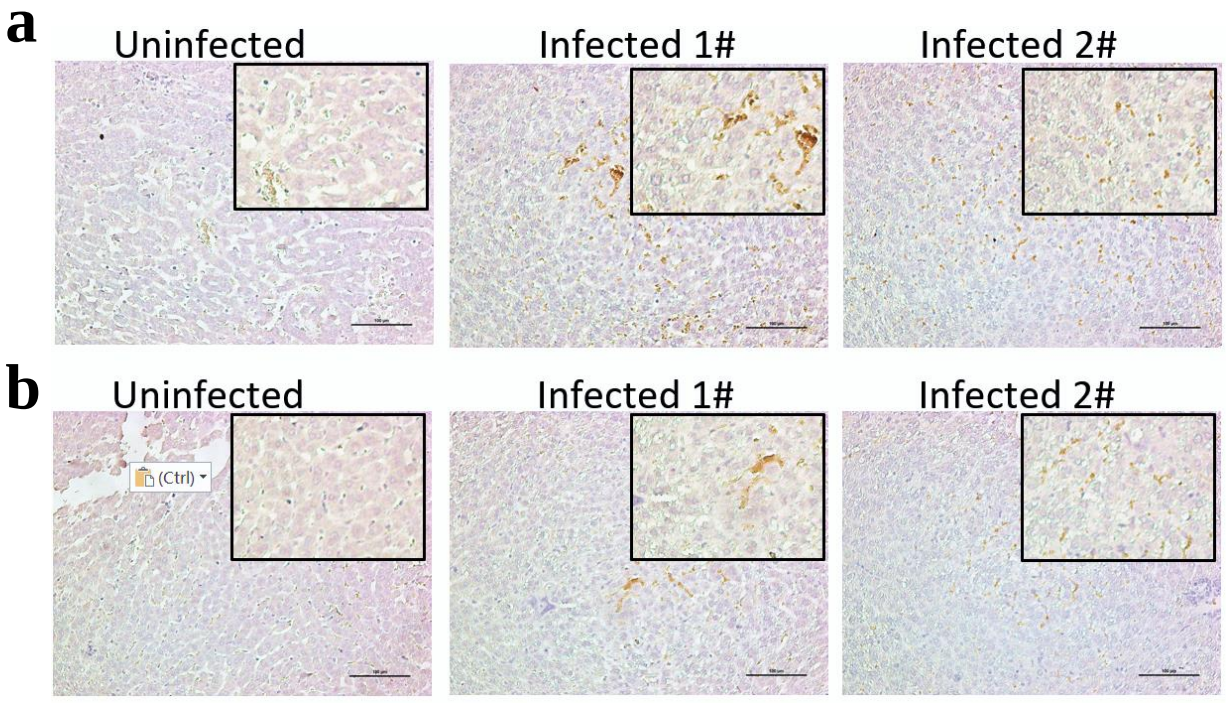
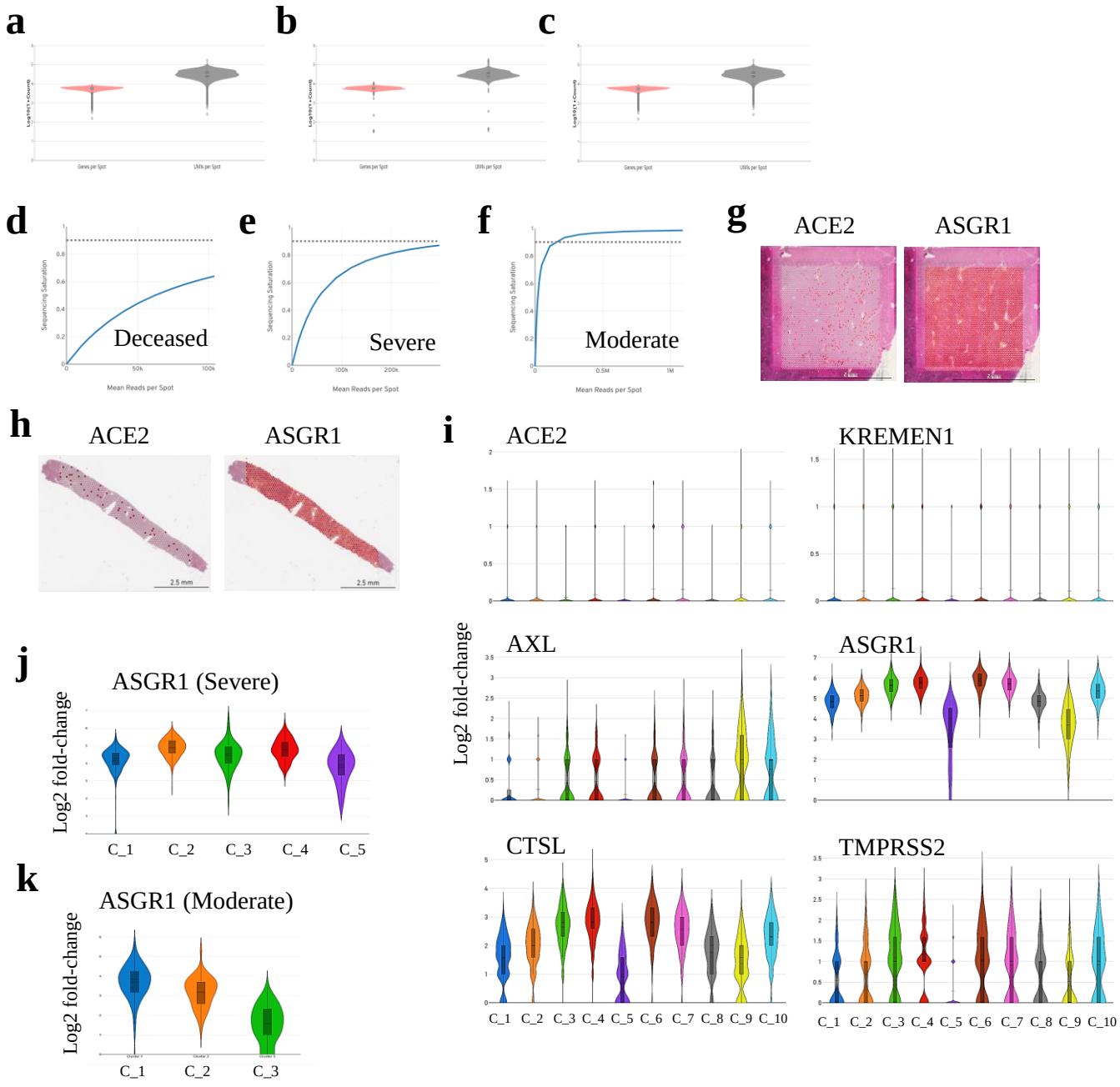
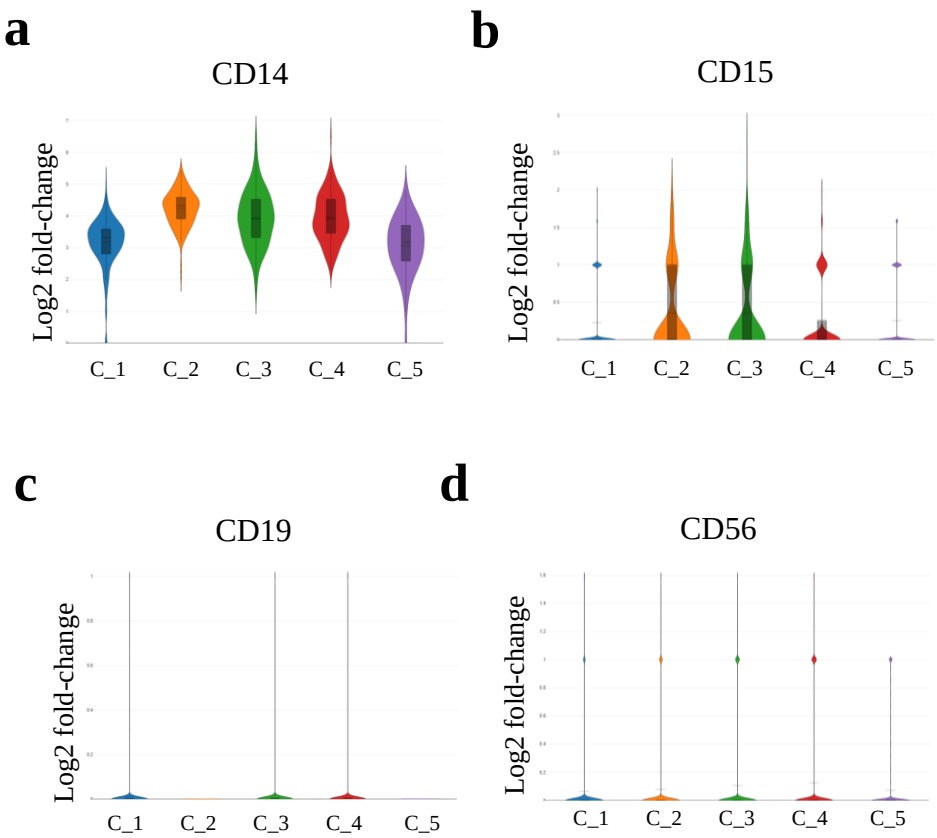


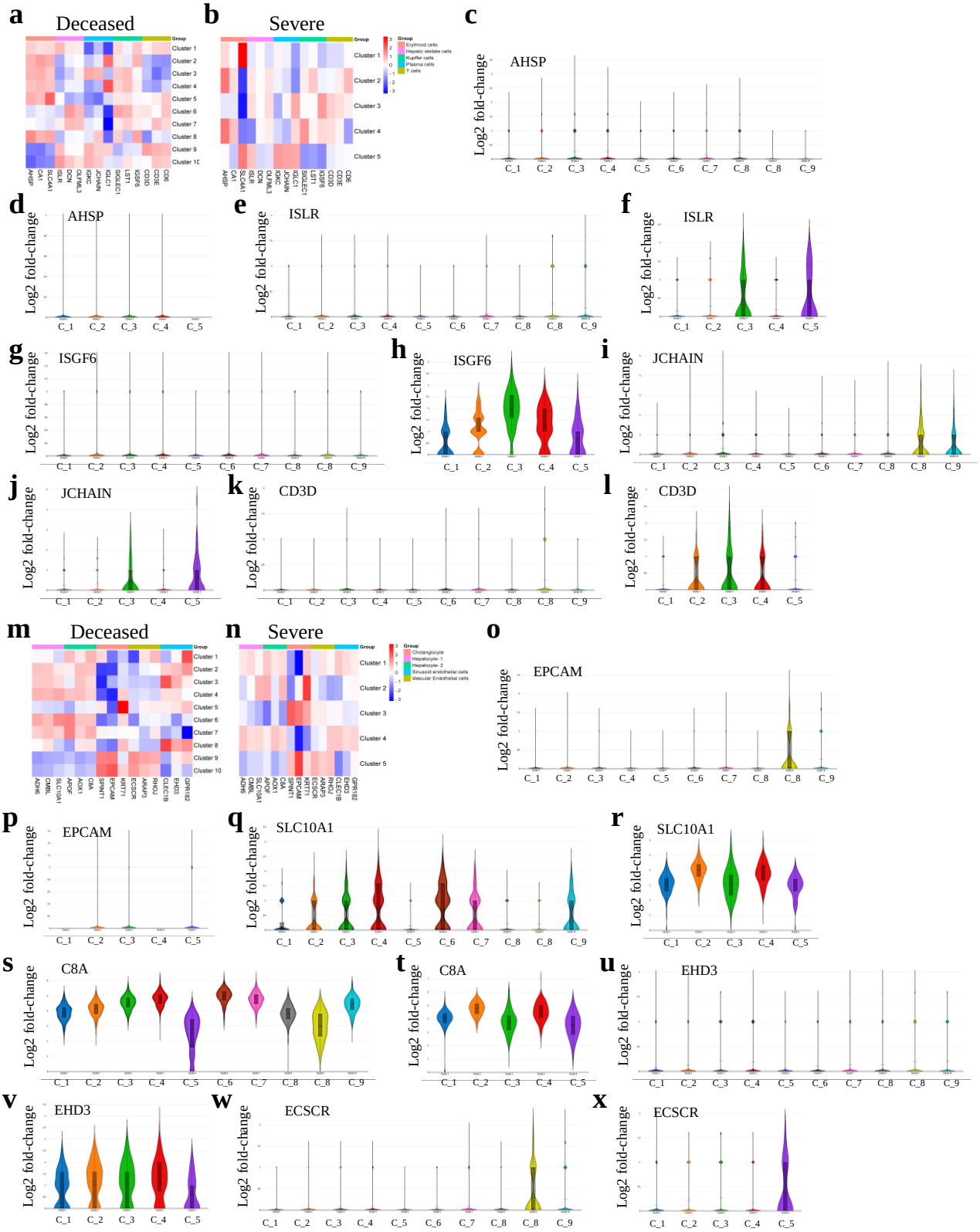
Supplementary Figure S1: Detection SARS-COV-2 proteins in natural infected golden (Syrian) hamsters. (a) Immunohistochemistry (IHC) staining SARS-COV-2 spike (S) protein in liver tissues from golden (Syrian) hamsters. (b) IHC staining SARS-COV-2 nucleocapsid (N) protein in liver tissues from golden (Syrian) hamsters. Viral S and N proteins were visualized in yellow/brown.



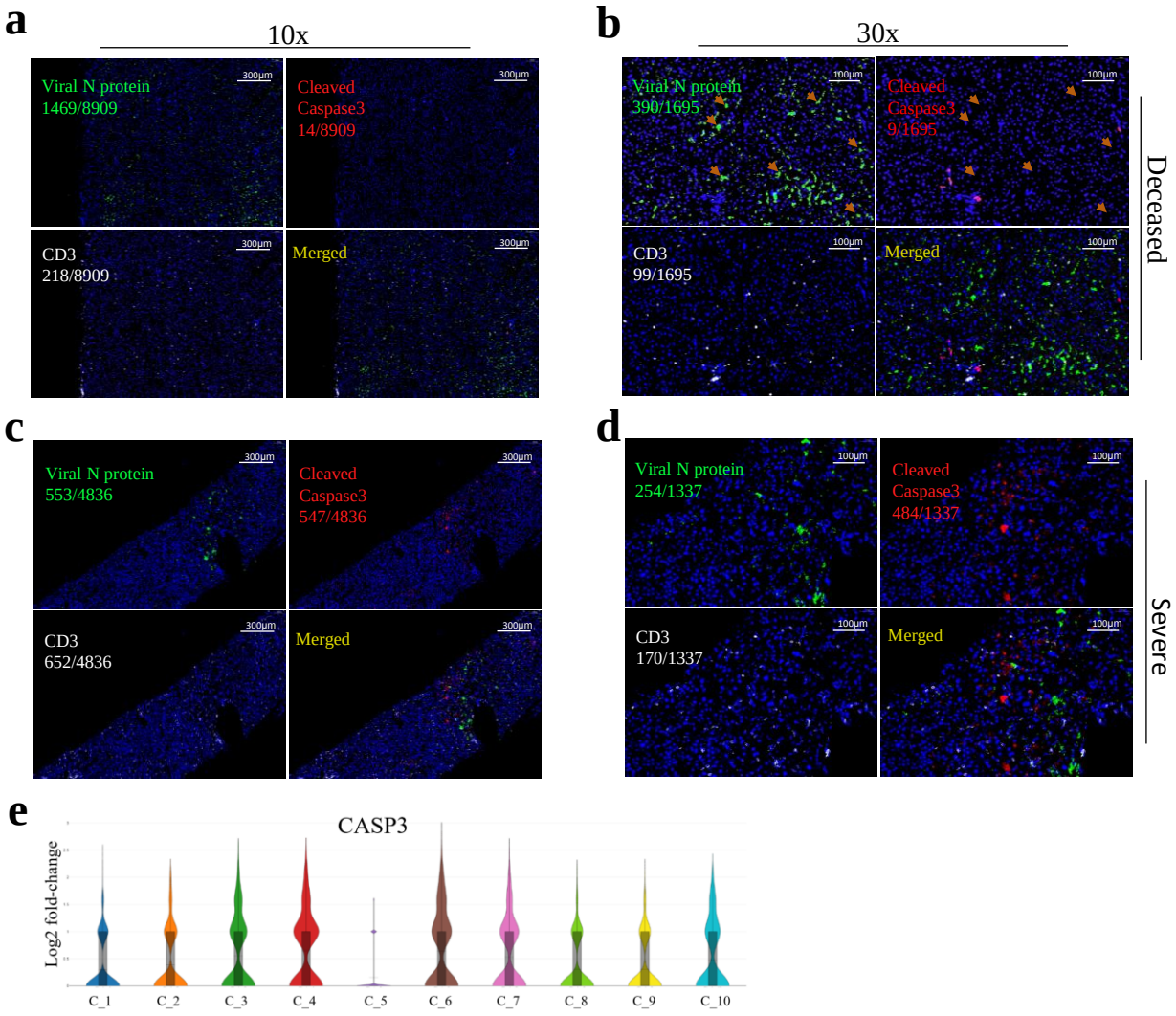
Supplementary Figure S2: Spatial transcriptomics analysis liver tissues from patients. Medians of genes and transcripts unique molecular identifiers (UMIs) per spot in spatial transcription analysis of deceased (a), severe (b) and moderate (c) subjects with COVID-19. Sequencing Saturation in deceased (d), severe (e) and moderate (f) liver tissues. Spatial distribution of ACE2 and ASGR1 in liver tissue from deceased (g) and severe (h) cases. ACE2, KREMEN1, AXL, ASGR1, CTSL and TMPRSS2 in clusters from deceased case(i). ASGR1 in clusters from severe (j) and moderate (k) patients.



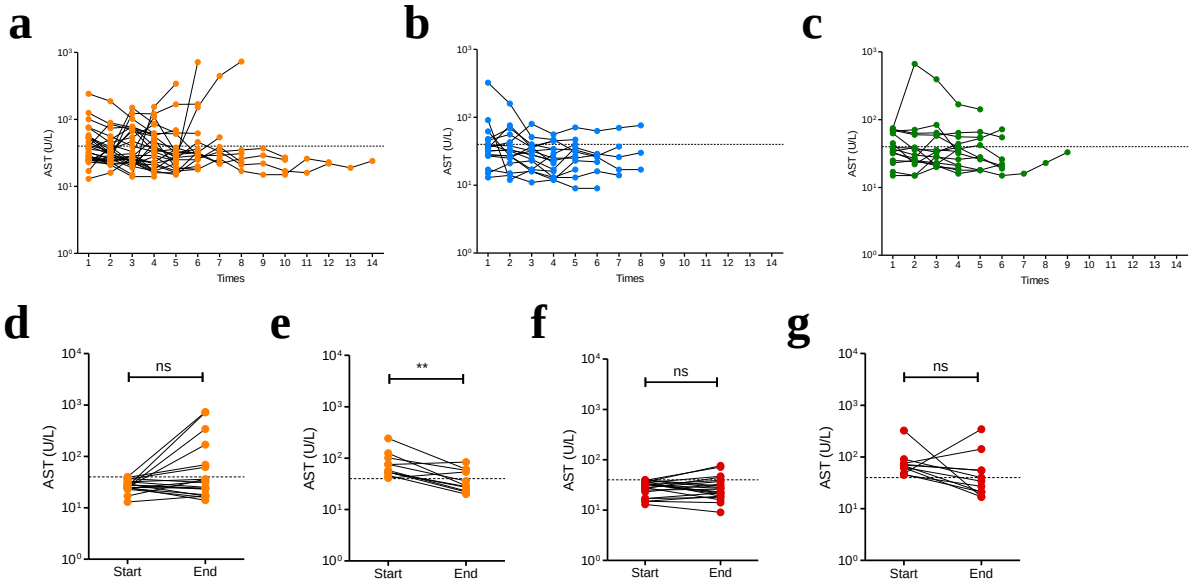
Supplementary Figure S3: Immune features in liver from patients. Transcription level of CD14 (a), CD15 (b), CD19 (c) and CD56 (d) in clusters from the severe patient.



Supplementary Figure S4: Feature of livers from patients with COVID-19. Distribution of erythroid, hepatic stellate, Kupffer, plasma and T cells-specific genes in clusters from severe (a) and deceased (b) cases. Violin plots showing feature genes for erythroid (AHSP), hepatic stellate (ISLR), Kupffer (ISGF6), plasma (JCHAIN) and T (CD3D) cells (c-l). Distribution of hepatocyte-1, hepatocyte-2, cholangiocyte, vascular endothelial and sinusoid endothelial cells-specific genes in clusters from severe (c) and deceased (d) cases. Violin plots showing feature genes for cholangiocyte (AHSP), hepatocyte-1 (SLC10A1), hepatocyte-2 (C8A), sinusoid endothelial (EHD3)and vascular endothelial (ECSCR) cells (o-x).



Supplementary Figure S5: Caspase 3 in livers from patients with COVID-19. Immunofluorescence staining viral N (Green), cleaved caspase3 (Red) and CD3 (white) in liver tissues from deceased (a, b) and severe (c, d) patients. Orange arrows show viral N protein and its corresponding area. Positive dots were counted using *QuPath-0.5.1*. The numbers depict viral positive dots/ nucleuses. (e) Transcription level of Caspase-3 gene (CASP3) in clusters from the deceased patient.



Supplementary Figure S6: Dynamic change of serum AST in COVID-19 clinical cohorts. (a) Dynamic monitor of serum AST in 30 deceased cases. (b) Dynamic monitor of AST in 17 severe cases. (c) Dynamic monitor of AST in 15 moderate cases. Change of AST between start and end points in deceased cases, with normal AST (d) or elevated AST (e) at the beginning. Change of AST between start and end points in survived cases, with normal AST (f) or elevated AST (g) at the beginning. Statistical significance was assessed by paired two-tailed t tests (d-g), $^{**}p<0.01$.