Figure S1. The newly developed mAb #7 detects HBc in HBV-infected HepG2-hNTCP-C4 cells. (A) The lysates of HepG2-hNTCP-C4 cells infected or uninfected (mock) with HBV were analyzed by immunoblotting with mAb #7. (B) The lysates of HepG2-hNTCP-C4 cells infected with HBV were immunoprecipitated with mAb #7. Bound proteins were subsequently analyzed by immunoblotting with mAb #7. (C) HepG2-hNTCP-C4 cells infected or uninfected (mock) with HBV were fixed with 4% PFA and then stained with mAb #7 (red) and DAPI (blue). Scale bar, 50 μm.
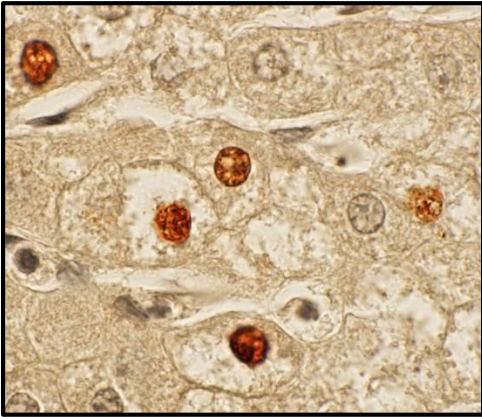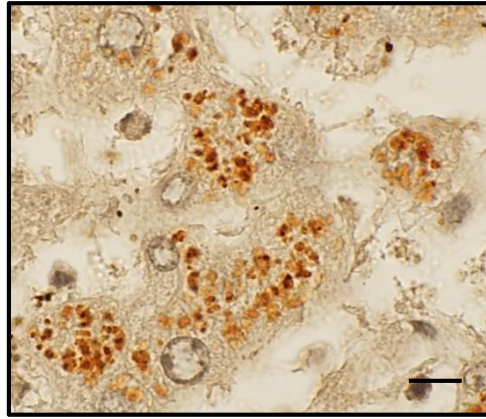
A

B

Figure S2. The newly developed mAb #7 allows for visualization of the subcellular localization of HBc in HBV-infected liver tissues. HBV-positive paraffin-embedded human liver tissues were stained with mAb #7 using peroxidase conjugate and DAB chromogen, and then counterstained with hematoxylin. mAb#7 detects nuclear (A) and cytoplasmic (B) localization of HBc. Scale bar, 10 μm.
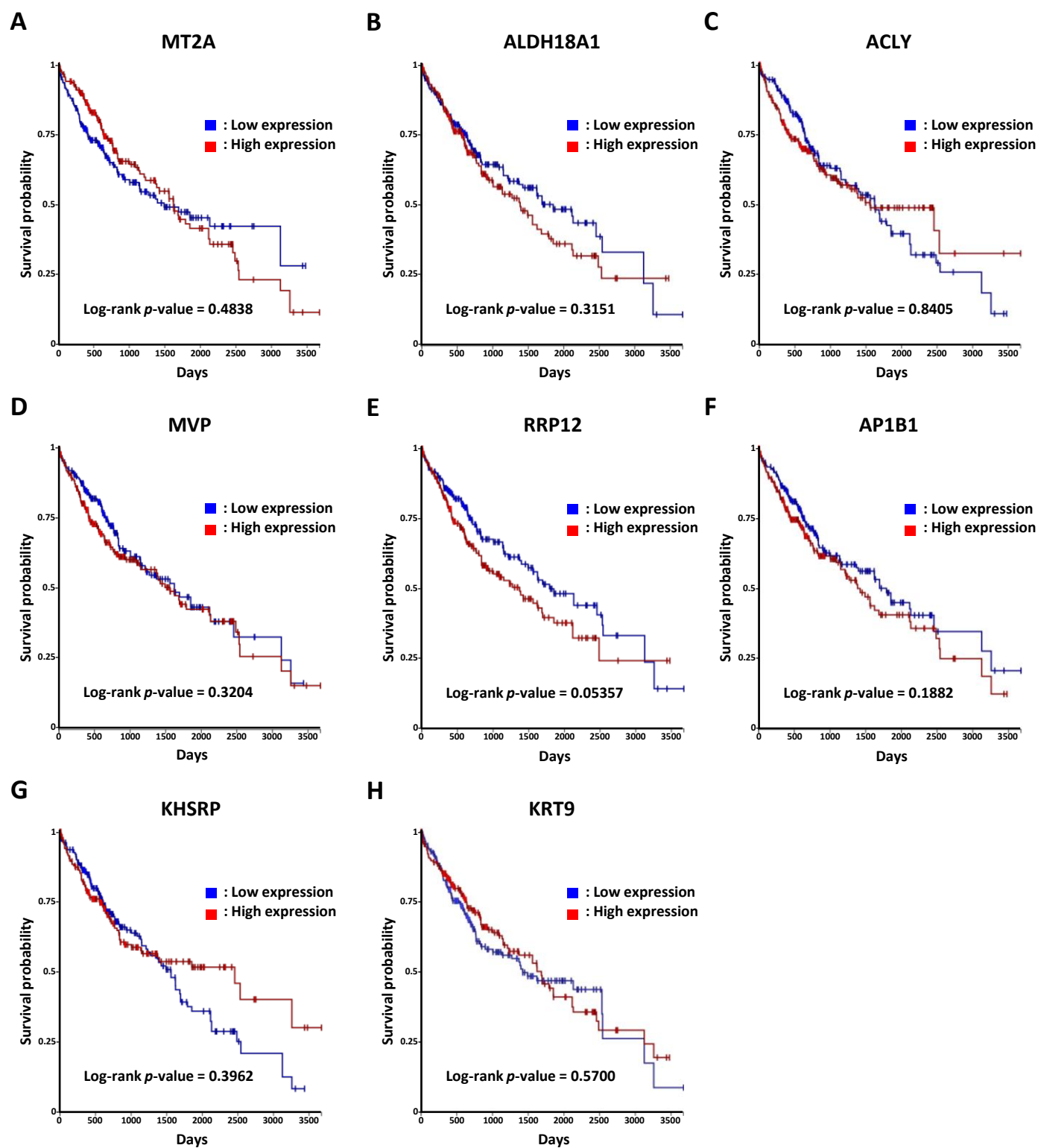
Figure S3. Kaplan-Meier analysis of eight proteins was performed using the UCSC Xena platform and mRNA sequence databases of the Cancer Genome Atlas Program (TCGA). (A) MT2A, log-rank p = 0.4838. (B) ALDH18A1, log-rank p = 0.3151. (C) ACLY, log-rank p = 0.8405. (D) MVP, log-rank p = 0.3204. (E) RRP12, log-rank p = 0.05357. (F) AP1B1, log-rank p = 0.1882. (G) KHSRP, log-rank p = 0.3962. (H) KRT9, log-rank p = 0.5700. log-rank p-value < 0.05 was regarded as statistically significant. The x-axis indicates the days and the y-axis indicates the survival probability.