

Supplementary Materials: IGF2BP1 - an oncofetal RNA-binding protein fuels tumor virus propagation

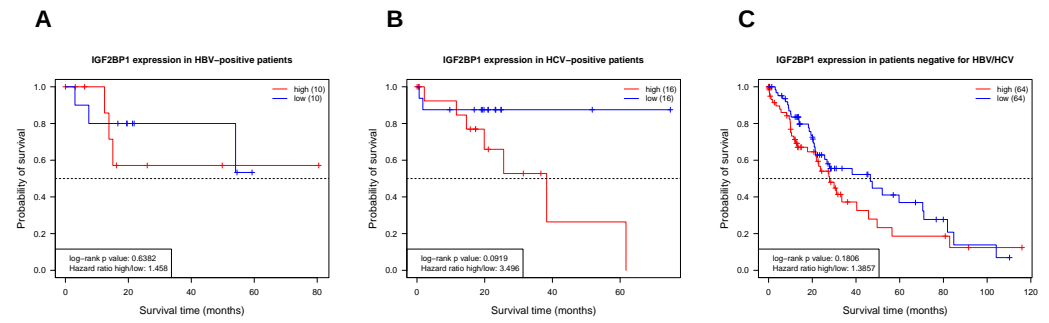


Figure S2. Kaplan-Meier curves describing overall survival probabilities depending on IGF2BP1 RNA expression in hepatocarcinoma derived RNA-seq data, provided by the TCGA (cohort LIHC). **A** Patients positive for HBV but not HCV. **B** Patients positive for HCV but not HBV virus. **C** Patients neither positive for HBV nor HCV. Patients were separated by median IGF2BP1 RNA expression.

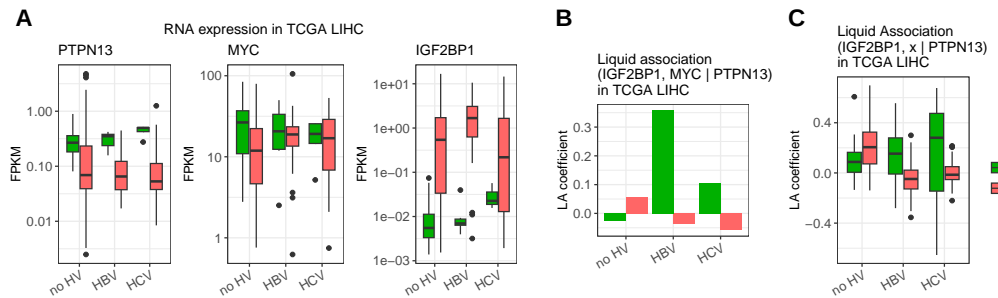


Figure S3. RNA expression and liquid association in in hepatocarcinoma derived RNA-seq data (HCC). **A** Distribution of RNA expression values of PTPN13, c-Myc and IGF2BP1 derived from HCC-RNA-seq samples (TCGA, cohort LIHC). **B** Liquid association (LA) coefficients of the correlation between IGF2BP1 and c-Myc in dependence of PTPN13 in TCGA HCC samples. **C** LA coefficient distributions of the correlation between IGF2BP1 and 117 published target candidates in dependence of PTPN13 in TCGA HCC samples. no HV - samples without detected Hepatitis virus infection, HBV - samples with exclusively detected Hepatitis B infection, HCV - samples with exclusively detected Hepatitis C infection, NT - normal tissue, PT - primary tumor tissue

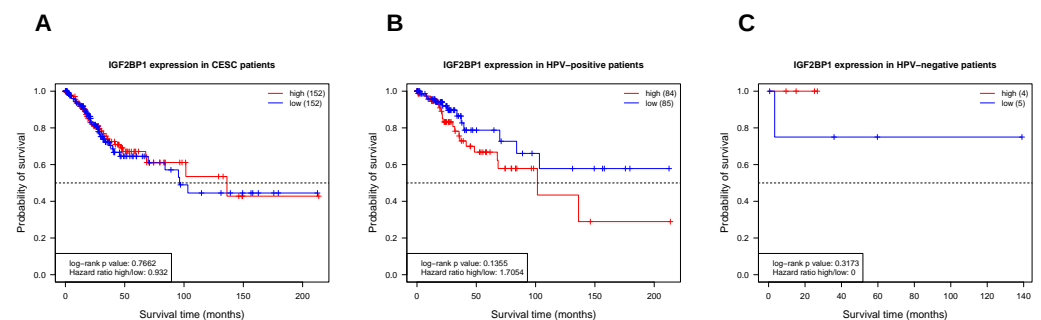


Figure S4. Kaplan-Meier curves describing overall survival probabilities depending on IGF2BP1 RNA expression in cervical carcinoma derived RNA-seq data, provided by the TCGA (cohort CESC). **A** Patients regardless of virus status. **B** Patients positive for HPV **C** Patients negative for HPV. Patients were separated by median IGF2BP1 RNA expression.

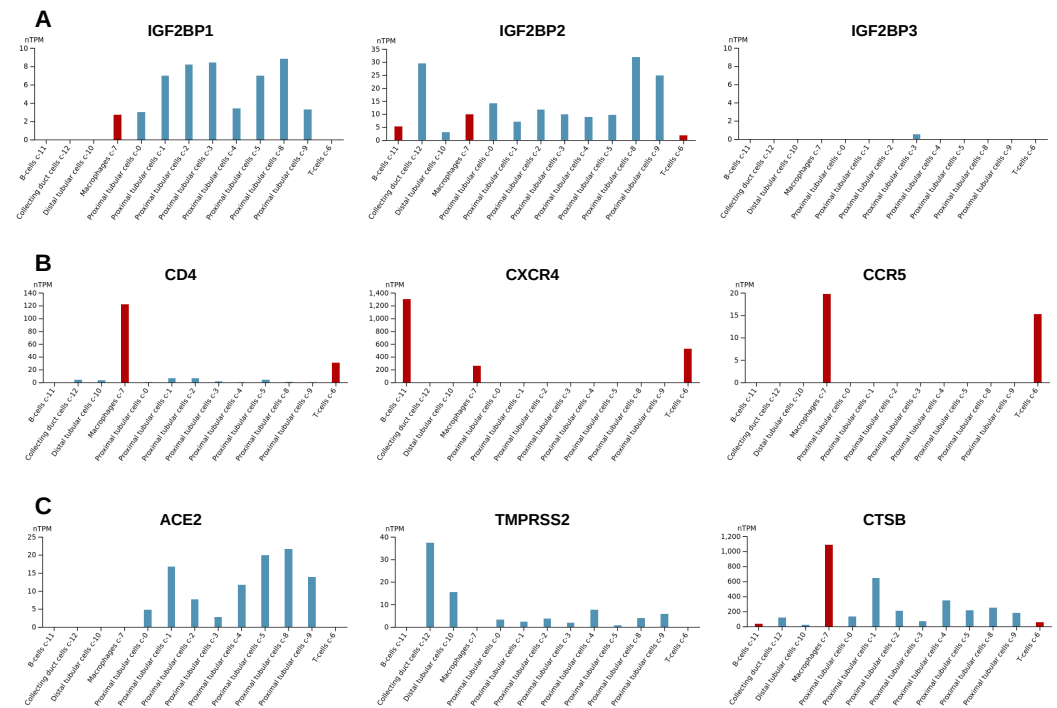


Figure S5. Average RNA expression in distinct kidney-resident cell types derived from single cell RNA-seq data provided by the Human protein atlas (www.proteinatlas.org). **A** IGF2BPs. **B** HIV-1 host (co)-receptors. **C** SARS-CoV-2 host receptor and priming proteases