



**SUPPLEMENTARY FIG. S7.** Overview of the 46 hepatocellular carcinoma genes detected in both proteomics and snRNA-seq experiments. **(A)** Number of probe-distal HiCap interactions associated to liver-specific ChromHMM annotations. **(B)** Expression levels from snRNA-seq in different liver cell types. The size of the dot represents the percentage of nuclei expressing the gene, while the color intensity the level of expression. **(C)** Heatmap comparing the expected and experimental levels of protein abundance from next-generation sequencing and MS experiments. The first column shows the  $\log_2$ -average expression of genes from the *in silico* bulk snRNA-seq. The second column illustrates the estimated protein abundance calculated from the *in silico* bulk snRNA-seq levels calibrated for tissue-independent gene-specific protein abundance estimation factors. The third column shows the experimental level of the protein abundance detected by MS. The last two columns show the estimated protein abundance from  $\log_2$ -average *in silico* bulk scRNA-seq levels and the  $\log_2$ -average number of reads of bulk RNA-seq adjusted for gene-specific protein abundance estimation factors (Lonsdale et al., 2013; MacParland et al., 2018).

### Supplementary References

- Lonsdale J, Thomas J, Salvatore M, et al. (2013). The genotype-tissue expression (GTEx) project. *Nat Genet* 45, 580–585.
- MacParland SA, Liu JC, Ma X-Z, et al. (2018). Single cell RNA sequencing of human liver reveals distinct intrahepatic macrophage populations. *Nat Commun* 9, 4383.