

Supplemental Material

Supplemental Figures

Figure S1: RNA-sequencing preprocessing of dataset GSE104766: A/voom transformation of the EdgeR normalized matrix; B/Densityplot by sample of the voom transformed data; C/Densityplot by sample after filtration of unexpressed genes; D/ Densityplot by sample after quantile normalization.

Figure S2: Harmonization of single transcriptome from human hepatoblastoma tissue samples: GSE180665, A/ Principal component analysis elbowplot of unintegrated single cell transcriptome data, B/ Unintegrated UMAP dimension reduction with original cell annotation, C/Unintegrated UMAP dimension reduction with sample origin annotation, D/ Dimension reduction post harmony integration with original cell annotation, E/Dimension reduction post harmony integration with sample origin annotation.

Figure S3: Single cell RNAseq preprocess for GSE180665 dataset: (A) UMAP dimension reduction post harmony with sample origin annotation (B) UMAP dimension reduction post harmony with group sample annotation (C) UMAP dimension reduction post harmony with original cluster annotation (D) UMAP dimension reduction post harmony with original cell annotation

Figure S4: Predictive values of activated metabolic markers in tumor cells from hepatoblastoma at single cell level: A/Elasticnet plot of fit with alpha fixed to 0.1; B/ ROC curve and area undercurve of the 41 metabolic markers with positive elasticnet coefficient for predicting tumor cell status in hepatoblastoma single cell transcriptome

Supplemental Table

Table S1: Differential expressed metabolic markers in human hepatoblastoma tumors (10.6084/m9.figshare.26413144) available at address: https://figshare.com/articles/dataset/Table_S1_Differential_expressed_metabolic_markers_in_human_hepatoblastoma_tumors/26413144?file=48042013 (accessed on 31 July 2024).

Figure S1

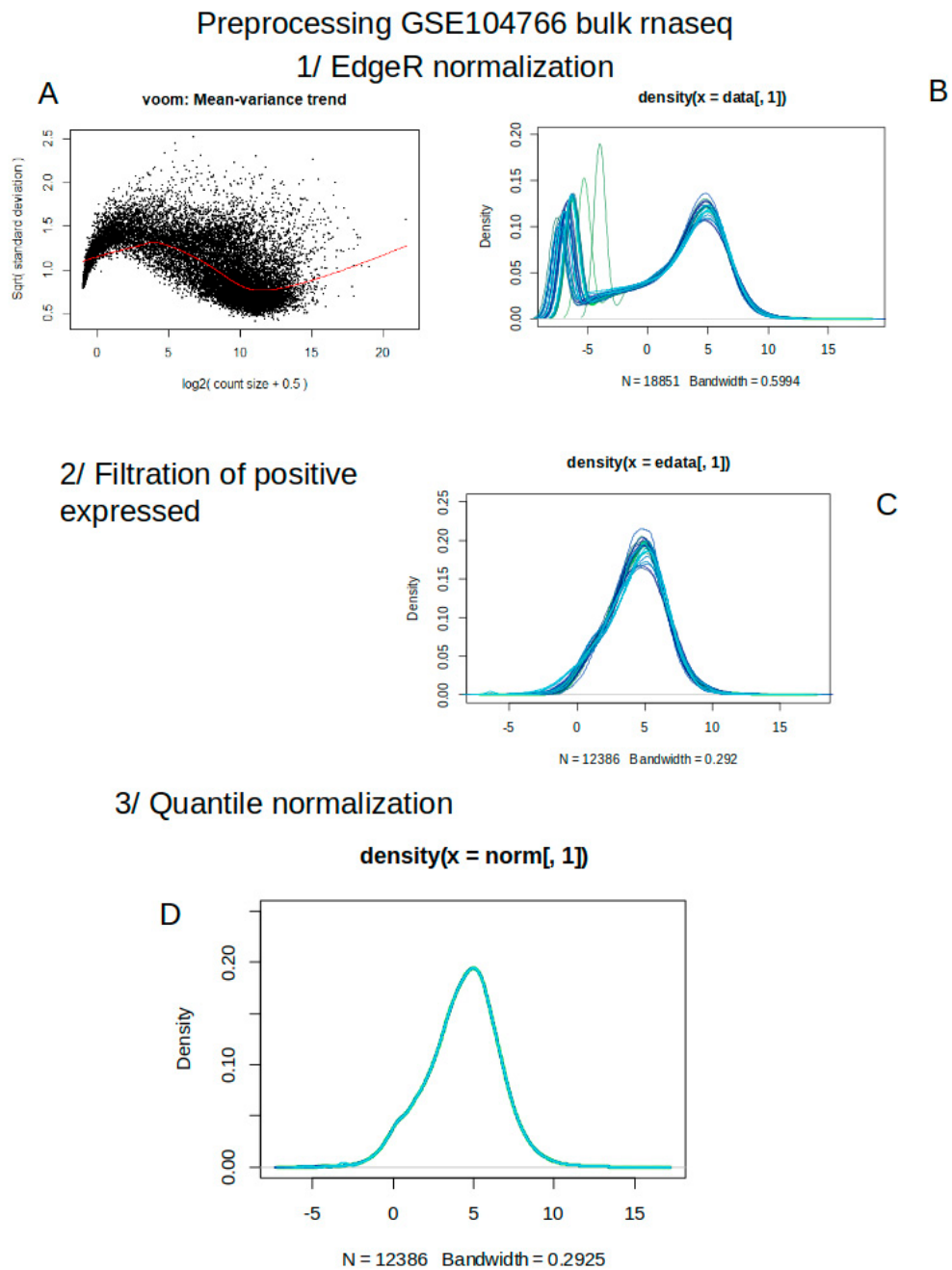


Figure S2

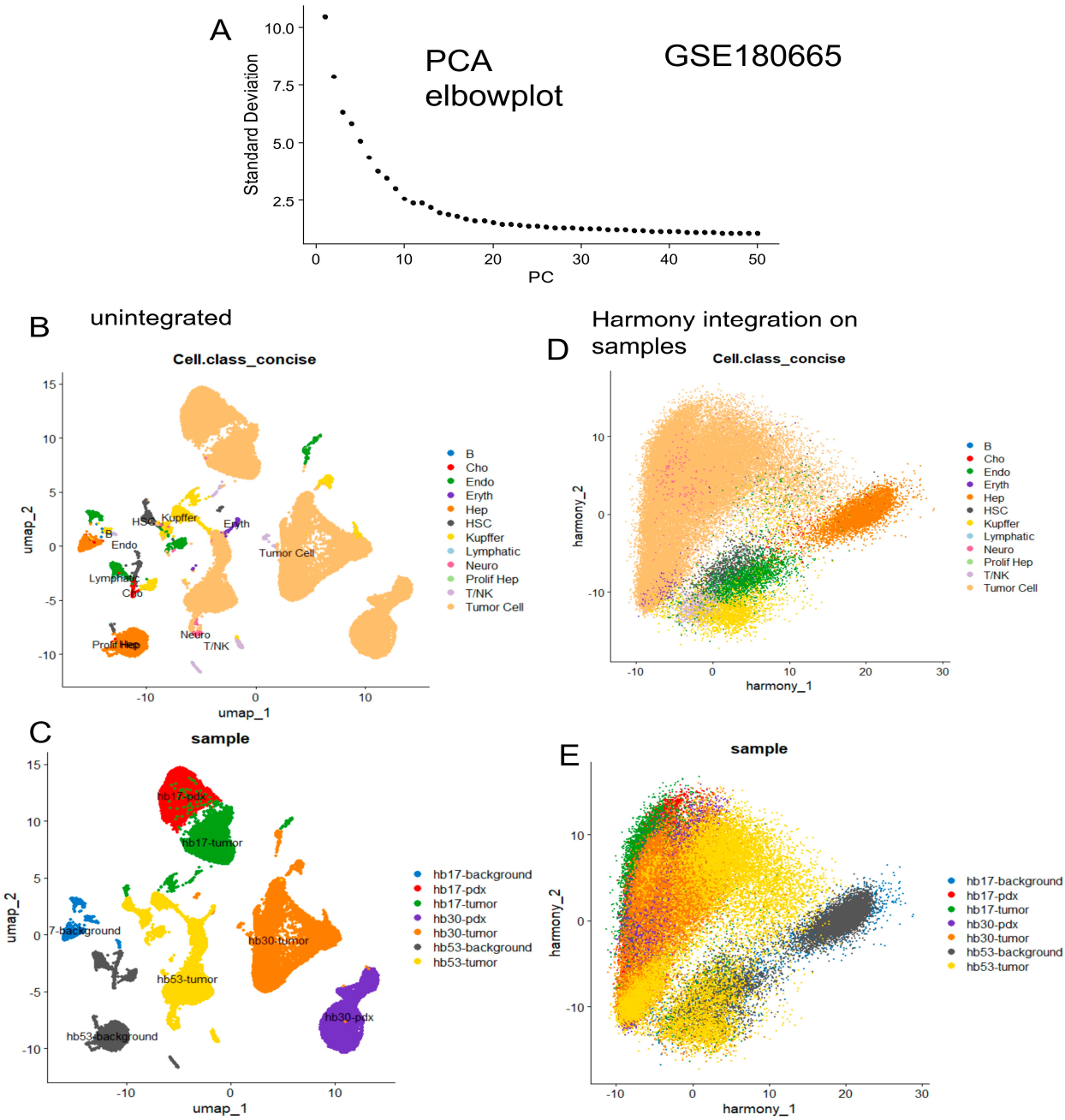


Figure S3

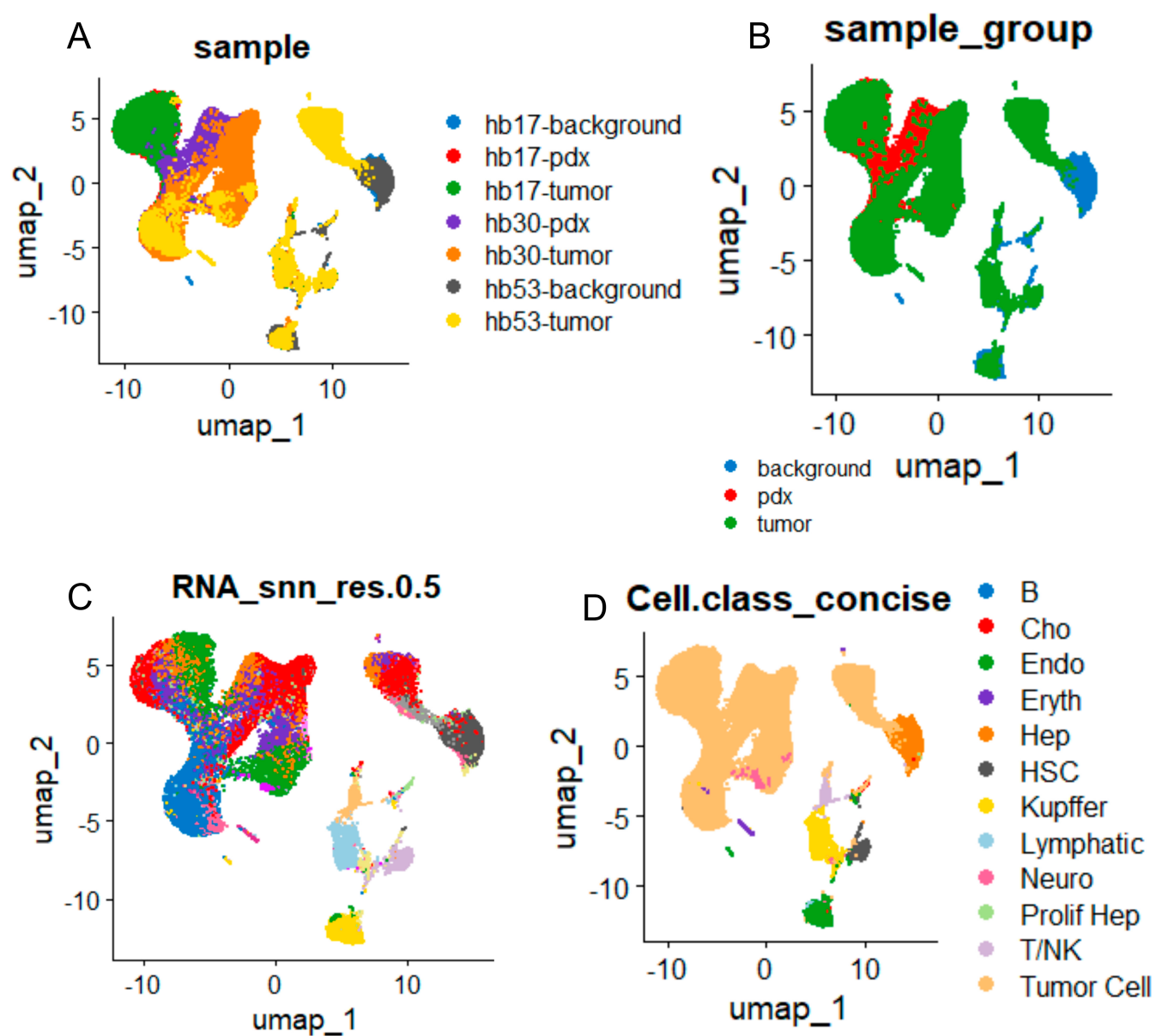


Figure S4

