Article (Supplemental data)

Activated metabolic transcriptional program in tumor cells from hepatoblastoma

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**Supplemental Material**

**Supplemental Figures**

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

**Figure S2: 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

Figure S1



Figure S2

