

Hepatocarcinoma Individual Transcriptomes Study

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Hepatocarcinoma



- most common primary liver tumor
- the most common causes: alcohol, hepatitis B and C

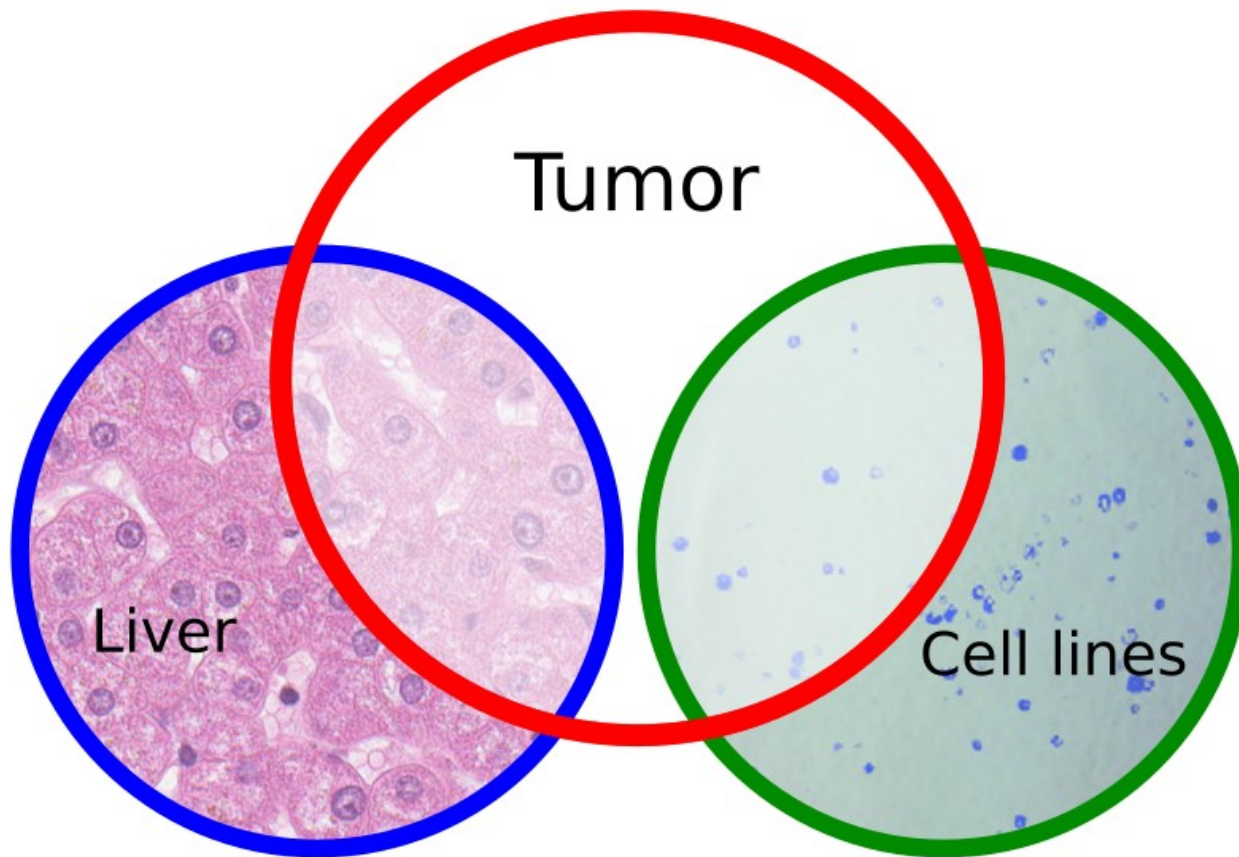
Purpose and Objective



Purpose: to find the genes responsible for the survival of hepatocarcinoma cells in the body

- Objective: Using the analysis of differential gene expression in hepatocarcinoma cells, cell lines derived from it, and tumor-associated normal liver, to find markers responsible for the interaction of the tumor with the surrounding tissue.

Survival markers



Methods



- DESeq2
- edgeR
- gage
- KEGG pathway
- kmplot

RNAseq samples



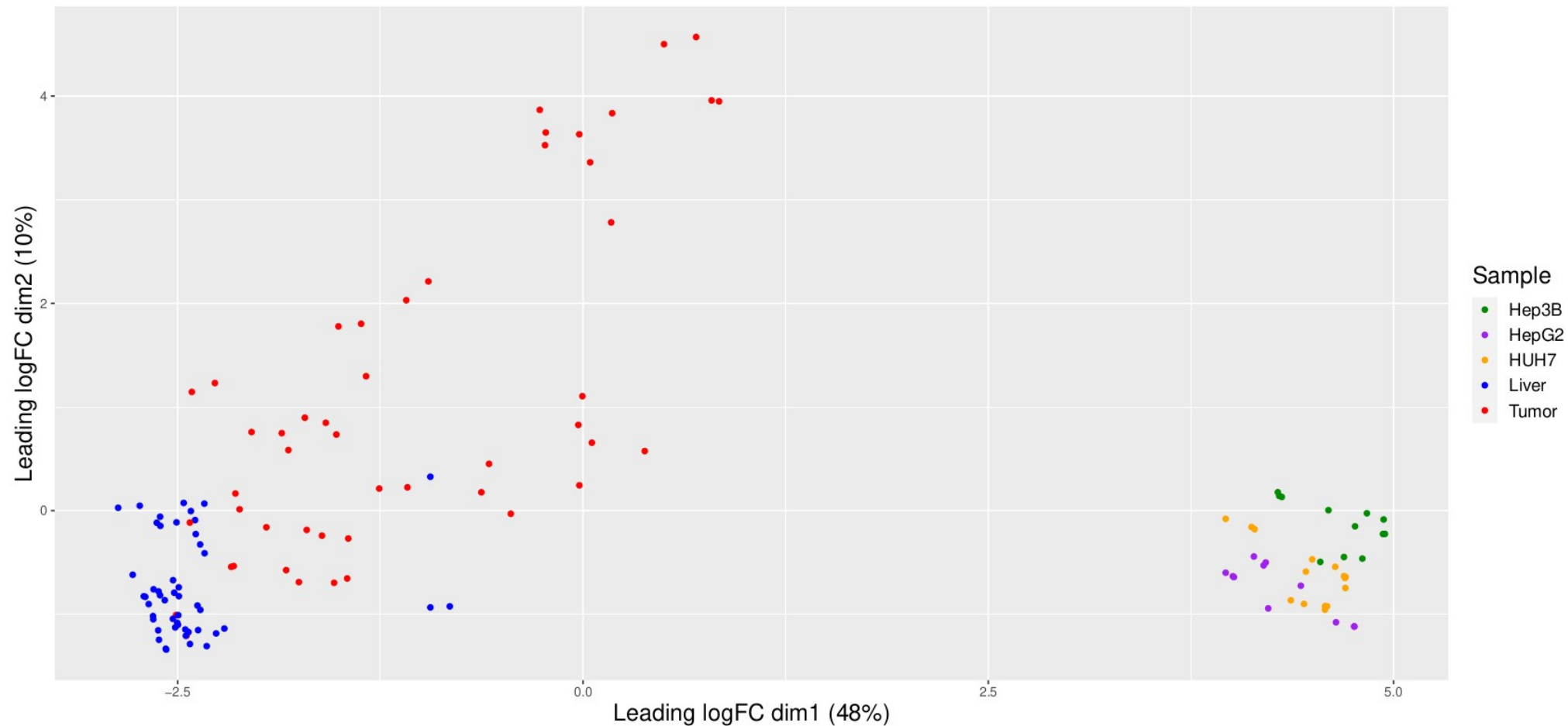
- 25 patients with hepatocarcinoma
- samples of tumor and normal tumor-associated liver tissue (normal liver)
- replicated data
- These samples were obtained from the Research Institute of Carcinogenesis

Cell lines

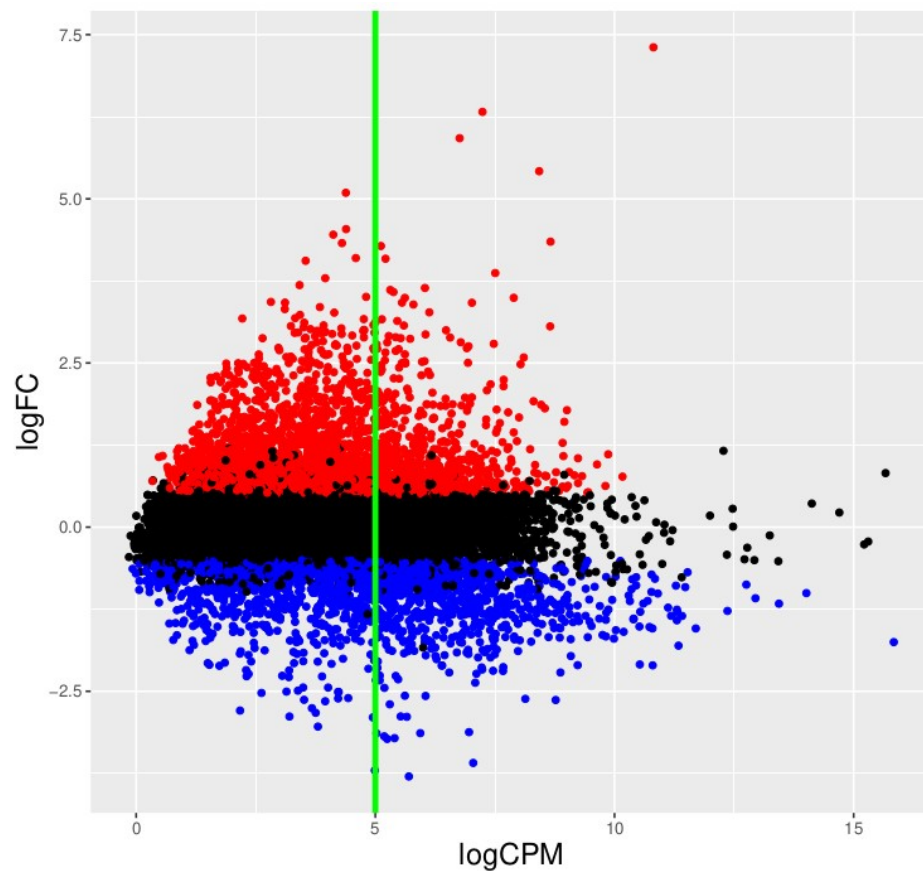
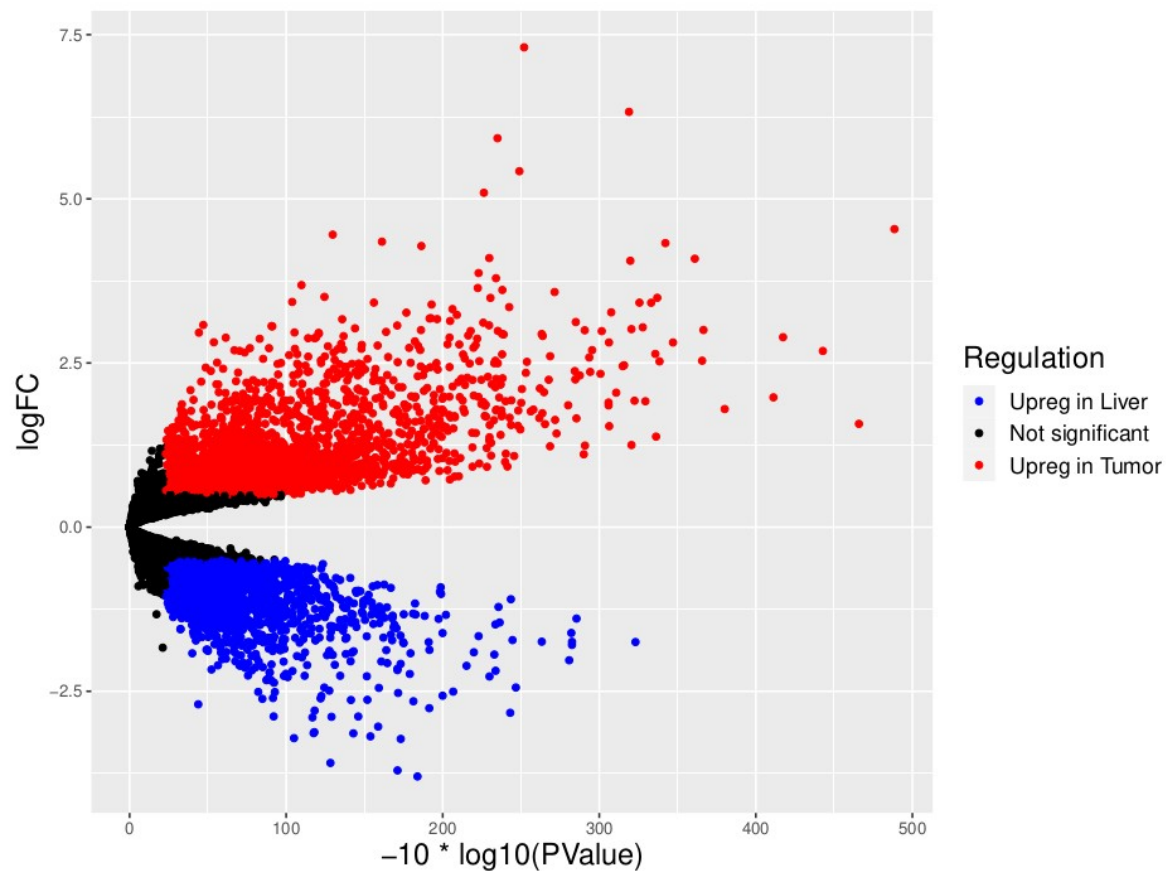
- Hep3B is a cell line with epithelial morphology and an integrated hepatitis B genome
- Huh7 - consists of epithelial-like and oncogenic cells isolated from hepatocytes
- HepG2 is a well-differentiated hepatocellular carcinoma showing an epithelial-like morphology.

The data was obtained from the open data bank GEO

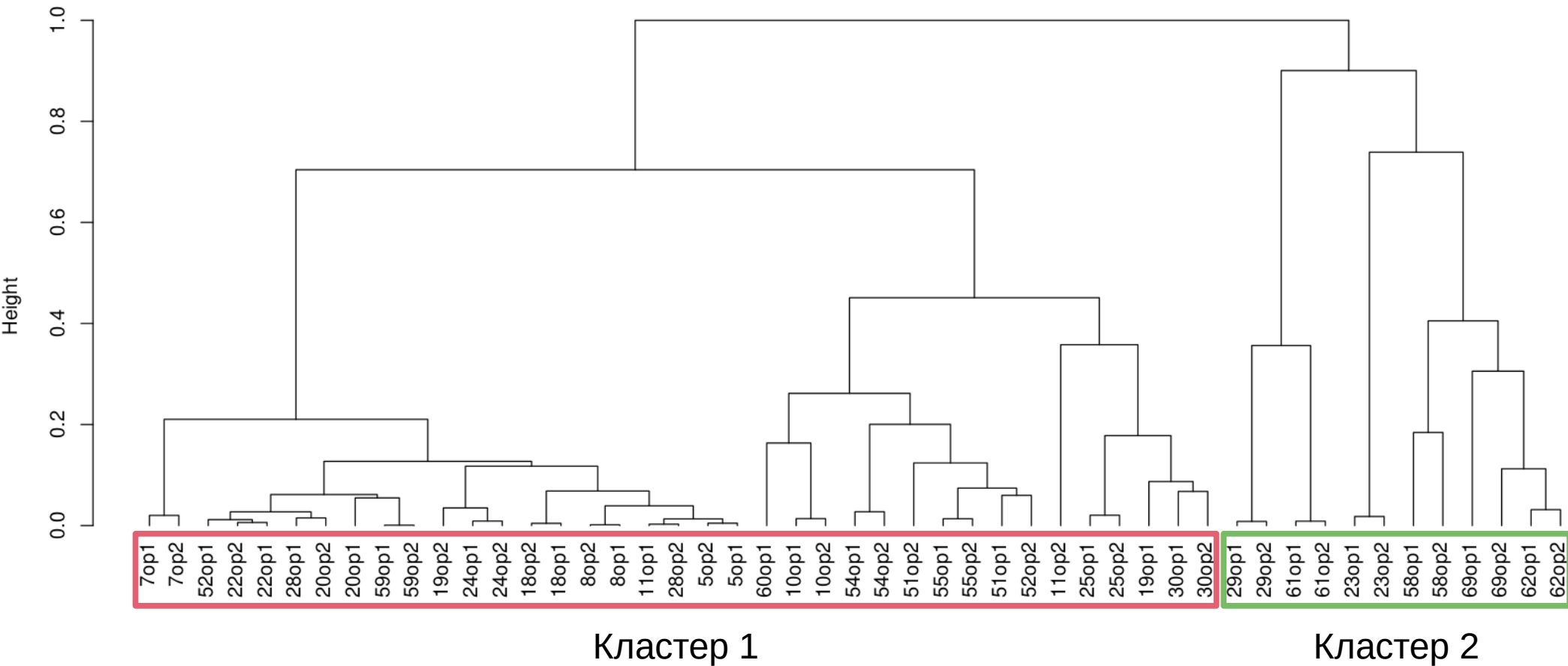
Expression profiles similarity



Choice of diffexpression markers

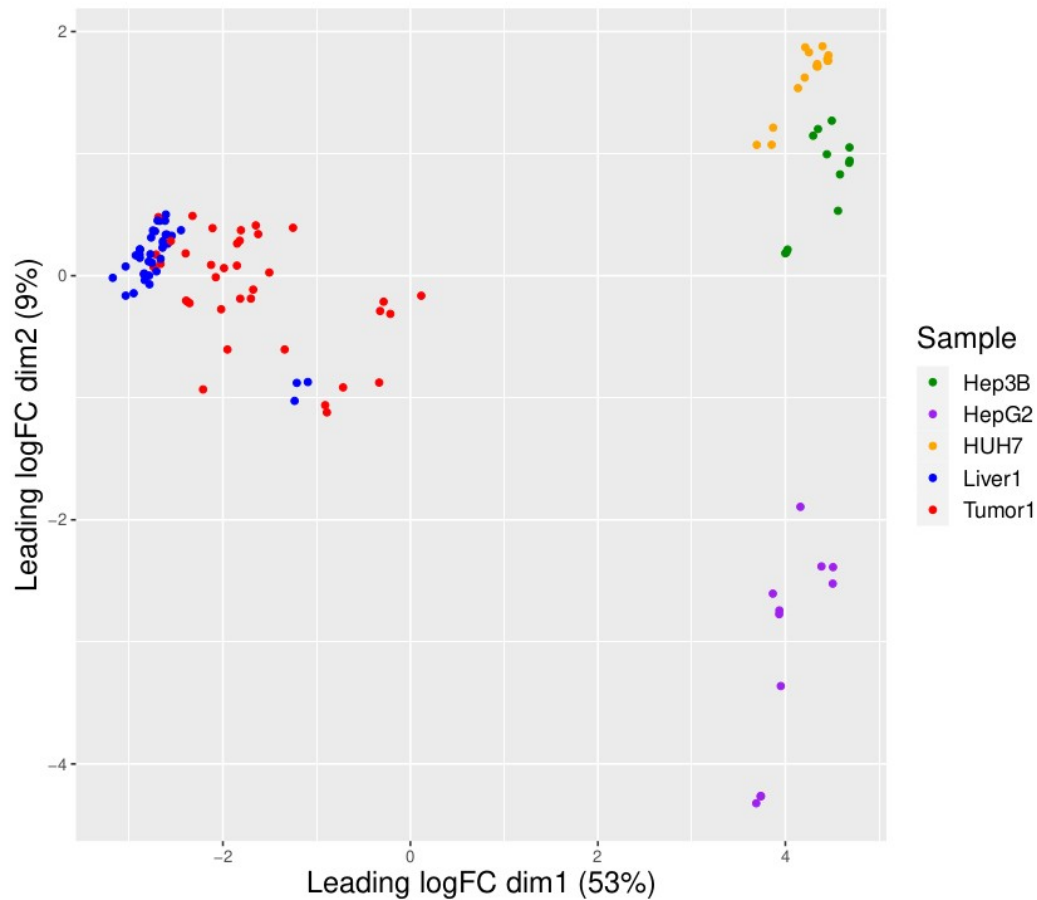


Hierarchical clustering

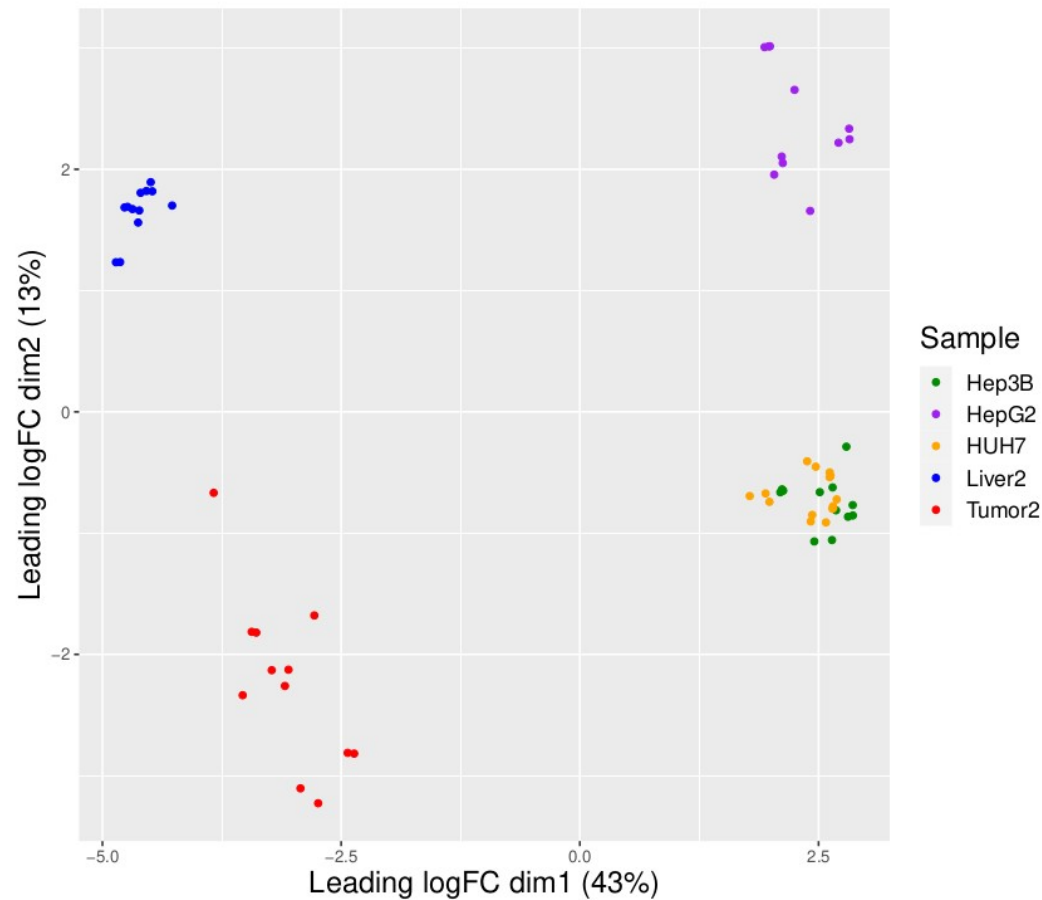


Different Similarity of Tumor Expression Profiles to Normal Tissue for Clusters

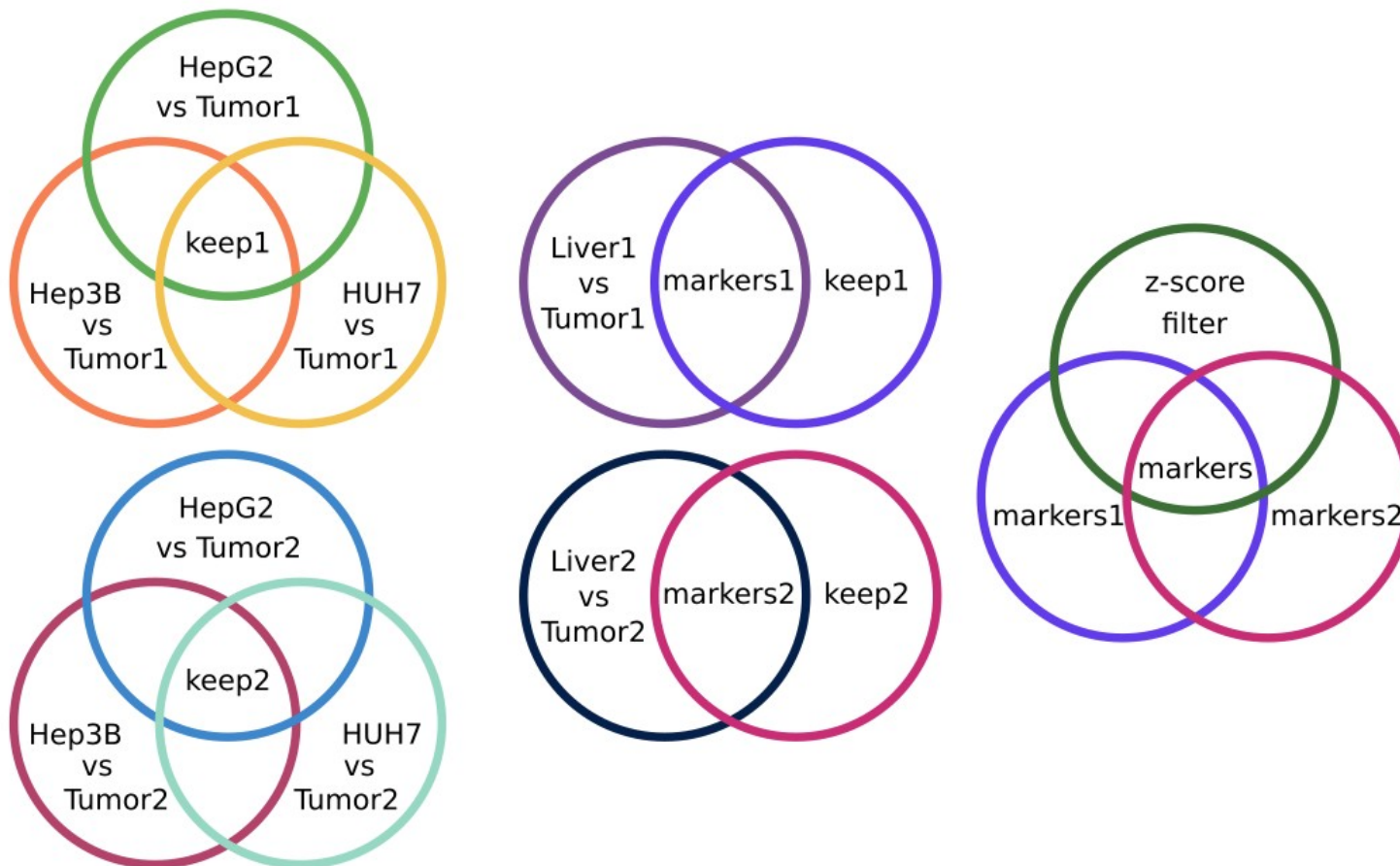
Кластер 1



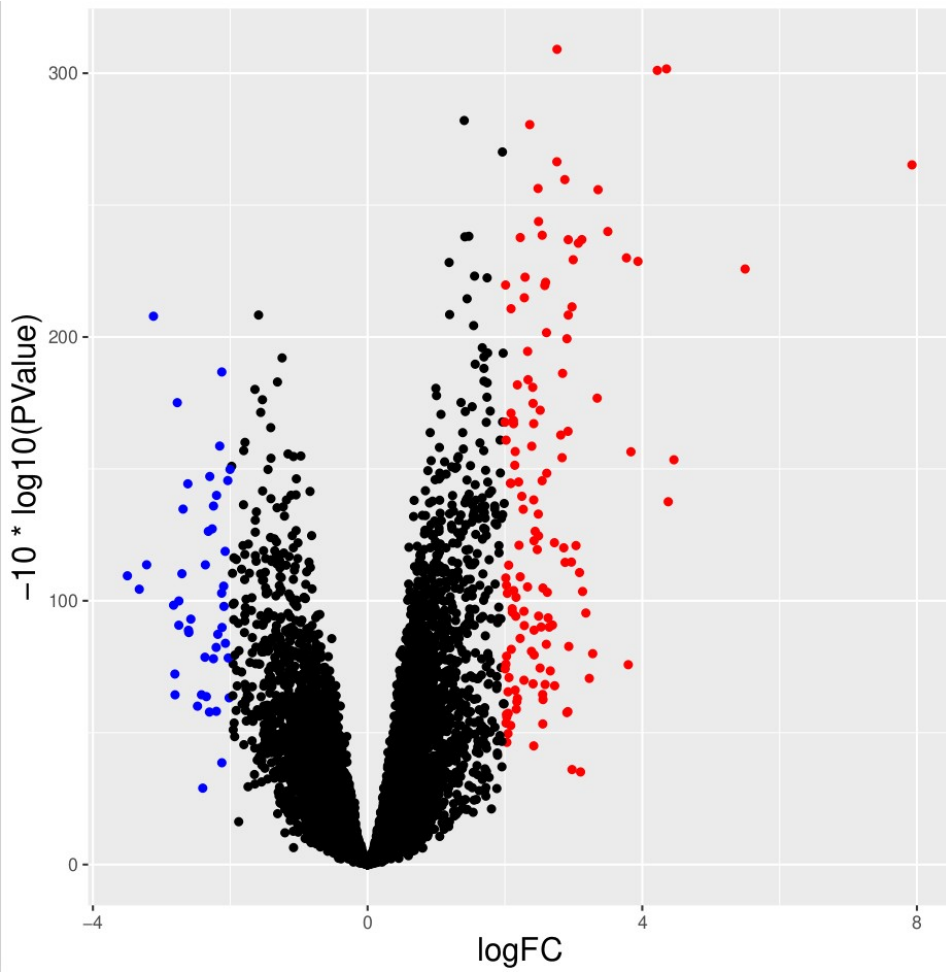
Кластер 2



Gene selection scheme

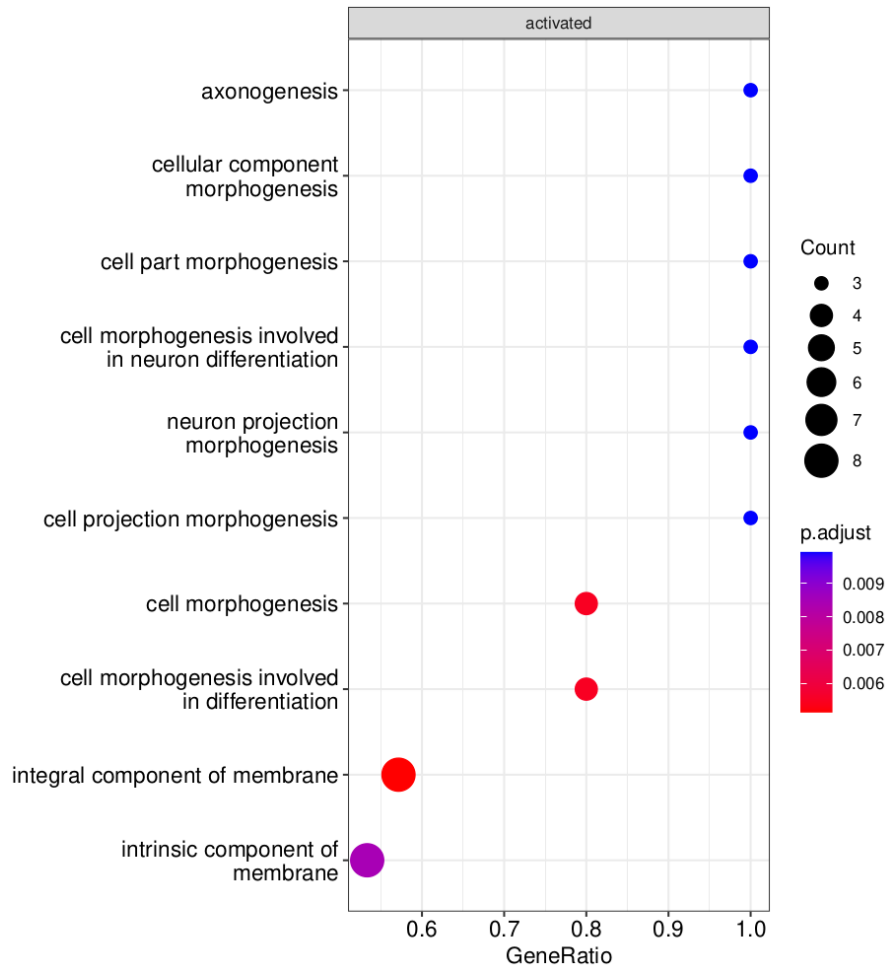


cluster №1

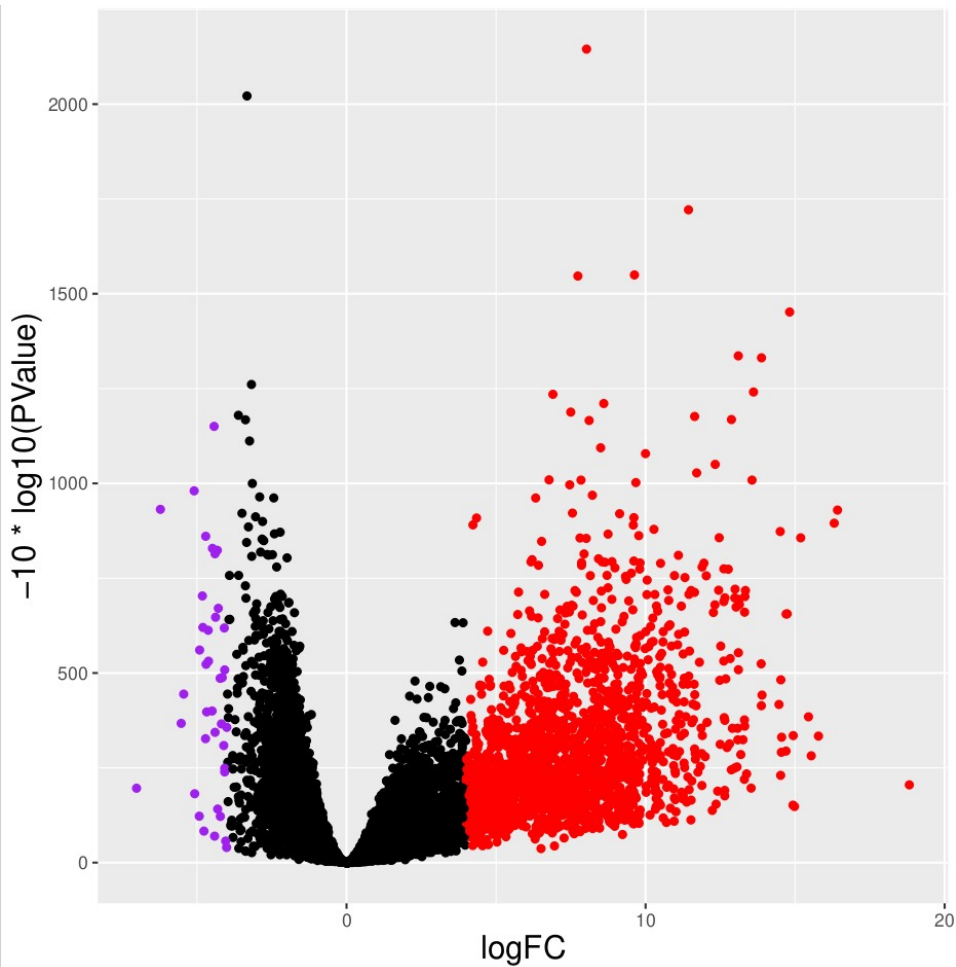


Regulation

- Upreg in Liver1
- Not significant
- Upreg in Tumor1

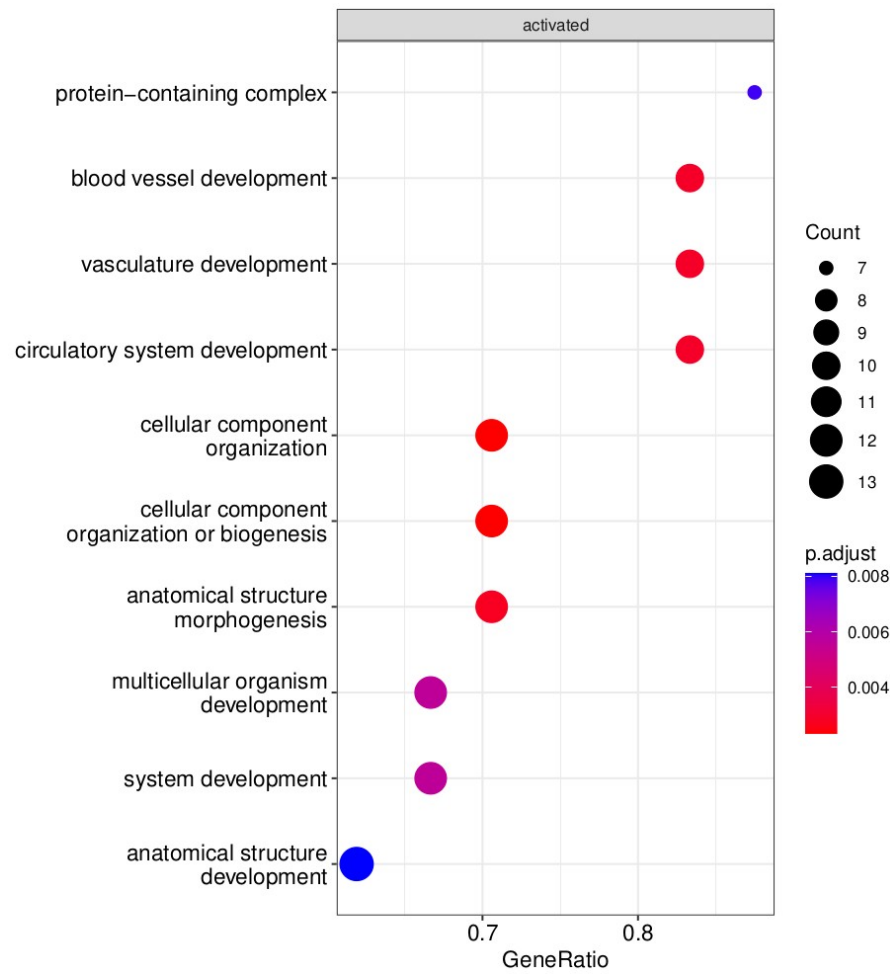


cluster №1

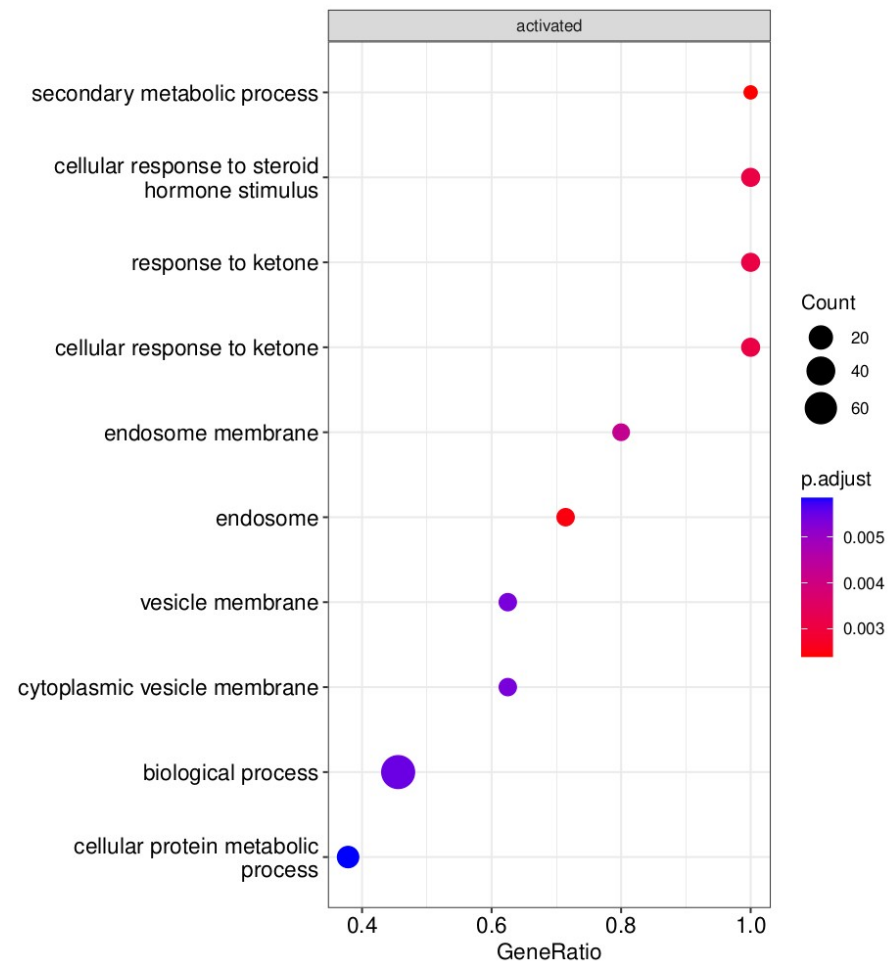
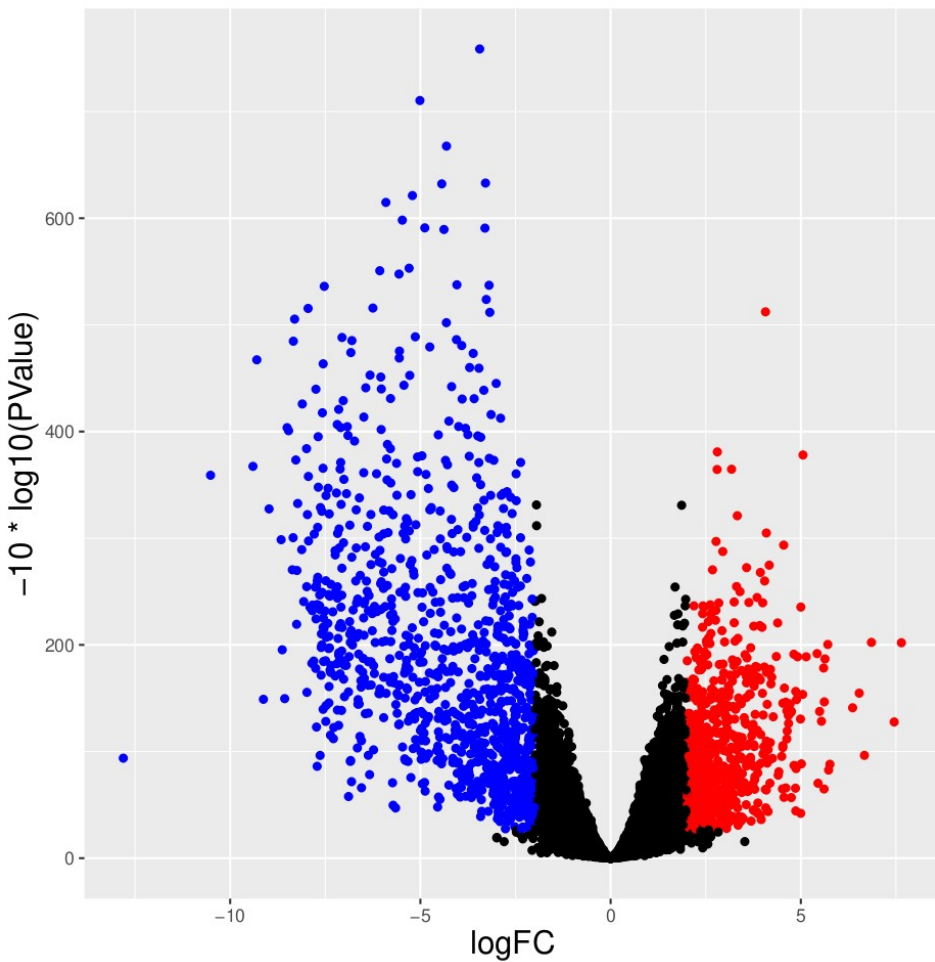


Regulation

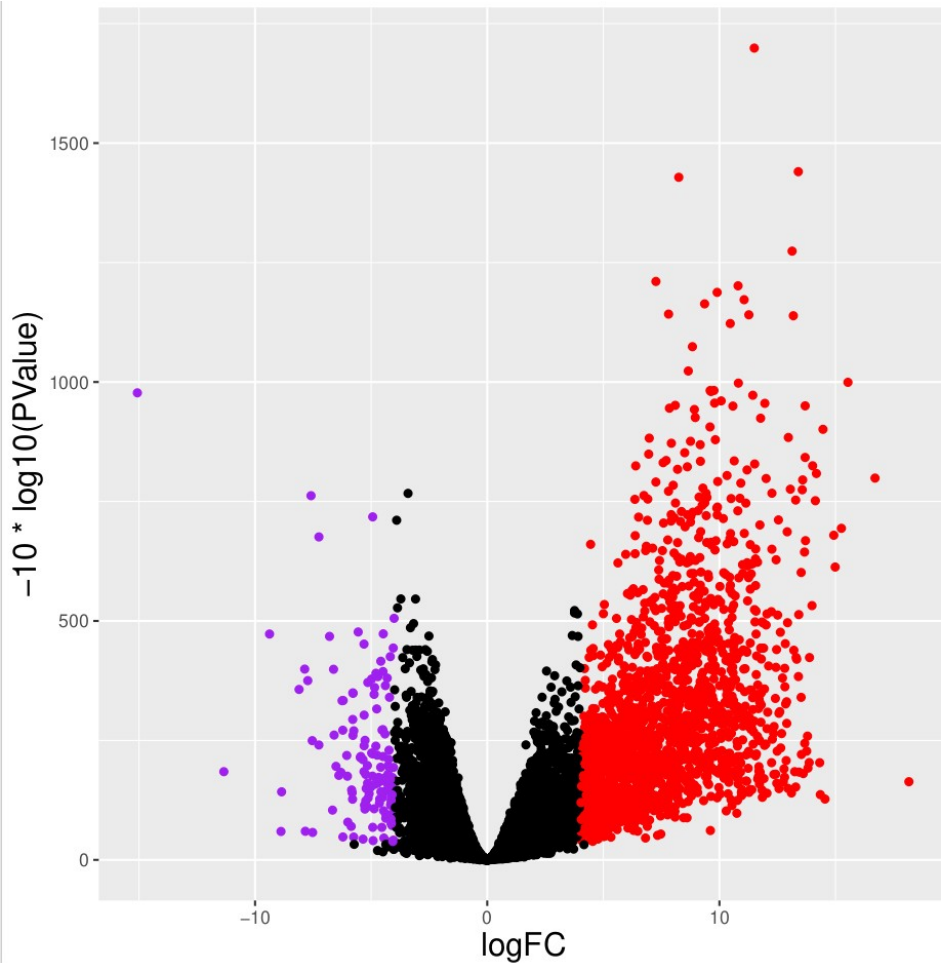
- Upreg in HepG2
- Not significant
- Upreg in Tumor1



cluster №2

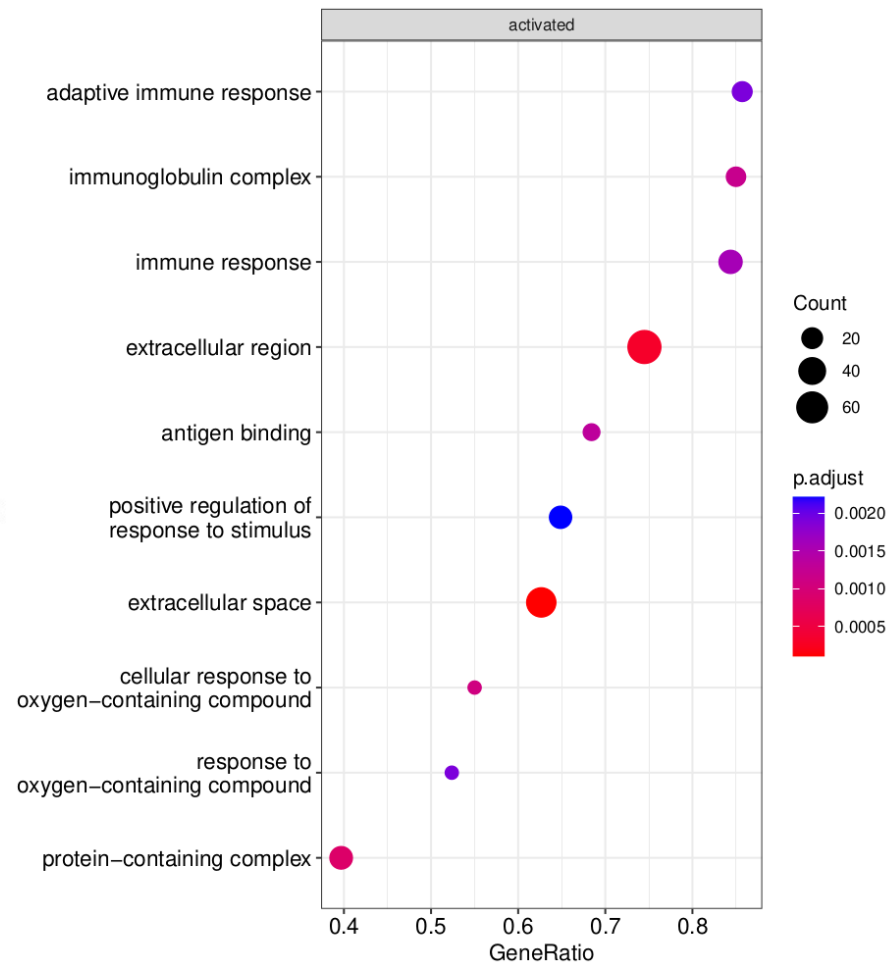


cluster №2

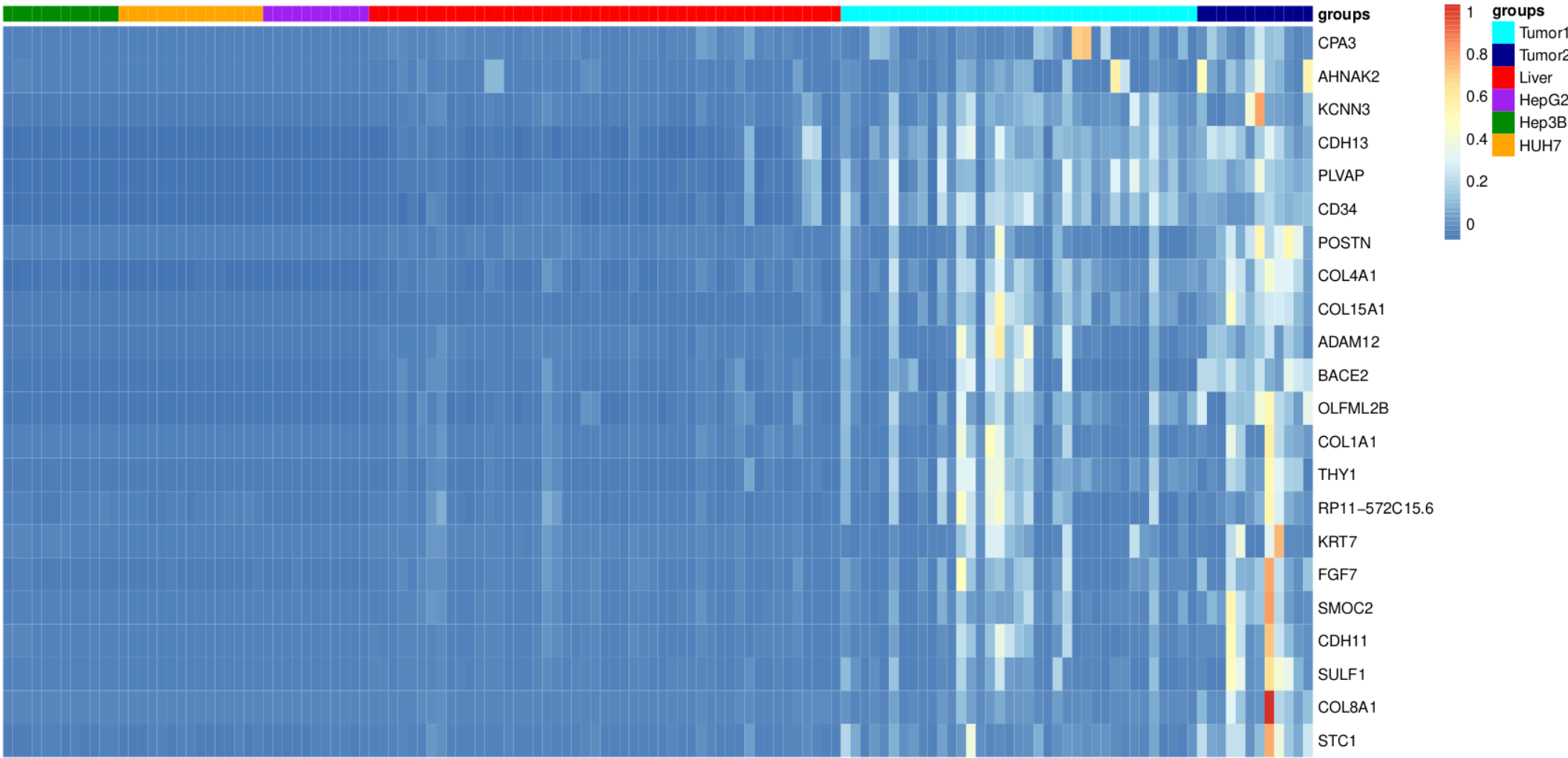


Regulation

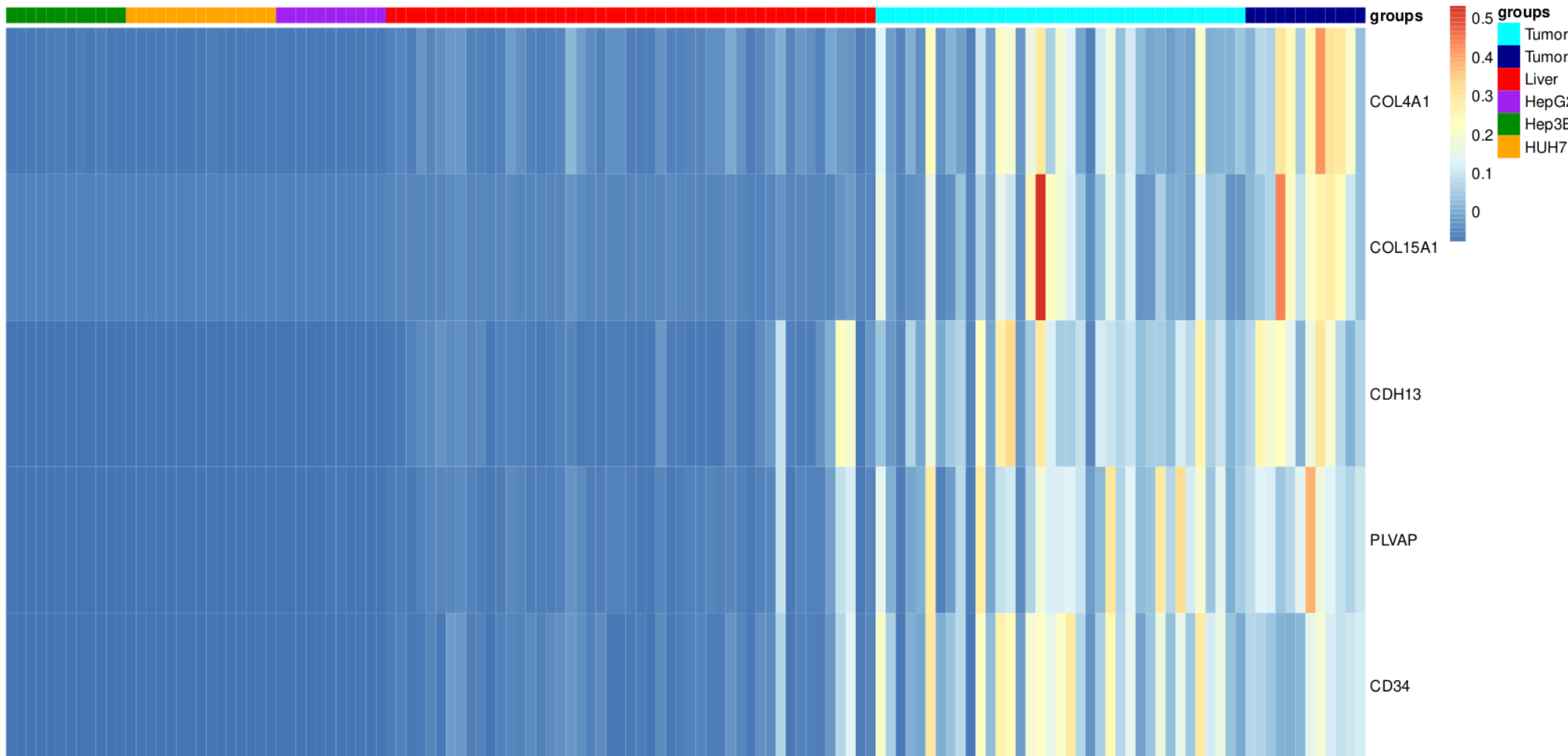
- Upreg in HepG2
- Not significant
- Upreg in Tumor2



Markers expression

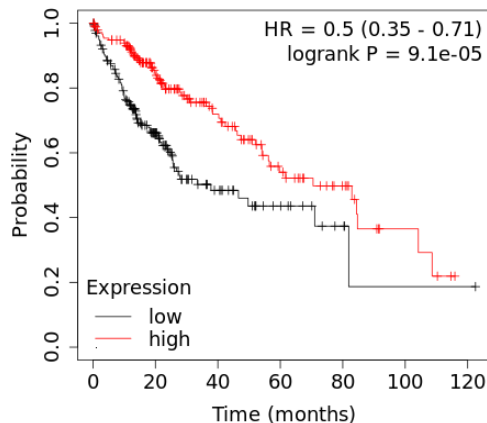


With z-score filter

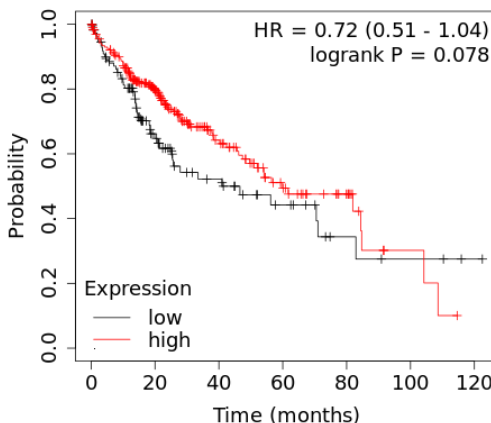


Patients survivability

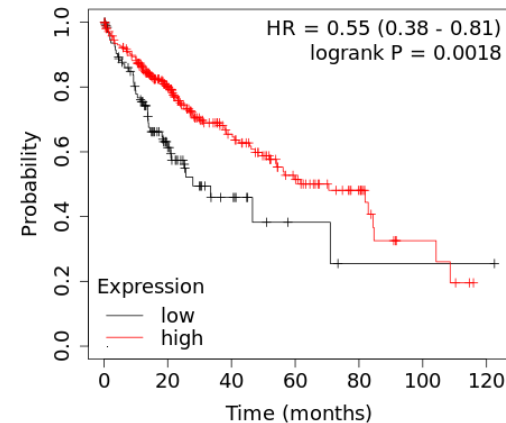
PLVAP (83483)



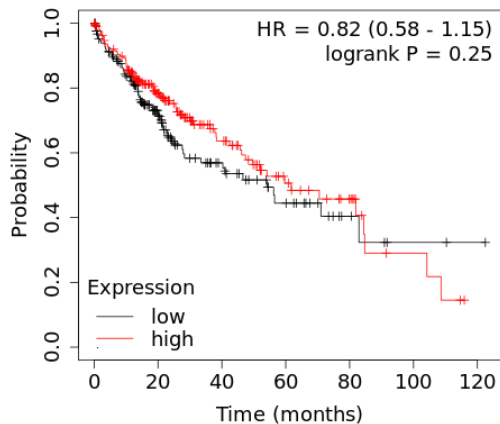
CDH13 (1012)



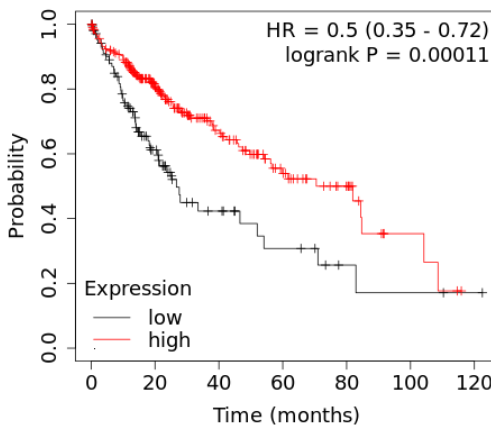
CD34 (947)



COL4A1 (1282)



COL15A1 (1306)



Conclusion



- According to RNA-seq data, genes were found whose expression is increased in hepatocarcinoma samples, both in comparison with healthy liver and in comparison with cell lines derived from hepatocarcinoma (interaction markers - tumor-organism).
- Increased expression of markers of tumor-organism interaction leads to better survival of patients with hepatocarcinoma.
- RNA-seq of surgical samples does not make it possible to determine which cells are responsible for the increased expression of markers - the tumor or the surrounding healthy tissue. ScRNA-seq studies are needed to answer this question.

Спасибо за внимание