

Supplementary Materials for

Glucose metabolism 3-gene signature associates with poor prognosis in hepatocellular carcinoma as a hallmark of tumor microenvironment evolution and progression

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Fig S1

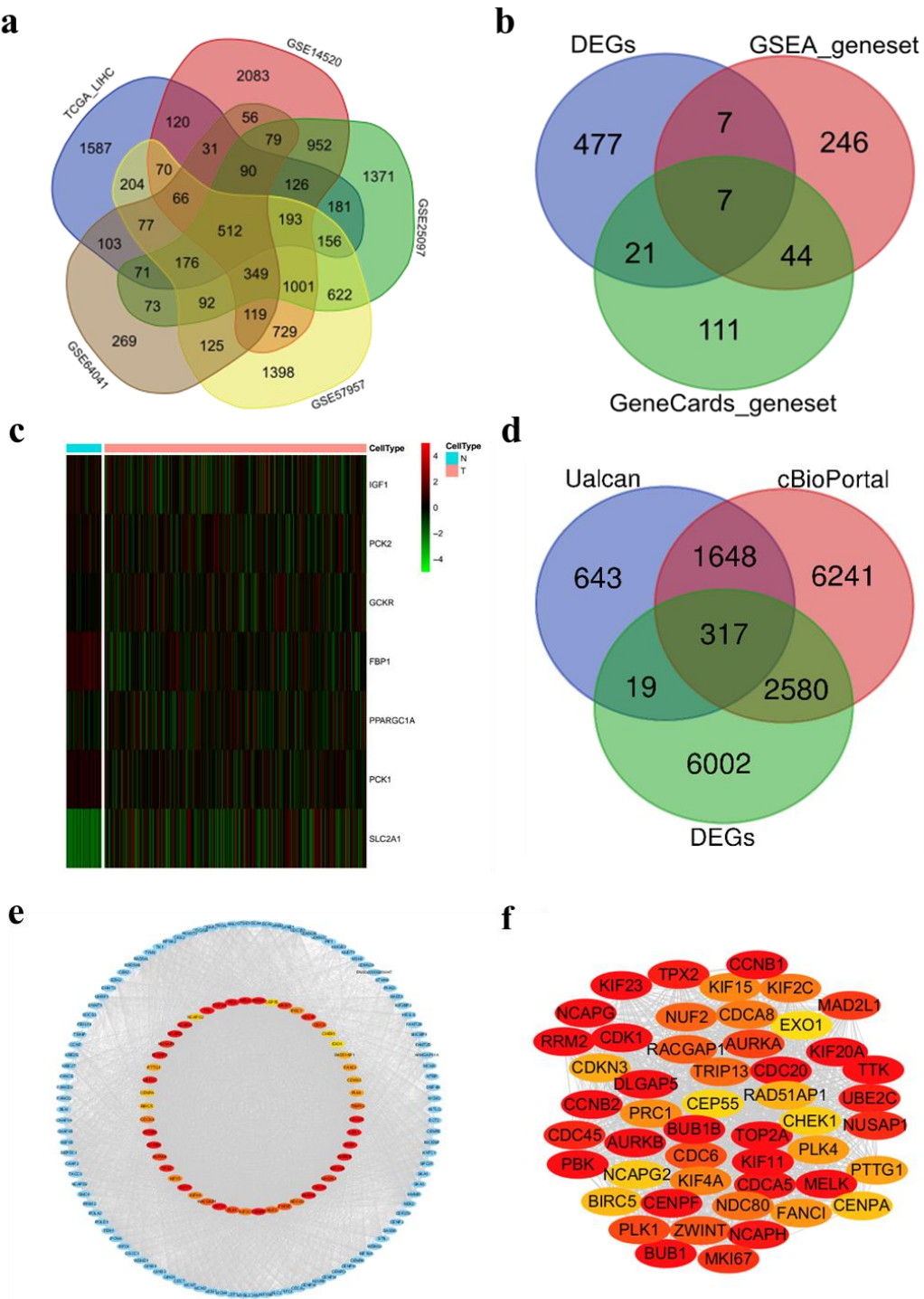


Fig. S1

a Differential expression analysis by TCGA and multiple GEO RNA-Seq data for intersection
b Discovery of glucose metabolism-related differentially expressed genes(DEGs)

c Heatmap of 7 glucose metabolism-related DEGs

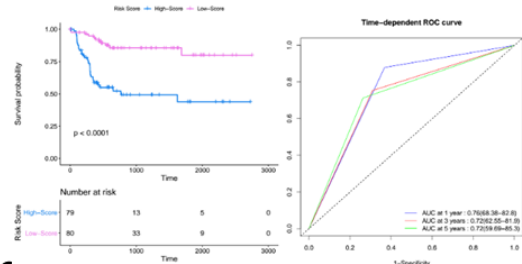
d finding 371 positively related genes for SLC2A1

e PPI of 371 positively related genes for SLC2A1

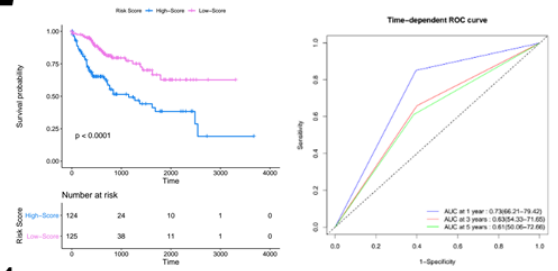
f 50 hubgene of positively related genes for SLC2A1

Fig S2

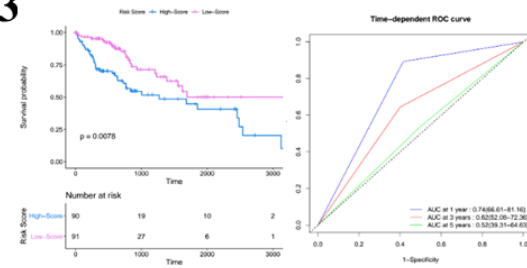
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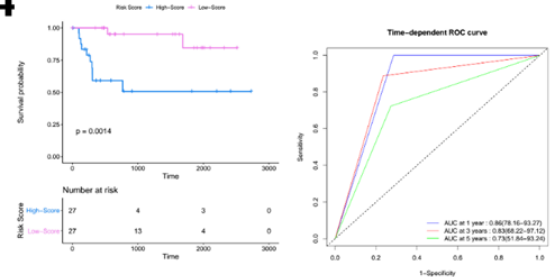
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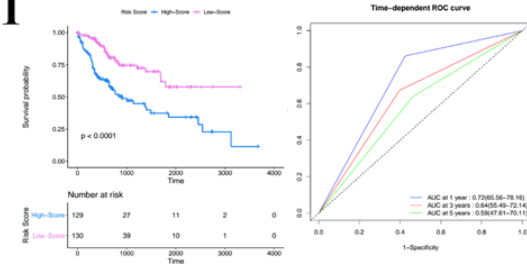
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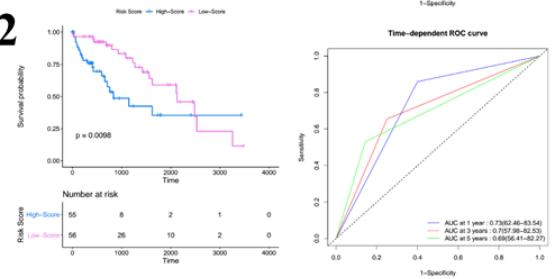
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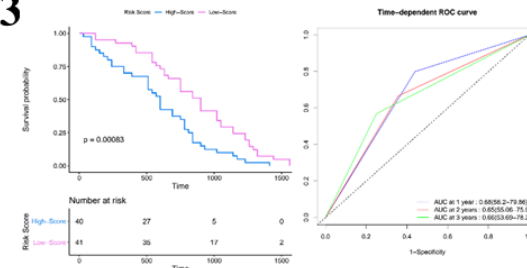
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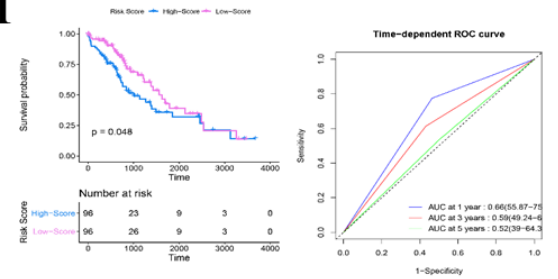
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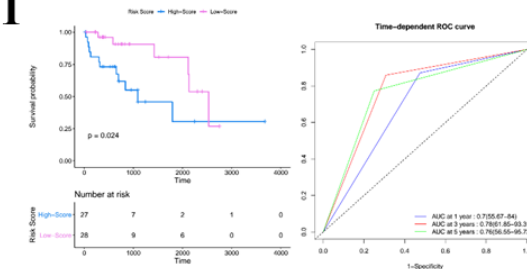
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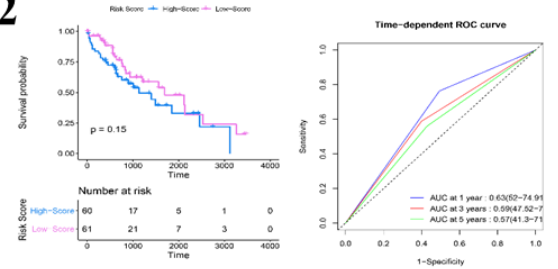
c-1



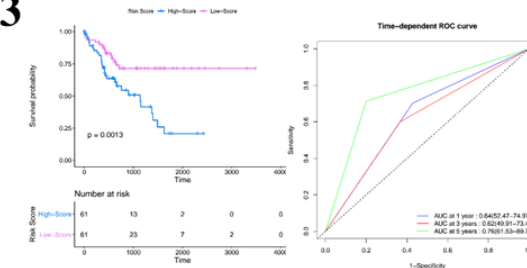
d-1



d-2



d-3



d-4

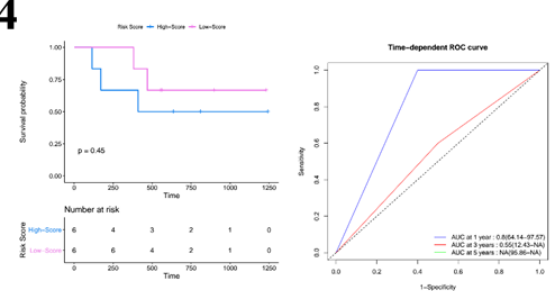


Fig. S2

Kaplan–Meier curves and ROC curves of patients in the low- and high-risk groups based on the 3 gene signature in clinical subtypes (a-1: Asian, a-2: Male, a-3: G2, a-4: Asian+Male+G2, b-1: train cohort, b-2: validation cohort, b-3:validation cohort2, c-1:White, d-1: G1, d-2: Female, d-3: G3, d-4: G4)

Fig S3

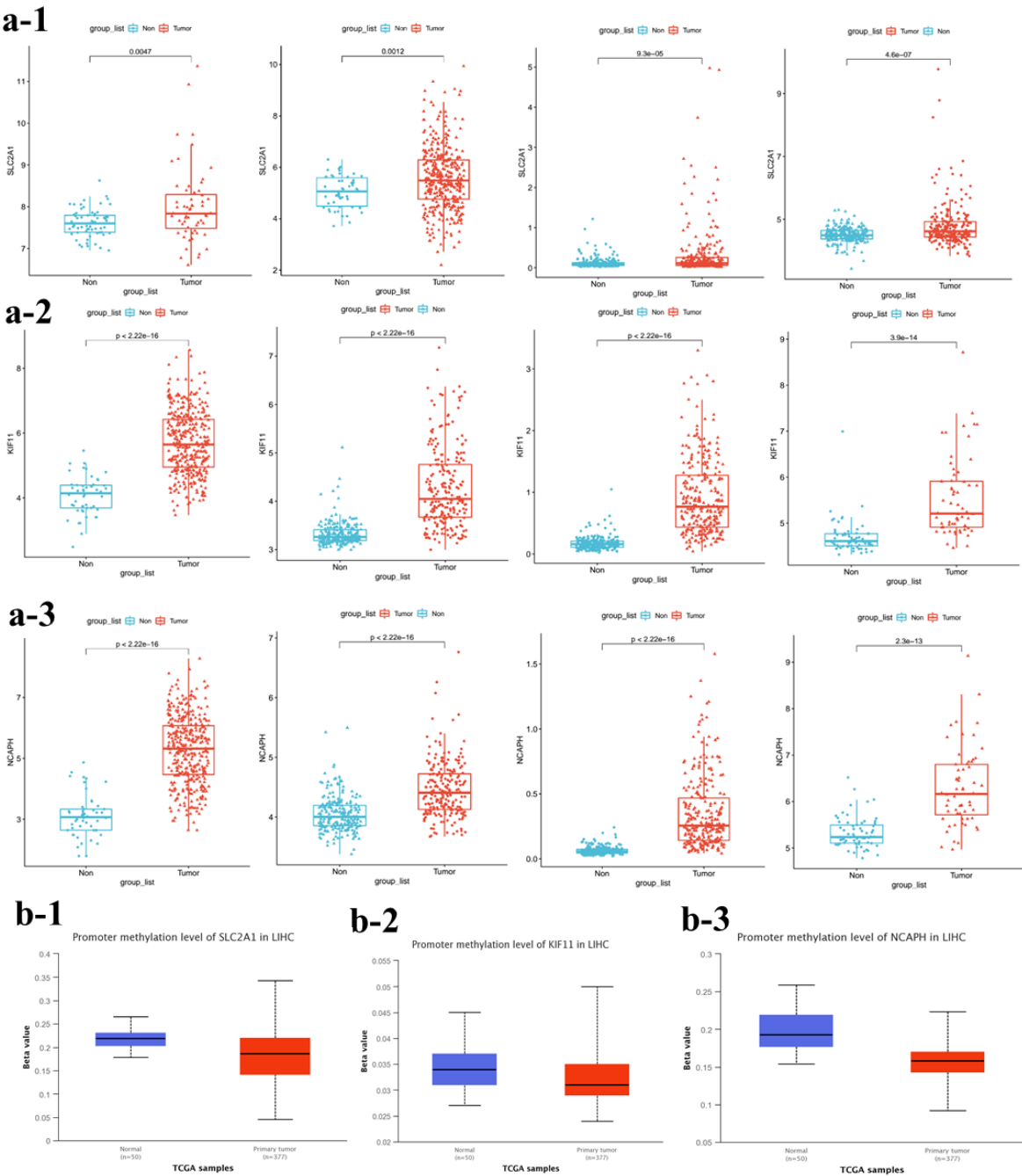


Fig. S3

b Promoter methylation of SLC2A1, NCAPH and KIF1 in LIHC(b-1 SLC2A1, b-2 KIF11, b-3 NCAPH)

Fig S4

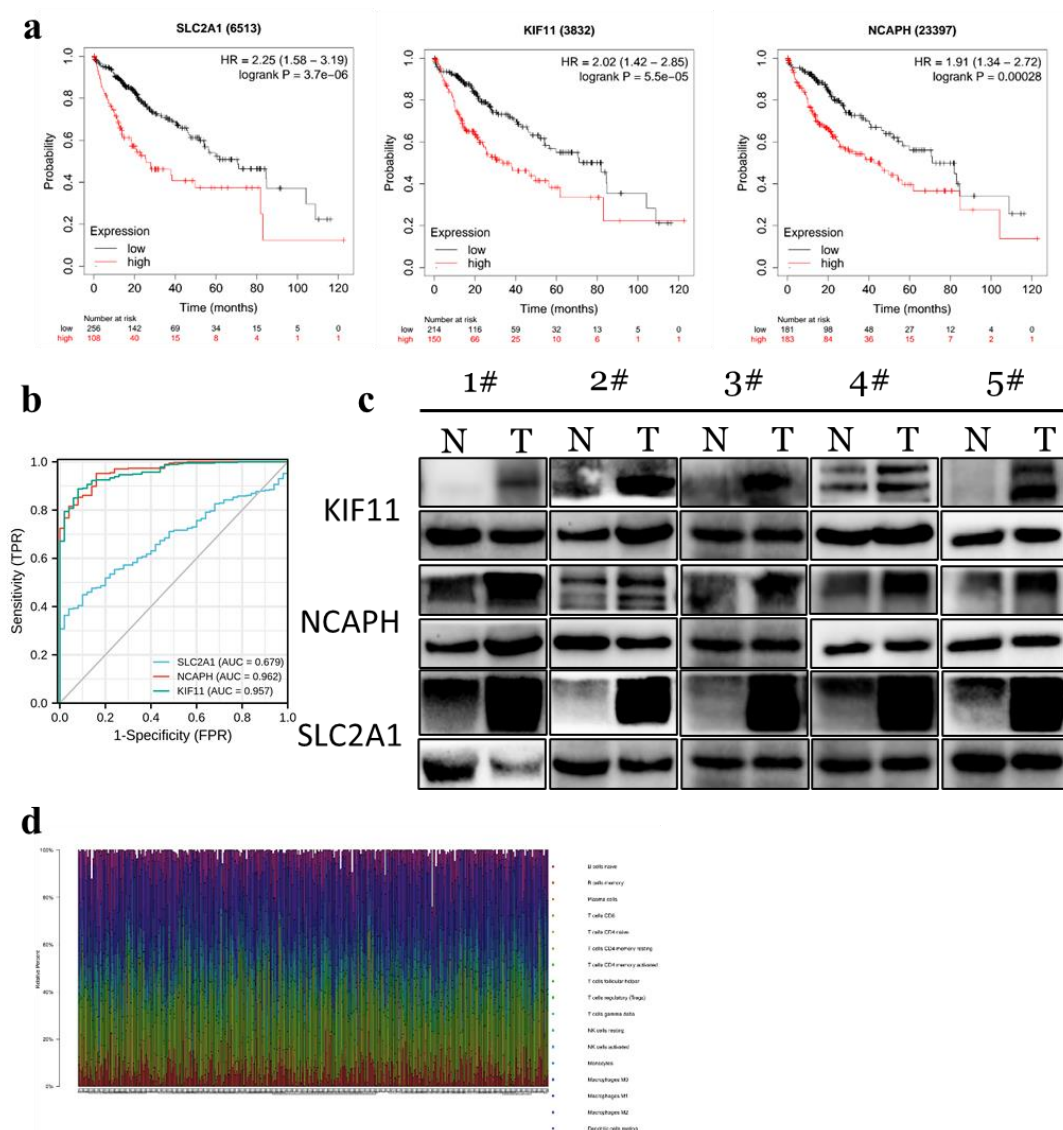


Fig. S4

a The Kaplan–Meier survival curves showing patients with higher expression levels of SLC2A1, NCAPH and KIF1 had a poor prognosis in LIHC

b ROC curves of the 3 signature genes in the hepatocellular carcinoma diagnostic model

c Representative Western blot showing 3 gene signature protein expression in liver normal (N) and matched cancer tissue (n=10)

d Histogram of the relative content of 22 immune cells in the hepatocellular carcinoma microenvironment, as determined by Cybersort

Fig S5

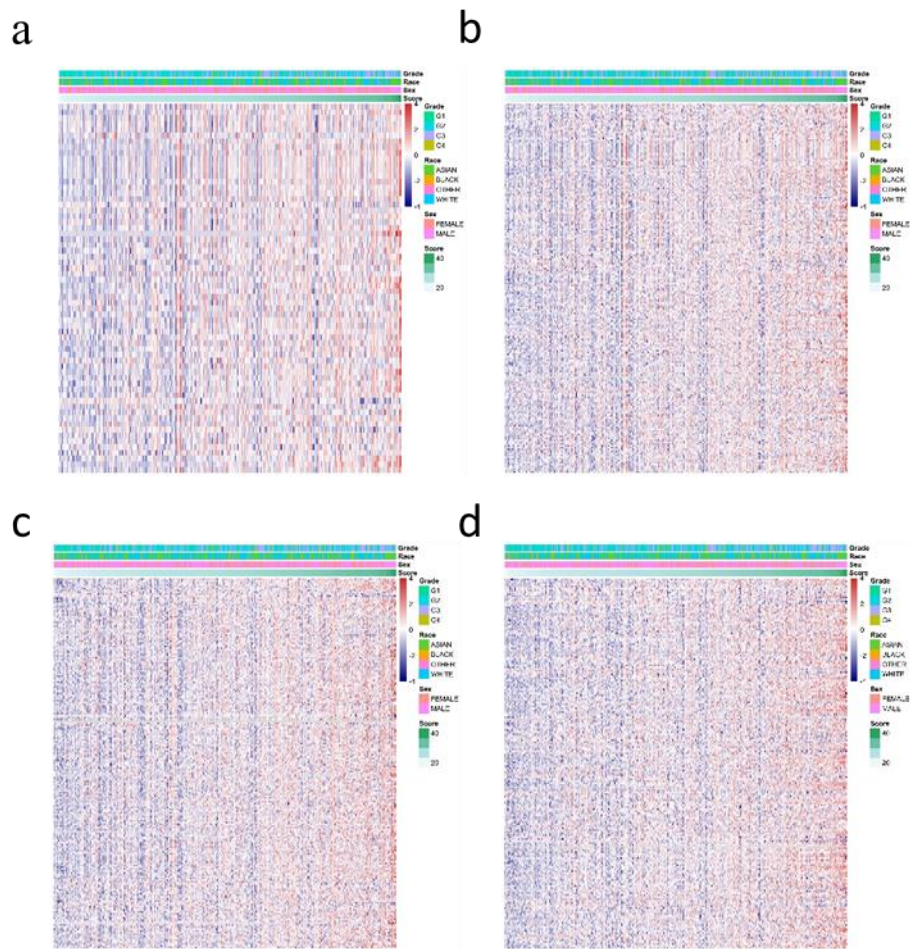


Fig. S5

Heat map of different phenotypic gene sets with ranking from low risk score to high risk score(a: Cell Cycle, b: EMT, c: Glycolysis,d: Inflammatory)