

## Supplementary Materials

### Methods

*Differentiation of metabolic status of the patients by the expression of corresponding rate-limiting enzymes*

Firstly, we used the average of the sum of HK1, HK2, and HK3 expression values to represent the expression value of hexokinase. This way, the expression value of phosphofructokinase-1 and pyruvate kinase were calculated. Secondly, the sum of the expression values of these three rate-limiting enzymes in glycolysis was calculated to represent the value of glycolysis pathway activity. Similarly, we calculated the sum of the expression values of corresponding rate-limiting enzymes of the TCA cycle pathway and fatty acid metabolism pathway. Thirdly, we calculated the sum of the values of glycolysis, fatty acid and, the TCA cycle activity to represent the metabolism value. Finally, we separated the TCGA-LAML training cohort into metabolism<sup>high</sup> and metabolism<sup>low</sup> groups by the median metabolism value. The Formula is as follows:

$$\text{Value of Glycolysis activity} = \frac{(E_{HK1} + E_{HK2} + E_{HK3})}{3} + \frac{(E_{PFKL} + E_{PFKM} + E_{PFKP})}{3} + \frac{(E_{PKLR} + E_{PKM})}{2}$$

$$\text{Value of TCA cycle activity} = E_{CS} + \frac{(E_{IDH1} + E_{IDH2} + E_{IDH3A} + E_{IDH3B} + E_{IDH3G})}{5} + \frac{(E_{OGDH} + E_{DLST} + E_{DLD})}{3}$$

$$\text{Value of Fatty acid metabolism activity} = \frac{(E_{CPT1A} + E_{CPT1B} + E_{CPT2})}{3}$$

Metabolism value = value of Glycolysis activity + value of TCA cycle activity + value of Fatty acid metabolism activity

Where  $E$  is the expression value of key rate-limiting enzyme genes.

**Table S1.** The overall features of the TCGA-LAML, Beat-AML, GSE37642, GSE10358, and GSE12417 databases.

	TCGA-LAML	Beat-AML	GSE37642	GSE10358	GSE12417
Number of cases	131	252	91	73	136
The time frames when diagnosed	2001-2010	NA	NA	NA	NA
Created in the year	2007	2015	2012	2008	2008

NA, not available.

**Table S2.** Metabolic pathways that were significantly enriched (FDR<0.25) in the gene expression data of the group with short-term survival (OS<12 months) compared with the group with long-term survival (OS>12 months) in the TCGA-LAML database.

Gene set name from Molecular Signature Database	Description of Gene set	Size <sup>1</sup>	NES <sup>2</sup>	FD <sup>3</sup>
GOBP_FRUCTOSE_1_6_BISPHOSPHATE_METABOLIC_PROCESS <sup>4</sup>	Genes involved in the chemical reactions and pathways involving fructose 1,6-bisphosphate collected by Gene Ontology	9	- 1.76	0.24 6

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MOOTHA_GLUONEOGENESIS <sup>5</sup>	Genes involved in gluconeogenesis collected by Broad Institute	29	-	0.24	1.56	6
MODULE_152 <sup>6</sup>	Genes involved in metabolism in Cancer collected by Broad Institute	122	-	0.22	1.55	8
REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE <sup>7</sup>	Pyruvate metabolism and TCA cycle collected by Reactome Database	54	-	0.22	1.54	4
MOOTHA_TCA	Genes involved in TCA cycle collected by Broad Institute	16	-	0.21	1.53	2
MODULE_307	Genes involved in metabolism in Cancer collected by Broad Institute	25	-	0.20	1.53	3
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION	Genes involved in Mitochondrial Fatty Acid Beta-Oxidation collected by Reactome Database	37	-	0.19	1.52	7
BIOCARTA_ETC_PATHWAY <sup>8</sup>	Genes involved in Electron Transport Reaction in Mitochondria collected by BioCarta Database	10	-	0.18	1.52	3
KEGG_OXIDATIVE_PHOSPHORYLATION <sup>9</sup>	Genes involved in Oxidative phosphorylation collected by Kyoto Encyclopedia of Genes and Genomes	125	-	0.17	1.51	9
WP_TCA_CYCLE_AKA_KREBS_OR_CITRIC_ACID_CYCLE <sup>10</sup>	Genes involved in TCA cycle collected by WikiPathways Database	18	-	0.18	1.50	0
REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE	Genes involved in TCA cycle collected by Reactome Database	22	-	0.19	1.48	3
WP_AEROBIC_GLYCOLYSIS	Genes involved in aerobic glycolysis collected by WikiPathways Database	11	-	0.18	1.48	5
MOOTHA_FFA_OXYDATION	Genes involved in free fatty acid oxidation collectdy by Broad Institute	23	-	0.20	1.45	6
MOOTHA_ROS	Genes involved in Reactive oxidative species collected by Broad Institute	7	-	0.21	1.43	8

WP_OXIDATIVE_STRESS_RESPONSE	Genes involved in oxidative stress resoiobse by WikiPathways	28	-	0.21	1.43	3
REACTOME_FATTY_ACID_METABOLISM	Genes involved in fatty acid metabolism collected by Reactome	171	-	0.24	1.40	6

1. Size, the number of genes enriched in the gene set; 2. FDR, false discovery rate; 3. NES, normalized enriched score; 4. GOBP, Gene Ontology Biological Process; 5. MOOTHA, gene set created by Broad Institute; 6. MODULE, gene involved in cancer collected by Broad Institute; 7. REACTOMEN, Reactome Database; 8. BIOCARTA, BioCarta Database; 9. KEGG, Kyoto Encyclopedia of Genes and Genomes; 10. WP, WikiPathways database.

**Table S3.** Metabolic pathways that were significantly enriched (FDR<0.2 and |NES|>1.5) in the gene expression data of the metabolism<sup>high</sup> compared with metabolism<sup>low</sup> group in the TCGA-LAML.

Gene set name from MSigDB	Description of Gene set	Size <sup>1</sup>	NES <sup>2</sup>	FDR <sup>3</sup>
GOBP_FATTY_ACID_BETA_OXIDATION <sup>4</sup>	Genes involved in the fatty acid beta oxidation collected by Gene Ontology	75	1.83	0.042
GOBP_GLUCOSE_IMPORT	Genes involved in glucose import collected by Gene Ontology	63	1.76	0.042
KEGG_CITRATE_CYCLE_TCA_CYCLE <sup>5</sup>	Genes involved in citrate cycle TCA cycle collected by Kyoto Encyclopedia of Genes and Genomes	30	1.57	0.081
KEGG_GLYCOLYSIS_GLUONEOGENESIS	Genes involved in Glycolysis Gluconeogenesis collected by Kyoto Encyclopedia of Genes and Genomes	54	1.61	0.080
KEGG_OXIDATIVE_PHOSPHORYLATION	Genes involved in oxidative phosphorylation collected by Kyoto Encyclopedia of Genes and Genomes	125	1.59	0.082
REACTOME_GLYCOLYSIS <sup>6</sup>	Genes involved in glycolysis collected by Reactome	69	2.04	0.007
REACTOME_GLUCOSE_METABOLISM	Genes involved in glucose metabolism by Reactome	87	2.06	0.007

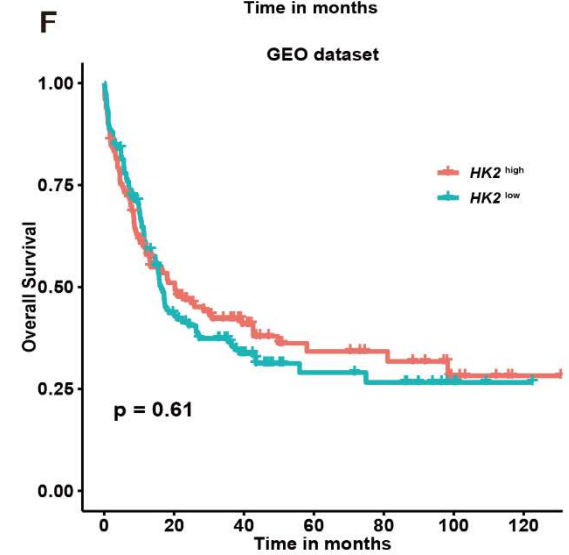
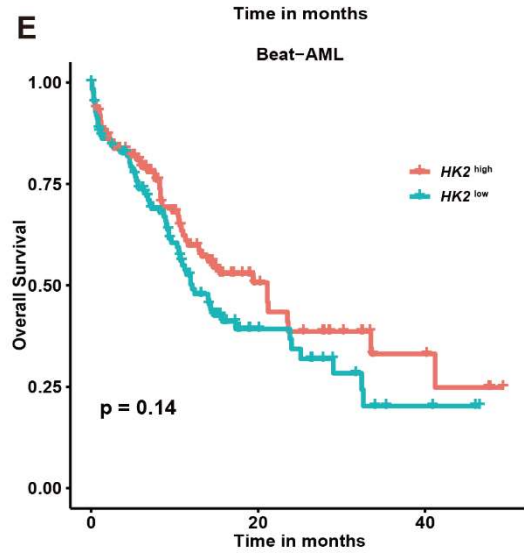
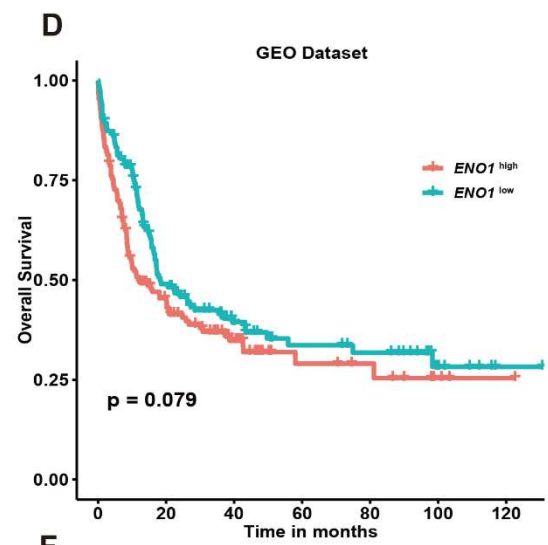
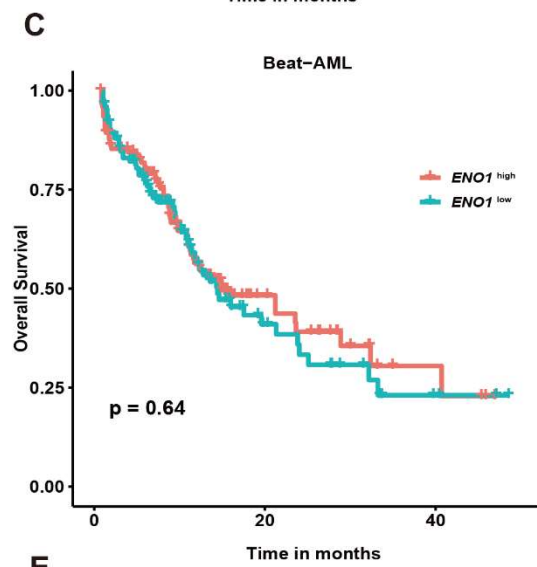
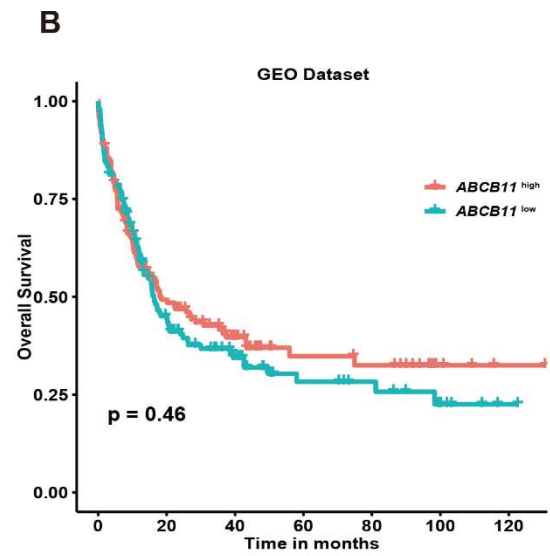
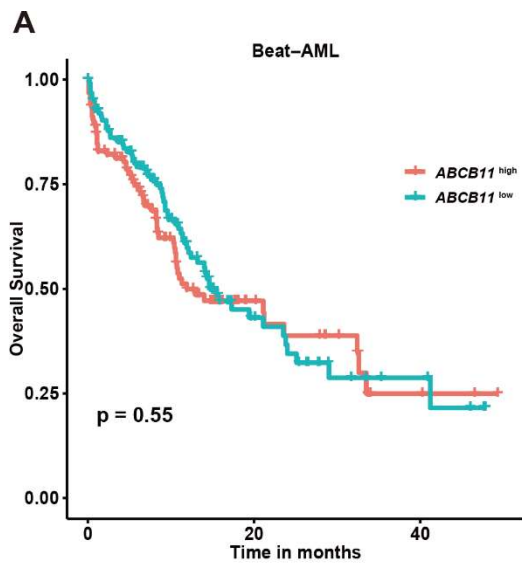
1. Size, the number of genes enriched in the gene set; 2. FDR, false discovery rate; 3. NES, normalized enriched score; 4. GOBP, Gene Ontology Biological Process; 5. KEGG, Kyoto Encyclopedia of Genes and Genomes; 6. REACTOMEN, Reactome Database.

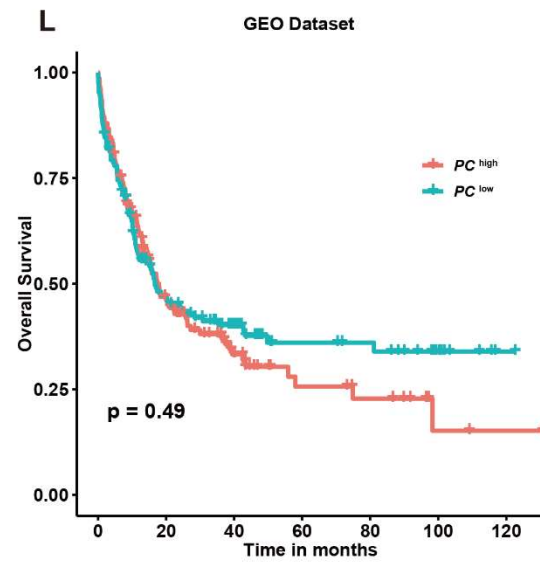
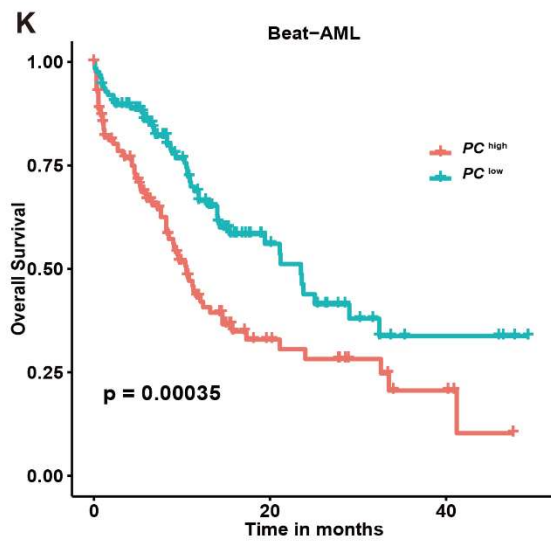
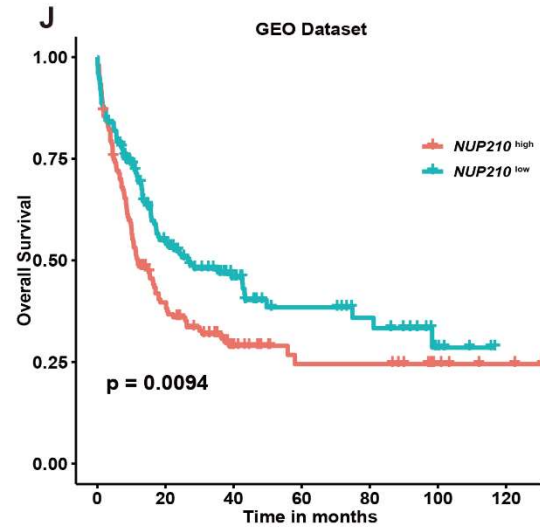
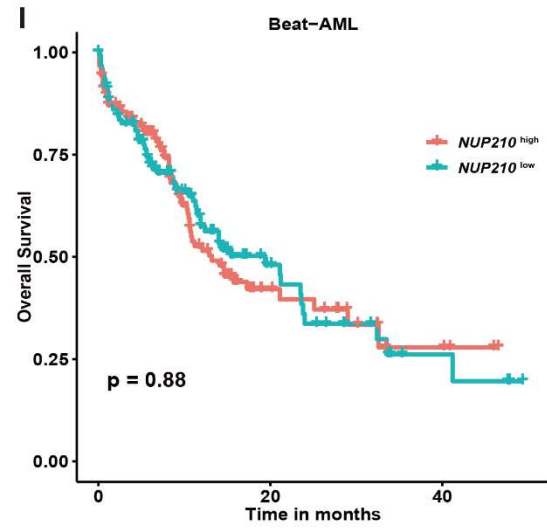
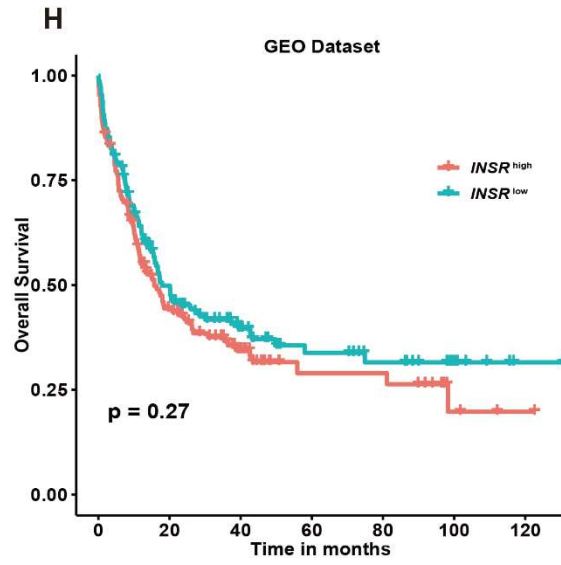
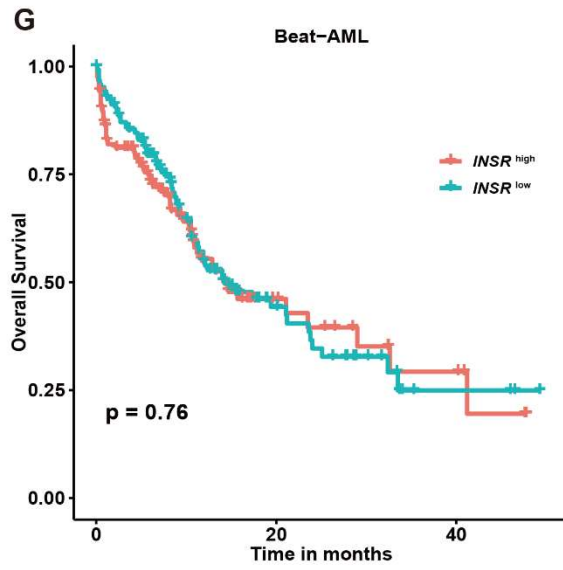
**Table S4.** The metabolism pathways of 33 prognosis-related genes identified by univariate Cox regression analysis

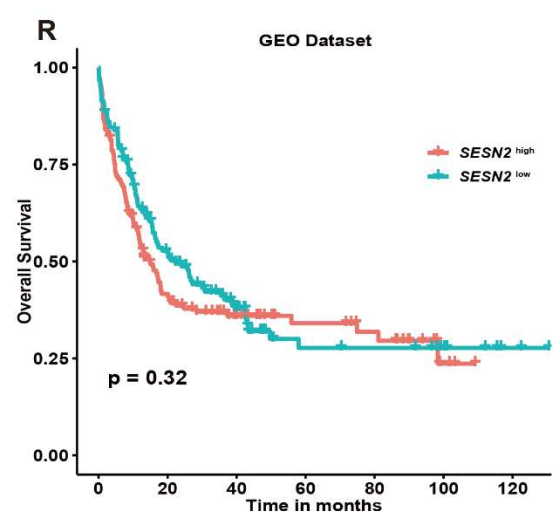
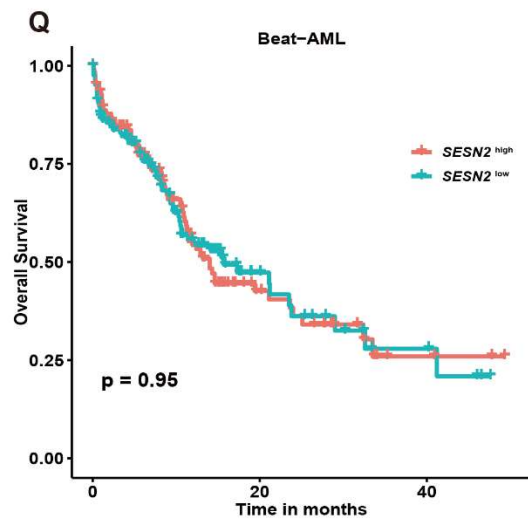
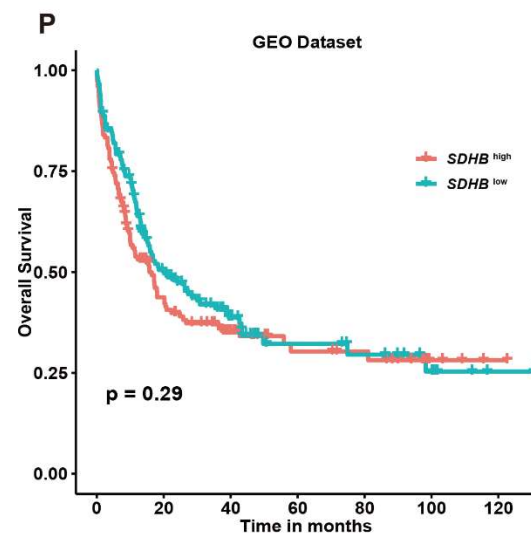
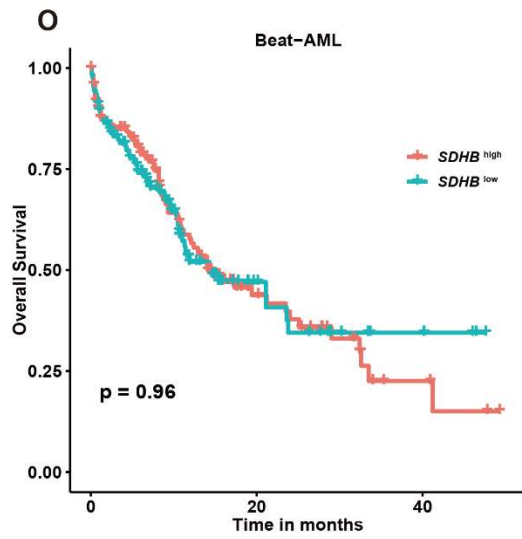
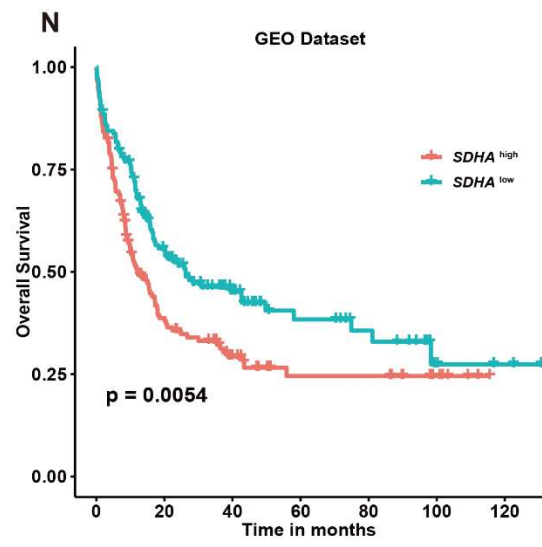
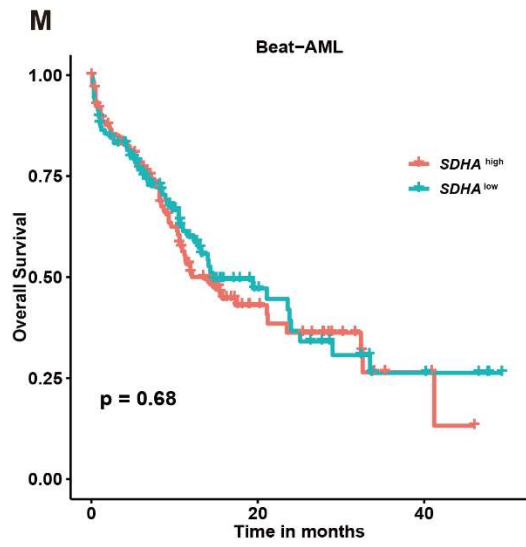
Gene	Full name of gene	Related Metabolism pathway
<i>ACOXL</i>	Acyl-CoA Oxidase Like	Fatty acid metabolism
<i>CRAT</i>	Carnitine O-Acetyltransferase	Fatty acid metabolism
<i>SESN2</i>	Sestrin 2	Fatty acid metabolism
<i>ABCD1</i>	ATP Binding Cassette Subfamily D Member 1	Fatty acid metabolism
<i>HSD17B10</i>	Hydroxysteroid 17-Beta Dehydrogenase 10	Fatty acid metabolism
<i>ECH1</i>	Enoyl-CoA Hydratase 1	Fatty acid metabolism
<i>ECHS1</i>	Enoyl-CoA Hydratase, Short Chain 1	Fatty acid metabolism
<i>ETFB</i>	Electron Transfer Flavoprotein Subunit Beta	Fatty acid metabolism
<i>ABCB11</i>	ATP Binding Cassette Subfamily B Member 11	Fatty acid metabolism
<i>SORT1</i>	Sortilin 1	Glycolysis
<i>C1QTNF12</i>	C1q And TNF Related 12	Glycolysis
<i>PEA15</i>	Proliferation And Apoptosis Adaptor Protein 15	Glycolysis
<i>SLC27A4</i>	Solute Carrier Family 27 Member 4	Glycolysis
<i>INSR</i>	Insulin Receptor	Glycolysis
<i>PC</i>	Pyruvate Carboxylase	Glycolysis
<i>IDH3G</i>	Isocitrate Dehydrogenase (NAD(+)) 3 Non-Catalytic Subunit Gamma	TCA cycle
<i>IDH3B</i>	Isocitrate Dehydrogenase (NAD(+)) 3 Non-Catalytic Subunit Beta	TCA cycle
<i>SDHB</i>	Succinate Dehydrogenase Complex Iron Sulfur Subunit B	TCA cycle
<i>ACO2</i>	Aconitase 2	TCA cycle
<i>SUCLG1</i>	Succinate-CoA Ligase GDP/ADP-Forming Subunit Alpha	TCA cycle
<i>PGM1</i>	Phosphoglucomutase 1	Glycolysis
<i>HK1</i>	Hexokinase 1	Glycolysis
<i>ALDOC</i>	Aldolase, Fructose-Bisphosphate C	Glycolysis
<i>ALDH2</i>	Aldehyde Dehydrogenase 2	Fatty acid metabolism
<i>PFKL</i>	Phosphofructokinase, Liver Type	Glycolysis
<i>ENO1</i>	$\alpha$ -Enolase 1	Glycolysis
<i>PFKP</i>	Phosphofructokinase, Platelet	Glycolysis

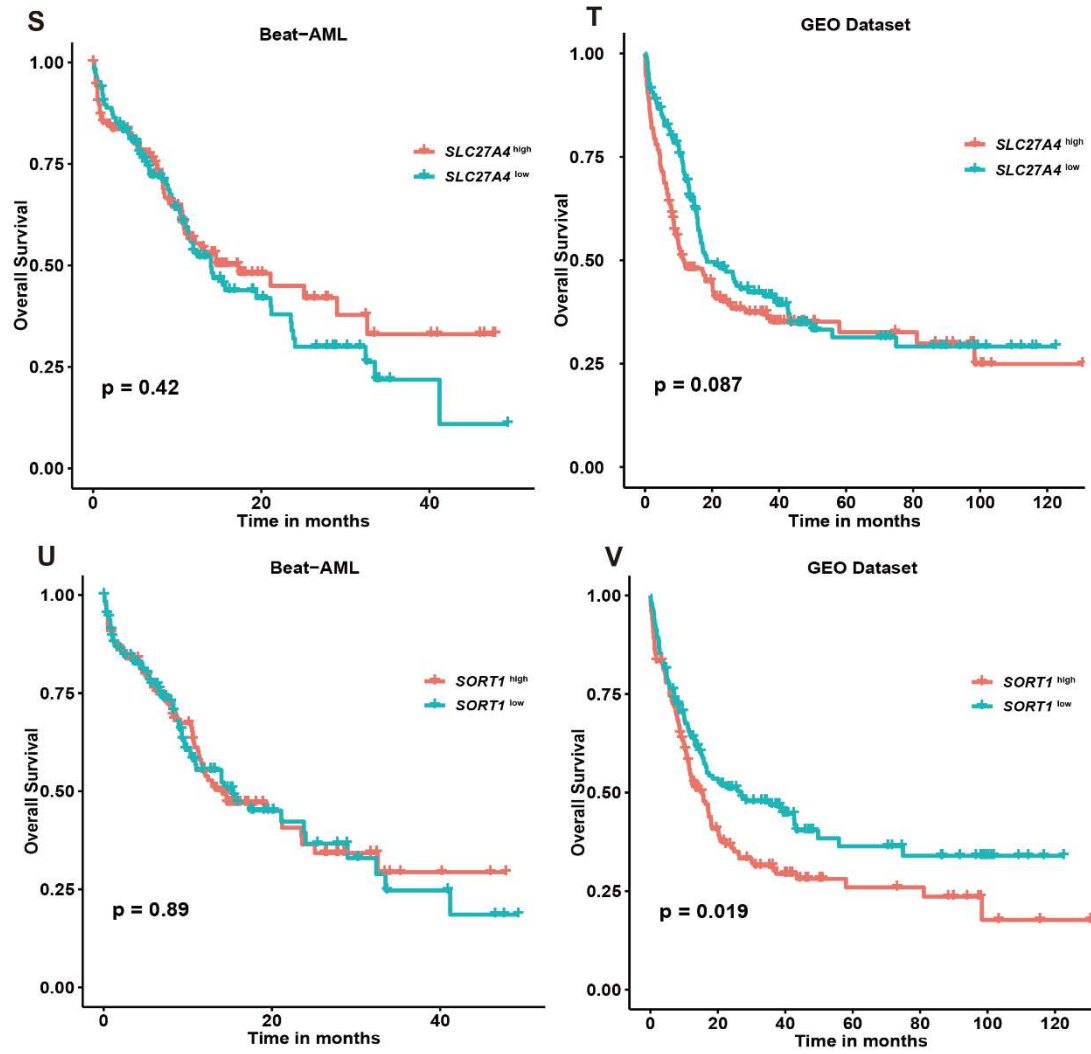
<i>AKR1A1</i>	Aldo-Keto Reductase Family 1 Member A1	Glycolysis
<i>CYC1</i>	Cytochrome C1	TCA cycle
<i>SDHA</i>	Succinate Dehydrogenase Complex Flavoprotein Subunit A	TCA cycle
<i>NUP210</i>	Nucleoporin 210	Glycolysis
<i>PPP2R1A</i>	Protein Phosphatase 2 Scaffold Subunit Aalpha	Glycolysis
<i>HK2</i>	Hexokinase 2	Glycolysis

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**Figure S1.** Kaplan–Meier curves for overall survival of AML patients with high and low expression of *ABCB11*, *ENO1*, *HK2*, *INSR*, *NUP210*, *PC*, *SDHA*, *SDHB*, *SESN2*, *SLC27A4* and *SORT1* in the Beat-AML (A, C, E, G, I, K, M, O, Q, S, U) and GEO cohorts (B, D, F, H, J, L, N, P, R, T, V).