

Muti-omics insights into PDHA1 as a predictive biomarker for prognosis, immunotherapy efficacy, and drug sensitivity in hepatocellular carcinoma

Yong Pan^{1,2}, Yiru Zhang², Daiwen Mao¹, Zhou Fang¹, Yingqiu Ma¹, Danwen Jin³, Shibo Li^{1*}

1 Department of Infectious Diseases, Zhoushan Hospital, Wenzhou Medical University, Zhoushan, China

2 State Key Laboratory for the Diagnosis and Treatment of Infectious Diseases, The First Affiliated Hospital of Zhejiang University, Hangzhou, China

3 Pathological Diagnosis Center, Zhoushan Hospital, Wenzhou Medical University, Zhoushan, China

Corresponding author:

Shibo Li

Department of Infectious Diseases, Zhoushan Hospital, Wenzhou Medical University, Zhoushan, China. lsb0398@126.com

Table S1 Baseline characteristics of the patients in TCGA cohort.

characteristics	TCGA-LIHC cohort
Number of patients	374
Gender (%)	
Female	121(32.4)
Male	253(67.6)
Age (median, range)	61(16-90)
Tumor grade (%)	
G1+G2	233(62.3)
G3+G4	136(36.4)
Unknown	5(1.3)
Stage (%)	
I+II	260(69.5)
III+IV	90(24.1)
Unknown	24(6.4)
AFP (%)	

≤400ng/L	215(57.5)
> 400ng/L	65(17.4)
Unknown	94(25.1)
Vascular Invasion (%)	
Yes	110(29.4)
No	208(55.6)
Unknown	56(15.0)

Table S2 The detailed information of enriched terms by GSEA.

ID	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalue	rank	leading_edge
REACTOME_BIOLOGICAL_OXIDATIONS	15	-0.44549975	-2.02623259	0.00744734	0.10612466	0.08427258	121	tags=53%, list=14%, signal=47%
REACTOME_CELLULAR_RESPONSES_TO_STIMULI	16	-0.41944866	-1.99498031	0.00566199	0.10612466	0.08427258	140	tags=62%, list=16%, signal=54%

REACTOME _NERVOUS _SYSTEM_ DEVELOPM ENT	21	0.43717274	1.87930225	0.00590846	0.10612466	0.08427258	367	tags=76%, list=41%, signal=46%
REACTOME _NEURONA L_SYSTEM	30	0.38539483	1.8745877	0.00545236	0.10612466	0.08427258	312	tags=63%, list=35%, signal=43%
REACTOME _EXTRACE LLULAR_M ATRIX_OR GANIZATIO N	12	0.50831014	1.78614752	0.01050422	0.11974807	0.0950908	236	tags=67%, list=26%, signal=50%
KEGG_MET ABOLISM_ OF_XENOB IOTICS_BY _CYTOCHR OME_P450	10	-0.47390995	-1.80347701	0.01699811	0.13110268	0.10410739	162	tags=70%, list=18%, signal=58%
REACTOME _RNA_POL YMERASE_ II_TRANSC RIPTION	15	0.46391138	1.77761094	0.01803118	0.13110268	0.10410739	153	tags=53%, list=17%, signal=45%
REACTOME	37	0.33254128	1.75863591	0.01840038	0.13110268	0.10410739	367	tags=65%,

_DEVELOP MENTAL_B IOLOGY								list=41%, signal=40%
WP_METAP ATHWAY_ BIOTRANS FORMATIO N_PHASE_I _AND_II	16	-0.37627795	-1.78965189	0.02070679	0.13114302	0.10413942	121	tags=50%, list=14%, signal=44%
REACTOME _TRANSMI SSION_ACR OSS_CHEM ICAL_SYN APSES	19	0.3980214	1.66360856	0.03891066	0.17916793	0.14227555	299	tags=63%, list=33%, signal=43%
REACTOME _BINDING_ _AND_UPTA KE_OF_LIG ANDS_BY_ SCAVENGE R_RECEPT ORS	10	-0.43026828	-1.63739747	0.03996969	0.17916793	0.14227555	401	tags=90%, list=45%, signal=50%
REACTOME _METABOL ISM_OF_LI	24	-0.28458461	-1.62416765	0.03633342	0.17916793	0.14227555	121	tags=33%, list=14%, signal=30%

PIDS								
KEGG_PATHWAYS_IN_CANCER	10	-0.4259887	-1.62111141	0.04086286	0.17916793	0.14227555	519	tags=100%, list=58%, signal=42%

Table S3 P value and correlation coefficient of the top 10 related genes.

id	Correlation pearson	P value pearson	P adj pearson	Correlation spearman	P value spearman	P adj spearman	Gene name	Gene type
ENSG00000184831.14	0.759068399	8.93424e-71	2.51356e-66	0.726308641	0	0	APOO	Protein coding
ENSG00000004961.15	0.670670857	8.24781e-50	1.54696e-45	0.664533675	1.27309e-48	2.06438e-46	HCCS	Protein coding
ENSG00000110955.9	0.660356175	7.9043e-48	1.1119e-43	0.635635209	0	0	ATP5F1B	Protein coding
ENSG00000102054.18	0.624387173	1.70881e-41	1.92303e-37	0.615732827	0	0	RBBP7	Protein coding
ENSG00000130985.17	0.62024254	8.1311e-41	7.62534e-37	0.607709788	0	0	UBA1	Protein coding
ENSG00000069509.6	0.609970558	3.51761e-39	2.82755e-35	0.584970789	1.94184e-35	3.13975e-33	FUNDC1	Protein coding
ENSG00000132305.21	0.607929527	7.31563e-39	4.57373e-35	0.58246122	0	0	IMMT	Protein coding
ENSG00000182220.15	0.580460635	8.49653e-35	3.98402e-31	0.573317949	0	0	ATP6AP2	Protein coding
ENSG00000152234.1	0.60925001	4.55801e-39	3.20588e-35	0.569459295	0	0	ATP5F1A	Protein

6	8							coding
ENSG00000102144.1	0.56718816	5.74131e-33	2.15368e-29	0.564592268	0	0	PGK1	Protein coding
5	8							