The Combined Signatures of Hypoxia and Cellular Landscape Provides a Prognostic and Therapeutic Biomarker in HBV-Related Hepatocellular Carcinoma

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S1. Basical information of HBV-related HCC cohorts and other included datasets

Source	Platform	Platforms	Total number of patients	HBV-related HCC	HCV-related HCC	Prognosis data	Notes
Four different sets							
GSE14520	Affymetrix Human Genome U133A 2.0 Array	GPL571	221	221	0	Yes	mRNA data,clinical data
GSE10143	Human 6k Transcriptionally Informative Gene Panel for DASL	GPL5474	80	19	58	Yes	mRNA data,clinical data
ICGC-LIRI-JP	RNA-Seq	-	212	53	117	Yes	mRNA data,clinical data
Gao_fudan	RNA-Seq	-	159	159	0	Yes	mRNA data,SNV data,clinical data,doi.org/10.1016/j.cell.2019.08.052
Validataion set							
TCGA-LIHC	RNA-Seq	-	368	144	95	Yes	mRNA data,SNV data,clinical data
Treatment sets							
GSE109211	Illumina HumanHT-12 WG-DASL V4.0 expression bead chip	GPL13938	140	NA	NA	NO	SorafenibTtreatment
GSE35640	[HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array	GPL570	65	NA	NA	NO	MAGE-A3 immunotherapy
Pan-Cancer data							
TCGA-PanCancer	RNA-Seq	-	8834	NA	NA	Yes	Download from https://xenabrowser.net/
Other HCC sets							
GSE76427	Illumina HumanHT-12 V4.0 expression bead chip	GPL10558	115	NA	NA	Yes	mRNA data,clinical data
GSE112790	Affymetrix Human Genome U133 Plus 2.0 Array	GPL570	198	NA	NA	No	mRNA data
GSE9843	Affymetrix Human Genome U133 Plus 2.0 Array	GPL570	91	NA	NA	No	mRNA data
GSE19977	Illumina HumanRef-8 WG-DASL v3.0	GPL8432	164	NA	NA	No	mRNA data
GSE22058	Rosetta/Merck Human RSTA Custom Affymetrix 1.0 microarray	GPL6793	96	NA	NA	No	mRNA data
GSE25097	Rosetta/Merck Human RSTA Affymetrix 1.0 microarray	GPL10687	268	NA	NA	No	mRNA data
GSE43619	Illumina HumanHT-12 V4.0 expression bead chip	GPL10558	88	NA	NA	No	mRNA data
GSE45267	Affymetrix Human Genome U133 Plus 2.0 Array	GPL570	87	NA	NA	No	mRNA data
GSE46444	Illumina Human Whole-Genome DASL HT	GPL13369	88	NA	NA	No	mRNA data
GSE54236	Agilent-014850 Whole Human Genome Microarray 4x44K G4112F	GPL6480	81	NA	NA	No	mRNA data
GSE63898	Affymetrix Human Genome U219 Array	GPL13667	228	NA	NA	No	mRNA data
GSE64041	Affymetrix Human Gene 1.0 ST Array	GPL6244	60	NA	NA	No	mRNA data
GSE84402	Affymetrix Human Genome U133 Plus 2.0 Array	GPL570	14	NA	NA	No	mRNA data

S2. Prognostic value of Hypoxia-related genes in five HBV-related HCC cohorts (n=596)

Hypoxia-related genes	Description	Four training cohorts								Validation cohort	
		GSE14520(n=221)		Gao et al(n=159)		ICGC_LIRI_JP(n=53)		GSE10143(n=19)		TCGA_LIHC(n=144)	
		HR95%CI	P	HR95%CI	P	HR95%CI	P	HR95%CI	P	HR95%CI	P
AKT1	AKT serine/threonine kinase 1 [KO:K04456] [EC:2.7.11.1]	0.553(0.354-0.863)	0.009	1.342(0.793-2.272)	0.273	/	/	0.616(0.152-2.492)	0.497	1.844(0.875-3.886)	0.108
AKT2	AKT serine/threonine kinase 2 [KO:K04456] [EC:2.7.11.1]	0.701(0.388-1.267)	0.24	1.124(0.65-1.943)	0.676	0.255(0.031-2.073)	0.201	1.318(0.327-5.316)	0.698	0.501(0.248-1.014)	0.055
AKT3	AKT serine/threonine kinase 3 [KO:K04456] [EC:2.7.11.1]	1.585(0.959-2.617)	0.072	/	/	0.197(0.049-0.794)	0.022	3.47(0.697-17.279)	0.129	0.679(0.346-1.333)	0.26
ALDOA	aldolase, fructose-bisphosphate A [KO:K01623] [EC:4.1.2.13]	1.841(0.453-7.487)	0.394	3.058(1.798-5.203)	<0.001	0.278(0.056-1.378)	0.117	2.709(0.555-13.219)	0.218	2.53(1.434-4.463)	0.001
ALDOB	aldolase, fructose-bisphosphate B [KO:K01623] [EC:4.1.2.13]	0.505(0.324-0.786)	0.002	1.822(1.039-3.196)	0.036	0.341(0.042-2.769)	0.314	4.192(1.014-17.334)	0.048	0.708(0.394-1.27)	0.247
ALDOC	aldolase, fructose-bisphosphate C [KO:K01623] [EC:4.1.2.13]	1.921(1.02-3.621)	0.043	0.838(0.493-1.423)	0.512	0.211(0.046-0.982)	0.047	1.098(0.273-4.417)	0.895	2.078(1.236-3.496)	0.006
ANGPT1	angiopoietin 1 [KO:K05465]	2.219(1.302-3.78)	0.003	/	/	2.154(0.538-8.617)	0.278	0.463(0.096-2.236)	0.338	2.436(1.312-4.523)	0.005
ANGPT2	angiopoietin 2 [KO:K05466]	4.303(1.742-10.629)	0.002	/	/	/	/	0.445(0.084-2.361)	0.342	2.397(1.221-4.707)	0.011
ANGPT4	angiopoietin 4 [KO:K05467]	0.498(0.289-0.858)	0.012	/	/	/	/	/	/	0.374(0.227-0.616)	<0.001
ARNT	aryl hydrocarbon receptor nuclear translocator [KO:K09097]	2.37(1.033-5.437)	0.042	1.698(0.999-2.888)	0.05	0.22(0.044-1.102)	0.065	0.257(0.032-2.061)	0.201	3.632(1.273-10.361)	0.016
BCL2	BCL2 apoptosis regulator [KO:K02161]	0.669(0.363-1.231)	0.196	/	/	0.291(0.058-1.448)	0.132	0.398(0.082-1.933)	0.253	0.736(0.45-1.203)	0.221
CAMK2A	calcium/calmodulin dependent protein kinase II alpha [KO:K04515] [EC:2.7.11.17]	0.54(0.351-0.83)	0.005	/	/	5.067(1.022-25.115)	0.047	3.304(0.8-13.639)	0.099	0.602(0.272-1.331)	0.21
CAMK2B	calcium/calmodulin dependent protein kinase II beta [KO:K04515] [EC:2.7.11.17]	0.447(0.28-0.715)	0.001	1.358(0.188-9.823)	0.762	0.157(0.019-1.283)	0.084	/	/	0.332(0.161-0.683)	0.003
CAMK2D	calcium/calmodulin dependent protein kinase II delta [KO:K04515] [EC:2.7.11.17]	/	/	0.403(0.207-0.782)	0.007	4.41(0.542-35.873)	0.165	/	/	1.717(1.011-2.916)	0.046
CAMK2G	calcium/calmodulin dependent protein kinase II gamma [KO:K04515] [EC:2.7.11.17]	1.431(0.83-2.465)	0.197	1.013(0.524-1.959)	0.969	0.346(0.07-1.717)	0.194	0.531(0.14-2.02)	0.353	2.131(0.937-4.846)	0.071
CDKN1A	cyclin dependent kinase inhibitor 1A [KO:K06625]	1.22(0.784-1.898)	0.378	/	/	4.146(0.99-17.368)	0.052	8.135(0.737-89.855)	0.087	0.397(0.239-0.66)	<0.001
CDKN1B	cyclin dependent kinase inhibitor 1B [KO:K06624]	0.578(0.374-0.892)	0.013	2.087(1.052-4.138)	0.035	/	/	/(/-/)	/	2.188(1.255-3.813)	0.006
CREBBP	CREB binding protein [KO:K04498] [EC:2.3.1.48]	0.509(0.33-0.785)	0.002	0.667(0.327-1.362)	0.266	/	/	0.844(0.21-3.385)	0.811	1.71(1.025-2.854)	0.04
CUL2	cullin 2 [KO:K03870]	0.715(0.459-1.112)	0.136	1.844(1.077-3.158)	0.026	0.239(0.048-1.197)	0.082	0.632(0.157-2.533)	0.517	2.612(1.514-4.506)	0.001
CYBB	cytochrome b-245 beta chain [KO:K21421] [EC:1.-.-.-]	0.758(0.489-1.176)	0.217	2.153(1.054-4.398)	0.035	2.492(0.502-12.376)	0.264	1.631(0.403-6.597)	0.493	1.755(1.05-2.935)	0.032
EDN1	endothelin 1 [KO:K16366]	1.613(0.968-2.688)	0.066	/	/	/	/	/	/	2.182(1.107-4.298)	0.024
EGF	epidermal growth factor [KO:K04357]	2.044(1.318-3.169)	0.001	/	/	/	/	/	/	2.044(1.211-3.449)	0.007
EGFR	epidermal growth factor receptor [KO:K04361] [EC:2.7.10.1]	0.1(0.014-0.721)	0.022	1.203(0.568-2.544)	0.629	/	/	/	/	0.652(0.383-1.108)	0.114
EGLN1	egl-9 family hypoxia inducible factor 1 [KO:K09592] [EC:1.14.11.29]	2.129(1.216-3.728)	0.008	1.575(0.915-2.71)	0.101	82434629.391(0-Inf)	0.998	/	/	2.289(1.114-4.7)	0.024
EGLN2	egl-9 family hypoxia inducible factor 2 [KO:K09592] [EC:1.14.11.29]	/	/	/	/	0.288(0.069-1.205)	0.088	/	/	0.79(0.39-1.599)	0.513
EGLN3	egl-9 family hypoxia inducible factor 3 [KO:K09592] [EC:1.14.11.29]	2.505(1.625-3.86)	<0.001	/	/	0.24(0.057-1.003)	0.05	/	/	0.404(0.169-0.963)	0.041
EIF4E	eukaryotic translation initiation factor 4E [KO:K03259]	1.429(0.927-2.201)	0.106	0.699(0.353-1.385)	0.305	0.34(0.068-1.691)	0.187	/	/	2.55(1.551-4.193)	<0.001
EIF4E1B	eukaryotic translation initiation factor 4E family member 1B [KO:K03259]	/	/	/	/	/	/	/	/	1.458(0.836-2.543)	0.184
EIF4E2	eukaryotic translation initiation factor 4E family member 2 [KO:K03259]	1.484(0.969-2.275)	0.07	2.641(1.543-4.523)	<0.001	/	/	/	/	2.486(1.475-4.191)	0.001
EIF4EBP1	eukaryotic translation initiation factor 4E binding protein 1 [KO:K07205]	1.482(0.905-2.427)	0.118	1.459(0.86-2.473)	0.161	3.349(0.783-14.322)	0.103	/	/	1.457(0.756-2.806)	0.261
ELOB	elongin B [KO:K03873]	0.565(0.368-0.87)	0.009	1.652(0.914-2.986)	0.096	/	/	/	/	2.302(1.378-3.845)	0.001
ELOC	elongin C [KO:K03872]	1.606(0.98-2.631)	0.06	1.368(0.779-2.403)	0.275	/	/	/	/	2.308(1.405-3.789)	0.001
ENO1	enolase 1 [KO:K01689] [EC:4.2.1.11]	1.271(0.613-2.633)	0.519	2.534(1.306-4.915)	0.006	0.234(0.047-1.179)	0.078	/	/	/	/
ENO2	enolase 2 [KO:K01689] [EC:4.2.1.11]	2.786(1.775-4.372)	<0.001	3.099(1.747-5.497)	<0.001	0.082(0.01-0.668)	0.019	0.396(0.08-1.962)	0.256	0.408(0.237-0.704)	0.001
ENO3	enolase 3 [KO:K01689] [EC:4.2.1.11]	2.024(1.261-3.248)	0.003	3.129(1.845-5.307)	<0.001	0.173(0.041-0.729)	0.017	9.415(1.117-79.339)	0.039	2.651(1.597-4.399)	<0.001
ENO4	enolase 4 [KO:K01689] [EC:4.2.1.11]	/	/	/	/	0.214(0.043-1.069)	0.06	/	/	2.205(1.342-3.625)	0.002
EP300	E1A binding protein p300 [KO:K04498] [EC:2.3.1.48]	1.68(1.047-2.695)	0.031	2.283(1.35-3.859)	0.002	0.37(0.092-1.493)	0.162	0.137(0.016-1.19)	0.071	0.598(0.357-1.001)	0.051
EPO	erythropoietin [KO:K05437]	3.357(2.065-5.456)	<0.001	/	/	3.009(0.752-12.05)	0.12	/	/	0.649(0.389-1.083)	0.098
ERBB2	erb-b2 receptor tyrosine kinase 2 [KO:K05083] [EC:2.7.10.1]	0.658(0.382-1.133)	0.131	1.55(0.884-2.718)	0.126	0.229(0.055-0.959)	0.044	0.419(0.103-1.71)	0.225	1.636(0.962-2.782)	0.069
FLT1	fms related tyrosine kinase 1 [KO:K05096] [EC:2.7.10.1]	1.639(1.064-2.525)	0.025	/	/	0.286(0.058-1.422)	0.126	/	/	3.999(1.243-12.862)	0.02
GAPDH	glyceraldehyde-3-phosphate dehydrogenase [KO:K00134] [EC:1.2.1.12]	2.337(1.484-3.682)	<0.001	0.987(0.546-1.783)	0.964	0.525(0.131-2.1)	0.362	0.334(0.069-1.627)	0.175	1.33(0.764-2.315)	0.314
HIF1A	hypoxia inducible factor 1 subunit alpha [KO:K08268]	1.637(0.962-2.786)	0.069	/	/	0.261(0.053-1.296)	0.1	0.15(0.03-0.741)	0.02	2.031(1.248-3.306)	0.004

S2. Prognostic value of Hypoxia-related genes in five HBV-related HCC cohorts (n=596)

Hypoxia-related genes	Description	Four training cohorts								Validation cohort	
		GSE14520(n=221)		Gao et al(n=159)		ICGC_LIRI_JP(n=53)		GSE10143(n=19)		TCGA_LIHC(n=144)	
		HR95%CI	P	HR95%CI	P	HR95%CI	P	HR95%CI	P	HR95%CI	P
HK1	hexokinase 1 [KO:K00844] [EC:2.7.1.1]	0.491(0.311-0.776)	0.002	2.98(1.537-5.776)	0.001	0.111(0.014-0.903)	0.04	0.515(0.138-1.919)	0.323	0.991(0.584-1.684)	0.975
HK2	hexokinase 2 [KO:K00844] [EC:2.7.1.1]	2.795(1.659-4.709)	<0.001	2.742(1.62-4.642)	<0.001	0.208(0.049-0.875)	0.032	6.287(0.777-50.872)	0.085	0.473(0.289-0.774)	0.003
HK3	hexokinase 3 [KO:K00844] [EC:2.7.1.1]	0.558(0.303-1.028)	0.061	2.103(1.087-4.07)	0.027	0.245(0.058-1.047)	0.058	0.803(0.098-6.585)	0.838	2.08(1.2-3.604)	0.009
HKDC1	hexokinase domain containing 1 [KO:K00844] [EC:2.7.1.1]	1.535(0.957-2.463)	0.076	1.687(0.723-3.936)	0.227	3.211(0.648-15.914)	0.153	/	/	1.331(0.772-2.293)	0.303
HMOX1	heme oxygenase 1 [KO:K00510] [EC:1.14.14.18]	2.193(1.315-3.659)	0.003	1.419(0.443-4.545)	0.555	6.269(1.264-31.093)	0.025	3.765(0.775-18.293)	0.1	2.196(1.245-3.873)	0.007
IFNG	interferon gamma [KO:K04687]	0.577(0.339-0.983)	0.043	/	/	0.18(0.022-1.467)	0.109	/	/	2.174(1.295-3.649)	0.003
IFNGR1	interferon gamma receptor 1 [KO:K05132]	0.759(0.488-1.18)	0.22	/	/	4.457(1.063-18.683)	0.041	0.306(0.074-1.267)	0.102	0.866(0.373-2.013)	0.739
IFNGR2	interferon gamma receptor 2 [KO:K05133]	2.073(1.168-3.679)	0.013	/	/	0.411(0.103-1.646)	0.209	0.28(0.074-1.062)	0.061	0.476(0.173-1.312)	0.151
IGF1	insulin like growth factor 1 [KO:K05459]	0.519(0.339-0.796)	0.003	/	/	6.99(0.858-56.982)	0.069	0.278(0.056-1.388)	0.119	1.678(0.998-2.82)	0.051
IGF1R	insulin like growth factor 1 receptor [KO:K05087] [EC:2.7.10.1]	0.558(0.309-1.007)	0.053	/	/	0.101(0.012-0.82)	0.032	1.956(0.486-7.872)	0.345	1.805(0.718-4.532)	0.209
IL6	interleukin 6 [KO:K05405]	0.573(0.374-0.877)	0.01	/	/	2.497(0.503-12.393)	0.263	/	/	1.829(1.115-3)	0.017
IL6R	interleukin 6 receptor [KO:K05055]	0.52(0.288-0.939)	0.03	/	/	0.447(0.107-1.873)	0.271	/	/	0.373(0.227-0.615)	<0.001
INS	insulin [KO:K04526]	1.569(0.869-2.833)	0.135	/	/	/	/	/	/	1.534(0.926-2.542)	0.097
INSR	insulin receptor [KO:K04527] [EC:2.7.10.1]	2.155(0.994-4.671)	0.052	1.367(0.722-2.59)	0.337	/	/	/	/	0.685(0.415-1.13)	0.139
LDHA	lactate dehydrogenase A [KO:K00016] [EC:1.1.1.27]	2.055(1.3-3.247)	0.002	2.418(1.217-4.803)	0.012	2.528(0.509-12.547)	0.256	5.378(1.329-21.763)	0.018	0.795(0.343-1.847)	0.595
LDHAL6A	lactate dehydrogenase A like 6A [KO:K00016] [EC:1.1.1.27]	/	/	/	/	/	/	/	/	2.932(1.68-5.117)	<0.001
LDHAL6B	lactate dehydrogenase A like 6B [KO:K00016] [EC:1.1.1.27]	1.516(0.925-2.483)	0.099	/	/	0.095(0.019-0.473)	0.004	/	/	0.724(0.4-1.311)	0.287
LDHB	lactate dehydrogenase B [KO:K00016] [EC:1.1.1.27]	1.878(1.039-3.394)	0.037	2.434(1.328-4.464)	0.004	0.362(0.086-1.523)	0.166	0.077(0.009-0.63)	0.017	1.83(0.87-3.85)	0.111
LDHC	lactate dehydrogenase C [KO:K00016] [EC:1.1.1.27]	0.646(0.407-1.025)	0.064	/	/	/	/	/	/	2.932(1.689-5.089)	<0.001
LTBR	lymphotoxin beta receptor [KO:K03159]	0.557(0.308-1.007)	0.053	/	/	0.312(0.038-2.538)	0.276	0.135(0.022-0.823)	0.03	1.506(0.911-2.49)	0.11
MAP2K1	mitogen-activated protein kinase kinase 1 [KO:K04368] [EC:2.7.12.2]	0.551(0.299-1.015)	0.056	1.257(0.722-2.187)	0.419	0.324(0.077-1.36)	0.124	24.467(2.472-242.195)	0.006	0.317(0.187-0.537)	<0.001
MAP2K2	mitogen-activated protein kinase kinase 2 [KO:K04369] [EC:2.7.12.2]	1.84(1.114-3.041)	0.017	1.851(0.907-3.779)	0.091	2.518(0.505-12.565)	0.26	/	/	0.886(0.539-1.457)	0.634
MAPK1	mitogen-activated protein kinase 1 [KO:K04371] [EC:2.7.11.24]	1.736(0.921-3.271)	0.088	2.91(1.425-5.944)	0.003	2.226(0.557-8.903)	0.258	/	/	0.962(0.587-1.577)	0.877
MAPK3	mitogen-activated protein kinase 3 [KO:K04371] [EC:2.7.11.24]	0.656(0.419-1.029)	0.066	2.59(1.53-4.383)	<0.001	2.437(0.486-12.208)	0.279	0.359(0.074-1.735)	0.202	0.353(0.128-0.975)	0.045
MKNK1	MAPK interacting serine/threonine kinase 1 [KO:K04372] [EC:2.7.11.1]	0.402(0.23-0.705)	0.001	/	/	0.151(0.019-1.229)	0.077	/	/	1.12(0.58-2.162)	0.736
MKNK2	MAPK interacting serine/threonine kinase 2 [KO:K04372] [EC:2.7.11.1]	1.362(0.739-2.51)	0.322	/	/	0.198(0.047-0.833)	0.027	/	/	0.477(0.278-0.818)	0.007
MTOR	mechanistic target of rapamycin kinase [KO:K07203] [EC:2.7.11.1]	0.542(0.344-0.852)	0.008	1.231(0.681-2.225)	0.491	0.116(0.029-0.472)	0.003	/	/	1.799(1.016-3.186)	0.044
NFKB1	nuclear factor kappa B subunit 1 [KO:K02580]	0.306(0.112-0.837)	0.021	0.687(0.407-1.161)	0.161	2.434(0.49-12.082)	0.277	0.116(0.014-0.992)	0.049	0.619(0.377-1.018)	0.059
NOS2	nitric oxide synthase 2 [KO:K13241] [EC:1.14.13.39]	1.574(1.005-2.467)	0.048	/	/	0.186(0.044-0.781)	0.022	/	/	1.482(0.669-3.283)	0.332
NOS3	nitric oxide synthase 3 [KO:K13242] [EC:1.14.13.39]	0.542(0.328-0.895)	0.017	1.34(0.792-2.268)	0.275	0.234(0.047-1.16)	0.075	/	/	1.685(1.016-2.794)	0.043
NPPA	natriuretic peptide A [KO:K12334]	0.454(0.264-0.784)	0.005	/	/	0.191(0.046-0.805)	0.024	/	/	0.482(0.284-0.819)	0.007
PDHA1	pyruvate dehydrogenase E1 alpha 1 subunit [KO:K00161] [EC:1.2.4.1]	0.599(0.392-0.918)	0.018	1.933(0.914-4.089)	0.085	0.218(0.052-0.914)	0.037	/	/	1.508(0.894-2.542)	0.123
PDHA2	pyruvate dehydrogenase E1 alpha 2 subunit [KO:K00161] [EC:1.2.4.1]	1.84(1.113-3.041)	0.017	/	/	/	/	6.871(0.844-55.912)	0.072	0.557(0.306-1.014)	0.056
PDHB	pyruvate dehydrogenase E1 beta subunit [KO:K00162] [EC:1.2.4.1]	0.791(0.396-1.579)	0.506	1.614(0.393-6.624)	0.506	0.301(0.061-1.497)	0.143	6.029(1.234-29.469)	0.026	2.607(0.942-7.217)	0.065
PDK1	pyruvate dehydrogenase kinase 1 [KO:K12077] [EC:2.7.11.2]	1.774(0.889-3.541)	0.104	0.402(0.202-0.798)	0.009	0.205(0.048-0.865)	0.031	/	/	0.786(0.374-1.649)	0.524
PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 [KO:K01103] [EC:3.1.3.46 2.7.1.105]	2.199(1.398-3.46)	0.001	/	/	0.38(0.09-1.594)	0.186	/	/	1.09(0.555-2.144)	0.802
PFKL	phosphofructokinase, liver type [KO:K00850] [EC:2.7.1.11]	1.573(1.014-2.441)	0.043	0.716(0.422-1.213)	0.214	0.407(0.097-1.706)	0.219	/	/	1.928(1.173-3.167)	0.01
PFKM	phosphofructokinase, muscle [KO:K00850] [EC:2.7.1.11]	1.572(1.026-2.406)	0.038	2.523(1.48-4.303)	0.001	0.135(0.027-0.675)	0.015	/	/	1.641(0.997-2.701)	0.051
PFKP	phosphofructokinase, platelet [KO:K00850] [EC:2.7.1.11]	1.565(0.929-2.636)	0.092	2.334(1.357-4.013)	0.002	0.168(0.021-1.365)	0.095	0.887(0.22-3.583)	0.866	0.665(0.338-1.312)	0.239
PGK1	phosphoglycerate kinase 1 [KO:K00927] [EC:2.7.2.3]	1.553(0.923-2.615)	0.097	2.535(1.308-4.913)	0.006	/	/	2.231(0.553-8.994)	0.259	2.019(1.154-3.531)	0.014
PGK2	phosphoglycerate kinase 2 [KO:K00927] [EC:2.7.2.3]	0.729(0.46-1.158)	0.181	/	/	0.355(0.044-2.896)	0.334	/	/	2.016(1.216-3.342)	0.007

S2. Prognostic value of Hypoxia-related genes in five HBV-related HCC cohorts (n=596)

Hypoxia-related genes	Description	Four training cohorts								Validation cohort	
		GSE14520(n=221)		Gao et al(n=159)		ICGC_LIRI_JP(n=53)		GSE10143(n=19)		TCGA_LIHC(n=144)	
		HR95%CI	P	HR95%CI	P	HR95%CI	P	HR95%CI	P	HR95%CI	P
PIK3CA	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit alpha [KO:K00922] [EC:2.7.1.153]	1.641(1.072-2.511)	0.023	0.29(0.091-0.928)	0.037	0.184(0.023-1.508)	0.115	0.532(0.126-2.25)	0.391	1.993(1.116-3.559)	0.02
PIK3CB	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit beta [KO:K00922] [EC:2.7.1.153]	1.596(0.899-2.835)	0.111	2.963(1.071-8.196)	0.036	4.624(0.569-37.596)	0.152	/	/	2.47(1.414-4.315)	0.001
PIK3CD	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit delta [KO:K00922] [EC:2.7.1.153]	0.718(0.466-1.106)	0.133	1.882(1.01-3.504)	0.046	0.211(0.052-0.853)	0.029	/	/	2.185(1.215-3.929)	0.009
PIK3R1	phosphoinositide-3-kinase regulatory subunit 1 [KO:K02649]	0.376(0.182-0.78)	0.009	1.327(0.724-2.431)	0.36	2.694(0.543-13.376)	0.225	0.201(0.039-1.042)	0.056	1.891(0.985-3.628)	0.056
PIK3R2	phosphoinositide-3-kinase regulatory subunit 2 [KO:K02649]	0.619(0.363-1.055)	0.078	/	/	0.395(0.094-1.66)	0.205	0.116(0.019-0.701)	0.019	1.887(1.017-3.502)	0.044
PIK3R3	phosphoinositide-3-kinase regulatory subunit 3 [KO:K02649]	0.453(0.29-0.707)	<0.001	/	/	/	/	12.338(1.498-101.594)	0.019	2.602(1.092-6.197)	0.031
PLCG1	phospholipase C gamma 1 [KO:K01116] [EC:3.1.4.11]	2.211(1.338-3.654)	0.002	2.485(1.251-4.933)	0.009	0.13(0.026-0.645)	0.013	0.802(0.209-3.071)	0.747	1.695(1.028-2.796)	0.039
PLCG2	phospholipase C gamma 2 [KO:K05859] [EC:3.1.4.11]	0.297(0.179-0.494)	<0.001	2.065(0.824-5.177)	0.122	0.204(0.049-0.855)	0.03	5.116(0.627-41.746)	0.127	0.59(0.351-0.992)	0.046
PRKCA	protein kinase C alpha [KO:K02677] [EC:2.7.11.13]	0.52(0.338-0.799)	0.003	0.62(0.266-1.447)	0.269	0.138(0.033-0.581)	0.007	/	/	0.377(0.231-0.617)	<0.001
PRKCB	protein kinase C beta [KO:K19662] [EC:2.7.11.13]	0.376(0.214-0.66)	0.001	1.453(0.855-2.47)	0.168	0.186(0.023-1.515)	0.116	/	/	3.32(1.767-6.24)	<0.001
PRKCG	protein kinase C gamma [KO:K19663] [EC:2.7.11.13]	0.584(0.329-1.038)	0.067	/	/	0.22(0.044-1.092)	0.064	5.967(1.175-30.314)	0.031	0.508(0.3-0.861)	0.012
RBX1	ring-box 1 [KO:K03868] [EC:2.3.2.32]	1.899(1.102-3.273)	0.021	/	/	0.257(0.052-1.273)	0.096	/	/	1.566(0.926-2.649)	0.094
RELA	RELA proto-oncogene, NF-kB subunit [KO:K04735]	1.528(0.946-2.467)	0.083	0.803(0.363-1.776)	0.588	0.336(0.08-1.408)	0.136	0.192(0.02-1.846)	0.153	1.998(1.163-3.432)	0.012
RPS6	ribosomal protein S6 [KO:K02991]	1.737(1.043-2.895)	0.034	2.203(1.183-4.104)	0.013	1.275(0.257-6.325)	0.766	0.09(0.011-0.725)	0.024	1.616(0.964-2.707)	0.069
RPS6KB1	ribosomal protein S6 kinase B1 [KO:K04688] [EC:2.7.11.1]	2.129(1.39-3.259)	0.001	1.892(1.109-3.23)	0.019	/	/	2.232(0.556-8.955)	0.257	2.28(1.376-3.778)	0.001
RPS6KB2	ribosomal protein S6 kinase B2 [KO:K04688] [EC:2.7.11.1]	1.8(1.055-3.071)	0.031	1.573(0.793-3.118)	0.195	0.465(0.093-2.319)	0.351	2.08(0.517-8.376)	0.303	2.094(1.183-3.708)	0.011
SERPINE1	serpin family E member 1 [KO:K03982]	2.482(1.562-3.944)	<0.001	/	/	4.526(1.075-19.046)	0.039	0.297(0.078-1.134)	0.076	2.107(1.227-3.62)	0.007
SLC2A1	solute carrier family 2 member 1 [KO:K07299]	1.873(1.221-2.873)	0.004	3.181(1.732-5.845)	<0.001	0.267(0.066-1.077)	0.063	/	/	2.355(1.256-4.416)	0.008
STAT3	signal transducer and activator of transcription 3 [KO:K04692]	0.476(0.285-0.795)	0.005	0.725(0.355-1.48)	0.377	0.41(0.098-1.721)	0.223	0.137(0.016-1.19)	0.071	4.529(1.359-15.097)	0.014
TEK	TEK receptor tyrosine kinase [KO:K05121] [EC:2.7.10.1]	0.454(0.283-0.729)	0.001	/	/	0.485(0.098-2.405)	0.376	1.785(0.445-7.168)	0.414	1.374(0.83-2.274)	0.217
TF	transferrin [KO:K14736]	0.304(0.111-0.829)	0.02	2.248(1.161-4.352)	0.016	2.13(0.429-10.575)	0.355	10.238(1.225-85.559)	0.032	2.957(1.778-4.92)	<0.001
TFRC	transferrin receptor [KO:K06503]	1.399(0.908-2.156)	0.128	2.438(1.345-4.42)	0.003	0.216(0.052-0.904)	0.036	/	/	1.796(1.08-2.987)	0.024
TIMP1	TIMP metallopeptidase inhibitor 1 [KO:K16451]	1.23(0.803-1.883)	0.341	2.605(1.346-5.04)	0.004	0.47(0.112-1.969)	0.301	0.3(0.075-1.205)	0.09	5.346(1.304-21.911)	0.02
TLR4	toll like receptor 4 [KO:K10160]	0.617(0.403-0.945)	0.026	/	/	2.425(0.577-10.189)	0.226	/	/	2.117(1.239-3.617)	0.006
VEGFA	vascular endothelial growth factor A [KO:K05448]	/	0.996	/	/	0.17(0.041-0.714)	0.015	0.411(0.084-2.019)	0.273	1.342(0.751-2.399)	0.32
VHL	von Hippel-Lindau tumor suppressor [KO:K03871]	1.754(0.988-3.117)	0.055	/	/	0.242(0.058-1.016)	0.053	/	/	2.05(1.044-4.027)	0.037

S3. Prognostic value of 64 TME cells in five HBV-related HCC cohorts (n=596)

TME cells	Subgroup	Full Names	Four training cohorts								Validation cohort	
			GSE14520(n=221)		Gao et al(n=159)		ICGC_LIRI_JP (n=53)		GSE10143(n=19)		TCGA_LIHC(n=144)	
			HR95%CI	P	HR95%CI	P	HR95%CI	P	HR95%CI	P	HR95%CI	P
aDC	Myeloid	Activated dendritic cells	0.51(0.207-1.259)	0.144	1.095(0.643-1.866)	0.738	0.172(0.035-0.852)	0.031	0.312(0.06-1.626)	0.167	/	/
Adipocytes	Stroma	Adipocytes	0.552(0.331-0.919)	0.022	0.376(0.091-1.547)	0.175	/	/	1.151(0.308-4.306)	0.834	0.438(0.252-0.761)	0.003
Astrocytes	Epithelial	Astrocytes	1.506(0.978-2.321)	0.063	1.169(0.617-2.215)	0.632	0.355(0.043-2.899)	0.334	0.227(0.045-1.141)	0.072	1.274(0.774-2.095)	0.341
Basophils	Myeloid	Basophils	1.532(0.943-2.49)	0.085	1.388(0.798-2.414)	0.246	/	/	13.017(1.806-93.817)	0.011	0.635(0.088-4.605)	0.654
B-cells	Lymphoid	B-cells	0.387(0.249-0.603)	<0.001	1.464(0.717-2.989)	0.295	0.354(0.072-1.756)	0.204	/	/	0.487(0.293-0.809)	0.006
CD4+ memory T-cells	Lymphoid	CD4+ memory T-cells	0.877(0.573-1.343)	0.546	2.734(0.854-8.75)	0.09	/	/	/	/	1.436(0.879-2.348)	0.149
CD4+ naive T-cells	Lymphoid	CD4+ naive T-cells	0.56(0.359-0.876)	0.011	1.864(0.881-3.941)	0.103	0.564(0.135-2.36)	0.433	/	/	0.582(0.352-0.961)	0.034
CD4+ T-cells	Lymphoid	CD4+ T-cells	0.382(0.053-2.748)	0.339	2.068(0.936-4.567)	0.072	0.262(0.032-2.135)	0.211	/	/	0.691(0.39-1.225)	0.205
CD4+ Tcm	Lymphoid	CD4+ central memory T-cells	0.647(0.419-1)	0.05	1.185(0.429-3.279)	0.743	/	/	/	/	0.551(0.297-1.023)	0.059
CD4+ Tem	Lymphoid	CD4+ effector memory T-cells	0.748(0.471-1.188)	0.218	0.765(0.186-3.143)	0.71	/	/	/	/	0.697(0.391-1.243)	0.222
CD8+ naive T-cells	Lymphoid	CD8+ naive T-cells	1.363(0.867-2.143)	0.18	2.227(1.121-4.424)	0.022	/	/	0.276(0.067-1.132)	0.074	0.595(0.309-1.147)	0.121
CD8+ T-cells	Lymphoid	CD8+ T-cells	0.58(0.362-0.932)	0.024	2.334(1.142-4.77)	0.02	/	/	/	/	0.467(0.283-0.772)	0.003
CD8+ Tcm	Lymphoid	CD8+ central memory T-cells	0.583(0.353-0.964)	0.035	0.483(0.243-0.96)	0.038	0.082(0.01-0.667)	0.019	/	/	0.52(0.257-1.052)	0.069
CD8+ Tem	Lymphoid	CD8+ effector memory T-cells	0.446(0.291-0.684)	<0.001	0.265(0.083-0.851)	0.026	0.384(0.077-1.917)	0.243	0.302(0.062-1.471)	0.138	0.57(0.257-1.263)	0.166
cDC	Myeloid	Conventional dendritic cells	0.259(0.112-0.597)	0.002	2.646(1.464-4.781)	0.001	/	/	/	/	0.984(0.561-1.729)	0.957
Chondrocytes	Stroma	Chondrocytes	0.73(0.474-1.123)	0.152	0.568(0.328-0.983)	0.043	/	/	/	/	0.683(0.388-1.201)	0.186
Class-switched memory B-cells	Lymphoid	Class-switched memory B-cells	0.661(0.412-1.06)	0.085	0.888(0.514-1.535)	0.671	0.449(0.091-2.229)	0.327	/	/	1.017(0.14-7.393)	0.986
CLP	HSC	Common lymphoid progenitors	1.809(1.159-2.825)	0.009	0.714(0.395-1.29)	0.264	0.181(0.022-1.475)	0.11	/	/	3.595(1.441-8.972)	0.006
CMP	HSC	Common myeloid progenitors	0.376(0.204-0.692)	0.002	1.72(0.907-3.261)	0.097	/	/	3.173(0.783-12.862)	0.106	0.815(0.487-1.365)	0.437
DC	Myeloid	Dendritic cells	0.737(0.416-1.308)	0.297	1.455(0.856-2.475)	0.166	/	/	/	/	0.505(0.07-3.649)	0.498
Endothelial cells	Stroma	Endothelial cells	0.629(0.36-1.099)	0.104	/	/	2.519(0.601-10.557)	0.206	/	/	/	/
Eosinophils	Myeloid	Eosinophils	0.487(0.303-0.781)	0.003	0.595(0.352-1.006)	0.053	2.669(0.667-10.677)	0.165	/	/	2.35(1.402-3.94)	0.001
Epithelial cells	Epithelial	Epithelial cells	1.21(0.682-2.148)	0.514	1.758(1.038-2.978)	0.036	0.407(0.05-3.313)	0.401	0.377(0.094-1.518)	0.17	0.765(0.461-1.269)	0.299
Erythrocytes	HSC	Erythrocytes	1.738(0.898-3.362)	0.101	1.494(0.364-6.135)	0.577	2.806(0.562-14.016)	0.209	0.123(0.011-1.358)	0.087	2.029(1.219-3.376)	0.006
Fibroblasts	Stroma	Fibroblasts	0.743(0.484-1.138)	0.172	0.698(0.278-1.75)	0.443	1.859(0.229-15.126)	0.562	0.177(0.039-0.802)	0.025	2.402(1.46-3.952)	0.001
GMP	HSC	Granulocyte-macrophage progenitors	0.714(0.442-1.153)	0.168	1.316(0.779-2.224)	0.305	/	/	/	/	0.391(0.232-0.657)	<0.001
Hepatocytes	Epithelial	Hepatocytes	0.435(0.261-0.724)	0.001	0.432(0.236-0.793)	0.007	/	/	2.988(0.791-11.282)	0.106	0.567(0.227-1.413)	0.223
HSC	HSC	Hematopoietic stem cells	0.698(0.426-1.143)	0.153	0.598(0.35-1.021)	0.059	2.673(0.668-10.703)	0.165	1.911(0.512-7.135)	0.335	1.677(0.875-3.213)	0.119
iDC	Myeloid	Immature dendritic cells	0.488(0.283-0.842)	0.01	1.756(0.752-4.1)	0.193	2.403(0.573-10.081)	0.231	2.101(0.262-16.825)	0.484	2.428(1.458-4.046)	0.001
Keratinocytes	Epithelial	Keratinocytes	1.09(0.624-1.905)	0.761	1.506(0.89-2.547)	0.127	/	/	0.322(0.04-2.599)	0.288	2.18(1.091-4.354)	0.027
Ly Endothelial cells	Stroma	Lymphatic endothelial cells	/	/	0.817(0.199-3.357)	0.779	0.179(0.045-0.719)	0.015	/	/	0.455(0.25-0.829)	0.01
Macrophages	Myeloid	Macrophages	0.667(0.435-1.022)	0.063	0.831(0.492-1.402)	0.487	0.279(0.056-1.383)	0.118	0.371(0.098-1.399)	0.143	1.714(1.019-2.883)	0.042
Macrophages M1	Myeloid	Macrophages M1	0.679(0.404-1.143)	0.145	0.897(0.508-1.586)	0.709	4.092(0.816-20.51)	0.087	0.37(0.077-1.788)	0.216	1.55(0.806-2.978)	0.189
Macrophages M2	Myeloid	Macrophages M2	0.564(0.283-1.127)	0.105	0.725(0.355-1.48)	0.377	/	/	3.023(0.352-25.952)	0.313	3.328(1.968-5.626)	<0.001
Mast cells	Myeloid	Mast cells	1.277(0.819-1.993)	0.281	2.726(1.408-5.28)	0.003	4.92(1.175-20.602)	0.029	4.979(0.959-25.841)	0.056	1.55(0.677-3.551)	0.3
Megakaryocytes	HSC	Megakaryocytes	0.78(0.508-1.196)	0.254	1.486(0.879-2.511)	0.139	2.445(0.301-19.88)	0.403	6.213(0.767-50.342)	0.087	2.532(1.545-4.149)	<0.001
Melanocytes	Epithelial	Melanocytes	0.728(0.471-1.127)	0.155	0.85(0.207-3.489)	0.822	3.214(0.803-12.871)	0.099	/	/	2.669(1.191-5.977)	0.017
Memory B-cells	Lymphoid	Memory B-cells	0.551(0.358-0.846)	0.007	0.541(0.32-0.915)	0.022	/	/	/	/	2.932(1.555-5.53)	0.001
MEP	HSC	Megakaryocyte–erythroid progenitors	2.143(0.866-5.302)	0.099	1.825(1.009-3.301)	0.047	5.572(0.612-50.764)	0.128	/	/	0.531(0.291-0.968)	0.039
Mesangial cells	Stroma	Mesangial cells	1.799(1.099-2.946)	0.02	2.483(0.898-6.867)	0.08	0.627(0.157-2.507)	0.509	/	/	0.3(0.041-2.191)	0.235
Monocytes	Myeloid	Monocytes	0.621(0.398-0.97)	0.036	1.815(0.822-4.008)	0.14	/	/	0.155(0.019-1.253)	0.08	1.617(0.994-2.633)	0.053
MPP	HSC	Multipotent rogenitors	0.536(0.347-0.829)	0.005	1.419(0.643-3.134)	0.386	1.169(0.292-4.688)	0.825	/	/	0.897(0.53-1.517)	0.684
MSC	Stroma	Mesenchymal stem cells	0.71(0.457-1.101)	0.126	1.265(0.739-2.166)	0.392	/	/	0.316(0.077-1.296)	0.11	2.512(1.474-4.282)	0.001
mv Endothelial cells	Stroma	Microvascular endothelial cells	0.809(0.498-1.315)	0.393	0.537(0.308-0.934)	0.028	1.641(0.392-6.871)	0.497	/	/	0.658(0.369-1.174)	0.156

S3. Prognostic value of 64 TME cells in five HBV-related HCC cohorts (n=596)

TME cells	Subgroup	Full Names	Four training cohorts								Validation cohort	
			GSE14520(n=221)		Gao et al(n=159)		ICGC_LIRI_JP (n=53)		GSE10143(n=19)		TCGA_LIHC(n=144)	
			HR95%CI	P	HR95%CI	P	HR95%CI	P	HR95%CI	P	HR95%CI	P
Myocytes	Stroma	Myocytes	0.763(0.497-1.172)	0.217	2.054(1.179-3.58)	0.011	2.626(0.323-21.35)	0.367	0.647(0.159-2.625)	0.542	0.626(0.226-1.732)	0.367
naive B-cells	Lymphoid	naive B-cells	0.511(0.311-0.838)	0.008	2.085(0.754-5.767)	0.157	/	/	/	/	1.629(0.995-2.669)	0.053
Neurons	Epithelial	Neurons	1.493(0.854-2.608)	0.159	0.563(0.255-1.244)	0.156	0.598(0.073-4.868)	0.63	2.661(0.543-13.025)	0.227	1.518(0.899-2.562)	0.119
Neutrophils	Myeloid	Neutrophils	1.283(0.47-3.502)	0.627	1.491(0.875-2.539)	0.142	0.516(0.123-2.163)	0.365	2.587(0.528-12.672)	0.241	0.529(0.166-1.692)	0.283
NK cells	Lymphoid	NK cells	0.552(0.349-0.872)	0.011	0.805(0.455-1.425)	0.457	0.244(0.03-1.988)	0.187	/	/	1.799(0.773-4.186)	0.173
NKT	Lymphoid	Natural killer T-cells	0.681(0.445-1.042)	0.077	5.023(0.695-36.31)	0.11	2.297(0.282-18.691)	0.437	/	/	0.558(0.339-0.918)	0.022
Osteoblast	Stroma	Osteoblasts	2.27(0.717-7.187)	0.163	0.662(0.385-1.137)	0.135	6.712(0.823-54.751)	0.075	0.123(0.011-1.358)	0.087	0.631(0.312-1.277)	0.201
pDC	Myeloid	Plasmacytoid dendritic cells	0.797(0.519-1.224)	0.3	0.45(0.213-0.952)	0.037	0.63(0.127-3.125)	0.572	/	/	0.559(0.308-1.013)	0.055
Pericytes	Stroma	Pericytes	1.727(0.973-3.064)	0.062	0.561(0.31-1.014)	0.055	2.507(0.599-10.503)	0.208	2.824(0.681-11.719)	0.153	1.966(1.083-3.569)	0.026
Plasma cells	Lymphoid	Plasma cells	0.503(0.32-0.792)	0.003	0.824(0.482-1.41)	0.48	0.107(0.013-0.869)	0.037	/	/	1.377(0.831-2.282)	0.214
Platelets	HSC	Platelets	0.605(0.395-0.926)	0.021	1.334(0.767-2.321)	0.307	4.082(1.02-16.34)	0.047	5.329(1.182-24.02)	0.029	0.441(0.27-0.718)	0.001
Preadipocytes	Stroma	Preadipocytes	0.462(0.245-0.87)	0.017	0.239(0.139-0.412)	<0.001	1.572(0.317-7.804)	0.58	/	/	0.588(0.353-0.978)	0.041
pro B-cells	Lymphoid	pro B-cells	1.395(0.773-2.518)	0.27	1.816(1.025-3.217)	0.041	0.481(0.12-1.926)	0.301	/	/	0.762(0.456-1.275)	0.301
Sebocytes	Epithelial	Sebocytes	1.828(1.074-3.112)	0.026	1.358(0.78-2.362)	0.279	0.681(0.163-2.857)	0.6	0.646(0.081-5.187)	0.681	4.813(1.51-15.343)	0.008
Skeletal muscle cells	Stroma	Skeletal muscle cells	2.2(1.102-4.391)	0.025	0.478(0.233-0.977)	0.043	/	/	0.385(0.076-1.946)	0.248	1.802(1.087-2.986)	0.022
Smooth muscle cells	Stroma	Smooth muscle cells	1.391(0.51-3.797)	0.52	1.699(0.951-3.036)	0.073	0.467(0.117-1.869)	0.282	/	/	1.442(0.351-5.921)	0.612
Tgd cells	Lymphoid	Gamma delta T-cells	1.619(0.972-2.698)	0.064	2.235(1.274-3.92)	0.005	3.394(0.809-14.24)	0.095	0.248(0.057-1.088)	0.065	0.514(0.267-0.989)	0.046
Th1 cells	Lymphoid	Type 1 T-helper cells	1.783(1.164-2.731)	0.008	1.245(0.721-2.151)	0.432	6.18(0.757-50.423)	0.089	3.406(0.898-12.918)	0.072	0.403(0.242-0.67)	<0.001
Th2 cells	Lymphoid	Type 2 T-helper cells	1.705(1.056-2.753)	0.029	2.008(1.173-3.438)	0.011	2.34(0.288-19.033)	0.426	/	/	1.694(0.767-3.742)	0.193
Tregs	Lymphoid	Regulatory T-cells	0.819(0.531-1.261)	0.364	1.856(0.96-3.589)	0.066	0.039(0.004-0.433)	0.008	/	/	1.636(0.968-2.768)	0.066

S4. Pooled prognostic value of Hypoxia-related genes based on pooled four training cohorts (meta-analysis,n=452)

Hypoxia-related genes	Pooled results(n=452)						Included in Hypoxia Score Model
	Freq of cohorts	HR	95CI_L	95CI_U	pvalue	FDR	
EPO	3	3.317	2.097	5.246	<0.001	<0.001	YES
HK2	4	2.424	1.702	3.452	<0.001	<0.001	YES
ENO2	4	2.413	1.715	3.394	<0.001	<0.001	YES
ALDOA	4	2.367	1.502	3.729	<0.001	0.003	YES
HMOX1	4	2.321	1.506	3.577	<0.001	0.002	YES
LDHA	4	2.311	1.616	3.307	<0.001	<0.001	YES
ENO3	4	2.196	1.566	3.079	<0.001	<0.001	YES
MAPK1	4	2.184	1.394	3.42	0.001	0.005	YES
SERPINE1	3	2.123	1.397	3.227	<0.001	0.004	YES
EGLN3	2	2.058	1.36	3.114	0.001	0.005	YES
RPS6KB1	4	2.045	1.479	2.827	<0.001	<0.001	YES
EGF	3	2.044	1.318	3.169	0.001	0.008	YES
PDHA2	3	1.977	1.213	3.223	0.006	0.023	YES
SLC2A1	4	1.968	1.402	2.764	<0.001	0.002	YES
PIK3CB	3	1.948	1.197	3.168	0.007	0.024	YES
ANGPT1	3	1.918	1.194	3.082	0.007	0.024	YES
PGK1	4	1.899	1.282	2.812	0.001	0.008	YES
MAP2K2	3	1.88	1.263	2.798	0.002	0.01	YES
PFKFB3	3	1.875	1.217	2.889	0.004	0.017	YES
EIF4E2	3	1.854	1.327	2.591	<0.001	0.004	YES
EGLN1	3	1.823	1.234	2.691	0.003	0.011	YES
PLCG1	4	1.808	1.24	2.636	0.002	0.01	YES
PFKM	4	1.696	1.224	2.349	0.002	0.008	YES
RPS6	4	1.692	1.161	2.467	0.006	0.023	YES
PFKP	4	1.681	1.176	2.403	0.004	0.017	YES
LDHB	4	1.651	1.108	2.46	0.014	0.041	YES
EP300	4	1.642	1.173	2.299	0.004	0.016	YES
HKDC1	3	1.642	1.101	2.449	0.015	0.042	YES
RPS6KB2	4	1.608	1.088	2.378	0.017	0.045	YES
EIF4EBP1	3	1.543	1.088	2.189	0.015	0.042	YES
TFRC	4	1.509	1.075	2.12	0.018	0.045	YES
MTOR	3	0.654	0.462	0.927	0.017	0.045	YES
CREBBP	4	0.563	0.394	0.805	0.002	0.009	YES
IGF1	3	0.55	0.367	0.824	0.004	0.016	YES
IFNG	2	0.538	0.321	0.901	0.018	0.046	YES
PIK3R2	3	0.522	0.322	0.845	0.008	0.027	YES
PIK3R3	3	0.522	0.337	0.807	0.003	0.015	YES
TEK	3	0.521	0.338	0.802	0.003	0.013	YES
STAT3	4	0.513	0.347	0.761	0.001	0.006	YES
IL6R	3	0.509	0.295	0.878	0.015	0.042	YES
ANGPT4	2	0.498	0.289	0.858	0.012	0.037	YES
PRKCA	4	0.492	0.34	0.712	<0.001	0.003	YES
PLCG2	4	0.48	0.316	0.727	0.001	0.005	YES
LTBR	3	0.471	0.274	0.812	0.007	0.023	YES
CAMK2B	3	0.451	0.289	0.705	<0.001	0.004	YES
NPPA	3	0.408	0.245	0.678	0.001	0.005	YES
MKNK1	3	0.377	0.22	0.648	<0.001	0.004	YES
VEGFA	3	0.252	0.087	0.733	0.011	0.036	YES
AKT1	4	0.789	0.567	1.098	0.16	0.247	NO
AKT2	4	0.892	0.61	1.304	0.555	0.638	NO
AKT3	3	1.353	0.86	2.129	0.191	0.278	NO
ALDOB	4	0.882	0.632	1.231	0.46	0.554	NO
ALDOC	4	1.056	0.724	1.542	0.776	0.81	NO
ANGPT2	3	2.57	1.16	5.691	0.02	0.05	NO
ARNT	4	1.489	0.977	2.271	0.064	0.126	NO
BCL2	3	0.574	0.335	0.981	0.042	0.096	NO
CAMK2A	3	0.715	0.48	1.066	0.1	0.173	NO
CAMK2D	2	0.501	0.266	0.943	0.032	0.076	NO
CAMK2G	4	1.074	0.728	1.583	0.72	0.766	NO
CDKN1A	3	1.432	0.945	2.17	0.091	0.165	NO
CDKN1B	4	0.835	0.579	1.205	0.336	0.43	NO
CUL2	4	0.959	0.693	1.327	0.801	0.83	NO
CYBB	4	1.087	0.764	1.546	0.643	0.705	NO
EDN1	2	1.613	0.968	2.688	0.067	0.128	NO
EGFR	4	0.879	0.436	1.77	0.717	0.766	NO
EIF4E	4	1.097	0.768	1.566	0.612	0.685	NO
ELOB	2	0.82	0.579	1.161	0.264	0.359	NO
ELOC	2	1.499	1.034	2.172	0.033	0.076	NO

S4. Pooled prognostic value of Hypoxia-related genes based on pooled four training cohorts (meta-analysis,n=452)

Hypoxia-related genes	Pooled results(n=452)						Included in Hypoxia Score Model
	Freq of cohorts	HR	95CI_L	95CI_U	pvalue	FDR	
ENO1	4	1.558	0.975	2.49	0.064	0.126	NO
ERBB2	4	0.855	0.594	1.23	0.398	0.498	NO
FLT1	3	1.456	0.959	2.21	0.078	0.144	NO
GAPDH	4	1.466	1.043	2.061	0.028	0.067	NO
HIF1A	3	1.116	0.69	1.806	0.654	0.708	NO
HK1	4	0.796	0.558	1.138	0.211	0.302	NO
HK3	4	0.904	0.594	1.375	0.636	0.703	NO
IFNGR1	3	0.812	0.542	1.217	0.312	0.408	NO
IFNGR2	3	1.287	0.786	2.106	0.316	0.408	NO
IGF1R	3	0.599	0.354	1.014	0.057	0.118	NO
IL6	3	0.631	0.418	0.953	0.029	0.068	NO
INS	3	1.57	0.87	2.834	0.135	0.215	NO
INSR	4	1.644	1.005	2.691	0.048	0.105	NO
LDHAL6B	2	1.194	0.745	1.914	0.462	0.554	NO
LDHC	3	0.646	0.407	1.025	0.064	0.126	NO
MAP2K1	4	0.887	0.601	1.308	0.544	0.634	NO
MAPK3	4	1.147	0.827	1.591	0.411	0.503	NO
MKNK2	2	1.014	0.578	1.779	0.962	0.974	NO
NFKB1	4	0.602	0.389	0.932	0.023	0.056	NO
NOS2	2	1.302	0.848	1.999	0.228	0.321	NO
NOS3	4	0.784	0.55	1.117	0.178	0.262	NO
PDHA1	3	0.736	0.514	1.053	0.093	0.167	NO
PDHB	4	0.999	0.58	1.72	0.996	0.996	NO
PDK1	4	0.727	0.458	1.153	0.175	0.262	NO
PFKL	4	1.079	0.777	1.499	0.65	0.708	NO
PGK2	2	0.706	0.45	1.108	0.13	0.213	NO
PIK3CA	4	1.176	0.805	1.718	0.401	0.498	NO
PIK3CD	4	0.895	0.634	1.263	0.527	0.619	NO
PIK3R1	4	0.789	0.512	1.214	0.281	0.377	NO
PRKCB	3	0.734	0.502	1.073	0.11	0.188	NO
PRKCG	3	0.666	0.399	1.113	0.121	0.201	NO
RBX1	2	1.543	0.922	2.583	0.099	0.173	NO
RELA	4	1.103	0.748	1.626	0.622	0.692	NO
TF	4	1.464	0.882	2.43	0.14	0.222	NO
TIMP1	4	1.305	0.932	1.828	0.121	0.201	NO
TLR4	2	0.69	0.459	1.038	0.075	0.142	NO
VHL	3	1.334	0.782	2.273	0.29	0.384	NO

S5. Pooled prognostic value of TME cells based on pooled four training cohorts (meta-analysis,n=452)

TME cells	Subgroup	Pooled results(n=452)						Included in TME Score Model
		Freq of cohorts	HR	95CI_L	95CI_U	pvalue	FDR	
aDC	Myeloid	4	0.745	0.487	1.142	0.177	0.262	NO
Adipocytes	Stroma	4	0.578	0.368	0.908	0.017	0.045	YES
Astrocytes	Epithelial	4	1.235	0.875	1.743	0.231	0.323	NO
Basophils	Myeloid	4	1.578	1.102	2.259	0.013	0.039	YES
B-cells	Lymphoid	4	0.547	0.379	0.789	0.001	0.008	YES
CD4+ memory T-cells	Lymphoid	4	1.004	0.673	1.497	0.986	0.992	NO
CD4+ naive T-cells	Lymphoid	4	0.752	0.52	1.09	0.132	0.213	NO
CD4+ T-cells	Lymphoid	4	1.339	0.669	2.68	0.41	0.503	NO
CD4+ Tcm	Lymphoid	4	0.711	0.476	1.06	0.094	0.167	NO
CD4+ Tem	Lymphoid	4	0.75	0.483	1.163	0.199	0.287	NO
CD8+ naive T-cells	Lymphoid	4	1.407	0.977	2.027	0.067	0.128	NO
CD8+ T-cells	Lymphoid	4	0.887	0.598	1.316	0.552	0.638	NO
CD8+ Tcm	Lymphoid	4	0.51	0.343	0.759	0.001	0.006	YES
CD8+ Tem	Lymphoid	4	0.41	0.281	0.598	<0.001	<0.001	YES
cDC	Myeloid	4	1.219	0.752	1.977	0.422	0.513	NO
Chondrocytes	Stroma	4	0.663	0.473	0.931	0.018	0.045	YES
Class-switched memory B-cells	Lymphoid	4	0.732	0.516	1.037	0.079	0.146	NO
CLP	HSC	4	1.223	0.861	1.738	0.26	0.358	NO
CMP	HSC	4	0.882	0.579	1.344	0.559	0.638	NO
DC	Myeloid	4	1.063	0.72	1.569	0.758	0.796	NO
Endothelial cells	Stroma	4	0.756	0.449	1.271	0.291	0.384	NO
Eosinophils	Myeloid	4	0.587	0.418	0.825	0.002	0.011	YES
Epithelial cells	Epithelial	4	1.294	0.896	1.87	0.169	0.255	NO
Erythrocytes	HSC	4	1.566	0.908	2.704	0.107	0.185	NO
Fibroblasts	Stroma	4	0.694	0.48	1.004	0.053	0.114	NO
GMP	HSC	4	0.943	0.662	1.343	0.745	0.787	NO
Hepatocytes	Epithelial	4	0.506	0.348	0.736	<0.001	0.004	YES
HSC	HSC	4	0.759	0.541	1.066	0.112	0.189	NO
iDC	Myeloid	4	0.828	0.54	1.27	0.387	0.489	NO
Keratinocytes	Epithelial	4	1.237	0.849	1.802	0.269	0.363	NO
ly Endothelial cells	Stroma	4	0.378	0.14	1.016	0.054	0.115	NO
Macrophages	Myeloid	4	0.675	0.493	0.925	0.015	0.042	YES
Macrophages M1	Myeloid	4	0.807	0.561	1.161	0.248	0.344	NO
Macrophages M2	Myeloid	4	0.689	0.425	1.118	0.132	0.213	NO
Mast cells	Myeloid	4	1.819	1.282	2.579	0.001	0.006	YES
Megakaryocytes	HSC	4	1.076	0.778	1.487	0.658	0.708	NO
Melanocytes	Epithelial	4	0.834	0.559	1.243	0.373	0.474	NO
Memory B-cells	Lymphoid	4	0.547	0.392	0.762	<0.001	0.004	YES
MEP	HSC	4	2.016	1.243	3.272	0.005	0.017	YES
Mesangial cells	Stroma	4	1.724	1.13	2.631	0.012	0.036	YES
Monocytes	Myeloid	4	0.761	0.519	1.114	0.16	0.247	NO
MPP	HSC	4	0.698	0.483	1.009	0.056	0.118	NO
MSC	Stroma	4	0.845	0.607	1.176	0.317	0.408	NO
mv Endothelial cells	Stroma	4	0.715	0.502	1.018	0.063	0.126	NO
Myocytes	Stroma	4	1.096	0.791	1.517	0.583	0.661	NO
naive B-cells	Lymphoid	4	0.669	0.429	1.045	0.077	0.144	NO
Neurons	Epithelial	4	1.126	0.733	1.73	0.587	0.662	NO
Neutrophils	Myeloid	4	1.372	0.892	2.11	0.15	0.234	NO
NK cells	Lymphoid	4	0.623	0.438	0.885	0.008	0.027	YES
NKT	Lymphoid	4	0.776	0.516	1.167	0.223	0.317	NO
Osteoblast	Stroma	4	0.854	0.535	1.363	0.508	0.6	NO
pDC	Myeloid	4	0.689	0.479	0.99	0.044	0.097	NO
Pericytes	Stroma	4	1.152	0.787	1.687	0.467	0.556	NO
Plasma cells	Lymphoid	4	0.59	0.419	0.83	0.002	0.011	YES
Platelets	HSC	4	0.963	0.699	1.327	0.82	0.845	NO
Preadipocytes	Stroma	4	0.349	0.234	0.52	<0.001	<0.001	YES
pro B-cells	Lymphoid	4	1.451	0.979	2.152	0.064	0.126	NO
Sebocytes	Epithelial	4	1.46	1.013	2.102	0.042	0.096	NO
Skeletal muscle cells	Stroma	4	0.965	0.6	1.553	0.885	0.901	NO
Smooth muscle cells	Stroma	4	1.399	0.873	2.244	0.163	0.249	NO
Tgd cells	Lymphoid	4	1.729	1.213	2.465	0.002	0.011	YES
Th1 cells	Lymphoid	4	1.683	1.219	2.322	0.002	0.008	YES
Th2 cells	Lymphoid	4	1.845	1.297	2.625	0.001	0.005	YES
Tregs	Lymphoid	4	0.973	0.681	1.391	0.882	0.901	NO

S6. The enrichment score of immune-related gene sets for HBV-related HCC cohorts

Cohort	ID	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalues	rank	leading_edge
Gao，Fudan	IMMUNE_SYSTEM_PROCESS	101.000	0.402	1.690	0.002	0.041	0.031	854	tags=29%, list=13%, signal=25%
Gao，Fudan	IMMUNE_RESPONSE	65.000	0.450	1.749	0.002	0.041	0.031	854	tags=31%, list=13%, signal=27%
Gao，Fudan	GO_SOMATIC_DIVERSIFICATION_OF_IMMUNE_RECEPTORS_VIA_GERMLINE_RECOMBINATION_WITHIN_A_SINGLE_LOCUS	28.000	-0.603	-1.919	0.002	0.041	0.031	1106	tags=43%, list=17%, signal=36%
GSE14520	GO_IMMUNE_RESPONSE_REGULATING_SIGNALING_PATHWAY	471.000	0.378	1.566	0.001	0.010	0.006	2465	tags=32%, list=20%, signal=27%
GSE14520	IMMUNE_SYSTEM_PROCESS	301.000	0.494	1.962	0.001	0.010	0.006	1859	tags=32%, list=15%, signal=28%
GSE14520	GO_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	369.000	0.416	1.680	0.002	0.010	0.006	2416	tags=36%, list=19%, signal=30%
GSE14520	GO_ADAPTIVE_IMMUNE_RESPONSE	351.000	0.582	2.343	0.002	0.010	0.006	1971	tags=40%, list=16%, signal=34%
GSE14520	GO_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	333.000	0.532	2.133	0.002	0.010	0.006	1472	tags=29%, list=12%, signal=26%
GSE14520	GO_ADAPTIVE_IMMUNE_RESPONSE_BASED_ON_SOMATIC_RECOMBINATION_OF_IMMUNE_RECEPTORS_BUILT_FROM_IMMUNOGLOBULIN_SUPERFAMILY_DOMAINS	221.000	0.571	2.202	0.002	0.010	0.006	1259	tags=31%, list=10%, signal=29%
GSE14520	IMMUNE_RESPONSE	214.000	0.556	2.138	0.002	0.010	0.006	1859	tags=36%, list=15%, signal=31%
GSE14520	GO_HUMORAL_IMMUNE_RESPONSE	207.000	0.682	2.608	0.002	0.010	0.006	1462	tags=38%, list=12%, signal=34%
GSE14520	GO_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	136.000	0.469	1.705	0.002	0.010	0.006	2116	tags=36%, list=17%, signal=30%
GSE14520	GO_IMMUNE_RECEPTOR_ACTIVITY	113.000	0.565	2.006	0.002	0.010	0.006	2710	tags=42%, list=22%, signal=33%
GSE14520	GO_NEGATIVE_REGULATION_OF_IMMUNE_RESPONSE	129.000	0.466	1.683	0.002	0.010	0.006	2403	tags=37%, list=19%, signal=30%
GSE14520	GO_REGULATION_OF_HUMORAL_IMMUNE_RESPONSE	66.000	0.800	2.576	0.002	0.010	0.006	939	tags=53%, list=8%, signal=49%
GSE14520	GO_NEGATIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	41.000	0.614	1.804	0.002	0.010	0.006	2082	tags=41%, list=17%, signal=35%
GSE14520	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	41.000	0.689	2.026	0.002	0.010	0.006	1969	tags=44%, list=16%, signal=37%
GSE14520	GO_HUMORAL_IMMUNE_RESPONSE_MEDIATED_BY_CIRCULATING_IMMUNOGLOBULIN	49.000	0.844	2.537	0.002	0.010	0.006	536	tags=59%, list=4%, signal=57%
GSE14520	GO_IMMUNE_RESPONSE_REGULATING_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY	340.000	0.375	1.507	0.003	0.015	0.009	2278	tags=30%, list=18%, signal=25%
GSE14520	GO_NEGATIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	109.000	0.503	1.781	0.003	0.015	0.009	2410	tags=40%, list=19%, signal=33%
GSE14520	GO_NEGATIVE_REGULATION_OF_HUMORAL_IMMUNE_RESPONSE	12.000	0.818	1.818	0.004	0.018	0.011	1431	tags=67%, list=12%, signal=59%
GSE14520	GO_REGULATION_OF_HUMORAL_IMMUNE_RESPONSE_MEDIATED_BY_CIRCULATING_IMMUNOGLOBULIN	11.000	0.815	1.775	0.006	0.025	0.015	1356	tags=55%, list=11%, signal=49%
GSE14520	GO_POSITIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	181.000	0.391	1.476	0.006	0.025	0.015	2274	tags=31%, list=18%, signal=26%
GSE14520	HUMORAL_IMMUNE_RESPONSE	30.000	0.630	1.751	0.008	0.030	0.018	1462	tags=33%, list=12%, signal=29%
GSE14520	GO_ANTIMICROBIAL_HUMORAL_IMMUNE_RESPONSE_MEDIATED_BY_ANTIMICROBIAL_PEPTIDE	52.000	0.522	1.600	0.011	0.039	0.023	1082	tags=19%, list=9%, signal=18%
GSE14520	GO_TYPE_2_IMMUNE_RESPONSE	34.000	0.597	1.705	0.011	0.039	0.023	2316	tags=50%, list=19%, signal=41%
GSE14520	GO_REGULATION_OF_TYPE_2_IMMUNE_RESPONSE	30.000	0.619	1.720	0.012	0.039	0.023	2316	tags=53%, list=19%, signal=43%
GSE14520	IMMUNE_EFFECTOR_PROCESS	33.000	0.586	1.671	0.013	0.042	0.025	1830	tags=33%, list=15%, signal=28%
GSE10143	GO_INNATE_IMMUNE_RESPONSE	478.000	0.327	1.523	0.001	0.006	0.003	1166	tags=26%, list=19%, signal=22%
GSE10143	GO_POSITIVE_REGULATION_OF_IMMUNE_RESPONSE	425.000	0.393	1.816	0.001	0.006	0.003	1166	tags=29%, list=19%, signal=25%
GSE10143	GO_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	421.000	0.346	1.593	0.001	0.006	0.003	1142	tags=26%, list=19%, signal=23%
GSE10143	REACTOME_ADAPTIVE_IMMUNE_SYSTEM	375.000	0.368	1.675	0.001	0.006	0.003	1119	tags=29%, list=18%, signal=26%
GSE10143	GO_IMMUNE_RESPONSE_REGULATING_SIGNALING_PATHWAY	300.000	0.422	1.878	0.001	0.006	0.003	1119	tags=30%, list=18%, signal=26%
GSE10143	GO_ACTIVATION_OF_IMMUNE_RESPONSE	326.000	0.421	1.879	0.001	0.006	0.003	1142	tags=29%, list=19%, signal=25%
GSE10143	GO_ADAPTIVE_IMMUNE_RESPONSE	237.000	0.527	2.283	0.001	0.006	0.003	1173	tags=40%, list=19%, signal=34%
GSE10143	GO_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	250.000	0.406	1.768	0.001	0.006	0.003	1302	tags=32%, list=21%, signal=27%
GSE10143	IMMUNE_SYSTEM_PROCESS	209.000	0.598	2.544	0.001	0.006	0.003	1054	tags=43%, list=17%, signal=37%
GSE10143	GO_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	226.000	0.404	1.735	0.001	0.006	0.003	1157	tags=29%, list=19%, signal=24%
GSE10143	GO_IMMUNE_RESPONSE_REGULATING_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY	227.000	0.452	1.942	0.001	0.006	0.003	1119	tags=32%, list=18%, signal=27%
GSE10143	GO_ADAPTIVE_IMMUNE_RESPONSE_BASED_ON_SOMATIC_RECOMBINATION_OF_IMMUNE_RECEPTORS_BUILT_FROM_IMMUNOGLOBULIN_SUPERFAMILY_DOMAINS	164.000	0.427	1.770	0.001	0.006	0.003	1166	tags=34%, list=19%, signal=28%
GSE10143	GO_HUMORAL_IMMUNE_RESPONSE	153.000	0.428	1.759	0.002	0.006	0.003	1155	tags=32%, list=19%, signal=27%

S6. The enrichment score of immune-related gene sets for HBV-related HCC cohorts

Cohort	ID	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalues	rank	leading_edge
GSE10143	IMMUNE_RESPONSE	153.000	0.614	2.524	0.002	0.006	0.003	948	tags=43%, list=16%, signal=37%
GSE10143	GO_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	100.000	0.466	1.806	0.002	0.006	0.003	1647	tags=48%, list=27%, signal=36%
GSE10143	GO_IMMUNE_RECEPTOR_ACTIVITY	81.000	0.542	2.009	0.002	0.006	0.003	906	tags=38%, list=15%, signal=33%
GSE10143	GO_NEGATIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	72.000	0.470	1.700	0.002	0.006	0.003	1344	tags=33%, list=22%, signal=26%
GSE10143	GO_T_CELL_DIFFERENTIATION_INVOLVED_IN_IMMUNE_RESPONSE	36.000	0.560	1.804	0.002	0.006	0.003	424	tags=33%, list=7%, signal=31%
GSE10143	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	35.000	0.643	2.058	0.002	0.006	0.003	1320	tags=66%, list=22%, signal=52%
GSE10143	REGULATION_OF_IMMUNE_SYSTEM_PROCESS	37.000	0.599	1.943	0.002	0.006	0.003	1529	tags=59%, list=25%, signal=45%
GSE10143	POSITIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	28.000	0.682	2.084	0.002	0.006	0.003	1023	tags=54%, list=17%, signal=45%
GSE10143	GO_T_HELPER_1_TYPE_IMMUNE_RESPONSE	25.000	0.595	1.761	0.002	0.006	0.003	948	tags=48%, list=16%, signal=41%
GSE10143	HUMORAL_IMMUNE_RESPONSE	24.000	0.616	1.828	0.003	0.011	0.006	1416	tags=62%, list=23%, signal=48%
GSE10143	GO_POSITIVE_REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONSE	12.000	0.724	1.823	0.004	0.011	0.006	805	tags=50%, list=13%, signal=43%
GSE10143	GO_T_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	61.000	0.467	1.655	0.008	0.024	0.013	424	tags=23%, list=7%, signal=22%
GSE10143	GO_REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONSE	16.000	0.651	1.754	0.009	0.026	0.014	424	tags=38%, list=7%, signal=35%
GSE10143	GO_LYMPHOCYTE_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	96.000	0.388	1.485	0.011	0.030	0.016	557	tags=20%, list=9%, signal=18%
GSE10143	GO_POSITIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	65.000	0.427	1.515	0.011	0.030	0.016	1335	tags=40%, list=22%, signal=32%
GSE10143	GO_HUMORAL_IMMUNE_RESPONSE_MEDIATED_BY_CIRCULATING_IMMUNOGLOBULIN	36.000	0.500	1.609	0.015	0.038	0.020	1155	tags=36%, list=19%, signal=29%
GSE10143	GO_POSITIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	129.000	0.346	1.386	0.017	0.041	0.022	1573	tags=40%, list=26%, signal=31%
GSE10143	POSITIVE_REGULATION_OF_IMMUNE_RESPONSE	15.000	0.610	1.630	0.018	0.043	0.023	948	tags=47%, list=16%, signal=40%
GSE10143	GO_NEGATIVE_REGULATION_OF_IMMUNE_RESPONSE	93.000	0.381	1.450	0.019	0.043	0.023	1137	tags=28%, list=19%, signal=23%
TCGA	GO_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	430.000	0.449	1.574	0.001	0.009	0.005	3406	tags=35%, list=17%, signal=30%
TCGA	GO_ADAPTIVE_IMMUNE_RESPONSE	395.000	0.571	1.989	0.001	0.009	0.005	3414	tags=43%, list=17%, signal=36%
TCGA	GO_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	375.000	0.579	2.008	0.001	0.009	0.005	3159	tags=37%, list=16%, signal=32%
TCGA	IMMUNE_SYSTEM_PROCESS	326.000	0.532	1.825	0.001	0.009	0.005	3331	tags=40%, list=17%, signal=33%
TCGA	GO_ADAPTIVE_IMMUNE_RESPONSE_BASED_ON_SOMATIC_RECOMBINATION_OF_IMMUNE_RECEPTORS_BUILT_FROM_IMMUNOGLOBULIN_SUPERFAMILY_DOMAINS	244.000	0.578	1.942	0.001	0.009	0.005	2598	tags=36%, list=13%, signal=32%
TCGA	GO_HUMORAL_IMMUNE_RESPONSE	235.000	0.638	2.136	0.001	0.009	0.005	1967	tags=33%, list=10%, signal=30%
TCGA	IMMUNE_RESPONSE	229.000	0.610	2.038	0.001	0.009	0.005	3314	tags=44%, list=17%, signal=37%
TCGA	GO_POSITIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	201.000	0.480	1.585	0.001	0.009	0.005	3386	tags=36%, list=17%, signal=30%
TCGA	GO_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	153.000	0.520	1.666	0.001	0.009	0.005	3314	tags=37%, list=17%, signal=31%
TCGA	GO_IMMUNE_RECEPTOR_ACTIVITY	126.000	0.600	1.886	0.001	0.009	0.005	3279	tags=41%, list=17%, signal=35%
TCGA	GO_NEGATIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	117.000	0.556	1.717	0.001	0.009	0.005	3222	tags=39%, list=16%, signal=33%
TCGA	GO_REGULATION_OF_HUMORAL_IMMUNE_RESPONSE	70.000	0.814	2.330	0.002	0.009	0.005	1739	tags=63%, list=9%, signal=57%
TCGA	GO_HUMORAL_IMMUNE_RESPONSE_MEDIATED_BY_CIRCULATING_IMMUNOGLOBULIN	47.000	0.827	2.239	0.002	0.009	0.005	916	tags=62%, list=5%, signal=59%
TCGA	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	46.000	0.721	1.939	0.002	0.009	0.005	3314	tags=57%, list=17%, signal=47%
TCGA	GO_NATURAL_KILLER_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	31.000	0.748	1.863	0.002	0.009	0.005	2553	tags=23%, list=13%, signal=20%
TCGA	GO_NEGATIVE_REGULATION_OF_IMMUNE_RESPONSE	146.000	0.520	1.659	0.003	0.014	0.008	2895	tags=35%, list=15%, signal=30%
TCGA	IMMUNE_EFFECTOR_PROCESS	38.000	0.666	1.726	0.003	0.015	0.009	1383	tags=32%, list=7%, signal=29%
TCGA	GO_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	85.000	0.521	1.541	0.006	0.026	0.015	3222	tags=38%, list=16%, signal=32%
TCGA	GO_TYPE_2_IMMUNE_RESPONSE	38.000	0.645	1.671	0.006	0.026	0.015	3620	tags=50%, list=19%, signal=41%
TCGA	GO_REGULATION_OF_TYPE_2_IMMUNE_RESPONSE	31.000	0.672	1.673	0.006	0.026	0.015	3620	tags=58%, list=19%, signal=47%
TCGA	GO_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	135.000	0.469	1.487	0.008	0.032	0.018	3386	tags=36%, list=17%, signal=30%
TCGA	GO_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	195.000	0.428	1.413	0.009	0.033	0.019	3386	tags=32%, list=17%, signal=27%
TCGA	GO_NEGATIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	46.000	0.612	1.647	0.010	0.033	0.019	3222	tags=43%, list=16%, signal=36%
TCGA	GO_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	103.000	0.489	1.486	0.012	0.040	0.023	3222	tags=36%, list=16%, signal=30%

S7. The correlationship of Hypoxia score and TME score in 21 HCC cohrots and 5 HBV-related HCC cohorts

All HCC patients		HBV-related HCC patients			
dataset	**cor**	**p.value**	**dataset**	**cor**	**p.value**
GSE9843	-0.48904568	8.71E-07	TCGA_LIHC	-0.536237	4.30578E-12
GSE76427	-0.34721097	4.28E-06	ICGC_LIRI_JP	-0.3271352	0.01680316
GSE109211	-0.39330548	1.53E-06	GSE14520	-0.5393331	4.45143E-18
GSE10143	0.15191543	2.73E-03	Fudandata	-0.2284428	0.003776837
GSE19977	-0.18849548	1.56E-02	GSE10143	0.2549266	0.2922078
GSE22058	-0.39435432	9.82E-09			
GSE25097	-0.38628831	2.90E-21			
GSE43619	-0.38985494	1.74E-04			
GSE45267	-0.7447641	1.35E-16			
GSE46444	0.05217944	5.46E-01			
GSE54236	-0.30253769	9.59E-05			
GSE63898	-0.29264702	2.93E-09			
GSE64041	-0.37257905	1.88E-05			
GSE84402	-0.40995592	3.03E-02			
GSE112790	-0.58265132	2.16E-19			
ICGC_LIRI_JP	-0.35063656	1.07E-12			
TCGA_LIHC	-0.44779741	2.67E-22			
GSE14520	-0.53933307	4.45E-18			
Fudandata	-0.27305123	7.64E-07			
GSE124751	-0.53528312	1.14E-16			
GSE15654	0.0599063	3.81E-01			

S8. The detailed Hypoxia-TME score of all included HBV-related HCC patients (n=596)

Sample_names	OS_time	OS	TME score	Hypoxia Score	TME subgroup	Hypoxia subgroup	Hypoxia-TME subgroup	Dataset
T1013	10.43	1.00	-1.04	0.16	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T1015	29.60	0.00	1.21	-1.23	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T1021	11.03	1.00	-1.20	-0.29	FALSE	FALSE	Mixed	Fudandata
T1025	29.67	0.00	0.01	0.28	TRUE	TRUE	Mixed	Fudandata
T1027	18.80	1.00	-0.10	1.35	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T1031	32.77	0.00	0.46	0.05	TRUE	TRUE	Mixed	Fudandata
T1041	32.43	0.00	-0.38	-0.73	FALSE	FALSE	Mixed	Fudandata
T1043	32.60	0.00	1.13	0.68	TRUE	TRUE	Mixed	Fudandata
T1045	32.53	0.00	1.68	-0.36	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T112	47.90	0.00	-0.18	-0.46	FALSE	FALSE	Mixed	Fudandata
T113	49.60	0.00	0.02	0.18	TRUE	TRUE	Mixed	Fudandata
T123	15.67	1.00	0.15	-0.94	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T125	9.30	1.00	-0.46	1.91	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T127	48.30	0.00	0.09	-1.07	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T131	48.30	0.00	-1.00	-0.29	FALSE	FALSE	Mixed	Fudandata
T135	25.33	1.00	0.74	0.86	TRUE	TRUE	Mixed	Fudandata
T137	48.10	0.00	1.30	-0.18	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T141	49.77	0.00	1.35	-0.20	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T145	49.83	0.00	0.97	-0.07	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T147	30.00	1.00	0.54	-0.65	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T161	47.80	0.00	-1.92	-1.00	FALSE	FALSE	Mixed	Fudandata
T171	14.53	1.00	-0.27	-0.87	FALSE	FALSE	Mixed	Fudandata
T187	47.10	0.00	1.85	-0.21	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T191	47.10	0.00	0.92	0.51	TRUE	TRUE	Mixed	Fudandata
T195	47.00	0.00	0.90	0.31	TRUE	TRUE	Mixed	Fudandata
T211	10.00	1.00	0.67	1.23	TRUE	TRUE	Mixed	Fudandata
T217	46.80	0.00	1.57	0.43	TRUE	TRUE	Mixed	Fudandata
T221	46.80	0.00	-0.11	-0.77	FALSE	FALSE	Mixed	Fudandata
T223	46.90	0.00	2.16	1.15	TRUE	TRUE	Mixed	Fudandata
T227	46.70	0.00	0.18	0.56	TRUE	TRUE	Mixed	Fudandata
T231	46.87	0.00	-0.56	-0.68	FALSE	FALSE	Mixed	Fudandata
T257	46.23	0.00	0.08	2.44	TRUE	TRUE	Mixed	Fudandata
T261	46.23	0.00	0.64	-1.35	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T267	45.43	1.00	-1.09	-0.26	FALSE	FALSE	Mixed	Fudandata
T271	46.10	0.00	0.05	-0.39	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T277	42.40	1.00	-1.24	-0.64	FALSE	FALSE	Mixed	Fudandata
T283	4.77	1.00	-0.34	2.22	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T285	10.57	1.00	-1.42	1.75	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T311	8.97	1.00	-0.28	0.75	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T313	19.77	1.00	-1.12	2.47	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T327	44.83	0.00	0.21	-0.97	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T331	4.67	1.00	-1.32	1.16	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T341	44.73	0.00	0.26	-0.65	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T343	43.93	1.00	0.35	0.88	TRUE	TRUE	Mixed	Fudandata
T351	10.83	1.00	-1.82	0.96	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T353	45.90	0.00	1.52	-0.92	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T355	44.37	0.00	-1.39	-0.01	FALSE	FALSE	Mixed	Fudandata
T357	44.37	0.00	-0.84	-1.37	FALSE	FALSE	Mixed	Fudandata
T361	45.30	0.00	0.18	0.00	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T363	44.30	0.00	0.16	0.28	TRUE	TRUE	Mixed	Fudandata
T365	44.00	0.00	1.55	-0.38	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T367	44.30	0.00	-0.58	1.51	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T375	44.67	0.00	-0.82	1.62	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T383	10.37	1.00	1.02	-0.66	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T385	44.00	0.00	-0.17	2.08	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T387	43.97	0.00	-0.82	1.71	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T391	43.93	0.00	-0.38	1.66	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T393	43.93	0.00	-0.17	0.58	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T395	43.87	0.00	-0.06	0.01	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T411	43.80	0.00	-0.32	-0.96	FALSE	FALSE	Mixed	Fudandata
T413	10.30	1.00	-1.31	1.28	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T415	43.23	0.00	1.54	-0.14	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T421	26.53	1.00	0.96	0.18	TRUE	TRUE	Mixed	Fudandata
T423	43.23	0.00	0.15	-1.26	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T425	43.30	0.00	-0.81	-1.69	FALSE	FALSE	Mixed	Fudandata
T427	44.73	0.00	-1.01	-0.03	FALSE	FALSE	Mixed	Fudandata
T431	43.00	0.00	0.29	-1.49	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T433	43.00	0.00	-0.87	-1.05	FALSE	FALSE	Mixed	Fudandata
T435	44.70	0.00	1.34	-2.20	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T443	44.20	0.00	0.25	-0.13	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T445	14.03	1.00	0.37	-1.39	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T451	23.83	1.00	0.07	-0.99	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T455	36.47	1.00	-0.07	0.67	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata

T461	42.87	0.00	1.85	-0.30	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T463	17.73	1.00	-1.20	0.60	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T465	43.23	0.00	0.21	-1.19	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T467	42.83	0.00	1.22	-0.51	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T471	42.83	0.00	1.01	-0.07	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T473	42.20	0.00	-0.83	-0.42	FALSE	FALSE	Mixed	Fudandata
T477	29.63	1.00	-0.41	-0.92	FALSE	FALSE	Mixed	Fudandata
T481	42.63	0.00	1.58	-0.37	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T483	42.70	0.00	-0.65	-0.64	FALSE	FALSE	Mixed	Fudandata
T487	42.60	0.00	0.70	0.24	TRUE	TRUE	Mixed	Fudandata
T491	15.30	1.00	0.98	0.58	TRUE	TRUE	Mixed	Fudandata
T493	0.40	1.00	-1.11	-0.53	FALSE	FALSE	Mixed	Fudandata
T497	9.23	1.00	-1.36	-1.01	FALSE	FALSE	Mixed	Fudandata
T513	41.93	0.00	0.83	-1.99	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T515	42.33	0.00	1.59	-0.59	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T517	6.90	1.00	-1.27	1.18	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T523	33.23	1.00	-0.86	0.60	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T525	25.10	1.00	-0.94	-0.32	FALSE	FALSE	Mixed	Fudandata
T527	16.60	1.00	-0.45	1.67	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T533	43.87	0.00	0.15	-1.56	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T537	43.80	0.00	-1.55	2.29	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T545	43.63	0.00	-0.99	-0.03	FALSE	FALSE	Mixed	Fudandata
T553	4.93	1.00	-0.40	-0.16	FALSE	FALSE	Mixed	Fudandata
T557	18.43	1.00	-1.02	-0.12	FALSE	FALSE	Mixed	Fudandata
T563	41.03	0.00	0.97	-0.21	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T567	16.27	1.00	-1.27	1.73	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T571	42.70	0.00	-0.73	-0.34	FALSE	FALSE	Mixed	Fudandata
T573	11.43	1.00	0.23	0.55	TRUE	TRUE	Mixed	Fudandata
T615	37.37	0.00	2.23	0.23	TRUE	TRUE	Mixed	Fudandata
T617	38.70	0.00	-0.48	0.33	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T627	37.17	0.00	1.20	-0.55	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T635	18.23	1.00	-0.27	-0.69	FALSE	FALSE	Mixed	Fudandata
T641	27.50	1.00	0.17	0.12	TRUE	TRUE	Mixed	Fudandata
T647	36.97	0.00	-0.20	-0.98	FALSE	FALSE	Mixed	Fudandata
T661	36.70	0.00	0.03	0.34	TRUE	TRUE	Mixed	Fudandata
T663	36.73	0.00	-0.81	0.75	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T665	10.50	1.00	0.32	-0.09	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T671	20.43	1.00	-0.86	1.07	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T685	23.07	1.00	-1.65	0.69	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T695	12.17	1.00	-1.31	-0.99	FALSE	FALSE	Mixed	Fudandata
T713	15.83	1.00	1.69	0.97	TRUE	TRUE	Mixed	Fudandata
T715	36.10	0.00	-0.98	0.42	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T721	35.47	0.00	2.16	-0.36	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T724	35.47	0.00	1.57	-0.41	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T727	35.43	0.00	-0.35	0.23	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T737	35.27	0.00	-1.45	0.55	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T741	34.37	0.00	0.35	-3.04	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T743	17.17	1.00	-1.92	0.74	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T745	36.33	0.00	1.09	0.27	TRUE	TRUE	Mixed	Fudandata
T755	34.97	0.00	0.00	-0.43	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T777	34.47	0.00	0.72	-1.51	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T785	7.37	1.00	-0.80	-0.40	FALSE	FALSE	Mixed	Fudandata
T813	12.53	1.00	-0.44	0.21	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T815	7.37	1.00	-0.12	2.05	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T817	34.00	0.00	-0.54	-0.17	FALSE	FALSE	Mixed	Fudandata
T823	33.90	0.00	1.08	0.14	TRUE	TRUE	Mixed	Fudandata
T851	16.97	1.00	0.54	1.62	TRUE	TRUE	Mixed	Fudandata
T857	33.90	0.00	1.93	0.11	TRUE	TRUE	Mixed	Fudandata
T861	34.13	0.00	1.26	-1.70	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T863	34.07	0.00	1.17	0.41	TRUE	TRUE	Mixed	Fudandata
T865	33.90	0.00	-1.99	-0.18	FALSE	FALSE	Mixed	Fudandata
T867	33.67	0.00	1.28	-1.19	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T873	33.90	0.00	-0.14	-0.02	FALSE	FALSE	Mixed	Fudandata
T877	28.20	1.00	-1.17	1.53	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T881	34.03	0.00	0.28	-0.43	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T883	33.90	0.00	-0.39	0.21	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T911	30.20	0.00	0.62	-1.88	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T913	24.13	1.00	0.38	-0.66	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T915	31.27	0.00	0.41	-0.82	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T917	31.30	0.00	0.48	0.88	TRUE	TRUE	Mixed	Fudandata
T921	31.23	0.00	-0.76	-0.60	FALSE	FALSE	Mixed	Fudandata
T923	4.17	1.00	-1.80	0.52	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T925	29.47	0.00	-0.37	-0.36	FALSE	FALSE	Mixed	Fudandata
T937	30.57	0.00	-0.03	-0.73	FALSE	FALSE	Mixed	Fudandata
T943	3.63	1.00	-0.64	0.44	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T951	18.80	1.00	-1.49	-0.20	FALSE	FALSE	Mixed	Fudandata
T953	30.07	0.00	-0.34	-0.01	FALSE	FALSE	Mixed	Fudandata
T955	30.73	0.00	1.40	-0.60	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata

T957	30.73	0.00	-1.21	-0.25	FALSE	FALSE	Mixed	Fudandata
T963	30.83	0.00	0.77	0.13	TRUE	TRUE	Mixed	Fudandata
T965	15.87	1.00	-0.76	0.57	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T967	30.03	0.00	-0.91	0.88	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
T975	29.90	0.00	0.77	-0.41	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T977	29.87	0.00	-0.72	-1.51	FALSE	FALSE	Mixed	Fudandata
T981	29.90	0.00	1.45	-0.52	TRUE	FALSE	Hypoxia^{low}/TME^{high}	Fudandata
T983	26.67	1.00	-0.23	2.19	FALSE	TRUE	Hypoxia^{high}/TME^{low}	Fudandata
GSM256428	71.50	1.00	0.59	-0.67	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE10143
GSM256439	129.67	0.00	-0.33	0.99	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE10143
GSM256442	107.90	0.00	-0.35	1.90	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE10143
GSM256445	94.97	1.00	0.57	-0.53	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE10143
GSM256446	132.43	0.00	-0.39	0.17	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE10143
GSM256448	67.30	1.00	1.14	0.87	TRUE	TRUE	Mixed	GSE10143
GSM256450	119.40	0.00	1.43	-0.07	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE10143
GSM256453	113.33	0.00	-0.59	-1.04	FALSE	FALSE	Mixed	GSE10143
GSM256455	124.53	1.00	-1.65	-2.19	FALSE	FALSE	Mixed	GSE10143
GSM256456	80.17	1.00	-0.97	0.34	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE10143
GSM256468	106.10	0.00	-1.15	-1.19	FALSE	FALSE	Mixed	GSE10143
GSM256469	95.30	1.00	0.43	0.40	TRUE	TRUE	Mixed	GSE10143
GSM256476	14.60	0.00	0.74	0.77	TRUE	TRUE	Mixed	GSE10143
GSM256479	38.00	1.00	-0.10	0.18	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE10143
GSM256482	93.73	0.00	0.68	-1.11	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE10143
GSM256490	13.60	1.00	-1.12	1.29	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE10143
GSM256497	70.20	1.00	-1.10	-0.24	FALSE	FALSE	Mixed	GSE10143
GSM256498	182.20	0.00	2.14	0.67	TRUE	TRUE	Mixed	GSE10143
GSM256504	184.27	0.00	0.04	-0.54	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE10143
GSM362958	28.20	1.00	-0.28	0.37	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM362959	9.50	1.00	0.08	0.67	TRUE	TRUE	Mixed	GSE14520
GSM362960	66.10	0.00	0.36	-0.02	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM362964	67.40	0.00	1.40	-0.79	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM362965	66.60	0.00	0.51	-0.47	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM362966	66.10	0.00	0.86	-1.34	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM362970	67.30	0.00	0.26	-1.53	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM362971	48.10	1.00	1.76	-0.53	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM362972	66.00	0.00	1.24	-1.34	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM362976	67.00	0.00	1.48	-1.45	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM362977	66.30	0.00	1.57	-1.66	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM362978	28.80	1.00	0.32	-0.81	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM362982	64.60	0.00	-0.39	-0.37	FALSE	FALSE	Mixed	GSE14520
GSM362983	64.20	0.00	-0.55	-0.11	FALSE	FALSE	Mixed	GSE14520
GSM362984	51.40	0.00	1.94	-2.02	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM362986	64.50	0.00	0.83	-0.40	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM362987	60.40	0.00	0.34	-1.58	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM362988	51.10	0.00	-0.50	-0.96	FALSE	FALSE	Mixed	GSE14520
GSM362992	64.30	0.00	0.28	-1.08	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM362993	3.80	0.00	-0.71	-0.54	FALSE	FALSE	Mixed	GSE14520
GSM362994	54.80	0.00	0.48	-1.73	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363008	58.40	0.00	1.03	0.48	TRUE	TRUE	Mixed	GSE14520
GSM363009	58.90	0.00	-0.95	1.45	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363010	62.00	0.00	0.60	1.79	TRUE	TRUE	Mixed	GSE14520
GSM363011	17.60	1.00	-1.50	1.21	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363012	4.50	1.00	0.94	-0.61	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363013	7.70	1.00	0.41	1.35	TRUE	TRUE	Mixed	GSE14520
GSM363014	60.70	0.00	0.59	-0.50	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363015	59.70	0.00	-0.37	0.40	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363016	2.00	0.00	0.55	-1.09	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363017	12.70	1.00	-0.97	0.93	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363029	51.30	0.00	1.41	0.51	TRUE	TRUE	Mixed	GSE14520
GSM363030	4.50	1.00	-1.55	2.01	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363031	52.80	0.00	0.05	-0.34	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363032	24.90	0.00	-0.18	1.60	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363033	36.40	1.00	0.02	0.22	TRUE	TRUE	Mixed	GSE14520
GSM363034	45.90	1.00	0.32	0.45	TRUE	TRUE	Mixed	GSE14520
GSM363035	56.10	0.00	2.09	-0.48	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363036	32.70	1.00	-0.02	-0.23	FALSE	FALSE	Mixed	GSE14520
GSM363037	61.20	0.00	-0.53	0.66	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363038	15.10	1.00	-0.34	0.85	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363039	52.80	0.00	0.71	-0.90	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363048	20.30	1.00	-0.62	1.05	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363049	62.40	0.00	-0.28	-0.16	FALSE	FALSE	Mixed	GSE14520
GSM363050	54.20	0.00	-0.05	-0.19	FALSE	FALSE	Mixed	GSE14520
GSM363051	20.60	0.00	1.09	1.30	TRUE	TRUE	Mixed	GSE14520
GSM363052	14.30	1.00	-0.86	3.45	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363053	57.00	0.00	-0.21	-0.52	FALSE	FALSE	Mixed	GSE14520
GSM363054	53.80	0.00	-0.96	0.28	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363055	7.30	0.00	-0.18	1.07	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363056	19.20	1.00	-0.83	1.21	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520

GSM363057	60.50	1.00	-0.51	0.54	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363069	13.60	1.00	-1.34	0.87	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363070	57.00	0.00	-1.48	2.39	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363071	13.80	1.00	-0.44	1.65	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363072	10.40	0.00	1.58	-1.20	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363073	26.50	1.00	1.14	1.35	TRUE	TRUE	Mixed	GSE14520
GSM363074	57.70	0.00	0.96	0.44	TRUE	TRUE	Mixed	GSE14520
GSM363075	18.00	1.00	-0.20	0.05	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363076	23.00	1.00	0.80	0.25	TRUE	TRUE	Mixed	GSE14520
GSM363077	52.70	0.00	0.02	-0.21	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363078	57.90	1.00	0.22	0.00	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363079	7.80	1.00	-1.30	0.37	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363080	2.30	1.00	-0.87	1.79	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363081	5.20	1.00	-1.18	0.70	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363082	57.00	0.00	0.62	-1.39	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363083	53.30	0.00	-1.27	1.13	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363084	62.60	0.00	0.28	-0.10	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363085	54.80	1.00	-1.47	0.85	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363086	60.50	0.00	-0.62	-0.18	FALSE	FALSE	Mixed	GSE14520
GSM363087	54.00	0.00	0.85	-0.72	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363098	56.90	0.00	1.47	0.71	TRUE	TRUE	Mixed	GSE14520
GSM363099	30.90	1.00	0.05	3.18	TRUE	TRUE	Mixed	GSE14520
GSM363100	3.40	1.00	-2.43	0.86	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363101	56.30	0.00	-0.13	-0.35	FALSE	FALSE	Mixed	GSE14520
GSM363102	37.90	1.00	0.43	-0.19	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363104	35.90	1.00	0.99	-1.23	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363105	9.50	0.00	-0.95	0.13	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363106	14.60	1.00	-0.42	0.15	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363107	7.00	1.00	0.35	-0.79	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363108	48.80	0.00	1.00	-0.89	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363109	55.20	0.00	-0.74	0.15	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363115	66.60	0.00	1.15	-0.56	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363121	51.20	0.00	1.92	0.25	TRUE	TRUE	Mixed	GSE14520
GSM363122	55.40	0.00	0.56	0.08	TRUE	TRUE	Mixed	GSE14520
GSM363123	42.70	0.00	0.16	-0.15	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363124	53.50	0.00	1.10	-1.57	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363125	16.50	1.00	0.23	0.31	TRUE	TRUE	Mixed	GSE14520
GSM363126	59.50	0.00	0.33	-0.24	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363127	22.20	1.00	-1.43	1.77	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363128	30.10	1.00	-0.34	1.22	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363129	3.50	1.00	-2.26	2.27	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363130	61.80	0.00	-0.31	-1.44	FALSE	FALSE	Mixed	GSE14520
GSM363142	46.10	1.00	0.46	0.53	TRUE	TRUE	Mixed	GSE14520
GSM363143	32.60	1.00	1.68	1.45	TRUE	TRUE	Mixed	GSE14520
GSM363144	51.10	0.00	0.24	0.22	TRUE	TRUE	Mixed	GSE14520
GSM363145	33.00	1.00	-0.21	0.53	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363146	54.90	0.00	1.27	-0.31	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363147	28.70	1.00	-0.47	0.70	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363148	52.40	0.00	0.83	-0.43	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363149	14.40	0.00	-0.26	-0.86	FALSE	FALSE	Mixed	GSE14520
GSM363150	3.30	1.00	-2.44	1.99	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363151	67.10	0.00	-0.31	0.27	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363152	8.30	1.00	-0.73	-0.68	FALSE	FALSE	Mixed	GSE14520
GSM363164	55.20	0.00	-0.13	-1.04	FALSE	FALSE	Mixed	GSE14520
GSM363166	53.80	0.00	-0.82	-1.55	FALSE	FALSE	Mixed	GSE14520
GSM363168	53.80	0.00	-0.13	-1.07	FALSE	FALSE	Mixed	GSE14520
GSM363169	39.40	0.00	-0.77	1.39	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363170	53.30	0.00	-0.42	0.46	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363172	6.70	1.00	-0.90	0.43	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363174	67.10	0.00	0.85	-0.15	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363176	50.70	0.00	1.25	-0.85	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363178	57.30	0.00	-0.17	-1.07	FALSE	FALSE	Mixed	GSE14520
GSM363180	47.10	1.00	0.77	-0.54	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363182	52.70	0.00	-0.53	-0.47	FALSE	FALSE	Mixed	GSE14520
GSM363184	16.30	0.00	-2.22	2.91	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363186	7.60	1.00	0.84	-1.47	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363188	57.30	0.00	0.38	-0.92	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363190	4.80	0.00	-1.00	-0.08	FALSE	FALSE	Mixed	GSE14520
GSM363192	52.20	0.00	-0.44	0.43	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363194	4.50	0.00	-1.44	2.00	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363196	57.70	0.00	2.34	-0.49	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363198	57.90	0.00	-0.16	-0.96	FALSE	FALSE	Mixed	GSE14520
GSM363200	23.90	1.00	-0.01	-1.04	FALSE	FALSE	Mixed	GSE14520
GSM363202	60.00	0.00	-0.04	-0.98	FALSE	FALSE	Mixed	GSE14520
GSM363204	14.10	1.00	-1.16	-0.17	FALSE	FALSE	Mixed	GSE14520
GSM363205	58.00	0.00	0.56	-1.21	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363207	53.30	1.00	-1.06	0.75	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363209	60.80	0.00	0.58	-0.59	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520

GSM363211	8.90	1.00	-1.12	0.56	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363213	57.60	0.00	0.31	-0.75	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363215	18.60	0.00	-0.32	-0.39	FALSE	FALSE	Mixed	GSE14520
GSM363217	54.50	0.00	-1.81	0.23	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363218	15.20	1.00	-1.91	0.93	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363220	54.20	0.00	0.55	0.06	TRUE	TRUE	Mixed	GSE14520
GSM363222	48.40	0.00	-1.18	0.60	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363224	57.90	0.00	-0.09	-0.29	FALSE	FALSE	Mixed	GSE14520
GSM363226	60.40	0.00	0.74	-0.80	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363230	4.80	0.00	-0.52	-0.68	FALSE	FALSE	Mixed	GSE14520
GSM363232	57.90	0.00	0.58	-0.42	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363235	32.80	0.00	-1.07	1.52	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363237	57.50	0.00	-0.20	0.91	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363239	42.20	1.00	-0.24	-0.75	FALSE	FALSE	Mixed	GSE14520
GSM363241	54.20	0.00	1.22	-0.82	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363243	55.80	0.00	1.93	-1.48	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363245	57.50	0.00	-0.85	1.04	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363247	52.90	0.00	0.42	-0.91	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363249	59.20	0.00	-0.71	-0.25	FALSE	FALSE	Mixed	GSE14520
GSM363251	19.60	1.00	-0.78	0.12	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363263	3.00	1.00	-1.47	1.06	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363264	17.80	1.00	0.63	-0.88	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363265	65.10	0.00	0.63	0.24	TRUE	TRUE	Mixed	GSE14520
GSM363266	2.50	1.00	-0.09	0.38	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363267	47.90	1.00	1.79	-0.62	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363268	56.00	0.00	0.22	0.26	TRUE	TRUE	Mixed	GSE14520
GSM363269	52.70	1.00	0.37	-1.51	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363270	21.30	1.00	-0.76	0.16	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363271	28.70	0.00	-0.61	1.56	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363272	56.30	0.00	0.80	-0.59	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363273	58.00	0.00	0.88	-1.22	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363274	26.90	1.00	-1.39	-1.01	FALSE	FALSE	Mixed	GSE14520
GSM363275	59.80	0.00	2.00	-0.58	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363288	60.30	0.00	0.49	-0.72	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363289	54.20	0.00	0.01	-0.48	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363290	54.70	0.00	0.49	-0.32	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363291	50.10	1.00	1.16	-0.33	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363292	59.90	0.00	-0.19	-0.17	FALSE	FALSE	Mixed	GSE14520
GSM363293	61.50	0.00	0.66	-0.60	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363294	62.60	0.00	-0.52	0.06	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363295	54.90	0.00	1.15	-1.36	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363296	27.50	1.00	-1.22	0.48	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363297	3.00	0.00	-0.03	1.00	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363298	53.60	0.00	0.41	-0.22	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363309	53.00	1.00	-0.76	-0.42	FALSE	FALSE	Mixed	GSE14520
GSM363310	23.50	1.00	-0.55	-0.09	FALSE	FALSE	Mixed	GSE14520
GSM363311	19.00	0.00	-0.45	-0.15	FALSE	FALSE	Mixed	GSE14520
GSM363312	55.30	0.00	0.81	-1.00	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363313	36.60	0.00	0.48	-0.75	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363314	57.10	0.00	0.61	-0.38	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363315	65.40	0.00	-0.12	-0.87	FALSE	FALSE	Mixed	GSE14520
GSM363316	54.70	0.00	-1.20	0.00	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363317	62.80	0.00	-0.79	0.90	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363326	37.20	1.00	0.96	0.55	TRUE	TRUE	Mixed	GSE14520
GSM363327	60.10	0.00	1.07	-0.94	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363328	12.00	1.00	-0.34	2.20	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363329	53.20	0.00	-0.04	0.13	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363330	12.60	1.00	-1.65	1.81	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363331	36.50	1.00	1.18	0.25	TRUE	TRUE	Mixed	GSE14520
GSM363332	12.60	1.00	-1.80	0.14	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363333	13.50	1.00	-0.93	1.01	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363335	59.40	0.00	0.91	-1.06	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363336	8.00	1.00	0.70	-1.04	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363337	65.50	0.00	-0.80	0.09	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363339	65.40	0.00	-0.55	0.84	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363341	65.40	0.00	-0.32	-0.39	FALSE	FALSE	Mixed	GSE14520
GSM363343	65.10	0.00	1.15	-0.54	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363344	38.70	0.00	-0.07	-0.85	FALSE	FALSE	Mixed	GSE14520
GSM363346	14.30	1.00	-0.99	-0.44	FALSE	FALSE	Mixed	GSE14520
GSM363348	14.30	0.00	-2.06	1.19	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363350	62.90	0.00	-2.26	1.09	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363352	16.20	1.00	1.37	0.35	TRUE	TRUE	Mixed	GSE14520
GSM363354	10.40	1.00	-3.13	1.60	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363355	9.10	1.00	-0.71	0.23	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363357	8.80	1.00	-0.66	0.52	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363358	53.90	0.00	-0.04	-0.63	FALSE	FALSE	Mixed	GSE14520
GSM363360	53.30	0.00	-0.84	-0.27	FALSE	FALSE	Mixed	GSE14520
GSM363362	5.80	1.00	-0.31	-0.03	FALSE	FALSE	Mixed	GSE14520

GSM363364	27.10	1.00	1.80	-1.80	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363366	52.30	0.00	0.82	-1.91	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363368	15.40	1.00	0.28	-0.10	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363371	66.30	0.00	0.74	-1.00	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363376	61.50	0.00	0.73	-0.69	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363378	31.90	1.00	1.17	-0.68	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363384	51.60	1.00	-0.47	0.82	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363386	10.00	1.00	-0.55	1.41	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
GSM363388	57.30	0.00	2.99	-0.15	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363391	57.30	0.00	0.15	-0.55	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363393	4.00	1.00	0.46	-0.85	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM363400	55.60	0.00	-0.18	-0.59	FALSE	FALSE	Mixed	GSE14520
GSM363404	12.00	1.00	0.83	-0.09	TRUE	FALSE	Hypoxia^{low}/TME^{high}	GSE14520
GSM712542	7.50	1.00	-0.48	1.16	FALSE	TRUE	Hypoxia^{high}/TME^{low}	GSE14520
HCCDB.18.S10	19.00	0.00	-1.68	0.08	FALSE	TRUE	Hypoxia^{high}/TME^{low}	ICGC_LIRI_JP
HCCDB.18.S100	15.00	0.00	0.50	-1.35	TRUE	FALSE	Hypoxia^{low}/TME^{high}	ICGC_LIRI_JP
HCCDB.18.S102	56.00	0.00	0.32	-0.03	TRUE	FALSE	Hypoxia^{low}/TME^{high}	ICGC_LIRI_JP
HCCDB.18.S104	39.00	0.00	-0.23	-0.95	FALSE	FALSE	Mixed	ICGC_LIRI_JP
HCCDB.18.S105	42.00	0.00	1.01	-0.42	TRUE	FALSE	Hypoxia^{low}/TME^{high}	ICGC_LIRI_JP
HCCDB.18.S11	17.00	0.00	-0.54	-0.93	FALSE	FALSE	Mixed	ICGC_LIRI_JP
HCCDB.18.S119	18.00	0.00	0.24	0.01	TRUE	TRUE	Mixed	ICGC_LIRI_JP
HCCDB.18.S12	13.00	0.00	-0.76	-0.74	FALSE	FALSE	Mixed	ICGC_LIRI_JP
HCCDB.18.S121	8.00	0.00	-1.60	2.05	FALSE	TRUE	Hypoxia^{high}/TME^{low}	ICGC_LIRI_JP
HCCDB.18.S124	24.00	0.00	0.98	-0.13	TRUE	FALSE	Hypoxia^{low}/TME^{high}	ICGC_LIRI_JP
HCCDB.18.S136	23.00	1.00	0.03	0.20	TRUE	TRUE	Mixed	ICGC_LIRI_JP
HCCDB.18.S138	27.00	0.00	0.14	-0.11	TRUE	FALSE	Hypoxia^{low}/TME^{high}	ICGC_LIRI_JP
HCCDB.18.S149	30.00	0.00	-1.34	3.43	FALSE	TRUE	Hypoxia^{high}/TME^{low}	ICGC_LIRI_JP
HCCDB.18.S15	17.00	0.00	-0.80	-0.84	FALSE	FALSE	Mixed	ICGC_LIRI_JP
HCCDB.18.S152	30.00	0.00	1.40	0.67	TRUE	TRUE	Mixed	ICGC_LIRI_JP
HCCDB.18.S153	53.00	0.00	-0.77	-1.06	FALSE	FALSE	Mixed	ICGC_LIRI_JP
HCCDB.18.S154	54.00	0.00	-0.63	0.47	FALSE	TRUE	Hypoxia^{high}/TME^{low}	ICGC_LIRI_JP
HCCDB.18.S166	30.00	1.00	-0.79	-0.40	FALSE	FALSE	Mixed	ICGC_LIRI_JP
HCCDB.18.S170	30.00	0.00	0.18	-1.57	TRUE	FALSE	Hypoxia^{low}/TME^{high}	ICGC_LIRI_JP
HCCDB.18.S173	6.00	1.00	1.20	0.66	TRUE	TRUE	Mixed	ICGC_LIRI_JP
HCCDB.18.S184	40.00	0.00	-0.08	-1.28	FALSE	FALSE	Mixed	ICGC_LIRI_JP
HCCDB.18.S185	1.00	1.00	0.35	-0.01	TRUE	FALSE	Hypoxia^{low}/TME^{high}	ICGC_LIRI_JP
HCCDB.18.S186	41.00	0.00	-0.78	2.51	FALSE	TRUE	Hypoxia^{high}/TME^{low}	ICGC_LIRI_JP
HCCDB.18.S192	21.00	0.00	0.02	0.45	TRUE	TRUE	Mixed	ICGC_LIRI_JP
HCCDB.18.S194	35.00	0.00	-0.31	-1.69	FALSE	FALSE	Mixed	ICGC_LIRI_JP
HCCDB.18.S196	35.00	0.00	1.60	-1.22	TRUE	FALSE	Hypoxia^{low}/TME^{high}	ICGC_LIRI_JP
HCCDB.18.S199	36.00	0.00	-0.83	-0.73	FALSE	FALSE	Mixed	ICGC_LIRI_JP
HCCDB.18.S22	18.00	0.00	-0.12	-1.29	FALSE	FALSE	Mixed	ICGC_LIRI_JP
HCCDB.18.S24	24.00	1.00	0.43	0.65	TRUE	TRUE	Mixed	ICGC_LIRI_JP
HCCDB.18.S37	3.00	1.00	-0.92	-0.14	FALSE	FALSE	Mixed	ICGC_LIRI_JP
HCCDB.18.S38	23.00	0.00	0.12	0.60	TRUE	TRUE	Mixed	ICGC_LIRI_JP
HCCDB.18.S47	27.00	0.00	1.51	0.01	TRUE	TRUE	Mixed	ICGC_LIRI_JP
HCCDB.18.S48	11.00	0.00	1.46	-0.05	TRUE	FALSE	Hypoxia^{low}/TME^{high}	ICGC_LIRI_JP
HCCDB.18.S49	29.00	0.00	-0.32	-0.12	FALSE	FALSE	Mixed	ICGC_LIRI_JP
HCCDB.18.S51	7.00	0.00	-0.64	1.20	FALSE	TRUE	Hypoxia^{high}/TME^{low}	ICGC_LIRI_JP
HCCDB.18.S52	36.00	0.00	0.13	1.20	TRUE	TRUE	Mixed	ICGC_LIRI_JP
HCCDB.18.S53	29.00	0.00	-0.76	0.41	FALSE	TRUE	Hypoxia^{high}/TME^{low}	ICGC_LIRI_JP
HCCDB.18.S54	30.00	0.00	1.03	-0.21	TRUE	FALSE	Hypoxia^{low}/TME^{high}	ICGC_LIRI_JP
HCCDB.18.S55	30.00	0.00	-0.41	1.00	FALSE	TRUE	Hypoxia^{high}/TME^{low}	ICGC_LIRI_JP
HCCDB.18.S56	34.00	0.00	1.17	-0.62	TRUE	FALSE	Hypoxia^{low}/TME^{high}	ICGC_LIRI_JP
HCCDB.18.S57	34.00	0.00	-0.90	0.28	FALSE	TRUE	Hypoxia^{high}/TME^{low}	ICGC_LIRI_JP
HCCDB.18.S60	9.00	1.00	-0.37	-0.03	FALSE	FALSE	Mixed	ICGC_LIRI_JP
HCCDB.18.S62	40.00	0.00	1.35	-0.68	TRUE	FALSE	Hypoxia^{low}/TME^{high}	ICGC_LIRI_JP
HCCDB.18.S63	39.00	0.00	1.87	-0.13	TRUE	FALSE	Hypoxia^{low}/TME^{high}	ICGC_LIRI_JP
HCCDB.18.S65	35.00	0.00	1.66	0.06	TRUE	TRUE	Mixed	ICGC_LIRI_JP
HCCDB.18.S67	39.00	0.00	0.71	-0.23	TRUE	FALSE	Hypoxia^{low}/TME^{high}	ICGC_LIRI_JP
HCCDB.18.S68	30.00	0.00	-2.33	2.10	FALSE	TRUE	Hypoxia^{high}/TME^{low}	ICGC_LIRI_JP
HCCDB.18.S75	49.00	0.00	-1.53	-0.16	FALSE	FALSE	Mixed	ICGC_LIRI_JP
HCCDB.18.S77	66.00	0.00	-1.21	0.04	FALSE	TRUE	Hypoxia^{high}/TME^{low}	ICGC_LIRI_JP
HCCDB.18.S83	44.00	0.00	0.86	-0.12	TRUE	FALSE	Hypoxia^{low}/TME^{high}	ICGC_LIRI_JP
HCCDB.18.S91	51.00	0.00	0.82	-0.92	TRUE	FALSE	Hypoxia^{low}/TME^{high}	ICGC_LIRI_JP
HCCDB.18.S93	17.00	1.00	-1.28	0.34	FALSE	TRUE	Hypoxia^{high}/TME^{low}	ICGC_LIRI_JP
HCCDB.18.S97	52.00	0.00	0.84	-0.24	TRUE	FALSE	Hypoxia^{low}/TME^{high}	ICGC_LIRI_JP
TCGA.2Y.A9GS.01A	24.13	1.00	-0.07	0.09	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.2Y.A9GT.01A	54.13	1.00	2.12	-1.82	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.2Y.A9GU.01A	64.63	0.00	0.08	-0.77	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.2Y.A9GV.01A	84.40	1.00	1.29	-1.49	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.2Y.A9GX.01A	81.40	0.00	1.51	0.01	TRUE	TRUE	Mixed	TCGA_LIHC
TCGA.2Y.A9GZ.01A	28.27	1.00	0.66	-1.15	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.2Y.A9H2.01A	57.70	0.00	-0.99	0.20	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.2Y.A9H3.01A	50.53	0.00	1.38	-0.54	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.2Y.A9H4.01A	48.40	0.00	0.32	-0.60	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.2Y.A9H7.01A	38.93	0.00	-0.29	0.30	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.2Y.A9H8.01A	21.10	1.00	0.17	0.18	TRUE	TRUE	Mixed	TCGA_LIHC

TCGA.4R.AA8I.01A	8.73	1.00	0.32	-1.04	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.5C.AAPD.01A	0.67	0.00	1.54	-0.07	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.5R.AA1C.01A	17.33	0.00	0.23	-0.14	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.5R.AA1D.01A	14.97	0.00	1.05	-0.05	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.5R.AAAM.01A	1.53	1.00	1.36	-0.22	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.BC.A10W.01A	3.03	1.00	-0.88	0.01	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.BD.A2L6.01A	45.43	0.00	-0.15	-0.69	FALSE	FALSE	Mixed	TCGA_LIHC
TCGA.BD.A3ER.01A	37.17	0.00	0.19	0.34	TRUE	TRUE	Mixed	TCGA_LIHC
TCGA.CC.5258.01A	4.30	1.00	-0.56	0.76	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.CC.5259.01A	8.33	0.00	-0.28	1.06	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.CC.5260.01A	2.90	1.00	-1.87	1.12	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.CC.5261.01A	3.23	1.00	0.97	-0.18	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.CC.5262.01A	3.43	1.00	-0.01	0.91	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.CC.5263.01A	4.30	1.00	-1.80	2.07	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.CC.5264.01A	3.40	1.00	-1.45	1.23	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.CC.A123.01A	7.30	0.00	-0.81	0.74	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.CC.A1HT.01A	3.37	1.00	-0.54	1.19	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.CC.A3M9.01A	10.00	1.00	-0.47	1.66	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.CC.A3MA.01A	10.10	1.00	-1.84	0.58	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.CC.A3MB.01A	10.50	1.00	-0.08	1.07	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.CC.A3MC.01A	12.10	0.00	-0.46	0.48	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.CC.A5UC.01A	11.57	1.00	-0.15	1.45	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.CC.A5UD.01A	10.13	1.00	-1.79	-0.65	FALSE	FALSE	Mixed	TCGA_LIHC
TCGA.CC.A5UE.01A	9.07	1.00	-0.86	0.52	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.CC.A7IE.01A	7.23	1.00	0.51	1.08	TRUE	TRUE	Mixed	TCGA_LIHC
TCGA.CC.A7IF.01A	21.63	1.00	0.21	-0.83	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.CC.A7IG.01A	9.97	1.00	-1.58	0.53	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.CC.A7IH.01A	12.17	0.00	-0.22	-1.16	FALSE	FALSE	Mixed	TCGA_LIHC
TCGA.CC.A7II.01A	13.30	0.00	-2.68	3.28	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.CC.A7IJ.01A	12.73	0.00	-1.04	1.41	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.CC.A7IK.01A	8.73	1.00	-0.13	-0.75	FALSE	FALSE	Mixed	TCGA_LIHC
TCGA.CC.A7IL.01A	9.27	1.00	0.21	-0.30	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.CC.A8HS.01A	10.00	1.00	-1.02	0.56	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.CC.A8HT.01A	4.67	1.00	-0.47	0.82	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.CC.A8HU.01A	11.47	1.00	-1.26	0.63	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.CC.A8HV.01A	9.30	1.00	-0.93	-0.18	FALSE	FALSE	Mixed	TCGA_LIHC
TCGA.CC.A9FS.01A	7.03	0.00	0.29	-0.78	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.CC.A9FU.01A	26.97	0.00	-0.78	1.54	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.CC.A9FV.01A	26.97	0.00	0.03	-0.42	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.CC.A9FW.01A	8.27	0.00	-0.29	1.14	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.DD.A113.01A	80.83	0.00	-0.37	-0.79	FALSE	FALSE	Mixed	TCGA_LIHC
TCGA.DD.A114.01A	38.30	1.00	0.50	0.25	TRUE	TRUE	Mixed	TCGA_LIHC
TCGA.DD.A115.01A	84.73	1.00	0.18	-0.38	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.DD.A116.01A	54.07	1.00	0.23	-0.18	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.DD.A118.01A	114.57	0.00	-0.50	-0.81	FALSE	FALSE	Mixed	TCGA_LIHC
TCGA.DD.A119.01A	7.43	1.00	-0.04	0.30	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.DD.A11B.01A	0.47	1.00	0.50	-0.42	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.DD.A11C.01A	22.07	0.00	0.44	-1.09	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.DD.A1EA.01A	80.50	0.00	1.43	-1.23	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.DD.A1EB.01A	67.23	0.00	1.00	-2.17	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.DD.A1ED.01A	76.70	0.00	1.00	-0.43	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.DD.A1EE.01A	11.63	1.00	-0.43	0.38	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.DD.A1EF.01A	13.13	1.00	0.24	0.35	TRUE	TRUE	Mixed	TCGA_LIHC
TCGA.DD.A1EG.01A	45.73	1.00	0.65	0.30	TRUE	TRUE	Mixed	TCGA_LIHC
TCGA.DD.A1EH.01A	49.83	0.00	-0.22	0.34	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.DD.A1EI.01A	6.10	0.00	0.11	0.20	TRUE	TRUE	Mixed	TCGA_LIHC
TCGA.DD.A1EJ.01A	33.50	1.00	-0.08	1.70	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.DD.A1EK.01A	18.60	1.00	0.77	0.46	TRUE	TRUE	Mixed	TCGA_LIHC
TCGA.DD.A1EL.01A	13.83	1.00	-0.34	1.16	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.DD.A39X.01A	56.47	1.00	-0.61	-0.21	FALSE	FALSE	Mixed	TCGA_LIHC
TCGA.DD.A39Y.01A	5.70	1.00	-1.32	1.66	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.DD.A3A6.01A	108.60	1.00	-0.05	-1.81	FALSE	FALSE	Mixed	TCGA_LIHC
TCGA.DD.A3A7.01A	13.97	1.00	-0.42	1.07	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.DD.A3A8.01A	0.37	1.00	-0.21	-0.83	FALSE	FALSE	Mixed	TCGA_LIHC
TCGA.DD.A4NA.01A	33.60	0.00	-1.21	1.20	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.DD.A4NE.01A	22.00	1.00	-0.56	-0.22	FALSE	FALSE	Mixed	TCGA_LIHC
TCGA.DD.A4NF.01A	31.40	0.00	-0.01	-1.10	FALSE	FALSE	Mixed	TCGA_LIHC
TCGA.DD.A4NG.01A	26.73	1.00	0.19	0.34	TRUE	TRUE	Mixed	TCGA_LIHC
TCGA.DD.A4NH.01A	30.57	0.00	-0.53	1.48	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.DD.A4NI.01A	27.20	0.00	2.04	-0.71	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.DD.A4NJ.01A	30.93	0.00	0.09	-0.54	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.DD.A4NK.01A	40.33	1.00	0.51	-1.43	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.DD.A4NL.01A	57.03	0.00	1.00	-0.94	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.DD.A4NO.01A	74.83	0.00	0.90	-0.69	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.DD.A4NP.01A	110.27	0.00	0.29	-0.93	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.DD.A4NQ.01A	12.43	1.00	-0.98	1.61	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.DD.A4NR.01A	0.30	1.00	1.22	0.58	TRUE	TRUE	Mixed	TCGA_LIHC
TCGA.DD.A4NS.01A	81.87	1.00	1.15	-0.45	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC

TCGA.DD.A4NV.01A	79.93	0.00	1.17	-2.02	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.DD.A73A.01A	24.27	0.00	0.90	-0.49	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.DD.A73B.01A	9.43	1.00	0.01	-0.25	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.DD.A73C.01A	23.37	0.00	1.38	-1.59	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.DD.A73D.01A	23.10	0.00	0.27	-0.44	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.DD.A73E.01A	1.47	0.00	-0.67	-1.34	FALSE	FALSE	Mixed	TCGA_LIHC
TCGA.DD.A73G.01A	115.93	0.00	-0.77	0.39	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.DD.AA3A.01A	13.67	1.00	-2.14	1.65	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.ED.A459.01A	30.33	0.00	0.06	1.05	TRUE	TRUE	Mixed	TCGA_LIHC
TCGA.ED.A4XI.01A	27.30	0.00	0.92	-0.73	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.ED.A5KG.01A	28.47	0.00	4.18	0.60	TRUE	TRUE	Mixed	TCGA_LIHC
TCGA.ED.A627.01A	14.10	0.00	2.34	0.15	TRUE	TRUE	Mixed	TCGA_LIHC
TCGA.ED.A66X.01A	13.53	0.00	0.09	0.31	TRUE	TRUE	Mixed	TCGA_LIHC
TCGA.ED.A66Y.01A	9.87	1.00	-1.35	-0.08	FALSE	FALSE	Mixed	TCGA_LIHC
TCGA.ED.A7PX.01A	0.20	0.00	-1.20	0.59	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.ED.A7PY.01A	13.00	0.00	-0.35	-0.72	FALSE	FALSE	Mixed	TCGA_LIHC
TCGA.ED.A7PZ.01A	0.20	0.00	-0.88	1.30	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.ED.A7XO.01A	14.23	0.00	0.72	-0.35	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.ED.A7XP.01A	13.33	0.00	0.63	-0.45	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.ED.A82E.01A	13.60	0.00	-1.82	1.69	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.ED.A8O5.01A	13.53	0.00	-0.28	-0.30	FALSE	FALSE	Mixed	TCGA_LIHC
TCGA.ED.A8O6.01A	1.87	1.00	-0.82	0.38	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.ED.A97K.01A	0.20	0.00	-0.41	1.04	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.FV.A3I1.01A	8.23	1.00	0.38	-0.01	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.FV.A3R2.01A	6.47	1.00	0.05	0.29	TRUE	TRUE	Mixed	TCGA_LIHC
TCGA.G3.A6UC.01A	22.37	0.00	0.30	-1.59	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.G3.A7M5.01A	14.90	0.00	0.57	-1.33	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.G3.A7M7.01A	12.03	0.00	0.44	-0.14	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.G3.A7M8.01A	14.33	0.00	0.73	-0.67	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.G3.A7M9.01A	1.87	1.00	-2.74	2.41	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.G3.AAUZ.01A	16.00	0.00	0.61	0.31	TRUE	TRUE	Mixed	TCGA_LIHC
TCGA.G3.AAV0.01A	15.87	0.00	0.76	-1.33	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.G3.AAV1.01A	11.97	1.00	0.57	0.05	TRUE	TRUE	Mixed	TCGA_LIHC
TCGA.G3.AAV2.01A	12.40	0.00	0.40	-1.52	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.G3.AAV5.01A	11.80	0.00	-0.20	0.56	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.G3.AAV6.01A	2.17	1.00	-1.56	1.64	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.G3.AAV7.01A	12.03	0.00	-1.86	1.42	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.HP.A5MZ.01A	3.03	1.00	1.14	-0.22	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.MI.A75C.01A	9.70	0.00	-0.41	-0.18	FALSE	FALSE	Mixed	TCGA_LIHC
TCGA.MR.A520.01A	7.63	0.00	0.84	-0.53	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.MR.A8JO.01A	11.00	0.00	0.94	0.14	TRUE	TRUE	Mixed	TCGA_LIHC
TCGA.UB.A7MA.01A	28.27	0.00	-1.78	0.33	FALSE	TRUE	Hypoxia^{high}/TME^{low}	TCGA_LIHC
TCGA.UB.A7MB.01A	20.03	0.00	-0.56	-2.02	FALSE	FALSE	Mixed	TCGA_LIHC
TCGA.UB.A7MC.01A	16.67	0.00	-0.33	-0.19	FALSE	FALSE	Mixed	TCGA_LIHC
TCGA.UB.A7MD.01A	1.73	1.00	0.46	0.20	TRUE	TRUE	Mixed	TCGA_LIHC
TCGA.UB.A7ME.01A	16.20	0.00	1.18	-0.18	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.UB.A7MF.01A	7.13	1.00	0.26	0.34	TRUE	TRUE	Mixed	TCGA_LIHC
TCGA.UB.AA0U.01A	10.90	0.00	-0.19	-0.42	FALSE	FALSE	Mixed	TCGA_LIHC
TCGA.UB.AA0V.01A	10.47	0.00	0.95	-0.59	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.WJ.A86L.01A	11.50	0.00	0.37	-1.40	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.ZP.A9CZ.01A	23.53	0.00	0.49	-0.26	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.ZS.A9CD.01A	46.20	1.00	0.26	-0.42	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.ZS.A9CE.01A	41.37	0.00	0.28	-2.42	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.ZS.A9CF.01A	80.40	0.00	0.01	-0.90	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC
TCGA.ZS.A9CG.01A	11.37	0.00	0.39	-0.95	TRUE	FALSE	Hypoxia^{low}/TME^{high}	TCGA_LIHC

S9. The cox regression analysis of Hypoxia-TME score in all HBV-related HCC cohorts

Training Sets	**GSE14520(n=221)**	**Univariate anysis**			**Multivariate analysis**		
	Characteristics	HR	95%CI	P	HR	95%CI	P
	Gender,M vs F	1.7	0.821-3.522	0.153			
	Age,years	0.992	0.973-1.011	0.405			
	HBV_status,CC vs SVR-CC	0.748	0.467-1.197	0.226			
	ALT,U/L	0.926	0.603-1.422	0.727			
	Tumor.size..cm.	1.943	1.265-2.985	0.002	0.928	0.521-1.653	0.799
	Tumor.number,multi vs single	1.592	0.986-2.571	0.057			
	Liver.cirrhosis, YES vs NO	4.624	1.137-18.802	0.032	3.939	0.96-16.16	0.057
	TNM, III-IV vs I-II	3.424	2.193-5.346	<0.001	1.794	0.803-4.008	0.154
	BCLC,B-C vs 0-A	3.457	2.222-5.378	<0.001	1.727	0.849-3.514	0.132
	AFP,>400 vs <=400	1.684	1.099-2.582	0.017	1.085	0.688-1.71	0.726
	Hypoxia-TME classifier，per	2.048	1.56-2.688	<0.001	**1.762**	**1.32-2.352**	**<0.001**
	Gao-Fudan(n=159)						
	Hypoxia-TME classifier，per	2.605	1.773-3.828	<0.001	**1.674**	**1.101-2.546**	**0.016**
	Gender,M vs F	0.757	0.406-1.41	0.381			
	Age,years	0.972	0.949-0.995	0.018	0.981	0.959-1.004	0.099
	Liver.cirrhosis, YES vs NO	1.282	0.699-2.35	0.422			
	Tumor.number,multi vs single	1.051	0.954-1.157	0.316			
	Tumor.size.cm.	1.163	1.103-1.226	<0.001	1.105	1.027-1.189	0.008
	Lymph.node.metastasis, YES vs NO	1.752	0.242-12.692	0.579			
	Tumor.thrombus, YES vs NO	2.19	1.262-3.803	0.005	1.223	0.436-3.433	0.702
	Tumour.epsulation, YES vs NO	0.848	0.483-1.489	0.566			
	PT.s.	1.022	0.868-1.204	0.792			
	ALB,g.L.	0.935	0.866-1.01	0.089			
	ALT,U/L	0.999	0.995-1.003	0.566			
	γ.GT,U/L	1.001	0.998-1.005	0.431			
	AFP,>400 vs <=400	3.528	2.065-6.027	<0.001	2.367	1.345-4.163	0.003
	BCLC,B-C vs 0-A	2.774	1.51-5.096	0.001	1.133	0.467-2.748	0.782
	TNM, III-IV vs I-II	1.738	1.024-2.953	0.041	0.64	0.233-1.759	0.387
	ICGC_LIRI_JP(n=53)						
	Hypoxia-TME classifier，per	1.24	0.495-3.108	0.647			
	GSE10143(n=19)						
	Hypoxia-TME classifier，per	1.179	0.495-2.807	0.71			
Validation Set	**TCGA(n=144)**						
	Characteristics	HR	95%CI	P	HR	95%CI	P
	Hypoxia-TME classifier，per	1.838	1.351-2.501	<0.001	**1.571**	**1.124-2.194**	**0.008**
	Gender,M vs F	1.247	0.735-2.117	0.413			
	Vascular invasion, YES vs NO,	1.134	0.59-2.177	0.707			
	TNM, III-IV vs I-II	2.84	1.692-4.769	<0.001	1.762	0.982-3.161	0.057
	GradeG3-G4	1.328	0.787-2.242	0.288			
	Child_pughB-C vs 0-A	0.809	0.348-1.882	0.622			
	TMB	1.014	0.979-1.05	0.446			
	family_cancer_history YES vs NO	0.954	0.55-1.653	0.866			
	Alcohol.YES vs NO	0.849	0.5-1.441	0.544			
	Hepatitis. YES vs NO	0.895	0.464-1.727	0.741			
	NAFLD,YES vs NO	0.538	0.131-2.206	0.389			
	Smoking,YES vs NO	0.44	0.158-1.226	0.116			
	Liver Cirrhosis,YES vs NO	0.133	0.018-1.001	0.05			
	Alb	0.88	0.771-1.005	0.059			
	Cr	0.996	0.979-1.013	0.646			
	PT	0.911	0.861-0.964	0.001	0.946	0.89-1.006	0.079
	PLT	0.996	0.994-0.998	<0.001	0.998	0.996-1	0.026
	AFP	1	1-1	0.413			

S10. Pan-cancer cox results of Hypoxia-TME classifier with overall survival (32 cohorts)

Characteristics	HR	95%CI	P.value	coeff	se	number
TCGA-KICH	8.162	1.961-33.963	0.004	2.099	0.727	64
TCGA-PCPG	2.735	0.738-10.134	0.132	1.006	0.668	175
TCGA-ACC	2.026	1.253-3.277	0.004	0.706	0.245	79
TCGA-MESO	1.781	1.243-2.551	0.002	0.577	0.183	79
TCGA-LIHC	1.776	1.417-2.227	<0.001	0.575	0.115	363
TCGA-PRAD	1.698	0.669-4.311	0.266	0.529	0.475	481
TCGA-CESC	1.525	1.102-2.11	0.011	0.422	0.166	283
TCGA-LUAD	1.419	1.179-1.707	<0.001	0.35	0.095	497
TCGA-UCEC	1.404	1.057-1.865	0.019	0.339	0.145	533
TCGA-SARC	1.402	1.099-1.789	0.007	0.338	0.124	255
TCGA-CHOL	1.311	0.678-2.538	0.421	0.271	0.337	36
TCGA-PAAD	1.303	1.012-1.676	0.04	0.264	0.129	176
TCGA-THCA	1.256	0.642-2.458	0.506	0.228	0.342	496
TCGA-BLCA	1.18	0.974-1.429	0.091	0.165	0.098	400
TCGA-HNSC	1.171	0.994-1.381	0.059	0.158	0.084	494
TCGA-BRCA	1.158	0.946-1.418	0.155	0.147	0.103	1050
TCGA-COAD	1.133	0.87-1.476	0.354	0.125	0.135	430
TCGA-DLBC	1.119	0.493-2.541	0.788	0.112	0.418	46
TCGA-KIRC	1.045	0.847-1.29	0.68	0.044	0.107	522
TCGA-OV	1.016	0.856-1.206	0.857	0.016	0.088	353
TCGA-READ	0.995	0.6-1.649	0.983	-0.005	0.258	154
TCGA-SKCM	0.983	0.628-1.539	0.94	-0.017	0.229	98
TCGA-KIRP	0.982	0.665-1.452	0.929	-0.018	0.199	284
TCGA-STAD	0.96	0.791-1.166	0.681	-0.041	0.099	348
TCGA-ESCA	0.96	0.699-1.319	0.803	-0.04	0.162	151
TCGA-LUSC	0.928	0.783-1.099	0.386	-0.075	0.086	489
TCGA-GBM	0.894	0.706-1.133	0.353	-0.112	0.121	143
TCGA-LGG	0.829	0.665-1.033	0.095	-0.187	0.112	495
TCGA-UVM	0.778	0.42-1.439	0.423	-0.251	0.314	77
TCGA-UCS	0.728	0.461-1.15	0.174	-0.317	0.233	54
TCGA-TGCT	0.562	0.138-2.281	0.42	-0.577	0.715	133
TCGA-THYM	0.318	0.12-0.846	0.022	-1.145	0.499	118

S11. The KEGG pathway analysis of High hypoxia score vs Low hypoxia score in HBV-related HCC cohorts

Cohorts	ID	Description	setSize	enrichment Score	NES	pvalue	p.adjust	qvalues	rank
GSE14520	hsa04110	Cell cycle	114	0.645	2.372	0.003	0.012	0.007	1764
GSE14520	hsa03030	DNA replication	34	0.621	1.846	0.002	0.011	0.007	2996
GSE14520	hsa03010	Ribosome	99	0.568	2.067	0.003	0.012	0.007	2609
GSE14520	hsa03040	Spliceosome	102	0.559	2.030	0.003	0.012	0.007	2355
GSE14520	hsa03013	RNA transport	127	0.496	1.858	0.003	0.012	0.007	3191
GSE14520	hsa04512	ECM-receptor interaction	79	0.493	1.712	0.002	0.012	0.007	1793
GSE14520	hsa04115	p53 signaling pathway	64	0.484	1.623	0.005	0.019	0.012	1591
GSE14520	hsa04350	TGF-beta signaling pathway	84	0.473	1.659	0.005	0.019	0.012	2558
GSE14520	hsa04218	Cellular senescence	145	0.437	1.674	0.003	0.012	0.008	1832
GSE14520	hsa03008	Ribosome biogenesis in eukaryotes	56	0.434	1.425	0.034	0.096	0.062	2847
GSE14520	hsa03018	RNA degradation	57	0.432	1.419	0.027	0.078	0.051	2123
GSE14520	hsa04390	Hippo signaling pathway	130	0.420	1.573	0.005	0.019	0.013	3051
GSE14520	hsa04066	HIF-1 signaling pathway	104	0.408	1.483	0.005	0.019	0.013	1826
GSE14520	hsa04145	Phagosome	132	0.405	1.522	0.005	0.019	0.013	1346
GSE14520	hsa04114	Oocyte meiosis	96	0.383	1.379	0.025	0.075	0.049	1413
GSE14520	hsa04061	Viral protein interaction with cytokine and cytokine receptor	86	0.371	1.305	0.056	0.140	0.091	1156
GSE14520	hsa04510	Focal adhesion	184	0.367	1.448	0.006	0.020	0.013	2251
GSE14520	hsa04120	Ubiquitin mediated proteolysis	116	0.345	1.277	0.065	0.153	0.099	2391
GSE14520	hsa04310	Wnt signaling pathway	131	0.339	1.272	0.043	0.118	0.077	3199
GSE14520	hsa04062	Chemokine signaling pathway	164	0.317	1.235	0.048	0.126	0.082	2626
GSE14520	hsa04360	Axon guidance	154	0.309	1.195	0.070	0.162	0.105	2797
GSE14520	hsa04015	Rap1 signaling pathway	189	0.302	1.199	0.089	0.196	0.128	2810
GSE14520	hsa04060	Cytokine-cytokine receptor interaction	245	0.300	1.217	0.056	0.140	0.091	2348
GSE14520	hsa04211	Longevity regulating pathway	77	(0.424)	(1.370)	0.058	0.141	0.092	1339
GSE14520	hsa04068	FoxO signaling pathway	120	(0.441)	(1.516)	0.005	0.019	0.012	1458
GSE14520	hsa00564	Glycerophospholipid metabolism	71	(0.454)	(1.446)	0.035	0.096	0.062	1864
GSE14520	hsa04213	Longevity regulating pathway - multiple species	53	(0.459)	(1.396)	0.053	0.136	0.088	1339
GSE14520	hsa04152	AMPK signaling pathway	105	(0.501)	(1.700)	0.002	0.010	0.007	1339
GSE14520	hsa01230	Biosynthesis of amino acids	63	(0.505)	(1.590)	0.014	0.042	0.027	675
GSE14520	hsa00500	Starch and sucrose metabolism	28	(0.534)	(1.447)	0.059	0.141	0.092	1026
GSE14520	hsa00010	Glycolysis / Gluconeogenesis	60	(0.536)	(1.675)	0.007	0.024	0.015	1067
GSE14520	hsa01200	Carbon metabolism	105	(0.552)	(1.874)	0.002	0.010	0.007	779
GSE14520	hsa00760	Nicotinate and nicotinamide metabolism	25	(0.555)	(1.475)	0.046	0.123	0.080	1427
GSE14520	hsa02010	ABC transporters	37	(0.568)	(1.619)	0.011	0.034	0.022	1001
GSE14520	hsa00561	Glycerolipid metabolism	46	(0.574)	(1.702)	0.006	0.020	0.013	1739
GSE14520	hsa01040	Biosynthesis of unsaturated fatty acids	19	(0.590)	(1.459)	0.071	0.162	0.105	1259
GSE14520	hsa00790	Folate biosynthesis	22	(0.604)	(1.550)	0.034	0.096	0.062	1523
GSE14520	hsa00310	Lysine degradation	49	(0.612)	(1.841)	0.002	0.010	0.007	923
GSE14520	hsa00250	Alanine, aspartate and glutamate metabolism	28	(0.617)	(1.672)	0.007	0.024	0.016	776
GSE14520	hsa00330	Arginine and proline metabolism	38	(0.621)	(1.786)	0.004	0.015	0.010	909
GSE14520	hsa01210	2-Oxocarboxylic acid metabolism	13	(0.631)	(1.466)	0.064	0.151	0.098	2035
GSE14520	hsa00860	Porphyrin and chlorophyll metabolism	25	(0.635)	(1.686)	0.009	0.030	0.019	432
GSE14520	hsa00983	Drug metabolism - other enzymes	54	(0.644)	(1.967)	0.002	0.010	0.007	1750
GSE14520	hsa00270	Cysteine and methionine metabolism	43	(0.648)	(1.929)	0.002	0.010	0.007	613
GSE14520	hsa01212	Fatty acid metabolism	47	(0.651)	(1.941)	0.002	0.010	0.007	1370
GSE14520	hsa00590	Arachidonic acid metabolism	48	(0.654)	(1.958)	0.002	0.010	0.007	519
GSE14520	hsa00920	Sulfur metabolism	10	(0.664)	(1.443)	0.085	0.190	0.124	961
GSE14520	hsa00620	Pyruvate metabolism	34	(0.680)	(1.926)	0.002	0.010	0.007	709
GSE14520	hsa00020	Citrate cycle (TCA cycle)	29	(0.683)	(1.875)	0.002	0.010	0.007	1896
GSE14520	hsa03320	PPAR signaling pathway	66	(0.687)	(2.174)	0.002	0.010	0.007	651
GSE14520	hsa00040	Pentose and glucuronate interconversions	17	(0.722)	(1.746)	0.012	0.036	0.023	852
GSE14520	hsa04146	Peroxisome	71	(0.757)	(2.413)	0.002	0.010	0.007	1171
GSE14520	hsa00640	Propanoate metabolism	30	(0.778)	(2.154)	0.002	0.010	0.007	920
GSE14520	hsa00630	Glyoxylate and dicarboxylate metabolism	24	(0.786)	(2.052)	0.002	0.010	0.007	621
GSE14520	hsa00360	Phenylalanine metabolism	15	(0.801)	(1.902)	0.002	0.010	0.007	1067
GSE14520	hsa00410	beta-Alanine metabolism	28	(0.806)	(2.184)	0.002	0.010	0.007	1476
GSE14520	hsa00220	Arginine biosynthesis	17	(0.810)	(1.960)	0.002	0.010	0.007	567
GSE14520	hsa00280	Valine, leucine and isoleucine degradation	42	(0.817)	(2.419)	0.002	0.010	0.007	1361
GSE14520	hsa00980	Metabolism of xenobiotics by cytochrome P450	51	(0.818)	(2.483)	0.002	0.010	0.007	1157
GSE14520	hsa00340	Histidine metabolism	18	(0.820)	(2.001)	0.002	0.010	0.007	1476
GSE14520	hsa00982	Drug metabolism - cytochrome P450	49	(0.821)	(2.471)	0.002	0.010	0.007	1157
GSE14520	hsa00650	Butanoate metabolism	23	(0.824)	(2.122)	0.002	0.010	0.007	1031
GSE14520	hsa00260	Glycine, serine and threonine metabolism	33	(0.824)	(2.324)	0.002	0.010	0.007	909
GSE14520	hsa00591	Linoleic acid metabolism	20	(0.832)	(2.072)	0.002	0.010	0.007	307
GSE14520	hsa00350	Tyrosine metabolism	32	(0.841)	(2.356)	0.002	0.010	0.007	659
GSE14520	hsa00053	Ascorbate and aldarate metabolism	12	(0.847)	(1.913)	0.002	0.010	0.007	709
GSE14520	hsa00140	Steroid hormone biosynthesis	43	(0.850)	(2.532)	0.002	0.010	0.007	855
GSE14520	hsa00380	Tryptophan metabolism	34	(0.852)	(2.414)	0.002	0.010	0.007	709
GSE14520	hsa00071	Fatty acid degradation	40	(0.853)	(2.485)	0.002	0.010	0.007	775

S11. The KEGG pathway analysis of High hypoxia score vs Low hypoxia score in HBV-related HCC cohorts

Cohorts	ID	Description	setSize	enrichment Score	NES	pvalue	p.adjust	qvalues	rank
GSE14520	hsa00830	Retinol metabolism	39	(0.863)	(2.498)	0.002	0.010	0.007	1047
GSE14520	hsa00120	Primary bile acid biosynthesis	15	(0.918)	(2.177)	0.002	0.010	0.007	520
TCGA	hsa03010	Ribosome	134	0.763	2.675	0.003	0.012	0.007	2028
TCGA	hsa03030	DNA replication	36	0.690	1.909	0.002	0.012	0.007	3103
TCGA	hsa03040	Spliceosome	131	0.627	2.202	0.003	0.012	0.007	4496
TCGA	hsa04110	Cell cycle	124	0.624	2.168	0.003	0.012	0.007	2258
TCGA	hsa03430	Mismatch repair	23	0.549	1.372	0.075	0.146	0.083	2834
TCGA	hsa03008	Ribosome biogenesis in eukaryotes	72	0.549	1.769	0.002	0.012	0.007	3308
TCGA	hsa04512	ECM-receptor interaction	87	0.537	1.777	0.003	0.012	0.007	1528
TCGA	hsa03020	RNA polymerase	31	0.524	1.413	0.051	0.109	0.062	4517
TCGA	hsa03050	Proteasome	44	0.523	1.515	0.021	0.055	0.031	4747
TCGA	hsa04145	Phagosome	148	0.520	1.855	0.003	0.012	0.007	2613
TCGA	hsa03440	Homologous recombination	37	0.509	1.412	0.057	0.121	0.069	6374
TCGA	hsa03013	RNA transport	157	0.496	1.775	0.003	0.012	0.007	4408
TCGA	hsa03015	mRNA surveillance pathway	90	0.496	1.650	0.003	0.012	0.007	4764
TCGA	hsa04390	Hippo signaling pathway	154	0.483	1.730	0.003	0.012	0.007	3355
TCGA	hsa04066	HIF-1 signaling pathway	107	0.455	1.563	0.003	0.012	0.007	895
TCGA	hsa04380	Osteoclast differentiation	124	0.454	1.576	0.003	0.012	0.007	3197
TCGA	hsa04218	Cellular senescence	157	0.443	1.585	0.003	0.012	0.007	2642
TCGA	hsa03460	Fanconi anemia pathway	49	0.435	1.293	0.093	0.170	0.097	3411
TCGA	hsa04144	Endocytosis	237	0.430	1.604	0.003	0.012	0.007	4757
TCGA	hsa04510	Focal adhesion	196	0.421	1.545	0.006	0.020	0.012	3752
TCGA	hsa04260	Cardiac muscle contraction	82	0.415	1.355	0.026	0.063	0.036	2428
TCGA	hsa03018	RNA degradation	75	0.402	1.306	0.060	0.122	0.069	4530
TCGA	hsa04115	p53 signaling pathway	70	0.402	1.286	0.074	0.146	0.083	2532
TCGA	hsa04064	NF-kappa B signaling pathway	102	0.399	1.362	0.026	0.064	0.036	3022
TCGA	hsa04061	Viral protein interaction with cytokine and cytokine receptor	98	0.396	1.336	0.038	0.086	0.049	4227
TCGA	hsa04114	Oocyte meiosis	123	0.396	1.370	0.020	0.054	0.031	1854
TCGA	hsa04350	TGF-beta signaling pathway	92	0.378	1.263	0.060	0.122	0.069	5214
TCGA	hsa04210	Apoptosis	134	0.368	1.291	0.041	0.093	0.053	2148
TCGA	hsa04514	Cell adhesion molecules (CAMs)	138	0.364	1.283	0.047	0.103	0.059	2913
TCGA	hsa04060	Cytokine-cytokine receptor interaction	289	0.360	1.366	0.007	0.022	0.013	3322
TCGA	hsa04015	Rap1 signaling pathway	207	0.359	1.324	0.010	0.028	0.016	3825
TCGA	hsa04217	Necroptosis	132	0.355	1.236	0.075	0.146	0.083	3627
TCGA	hsa04062	Chemokine signaling pathway	185	0.349	1.275	0.034	0.080	0.045	4311
TCGA	hsa04310	Wnt signaling pathway	158	0.342	1.222	0.077	0.147	0.084	2807
TCGA	hsa04151	PI3K-Akt signaling pathway	351	0.337	1.315	0.011	0.031	0.018	2026
TCGA	hsa04270	Vascular smooth muscle contraction	130	(0.406)	(1.295)	0.047	0.103	0.059	3388
TCGA	hsa04068	FoxO signaling pathway	130	(0.438)	(1.397)	0.015	0.041	0.023	2520
TCGA	hsa04152	AMPK signaling pathway	120	(0.515)	(1.625)	0.002	0.011	0.006	2544
TCGA	hsa04213	Longevity regulating pathway - multiple species	62	(0.519)	(1.481)	0.022	0.057	0.033	2520
TCGA	hsa00500	Starch and sucrose metabolism	34	(0.564)	(1.453)	0.039	0.089	0.050	1246
TCGA	hsa01230	Biosynthesis of amino acids	72	(0.570)	(1.675)	0.003	0.012	0.007	731
TCGA	hsa01040	Biosynthesis of unsaturated fatty acids	23	(0.571)	(1.366)	0.093	0.170	0.097	1674
TCGA	hsa01200	Carbon metabolism	114	(0.582)	(1.831)	0.002	0.011	0.006	1626
TCGA	hsa00010	Glycolysis / Gluconeogenesis	67	(0.596)	(1.737)	0.003	0.012	0.007	1152
TCGA	hsa00330	Arginine and proline metabolism	48	(0.600)	(1.643)	0.010	0.029	0.017	1082
TCGA	hsa00900	Terpenoid backbone biosynthesis	22	(0.619)	(1.467)	0.058	0.121	0.069	3141
TCGA	hsa00561	Glycerolipid metabolism	52	(0.621)	(1.714)	0.007	0.021	0.012	2122
TCGA	hsa00670	One carbon pool by folate	19	(0.623)	(1.414)	0.083	0.156	0.089	940
TCGA	hsa00270	Cysteine and methionine metabolism	46	(0.627)	(1.692)	0.005	0.017	0.010	829
TCGA	hsa00760	Nicotinate and nicotinamide metabolism	37	(0.628)	(1.660)	0.009	0.025	0.014	2382
TCGA	hsa01212	Fatty acid metabolism	52	(0.631)	(1.740)	0.005	0.017	0.010	1994
TCGA	hsa00061	Fatty acid biosynthesis	17	(0.633)	(1.407)	0.086	0.160	0.091	1994
TCGA	hsa02010	ABC transporters	45	(0.634)	(1.709)	0.003	0.012	0.007	1117
TCGA	hsa00590	Arachidonic acid metabolism	61	(0.646)	(1.844)	0.003	0.012	0.007	503
TCGA	hsa00310	Lysine degradation	56	(0.648)	(1.814)	0.002	0.011	0.006	995
TCGA	hsa00790	Folate biosynthesis	24	(0.650)	(1.571)	0.024	0.060	0.034	919
TCGA	hsa00250	Alanine, aspartate and glutamate metabolism	34	(0.678)	(1.747)	0.005	0.017	0.010	881
TCGA	hsa00860	Porphyrin and chlorophyll metabolism	41	(0.689)	(1.842)	0.002	0.011	0.006	1971
TCGA	hsa00020	Citrate cycle (TCA cycle)	30	(0.693)	(1.730)	0.004	0.013	0.007	1867
TCGA	hsa00983	Drug metabolism - other enzymes	77	(0.702)	(2.092)	0.002	0.011	0.006	817
TCGA	hsa01210	2-Oxocarboxylic acid metabolism	18	(0.703)	(1.567)	0.028	0.066	0.037	665
TCGA	hsa00430	Taurine and hypotaurine metabolism	11	(0.711)	(1.440)	0.061	0.122	0.069	315
TCGA	hsa00620	Pyruvate metabolism	39	(0.722)	(1.913)	0.002	0.011	0.006	1135
TCGA	hsa03320	PPAR signaling pathway	76	(0.757)	(2.254)	0.002	0.011	0.006	1054
TCGA	hsa04146	Peroxisome	82	(0.766)	(2.303)	0.002	0.011	0.006	1277
TCGA	hsa00040	Pentose and glucuronate interconversions	33	(0.772)	(1.972)	0.002	0.011	0.006	944

S11. The KEGG pathway analysis of High hypoxia score vs Low hypoxia score in HBV-related HCC cohorts

Cohorts	ID	Description	setSize	enrichment Score	NES	pvalue	p.adjust	qvalues	rank
TCGA	hsa00130	Ubiquinone and other terpenoid-quinone biosynthesis	11	(0.775)	(1.570)	0.025	0.063	0.036	2179
TCGA	hsa00360	Phenylalanine metabolism	17	(0.789)	(1.755)	0.007	0.022	0.013	1106
TCGA	hsa00640	Propanoate metabolism	33	(0.790)	(2.018)	0.002	0.011	0.006	1173
TCGA	hsa00630	Glyoxylate and dicarboxylate metabolism	29	(0.797)	(1.958)	0.002	0.011	0.006	1050
TCGA	hsa00280	Valine, leucine and isoleucine degradation	47	(0.814)	(2.212)	0.002	0.011	0.006	2040
TCGA	hsa00410	beta-Alanine metabolism	31	(0.819)	(2.061)	0.002	0.011	0.006	946
TCGA	hsa00350	Tyrosine metabolism	36	(0.820)	(2.157)	0.002	0.011	0.006	1353
TCGA	hsa00260	Glycine, serine and threonine metabolism	38	(0.822)	(2.183)	0.002	0.011	0.006	2001
TCGA	hsa00340	Histidine metabolism	22	(0.834)	(1.974)	0.002	0.011	0.006	1793
TCGA	hsa00220	Arginine biosynthesis	21	(0.834)	(1.956)	0.002	0.011	0.006	731
TCGA	hsa00140	Steroid hormone biosynthesis	59	(0.841)	(2.387)	0.002	0.011	0.006	1022
TCGA	hsa00072	Synthesis and degradation of ketone bodies	10	(0.842)	(1.683)	0.014	0.037	0.021	1623
TCGA	hsa00980	Metabolism of xenobiotics by cytochrome P450	71	(0.844)	(2.483)	0.002	0.011	0.006	699
TCGA	hsa00380	Tryptophan metabolism	40	(0.845)	(2.252)	0.002	0.011	0.006	1685
TCGA	hsa00982	Drug metabolism - cytochrome P450	67	(0.854)	(2.489)	0.002	0.011	0.006	699
TCGA	hsa00591	Linoleic acid metabolism	28	(0.854)	(2.094)	0.002	0.011	0.006	503
TCGA	hsa00053	Ascorbate and aldarate metabolism	27	(0.856)	(2.085)	0.002	0.011	0.006	946
TCGA	hsa00071	Fatty acid degradation	44	(0.867)	(2.328)	0.002	0.011	0.006	1353
TCGA	hsa00650	Butanoate metabolism	28	(0.883)	(2.164)	0.002	0.011	0.006	760
TCGA	hsa00830	Retinol metabolism	65	(0.884)	(2.560)	0.002	0.011	0.006	699
TCGA	hsa00120	Primary bile acid biosynthesis	17	(0.929)	(2.064)	0.002	0.011	0.006	865
Fudan	hsa03030	DNA replication	22	0.719	2.099	0.002	0.008	0.005	1201
Fudan	hsa04080	Neuroactive ligand-receptor interaction	13	0.689	1.755	0.002	0.008	0.005	719
Fudan	hsa04145	Phagosome	95	0.635	2.436	0.002	0.008	0.005	1277
Fudan	hsa04066	HIF-1 signaling pathway	65	0.592	2.147	0.002	0.008	0.005	541
Fudan	hsa04216	Ferroptosis	28	0.554	1.716	0.010	0.027	0.017	582
Fudan	hsa04512	ECM-receptor interaction	46	0.545	1.849	0.002	0.008	0.005	1390
Fudan	hsa04380	Osteoclast differentiation	53	0.542	1.877	0.002	0.008	0.005	1196
Fudan	hsa04514	Cell adhesion molecules (CAMs)	51	0.537	1.853	0.002	0.008	0.005	918
Fudan	hsa03008	Ribosome biogenesis in eukaryotes	61	0.514	1.826	0.004	0.014	0.008	2157
Fudan	hsa04110	Cell cycle	58	0.477	1.675	0.010	0.029	0.017	2266
Fudan	hsa04142	Lysosome	81	0.469	1.759	0.004	0.014	0.008	1765
Fudan	hsa04015	Rap1 signaling pathway	88	0.442	1.680	0.006	0.019	0.011	792
Fudan	hsa04062	Chemokine signaling pathway	79	0.430	1.603	0.012	0.034	0.020	1404
Fudan	hsa04510	Focal adhesion	115	0.384	1.538	0.006	0.019	0.011	1404
Fudan	hsa04144	Endocytosis	158	0.374	1.563	0.002	0.008	0.005	1766
Fudan	hsa03013	RNA transport	116	0.356	1.430	0.014	0.038	0.023	2705
Fudan	hsa01200	Carbon metabolism	105	(0.387)	(1.518)	0.008	0.023	0.014	912
Fudan	hsa00190	Oxidative phosphorylation	83	(0.473)	(1.784)	0.002	0.008	0.005	1924
Fudan	hsa03050	Proteasome	41	(0.529)	(1.802)	0.006	0.019	0.011	2687
Fudan	hsa03320	PPAR signaling pathway	48	(0.537)	(1.875)	0.002	0.008	0.005	626
Fudan	hsa00620	Pyruvate metabolism	34	(0.554)	(1.800)	0.004	0.014	0.008	732
Fudan	hsa00983	Drug metabolism - other enzymes	59	(0.557)	(2.026)	0.002	0.008	0.005	713
Fudan	hsa00561	Glycerolipid metabolism	30	(0.571)	(1.796)	0.006	0.019	0.011	1250
Fudan	hsa00310	Lysine degradation	34	(0.621)	(2.016)	0.004	0.014	0.008	728
Fudan	hsa00340	Histidine metabolism	18	(0.636)	(1.786)	0.004	0.014	0.008	729
Fudan	hsa00640	Propanoate metabolism	30	(0.644)	(2.024)	0.002	0.008	0.005	912
Fudan	hsa00020	Citrate cycle (TCA cycle)	28	(0.658)	(2.038)	0.002	0.008	0.005	1772
Fudan	hsa00670	One carbon pool by folate	14	(0.659)	(1.753)	0.010	0.027	0.017	850
Fudan	hsa01212	Fatty acid metabolism	40	(0.660)	(2.232)	0.002	0.008	0.005	788
Fudan	hsa00260	Glycine, serine and threonine metabolism	35	(0.663)	(2.166)	0.002	0.008	0.005	871
Fudan	hsa00450	Selenocompound metabolism	14	(0.673)	(1.790)	0.006	0.019	0.011	1042
Fudan	hsa00360	Phenylalanine metabolism	15	(0.674)	(1.822)	0.002	0.008	0.005	223
Fudan	hsa02010	ABC transporters	25	(0.675)	(2.024)	0.002	0.008	0.005	884
Fudan	hsa00790	Folate biosynthesis	16	(0.679)	(1.840)	0.004	0.014	0.008	1126
Fudan	hsa00860	Porphyrin and chlorophyll metabolism	29	(0.689)	(2.153)	0.002	0.008	0.005	828
Fudan	hsa00630	Glyoxylate and dicarboxylate metabolism	29	(0.691)	(2.159)	0.002	0.008	0.005	1361
Fudan	hsa00350	Tyrosine metabolism	25	(0.692)	(2.073)	0.002	0.008	0.005	1023
Fudan	hsa00220	Arginine biosynthesis	17	(0.693)	(1.901)	0.002	0.008	0.005	407
Fudan	hsa00280	Valine, leucine and isoleucine degradation	45	(0.701)	(2.424)	0.002	0.008	0.005	728
Fudan	hsa00062	Fatty acid elongation	16	(0.706)	(1.913)	0.002	0.008	0.005	705
Fudan	hsa00970	Aminoacyl-tRNA biosynthesis	24	(0.719)	(2.136)	0.002	0.008	0.005	1323
Fudan	hsa00380	Tryptophan metabolism	32	(0.724)	(2.306)	0.002	0.008	0.005	783
Fudan	hsa00980	Metabolism of xenobiotics by cytochrome P450	51	(0.747)	(2.633)	0.002	0.008	0.005	783
Fudan	hsa00982	Drug metabolism - cytochrome P450	50	(0.758)	(2.676)	0.002	0.008	0.005	783
Fudan	hsa04146	Peroxisome	72	(0.760)	(2.824)	0.002	0.008	0.005	699
Fudan	hsa00140	Steroid hormone biosynthesis	34	(0.771)	(2.503)	0.002	0.008	0.005	836
Fudan	hsa00650	Butanoate metabolism	22	(0.783)	(2.304)	0.002	0.008	0.005	350
Fudan	hsa00071	Fatty acid degradation	38	(0.796)	(2.658)	0.002	0.008	0.005	788

S11. The KEGG pathway analysis of High hypoxia score vs Low hypoxia score in HBV-related HCC cohorts

Cohorts	ID	Description	setSize	enrichment Score	NES	pvalue	p.adjust	qvalues	rank
Fudan	hsa00410	beta-Alanine metabolism	23	(0.801)	(2.369)	0.002	0.008	0.005	788
Fudan	hsa00040	Pentose and glucuronate interconversions	21	(0.805)	(2.316)	0.002	0.008	0.005	814
Fudan	hsa00830	Retinol metabolism	39	(0.806)	(2.706)	0.002	0.008	0.005	783
Fudan	hsa00053	Ascorbate and aldarate metabolism	17	(0.881)	(2.418)	0.002	0.008	0.005	688
Fudan	hsa00120	Primary bile acid biosynthesis	15	(0.882)	(2.383)	0.002	0.008	0.005	673

S12. The KEGG pathway analysis of High TME score vs Low TME score in HBV-related HCC cohorts

Cohort	ID	Description	setSize	enrichment Score	NES	pvalue	p.adjust	qvalues	rank
GSE14520	hsa00120	Primary bile acid biosynthesis	15	0.882	2.201	0.002	0.008	0.004	1209
GSE14520	hsa00830	Retinol metabolism	39	0.869	2.607	0.002	0.008	0.004	806
GSE14520	hsa00380	Tryptophan metabolism	34	0.865	2.554	0.002	0.008	0.004	1004
GSE14520	hsa00650	Butanoate metabolism	23	0.833	2.247	0.002	0.008	0.004	779
GSE14520	hsa00071	Fatty acid degradation	40	0.830	2.490	0.002	0.008	0.004	842
GSE14520	hsa00220	Arginine biosynthesis	17	0.829	2.096	0.002	0.008	0.004	1300
GSE14520	hsa00140	Steroid hormone biosynthesis	43	0.828	2.527	0.002	0.008	0.004	1195
GSE14520	hsa00591	Linoleic acid metabolism	20	0.827	2.156	0.002	0.008	0.004	793
GSE14520	hsa00350	Tyrosine metabolism	32	0.814	2.353	0.002	0.008	0.004	895
GSE14520	hsa00980	Metabolism of xenobiotics by cytochrome P450	51	0.811	2.547	0.002	0.008	0.004	715
GSE14520	hsa00053	Ascorbate and aldarate metabolism	12	0.811	1.909	0.006	0.016	0.009	842
GSE14520	hsa00340	Histidine metabolism	18	0.808	2.076	0.002	0.008	0.004	1714
GSE14520	hsa00630	Glyoxylate and dicarboxylate metabolism	24	0.807	2.194	0.002	0.008	0.004	848
GSE14520	hsa00982	Drug metabolism - cytochrome P450	49	0.801	2.505	0.002	0.008	0.004	895
GSE14520	hsa00360	Phenylalanine metabolism	15	0.794	1.979	0.004	0.013	0.007	1747
GSE14520	hsa00280	Valine, leucine and isoleucine degradation	42	0.793	2.407	0.002	0.008	0.004	1485
GSE14520	hsa00410	beta-Alanine metabolism	28	0.780	2.206	0.002	0.008	0.004	1747
GSE14520	hsa00260	Glycine, serine and threonine metabolism	33	0.769	2.230	0.002	0.008	0.004	1020
GSE14520	hsa00040	Pentose and glucuronate interconversions	17	0.755	1.909	0.006	0.016	0.009	919
GSE14520	hsa00640	Propanoate metabolism	30	0.754	2.159	0.002	0.008	0.004	1192
GSE14520	hsa04146	Peroxisome	71	0.700	2.310	0.002	0.008	0.004	1187
GSE14520	hsa00590	Arachidonic acid metabolism	48	0.700	2.180	0.002	0.008	0.004	2123
GSE14520	hsa00020	Citrate cycle (TCA cycle)	29	0.689	1.965	0.004	0.013	0.007	959
GSE14520	hsa03320	PPAR signaling pathway	66	0.686	2.242	0.002	0.008	0.004	1060
GSE14520	hsa00760	Nicotinate and nicotinamide metabolism	25	0.675	1.854	0.006	0.016	0.009	1547
GSE14520	hsa00860	Porphyrin and chlorophyll metabolism	25	0.668	1.836	0.006	0.016	0.009	1774
GSE14520	hsa00620	Pyruvate metabolism	34	0.641	1.891	0.002	0.008	0.004	1074
GSE14520	hsa04061	Viral protein interaction with cytokine and cytokine receptor	86	0.631	2.164	0.002	0.008	0.004	1660
GSE14520	hsa00790	Folate biosynthesis	22	0.630	1.685	0.012	0.031	0.017	2374
GSE14520	hsa02010	ABC transporters	37	0.630	1.876	0.002	0.008	0.004	1169
GSE14520	hsa00983	Drug metabolism - other enzymes	54	0.616	1.965	0.002	0.008	0.004	655
GSE14520	hsa00250	Alanine, aspartate and glutamate metabolism	28	0.599	1.696	0.014	0.032	0.018	1300
GSE14520	hsa01212	Fatty acid metabolism	47	0.585	1.816	0.002	0.008	0.004	1060
GSE14520	hsa00010	Glycolysis / Gluconeogenesis	60	0.584	1.889	0.002	0.008	0.004	1149
GSE14520	hsa00561	Glycerolipid metabolism	46	0.584	1.803	0.004	0.013	0.007	2144
GSE14520	hsa00500	Starch and sucrose metabolism	28	0.582	1.647	0.014	0.032	0.018	1019
GSE14520	hsa00270	Cysteine and methionine metabolism	43	0.579	1.766	0.002	0.008	0.004	1074
GSE14520	hsa01200	Carbon metabolism	105	0.558	1.988	0.002	0.008	0.004	968
GSE14520	hsa00310	Lysine degradation	49	0.547	1.711	0.006	0.016	0.009	842
GSE14520	hsa00330	Arginine and proline metabolism	38	0.536	1.601	0.019	0.043	0.024	1127
GSE14520	hsa04514	Cell adhesion molecules (CAMs)	122	0.518	1.874	0.002	0.008	0.004	1654
GSE14520	hsa04064	NF-kappa B signaling pathway	93	0.489	1.699	0.002	0.008	0.004	2154
GSE14520	hsa01230	Biosynthesis of amino acids	63	0.478	1.550	0.014	0.032	0.018	1031
GSE14520	hsa00564	Glycerophospholipid metabolism	71	0.467	1.539	0.011	0.029	0.016	2286
GSE14520	hsa04062	Chemokine signaling pathway	164	0.452	1.702	0.002	0.008	0.004	1897
GSE14520	hsa04060	Cytokine-cytokine receptor interaction	245	0.438	1.733	0.002	0.008	0.004	1660
GSE14520	hsa04145	Phagosome	132	0.426	1.545	0.005	0.016	0.009	1099
GSE14520	hsa04152	AMPK signaling pathway	105	0.397	1.413	0.022	0.048	0.027	1623
GSE14520	hsa04380	Osteoclast differentiation	121	0.387	1.399	0.018	0.043	0.024	3011
GSE14520	hsa04080	Neuroactive ligand-receptor interaction	295	0.386	1.552	0.002	0.008	0.004	4013
GSE14520	hsa04310	Wnt signaling pathway	131	(0.379)	(1.445)	0.011	0.028	0.016	3433
GSE14520	hsa04218	Cellular senescence	145	(0.397)	(1.525)	0.002	0.008	0.004	2531
GSE14520	hsa04390	Hippo signaling pathway	130	(0.429)	(1.633)	0.002	0.008	0.004	2430
GSE14520	hsa04120	Ubiquitin mediated proteolysis	116	(0.435)	(1.628)	0.004	0.013	0.007	4099
GSE14520	hsa04115	p53 signaling pathway	64	(0.444)	(1.510)	0.008	0.022	0.012	1149
GSE14520	hsa03018	RNA degradation	57	(0.506)	(1.666)	0.004	0.013	0.007	2590
GSE14520	hsa04114	Oocyte meiosis	96	(0.525)	(1.906)	0.002	0.008	0.004	1702
GSE14520	hsa03022	Basal transcription factors	36	(0.562)	(1.676)	0.004	0.013	0.007	3718
GSE14520	hsa03420	Nucleotide excision repair	42	(0.563)	(1.752)	0.002	0.008	0.004	2253
GSE14520	hsa03015	mRNA surveillance pathway	68	(0.570)	(1.965)	0.002	0.008	0.004	3158
GSE14520	hsa03460	Fanconi anemia pathway	38	(0.573)	(1.736)	0.004	0.013	0.007	2467
GSE14520	hsa03008	Ribosome biogenesis in eukaryotes	56	(0.575)	(1.888)	0.002	0.008	0.004	2747
GSE14520	hsa03010	Ribosome	99	(0.583)	(2.106)	0.002	0.008	0.004	2715
GSE14520	hsa03013	RNA transport	127	(0.589)	(2.237)	0.002	0.008	0.004	2875
GSE14520	hsa03440	Homologous recombination	38	(0.622)	(1.885)	0.002	0.008	0.004	2563
GSE14520	hsa03040	Spliceosome	102	(0.660)	(2.399)	0.002	0.008	0.004	3010
GSE14520	hsa03450	Non-homologous end-joining	12	(0.693)	(1.602)	0.018	0.041	0.023	2519
GSE14520	hsa04110	Cell cycle	114	(0.707)	(2.636)	0.002	0.008	0.004	1607
GSE14520	hsa03430	Mismatch repair	22	(0.723)	(1.965)	0.002	0.008	0.004	1449
GSE14520	hsa03030	DNA replication	34	(0.792)	(2.327)	0.002	0.008	0.004	1460

S12. The KEGG pathway analysis of High TME score vs Low TME score in HBV-related HCC cohorts

Cohort	ID	Description	setSize	enrichment Score	NES	pvalue	p.adjust	qvalues	rank
Gao et al	hsa00120	Primary bile acid biosynthesis	15	0.863	2.395	0.002	0.008	0.004	652
Gao et al	hsa00410	beta-Alanine metabolism	23	0.815	2.544	0.002	0.008	0.004	962
Gao et al	hsa00380	Tryptophan metabolism	32	0.811	2.694	0.002	0.008	0.004	999
Gao et al	hsa00830	Retinol metabolism	39	0.793	2.801	0.002	0.008	0.004	798
Gao et al	hsa00982	Drug metabolism - cytochrome P450	50	0.787	2.930	0.002	0.008	0.004	575
Gao et al	hsa00140	Steroid hormone biosynthesis	34	0.784	2.645	0.002	0.008	0.004	798
Gao et al	hsa00980	Metabolism of xenobiotics by cytochrome P450	51	0.773	2.899	0.002	0.008	0.004	552
Gao et al	hsa00053	Ascorbate and aldarate metabolism	17	0.772	2.213	0.002	0.008	0.004	955
Gao et al	hsa00040	Pentose and glucuronate interconversions	21	0.772	2.350	0.002	0.008	0.004	350
Gao et al	hsa00640	Propanoate metabolism	30	0.759	2.498	0.002	0.008	0.004	920
Gao et al	hsa00071	Fatty acid degradation	38	0.756	2.673	0.002	0.008	0.004	1003
Gao et al	hsa00350	Tyrosine metabolism	25	0.729	2.306	0.002	0.008	0.004	984
Gao et al	hsa02010	ABC transporters	25	0.728	2.304	0.002	0.008	0.004	556
Gao et al	hsa00591	Linoleic acid metabolism	10	0.717	1.774	0.017	0.045	0.025	625
Gao et al	hsa04146	Peroxisome	72	0.714	2.855	0.002	0.008	0.004	1333
Gao et al	hsa00020	Citrate cycle (TCA cycle)	28	0.707	2.308	0.002	0.008	0.004	1724
Gao et al	hsa00650	Butanoate metabolism	22	0.696	2.140	0.002	0.008	0.004	1011
Gao et al	hsa00280	Valine, leucine and isoleucine degradation	45	0.695	2.513	0.002	0.008	0.004	955
Gao et al	hsa00340	Histidine metabolism	18	0.693	2.035	0.006	0.018	0.010	990
Gao et al	hsa00360	Phenylalanine metabolism	15	0.692	1.921	0.004	0.013	0.007	984
Gao et al	hsa00860	Porphyrin and chlorophyll metabolism	29	0.686	2.239	0.002	0.008	0.004	825
Gao et al	hsa00220	Arginine biosynthesis	17	0.674	1.932	0.006	0.018	0.010	1256
Gao et al	hsa00630	Glyoxylate and dicarboxylate metabolism	29	0.648	2.116	0.002	0.008	0.004	999
Gao et al	hsa01212	Fatty acid metabolism	40	0.623	2.202	0.002	0.008	0.004	762
Gao et al	hsa03320	PPAR signaling pathway	48	0.619	2.276	0.002	0.008	0.004	1025
Gao et al	hsa00790	Folate biosynthesis	16	0.606	1.710	0.012	0.032	0.017	829
Gao et al	hsa00310	Lysine degradation	34	0.601	2.028	0.002	0.008	0.004	955
Gao et al	hsa00500	Starch and sucrose metabolism	22	0.581	1.787	0.008	0.022	0.012	807
Gao et al	hsa00590	Arachidonic acid metabolism	29	0.580	1.894	0.004	0.013	0.007	625
Gao et al	hsa00260	Glycine, serine and threonine metabolism	35	0.579	1.968	0.002	0.008	0.004	710
Gao et al	hsa00620	Pyruvate metabolism	34	0.574	1.937	0.002	0.008	0.004	955
Gao et al	hsa04130	SNARE interactions in vesicular transport	25	0.569	1.802	0.009	0.027	0.015	2014
Gao et al	hsa00760	Nicotinate and nicotinamide metabolism	27	0.565	1.826	0.007	0.022	0.012	777
Gao et al	hsa00983	Drug metabolism - other enzymes	59	0.556	2.151	0.002	0.008	0.004	587
Gao et al	hsa00561	Glycerolipid metabolism	30	0.544	1.791	0.008	0.022	0.012	1603
Gao et al	hsa00330	Arginine and proline metabolism	33	0.497	1.673	0.011	0.032	0.017	598
Gao et al	hsa00010	Glycolysis / Gluconeogenesis	55	0.468	1.781	0.004	0.013	0.007	838
Gao et al	hsa01200	Carbon metabolism	105	0.466	1.974	0.002	0.008	0.004	996
Gao et al	hsa00190	Oxidative phosphorylation	83	0.460	1.871	0.002	0.008	0.004	2523
Gao et al	hsa00270	Cysteine and methionine metabolism	42	0.426	1.520	0.017	0.045	0.025	688
Gao et al	hsa04217	Necroptosis	74	0.405	1.624	0.008	0.022	0.012	1769
Gao et al	hsa03010	Ribosome	115	(0.493)	(2.178)	0.002	0.008	0.004	2761
Gao et al	hsa03018	RNA degradation	52	(0.539)	(2.081)	0.002	0.008	0.004	2318
Gao et al	hsa03015	mRNA surveillance pathway	63	(0.581)	(2.332)	0.002	0.008	0.004	1843
Gao et al	hsa03013	RNA transport	116	(0.590)	(2.618)	0.002	0.008	0.004	1482
Gao et al	hsa03008	Ribosome biogenesis in eukaryotes	61	(0.640)	(2.553)	0.002	0.008	0.004	1531
Gao et al	hsa03022	Basal transcription factors	27	(0.653)	(2.157)	0.002	0.008	0.004	1882
Gao et al	hsa03020	RNA polymerase	20	(0.653)	(2.005)	0.002	0.008	0.004	2225
Gao et al	hsa03420	Nucleotide excision repair	33	(0.679)	(2.371)	0.002	0.008	0.004	1484
Gao et al	hsa04110	Cell cycle	58	(0.687)	(2.719)	0.002	0.008	0.004	888
Gao et al	hsa03040	Spliceosome	114	(0.709)	(3.144)	0.002	0.008	0.004	1704
Gao et al	hsa03410	Base excision repair	17	(0.797)	(2.331)	0.002	0.008	0.004	328
Gao et al	hsa03430	Mismatch repair	16	(0.824)	(2.349)	0.002	0.008	0.004	666
Gao et al	hsa03030	DNA replication	22	(0.876)	(2.726)	0.002	0.008	0.004	705
TCGA	hsa00120	Primary bile acid biosynthesis	17	0.915	2.052	0.002	0.008	0.004	991
TCGA	hsa00650	Butanoate metabolism	28	0.872	2.180	0.002	0.008	0.004	1141
TCGA	hsa00071	Fatty acid degradation	44	0.863	2.344	0.002	0.008	0.004	1206
TCGA	hsa00830	Retinol metabolism	65	0.860	2.500	0.002	0.008	0.004	1451
TCGA	hsa00260	Glycine, serine and threonine metabolism	38	0.860	2.294	0.002	0.008	0.004	1442
TCGA	hsa00380	Tryptophan metabolism	40	0.856	2.291	0.002	0.008	0.004	1630
TCGA	hsa00072	Synthesis and degradation of ketone bodies	10	0.856	1.706	0.006	0.016	0.008	1141
TCGA	hsa00350	Tyrosine metabolism	36	0.851	2.255	0.002	0.008	0.004	1451
TCGA	hsa00591	Linoleic acid metabolism	28	0.845	2.112	0.002	0.008	0.004	607
TCGA	hsa00982	Drug metabolism - cytochrome P450	67	0.845	2.458	0.002	0.008	0.004	1061
TCGA	hsa00360	Phenylalanine metabolism	17	0.837	1.876	0.002	0.008	0.004	999
TCGA	hsa00220	Arginine biosynthesis	21	0.831	1.969	0.002	0.008	0.004	1704
TCGA	hsa00280	Valine, leucine and isoleucine degradation	47	0.828	2.276	0.002	0.008	0.004	2134
TCGA	hsa00980	Metabolism of xenobiotics by cytochrome P450	71	0.826	2.408	0.002	0.008	0.004	1123
TCGA	hsa00640	Propanoate metabolism	33	0.817	2.125	0.002	0.008	0.004	1368
TCGA	hsa00053	Ascorbate and aldarate metabolism	27	0.816	2.028	0.002	0.008	0.004	1206

S12. The KEGG pathway analysis of High TME score vs Low TME score in HBV-related HCC cohorts

Cohort	ID	Description	setSize	enrichment Score	NES	pvalue	p.adjust	qvalues	rank
TCGA	hsa03320	PPAR signaling pathway	76	0.813	2.386	0.002	0.008	0.004	1505
TCGA	hsa00630	Glyoxylate and dicarboxylate metabolism	29	0.804	2.027	0.002	0.008	0.004	1557
TCGA	hsa00140	Steroid hormone biosynthesis	59	0.802	2.302	0.002	0.008	0.004	1061
TCGA	hsa00410	beta-Alanine metabolism	31	0.797	2.055	0.002	0.008	0.004	1428
TCGA	hsa00340	Histidine metabolism	22	0.782	1.859	0.002	0.008	0.004	2384
TCGA	hsa00040	Pentose and glucuronate interconversions	33	0.759	1.974	0.002	0.008	0.004	1061
TCGA	hsa04146	Peroxisome	82	0.758	2.264	0.001	0.008	0.004	2120
TCGA	hsa00270	Cysteine and methionine metabolism	46	0.739	2.026	0.002	0.008	0.004	1250
TCGA	hsa00620	Pyruvate metabolism	39	0.726	1.948	0.002	0.008	0.004	2134
TCGA	hsa00250	Alanine, aspartate and glutamate metabolism	34	0.722	1.886	0.003	0.012	0.006	846
TCGA	hsa00592	alpha-Linolenic acid metabolism	24	0.721	1.738	0.003	0.012	0.006	2241
TCGA	hsa00020	Citrate cycle (TCA cycle)	30	0.714	1.818	0.003	0.012	0.006	1776
TCGA	hsa00790	Folate biosynthesis	24	0.712	1.718	0.003	0.012	0.006	1613
TCGA	hsa00860	Porphyrin and chlorophyll metabolism	41	0.708	1.908	0.002	0.008	0.004	1061
TCGA	hsa01210	2-Oxocarboxylic acid metabolism	18	0.705	1.600	0.018	0.043	0.023	2834
TCGA	hsa00590	Arachidonic acid metabolism	61	0.691	1.995	0.002	0.008	0.004	1494
TCGA	hsa00983	Drug metabolism - other enzymes	77	0.685	2.017	0.002	0.008	0.004	1061
TCGA	hsa01212	Fatty acid metabolism	52	0.662	1.862	0.002	0.008	0.004	1146
TCGA	hsa02010	ABC transporters	45	0.650	1.778	0.002	0.008	0.004	3051
TCGA	hsa00330	Arginine and proline metabolism	48	0.650	1.798	0.002	0.008	0.004	1704
TCGA	hsa00561	Glycerolipid metabolism	52	0.648	1.824	0.002	0.008	0.004	2134
TCGA	hsa01200	Carbon metabolism	114	0.637	1.981	0.001	0.008	0.004	1630
TCGA	hsa00010	Glycolysis / Gluconeogenesis	67	0.632	1.840	0.002	0.008	0.004	1674
TCGA	hsa01230	Biosynthesis of amino acids	72	0.628	1.831	0.002	0.008	0.004	1080
TCGA	hsa00310	Lysine degradation	56	0.610	1.732	0.003	0.012	0.006	1206
TCGA	hsa00760	Nicotinate and nicotinamide metabolism	37	0.607	1.619	0.008	0.022	0.012	2298
TCGA	hsa04061	Viral protein interaction with cytokine and cytokine receptor	98	0.584	1.778	0.001	0.008	0.004	2324
TCGA	hsa04514	Cell adhesion molecules (CAMs)	138	0.570	1.806	0.001	0.008	0.004	3103
TCGA	hsa04152	AMPK signaling pathway	120	0.523	1.637	0.006	0.015	0.008	1698
TCGA	hsa00564	Glycerophospholipid metabolism	89	0.487	1.465	0.020	0.047	0.025	2241
TCGA	hsa04270	Vascular smooth muscle contraction	130	0.482	1.521	0.010	0.025	0.013	3332
TCGA	hsa04068	FoxO signaling pathway	130	0.475	1.498	0.014	0.034	0.018	2580
TCGA	hsa04060	Cytokine-cytokine receptor interaction	289	0.457	1.561	0.001	0.008	0.004	3170
TCGA	hsa04062	Chemokine signaling pathway	185	0.457	1.495	0.004	0.012	0.006	3682
TCGA	hsa04218	Cellular senescence	157	(0.363)	(1.334)	0.012	0.029	0.016	2288
TCGA	hsa04310	Wnt signaling pathway	158	(0.393)	(1.446)	0.004	0.012	0.006	3265
TCGA	hsa04114	Oocyte meiosis	123	(0.445)	(1.578)	0.004	0.012	0.006	1455
TCGA	hsa04390	Hippo signaling pathway	154	(0.457)	(1.681)	0.004	0.012	0.006	4220
TCGA	hsa04260	Cardiac muscle contraction	82	(0.469)	(1.589)	0.006	0.017	0.009	4515
TCGA	hsa03015	mRNA surveillance pathway	90	(0.559)	(1.906)	0.003	0.012	0.006	4589
TCGA	hsa03013	RNA transport	157	(0.560)	(2.060)	0.004	0.012	0.006	4597
TCGA	hsa03460	Fanconi anemia pathway	49	(0.563)	(1.708)	0.008	0.022	0.012	1765
TCGA	hsa03410	Base excision repair	33	(0.565)	(1.579)	0.018	0.042	0.023	2681
TCGA	hsa03420	Nucleotide excision repair	46	(0.570)	(1.705)	0.005	0.015	0.008	2852
TCGA	hsa03008	Ribosome biogenesis in eukaryotes	72	(0.572)	(1.893)	0.003	0.012	0.006	4337
TCGA	hsa03440	Homologous recombination	37	(0.599)	(1.711)	0.010	0.026	0.014	4843
TCGA	hsa03020	RNA polymerase	31	(0.622)	(1.728)	0.005	0.014	0.008	3962
TCGA	hsa03040	Spliceosome	131	(0.643)	(2.297)	0.004	0.012	0.006	3618
TCGA	hsa04110	Cell cycle	124	(0.662)	(2.343)	0.004	0.012	0.006	2260
TCGA	hsa03430	Mismatch repair	23	(0.682)	(1.789)	0.005	0.014	0.007	2678
TCGA	hsa03450	Non-homologous end-joining	12	(0.707)	(1.537)	0.019	0.044	0.024	1546
TCGA	hsa03030	DNA replication	36	(0.767)	(2.169)	0.003	0.011	0.006	2681
TCGA	hsa03010	Ribosome	134	(0.769)	(2.759)	0.004	0.012	0.006	1929
ICGC_LIRI_JP	hsa00072	Synthesis and degradation of ketone bodies	10	0.907	1.906	0.002	0.011	0.006	1170
ICGC_LIRI_JP	hsa00650	Butanoate metabolism	27	0.867	2.373	0.002	0.011	0.006	1381
ICGC_LIRI_JP	hsa00280	Valine, leucine and isoleucine degradation	47	0.863	2.635	0.002	0.011	0.006	1421
ICGC_LIRI_JP	hsa00071	Fatty acid degradation	44	0.832	2.523	0.002	0.011	0.006	1421
ICGC_LIRI_JP	hsa00640	Propanoate metabolism	33	0.831	2.354	0.002	0.011	0.006	1363
ICGC_LIRI_JP	hsa00120	Primary bile acid biosynthesis	17	0.803	1.948	0.002	0.011	0.006	1225
ICGC_LIRI_JP	hsa00380	Tryptophan metabolism	38	0.800	2.333	0.002	0.011	0.006	2269
ICGC_LIRI_JP	hsa00260	Glycine, serine and threonine metabolism	39	0.794	2.330	0.002	0.011	0.006	2390
ICGC_LIRI_JP	hsa00830	Retinol metabolism	65	0.778	2.526	0.002	0.011	0.006	1304
ICGC_LIRI_JP	hsa00630	Glyoxylate and dicarboxylate metabolism	29	0.738	2.028	0.002	0.011	0.006	2199
ICGC_LIRI_JP	hsa00770	Pantothenate and CoA biosynthesis	19	0.736	1.842	0.004	0.018	0.010	856
ICGC_LIRI_JP	hsa00500	Starch and sucrose metabolism	35	0.731	2.106	0.002	0.011	0.006	1222
ICGC_LIRI_JP	hsa00053	Ascorbate and aldarate metabolism	27	0.715	1.957	0.002	0.011	0.006	1421
ICGC_LIRI_JP	hsa00140	Steroid hormone biosynthesis	59	0.714	2.259	0.002	0.011	0.006	1079
ICGC_LIRI_JP	hsa00220	Arginine biosynthesis	21	0.707	1.819	0.004	0.018	0.010	1254
ICGC_LIRI_JP	hsa00982	Drug metabolism - cytochrome P450	69	0.698	2.298	0.002	0.011	0.006	1268
ICGC_LIRI_JP	hsa00020	Citrate cycle (TCA cycle)	30	0.696	1.936	0.002	0.011	0.006	2197

S12. The KEGG pathway analysis of High TME score vs Low TME score in HBV-related HCC cohorts

Cohort	ID	Description	setSize	enrichment Score	NES	pvalue	p.adjust	qvalues	rank
ICGC_LIRI_JP	hsa01212	Fatty acid metabolism	52	0.693	2.148	0.002	0.011	0.006	1293
ICGC_LIRI_JP	hsa04146	Peroxisome	83	0.687	2.313	0.002	0.011	0.006	2279
ICGC_LIRI_JP	hsa00410	beta-Alanine metabolism	31	0.683	1.909	0.002	0.011	0.006	1421
ICGC_LIRI_JP	hsa00620	Pyruvate metabolism	38	0.666	1.942	0.002	0.011	0.006	3009
ICGC_LIRI_JP	hsa00062	Fatty acid elongation	23	0.657	1.713	0.006	0.025	0.014	988
ICGC_LIRI_JP	hsa00350	Tyrosine metabolism	36	0.648	1.864	0.002	0.011	0.006	2181
ICGC_LIRI_JP	hsa00980	Metabolism of xenobiotics by cytochrome P450	73	0.635	2.101	0.002	0.011	0.006	1313
ICGC_LIRI_JP	hsa01200	Carbon metabolism	112	0.632	2.207	0.002	0.011	0.006	1946
ICGC_LIRI_JP	hsa00340	Histidine metabolism	21	0.625	1.608	0.014	0.048	0.029	2181
ICGC_LIRI_JP	hsa00900	Terpenoid backbone biosynthesis	22	0.617	1.590	0.014	0.048	0.029	1896
ICGC_LIRI_JP	hsa00250	Alanine, aspartate and glutamate metabolism	34	0.616	1.752	0.002	0.011	0.006	1254
ICGC_LIRI_JP	hsa01040	Biosynthesis of unsaturated fatty acids	23	0.613	1.596	0.014	0.048	0.029	1225
ICGC_LIRI_JP	hsa00270	Cysteine and methionine metabolism	46	0.600	1.819	0.002	0.011	0.006	3235
ICGC_LIRI_JP	hsa00310	Lysine degradation	47	0.595	1.818	0.002	0.011	0.006	1619
ICGC_LIRI_JP	hsa00040	Pentose and glucuronate interconversions	32	0.577	1.622	0.012	0.046	0.027	1102
ICGC_LIRI_JP	hsa03320	PPAR signaling pathway	76	0.576	1.901	0.002	0.011	0.006	1405
ICGC_LIRI_JP	hsa02010	ABC transporters	45	0.519	1.572	0.012	0.046	0.027	2521
ICGC_LIRI_JP	hsa00010	Glycolysis / Gluconeogenesis	67	0.517	1.688	0.002	0.011	0.006	2076
ICGC_LIRI_JP	hsa00590	Arachidonic acid metabolism	61	0.497	1.592	0.010	0.039	0.023	736
ICGC_LIRI_JP	hsa00983	Drug metabolism - other enzymes	79	0.493	1.642	0.004	0.018	0.010	1383
ICGC_LIRI_JP	hsa04152	AMPK signaling pathway	118	0.469	1.649	0.002	0.011	0.006	1861
ICGC_LIRI_JP	hsa01230	Biosynthesis of amino acids	71	0.449	1.476	0.014	0.048	0.029	2408
ICGC_LIRI_JP	hsa04151	PI3K-Akt signaling pathway	347	(0.334)	(1.343)	0.004	0.018	0.011	4169
ICGC_LIRI_JP	hsa04390	Hippo signaling pathway	151	(0.417)	(1.527)	0.004	0.018	0.010	3928
ICGC_LIRI_JP	hsa04510	Focal adhesion	193	(0.439)	(1.664)	0.002	0.011	0.006	2021
ICGC_LIRI_JP	hsa04110	Cell cycle	124	(0.477)	(1.712)	0.004	0.018	0.010	2042
ICGC_LIRI_JP	hsa04260	Cardiac muscle contraction	82	(0.493)	(1.657)	0.004	0.018	0.010	4124
ICGC_LIRI_JP	hsa03010	Ribosome	133	(0.495)	(1.788)	0.002	0.011	0.006	4203
ICGC_LIRI_JP	hsa04512	ECM-receptor interaction	86	(0.594)	(2.033)	0.002	0.011	0.006	3370
GSE10143	hsa04061	Viral protein interaction with cytokine and cytokine receptor	65	0.645	2.322	0.002	0.046	0.041	514
GSE10143	hsa04514	Cell adhesion molecules (CAMs)	88	0.528	2.010	0.002	0.046	0.041	1054
GSE10143	hsa04060	Cytokine-cytokine receptor interaction	171	0.488	2.016	0.001	0.046	0.041	932
GSE10143	hsa04062	Chemokine signaling pathway	129	0.470	1.884	0.002	0.046	0.041	1099
GSE10143	hsa04380	Osteoclast differentiation	95	0.430	1.650	0.003	0.049	0.043	818
GSE10143	hsa04110	Cell cycle	87	(0.452)	(1.844)	0.003	0.046	0.041	978
GSE10143	hsa04114	Oocyte meiosis	67	(0.459)	(1.790)	0.002	0.046	0.041	842
GSE10143	hsa03420	Nucleotide excision repair	33	(0.544)	(1.842)	0.002	0.046	0.041	1802
GSE10143	hsa03030	DNA replication	26	(0.584)	(1.859)	0.002	0.046	0.041	907

S13. The KEGG pathway analysis of Hypoxia-TME subgroups in HBV-related HCC cohorts

		Hypoxia-TME score high risk vs others							
cohort	**ID**	**Description**	**setSize**	**enrichmentScore**	**NES**	**pvalue**	**p.adjust**	**qvalues**	**rank**
GSE14520	hsa03030	DNA replication	34	0.742	2.153	0.022	0.071	0.045	2501
GSE14520	hsa03430	Mismatch repair	22	0.675	1.799	0.020	0.071	0.045	2501
GSE14520	hsa04110	Cell cycle	114	0.670	2.433	0.023	0.071	0.045	1663
GSE14520	hsa03040	Spliceosome	102	0.655	2.338	0.021	0.071	0.045	2380
GSE14520	hsa03010	Ribosome	99	0.608	2.181	0.022	0.071	0.045	2745
GSE14520	hsa03013	RNA transport	127	0.570	2.143	0.021	0.071	0.045	2271
GSE14520	hsa03460	Fanconi anemia pathway	38	0.552	1.587	0.024	0.071	0.045	3218
GSE14520	hsa03440	Homologous recombination	38	0.547	1.571	0.024	0.071	0.045	3296
GSE14520	hsa03410	Base excision repair	30	0.496	1.380	0.021	0.071	0.045	1990
GSE14520	hsa03015	mRNA surveillance pathway	68	0.496	1.603	0.025	0.073	0.046	2312
GSE14520	hsa03008	Ribosome biogenesis in eukaryotes	56	0.488	1.552	0.022	0.071	0.045	4077
GSE14520	hsa04115	p53 signaling pathway	64	0.460	1.488	0.024	0.071	0.045	1336
GSE14520	hsa03018	RNA degradation	57	0.450	1.445	0.022	0.071	0.045	1661
GSE14520	hsa04114	Oocyte meiosis	96	0.437	1.522	0.023	0.071	0.045	1601
GSE14520	hsa04390	Hippo signaling pathway	130	0.423	1.584	0.022	0.071	0.045	2929
GSE14520	hsa04512	ECM-receptor interaction	79	0.418	1.409	0.023	0.071	0.045	1722
GSE14520	hsa04350	TGF-beta signaling pathway	84	0.415	1.412	0.023	0.071	0.045	1992
GSE14520	hsa04218	Cellular senescence	145	0.404	1.521	0.023	0.071	0.045	2524
GSE14520	hsa00190	Oxidative phosphorylation	99	(0.432)	(1.484)	0.036	0.097	0.062	2394
GSE14520	hsa04152	AMPK signaling pathway	105	(0.469)	(1.590)	0.036	0.097	0.062	1570
GSE14520	hsa00564	Glycerophospholipid metabolism	71	(0.478)	(1.549)	0.032	0.091	0.058	990
GSE14520	hsa01230	Biosynthesis of amino acids	63	(0.524)	(1.671)	0.016	0.071	0.045	580
GSE14520	hsa00561	Glycerolipid metabolism	46	(0.538)	(1.625)	0.033	0.093	0.060	1813
GSE14520	hsa01200	Carbon metabolism	105	(0.567)	(1.926)	0.018	0.071	0.045	1040
GSE14520	hsa00010	Glycolysis / Gluconeogenesis	60	(0.568)	(1.756)	0.017	0.071	0.045	1160
GSE14520	hsa00310	Lysine degradation	49	(0.575)	(1.770)	0.016	0.071	0.045	663
GSE14520	hsa00330	Arginine and proline metabolism	38	(0.582)	(1.735)	0.017	0.071	0.045	1260
GSE14520	hsa02010	ABC transporters	37	(0.597)	(1.772)	0.016	0.071	0.045	1603
GSE14520	hsa00270	Cysteine and methionine metabolism	43	(0.607)	(1.842)	0.016	0.071	0.045	604
GSE14520	hsa01212	Fatty acid metabolism	47	(0.611)	(1.855)	0.016	0.071	0.045	1766
GSE14520	hsa00250	Alanine, aspartate and glutamate metabolism	28	(0.624)	(1.680)	0.020	0.071	0.045	751
GSE14520	hsa00790	Folate biosynthesis	22	(0.642)	(1.616)	0.038	0.099	0.063	1494
GSE14520	hsa00760	Nicotinate and nicotinamide metabolism	25	(0.642)	(1.676)	0.036	0.097	0.062	1601
GSE14520	hsa00983	Drug metabolism - other enzymes	54	(0.642)	(1.940)	0.018	0.071	0.045	464
GSE14520	hsa00620	Pyruvate metabolism	34	(0.661)	(1.876)	0.018	0.071	0.045	1035
GSE14520	hsa00590	Arachidonic acid metabolism	48	(0.681)	(2.084)	0.016	0.071	0.045	990
GSE14520	hsa03320	PPAR signaling pathway	66	(0.685)	(2.194)	0.017	0.071	0.045	795
GSE14520	hsa00020	Citrate cycle (TCA cycle)	29	(0.690)	(1.902)	0.020	0.071	0.045	885
GSE14520	hsa00860	Porphyrin and chlorophyll metabolism	25	(0.702)	(1.834)	0.018	0.071	0.045	425
GSE14520	hsa00040	Pentose and glucuronate interconversions	17	(0.730)	(1.716)	0.019	0.071	0.045	444
GSE14520	hsa04146	Peroxisome	71	(0.736)	(2.383)	0.016	0.071	0.045	1915
GSE14520	hsa00640	Propanoate metabolism	30	(0.755)	(2.128)	0.019	0.071	0.045	1069
GSE14520	hsa00630	Glyoxylate and dicarboxylate metabolism	24	(0.789)	(2.044)	0.019	0.071	0.045	656
GSE14520	hsa00260	Glycine, serine and threonine metabolism	33	(0.803)	(2.315)	0.018	0.071	0.045	656
GSE14520	hsa00410	beta-Alanine metabolism	28	(0.813)	(2.186)	0.020	0.071	0.045	1260
GSE14520	hsa00220	Arginine biosynthesis	17	(0.814)	(1.915)	0.019	0.071	0.045	580
GSE14520	hsa00071	Fatty acid degradation	40	(0.816)	(2.396)	0.017	0.071	0.045	797
GSE14520	hsa00982	Drug metabolism - cytochrome P450	49	(0.819)	(2.520)	0.016	0.071	0.045	955
GSE14520	hsa00980	Metabolism of xenobiotics by cytochrome P450	51	(0.824)	(2.506)	0.017	0.071	0.045	464
GSE14520	hsa00140	Steroid hormone biosynthesis	43	(0.824)	(2.500)	0.016	0.071	0.045	425
GSE14520	hsa00360	Phenylalanine metabolism	15	(0.827)	(1.912)	0.017	0.071	0.045	818
GSE14520	hsa00350	Tyrosine metabolism	32	(0.832)	(2.429)	0.018	0.071	0.045	1029
GSE14520	hsa00053	Ascorbate and aldarate metabolism	12	(0.834)	(1.852)	0.018	0.071	0.045	1035
GSE14520	hsa00591	Linoleic acid metabolism	20	(0.834)	(2.029)	0.021	0.071	0.045	990
GSE14520	hsa00280	Valine, leucine and isoleucine degradation	42	(0.844)	(2.547)	0.016	0.071	0.045	1064

S13. The KEGG pathway analysis of Hypoxia-TME subgroups in HBV-related HCC cohorts

GSE14520	hsa00340	Histidine metabolism	18	(0.851)	(2.035)	0.019	0.071	0.045	1260
GSE14520	hsa00650	Butanoate metabolism	23	(0.852)	(2.166)	0.019	0.071	0.045	797
GSE14520	hsa00380	Tryptophan metabolism	34	(0.858)	(2.436)	0.018	0.071	0.045	663
GSE14520	hsa00830	Retinol metabolism	39	(0.881)	(2.599)	0.017	0.071	0.045	782
GSE14520	hsa00120	Primary bile acid biosynthesis	15	(0.887)	(2.050)	0.017	0.071	0.045	275
		Hypoxia-TME score low risk vs others							
	ID	**Description**	**setSize**	**enrichmentScore**	**NES**	**pvalue**	**p.adjust**	**qvalues**	**rank**
GSE14520	hsa00120	Primary bile acid biosynthesis	15	0.903	2.192	0.022	0.083	0.058	572
GSE14520	hsa00380	Tryptophan metabolism	34	0.891	2.509	0.020	0.083	0.058	809
GSE14520	hsa00830	Retinol metabolism	39	0.867	2.457	0.020	0.083	0.058	952
GSE14520	hsa00071	Fatty acid degradation	40	0.864	2.458	0.019	0.083	0.058	809
GSE14520	hsa00220	Arginine biosynthesis	17	0.846	2.147	0.020	0.083	0.058	1282
GSE14520	hsa00591	Linoleic acid metabolism	20	0.839	2.139	0.021	0.083	0.058	219
GSE14520	hsa00140	Steroid hormone biosynthesis	43	0.836	2.439	0.018	0.083	0.058	474
GSE14520	hsa00260	Glycine, serine and threonine metabolism	33	0.834	2.331	0.020	0.083	0.058	528
GSE14520	hsa00280	Valine, leucine and isoleucine degradation	42	0.833	2.386	0.019	0.083	0.058	1277
GSE14520	hsa00053	Ascorbate and aldarate metabolism	12	0.833	1.882	0.026	0.088	0.061	789
GSE14520	hsa00982	Drug metabolism - cytochrome P450	49	0.832	2.467	0.020	0.083	0.058	1130
GSE14520	hsa00340	Histidine metabolism	18	0.828	2.099	0.020	0.083	0.058	789
GSE14520	hsa00350	Tyrosine metabolism	32	0.828	2.320	0.020	0.083	0.058	569
GSE14520	hsa00980	Metabolism of xenobiotics by cytochrome P450	51	0.828	2.415	0.020	0.083	0.058	1130
GSE14520	hsa00650	Butanoate metabolism	23	0.822	2.165	0.020	0.083	0.058	929
GSE14520	hsa00630	Glyoxylate and dicarboxylate metabolism	24	0.822	2.144	0.021	0.083	0.058	535
GSE14520	hsa00410	beta-Alanine metabolism	28	0.816	2.229	0.020	0.083	0.058	1232
GSE14520	hsa00640	Propanoate metabolism	30	0.794	2.163	0.020	0.083	0.058	890
GSE14520	hsa00040	Pentose and glucuronate interconversions	17	0.790	2.006	0.020	0.083	0.058	584
GSE14520	hsa00360	Phenylalanine metabolism	15	0.790	1.918	0.022	0.083	0.058	1232
GSE14520	hsa04146	Peroxisome	71	0.767	2.366	0.019	0.083	0.058	1512
GSE14520	hsa00590	Arachidonic acid metabolism	48	0.712	2.159	0.019	0.083	0.058	456
GSE14520	hsa00790	Folate biosynthesis	22	0.702	1.828	0.020	0.083	0.058	1405
GSE14520	hsa00020	Citrate cycle (TCA cycle)	29	0.699	1.916	0.020	0.083	0.058	1339
GSE14520	hsa03320	PPAR signaling pathway	66	0.690	2.098	0.019	0.083	0.058	799
GSE14520	hsa01212	Fatty acid metabolism	47	0.667	2.002	0.019	0.083	0.058	809
GSE14520	hsa00620	Pyruvate metabolism	34	0.663	1.867	0.020	0.083	0.058	789
GSE14520	hsa00983	Drug metabolism - other enzymes	54	0.653	1.973	0.019	0.083	0.058	1230
GSE14520	hsa00561	Glycerolipid metabolism	46	0.641	1.931	0.018	0.083	0.058	1501
GSE14520	hsa00270	Cysteine and methionine metabolism	43	0.635	1.853	0.018	0.083	0.058	379
GSE14520	hsa00860	Porphyrin and chlorophyll metabolism	25	0.633	1.654	0.022	0.083	0.058	552
GSE14520	hsa02010	ABC transporters	37	0.629	1.809	0.020	0.083	0.058	723
GSE14520	hsa00250	Alanine, aspartate and glutamate metabolism	28	0.622	1.697	0.020	0.083	0.058	1282
GSE14520	hsa00310	Lysine degradation	49	0.610	1.808	0.020	0.083	0.058	1051
GSE14520	hsa00330	Arginine and proline metabolism	38	0.596	1.723	0.019	0.083	0.058	1080
GSE14520	hsa00010	Glycolysis / Gluconeogenesis	60	0.566	1.700	0.020	0.083	0.058	974
GSE14520	hsa01200	Carbon metabolism	105	0.534	1.730	0.018	0.083	0.058	1080
GSE14520	hsa04310	Wnt signaling pathway	131	(0.416)	(1.475)	0.023	0.083	0.058	2528
GSE14520	hsa04218	Cellular senescence	145	(0.449)	(1.635)	0.022	0.083	0.058	1479
GSE14520	hsa04390	Hippo signaling pathway	130	(0.468)	(1.652)	0.023	0.083	0.058	3150
GSE14520	hsa04120	Ubiquitin mediated proteolysis	116	(0.471)	(1.628)	0.023	0.083	0.058	2673
GSE14520	hsa03013	RNA transport	127	(0.568)	(1.986)	0.025	0.085	0.059	2911
GSE14520	hsa03010	Ribosome	99	(0.569)	(1.912)	0.024	0.083	0.058	3324
GSE14520	hsa03040	Spliceosome	102	(0.638)	(2.209)	0.022	0.083	0.058	3349
GSE14520	hsa03430	Mismatch repair	22	(0.682)	(1.719)	0.020	0.083	0.058	1945
GSE14520	hsa04110	Cell cycle	114	(0.683)	(2.323)	0.024	0.083	0.058	2065
GSE14520	hsa03030	DNA replication	34	(0.747)	(2.049)	0.019	0.083	0.058	1945

		Hypoxia-TME score high risk vs others					

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	ID	Description	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalues	rank
Gao et al	hsa03030	DNA replication	22	0.862	2.475	0.025	0.080	0.048	351
Gao et al	hsa03430	Mismatch repair	16	0.784	2.087	0.026	0.080	0.048	758
Gao et al	hsa04080	Neuroactive ligand-receptor	13	0.703	1.928	0.025	0.080	0.048	892
Gao et al	hsa03410	Base excision repair	17	0.692	1.911	0.024	0.080	0.048	1205
Gao et al	hsa03420	Nucleotide excision repair	33	0.629	2.114	0.027	0.080	0.048	1777
Gao et al	hsa03022	Basal transcription factors	27	0.611	1.899	0.023	0.080	0.048	1997
Gao et al	hsa04110	Cell cycle	58	0.602	2.285	0.027	0.080	0.048	1426
Gao et al	hsa03020	RNA polymerase	20	0.591	1.702	0.025	0.080	0.048	2292
Gao et al	hsa03008	Ribosome biogenesis in eukaryotes	61	0.566	2.194	0.027	0.080	0.048	2006
Gao et al	hsa03040	Spliceosome	114	0.548	2.297	0.026	0.080	0.048	2395
Gao et al	hsa03013	RNA transport	116	0.521	2.180	0.026	0.080	0.048	2145
Gao et al	hsa03015	mRNA surveillance pathway	63	0.460	1.729	0.029	0.080	0.048	2128
Gao et al	hsa04066	HIF-1 signaling pathway	65	0.460	1.761	0.027	0.080	0.048	610
Gao et al	hsa04145	Phagosome	95	0.410	1.691	0.027	0.080	0.048	1804
Gao et al	hsa03010	Ribosome	115	0.381	1.593	0.026	0.080	0.048	2872
Gao et al	hsa00190	Oxidative phosphorylation	83	(0.365)	(1.417)	0.029	0.080	0.048	2163
Gao et al	hsa01200	Carbon metabolism	105	(0.434)	(1.695)	0.016	0.077	0.047	985
Gao et al	hsa00250	Alanine, aspartate and glutamate metabolism	28	(0.489)	(1.486)	0.032	0.080	0.048	599
Gao et al	hsa00760	Nicotinate and nicotinamide metabolism	27	(0.517)	(1.531)	0.034	0.084	0.051	1146
Gao et al	hsa00330	Arginine and proline metabolism	33	(0.524)	(1.655)	0.031	0.080	0.048	852
Gao et al	hsa00970	Aminoacyl-tRNA biosynthesis	24	(0.544)	(1.621)	0.032	0.080	0.048	2034
Gao et al	hsa03050	Proteasome	41	(0.545)	(1.738)	0.016	0.077	0.047	2184
Gao et al	hsa00620	Pyruvate metabolism	34	(0.575)	(1.795)	0.032	0.080	0.048	896
Gao et al	hsa00590	Arachidonic acid metabolism	29	(0.584)	(1.786)	0.031	0.080	0.048	597
Gao et al	hsa00983	Drug metabolism - other enzymes	59	(0.591)	(2.103)	0.015	0.077	0.047	497
Gao et al	hsa03320	PPAR signaling pathway	48	(0.597)	(2.022)	0.015	0.077	0.047	796
Gao et al	hsa01212	Fatty acid metabolism	40	(0.609)	(1.911)	0.016	0.077	0.047	857
Gao et al	hsa00561	Glycerolipid metabolism	30	(0.611)	(1.893)	0.016	0.077	0.047	1022
Gao et al	hsa00670	One carbon pool by folate	14	(0.632)	(1.596)	0.030	0.080	0.048	959
Gao et al	hsa00260	Glycine, serine and threonine metabolism	35	(0.633)	(2.013)	0.016	0.077	0.047	959
Gao et al	hsa00062	Fatty acid elongation	16	(0.635)	(1.663)	0.031	0.080	0.048	791
Gao et al	hsa00310	Lysine degradation	34	(0.647)	(2.017)	0.016	0.077	0.047	849
Gao et al	hsa00020	Citrate cycle (TCA cycle)	28	(0.661)	(2.008)	0.016	0.077	0.047	1365
Gao et al	hsa00360	Phenylalanine metabolism	15	(0.674)	(1.706)	0.016	0.077	0.047	664
Gao et al	hsa00340	Histidine metabolism	18	(0.682)	(1.808)	0.018	0.077	0.047	772
Gao et al	hsa00280	Valine, leucine and isoleucine degradation	45	(0.683)	(2.217)	0.016	0.077	0.047	849
Gao et al	hsa00450	Selenocompound metabolism	14	(0.702)	(1.772)	0.015	0.077	0.047	966
Gao et al	hsa00220	Arginine biosynthesis	17	(0.707)	(1.864)	0.016	0.077	0.047	563
Gao et al	hsa00640	Propanoate metabolism	30	(0.716)	(2.218)	0.016	0.077	0.047	985
Gao et al	hsa00920	Sulfur metabolism	10	(0.718)	(1.697)	0.031	0.080	0.048	1123
Gao et al	hsa02010	ABC transporters	25	(0.723)	(2.156)	0.016	0.077	0.047	976
Gao et al	hsa00630	Glyoxylate and dicarboxylate metabolism	29	(0.732)	(2.239)	0.016	0.077	0.047	1087
Gao et al	hsa00860	Porphyrin and chlorophyll metabolism	29	(0.736)	(2.250)	0.016	0.077	0.047	827
Gao et al	hsa04146	Peroxisome	72	(0.741)	(2.790)	0.015	0.077	0.047	981
Gao et al	hsa00350	Tyrosine metabolism	25	(0.751)	(2.240)	0.016	0.077	0.047	802
Gao et al	hsa00650	Butanoate metabolism	22	(0.754)	(2.173)	0.016	0.077	0.047	547
Gao et al	hsa00071	Fatty acid degradation	38	(0.772)	(2.506)	0.016	0.077	0.047	857
Gao et al	hsa00380	Tryptophan metabolism	32	(0.783)	(2.488)	0.015	0.077	0.047	849
Gao et al	hsa00980	Metabolism of xenobiotics by cytochrome P450	51	(0.825)	(2.802)	0.016	0.077	0.047	710
Gao et al	hsa00830	Retinol metabolism	39	(0.828)	(2.599)	0.017	0.077	0.047	580
Gao et al	hsa00982	Drug metabolism - cytochrome P450	50	(0.828)	(2.806)	0.015	0.077	0.047	494
Gao et al	hsa00410	beta-Alanine metabolism	23	(0.831)	(2.440)	0.016	0.077	0.047	796
Gao et al	hsa00140	Steroid hormone biosynthesis	34	(0.837)	(2.610)	0.016	0.077	0.047	517
Gao et al	hsa00053	Ascorbate and aldarate metabolism	17	(0.838)	(2.209)	0.016	0.077	0.047	702
Gao et al	hsa00040	Pentose and glucuronate interconversions	21	(0.840)	(2.326)	0.017	0.077	0.047	638
Gao et al	hsa00591	Linoleic acid metabolism	10	(0.847)	(2.001)	0.016	0.077	0.047	476
Gao et al	hsa00120	Primary bile acid biosynthesis	15	(0.909)	(2.303)	0.016	0.077	0.047	517

S13. The KEGG pathway analysis of Hypoxia-TME subgroups in HBV-related HCC cohorts

		Hypoxia-TME score low risk vs others							
	ID	**Description**	**setSize**	**enrichmentScore**	**NES**	**pvalue**	**p.adjust**	**qvalues**	**rank**
Gao et al	hsa00120	Primary bile acid biosynthesis	15	0.886	2.458	0.018	0.068	0.041	693
Gao et al	hsa00071	Fatty acid degradation	38	0.857	2.789	0.018	0.068	0.041	615
Gao et al	hsa00830	Retinol metabolism	39	0.850	2.787	0.018	0.068	0.041	541
Gao et al	hsa00053	Ascorbate and aldarate metabolism	17	0.846	2.340	0.019	0.068	0.041	794
Gao et al	hsa00410	beta-Alanine metabolism	23	0.841	2.503	0.020	0.068	0.041	615
Gao et al	hsa00380	Tryptophan metabolism	32	0.815	2.622	0.018	0.068	0.041	814
Gao et al	hsa00140	Steroid hormone biosynthesis	34	0.802	2.503	0.019	0.068	0.041	946
Gao et al	hsa00982	Drug metabolism - cytochrome P450	50	0.797	2.710	0.017	0.068	0.041	474
Gao et al	hsa00591	Linoleic acid metabolism	10	0.790	1.901	0.018	0.068	0.041	607
Gao et al	hsa00020	Citrate cycle (TCA cycle)	28	0.789	2.401	0.020	0.068	0.041	948
Gao et al	hsa00040	Pentose and glucuronate interconversions	21	0.788	2.265	0.021	0.068	0.041	350
Gao et al	hsa04146	Peroxisome	72	0.782	2.782	0.016	0.068	0.041	912
Gao et al	hsa00650	Butanoate metabolism	22	0.763	2.243	0.020	0.068	0.041	463
Gao et al	hsa00980	Metabolism of xenobiotics by cytochrome P450	51	0.750	2.577	0.016	0.068	0.041	794
Gao et al	hsa00630	Glyoxylate and dicarboxylate metabolism	29	0.750	2.282	0.020	0.068	0.041	1243
Gao et al	hsa00640	Propanoate metabolism	30	0.748	2.310	0.019	0.068	0.041	509
Gao et al	hsa00220	Arginine biosynthesis	17	0.745	2.061	0.019	0.068	0.041	627
Gao et al	hsa00280	Valine, leucine and isoleucine degradation	45	0.741	2.467	0.016	0.068	0.041	519
Gao et al	hsa01212	Fatty acid metabolism	40	0.737	2.417	0.018	0.068	0.041	502
Gao et al	hsa02010	ABC transporters	25	0.729	2.156	0.020	0.068	0.041	961
Gao et al	hsa00340	Histidine metabolism	18	0.726	1.971	0.020	0.068	0.041	1120
Gao et al	hsa00062	Fatty acid elongation	16	0.719	2.008	0.018	0.068	0.041	493
Gao et al	hsa00350	Tyrosine metabolism	25	0.717	2.119	0.020	0.068	0.041	663
Gao et al	hsa00860	Porphyrin and chlorophyll metabolism	29	0.715	2.178	0.020	0.068	0.041	813
Gao et al	hsa00970	Aminoacyl-tRNA biosynthesis	24	0.688	2.051	0.020	0.068	0.041	1359
Gao et al	hsa00790	Folate biosynthesis	16	0.687	1.919	0.018	0.068	0.041	1414
Gao et al	hsa00360	Phenylalanine metabolism	15	0.683	1.893	0.018	0.068	0.041	172
Gao et al	hsa00190	Oxidative phosphorylation	83	0.666	2.434	0.016	0.068	0.041	1431
Gao et al	hsa00450	Selenocompound metabolism	14	0.659	1.796	0.034	0.084	0.050	1359
Gao et al	hsa00260	Glycine, serine and threonine metabolism	35	0.657	2.080	0.019	0.068	0.041	695
Gao et al	hsa01040	Biosynthesis of unsaturated fatty	15	0.650	1.802	0.018	0.068	0.041	263
Gao et al	hsa03320	PPAR signaling pathway	48	0.641	2.203	0.016	0.068	0.041	502
Gao et al	hsa00561	Glycerolipid metabolism	30	0.635	1.962	0.019	0.068	0.041	1108
Gao et al	hsa01210	2-Oxocarboxylic acid metabolism	17	0.626	1.731	0.019	0.068	0.041	956
Gao et al	hsa00620	Pyruvate metabolism	34	0.614	1.918	0.019	0.068	0.041	728
Gao et al	hsa00310	Lysine degradation	34	0.613	1.915	0.019	0.068	0.041	615
Gao et al	hsa00061	Fatty acid biosynthesis	14	0.600	1.635	0.034	0.084	0.050	502
Gao et al	hsa04260	Cardiac muscle contraction	27	0.592	1.763	0.021	0.068	0.041	885
Gao et al	hsa00590	Arachidonic acid metabolism	29	0.561	1.709	0.020	0.068	0.041	751
Gao et al	hsa00250	Alanine, aspartate and glutamate metabolism	28	0.522	1.590	0.040	0.096	0.057	569
Gao et al	hsa00983	Drug metabolism - other enzymes	59	0.518	1.826	0.015	0.068	0.041	672
Gao et al	hsa01200	Carbon metabolism	105	0.501	1.914	0.015	0.068	0.041	841
Gao et al	hsa00330	Arginine and proline metabolism	33	0.475	1.505	0.038	0.092	0.055	844
Gao et al	hsa00230	Purine metabolism	70	(0.384)	(1.478)	0.024	0.073	0.044	626
Gao et al	hsa04015	Rap1 signaling pathway	88	(0.414)	(1.620)	0.026	0.074	0.044	688
Gao et al	hsa04145	Phagosome	95	(0.424)	(1.688)	0.026	0.074	0.044	1364
Gao et al	hsa04512	ECM-receptor interaction	46	(0.440)	(1.545)	0.025	0.073	0.044	631
Gao et al	hsa03015	mRNA surveillance pathway	63	(0.459)	(1.708)	0.027	0.075	0.045	2434
Gao et al	hsa03018	RNA degradation	52	(0.469)	(1.665)	0.025	0.073	0.044	2390
Gao et al	hsa04066	HIF-1 signaling pathway	65	(0.489)	(1.814)	0.025	0.073	0.044	782
Gao et al	hsa03013	RNA transport	116	(0.537)	(2.175)	0.033	0.084	0.050	2068
Gao et al	hsa03040	Spliceosome	114	(0.543)	(2.217)	0.032	0.084	0.050	2433
Gao et al	hsa03022	Basal transcription factors	27	(0.601)	(1.903)	0.019	0.068	0.041	2346
Gao et al	hsa03420	Nucleotide excision repair	33	(0.611)	(2.021)	0.020	0.068	0.041	1668
Gao et al	hsa03008	Ribosome biogenesis in eukaryotes	61	(0.624)	(2.272)	0.028	0.075	0.045	1979
Gao et al	hsa04110	Cell cycle	58	(0.627)	(2.198)	0.029	0.078	0.047	1141
Gao et al	hsa03410	Base excision repair	17	(0.729)	(1.976)	0.020	0.068	0.041	987

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Gao et al	hsa03430	Mismatch repair	16	(0.733)	(1.923)	0.022	0.070	0.042	333
Gao et al	hsa03030	DNA replication	22	(0.843)	(2.472)	0.019	0.068	0.041	456
		Hypoxia-TME score high risk vs others							
	ID	**Description**	**setSize**	**enrichmentScore**	**NES**	**pvalue**	**p.adjust**	**qvalues**	**rank**
TCGA	hsa03010	Ribosome	134	0.794	2.741	0.032	0.095	0.061	1696
TCGA	hsa03030	DNA replication	36	0.724	2.018	0.023	0.093	0.060	3217
TCGA	hsa04110	Cell cycle	124	0.664	2.253	0.033	0.095	0.061	2140
TCGA	hsa03040	Spliceosome	131	0.649	2.219	0.034	0.095	0.061	3470
TCGA	hsa03440	Homologous recombination	37	0.555	1.565	0.022	0.093	0.060	2520
TCGA	hsa03008	Ribosome biogenesis in eukaryotes	72	0.543	1.726	0.030	0.095	0.061	3704
TCGA	hsa03460	Fanconi anemia pathway	49	0.538	1.559	0.029	0.095	0.061	2943
TCGA	hsa03015	mRNA surveillance pathway	90	0.528	1.702	0.034	0.095	0.061	4521
TCGA	hsa03013	RNA transport	157	0.527	1.806	0.033	0.095	0.061	4333
TCGA	hsa04390	Hippo signaling pathway	154	0.494	1.703	0.031	0.095	0.061	3672
TCGA	hsa04260	Cardiac muscle contraction	82	0.484	1.512	0.034	0.095	0.061	1002
TCGA	hsa04512	ECM-receptor interaction	87	0.470	1.530	0.032	0.095	0.061	1392
TCGA	hsa04114	Oocyte meiosis	123	0.445	1.513	0.032	0.095	0.061	2055
TCGA	hsa03018	RNA degradation	75	0.436	1.397	0.029	0.095	0.061	4451
TCGA	hsa04218	Cellular senescence	157	0.436	1.493	0.033	0.095	0.061	2406
TCGA	hsa04310	Wnt signaling pathway	158	0.410	1.400	0.034	0.095	0.061	3656
TCGA	hsa04144	Endocytosis	237	0.397	1.453	0.034	0.095	0.061	4250
TCGA	hsa04510	Focal adhesion	196	0.380	1.353	0.037	0.098	0.063	2484
TCGA	hsa04152	AMPK signaling pathway	120	(0.519)	(1.577)	0.028	0.095	0.061	1623
TCGA	hsa01230	Biosynthesis of amino acids	72	(0.600)	(1.719)	0.014	0.078	0.050	1290
TCGA	hsa00010	Glycolysis / Gluconeogenesis	67	(0.620)	(1.764)	0.014	0.078	0.050	1633
TCGA	hsa00561	Glycerolipid metabolism	52	(0.621)	(1.638)	0.029	0.095	0.061	2708
TCGA	hsa01200	Carbon metabolism	114	(0.621)	(1.917)	0.013	0.078	0.050	1403
TCGA	hsa00310	Lysine degradation	56	(0.630)	(1.713)	0.014	0.078	0.050	1911
TCGA	hsa01212	Fatty acid metabolism	52	(0.636)	(1.679)	0.015	0.078	0.050	2359
TCGA	hsa00330	Arginine and proline metabolism	48	(0.642)	(1.676)	0.015	0.078	0.050	1512
TCGA	hsa00760	Nicotinate and nicotinamide metabolism	37	(0.646)	(1.560)	0.035	0.095	0.061	1877
TCGA	hsa00592	alpha-Linolenic acid metabolism	24	(0.659)	(1.550)	0.032	0.095	0.061	1558
TCGA	hsa00590	Arachidonic acid metabolism	61	(0.665)	(1.814)	0.015	0.078	0.050	1030
TCGA	hsa02010	ABC transporters	45	(0.677)	(1.764)	0.015	0.078	0.050	2367
TCGA	hsa00983	Drug metabolism - other enzymes	77	(0.690)	(1.997)	0.014	0.078	0.050	1266
TCGA	hsa01210	2-Oxocarboxylic acid metabolism	18	(0.704)	(1.553)	0.033	0.095	0.061	953
TCGA	hsa00250	Alanine, aspartate and glutamate metabolism	34	(0.706)	(1.729)	0.018	0.079	0.051	1478
TCGA	hsa00860	Porphyrin and chlorophyll metabolism	41	(0.707)	(1.784)	0.016	0.078	0.050	1314
TCGA	hsa00270	Cysteine and methionine metabolism	46	(0.708)	(1.829)	0.015	0.078	0.050	1255
TCGA	hsa00020	Citrate cycle (TCA cycle)	30	(0.710)	(1.729)	0.017	0.078	0.050	2992
TCGA	hsa00040	Pentose and glucuronate interconversions	33	(0.728)	(1.790)	0.017	0.078	0.050	1510
TCGA	hsa00620	Pyruvate metabolism	39	(0.737)	(1.827)	0.017	0.078	0.050	1383
TCGA	hsa04146	Peroxisome	82	(0.764)	(2.263)	0.014	0.078	0.050	2388
TCGA	hsa03320	PPAR signaling pathway	76	(0.770)	(2.219)	0.014	0.078	0.050	1428
TCGA	hsa00410	beta-Alanine metabolism	31	(0.804)	(1.966)	0.017	0.078	0.050	1512
TCGA	hsa00630	Glyoxylate and dicarboxylate metabolism	29	(0.805)	(1.969)	0.016	0.078	0.050	1075
TCGA	hsa00640	Propanoate metabolism	33	(0.812)	(1.994)	0.017	0.078	0.050	1058
TCGA	hsa00053	Ascorbate and aldarate metabolism	27	(0.816)	(1.954)	0.016	0.078	0.050	1358
TCGA	hsa00360	Phenylalanine metabolism	17	(0.818)	(1.807)	0.016	0.078	0.050	953
TCGA	hsa00140	Steroid hormone biosynthesis	59	(0.822)	(2.231)	0.015	0.078	0.050	1001
TCGA	hsa00220	Arginine biosynthesis	21	(0.830)	(1.886)	0.015	0.078	0.050	953
TCGA	hsa00280	Valine, leucine and isoleucine degradation	47	(0.836)	(2.186)	0.015	0.078	0.050	1421
TCGA	hsa00591	Linoleic acid metabolism	28	(0.836)	(2.029)	0.016	0.078	0.050	1558
TCGA	hsa00980	Metabolism of xenobiotics by cytochrome P450	71	(0.837)	(2.385)	0.014	0.078	0.050	1001
TCGA	hsa00350	Tyrosine metabolism	36	(0.841)	(2.050)	0.017	0.078	0.050	1083
TCGA	hsa00982	Drug metabolism - cytochrome P450	67	(0.844)	(2.401)	0.014	0.078	0.050	1001
TCGA	hsa00260	Glycine, serine and threonine metabolism	38	(0.846)	(2.067)	0.017	0.078	0.050	1626

S13. The KEGG pathway analysis of Hypoxia-TME subgroups in HBV-related HCC cohorts

TCGA	hsa00340	Histidine metabolism	22	(0.848)	(1.982)	0.015	0.078	0.050	1717
TCGA	hsa00071	Fatty acid degradation	44	(0.851)	(2.209)	0.015	0.078	0.050	1871
TCGA	hsa00380	Tryptophan metabolism	40	(0.857)	(2.140)	0.016	0.078	0.050	1358
TCGA	hsa00072	Synthesis and degradation of ketone bodies	10	(0.869)	(1.612)	0.019	0.083	0.053	1785
TCGA	hsa00830	Retinol metabolism	65	(0.874)	(2.453)	0.015	0.078	0.050	1001
TCGA	hsa00650	Butanoate metabolism	28	(0.879)	(2.135)	0.016	0.078	0.050	1352
TCGA	hsa00120	Primary bile acid biosynthesis	17	(0.924)	(2.041)	0.016	0.078	0.050	918
		Hypoxia-TME score low risk vs others							
	ID	**Description**	**setSize**	**enrichmentScore**	**NES**	**pvalue**	**p.adjust**	**qvalues**	**rank**
TCGA	hsa00120	Primary bile acid biosynthesis	17	0.920	2.084	0.018	0.071	0.044	880
TCGA	hsa00830	Retinol metabolism	65	0.887	2.497	0.018	0.071	0.044	748
TCGA	hsa00650	Butanoate metabolism	28	0.877	2.123	0.019	0.071	0.044	1147
TCGA	hsa00071	Fatty acid degradation	44	0.874	2.376	0.017	0.071	0.044	1365
TCGA	hsa00072	Synthesis and degradation of ketone bodies	10	0.868	1.742	0.018	0.071	0.044	1147
TCGA	hsa00380	Tryptophan metabolism	40	0.868	2.262	0.018	0.071	0.044	1156
TCGA	hsa00982	Drug metabolism - cytochrome P450	67	0.867	2.464	0.018	0.071	0.044	997
TCGA	hsa00053	Ascorbate and aldarate metabolism	27	0.865	2.129	0.018	0.071	0.044	906
TCGA	hsa00591	Linoleic acid metabolism	28	0.865	2.093	0.019	0.071	0.044	858
TCGA	hsa00350	Tyrosine metabolism	36	0.854	2.187	0.018	0.071	0.044	1218
TCGA	hsa00980	Metabolism of xenobiotics by cytochrome P450	71	0.853	2.454	0.017	0.071	0.044	997
TCGA	hsa00140	Steroid hormone biosynthesis	59	0.850	2.365	0.016	0.071	0.044	880
TCGA	hsa00260	Glycine, serine and threonine metabolism	38	0.843	2.184	0.018	0.071	0.044	1735
TCGA	hsa00340	Histidine metabolism	22	0.841	1.948	0.019	0.071	0.044	1189
TCGA	hsa00220	Arginine biosynthesis	21	0.835	1.922	0.019	0.071	0.044	1814
TCGA	hsa00630	Glyoxylate and dicarboxylate metabolism	29	0.826	2.024	0.019	0.071	0.044	1131
TCGA	hsa00280	Valine, leucine and isoleucine degradation	47	0.816	2.194	0.017	0.071	0.044	1588
TCGA	hsa00410	beta-Alanine metabolism	31	0.813	2.033	0.018	0.071	0.044	1535
TCGA	hsa00640	Propanoate metabolism	33	0.810	2.031	0.018	0.071	0.044	1397
TCGA	hsa00360	Phenylalanine metabolism	17	0.809	1.834	0.018	0.071	0.044	1218
TCGA	hsa00040	Pentose and glucuronate interconversions	33	0.804	2.018	0.018	0.071	0.044	749
TCGA	hsa03320	PPAR signaling pathway	76	0.799	2.334	0.017	0.071	0.044	1147
TCGA	hsa04146	Peroxisome	82	0.759	2.262	0.017	0.071	0.044	1829
TCGA	hsa00790	Folate biosynthesis	24	0.758	1.785	0.019	0.071	0.044	2018
TCGA	hsa00620	Pyruvate metabolism	39	0.738	1.911	0.018	0.071	0.044	1413
TCGA	hsa00860	Porphyrin and chlorophyll metabolism	41	0.720	1.888	0.018	0.071	0.044	2180
TCGA	hsa00250	Alanine, aspartate and glutamate metabolism	34	0.712	1.802	0.018	0.071	0.044	1715
TCGA	hsa00020	Citrate cycle (TCA cycle)	30	0.710	1.752	0.019	0.071	0.044	1156
TCGA	hsa00590	Arachidonic acid metabolism	61	0.707	1.985	0.017	0.071	0.044	858
TCGA	hsa00983	Drug metabolism - other enzymes	77	0.703	2.068	0.017	0.071	0.044	910
TCGA	hsa00592	alpha-Linolenic acid metabolism	24	0.701	1.651	0.019	0.071	0.044	2512
TCGA	hsa01210	2-Oxocarboxylic acid metabolism	18	0.694	1.577	0.037	0.092	0.057	797
TCGA	hsa00270	Cysteine and methionine metabolism	46	0.689	1.843	0.017	0.071	0.044	1684
TCGA	hsa00310	Lysine degradation	56	0.668	1.835	0.016	0.071	0.044	1156
TCGA	hsa01212	Fatty acid metabolism	52	0.665	1.794	0.017	0.071	0.044	1395
TCGA	hsa00561	Glycerolipid metabolism	52	0.659	1.776	0.017	0.071	0.044	2351
TCGA	hsa02010	ABC transporters	45	0.647	1.729	0.017	0.071	0.044	2896
TCGA	hsa00010	Glycolysis / Gluconeogenesis	67	0.636	1.807	0.018	0.071	0.044	1056
TCGA	hsa00330	Arginine and proline metabolism	48	0.627	1.667	0.018	0.071	0.044	2288
TCGA	hsa01200	Carbon metabolism	114	0.624	1.932	0.016	0.071	0.044	1156
TCGA	hsa00760	Nicotinate and nicotinamide metabolism	37	0.616	1.566	0.037	0.092	0.057	2400
TCGA	hsa01230	Biosynthesis of amino acids	72	0.597	1.709	0.017	0.071	0.044	797
TCGA	hsa04152	AMPK signaling pathway	120	0.516	1.603	0.016	0.071	0.044	1655
TCGA	hsa04213	Longevity regulating pathway - multiple species	62	0.513	1.456	0.033	0.085	0.053	3131
TCGA	hsa04270	Vascular smooth muscle contraction	130	0.499	1.582	0.015	0.071	0.044	2996

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TCGA	hsa04068	FoxO signaling pathway	130	0.471	1.492	0.015	0.071	0.044	2566
TCGA	hsa00564	Glycerophospholipid metabolism	89	0.456	1.368	0.033	0.085	0.053	2512
TCGA	hsa04510	Focal adhesion	196	(0.350)	(1.296)	0.029	0.079	0.049	2247
TCGA	hsa04144	Endocytosis	237	(0.353)	(1.351)	0.032	0.085	0.053	3859
TCGA	hsa04218	Cellular senescence	157	(0.404)	(1.433)	0.027	0.077	0.048	2689
TCGA	hsa04114	Oocyte meiosis	123	(0.424)	(1.394)	0.028	0.077	0.048	2049
TCGA	hsa03018	RNA degradation	75	(0.434)	(1.358)	0.023	0.073	0.045	3916
TCGA	hsa04260	Cardiac muscle contraction	82	(0.438)	(1.381)	0.023	0.073	0.045	2557
TCGA	hsa04390	Hippo signaling pathway	154	(0.466)	(1.647)	0.028	0.077	0.048	4098
TCGA	hsa04512	ECM-receptor interaction	87	(0.470)	(1.516)	0.023	0.073	0.045	2155
TCGA	hsa03460	Fanconi anemia pathway	49	(0.521)	(1.496)	0.022	0.073	0.045	2123
TCGA	hsa03013	RNA transport	157	(0.540)	(1.918)	0.027	0.077	0.048	4908
TCGA	hsa03015	mRNA surveillance pathway	90	(0.541)	(1.739)	0.023	0.073	0.045	4786
TCGA	hsa03008	Ribosome biogenesis in eukaryotes	72	(0.574)	(1.757)	0.023	0.073	0.045	3002
TCGA	hsa03440	Homologous recombination	37	(0.599)	(1.634)	0.021	0.073	0.045	5407
TCGA	hsa04110	Cell cycle	124	(0.638)	(2.120)	0.028	0.077	0.048	1999
TCGA	hsa03040	Spliceosome	131	(0.652)	(2.214)	0.029	0.079	0.049	3144
TCGA	hsa03030	DNA replication	36	(0.710)	(1.908)	0.021	0.073	0.045	3857
TCGA	hsa03010	Ribosome	134	(0.761)	(2.614)	0.028	0.077	0.048	1639

S14. Other HCC-related molecular classification gene sets signature (n=87) in the MSigDB used in current study

Signatures	Msigdb Names	Description
Andersen_good_survival	ANDERSEN_CHOLANGIOCARCINOMA_CLASS1	Genes overexpressed in cholangiocarcinoma class 1 associated with good prognosis
Andersen_poor_survival	ANDERSEN_CHOLANGIOCARCINOMA_CLASS2	Genes overexpressed in cholangiocarcinoma class 2 associated with poor prognosis.
Boyault_G123_dn	BOYAULT_LIVER_CANCER_SUBCLASS_G123_DN	Down-regulated genes in hepatocellular carcinoma (HCC) subclass G123, defined by unsupervised clustering.
Boyault_G123_up	BOYAULT_LIVER_CANCER_SUBCLASS_G123_UP	Up-regulated genes in hepatocellular carcinoma (HCC) subclass G123, defined by unsupervised clustering.
Boyault_G12_dn	BOYAULT_LIVER_CANCER_SUBCLASS_G12_DN	Down-regulated genes in hepatocellular carcinoma (HCC) subclass G12, defined by unsupervised clustering
Boyault_G12_up	BOYAULT_LIVER_CANCER_SUBCLASS_G12_UP	Up-regulated genes in hepatocellular carcinoma (HCC) subclass G12, defined by unsupervised clustering
Boyault_G1_dn	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN	Down-regulated genes in hepatocellular carcinoma (HCC) subclass G1, defined by unsupervised clustering
Boyault_G1_up	BOYAULT_LIVER_CANCER_SUBCLASS_G1_UP	Up-regulated genes in hepatocellular carcinoma (HCC) subclass G1, defined by unsupervised clustering
Boyault_G2	BOYAULT_LIVER_CANCER_SUBCLASS_G2	Genes in hepatocellular carcinoma (HCC) subclass G2, defined by unsupervised clustering.
Boyault_G23_dn	BOYAULT_LIVER_CANCER_SUBCLASS_G23_DN	Down-regulated genes in hepatocellular carcinoma (HCC) subclass G23, defined by unsupervised clustering.
Boyault_G23_up	BOYAULT_LIVER_CANCER_SUBCLASS_G23_UP	Up-regulated genes in hepatocellular carcinoma (HCC) subclass G23, defined by unsupervised clustering.
Boyault_G3_dn	BOYAULT_LIVER_CANCER_SUBCLASS_G3_DN	Down-regulated genes in hepatocellular carcinoma (HCC) subclass G3, defined by unsupervised clustering.
Boyault_G3_up	BOYAULT_LIVER_CANCER_SUBCLASS_G3_UP	Up-regulated genes in hepatocellular carcinoma (HCC) subclass G3, defined by unsupervised clustering.
Boyault_G56_dn	BOYAULT_LIVER_CANCER_SUBCLASS_G56_DN	Down-regulated genes in hepatocellular carcinoma (HCC) subclass G56, defined by unsupervised clustering.
Boyault_G56_up	BOYAULT_LIVER_CANCER_SUBCLASS_G56_UP	Up-regulated genes in hepatocellular carcinoma (HCC) subclass G56, defined by unsupervised clustering.
Boyault_G5_dn	BOYAULT_LIVER_CANCER_SUBCLASS_G5_DN	Down-regulated genes in hepatocellular carcinoma (HCC) subclass G5, defined by unsupervised clustering.
Boyault_G6_dn	BOYAULT_LIVER_CANCER_SUBCLASS_G6_DN	Down-regulated genes in hepatocellular carcinoma (HCC) subclass G6, defined by unsupervised clustering.
Boyault_G6_up	BOYAULT_LIVER_CANCER_SUBCLASS_G6_UP	Up-regulated genes in hepatocellular carcinoma (HCC) subclass G6, defined by unsupervised clustering.
Cavard_maligant	CAVARD_LIVER_CANCER_MALIGNANT_VS_BENIGN	Genes identified by subtractive hybridization comparing malignant and benign components of a hepatocellular carcinoma (HCC) in a pre-existing liver adenoma in a morphologically normal liver.
Coulouarn_TGFB1_dn	COULOUARN_TEMPORAL_TGFB1_SIGNATURE_DN	'Early-TGFB1 signature': genes overexpressed in primary hepatocytes at an early phase of TGFB1 [GeneID=7040] treatment; is associated with a less invasive phenotype.
Coulouarn_TGFB1_up	COULOUARN_TEMPORAL_TGFB1_SIGNATURE_UP	'Late-TGFB1 signature': genes overexpressed in primary hepatocytes at a late phase of TGFB1 [GeneID=7040] treatment; is associated with a more invasive phenotype.
Gho_ATF5_dn	GHO_ATF5_TARGETS_DN	Genes down-regulated in HEP3B cells (liver cancer) overexpressing ATF5 [GeneID=22809] off a plasmid vector.
Gho_ATF5_up	GHO_ATF5_TARGETS_UP	Genes up-regulated in HEP3B cells (liver cancer) overexpressing ATF5 [GeneID=22809] off a plasmid vector.
HO_vascular_invasion	HO_LIVER_CANCER_VASCULAR_INVASION	Gene expression signature of vascular invasion of hepatocellular carcinoma (HCC).
Hoshida_S1	HOSHIDA_LIVER_CANCER_SUBCLASS_S1	Genes from 'subtype S1' signature of hepatocellular carcinoma (HCC): aberrant activation of the WNT signaling pathway.
Hoshida_S2	HOSHIDA_LIVER_CANCER_SUBCLASS_S2	Genes from 'subtype S2' signature of hepatocellular carcinoma (HCC): proliferation, MYC and AKT1 [GeneID=4609;207] activation.
Hoshida_S3	HOSHIDA_LIVER_CANCER_SUBCLASS_S3	Genes from 'subtype S3' signature of hepatocellular carcinoma (HCC): hepatocyte differentiation.
Iizuka_progression_G1_G2_dn	IIZUKA_LIVER_CANCER_PROGRESSION_G1_G2_DN	Genes down-regulated during transition from G1 (well differentiated tumor, infected with HCV) to G2 (moderately differentiated tumor, infected with HCV) in the development of hepatocellular carcinoma.
Iizuka_progression__G1_G2_up	IIZUKA_LIVER_CANCER_PROGRESSION_G1_G2_UP	Genes up-regulated during transition from G1 (well differentiated tumor, infected with HCV) to G2 (moderately differentiated tumor, infected with HCV) in the development of hepatocellular carcinoma.
Iizuka_progression__G2_G3_dn	IIZUKA_LIVER_CANCER_PROGRESSION_G2_G3_DN	Genes down-regulated during transition from G2 (moderately differentiated tumor, infected with HCV) to G3 (poorly differentiated tumor, infected with HCV) in the development of hepatocellular carcinoma.

Iizuka_progression__G2_G3_up	IIZUKA_LIVER_CANCER_PROGRESSION_G2_G3_UP	Genes up-regulated during transition from G2 (moderately differentiated tumor, infected with HCV) to G3 (poorly differentiated tumor, infected with HCV) in the development of hepatocellular carcinoma.
Iizuka_progression__L0_L1_dn	IIZUKA_LIVER_CANCER_PROGRESSION_L0_L1_DN	Genes down-regulated during transition from L0 (non-tumor, not infected with HCV) to L1 (non-tumor, infected with HCV) in the development of hepatocellular carcinoma.
Iizuka_progression__L0_L1_up	IIZUKA_LIVER_CANCER_PROGRESSION_L0_L1_UP	Genes up-regulated during transition from L0 (non-tumor, not infected with HCV) to L1 (non-tumor, infected with HCV) in the development of hepatocellular carcinoma.
Iizuka_progression__L1_G1_dn	IIZUKA_LIVER_CANCER_PROGRESSION_L1_G1_DN	Genes down-regulated during transition from L1 (non-tumor, infected with HCV) to G1 (well differentiated tumor, infected with HCV) in the development of hepatocellular carcinoma.
Iizuka_progression__L1_G1_up	IIZUKA_LIVER_CANCER_PROGRESSION_L1_G1_UP	Genes up-regulated during transition from L1 (non-tumor, infected with HCV) to G1 (well differentiated tumor, infected with HCV) in the development of hepatocellular carcinoma.
Jiang_TIP30_dn	JIANG_TIP30_TARGETS_DN	Down-regulated genes in HepG2 cells (liver cancer) overexpressing an oncogenic variant of tumor suppressor TIP30 [GeneID=10553] compared to its wild type form.
Jiang_TIP30_up	JIANG_TIP30_TARGETS_UP	Up-regulated genes in HepG2 cells (liver cancer) overexpressing an oncogenic variant of tumor suppressor TIP30 [GeneID=10553] compared to its wild type form.
Kaposi_MET_dn	KAPOSI_LIVER_CANCER_MET_DN	Selected down-regulated MET [GeneID=4233] target genes from a classifier of hepatocellular carcinoma (HCC) cases; associated with poor survival.
Kaposi_MET_up	KAPOSI_LIVER_CANCER_MET_UP	Selected up-regulated MET [GeneID=4233] target genes from a classifier of hepatocellular carcinoma (HCC) cases; associated with poor survival.
Khetchoumian_TRIM24_dn	KHETCHOUMIAN_TRIM24_TARGETS_DN	Retinoic acid-responsive genes down-regulated in hepatocellular carcinoma (HCC) samples of TRIM24 [GeneID=8805] knockout mice.
Khetchoumian_TRIM24_up	KHETCHOUMIAN_TRIM24_TARGETS_UP	Retinoic acid-responsive genes up-regulated in hepatocellular carcinoma (HCC) samples of TRIM24 [GeneID=8805] knockout mice.
Kim_poor_survival_dn	KIM_LIVER_CANCER_POOR_SURVIVAL_DN	Genes under-expressed in hepatocellular carcinoma (HCC) with poor survival
Kim_poor_survival_up	KIM_LIVER_CANCER_POOR_SURVIVAL_UP	Genes over-expressed in hepatocellular carcinoma (HCC) with poor survival
Kurokawa_early_recurrence_dn	KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_DN	Genes down-regulated in hepatocellular carcinoma (HCC) with early recurrence.
Kurokawa_early_recurrence_up	KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP	Genes up-regulated in hepatocellular carcinoma (HCC) with early recurrence.
Lee_heaptoblast	LEE_LIVER_CANCER_HEPATOBLAST	Fig.5, Supplementary Fig.2 Genes overexpressed in human hepatocellular carcinoma with hepatoblast property
Lee_Survival_dn	LEE_LIVER_CANCER_SURVIVAL_DN	Genes highly expressed in hepatocellular carcinoma with poor survival.
Lee_Survival_up	LEE_LIVER_CANCER_SURVIVAL_UP	Genes highly expressed in hepatocellular carcinoma with good survival.
Liao_HAVE_SOX4	LIAO_HAVE_SOX4_BINDING_SITES	Genes up-regulated in the samples with intrahepatic metastatic hepatocellular carcinoma (HCC) vs primary HCC that also have putative binding sites for SOX4 [GeneID=6659].
Liao_metastasis	LIAO_METASTASIS	Genes up-regulated in the samples with intrahepatic metastatic hepatocellular carcinoma (HCC) vs primary HCC.
Midorikawa_amplified	MIDORIKAWA_AMPLIFIED_IN_LIVER_CANCER	Candidate genes in genomic amplification regions in hepatocellular carcinoma (HCC) samples.
Minguez_vascular_invasion_dn	MINGUEZ_LIVER_CANCER_VASCULAR_INVASION_DN	Genes under-expressed in hepatocellular carcinoma (HCC) with vascular invasion.
Minguez_vascular_invasion_up	MINGUEZ_LIVER_CANCER_VASCULAR_INVASION_UP	Genes over-expressed in hepatocellular carcinoma (HCC) with vascular invasion.
Patil_liver_cancer	PATIL_LIVER_CANCER	Genes up-regulated in hepatocellular carcinoma (HCC) compared to normal liver samples.
Roessler_metastasis_dn	ROESSLER_LIVER_CANCER_METASTASIS_DN	Genes down-regulated in liver samples containing tumor thrombi in the major branches of the portal vein at surgery (PT) compared to those from metastasis-free HCC patients (PN) at the time of surgery and at follow-up.
Roessler_metastasis_up	ROESSLER_LIVER_CANCER_METASTASIS_UP	Genes up-regulated in liver samples containing tumor thrombi in the major branches of the portal vein at surgery (PT) compared to those from metastasis-free HCC patients (PN) at the time of surgery and at follow-up.
Sakai_chronic_hepatitis_dn	SAKAI_CHRONIC_HEPATITIS_VS_LIVER_CANCER_DN	Selected genes down-regulated in peripheral blood monocytes (PBMC) of patients with hepatocellular carcinoma (HCC) compared to those with chronic hepatitis.
Sakai_chronic_hepatitis_up	SAKAI_CHRONIC_HEPATITIS_VS_LIVER_CANCER_UP	Selected genes up-regulated in peripheral blood monocytes (PBMC) of patients with hepatocellular carcinoma (HCC) compared to those with chronic hepatitis.
Sakai_monocytes_dn	SAKAI_TUMOR_INFILTRATING_MONOCYTES_DN	Selected genes down-regulated in inflammatory monocytes infiltrating hepatocellular carcinoma (HCC).
Sakai_monocytes_up	SAKAI_TUMOR_INFILTRATING_MONOCYTES_UP	Selected genes up-regulated in inflammatory monocytes infiltrating hepatocellular carcinoma (HCC).
SHETH_VS_TXNIP_LOSS_PAM1	SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM1	Cluster PAM1: genes up-regulated in hepatocellular carcinoma (HCC) vs normal liver tissue from mice deficient for TXNIP [GeneID=10628].
SHETH_VS_TXNIP_LOSS_PAM2	SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM2	Cluster PAM2: genes up-regulated in hepatocellular carcinoma (HCC) vs normal liver tissue from mice deficient for TXNIP [GeneID=10628].

SHETH_VS_TXNIP_LOSS_PAM3	SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM3	Cluster PAM3: genes most highly up-regulated in hepatocellular carcinoma (HCC) vs normal liver tissue from mice deficient for TXNIP [GeneID=10628].
SHETH_VS_TXNIP_LOSS_PAM4	SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM4	Cluster PAM4: genes down-regulated in hepatocellular carcinoma (HCC) vs normal liver tissue from mice deficient for TXNIP [GeneID=10628].
SHETH_VS_TXNIP_LOSS_PAM5	SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM5	Cluster PAM5: genes changed exclusively in hepatocellular carcinoma (HCC) samples from 27 month old mice deficient for TXNIP [GeneID=10628].
SHETH_VS_TXNIP_LOSS_PAM6	SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM6	Cluster PAM6: genes changed exclusively in normal liver tissue adjacent to hepatocellular carcinoma (HCC) from mice deficient for TXNIP [GeneID=10628].
Smith_liver_cancer	SMITH_LIVER_CANCER	Potential marker genes specifically up-regulated in the majority of hepatocellular carcinoma (HCC) tumors.
Villanueva_KRT19_dn	VILLANUEVA_LIVER_CANCER_KRT19_DN	Genes under-expressed in KRT19-positive [GeneID=3880] hepatocellular carcinoma (HCC).
Villanueva_KRT19_up	VILLANUEVA_LIVER_CANCER_KRT19_UP	Genes over-expressed in KRT19-positive [GeneID=3880] hepatocellular carcinoma (HCC).
Wang_recurrent_dn	WANG_RECURRENT_LIVER_CANCER_DN	Genes down-regulated in samples from patients with recurrent hepatocellular carcinoma (HCC).
Wang_recurrent_up	WANG_RECURRENT_LIVER_CANCER_UP	Genes up-regulated in samples from patients with recurrent hepatocellular carcinoma (HCC).
Woo_recurrence_dn	WOO_LIVER_CANCER_RECURRENCE_DN	Genes negatively correlated with recurrence free survival in patients with hepatitis B-related (HBV) hepatocellular carcinoma (HCC).
Woo_recurrence_up	WOO_LIVER_CANCER_RECURRENCE_UP	Genes positively correlated with recurrence free survival in patients with hepatitis B-related (HBV) hepatocellular carcinoma (HCC).
Wu_HBX_TARGETS_1_dn	WU_HBX_TARGETS_1_DN	Genes down-regulated by expression of HBV X protein (HBVgp3) [GeneID=944566] in SK-Hep-1 cells (hepatocellular carcinoma).
Wu_HBX_TARGETS_1_up	WU_HBX_TARGETS_1_UP	Genes up-regulated by expression of HBV X protein (HBVgp3) [GeneID=944566] in SK-Hep-1 cells (hepatocellular carcinoma).
Wu_HBX_TARGETS_2_dn	WU_HBX_TARGETS_2_DN	Genes down-regulated by expression of HBV X protein (HBVgp3) [GeneID=944566] in primary hepatocytes.
Wu_HBX_TARGETS_2_up	WU_HBX_TARGETS_2_UP	Genes up-regulated by expression of HBV X protein (HBVgp3) [GeneID=944566] in primary hepatocytes.
Wu_HBX_TARGETS_3_dn	WU_HBX_TARGETS_3_DN	Genes down-regulated by expression of HBV X protein (HBVgp3) [GeneID=944566] both in SK-Hep-1 cells (hepatocellular carcinoma) and normal primary hepatocytes.
Wu_HBX_TARGETS_3_up	WU_HBX_TARGETS_3_UP	Genes up-regulated by expression of HBV X protein (HBVgp3) [GeneID=944566] both in SK-Hep-1 cells (hepatocellular carcinoma) and normal primary hepatocytes.
Yamashita_dn	YAMASHITA_LIVER_CANCER_STEM_CELL_DN	Genes down-regulated in hepatocellular carcinoma (HCC) cells with hepatic stem cell properties.
Yamashita_up	YAMASHITA_LIVER_CANCER_STEM_CELL_UP	Genes up-regulated in hepatocellular carcinoma (HCC) cells with hepatic stem cell properties.
Yamashita_EPCAM_dn	YAMASHITA_LIVER_CANCER_WITH_EPCAM_DN	Down-regulated genes distinguishing hepatocellular carcinoma (HCC) samples positive for EPCAM [GeneID=4072] from the negative ones.
Yamashita_EPCAM_up	YAMASHITA_LIVER_CANCER_WITH_EPCAM_UP	Up-regulated genes distinguishing hepatocellular carcinoma (HCC) samples positive for EPCAM [GeneID=4072] from the negative ones.
Pinyol_146_Sora_Signature	NA	Molecular predictors of prevention of recurrence in HCC with sorafenib as adjuvant treatment and prognostic factors in the phase 3 STORM trial
Lachenmayer_CTNNB1_up	NA	Wnt-Pathway Activation in Two Molecular Classes of Hepatocellular Carcinoma and Experimental Modulation by Sorafenib
Lachenmayer_Wnt-TGFb_up	NA	Wnt-Pathway Activation in Two Molecular Classes of Hepatocellular Carcinoma and Experimental Modulation by Sorafenib
Moeini_ICF_signature	NA	An Immune Gene Expression Signature Associated With Development of Human Hepatocellular Carcinoma Identifies Mice That Respond to Chemopreventive Agents