

Supplementary Material

Supplementary Tables:

Table S1. Clinicopathological characteristics of Discovery cohort (204 HCC patients)

Characteristics	Total Patients=N=204
Diagnosis Age	
<60years	139(68.14%)
>=60years	65(31.86%)
Sex	
Female	152(74.51%)
Male	52(25.49%)
HBV vs non-HBV	
HBV	148(72.55%)
non-HBV	56(27.45%)
Tumor size	
<=5	142(69.61%)
>5	62(30.39%)
Edmonson most Grade	
<=2	130(63.73%)
>2	74(36.27%)
Alpha-fetoprotein level	
<10	127(62.25%)
>=10	77(37.75%)
Microvascular invasion	
No	147(72.06%)
Yes	57(27.94%)
Cirrhosis	
No	106(51.96%)
Yes	98(48.04%)
Overall survival	
Alive	175(85.78%)
Death	29(14.22%)
Disease Free survival	
Disease Free	118(57.84%)
Recurrence	86(42.16%)

Table S2. Clinicopathological characteristics of Validation cohort (372 HCC patients)

Characteristics	Total patients=N=372
Diagnosis Age	
<60years	169(45.43%)
>=60years	203(54.57%)
Sex	
Female	121(32.53%)
Male	251(67.47%)
HBV	
No	248(66.67%)
Yes	105(28.23%)
NA	19
HCV	
No	297(79.84%)
Yes	56(15.05%)
NA	19
HBV or HCV	
No	199(53.49%)
Yes	154(41.40%)
NA	19
HBV and HCV	
No	346(93.01%)
Yes	7(1.88%)
NA	19
Alcohol consumption	
No	236(63.44%)
Yes	117(31.45%)
NA	19
Grade	
G1-G2	233(62.63%)
G3-G4	134(36.02%)
NA	5
T stage	
T1-T2	276(74.19%)
T3-T4	93(25%)
NA	3
Residual tumor	
R0	325(87.37%)
R1-R2	18(4.84%)
NA	29
Alpha-fetoprotein level	
<200	202(54.30%)
>=200	76(20.43%)
NA	94
Node stage	

N0	253(68.01%)
N1	4(1.07%)
NA	115
Metastasis stage	
M0	267(71.77%)
M1	4(1.08%)
NA	101
Tumor stage	
Stage I-II	258(69.35%)
Stage III-IV	90(24.19%)
NA	24
Microvascular invasion	
No	16(4.30%)
Yes	93(25%)
NA	263
Macrovascular invasion	
No	93(25%)
Yes	16(4.30%)
NA	263
Cirrhosis	
Fibrosis	68(18.28%)
Cirrhosis	70(18.81%)
NA	234
Overall survival	
Alive	242(65.05%)
Death	130(34.95%)
Disease free survival	
Disease free	145(38.98%)
Recurrence	176(47.31%)
NA	51

*NA = Not Available

Table S3. Association of expression of HLA genes with clinical features in Discovery cohort

Gene ID	Sex	Age	Tumor size	HBV vs non-HBV	Edmonson most grade	Cirrhosis	Alpha-fetoprotein in level	Microvascular	Kaplan-Meier overall	Kaplan-Meier disease
<i>HLA-A</i>	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
<i>HLA-B</i>	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
<i>HLA-C</i>		NA	NA	NA		NA		NA	NA	NA
<i>HLA-DMA</i>	NA	NA	NA	NA	NA	NA	NA	NA	NA	
<i>HLA-DMB</i>	NA		NA	NA	NA	NA	NA	NA	NA	
<i>HLA-DOA</i>		NA	NA	NA	NA	NA	NA	NA	NA	
<i>HLA-DOB</i>	NA	NA	NA	NA			NA	NA	NA	
<i>HLA-DPA1</i>	NA		NA	NA	NA	NA	NA	NA	NA	NA
<i>HLA-DPB1</i>	NA		NA	NA	NA	NA	NA	NA	NA	
<i>HLA-DPB2</i>	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
<i>HLA-DQA1</i>	NA	NA	NA	NA	NA		NA	NA	NA	NA
<i>HLA-DQA2</i>	NA			NA		NA	NA	NA		
<i>HLA-DQB1</i>	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
<i>HLA-DQB2</i>	NA			NA		NA	NA	NA	NA	
<i>HLA-DRA</i>	NA		NA	NA	NA	NA	NA	NA	NA	NA
<i>HLA-DRB1</i>	NA	NA	NA	NA	NA		NA	NA	NA	NA
<i>HLA-DRB6</i>	NA			NA	NA	NA	NA		NA	
<i>HLA-E</i>	NA	NA	NA			NA	NA	NA	NA	
<i>HLA-F</i>	NA	NA	NA	NA	NA		NA	NA	NA	NA
<i>HLA-G</i>		NA	NA	NA	NA	NA		NA		
<i>HLA-H</i>	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
<i>HLA-J</i>	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
<i>HLA-L</i>		NA		NA	NA	NA	NA	NA	NA	NA



Upregulation in Female, age<60, non-HBV, no Cirrhosis



Upregulation in Male. Advance grade stage. Tumor size>=5. High Alpha-fetoprotein level



Upregulation in no Microvascular invasion, Tumor size<5, Good survival,

Table S4. Association of expression of HLA genes with clinical features in Validation cohort

Gene ID	Age	Sex	Grade	HBV	HCV	HBV or HCV	HBV and HCV	Alpha-fetoprotein	Alcohol consumption	Cirrhosis	Tumor stage	T stage	Kaplan-Meier overall	Kaplan-Meier disease free
<i>HLA-C</i>	NA		NA	NA		NA	NA				NA	NA	NA	NA
<i>HLA-DMA</i>	NA	NA	NA	NA	NA	NA	NA	NA		NA	NA	NA	NA	
<i>HLA-DMB</i>	NA	NA	NA	NA	NA	NA	NA	NA		NA	NA	NA	NA	
<i>HLA-DOA</i>	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA		NA	NA	
<i>HLA-DOB</i>	NA	NA	NA	NA			NA	NA		NA			NA	NA
<i>HLA-DPB1</i>	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
<i>HLA-DPB2</i>	NA		NA	NA	NA	NA	NA		NA	NA	NA	NA	NA	NA
<i>HLA-DQA1</i>	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
<i>HLA-DQA2</i>	NA	NA		NA		NA	NA	NA	NA	NA			NA	NA
<i>HLA-DQB1</i>	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
<i>HLA-DQB2</i>	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
<i>HLA-DRA</i>	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA		NA	NA	
<i>HLA-DRB1</i>	NA	NA	NA	NA		NA	NA	NA		NA	NA	NA	NA	
<i>HLA-DRB6</i>	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
<i>HLA-DRB5</i>	NA	NA	NA	NA		NA	NA	NA		NA	NA	NA	NA	NA
<i>HLA-E</i>	NA	NA				NA	NA			NA	NA			
<i>HLA-F</i>		NA	NA	NA		NA			NA	NA			NA	NA
<i>HLA-G</i>	NA	NA	NA	NA			NA	NA	NA	NA	NA		NA	NA
<i>HLA-H</i>			NA	NA			NA	NA	NA	NA				NA



Upregulation in Female Initial grade stage,, non-HBV, non-HBV, no Cirrhosis, Initial T stage, , Low Alpha-fetoprotein level, non-HCV



Upregulation in Male, age>=60, Advance grade stage, HCV, Alcohol consumption, HBV or HCV, High Alpha-fetoprotein level, HBV and HCV



Upregulation in Initial tumor stage, Good survival, Delayed recurrence

NA: No Association

Table S5. MHC gene and their correlated gene list

MHC Gene name	Correlated Genes
HLA-DMA	CD300A, CD74, CD79B, CLEC2B, CYBA, HCST, IFITM1, LAT, LILRB4, NCF4, NPDC1, PILRA, PSMB10, RASGRP2, SIGLEC1, TYROBP, UBE2L6, WAS and TNFRSF14
HLA-DMB	B2M, CD300A, CD4, CD74, CD79B, CLEC2B, CLEC2D, COL3A1, CYBA, CYBB, EVL, FCGR3A, FYN, HCST, IFITM1, INPP5D, ITGA4, ITGAL, ITGB2, ITGB7, LAT, LCP2, LILRB4, NCF4, NPDC1, PIK3CD, PILRA, PTPRC, RASGRP2, SIGLEC1, SOCS3, TYROBP, UBE2L6, WAS, ZAP70
HLA-DOA	B2M, CD300A, CD74, CD79B, CLEC2B, CYBA, EVL, FCGR3A, HCST, IFITM1, ITGAL, ITGB2, LAT, LILRB4, NCF4, NPDC1, PIK3CD, PILRA, PSMB10, RASGRP2, SIGLEC1, TYROBP, UBE2L6, WAS, ZAP70
HLA-DRB6	B2M, CD300A, CD74, CD79B, CLEC2B, CYBA, FCGR3A, HCST, IFITM1, ITGAL, ITGB2, LILRB4, NCF4, PIK3CD, PILRA, PSMB10, RASGRP2, SIGLEC1, TYROBP, UBE2L6, WAS, ZAP70
HLA-E	B2M, CD74, UBE2L6, WAS, ITGB2, LCP2, PTPRC, PILRA, SIGLEC1, CYBB, FCGR3A, LILRB4, HERC5, IFITM1, NCF4, HCST, TYROBP, PIK3CD, CLEC2B, ZAP70, ITGA4, FYN, INPP5D, ITGAL, CD300A, CTSB, CD4, ITGB7, EVL, CD79B, SOCS3

Table S6. Gene name and chromosomal location of 40 unique genes

HGNC symbol	Chromosome location	Gene description
B2M	15q21.1	beta-2-microglobulin
CD300A	17q25.1	CD300a molecule
CD4	12p13.31	CD4 molecule
CD74	5q33.1	CD74 molecule
CD79B	17q23.3	CD79b molecule
CLEC2B	12p13.31	C-type lectin domain family 2 member B
CLEC2D	12p13.31	C-type lectin domain family 2 member D
COL3A1	2q32.2	collagen type III alpha 1 chain
CTSB	21q22.3	cathepsin B
CYBA	16q24.2	cytochrome b-245 alpha chain
CYBB	Xp21.1-p11.4	cytochrome b-245 beta chain
EVL	14q32.2	Enah/Vasp-like
FCGR3A	1q23.3	Fc fragment of IgG receptor IIIa
FGFR1	8p11.23	fibroblast growth factor receptor 1
FYN	6q21	FYN proto-oncogene, Src family tyrosine kinase
HCST	19q13.12	hematopoietic cell signal transducer
HERC5	4q22.1	HECT and RLD domain containing E3 ubiquitin protein ligase 5
IFITM1	11p15.5	interferon induced transmembrane protein 1
INPP5D	2q37.1	inositol polyphosphate-5-phosphatase D
ITGA4	2q31.3	integrin subunit alpha 4
ITGAL	16p11.2	integrin subunit alpha L
ITGB2	21q22.3	integrin subunit beta 2
ITGB7	12q13.13	integrin subunit beta 7
LAT	16p11.2	linker for activation of T cells
LCP2	5q35.1	lymphocyte cytosolic protein 2
LILRB4	19q13.4	leukocyte immunoglobulin like receptor B4
NCF4	22q12.3	neutrophil cytosolic factor 4
NPDC1	9q34.3	neural proliferation, differentiation and control 1
PIK3CD	1p36.22	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit delta
PILRA	7q22.1	paired immunoglobulin like type 2 receptor alpha
PSMB10	16q22.1	proteasome subunit beta 10
PTPRC	1q31.3	protein tyrosine phosphatase receptor type C
RASGRP2	11q13.1	RAS guanyl releasing protein 2
SIGLEC1	20p13	sialic acid binding Ig like lectin 1
SOCS3	17q25.3	suppressor of cytokine signaling 3
TNFRSF14	1p36.32	TNF receptor superfamily member 14
TYROBP	19q13.12	TYRO protein tyrosine kinase binding protein
UBE2L6	11q12.1	ubiquitin conjugating enzyme E2 L6

WAS	Xp11.23	WASP actin nucleation promoting factor
ZAP70	2q11.2	zeta chain of T cell receptor associated protein kinase 70