



**Figure S1** PPI network of differentially expressed genes. Circles represent genes (the red represents  $\log FC > 0$ , the green represents  $\log FC < 0$ ), lines represent interactions between gene encoded proteins and line colors represent evidence of interactions between proteins. PPI, protein-protein interaction; FC, fold change.



**Table S2** Top GO enrichment terms of differentially expressed genes associated with hepatitis B-related hepatocellular carcinoma

Category	Term	Count	%	P value
BP	GO:0032787: monocarboxylic acid metabolic process	13	11.3	6.76083E-08
BP	GO:0009617: response to bacterium	12	10.43	3.38844E-05
BP	GO:1901652: response to peptide	11	9.57	1.28825E-06
BP	GO:0040008: regulation of growth	10	8.7	0.000141254
BP	GO:0071466: cellular response to xenobiotic stimulus	9	7.83	3.71535E-08
BP	GO:0034754: cellular hormone metabolic process	8	6.96	3.80189E-08
BP	GO:0000819: sister chromatid segregation	7	6.09	1.65959E-06
BP	GO:0002697: regulation of immune effector process	7	6.09	0.000645654
BP	GO:0015850: organic hydroxy compound transport	6	5.22	3.63078E-05
BP	GO:0045861: negative regulation of proteolysis	6	5.22	0.002344229
BP	GO:0044262: cellular carbohydrate metabolic process	5	4.35	0.000446684
BP	GO:0071902: positive regulation of protein serine/threonine kinase activity	5	4.35	0.001862087
BP	GO:0044070: regulation of anion transport	4	3.48	0.000446684
BP	GO:0051701: biological process involved in interaction with host	4	3.48	0.002951209
BP	GO:2000096: positive regulation of Wnt signaling pathway, planar cell polarity pathway	3	2.61	4.46684E-06
BP	GO:0019835: cytolysis	3	2.61	6.76083E-05
BP	GO:0042537: benzene-containing compound metabolic process	3	2.61	0.000147911
BP	GO:0009595: detection of biotic stimulus	3	2.61	0.000446684
BP	GO:0043277: apoptotic cell clearance	3	2.61	0.000630957
BP	GO:0040014: regulation of multicellular organism growth	3	2.61	0.001995262
CC	GO:0062023: collagen-containing extracellular matrix	10	8.7	6.45654E-06
CC	GO:0005819: spindle	8	6.96	0.000234423
CC	GO:0009897: external side of plasma membrane	7	6.09	0.001995262
CC	GO:0072562: blood microparticle	6	5.22	2.04174E-05
CC	GO:0016323: basolateral plasma membrane	5	4.35	0.001862087
CC	GO:0005579: membrane attack complex	3	2.61	1.86209E-06
CC	GO:0000940: outer kinetochore	3	2.61	1.14815E-05
CC	GO:0034358: plasma lipoprotein particle	3	2.61	0.000354813
MF	GO:0016491: oxidoreductase activity	16	13.91	2.0893E-08
MF	GO:0042803: protein homodimerization activity	9	7.83	0.00134896
MF	GO:0030246: carbohydrate binding	8	6.96	1.0965E-05
MF	GO:0033218: amide binding	8	6.96	0.00017378
MF	GO:0005319: lipid transporter activity	6	5.22	3.6308E-05
MF	GO:0016614: oxidoreductase activity, acting on CH-OH group of donors	5	4.35	0.00019055
MF	GO:1901618: organic hydroxy compound transmembrane transporter activity	4	3.48	5.1286E-05
MF	GO:0038024: cargo receptor activity	4	3.48	0.00028184
MF	GO:0031406: carboxylic acid binding	4	3.48	0.0042658
MF	GO:0005201: extracellular matrix structural constituent	4	3.48	0.00436516
MF	GO:0030414: peptidase inhibitor activity	4	3.48	0.0057544
MF	GO:0016829: lyase activity	4	3.48	0.00724436
MF	GO:0042834: peptidoglycan binding	3	2.61	4.2658E-05
MF	GO:0016709: oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen	3	2.61	0.00047863
MF	GO:0051213: dioxygenase activity	3	2.61	0.00549541
MF	GO:0004896: cytokine receptor activity	3	2.61	0.00616595

GO, Gene Ontology; BP, biological process; CC, cellular component; MF, molecular function.

**Table S3** KEGG pathway analysis of differentially expressed genes associated with hepatitis B-related hepatocellular carcinoma

Term	Count	%	P value
hsa04976: Bile secretion	6	5.22	1.20226E-06
hsa04060: Cytokine-cytokine receptor interaction	5	4.35	0.005495409
hsa00232: Caffeine metabolism	3	2.61	1.07152E-06
hsa00380: Tryptophan metabolism	3	2.61	0.000549541
hsa00140: Steroid hormone biosynthesis	3	2.61	0.001659587
hsa04610: Complement and coagulation cascades	3	2.61	0.004265795
hsa04657: IL-17 signaling pathway	3	2.61	0.005623413
hsa04922: Glucagon signaling pathway	3	2.61	0.007943282
hsa01200: Carbon metabolism	3	2.61	0.009772372

KEGG, Kyoto Encyclopedia of Genes and Genomes.