Supplementary Information

for

Serum Metabolomics to Identify the Liver Disease-Specific Biomarkers for the Progression of Hepatitis to Hepatocellular Carcinoma

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Duplicate	Pearson Correlation	Duplicate	Pearson Correlation
sample (DS)	Coefficient	Sample (DS)	Coefficient
DS-1	0.998268058	DS-16	0.999686837
DS-2	0.999072175	DS-17	0.985738252
DS-3	0.999426573	DS-18	0.999634599
DS-4	0.999664146	DS-19	0.999440753
DS-5	0.999856752	DS-20	0.999939986
DS-6	0.999243799	DS-21	0.999047992
DS-7	0.999481800	DS-22	0.999790789
DS-8	0.999781987	DS-23	0.999958316
DS-9	0.998400789	DS-24	0.999389796
DS-10	0.997037309	DS-25	0.999946129
DS-11	0.999941303	DS-26	0.999935874
DS-12	0.999931416	DS-27	0.969182726
DS-13	0.999990246	DS-28	0.987997904
DS-14	0.999800965	DS-29	0.994257984
DS-15	0.999827710	DS-30	0.978366691

Supplementary Table S1. The Pearson correlation coefficient of the randomly selected duplicate samples.

Metabolites	C*(CON)	C*(HBV)	C*(LC)	C*(HCC)
Boric acid	-3.84E-06	8.52E-06	-3.35E-06	-3.84E-06
Trans-1,2-cyclopropanecarboxylate	2.60E-06	8.98E-05	4.95E-05	2.60E-06
Valine	3.11E-06	-6.35E-06	-8.24E-07	3.11E-06
Oxalic acid	7.16E-06	4.00E-05	1.11E-06	7.16E-06
Isoleucine	-5.80E-06	-2.43E-06	2.49E-06	-5.80E-06
3-methyl-2-hydroxybutyric acid	-1.85E-06	-8.60E-06	-4.01E-06	-1.85E-06
Ethanolamine	1.03E-04	-3.62E-04	3.49E-05	1.03E-04
Leucine	1.64E-05	-2.37E-05	1.48E-05	1.64E-05
Succinic acid	-5.03E-06	-1.32E-05	5.76E-07	-5.03E-06
Salicylaldehyde	7.74E-04	6.22E-03	1.09E-03	7.74E-04
4-Hydroxy-Proline	-1.93E-06	-4.27E-05	-4.32E-06	-1.93E-06
Threitol	3.52E-05	6.37E-05	3.21E-05	3.52E-05
Methionine	3.72E-06	-1.57E-05	-6.48E-06	3.72E-06
Glutamate	2.33E-06	1.46E-05	3.47E-06	2.33E-06
Threonic acid	-3.40E-06	-6.19E-06	-2.07E-07	-3.40E-06
Glutamate	5.71E-06	-6.16E-06	2.08E-07	5.71E-06
Dodecanoic acid	2.78E-05	-2.07E-04	-5.97E-05	2.78E-05
Asparagine	-1.17E-04	1.42E-04	1.44E-04	-1.17E-04
9H-purine	-1.65E-05	-2.40E-04	-2.88E-05	-1.65E-05
Citrulline	1.61E-04	1.31E-05	-1.99E-06	1.61E-04
Methionine sulfoxide	-2.03E-05	2.98E-04	5.30E-05	-2.03E-05
Fructose	-8.55E-06	-4.19E-05	-1.71E-05	-8.55E-06
Glucose	5.56E-06	-2.60E-05	-1.87E-05	5.56E-06
Altrose	-1.56E-05	7.33E-05	-2.17E-05	-1.56E-05
Arachidic acid	2.66E-04	-3.50E-04	4.04E-05	2.66E-04
Methyl -β-D-galactopyranoside	-1.59E-07	8.61E-07	3.19E-06	-1.59E-07
Palmitic acid	2.60E-08	1.02E-05	3.64E-06	2.60E-08

Supplementary Table S2. The stepwise discriminant functions variables and	nd
classification function coefficients of the four groups.	

Noradrenaline	-7.71E-05	3.31E-04	-1.10E-04	-7.71E-05
Stearic acid	-1.05E-06	-9.35E-06	-1.04E-06	-1.05E-06
Sucrose	-2.70E-07	1.68E-05	-1.91E-06	-2.70E-07
Constant	-1.55E+03	-1.91E+03	-4.68E+02	-2.42E+02

				data sets.			
		group	group Predicted Group Membership				Total
		_	NC HBV		LC	LC HCC	
	Count	NC	40	0	0	0	40
		HBV	0	32	0	0	32
		LC	0	0	34	0	34
Training		HCC	0	0	0	26	26
data set	%	NC	100.00	0.00	0.00	0.00	100.00
		HBV	0.00	100.00	0.00	0.00	100.00
		LC	0.00	0.00	100.00	0.00	100.00
		HCC	0.00	0.00	0.00	100.00	100.00
	Count	NC	21	0	0	0	21
		HBV	1	16	0	0	17
		LC	0	0	18	0	18
Validation		HCC	0	0	3	10	13
data set	%	NC	100.00	0.00	0.00	0.00	100.00
		HBV	5.88	94.12	0.00	0.00	100.00
		LC	0.00	0.00	100.00	0.00	100.00
		HCC	0.00	0.00	23.08	76.92	100.00

Supplementary Table S3. The Bayes Classification Results of training and validation

		-			
Characteristics	NC (n=61)	HBV (n=49)	LC (n=52)	HCC (n=39)	
A = = (=)	$40.0~\pm9.8$	$43.9~{\pm}9.5$	$48.2\ \pm 10.0$	$54.7\ \pm 8.8$	
Age (years)	(18~71)	(20~76)	(20~76) (25~72)		
Male (%)	69.2	84.3	78.5	86.2	
AFP	1	51.85 ± 70.2	211.8 ±387.3	233.9 ±430.3	
(range),ng/ml	/	(1.88~210.2)	(2.08~1189.3)	(1.86~1210)	
HbsAg	Negative	Positive	Positive	Positive	

Supplementary Table S4. Characteristics of the healthy controls and patients with chronic hepatic diseases and HCC

NC: Healthy control; HBV: Hepatitis B virus; LC: Liver cirrhosis; HCC: Hepatocellular carcinoma; AFP: alpha fetal protein.



Figure S1. Metabolic profilings of representative serum samples. The GC-TOFMS TIC chromatograms for blank (black line), health control (CN, green line), HBV (blue line), LC (purple line) and HCC (red line). X axis and Y axis represent the retention time (s) and relative peak intensity, respectively.



Figure S2. Heat map based on the Pearson distance measure and the Ward cluster algorithm, providing intuitive visualization of the metabolic remodeling in disease groups compared to the control group. Red color indicates a high level of metabolites and green color indicates a low level of metabolites, while black color means an equal level in groups.



Figure S3. OPLS-DA scores plots for serum samples of (A) patients with HBV (\bullet) and NC (\bullet), (B) patients with LC (\bullet) and NC (\bullet), and (C) patients with HCC (\bullet) and NC (\bullet).

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		Pı	redicted HBV	Predicted 1	NC	Predicted LC	Predicted HB	V	Predicted H	CC Predicted LC
	True HI	BV	32	0	True LC	34	0	True HCC	C 26	0
	True NO	C	0	40	True HB	V 0	32	True LC	0	34

Figure S4. The top 30 ranked differential metabolites according to the mean decrease accuracy (MDA) and performance of Random Forest

(RFs) models discriminating (A) HBV from NC, (B) LC from HBV and (C) HCC from LC based on training data set serum.

Canonical Discriminant Functions



Figure S5. The discriminant function model based on Bayes' Rule by stepwise discriminant analysis.



Figure S6. Metabolic network of the detected metabolites in this study. The normalized contents of each metabolite in NC (green bar chart), HBV (blue bar chart), LC (purple bar chart) and HCC (red bar chart) are shown under the chemical name.



Figure S7. The ratio of BCAA (leucine, isoleucine, and valine) to ArAA (tyrosine, phenylalanine and tryptophan), the ratio of FFA C16:1 to FFA C16:0 and FFA C18:1 to FFA C18:0.