

**Table S1** The differentiated metabolites detected by serum metabolomics.

No.	Rt(min)	Ion mode	m/z	Error (ppm)	Proposed compound	Formula	Trend in model group	HMDB
1	0.56	M-H	187.1102	-0.5	Valyl-Alanine	C8H16N2O3	↓	HMDB29120
2	0.81	M-H	145.0602	-6.0	L-Glutamine	C5H10N2O3	↓	HMDB00641
3	1.02	M-H	191.0211	-0.5	Citric acid	C6H8O7	↓	HMDB00094
4	1.38	M+H	175.1221	2.0	L-Arginine	C6H14N4O2	↓	HMDB00517
5	1.49	M+H	215.0261	-0.5	Isocitric acid	C6H8O7	↓	HMDB00193
6	1.64	M+H	169.0423	2.0	Uric acid	C5H4N4O3	↑	HMDB00289
7	1.84	M-H	103.0440	-8.0	3-Hydroxybutyric acid	C4H8O3	↓	HMDB00357
8	2.07	M-H	130.0900	-8.6	L-Leucine	C6H13NO2	↑	HMDB0000687
9	2.21	M-H	190.0376	-3.3	γ-Carboxyglutamic acid	C6H9NO6	↑	HMDB41900
10	2.53	M-H	164.0752	-7.3	L-Phenylalanine	C9H11NO2	↓	HMDB00159
11	2.78	M-H	115.0439	-5.3	Pyruvate	C5H8O3	↑	HMDB31643
12	3.52	M+H	133.1085	-9.4	D-Ornithine	C5H12N2O2	↓	HMDB03374
13	3.96	M-H	464.3030	2.2	Glycocholic acid	C26H43NO6	↓	HMDB00138
14	4.25	M-H	498.2954	-5.1	Taurodeoxycholic acid	C26H45NO6S	↓	HMDB00896
15	4.57	M-H	785.6506	-4.0	SM(d18:1/22:0)	C45H91N2O6P	↑	HMDB12103
16	4.84	M-H	203.0858	-1.7	D-Tryptophan	C11H12N2O2	↓	HMDB13609
17	5.10	M-H	146.0574	-7.9	D-Glutamic acid	C5H9NO4	↓	HMDB03339
18	5.59	M-H	303.2316	-4.4	Arachidonic acid	C20H32O2	↑	HMDB01043
19	6.33	M+H	380.2608	3.9	Sphingosine	C18H38NO5P	↓	HMDB00252
20	6.84	M+H	532.3442	3.1	LysoPE(0:0/20:0)	C25H52NO7P	↑	HMDB11481
21	7.43	M-H	566.5542	-2.4	Cer(d18:0/18:0)	C36H73NO3	↓	HMDB11761
22	7.72	M+H	510.3637	3.1	LysoPC(17:0)	C25H52NO7P	↓	HMDB12108
23	8.09	M+H	810.6096	-5.4	PE(15:0/24:1(15Z))	C44H86NO8P	↓	HMDB08915
24	8.42	M-H	89.0205	-9.6	L-Lactic acid	C3H6O3	↓	HMDB00190
25	8.83	M-H	465.3523	-9.7	LysoSM(d18:0)	C23H51N2O5P	↓	HMDB12082
26	9.52	M+H	256.2647	4.4	Palmitic amide	C16H33NO	↑	HMDB12273

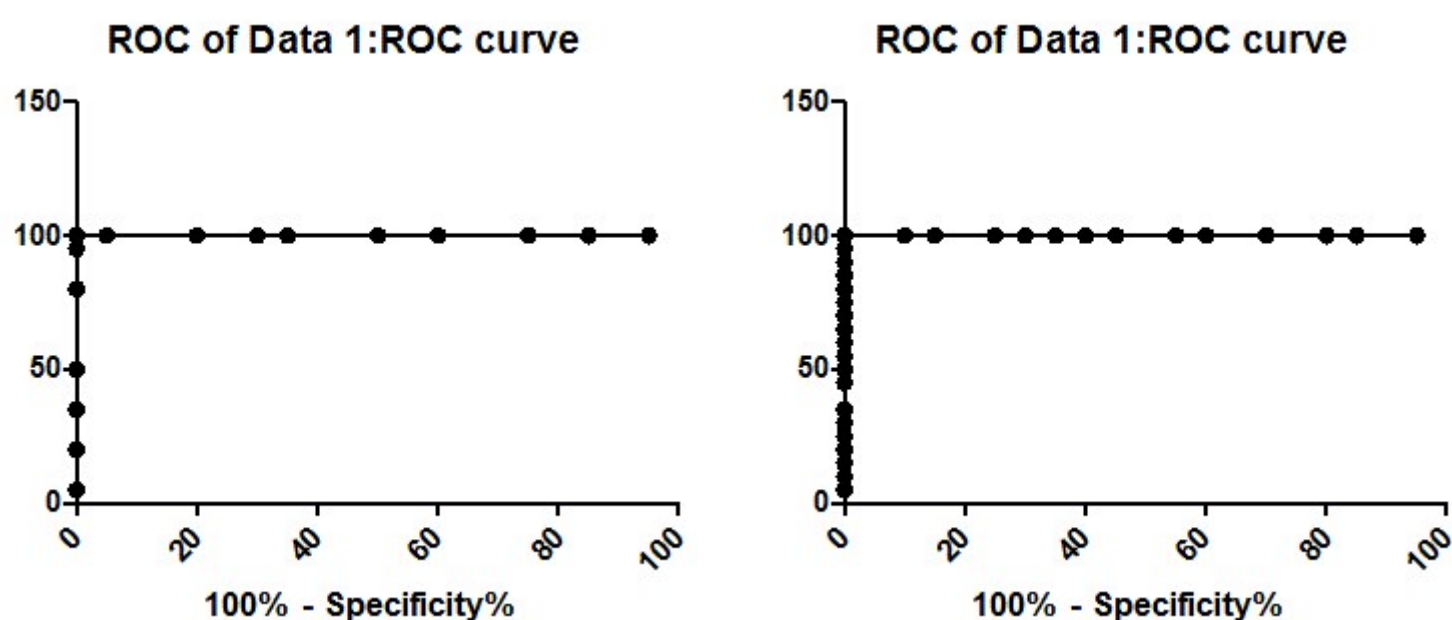


Fig.S1. The area under the curve for both plots is respectively 0.894 and 0.845.