

Fig S1. Chromatogram (A) and MS (B) optimization in positive ion mode.

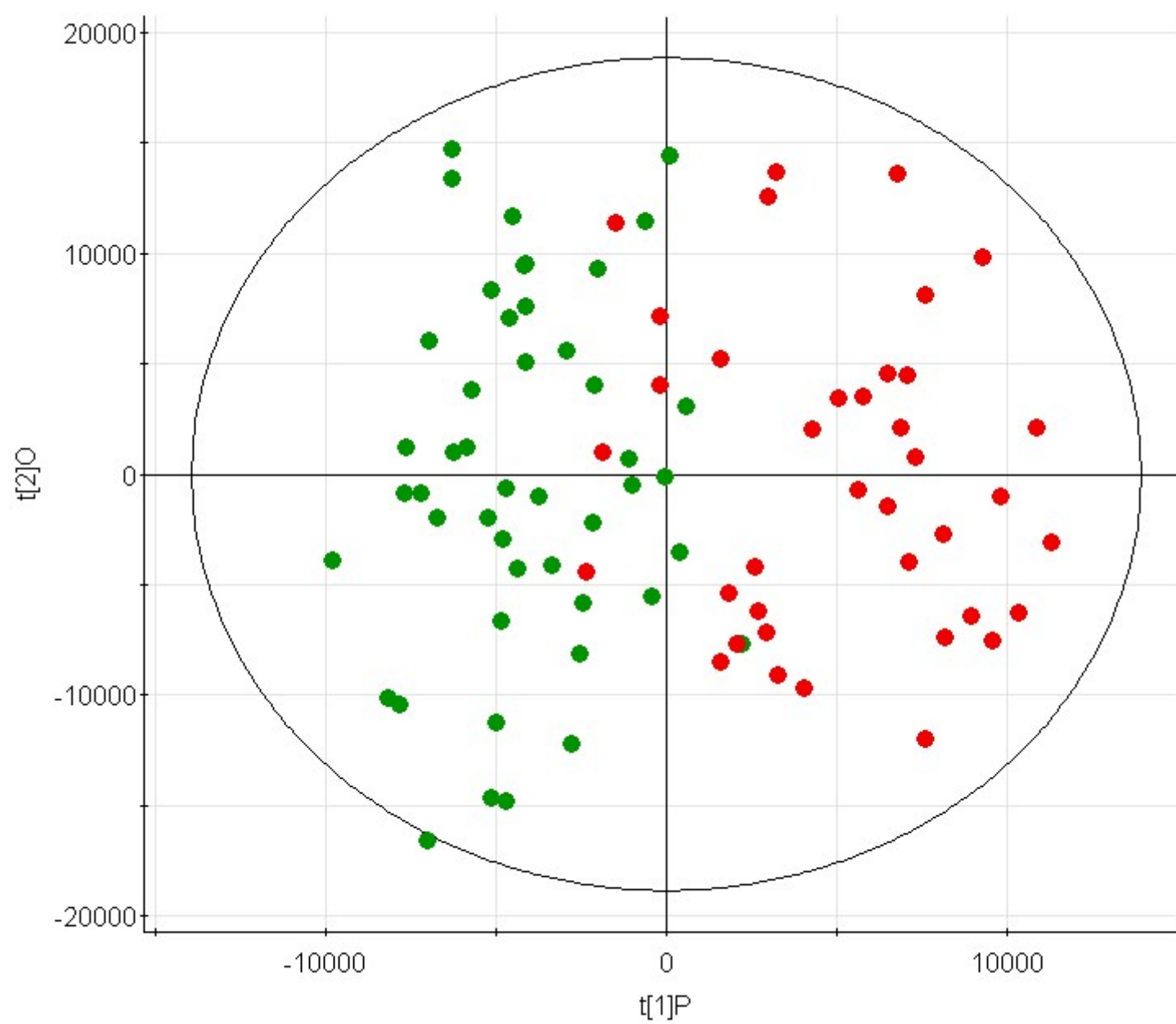


Fig.S2. Score plots of lipidomic profiles obtained for controls (red) and CHD (green) using ultra high-performance liquid chromatography coupled with quadrupole time-of-flight mass spectrometry at negative ESI mode.

Table S1. Biochemistry results in CHD group.

Group	SOD(U/ml)	MDA(nmol/ml)	cAMP(pmol/ml)	cGMP(pmol/ml)	ANF(ng/ml)	cTn-I (ng/ml)
Control	1.46±0.12	4.44±0.70	14.24±2.47	13.04±2.45	0.41±0.07	6.20±0.67
CHD	1.18±0.07**	5.85±0.69**	20.25±6.07*	16.93±4.02*	0.42±0.07	6.69±0.41

*Significant difference from control group at $p < 0.05$

Table S2. Identification of serum lipid in CHD cases.

No	Retention time (min)	m/z	Compound ID	Adducts	Formula	Mass Error (ppm)	VIP	Compound	Anova (p)	Trend
1	3.27	452.28	LMGP02050010	M+H	C ₂₁ H ₄₂ NO ₇ P	1.99	16.43	PE(16:1(9Z)/0:0)	0.0079	Up
2	0.44	361.20	LMST02030026	M+H	C ₂₁ H ₂₈ O ₅	1.48	16.39	Aldosterone	0.0034	Up
3	7.56	285.10	LMGP0105AA00	M+H	C ₉ H ₁₉ NO ₇ P	3.37	15.11	2-acyl-sn-glycero-3-phosphocholine	0.0024	Up
4	4.47	297.17	LMPR02020062	M+H	C ₁₆ H ₂₄ O ₅	-4.72	14.7	alpha-tocopheronic acid	0.0028	Up

Table S3. Result from ingenuity pathway analysis with MetPA.

Pathway	Total	Expected	Hits	Raw p	Holm adjust	Impact
Glycerophospholipid metabolism	39	0.0486082	0.00075984	0.060787	0.10746	
Glycerolipid metabolism	32	0.0398841	0.039372	1	0.01247	
Steroid hormone biosynthesis	99	0.123391	0.11843	1	0.01235	

Note: Total is the total number of compounds in the pathway; the Hits is the actually matched number from the user uploaded data; the Impact is the pathway impact value calculated from pathway topology analysis.