

Supplemental material:

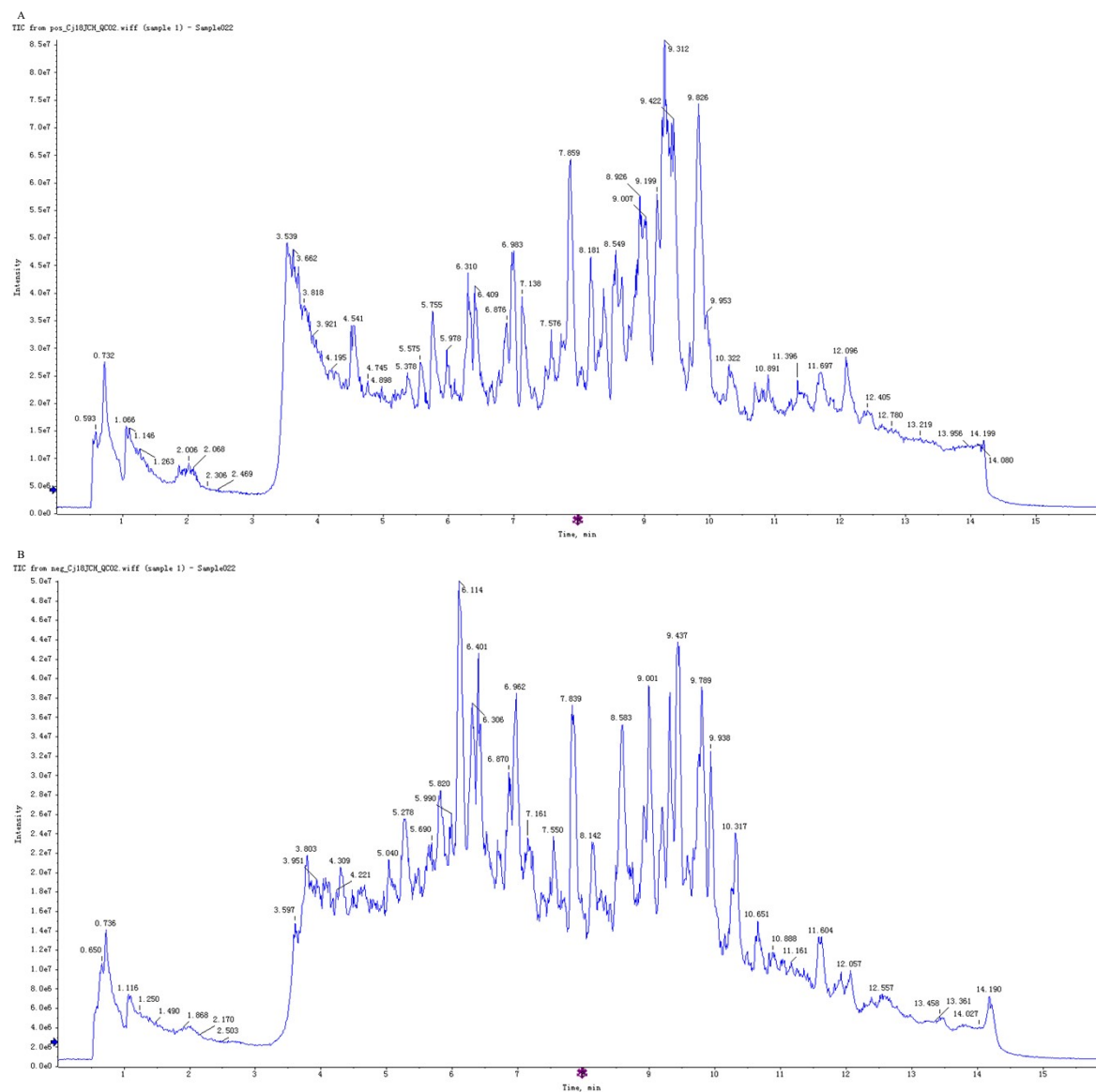


Fig. S1. Total ion chromatography of mass spectrometer in QC samples, (A) UPLC-TOF ESI (+), (B) UPLC-TOF ESI (-).

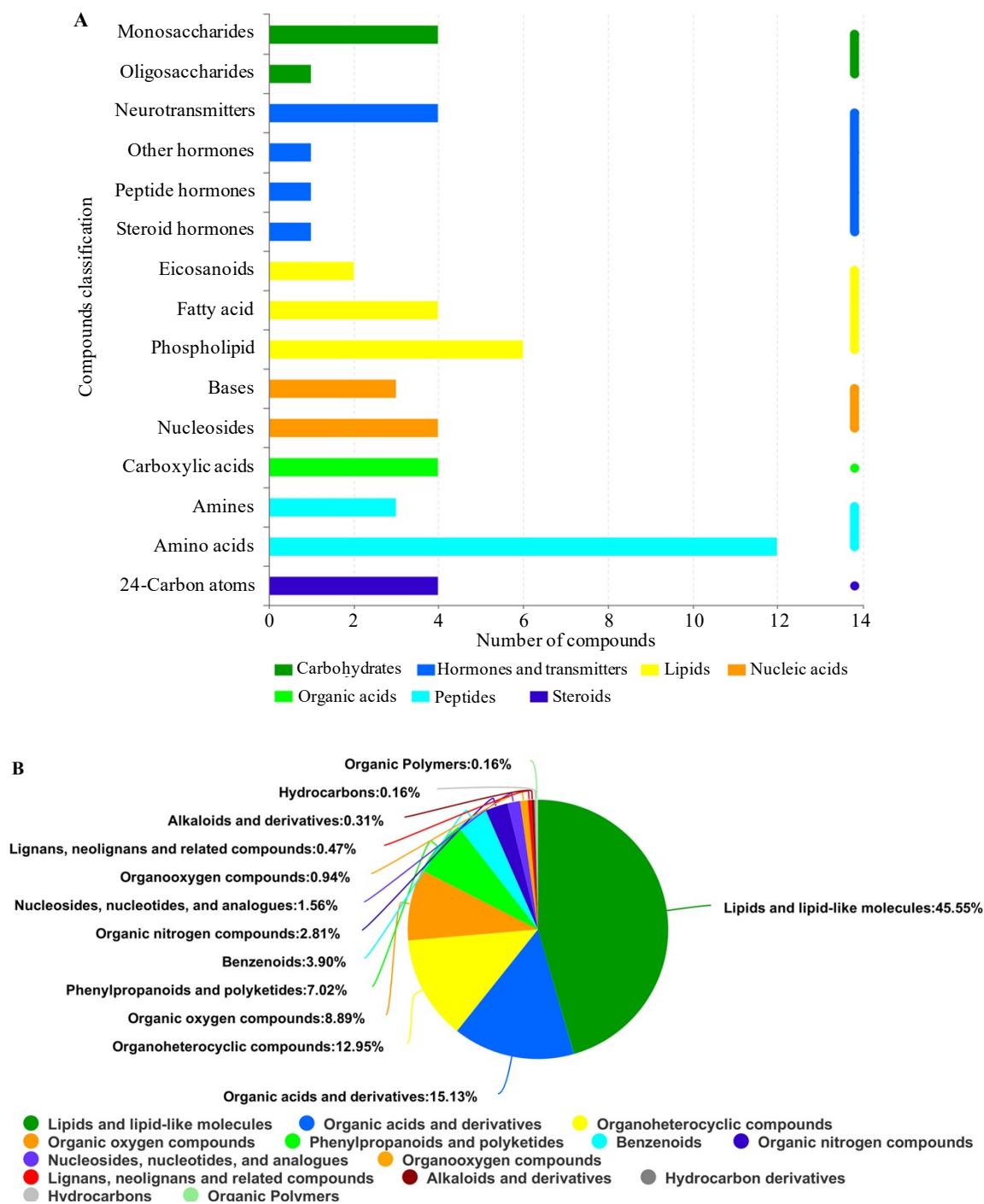


Fig. S2. Metabolites classification according to KEGG (A) and HMDB (B).

Table S1

Pathway description of KEGG topology for each metabolite set.

Pathway	DSS vs. NC		DSS+PSWP-I vs.DSS		DSS+PSAP-I vs.DSS	
	Impact value	P value	Impact value	P value	Impact value	P value
Cutin, suberine and wax biosynthesis	0.0357	0.0272	0.0357	0.0272	0.0357	0.0182
Biosynthesis of unsaturated fatty acids	0.0000	0.0325	0.0000	0.0325	0.0000	0.0218
Fatty acid biosynthesis	0.0000	0.0336	0.0000	0.0336	0.0000	0.0226
Steroid hormone biosynthesis	0.0955	0.0470	0.0955	0.0470	0.0955	0.0320