Supplementary Material

1 HPLC fingerprints of SMD

1.1 Sample preparation

One gram of SMD extract from 15 different batches was weighed accurately, respectively. Then the extract was sonicated extracted with 30 mL of water for 30 min. An equal volume of water-saturated n-butanol was added to perform liquid-liquid extraction twice, the n-butanol layer was combined and evaporated. The residue was dissolved with 10 mL methanol for HPLC analysis.

1.2 HPLC analysis

The separation of the SMD sample was conducted using an Agilent 1200 series LC system equipped with an Agilent ZorBax SB-C18 column (5 μm, 4.6 × 250 mm) at 30 °C with an injected volume of 3 μL. The mobile phase consisted of acetonitrile (phase A) and 0.1% phosphoric acid solution (phase B). It was carried out under the following gradient procedure: 0-2 min, 2%-4% A; 2-10 min, 4%-5% A; 10-20 min, 5%-8% A; 20-35 min, 8%-18% A; 35-50 min, 18%-19% A; 50-60 min, 19%-30% A; 60-70 min, 30%-40% A; 70-100 min, 40%-85% A; 100-110 min, 85%-100% A. The chromatogram was monitored at a wavelength of 210 nm.

1.3 Results of fingerprints analysis

The HPLC fingerprints of SMD obtained from 15 different batches were analyzed using the Similarity Evaluation System for Chromatographic Fingerprints of Traditional Chinese Medicine (Version, 2004A). Thirty-six common peaks in the HPLC fingerprint appeared in 15 samples (**Figure S1**). By comparing the retention times with reference standards, we identified eight peaks as ephedrine (peak 4), pseudoephedrine (peak 5), chlorogenic acid (peak 6), rutinum (peak 11), hesperidin (peak 16), irisflorentin (peak 24), schizandrin (peak 25), asarinin (30) and deoxyschizandrin (peak 34).

Table S1 The information on the signaling pathway highlighted in the joint pathway analysis

No.	Signaling pathways	P-value
P1	Serotonergic synapse	0.0036
P2	SLC-mediated transmembrane transport	0.0047
P3	PPAR signaling pathway	0.0108
P4	COPI-independent Golgi-to-ER retrograde traffic	0.0194
P5	Golgi-to-ER retrograde transport	0.0237
P6	Ca-dependent events	0.0237
P7	Cytochrome P450 - arranged by substrate type	0.0270
P8	Intra-Golgi and retrograde Golgi-to-ER traffic	0.0279
P9	PLC beta mediated events	0.0364
P10	G-protein mediated events	0.0364
P11	GPCR downstream signaling	0.0417

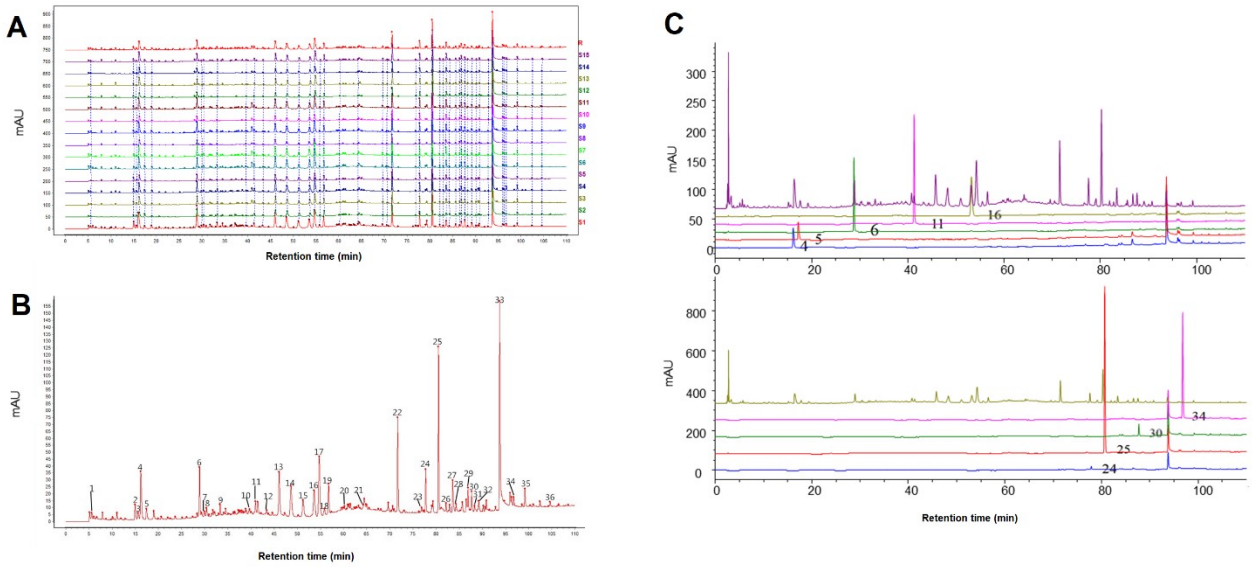

Figure S1 HPLC fingerprints of SMD from 15 different habitats (A), the SMD reference fingerprint (B), and the chromatograms of 9 standard references.

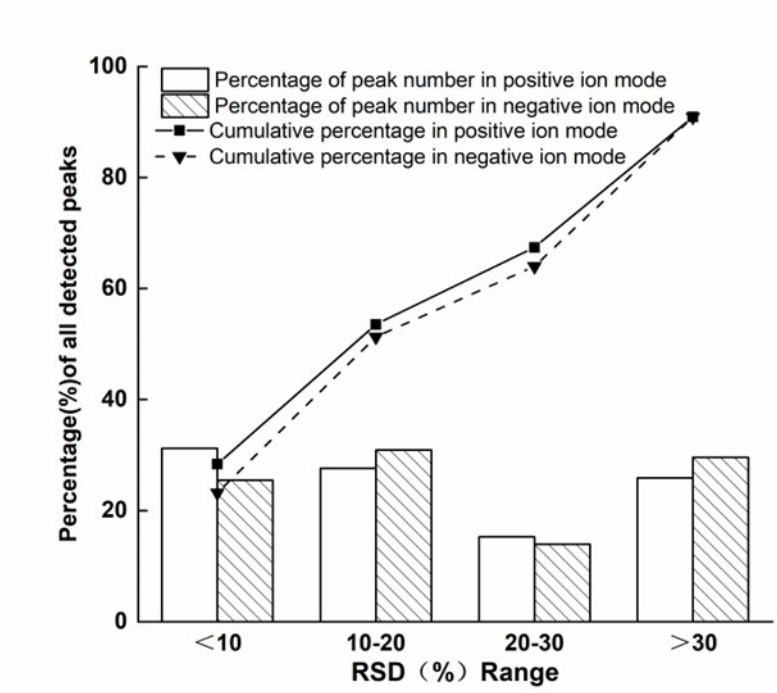

Figure S2. RSD (%) distribution of all metabolites in QC samples.

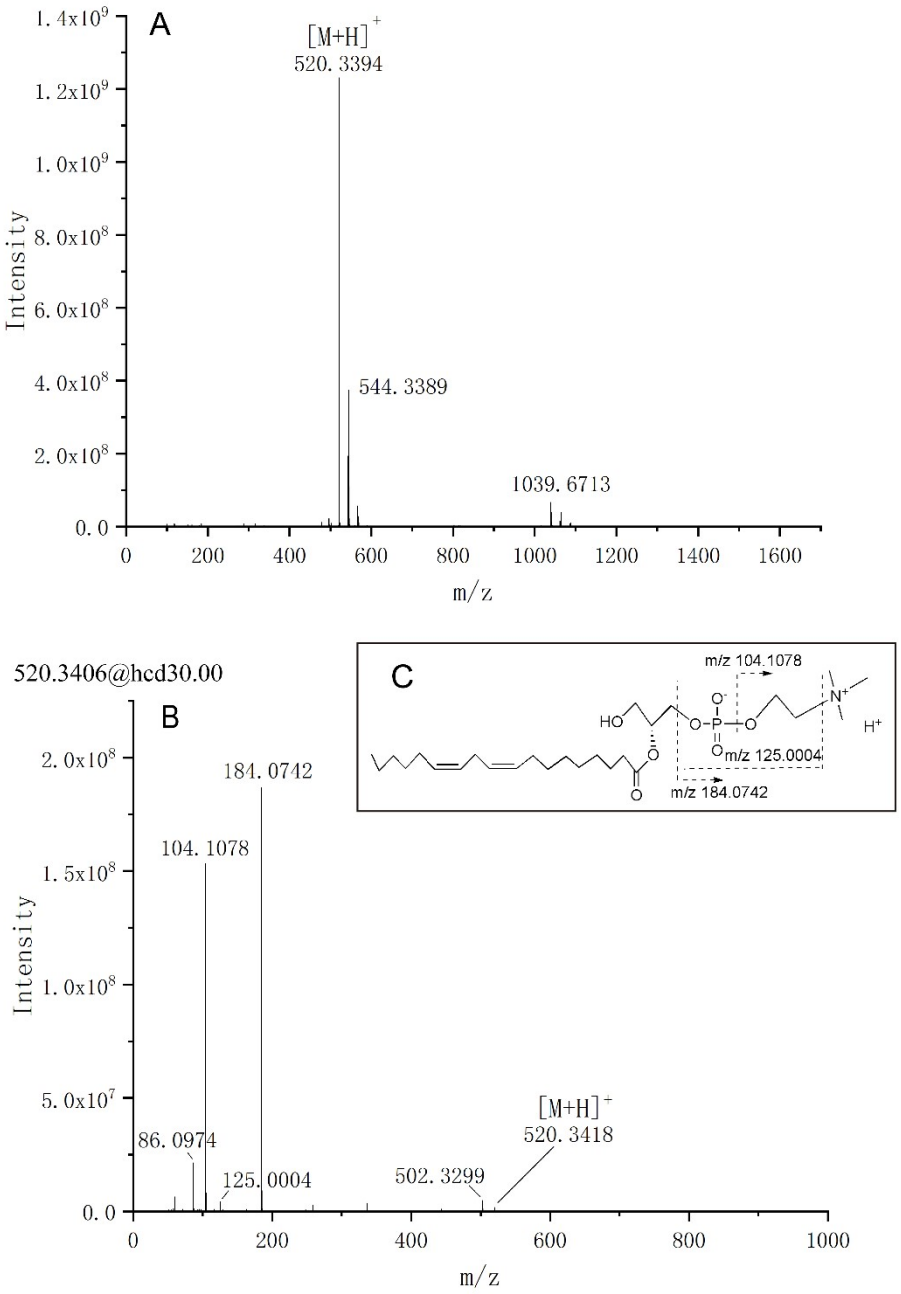

Figure S3. MS spectrum (A), tandem MS spectrum (B), and the probable fragmentation pathway (C) of the LysoPC (0:0/18:2) at RT 16.65_m/z 520.3394.