

SUPPLEMENTARY MATERIAL

Table S1. Processing parameters of LC-MS chromatograms using MzMine 2.0 (Pluskal et al., 2010). Chromatogram represents by the total ion current (TIC).

		(+H) Chromatograms	(-H) Chromatograms
1	Baseline correction		
	Chromatogram type	TIC	TIC
	MS level	1	1
	Smoothing	10E6	10E6
	Asymmetry	0.001	0.001
2	Mass detection (Exact Mass)		
	Noise level	4.5×10^5	4.5×10^5
3	Chromatogram builder		
	Min time span	0.05	0.05
	Min height	25000	25000
	m/z tolerance	0.002	0.002
4	Smoothing		
	Filter width	5	5
5	Chromatogram deconvolution (Local minimum search)		
	Chromatographic threshold	70%	70%
	Search minimum in RT range (min)	0.1	0.1
	Minimum relative height	7.0%	7.0%
	Minimum absolute height	30000	30000
	Min ratio of peak top/edge	2	2
	Peak duration range	0.0-2.0	0.0-2.0
6	Chromatogram alignment (join alignment)		
	m/z tolerance	0.001	0.001
	weight for m/z	80	80
	RT tolerance	0.3	0.3
	Weight for RT	20	20
7	Gap filling (Peak Finder)		
	Intensity tolerance	20%	20%
	m/z tolerance	0.001	0.001
	Retention time tolerance	0.1	0.1
	RT correction	marked	marked
8	Filtering		
	Minimum peaks in a row	25	25
	Ions excluded from database	<75 Between 0.0 and 1 min Between 28.5 and 30 min	<85 Between 0.0 and 1,1 min Between 27.0 and 30 min

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Pathway enrichment analysis floor soil versus suspended soil without epiphytes

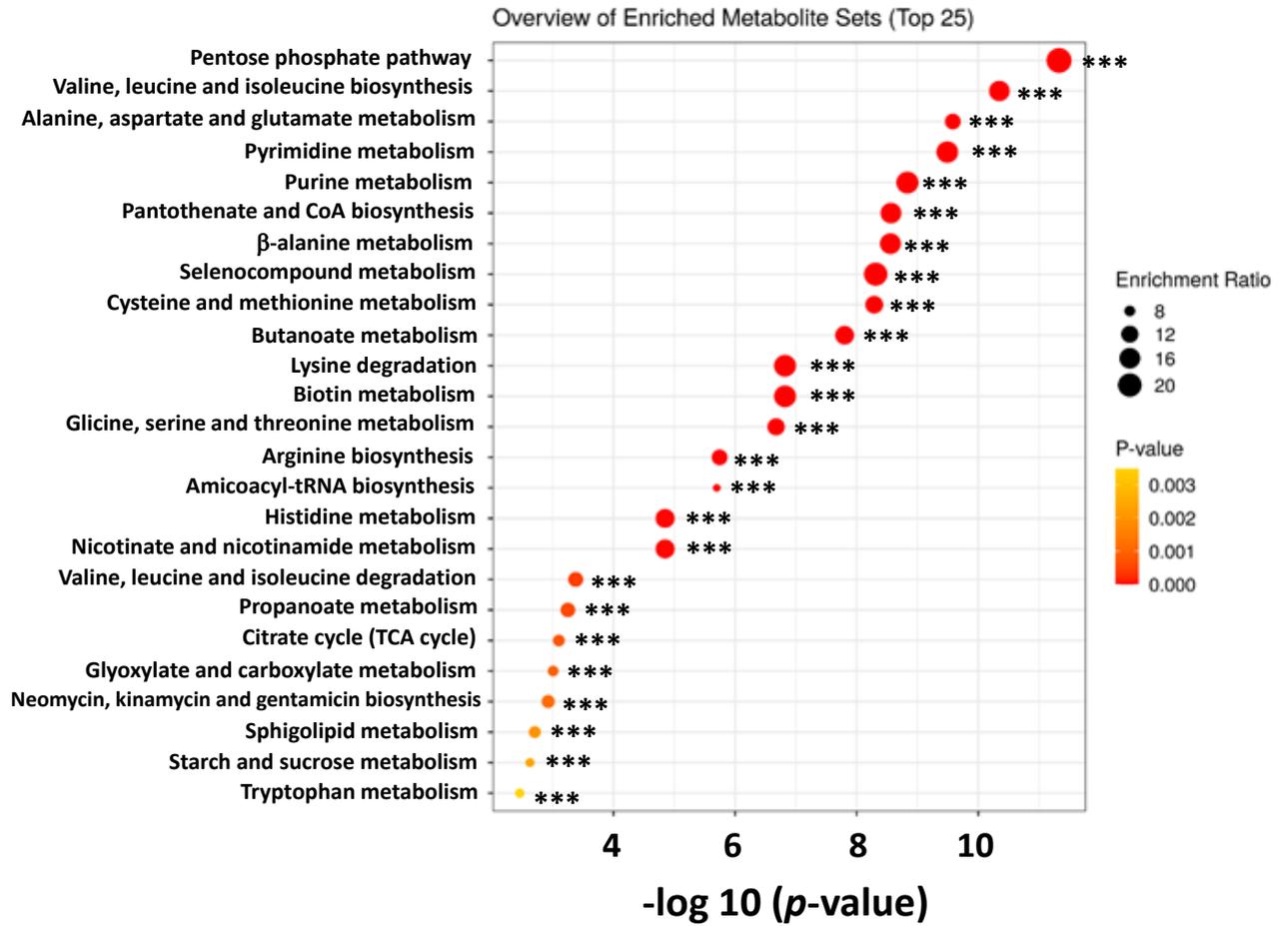


Figure S1. Enrichment pathway analysis of soil metabolomics profile versus suspended soils without epiphytes. *** ($P < 0.001$).