

Table S1. Parameter settings used for metabolomics data processing of *Pseudomonas* extract and wheat root samples

Step	Method	Parameters	Values wheat root samples	Values <i>Pseudomonas</i> strains culture samples
Peak detection (<i>Peakpicking</i>)^a	centWave	ppm	10	10
		mzdiff	0.05	0.05
		prefilter	3, 2500	3, 5000
		snthresh	10	10
		peakwidth	4, 15	4, 15
		noise	5000	10000
Peak grouping (<i>group</i>)^a	density	bw	4	3
		mzwid	0.25	0.25
		minfrac	0.05	0.01
FillPeaks	chrom			

^a data processed with xcms R-package on collaborative Galaxy platform "Workflow4metabolomics" version 3.3