Supplementary Table 3. Description of the processes and parameters applied to LC-MS chromatograms with MZmine ver.2.38 to obtain the metabolomic fingerprints of *Arabidopsis* root samples from both positive and negative ionization modes.

		Parameters
1	**Baseline correction – RollingBall baseline corrector**	
	Chromatogram type	TIC
	Use m/z bins	No
	wm	25
	ws	25
2	**Mass detection** (exact Mass)	
	Noise level	1×10^3
3	**FTMS shoulder peak filter**	
	Mass Resolution	60,000
	Peak model function	Lorentzian
4	**Chromatogram builder**	
	Minimum time span	0.04
	Minimum height	1×10^3
	m/z tolerance	0.0005 m/z or 7ppm
5	**Smoothing**	
	Filter width	5
6	**Chromatogram deconvolution (local minimum search)**	
	Chromatographic threshold	40%
	Search minimum in RT range (min)	0.3
	Minimum relative height	30%
	Minimum absolute height	3000
	Minimum ratio of peak top/edge	1.5
	Peak duration range	0-1
7	**Normalization – Retention time normalizer**	
	m/z tolerance	0.0005 m/z or 7ppm
	RT tolerance	0.3
	Minimum Standard Intensity	1×10^5
8	**Chromatogram alignment (join alignment)**	
	m/z tolerance	0.0005 m/z or 6ppm
	Weight for m/z	80
	RT tolerance	0.25
	Weight for RT	40
9	**Gap filling (Peak Finder)**	
	Intensity tolerance	30%
	m/z tolerance	0.0005 m/z or 6ppm
	Retention time tolerance	0.25
	RT correction	Yes
10	**Metabolite Assignation**	
	m/z tolerance	0.001 m/z or 15ppm*
	RT tolerance	0.45*
11	**Data Exported**	Peak Area

RT, retention time; m/z, mass to charge ratio

* Metabolite assignation filtered a posteriori (Supplementary Table 5)