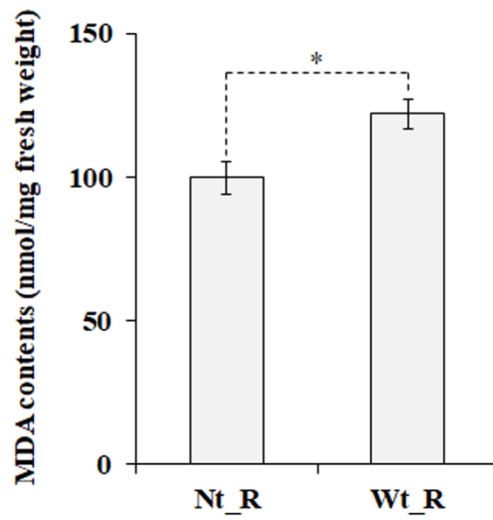


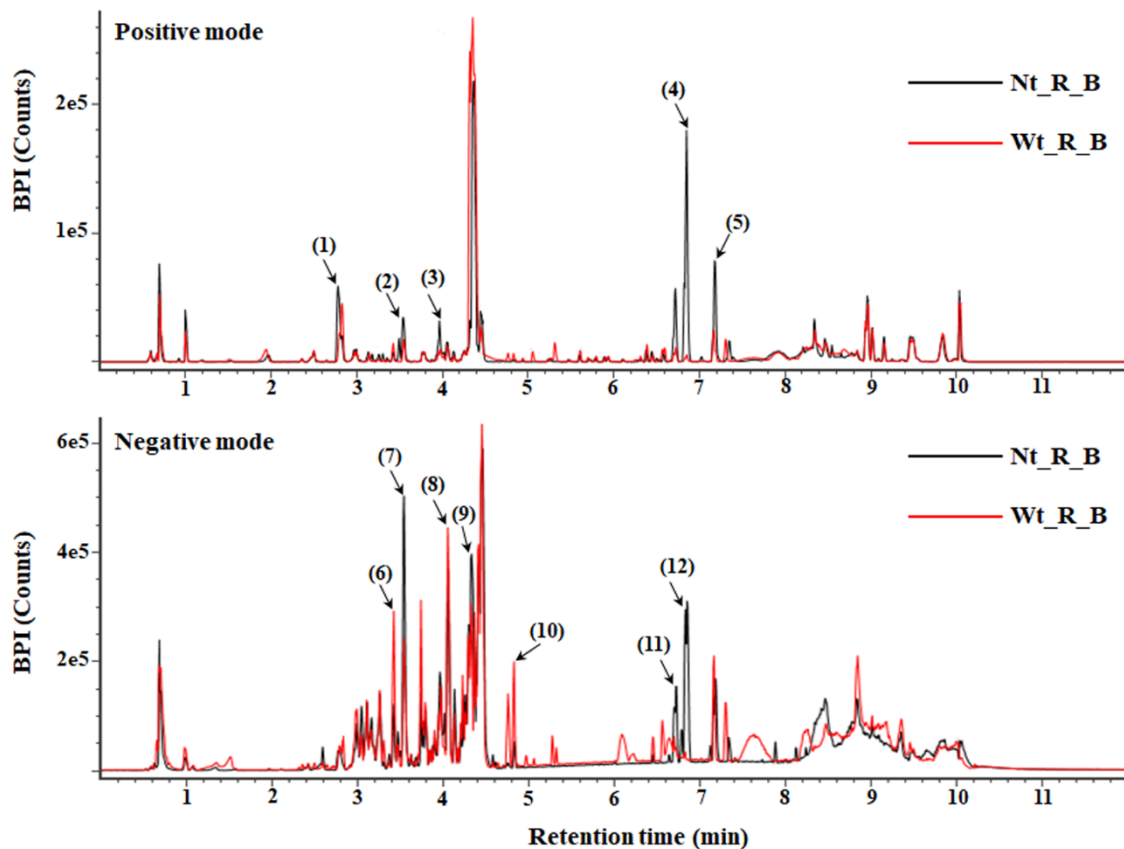
Supplementary materials

Supplementary Table 1. Primer list for quantitative real-time PCR analysis.

Source	Gene	Sequence (5'-3')
B16F10 cell	Tyrosinase	F-ATAGGTGCATTGGCTTCTGG R-CCAACGATCCCATTTTTCTT
	TRP1	F-GAGTGACATCCTGTGGCTCA R-CGATACCCTGGGAACACTTT
	TRP2	F-GCATCTGTGGAAGGGTTGTT R-ACTCCTTCTGAATGGGACC
	β -actin	F-CCCACTCCTAAGAGGAGGATG R-AGGGAGACCAAAGCCTTCAT
<i>Platycodon grandiflorus</i>	PlgSS1	F-GCCGGAAAAGTAACCGATAAATG R-TTGGCGATATAACAGCAGTGATG
	PlgSS2	F-CAATCGGAACGCTAGCTCTATGT R-TCAGCATGGAAGCAAAATCG
	PlgSE1	F-GCCCTGCTCTCTGGTCTGAA R-CCCAGATGCATTTCGAAATCA
	PlgSE2	F-TCGACAGGACCAGTATCTTTGCT R-AATCAATCTGGCTCCAATCCA
	Plg β -AS1	F-GGACTGCCAGGATAGGGAGAA R-ACGTCAACCGGTAAAGCGTAA
	Plg β -AS2	F-AACCAGGGAAGGGCAGAGA R-GGTTGACGGGTTCCAACAGA
	Plg β -A28O	F-GCCAACTCAACGCACAAAAAC R-AACTCGCGGCTACTCTTTTCC
	PlgGAPT	F-ACGTTCTTGAACCAGTTGCC R-GCACCCGGTATTTGTCCTTC
	PlgCAS	F-TTCGCAAGGCGTGTGATTT R-TGAGAGATAGCATAGCCCATCCA
	PlgActin	F-CCATACAGTCCCCATTTATGAAG R-GCTAACTTCTCCTTCATGTCTCTCA



Supplementary Fig. 1. Changes in root MDA content by waterlogging. Asterisks (* $p < 0.05$) indicate significant differences between non-treated (Nt_R) and waterlogging-treated roots (Wt_R). The data are presented as means \pm SE (n = 20).



Supplementary Fig. 2. Chromatograms of BuOH fractions of non-treated root extracts (Nt_R_B) and waterlogging-treated root extracts (Wt_R_B) by UPLC-ESI-Q-TOF-MS in positive and negative modes.