

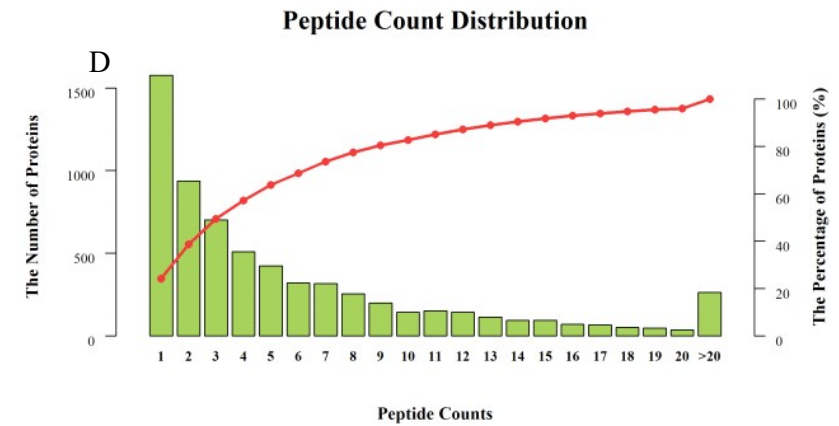
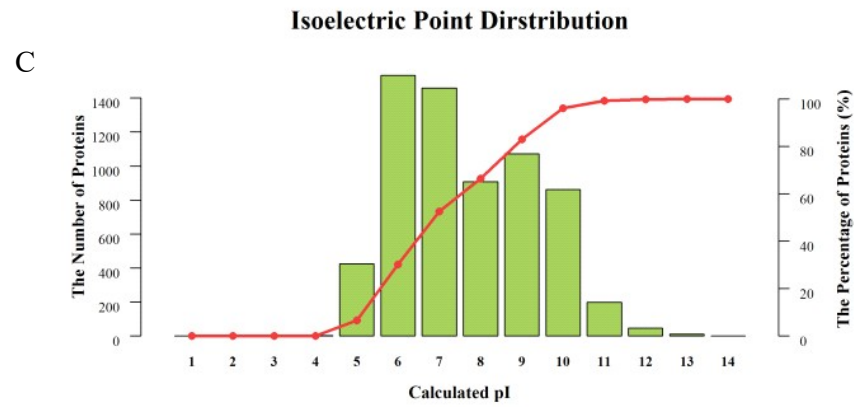
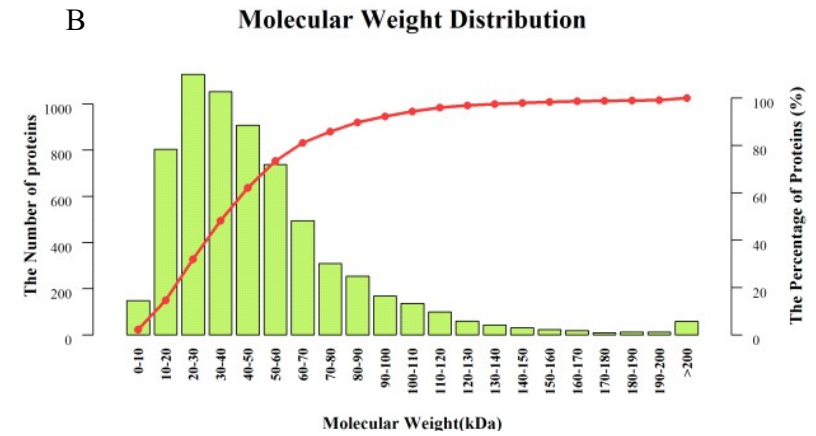
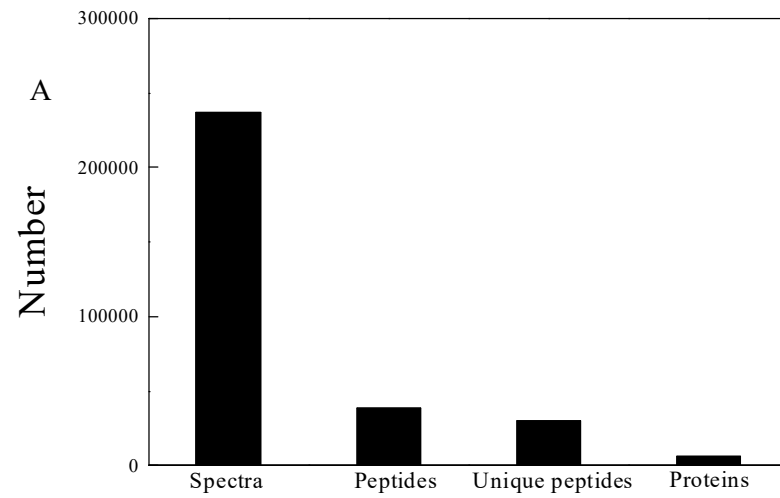


Fig S1. Identification and analysis of proteome in WT and the *nla* mutant. (A) Total spectra, peptides, unique peptides and identified proteins by iTRAQ proteomic analysis. (B) The molecular distribution, (C) Isoelectric point distribution, (D) Peptide count distribution.

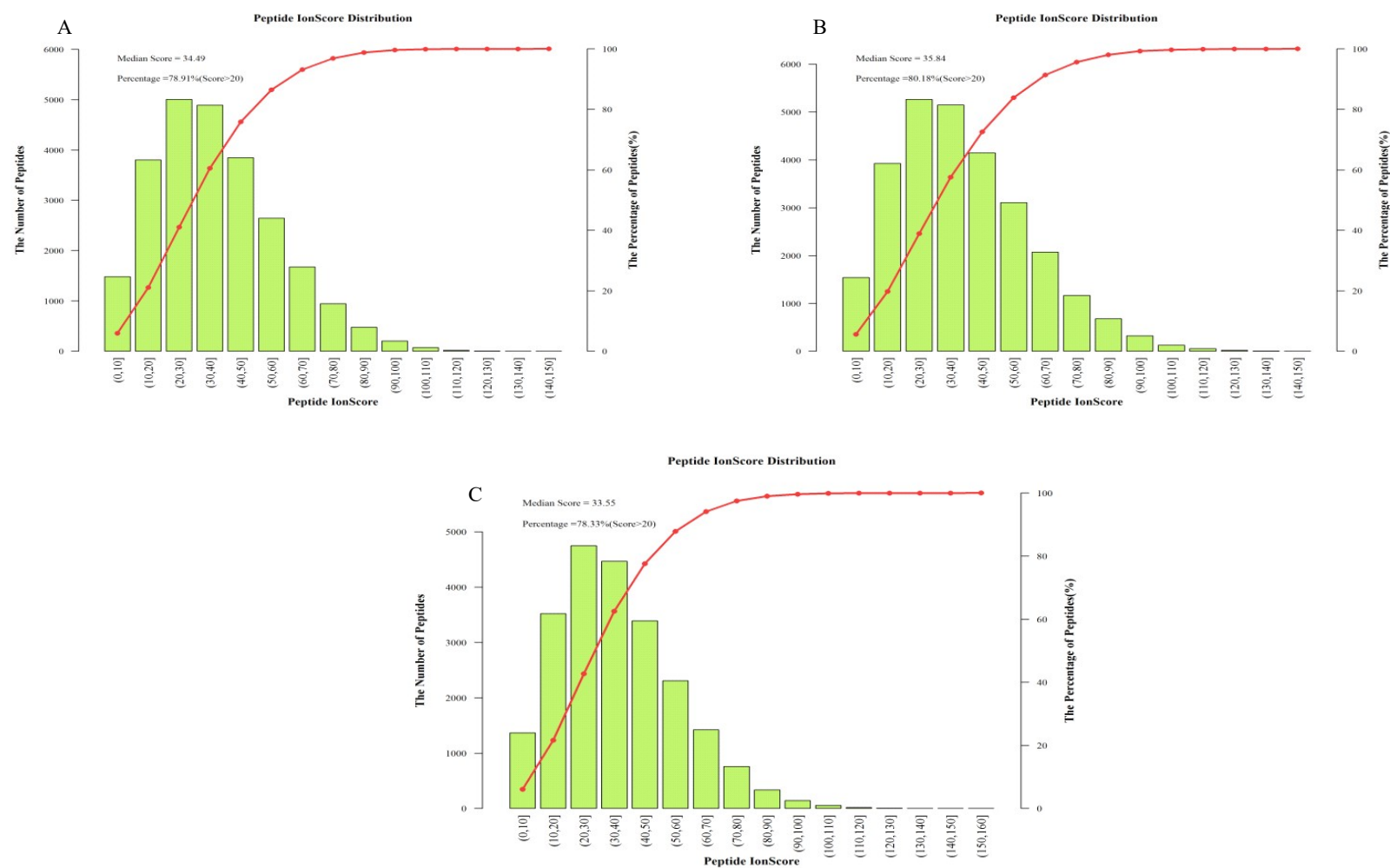


Fig S2. Peptide ionscore distribution of the detected peptides.

Table S1 The primers of the genes for q-PCR assays

Genes	Forward primer (5' to 3')	Reverse primer (5' to 3')
<i>AtActin2</i>	AGTGGTCGTACAACCGGTATTGT	GATGGCATGAGGAAGAGAGAAAC
<i>AtMYB2</i>	CAAACCTCTCCAACACATGAAG	CTCTTCTAACATCTGGACGTAAG
<i>AtNRT1.7</i>	GCAACAGCCAGGACCCACTCAG	AACCCCAAAAGGGATGCTACAA
<i>AtLHT1</i>	AGTCATCGTTGCTTACATCGTCGT	TGGCGATAGGACCATCAAGAAAAGA
<i>AtORE1</i>	CTTACCATGGAAGGCTAAGATGGG	TCGGGTATTTCCGGTCTCTCAC
<i>AtRNS3</i>	AAGCTGGTCTCAAGCTCAAACAG	TCCGGTTTGATCCCAGCATTGG
<i>AtSAG29</i>	TAAGCGCCGTTATGTGGTTCGC	ATCCCACCACGTTTGGAATCGC
<i>AtVIN2</i>	CAAAGGCAAACCACCTCATGGC	TCTGAGTGGGACCCATAGAACTCG