Supplemental Data

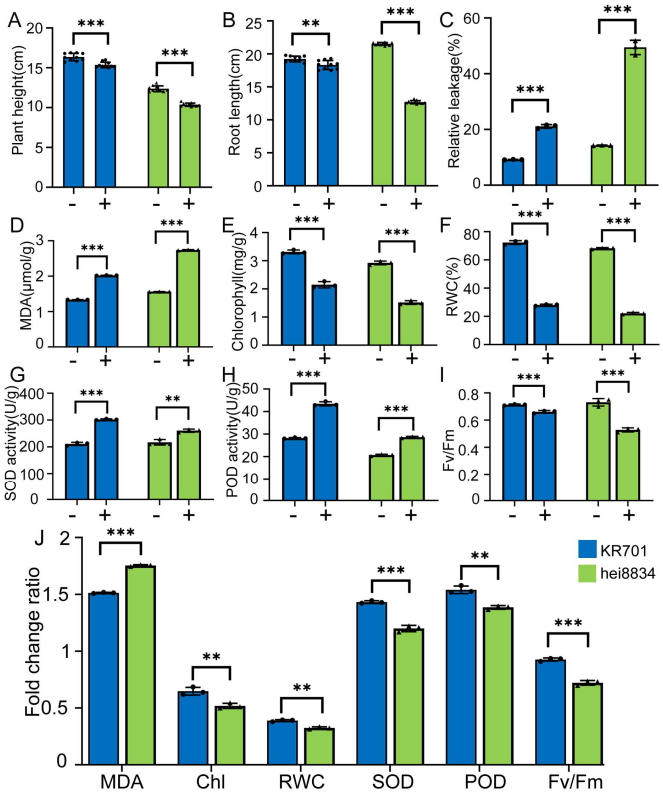

Figure S1. Changes in physiological traits of maize seedlings after chilling stress at the first leaf stage. (A-I) Changes in the measured values of ten physiological traits after chilling stress. Different stress treatments: -: uniformly growing seedlings were grown at normal condition for 24 h. +: uniformly growing seedlings were grown at 4°C for 24 h. **(J)** The fold change ratio of six representative traits. Fold change ratio: +chilling/-chilling. Blue square: KR701. Green square: hei8834. The plant height and root length data are the means ± SD of ten replicates. Other trait data are means ± SD of three replicates. ** and *** denote levels of significance at $p < 0.01$ and $p < 0.001$, respectively.

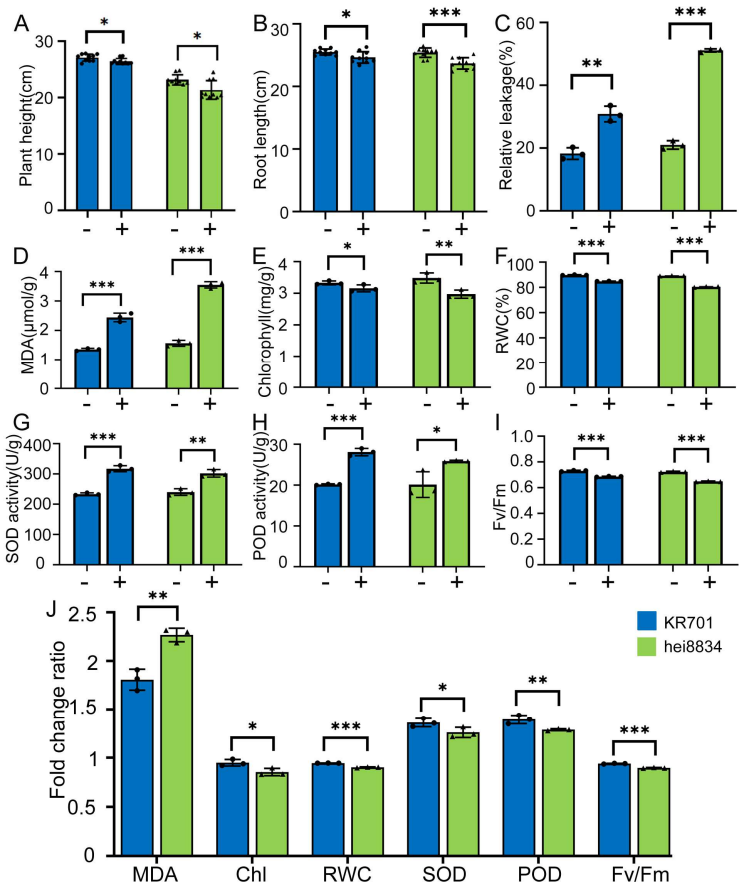

Figure S2. Changes in physiological traits of maize seedlings after chilling stress at the third leaf stage. (A-I) Changes in the measured values of ten physiological traits after chilling stress. Different stress treatments: -: uniformly growing seedlings were grown at normal condition for 24 h. +: uniformly growing seedlings were grown at 4°C for 24 h. **(J)** The fold change ratio of six representative traits. Fold change ratio: +chilling/-chilling. Blue square: KR701. Green square: hei8834. The plant height and root length data are the means ± SD of ten replicates. Other trait data are means ± SD of three replicates. *, ** and *** denote levels of significance at $p < 0.05$, $p < 0.01$ and $p < 0.001$, respectively.

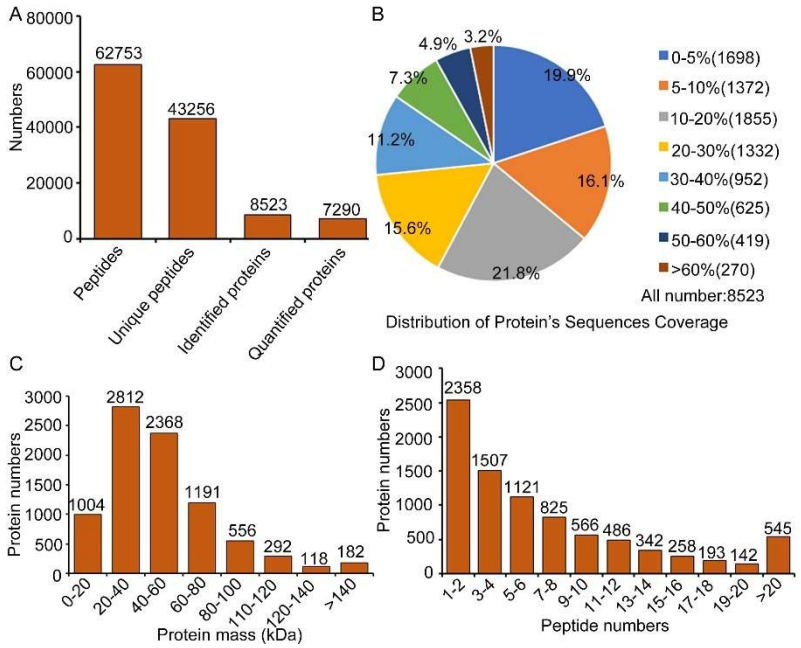

Figure S3. Display of the main data identified by proteomics. (A) The proportional distribution of the number of peptides and proteins identified in proteomics by searching the maize database. **(B)** The distribution of protein sequence coverage. **(C)** The distribution of the identified protein size. **(D)** Proportional distribution of the number of identified peptides.

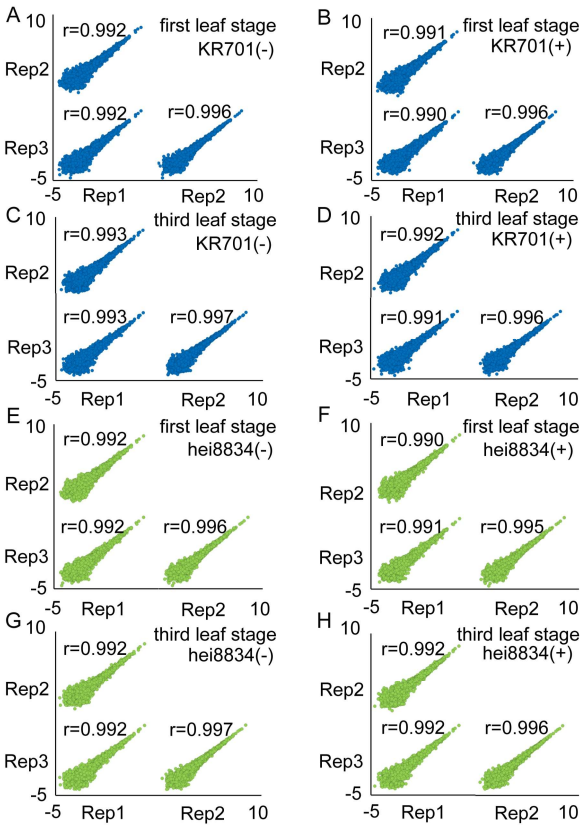

Figure S4. Sample correlation of proteomics data. The repeatability of the experiment was verified by data correlation analysis among three replicates. *Pearson* correlation coefficient analysis was used. **(A, B, C, D)** Tolerant line KR701. **(E, F, G, H)** Sensitive line hei8834. (-): uniformly growing seedlings were grown at normal condition for 24 h. (+): uniformly growing seedlings were grown at 4°C for 24 h.

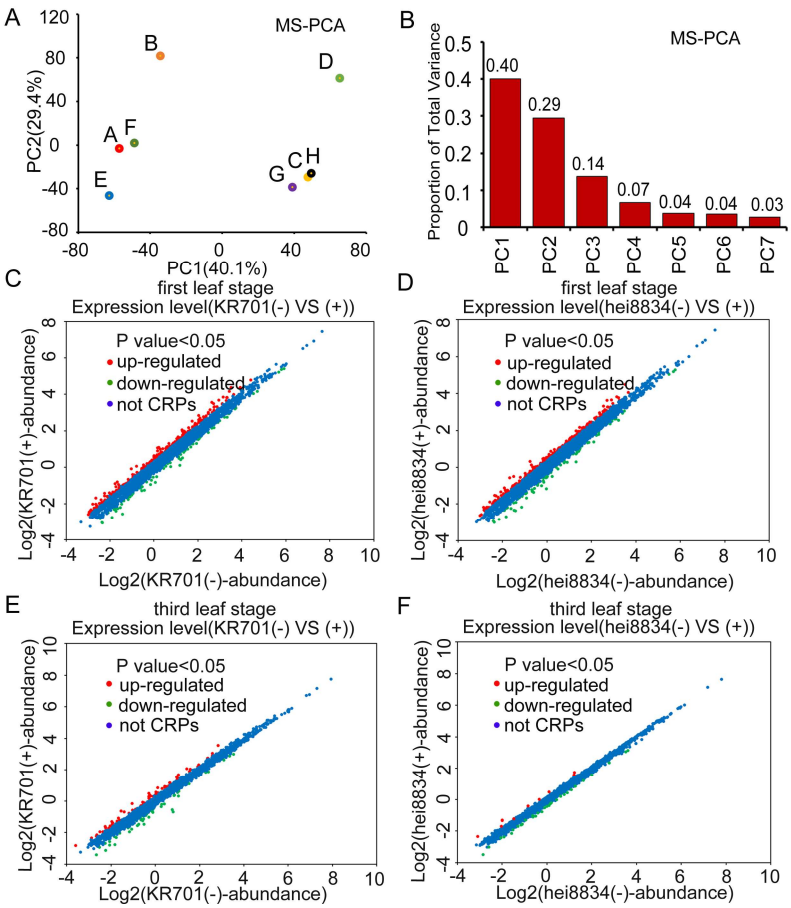

Figure S5. Summary of the proteomics data. (A) Principal component (PCA) analysis. Letters A-D: KR701(-), KR701(+), hei8834(-) and hei8834(+) at the first leaf stage. Letters E-H: KR701(-), KR701(+), hei8834(-) and hei8834(+) at the third leaf stage. **(B)** The proportion of the total variance of each principal component. **(C, D, E, F)** The overall distribution of protein abundance. The red, green and blue dots represent the upregulated CRPs, downregulated CRPs and non-CRPs, respectively. (-): uniformly growing seedlings were grown at normal condition for 24 h. (+): uniformly growing seedlings were grown at 4°C for 24 h.

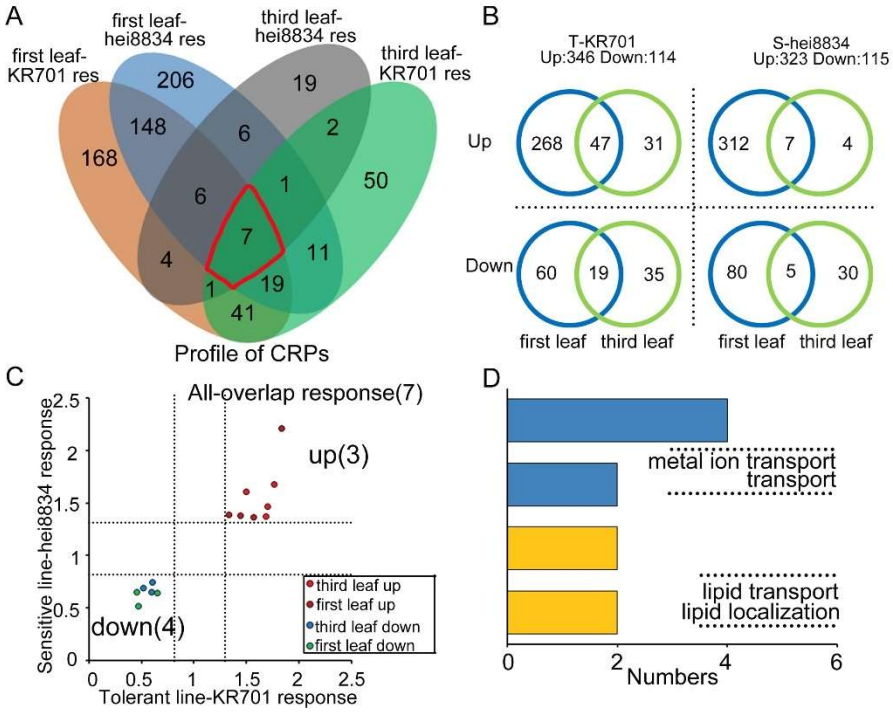

Figure S6. Co-expression analysis of CRPs. (A) Profile of CRPs. **(B)** Classification of CRPs. **(C)** The specific distribution of all overlapping CRPs. **(D)** GO enrichment analysis of all overlapping CRPs.

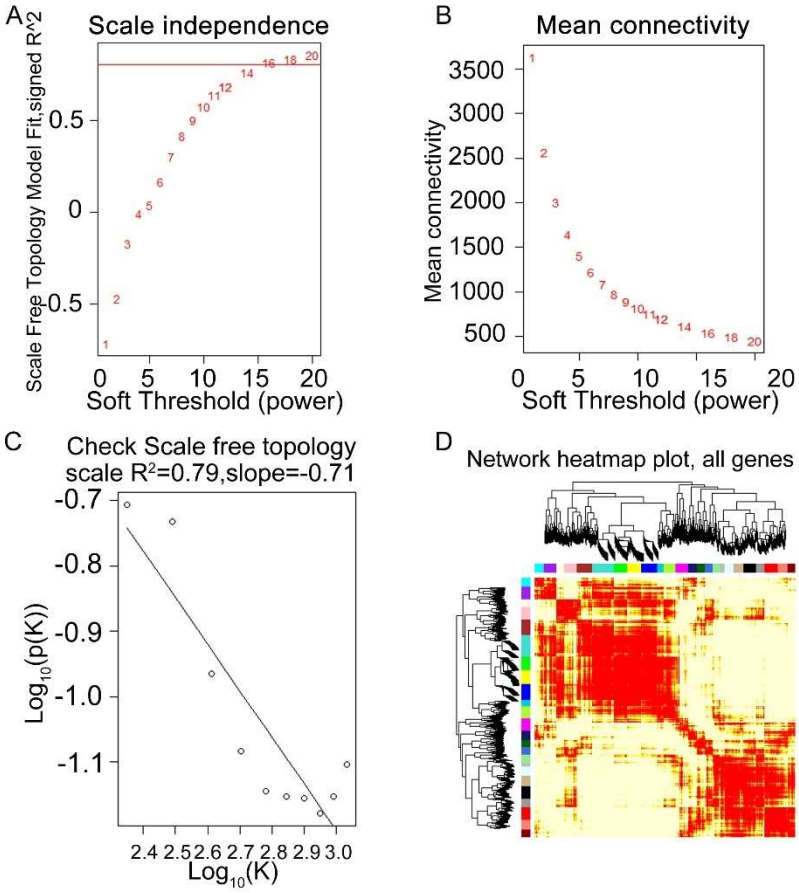

Figure S7. Assessment of soft thresholds used in WGCNA to generate coexpression networks. (A) Scale independence for the coexpression network. The red line shows the position where R^2 reaches 0.8. **(B)** Mean connectivity in the coexpression network. **(C)** Reliability verification of power selection. **(D)** Visualized gene network (TOM plot).

Supplemental Table S1

Physiological responses induced by chilling stress in maize inbred lines KR701 (chilling tolerant) and hei8834 (chilling sensitive) at the first leaf and third leaf stage.

Supplemental Table S2

Basic profiles of proteomics data.

Supplemental Table S3

Protein abundance of the tolerant line KR701 and sensitive line hei8834 at the first leaf and third leaf stage.

Supplemental Table S4

The average abundance of proteins in different materials from the tolerant line KR701 and sensitive line hei8834 at the first leaf and third leaf stage.

Supplemental table S5

The fold change ratio (abundance) of proteins in the tolerant line KR701 and sensitive line hei8834 at the first leaf and third leaf stage.

Supplemental Table S6

The $\log_2$ (fold change ratio) of responsive proteins at the first leaf and third leaf stage.

Supplemental Table S7

Distribution and GO enrichment analysis of CRPs.

Supplemental Table S8

Division of representative modules.