

Appendix

Appendix A Specific primer pairs used for qPCR expression analysis.

Appendix B Overview of quantitative proteomic analysis. (A) Repeatability between two biological replicates at Cd treatment time points of 12, 24, 48, and 72 h; (B) Basic iTRAQ information statistics of two replicates; (C) Distribution of proteins identified among different molecular weights (Means \pm SD, two replicates); (D) Sequence coverage of proteins by the identified peptides (two replicates' average).

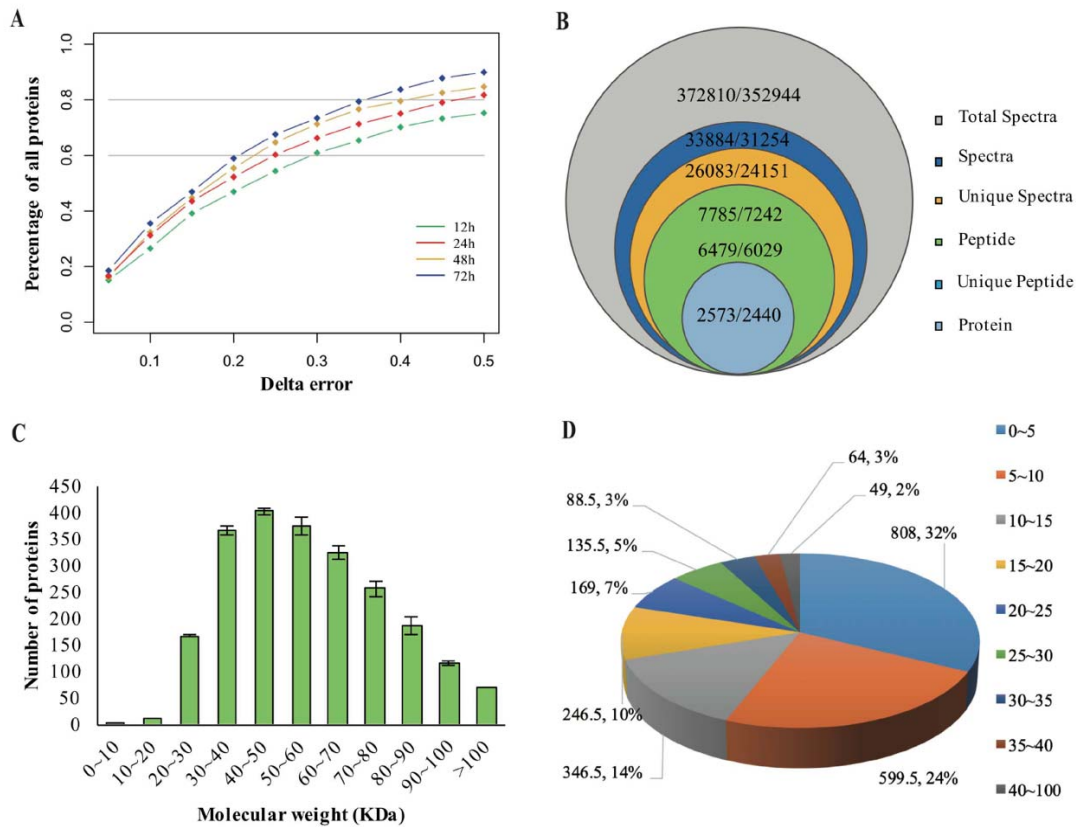
Appendix C Proteomic variation among differential time points of Cd treatment. Venn diagram of the differentially expressed proteins at 12, 24, 48 and 72 h (Left: up-regulated; right: down-regulated).

Appendix D Gene ontology categories for up-regulated (A) and down-regulated (B) proteins. The top 20 enriched GO-terms in three different clusters were shown. Green bar represented the percentage of genes compared with reference, brown bar represented the percentage of genes in differentially abundant proteins.

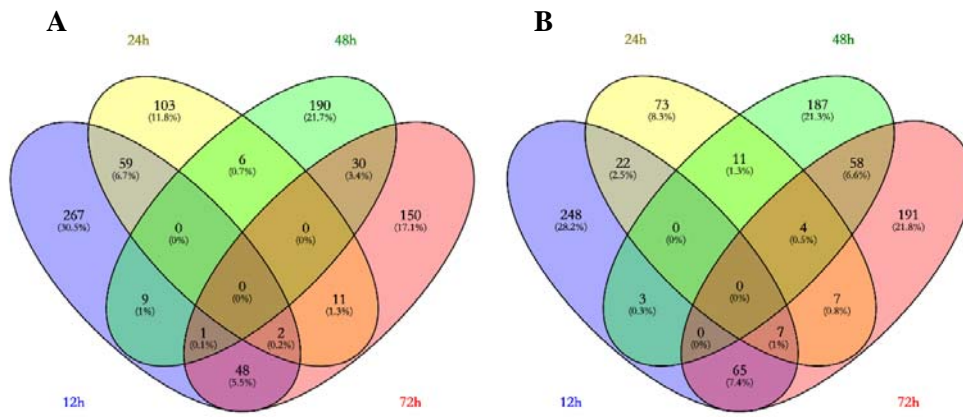
Appendix E Many up-regulated or down-regulated KEGG pathways of candidate regulated proteins in response to cadmium. The input number means the number of proteins found in this study matching with the pathway. The input number means the number of proteins found in this study matching with the pathway.

Appendix A Specific primer pairs used for qPCR expression analysis.

Gene	Forward primer (5'-3')	Reverse primer (5'-3')	Size (bp)
<i>GRMZM2G158034</i>	GGCAGAGGGACTCCTAAATGTA	TGGATGATGTCACACGAACACT	121
<i>GRMZM2G308687</i>	CGGGAGTAATAATGACGAACCA	ACAATAGAAAATACAACGACGACG	100
<i>GRMZM2G039639</i>	CCATCGAGCTGCTCAAACATA	CCAACCTTGAAGCTAGAAGAACA	164
<i>GRMZM2G047055</i>	GCCGCTTTCTCCTATTCATCA	CCTCATCAGGCATCTCATTAAAA	113
<i>GRMZM2G059693</i>	CGTAGCTTTTGGATTGCATGTT	GGAGAGGATGCATATATTCAACAA	127
<i>GRMZM2G146670</i>	GTCCTAGCATGACTGTTTGGGT	TCCTCAATGAAACATTTTCGCA	124
<i>GRMZM2G150616</i>	GGCATCTTTGTTTGCTGTAGTCA	CGAGCTTGAATTATTGTGAAGGT	122
<i>GRMZM2G156861</i>	GCACTAGTTGTTTGCGTTTCC	GCCTTATTACAACAGTCCTCACG	122
<i>GRMZM2G156684</i>	GCTTTTGAGGAGCGTGTTCTG	ATCAAATGCTATTTGCTGCACAT	125
<i>GRMZM2G178817</i>	CGTTTCAGGTGGACAAGAAGG	TGCATAAAACAATGACAATAGCG	103
<i>gpn1</i>	TGACCAAGGTGAAGAGCACTGT	CAAATCTCACGTGGCTATGAAAC	134



Appendix B Overview of quantitative proteomic analysis. (A) Repeatability between two biological replicates at Cd treatment time points of 12, 24, 48, and 72 h; (B) Basic iTRAQ information statistics of two replicates; (C) Distribution of proteins identified among different molecular weights (Means \pm SD, two replicates); (D) Sequence coverage of proteins by the identified peptides (two replicates' average).



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Appendix E Many up-regulated or down-regulated KEGG pathways of candidate regulated proteins in response to cadmium. The input number means the number of proteins found in this study matching with the pathway. The input number means the number of proteins found in this study matching with the pathway.

KEGG pathway	Regulation	Pathway ID	Input number	Background number	<i>p</i> -Value	Corrected <i>p</i> -Value
Ribosome	Up	zma03010	34	509	3.71E-24	1.30E-22
Proteasome	Up	zma03050	5	99	0.00070267	0.01229672
2-Oxocarboxylic acid metabolism	Up	zma01210	1	86	0.44792178	0.67497933
Glutathione metabolism	Up	zma00480	3	146	0.08075043	0.67497933
Protein processing in endoplasmic reticulum	Up	zma04141	4	333	0.19570278	0.67497933
Alanine, aspartate and glutamate metabolism	Up	zma00250	1	82	0.43259041	0.67497933
Arginine and proline metabolism	Up	zma00330	2	111	0.17867168	0.67497933
Biosynthesis of amino acids	Up	zma01230	4	378	0.26070606	0.67497933
beta-Alanine metabolism	Up	zma00410	1	57	0.32675592	0.67497933
Phenylalanine, tyrosine and tryptophan biosynthesis	Up	zma00400	1	75	0.40473979	0.67497933
Cyanoamino acid metabolism	Up	zma00460	1	58	0.33134212	0.67497933
Fructose and mannose metabolism	Up	zma00051	1	88	0.45543296	0.67497933
Galactose metabolism	Up	zma00052	1	85	0.44412783	0.67497933
Pentose and glucuronate interconversions	Up	zma00040	1	68	0.37553664	0.67497933
Glyoxylate and dicarboxylate metabolism	Up	zma00630	1	90	0.46284297	0.67497933
Pentose phosphate pathway	Up	zma00030	1	78	0.41683771	0.67497933
Nitrogen metabolism	Up	zma00910	1	54	0.31280969	0.67497933
One carbon pool by folate	Up	zma00670	1	21	0.13919481	0.67497933
Pantothenate and CoA biosynthesis	Up	zma00770	1	34	0.21224131	0.67497933
Photosynthesis	Up	zma00195	2	103	0.15941616	0.67497933
Plant-pathogen interaction	Up	zma04626	2	223	0.45298524	0.67497933
Selenocompound metabolism	Up	zma00450	1	30	0.19044451	0.67497933
SNARE interactions in vesicular transport	Up	zma04130	1	51	0.29857753	0.67497933
Ubiquitin mediated proteolysis	Up	zma04120	3	193	0.14820339	0.67497933
Glycine, serine and threonine metabolism	Up	zma00260	1	104	0.51199127	0.71678778
Cysteine and methionine metabolism	Up	zma00270	1	119	0.55971656	0.7534646
Pyrimidine metabolism	Up	zma00240	1	181	0.71259287	0.83135834
Carbon metabolism	Up	zma01200	2	346	0.68768864	0.83135834
KEGG pathway	Regulation	Pathway ID	Input	Background	<i>p</i> -Value	Corrected

			number	number		p-Value
Amino sugar and nucleotide sugar metabolism	Up	zma00520	1	168	0.68565737	0.83135834
RNA degradation	Up	zma03018	1	181	0.71259287	0.83135834
Starch and sucrose metabolism	Up	zma00500	1	226	0.78935491	0.89120716
RNA transport	Up	zma03013	1	252	0.82405014	0.90130484
Plant hormone signal transduction	Up	zma04075	1	371	0.92311867	0.97906526
Metabolic pathways	Up	zma01100	10	2519	0.98459453	0.98459453
Biosynthesis of secondary metabolites	Up	zma01110	5	1349	0.95878445	0.98459453
Phenylpropanoid biosynthesis	Down	zma00940	10	232	3.86E-06	0.00010409
Phenylalanine metabolism	Down	zma00360	8	182	3.30E-05	0.00044601
Endocytosis	Down	zma04144	6	207	0.00266976	0.0240278
Glycosaminoglycan degradation	Down	zma00531	2	19	0.0081315	0.05488763
Oxidative phosphorylation	Down	zma00190	4	180	0.03213356	0.17352124
Cyanoamino acid metabolism	Down	zma00460	2	58	0.05822745	0.26202351
Biosynthesis of secondary metabolites	Down	zma01110	13	1349	0.10353342	0.31555499
Spliceosome	Down	zma03040	4	271	0.10477546	0.31555499
Linoleic acid metabolism	Down	zma00591	1	16	0.105185	0.31555499
Ribosome	Down	zma03010	6	509	0.11934696	0.32223679
Lysine biosynthesis	Down	zma00300	1	27	0.1673323	0.41072473
Starch and sucrose metabolism	Down	zma00500	3	226	0.18754652	0.42197968
Metabolic pathways	Down	zma01100	19	2519	0.2892173	0.5861479
Amino sugar and nucleotide sugar metabolism	Down	zma00520	2	168	0.30392854	0.5861479
Inositol phosphate metabolism	Down	zma00562	1	83	0.42329491	0.74577337
Fructose and mannose metabolism	Down	zma00051	1	88	0.44193977	0.74577337
Carbon fixation in photosynthetic organisms	Down	zma00710	1	115	0.53277831	0.81739235
Cysteine and methionine metabolism	Down	zma00270	1	119	0.54492824	0.81739235
Glutathione metabolism	Down	zma00480	1	146	0.6191484	0.83645544
Phagosome	Down	zma04145	1	147	0.621654	0.83645544
Pyrimidine metabolism	Down	zma00240	1	181	0.6977929	0.83645544
Glycolysis / Gluconeogenesis	Down	zma00010	1	186	0.70762885	0.83645544
Biosynthesis of amino acids	Down	zma01230	2	378	0.71253612	0.83645544
Purine metabolism	Down	zma00230	1	234	0.78732039	0.87620113
RNA transport	Down	zma03013	1	252	0.81129735	0.87620113
Protein processing in endoplasmic reticulum	Down	zma04141	1	333	0.89004883	0.89920778
Carbon metabolism	Down	zma01200	1	346	0.89920778	0.89920778

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