## Transcriptome analysis of genes related to cadmium absorprion and transportation in pepper

Riyong Wang<sup>a</sup>, Xiongze Dai<sup>b</sup>, Junheng Lv<sup>c</sup>, Zhuqing Zhang<sup>a,\*</sup> and Lijun Ou<sup>b,\*</sup>

<sup>a</sup>Institute of Vegetable Research, Hunan Academy of Agricultural Science, Changsha, Hunan 410125,

China

<sup>b</sup>Horticulture College, Hunan Agricultural University, Changsha, Hunan 410128, China <sup>c</sup>Longping Branch, Graduate School of Hunan University, Changsha, Hunan 410006, China

\*Corresponding authors: <a href="mailto:cszzq@126.com">cszzq@126.com</a> / <a href="mailto:ou9572@126.com">ou9572@126.com</a> /

**Supplementary material** 

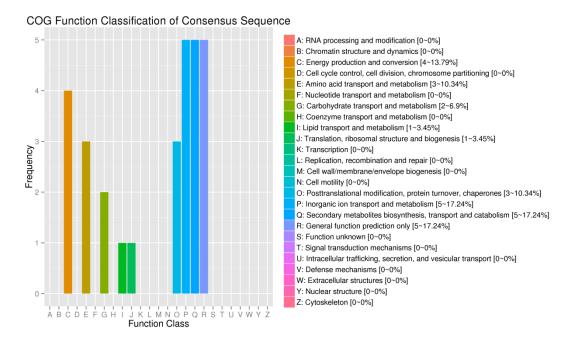


Figure S1. COG function classification of DEGs in the fruits.

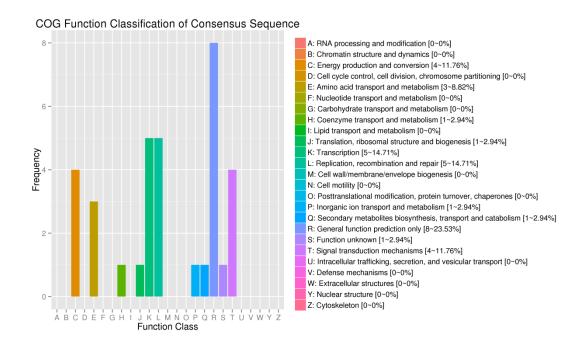


Figure S2. COG function classification of DEGs in the leaves.

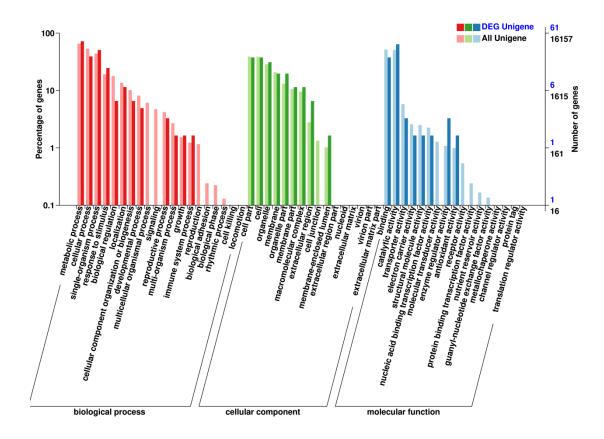


Figure S3. GO function classification of all unigenes and DEGs in the fruits.

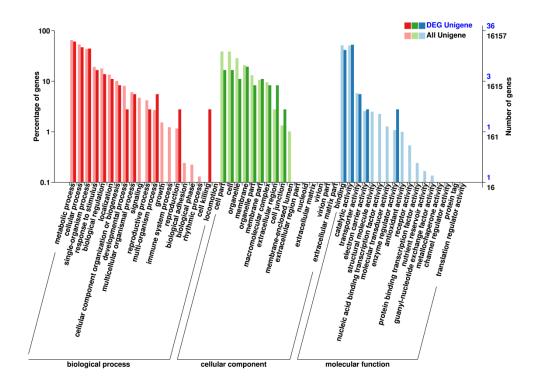


Figure S4. GO function classification of all unigenes and DEGs in the leaves.

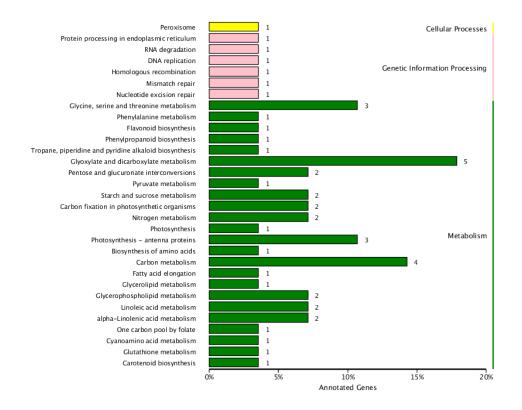


Figure S5. KEGG enrichment of DEGs in the fruits.

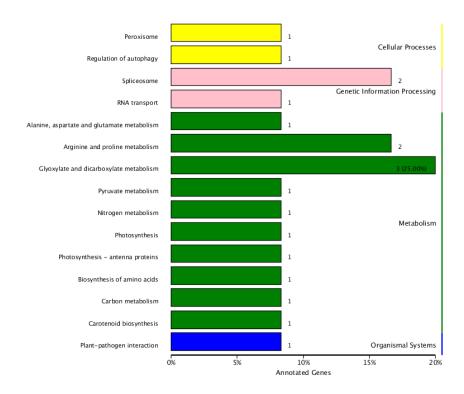


Figure S6. KEGG enrichment of DEGs in the leaves.

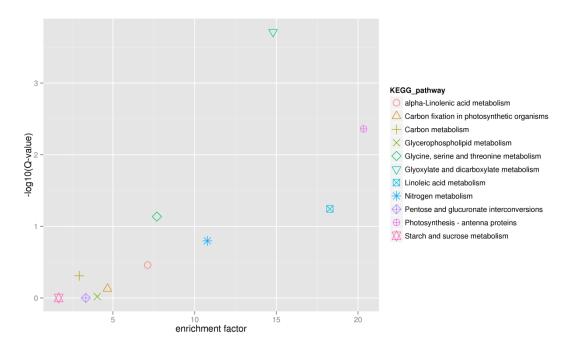


Figure S7. KEGG enrichment of differentially expressed genes in fruit between mutant and wild type.

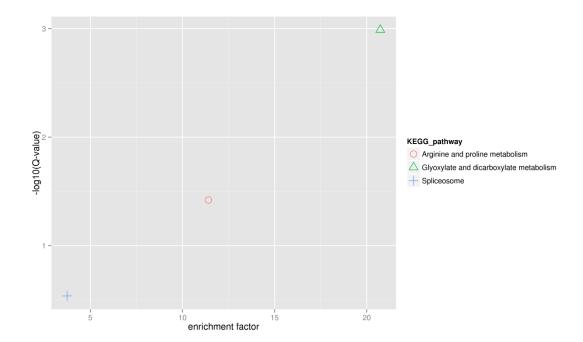


Figure S8. KEGG enrichment of differentially expressed genes in leaf between mutant and wild type.