

A qualitative proteome-wide lysine crotonylation profiling of papaya (*Carica papaya* L.)

Kaidong Liu^{1,3*}, Changchun Yuan¹, Haili Li¹, Kunyan Chen¹, Lishi Lu¹, Chenjia Shen⁴, Xiaolin Zheng^{2*}

¹ Life Science and Technology School, Lingnan Normal University, Zhanjiang, Guangdong 524048, China;

² College of Food Science and Biotechnology, Zhejiang Gongshang University, Hangzhou 310035, China;

³ College of Bioscience and Technology, Hunan Agricultural University, Changsha, Hunan 410128, China;

⁴ College of Life and Environmental Sciences, Hangzhou Normal University, Hangzhou, 310036, China.

*Correspondence

Kaidong Liu

Email: liukaidong2001@126.com

Xiaolin Zheng

Email: zheng9393@163.com

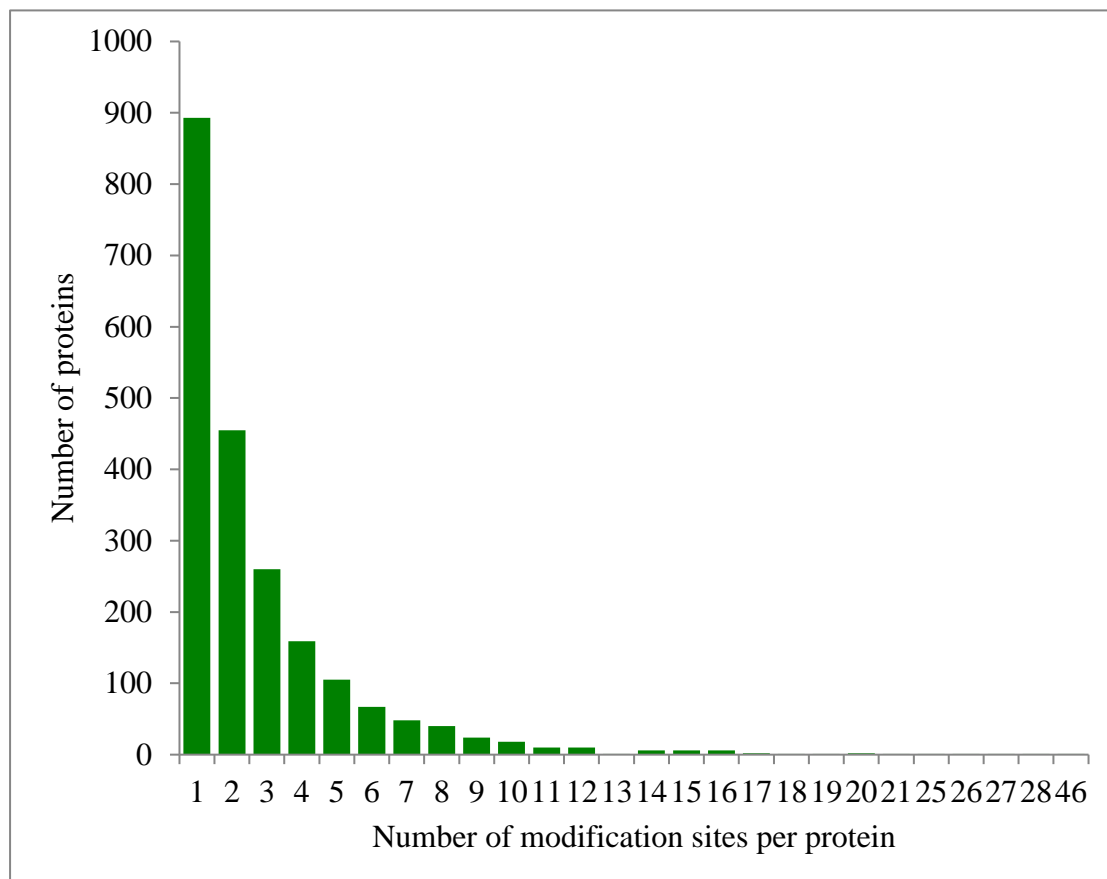


Figure S1 Number of crotonylation sites in each protein.

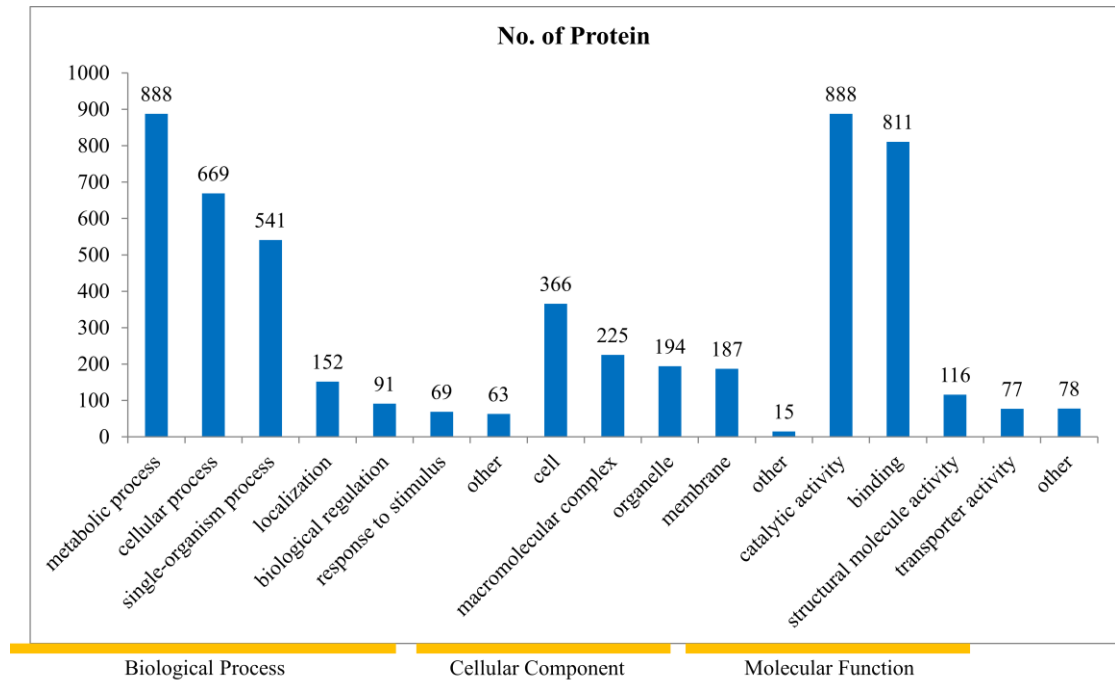


Figure S2 GO analysis of lysine crotonylated proteins in *C. papaya*.

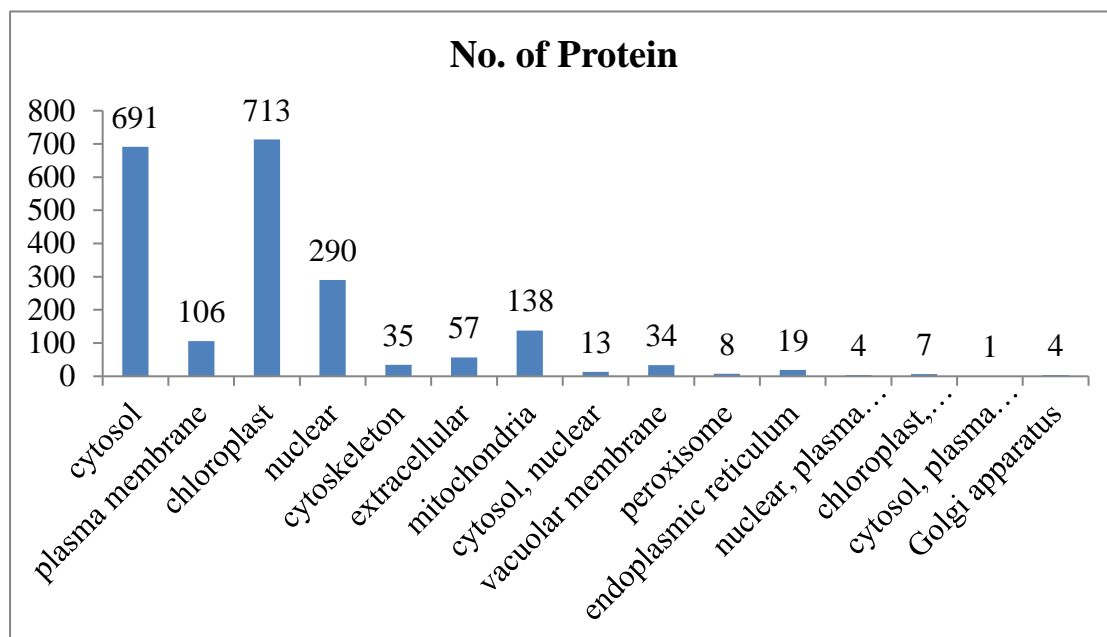


Figure S3 Subcellular localization analysis of lysine crotonylated proteins in *C. papaya*.

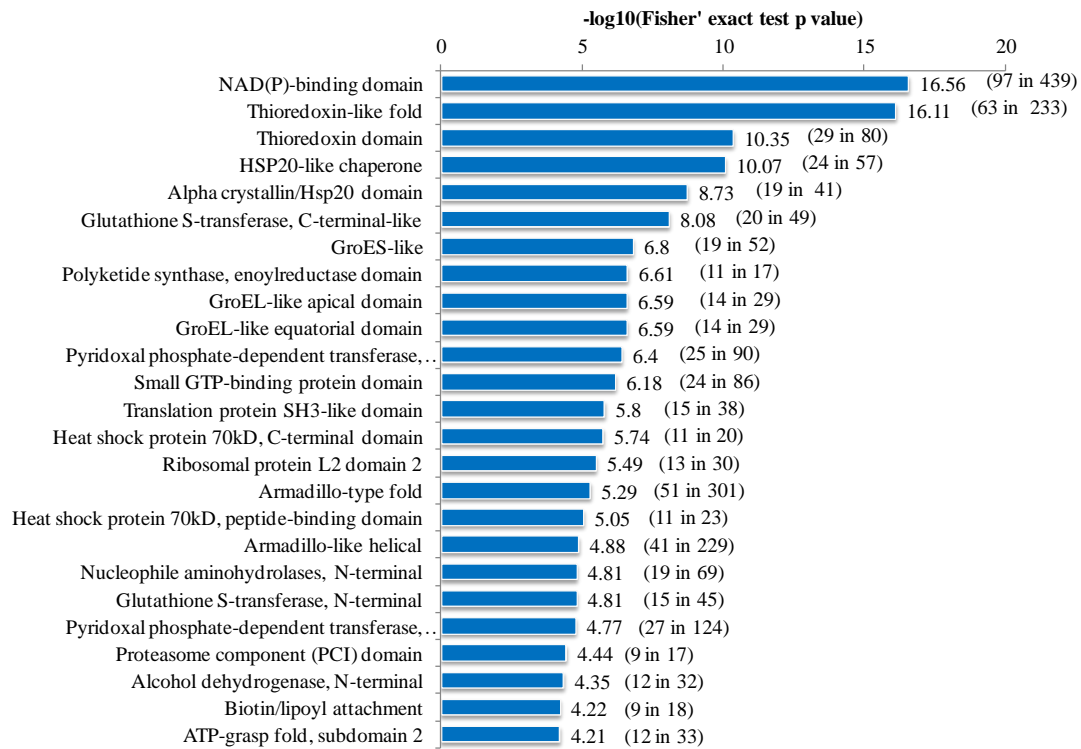


Figure S4 Domain enrichment analysis of all crotonylated proteins in *C. papaya*.