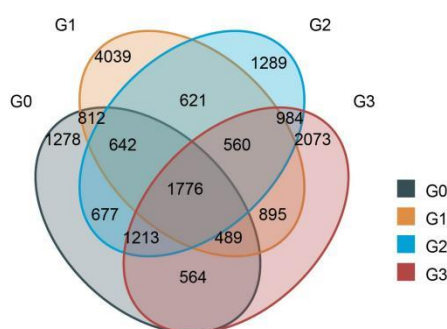


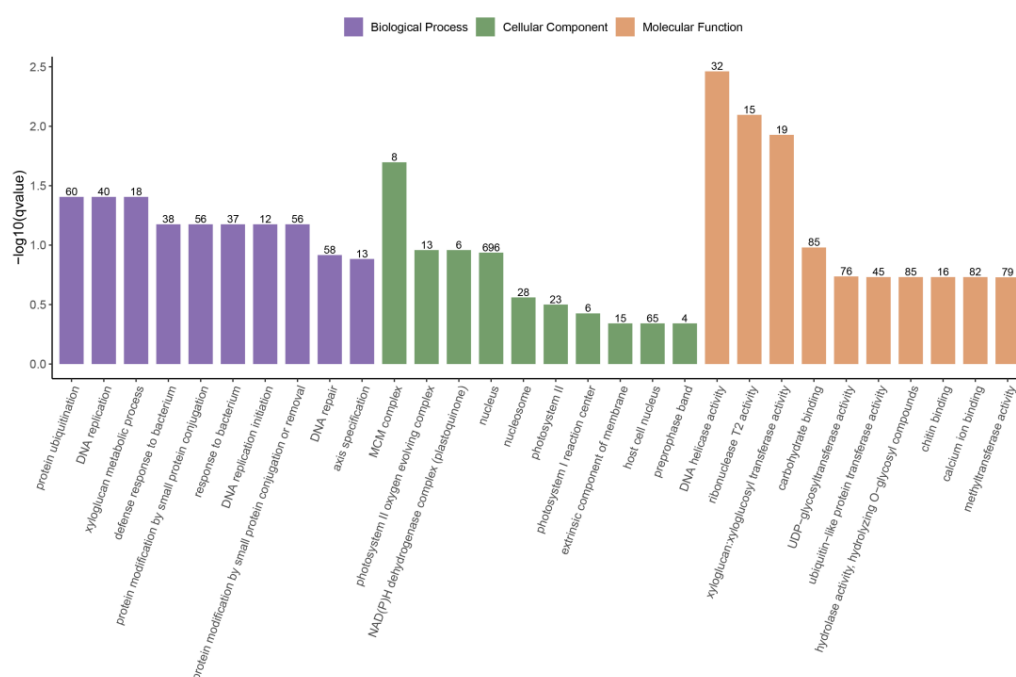
Article

# Fine Mapping and Candidate Gene Analysis of Two Major Quantitative Trait Loci, *qFW2.1* and *qFW3.1*, Controlling Fruit Weight in Pepper (*Capsicum annuum*)

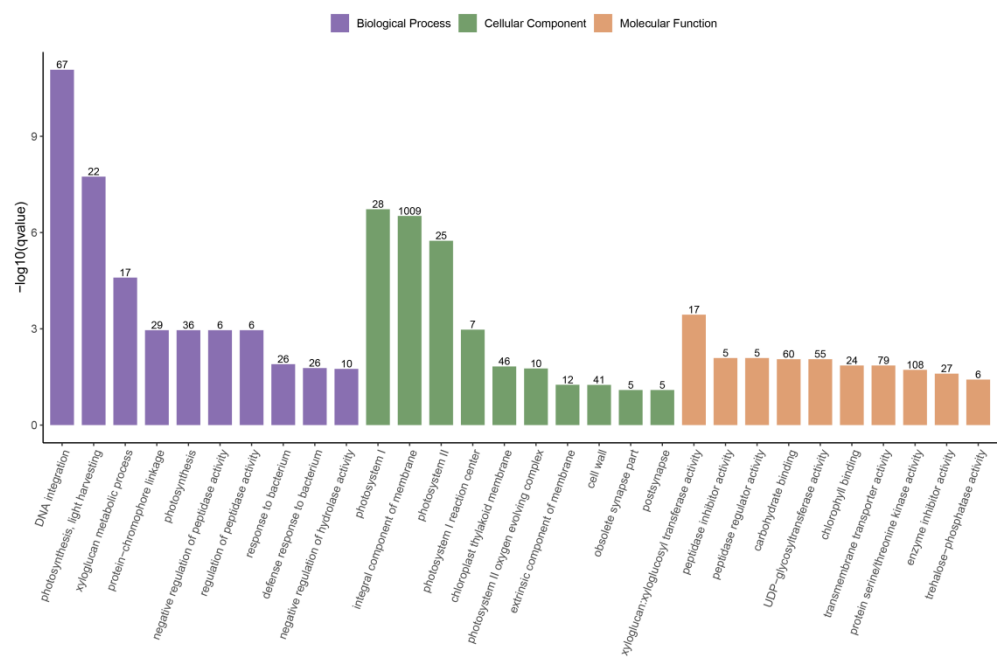
## Supplementary Figures



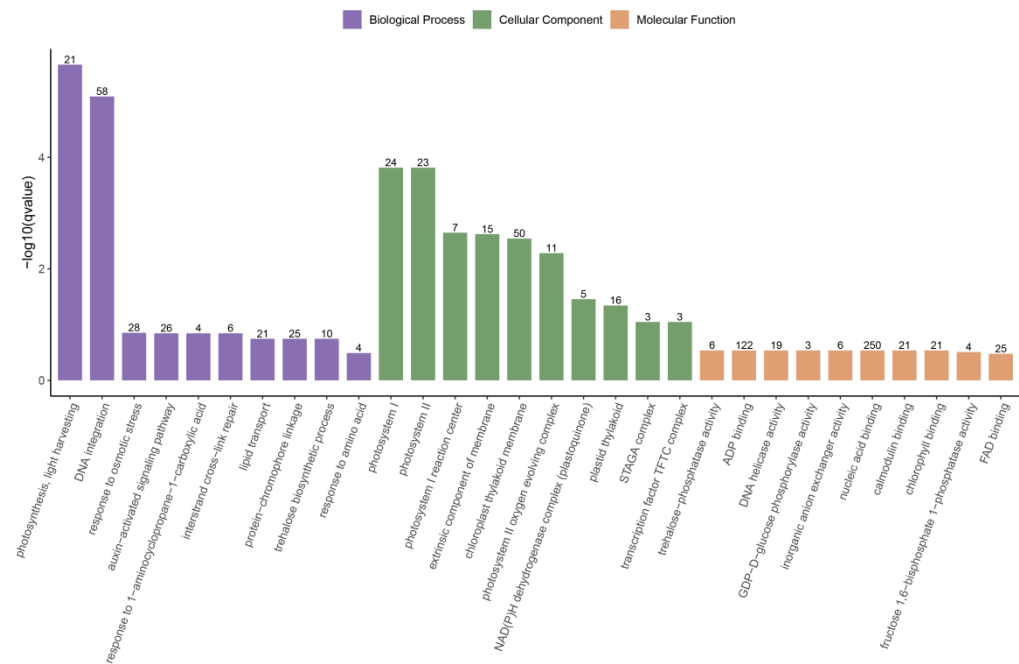
**Figure S1.** Venn diagram of differentially expressed genes by fruit weight. G0 represents the number of differentially expressed genes 15 DAP between Qiemen and 129-1; G1 represents the number of differentially expressed genes 1 DAP between Qiemen and 129-1; G2 represents the number of differentially expressed genes 25 DAP between Qiemen and 129-1; G3 represents the number of differentially expressed genes 35 DAP between Qiemen and 129-1.



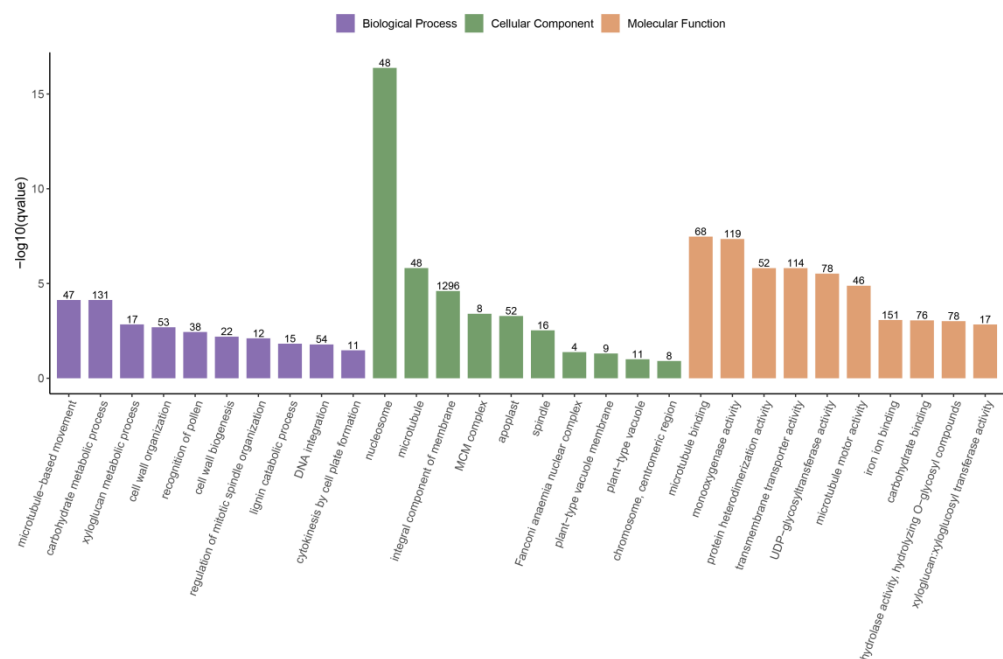
**Figure S2.** Go classification enrichment analysis of differentially expressed genes 1 day after pollination of between Qiemen and 129-1.



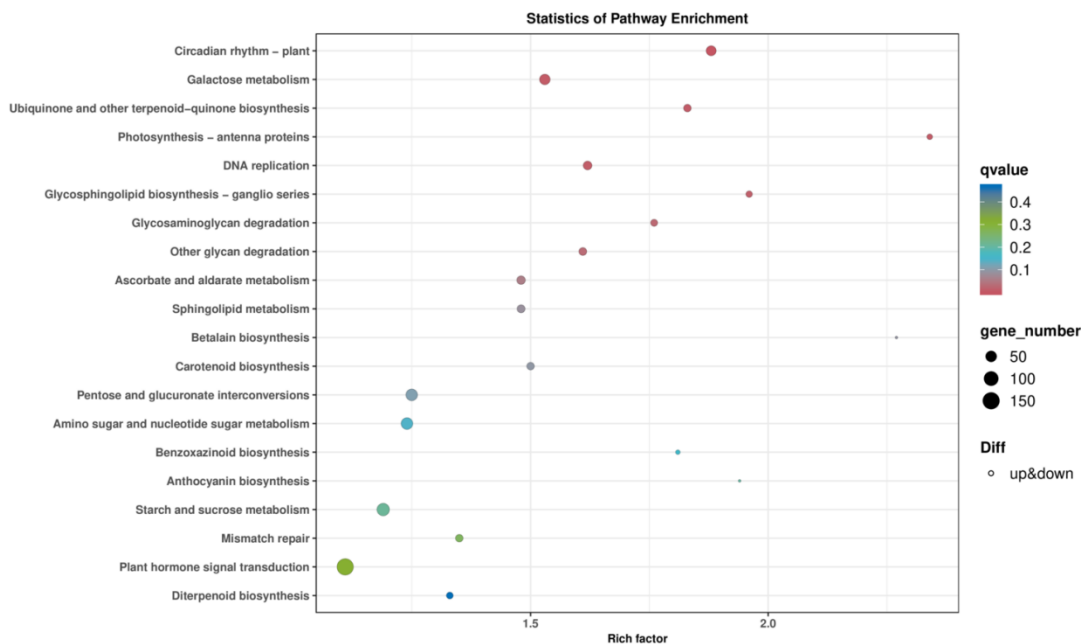
**Figure S3.** Go classification enrichment analysis of differentially expressed genes 15 day after pollination of between Qiemen and 129-1.



**Figure S4.** Go classification enrichment analysis of differentially expressed genes 25 day after pollination of between Qiemen and 129-1.



**Figure S5.** Go classification enrichment analysis of differentially expressed genes 35 day after pollination of between Qiemen and 129-1.



**Figure S6.** KEGG enrichment analysis of differentially expressed genes 1 day after pollination by between Qiemen and 129-1.

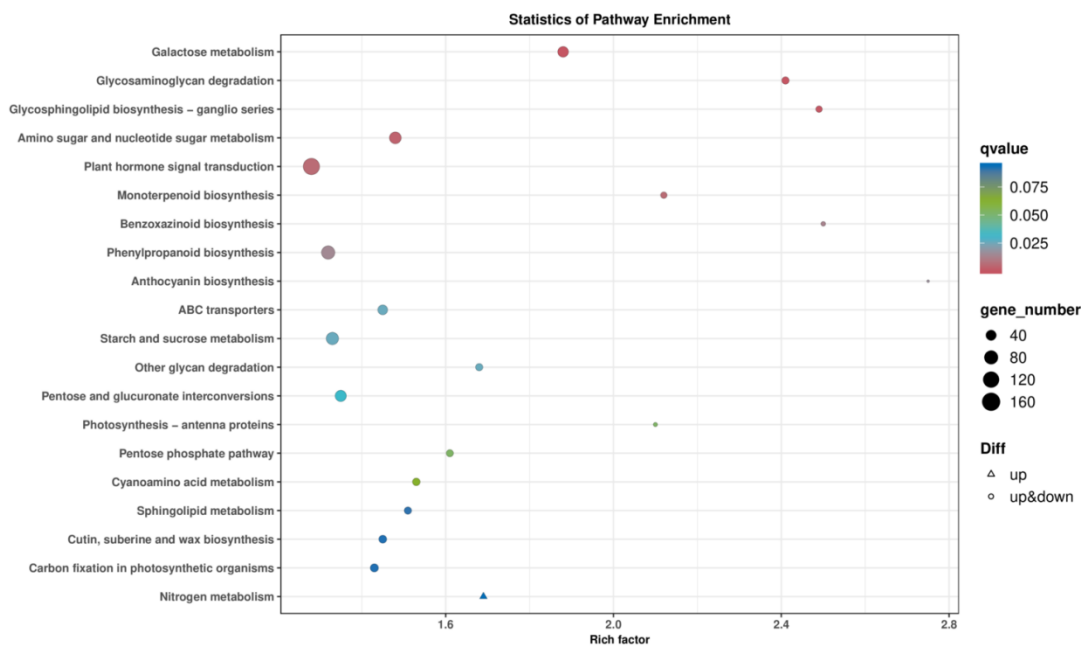


Figure S7. KEGG enrichment analysis of differentially expressed genes 15 day after pollination by between Qiemen and 129-1.

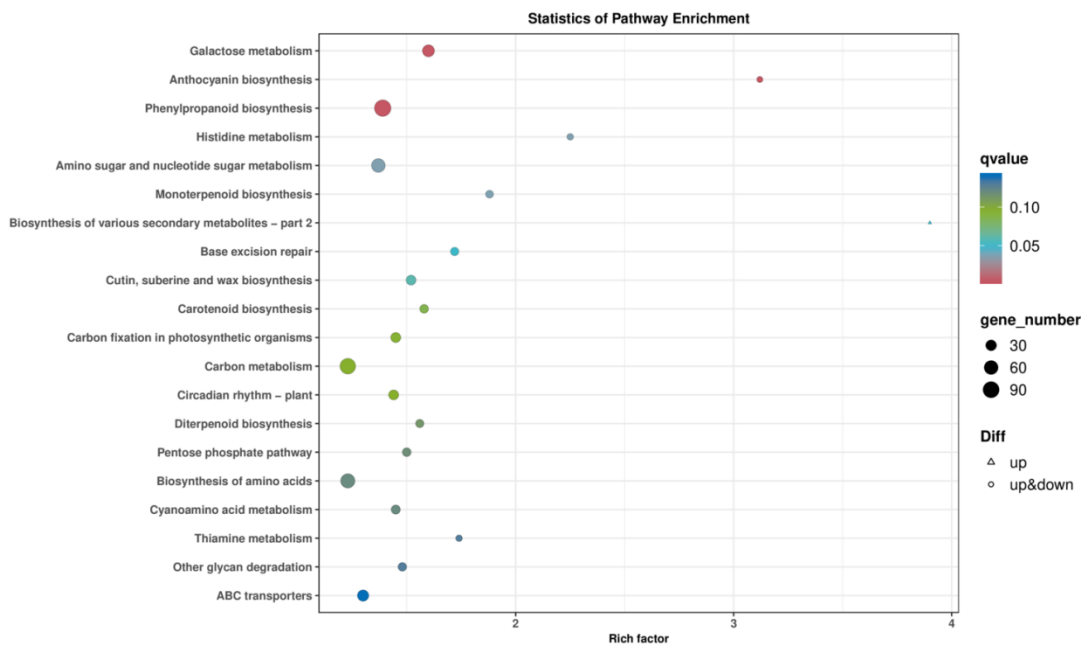


Figure S8. KEGG enrichment analysis of differentially expressed genes 25 day after pollination by between Qiemen and 129-1.

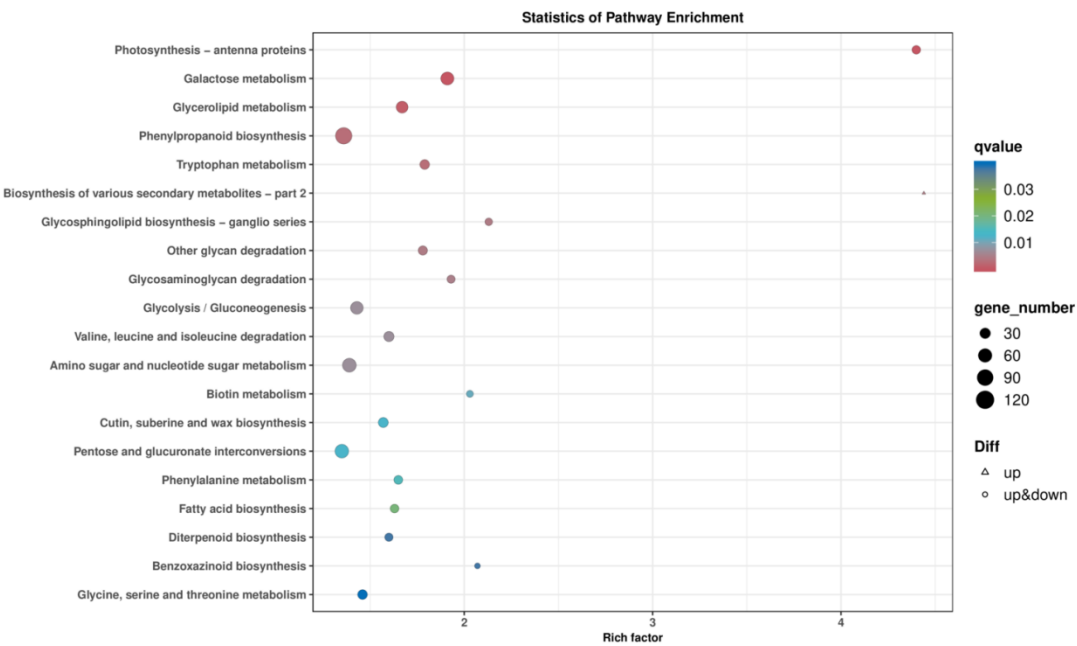


Figure S9. KEGG enrichment analysis of differentially expressed genes 35 day after pollination by between Qiemen and 129-1.

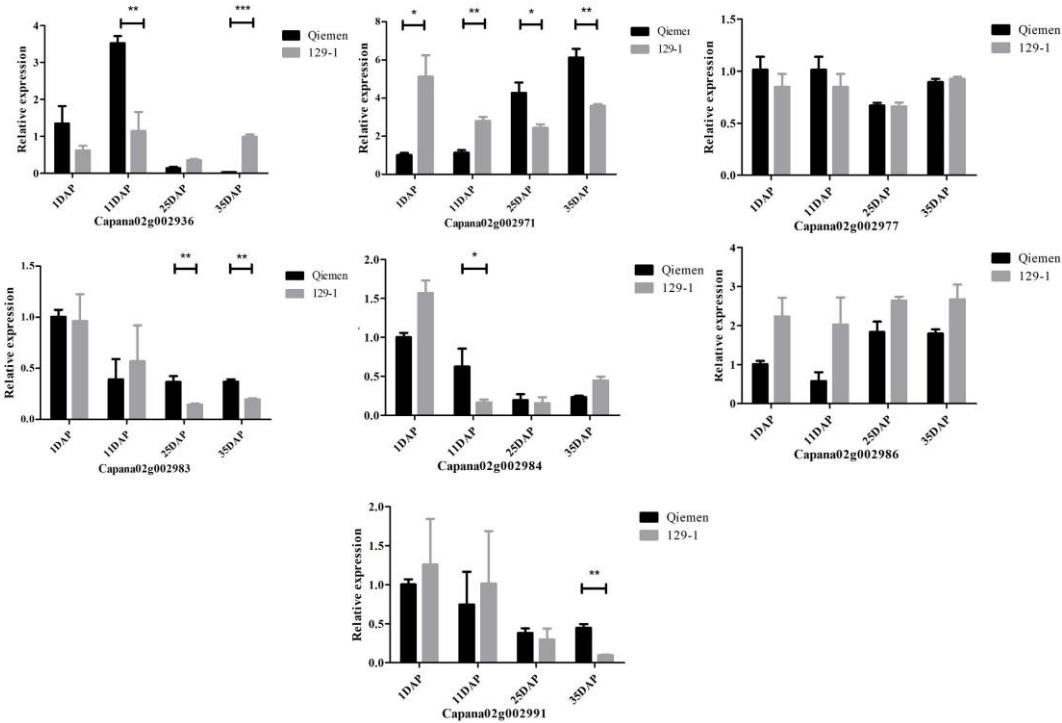


Figure S10. Expression patterns of other candidate genes in *qFW3.1* region.

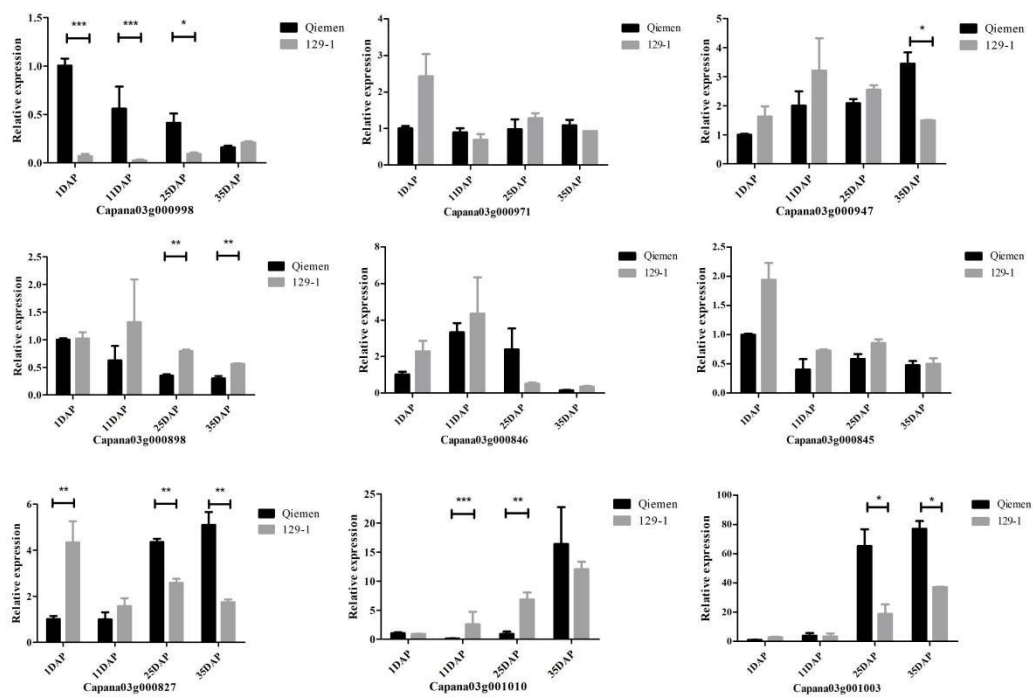


Figure S11. Expression patterns of other candidate genes in *qFW3.1* region.