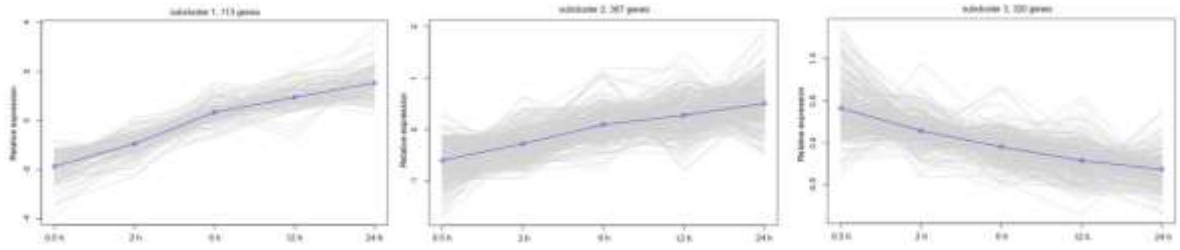
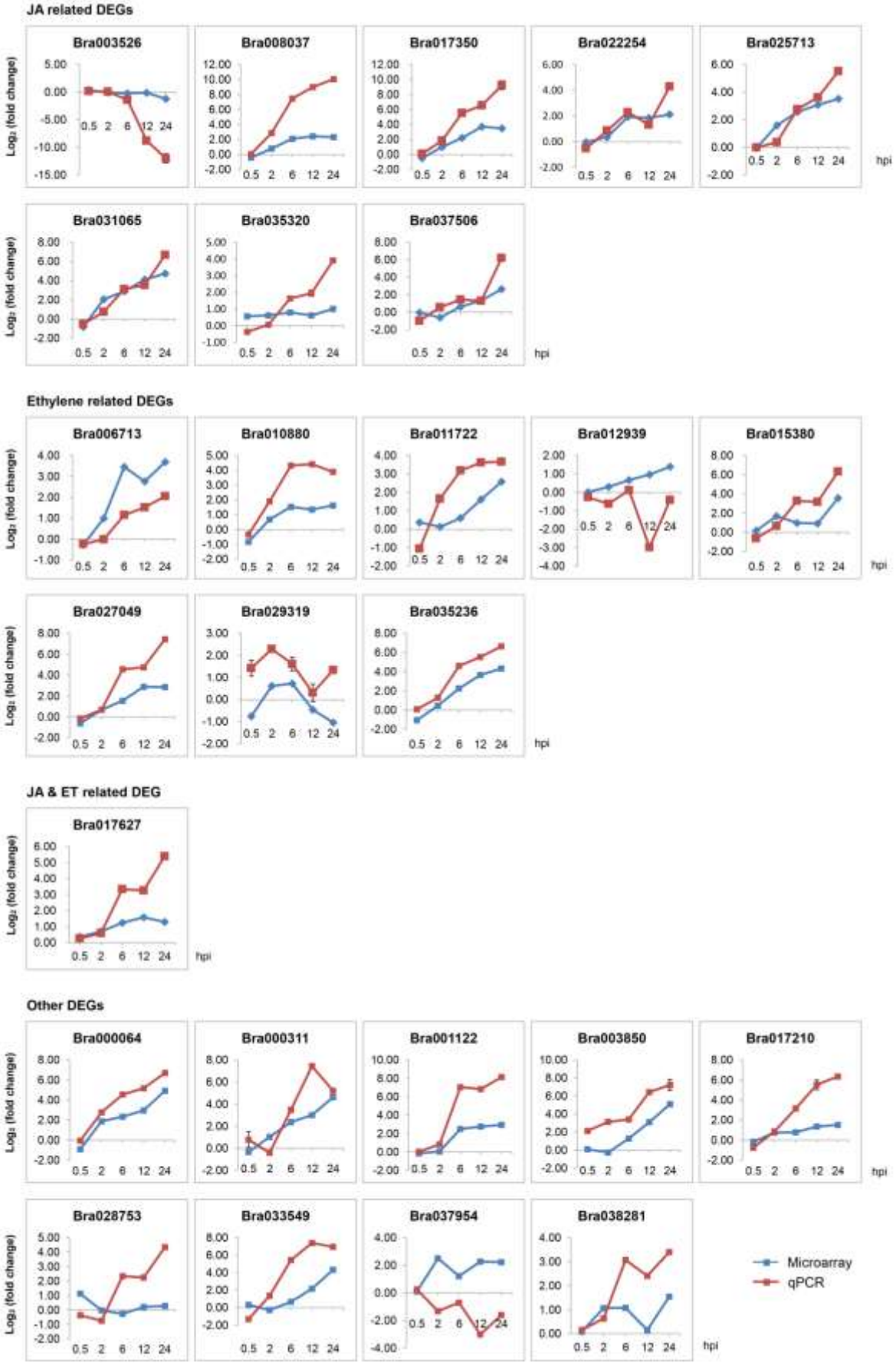
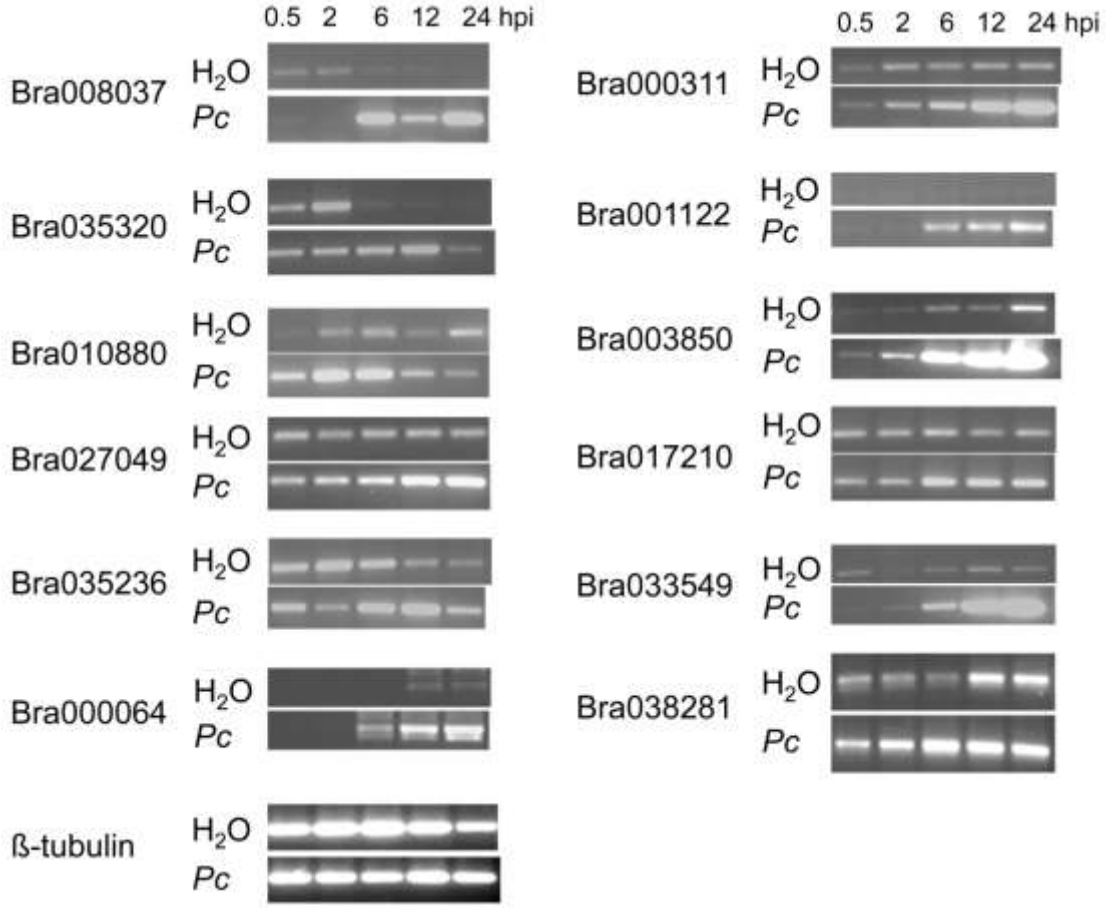


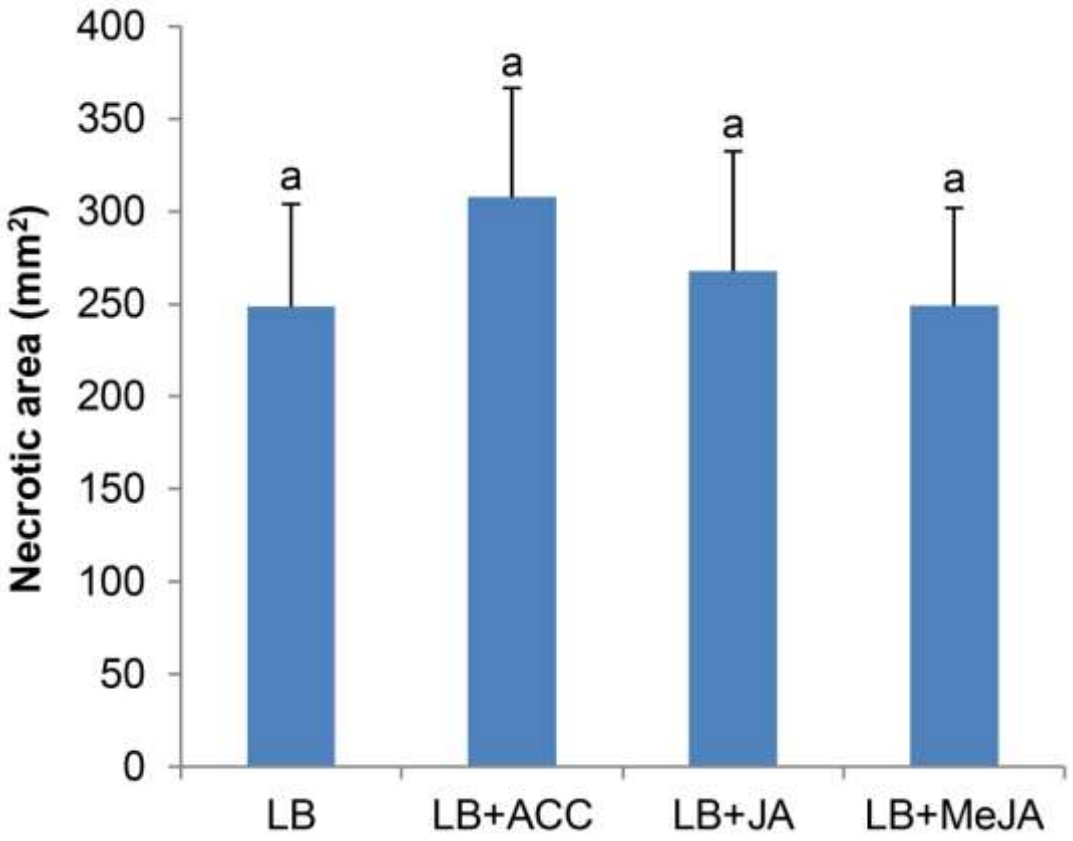
Appendix D The clustered expression patterns of differentially expressed genes (DEGs) in Chinese cabbage induced by *Pectobacterium carotovorum* infection analyzed by microarray. The three subclusters are indicated.


JA related DEGs
Bra003526
Bra008037
Bra017350
Bra022254
Bra025713
Bra031065
Bra035320
Bra037506
Ethylene related DEGs
Bra006713
Bra010880
Bra011722
Bra012939
Bra015380
Bra027049
Bra029319
Bra035236
JA & ET related DEG
Bra017627
Other DEGs
Bra000064
Bra000311
Bra001122
Bra003850
Bra017210
Bra028753
Bra033549
Bra037954
Bra038281
Log2 (fold change)
hpi
0.5 2 6 12 24
Microarray
qPCR

Appendix E Verification of gene expression regulation in Chinese cabbage infected with *P. carotovorum* by qPCR. Twenty-six DEGs (including 8 JA-related DEGs, 8 ET-related DEGs, 1 JA & ET-related DEG, and 9 other randomly selected DEGs) were used to validate the reliability of the microarray data. The fold change indicates the comparison of gene expression level in Chinese cabbage infected with *P. carotovorum* with that in the mock-inoculated control. JA, jasmonic acid; ET, ethylene.



Appendix F Verification of the expression levels of 12 selected genes in Chinese cabbage infected with *P. carotovorum* revealed by semi-quantitative RT-PCR analysis and agarose gel electrophoresis with β-tubulin as a reference gene.



Appendix G Direct effect of phytohormones on *Pc* virulence to Chinese cabbage petioles in vitro (n=9). Each column shows the mean and standard deviation. Statistical analyses were conducted by one-way ANOVA among different columns. The same letter indicates no significant difference among virulence of *Pc* cultures incubated in LB alone or addition with different phytohormones ($P > 0.05$). JA, jasmonic acid; MeJA, methyl jasmonate; ACC, 1-aminocyclopropane-1-carboxylate.