



Figure 3 The interaction network of AP2/ERF in Chinese cabbage according to the orthologs in Arabidopsis. The PCC represents the Pearson Correlation Coefficient.

AP2/ERF superfamily transcription factor expression patterns in Chinese cabbage

AP2/ERF transcription factors were integral in plant growth. Therefore, we constructed AP2/ERF transcription factor functional pathways for comprehensive research. The pathway diagrams showed that 65, 54, and 25 AP2/ERF proteins were involved in metabolic and regulatory pathways, and secondary metabolic biosynthesis, respectively (Additional file 2: Figure S10, Figure S11, Figure S12). AP2/ERF protein function in Chinese cabbage was examined by predicting tissue function and expression using ESTs. To date, 168,703 total ESTs, more than 30,000 unique genes, and a corresponding expression profile of Chinese cabbage have been published. These data provided us with rich resources for gene discovery, genome annotation, and studies of gene expression patterns. A total of 174 AP2/ERF transcription factors were obtained by expression profile tags

(Additional file 1: Table S4), which contained 96 (55.2%) ERF, 58 (33.3%) DREB, 12 (6.9%) AP2, 7 (4.0%) RAV, and 1 (0.6%) Soloist genes (Table 3, Additional file 2: Figure S13). The expression patterns of these AP2/ERF transcription factors in various tissues, and analysis of the overall similarities and differences among transcriptomes of different tissues or organs were obtained by performing coordinated gene expression analyses of Chinese cabbage ESTs derived from different tissue types. The AP2/ERF transcription factors were detected in six tissues, including buds, flowers, leaves, roots, seeds, and siliques. AP2/ERF transcription factor transcripts were most abundant in roots 42,027 (31.95%), followed by seeds 30,120 (22.90%), leaves 26,384 (20.06%), and flowers 17,288 (13.14%). Few AP2/ERF superfamily genes were detected in siliques 8,051 (6.12%) and buds 7,677 (5.84%) (Additional file 2: Figure S14).