



**Figure S4** Kyoto Encyclopedia of Genes and Genome (KEGG) enrichment circle plots for the top 30 enriched pathways of three comparisons: CD0 (*Agrobacterium* cells co-cultivated with phylloplane of *Camellia sinensis* for 30 min) vs. ND0 (*Agrobacterium* cells co-cultivated with phylloplane of *N. benthamiana* for 30 min); CD3 (*Agrobacterium* cells co-cultivated with phylloplane of *C. sinensis* for 3 d) vs. ND3 (*Agrobacterium* cells co-cultivated with phylloplane of *N. benthamiana* for 3 d); CD4 (*Agrobacterium* cells co-cultivated with phylloplane of *C. sinensis* for 4 d) vs. ND4 (*Agrobacterium* cells co-cultivated with phylloplane of *N. benthamiana* for 4 d). There are three circles from the inside to the outside: the first circle is the pathway ID, the length of the bar indicate the rich factor (the number of DEGs/the number of background genes of this pathway), different colors represent different classifications; the second circle is the number of up-regulated genes and the down-regulated ones; the outside circle shows the number of the background genes and the adjusted p-value ( $P_{adj}$ ) of the pathway.