



Figure S3 Gene Ontology (GO) enrichment bubble charts of three comparisons: CD0 (*Agrobacterium* cells co-cultivated with *Camellia sinensis* (leaves) for 30 min) vs. ND0 (*Agrobacterium* cells co-cultivated with *Nicotiana benthamiana* (leaves) for 30 min); CD3 (*Agrobacterium* cells co-cultivated with *C. sinensis* for 3 d) vs. ND3 (*Agrobacterium* cells co-cultivated with *N. benthamiana* for 3 d); CD4 (*Agrobacterium* cells co-cultivated with *C. sinensis* for 4 d) vs. ND4 (*Agrobacterium* cells co-cultivated with *N. benthamiana* for 4 d). Up-down normalization = (number of up-regulated genes - number of down-regulated genes)/(number of DEGs). Each bubble represents a GO term; different colors represent categories; the size of the bubble indicates the quantity of the genes annotated to the GO term; bubbles above the threshold line are considered significantly enriched GO terms.