

Table S2. Unigenes used for validation of gene expression profile in <i>C. cinerea</i> transcriptome data.					
Sample set	JGI Protein ID	Gene ID	Differential expression analysis based on RNA-Seq (log2 Fold Change)	Validation of the DEG by qRT-PCR (log2- $\Delta\Delta C$)	
LM1/HM	473005	CC1G_07486	1.48	1.77 \pm 0.22	
	411802	CC1G_04403	-1.95	-2.29 \pm 0.49	
	542232	CC1G_09477	1.53	1.92 \pm 0.26	
	375908	CC1G_00058	-1.95	-0.98 \pm 0.24	
	397251	CC1G_00620	-1.41	-1.92 \pm 0.48	
	461885	CC1G_01088	-1.15	-2.19 \pm 1.04	
LM2/HHK	467706	CC1G_00407	-2.54	-1.60 \pm 0.45	
	429272	CC1G_15600	4.02	3.82 \pm 0.80	
	444086	CC1G_10354	-1.38	-1.07 \pm 1.15	
	427679	CC1G_09588	-1.65	-2.59 \pm 1.82	

2- $\Delta\Delta C$, relative gene expression level with beta-tubulin serving as the reference gene using qRT-PCR. Data presented as mean \pm standard deviation (SD) in three replicates. HM, *C. cinerea* mycelium treated with water; LM1, *C. cinerea* treated with 70 mM LiCl; HHK, *C. cinerea* treated with water that formed hyphal knot under favorable environmental conditions for fruiting; LM2, *C. cinerea* treated with 70 mM LiCl that remained in mycelium under favorable environmental conditions for fruiting.