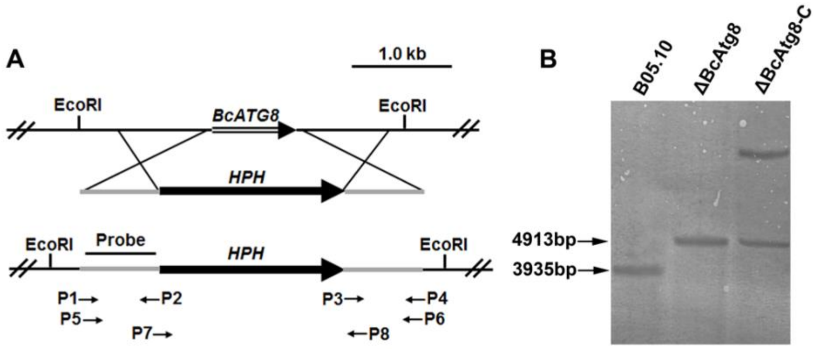

Fig. S1 Generation and identification of *BcATG8* gene deletion mutant. (A) Schematic diagram of the *BcATG8* gene replacement strategy. (B) Southern blot hybridization analysis of EcoRI-digested genomic DNA of the wild-type strain B05.10, the *BcATG8* deletion mutant ΔBcAtg8 and complemented strain ΔBcAtg8-C using the upstream fragment of *BcATG8* as a probe.

Table S1. Autophagy-related genes in *Botrytis cinerea*

Saccharomyces cerevisiae		***B. cinerea***
Protein	Gene	Gene
Atg1	YGL180W	BC1G_05432
Atg2	YNL242W	BC1G_09010
Atg3	YNR007C	BC1G_08793
Atg4	YNL223W	BC1G_11320
Atg6	YPL120W	BC1G_01844
Atg7	YHR171W	BC1G_09811
Atg8	YBL078C	BC1G_02467
Atg9	YDL149W	BC1G_15751
Atg11	YPR049C	BC1G_03242
Atg15	YCR068W	BC1G_07555
Atg17	YLR423C	BC1G_11270
Atg18	YFR021W	BC1G_12821
Atg21	YPL100W	BC1G_12821
Atg22	YCL038C	BC1G_07239
Atg23	YLR431C	BC1G_09995
Atg24	YJL036W	BC1G_01500
Atg26	YLR189C	BC1G_12424

Atg33	YLR356W	BC1G_00142
Irs4	YKR019C	BC1G_09584
Tax4	YJL083W	BC1G_09584
Tor1	YJR066W	BC1G_11880
Tor2	YKL203C	BC1G_11880
Mon1	YGL124C	BC1G_02219
Sec17	YBL050W	BC1G_12159
Sec18	YBR080C	BC1G_01819

Homologues were identified through BLAST searches of the *B. cinerea* genome database (http://www.broadinstitute.org) using the *S. cerevisiae* Atg proteins (http://www.yeastgenome.org) as a query. Sequences of the best hit with an E-value < 10^{-6} are shown as candidates.

Table S2 The lipid metabolism related genes in *Botrytis cinerea*.

Code	Gene locus	Putative function	Ortholog in *Saccharomyces cerevisiae*
A	BC1G_13009	Phosphatidic acid phosphohydrolase	Pah1
B	BC1G_11851	Diacylglycerol acyltransferase	Dga1
C	BC1G_10262	Acyl-coenzyme A: cholesterol acyl transferase-related enzyme	Are1
D	BC1G_07580	Lipid droplet hydrolase	Ldh1
E	BC1G_03357	Triacylglycerol lipase	Tgl3
F	BC1G_12236	1-Acyldihydroxyacetone-phosphate reductase	Ayr1
G	BC1G_09602	Triglyceride Lipase	Tgl1
H	BC1G_07986	Steryl ester hydrolase	Yeh2