

Figure S1. Analysis of *SsZNC1* transformants. **(A)** Schematic diagram of the *SsZNC1* gene knock-out strategy. **(B)** PCR validation of the *SsZNC1* knockout mutants and complemented strain. The verification of *SsZNC1* upstream (Lanes 1, 5, 9, 13, 17, 21); the verification of *SsZNC1* downstream (Lanes 2, 6, 10, 14, 18, and 22); the verification of *HYG* (Lanes 3, 7, 11, 15, 19, and 23); the verification of the full-length *SsZNC1* gene (Lanes 4, 8, 12, 16, 20, and 24). Lane M, DL5000 marker (3428Q, Takara, China). **(C)** RT-PCR analysis of the transcription of *SsZNC1* in different strains. The β -tubulin gene in *S. sclerotiorum* was used as the reference gene. Lane Marker, DL5000 marker. Primer sequences used were listed in Table S1. **(D)** Detection of protein of *SsZNC1* transformants by western blot. The protein expression of transformants through western blot using FLAG antibody (66008-4-Ig, Proteintech, China).

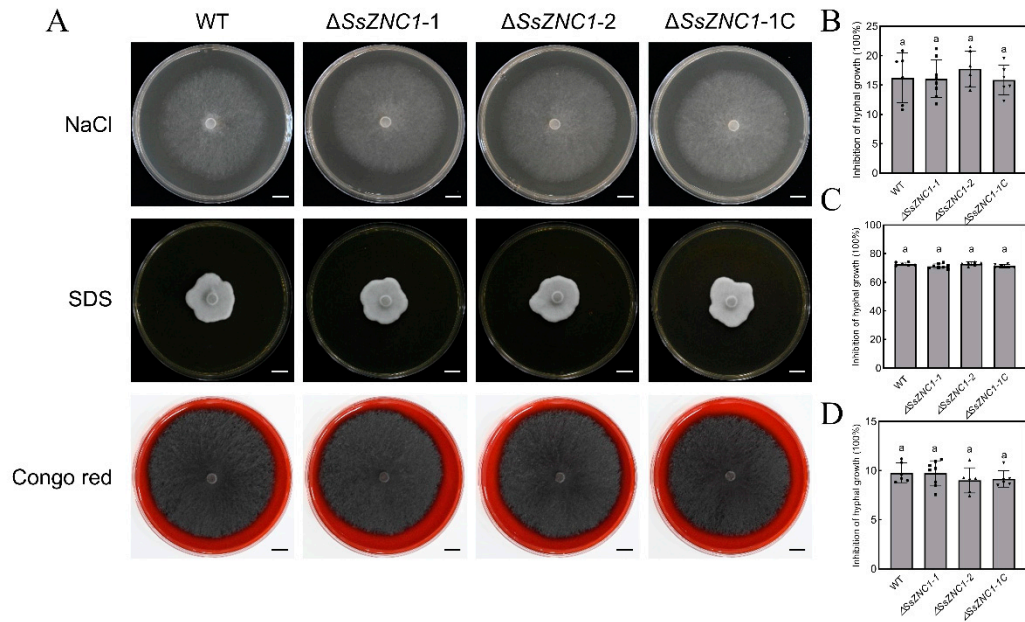


Figure S2. Survivability of the WT and *SsZNC1* transformants in stress media. **(A)** Growth observation of the WT and the *SsZNC1* transformants on PDA medium containing 0.5 M NaCl, 0.02% SDS, and 2.5 mg/mL Congo red. Bar, 1 cm. **(B-D)** The inhibition of hyphal growth of the WT and the *SsZNC1* transformants on PDA medium containing different stress factors. The values represent means derived from three independent replicates, and the error bars indicate \pm SD of the mean.

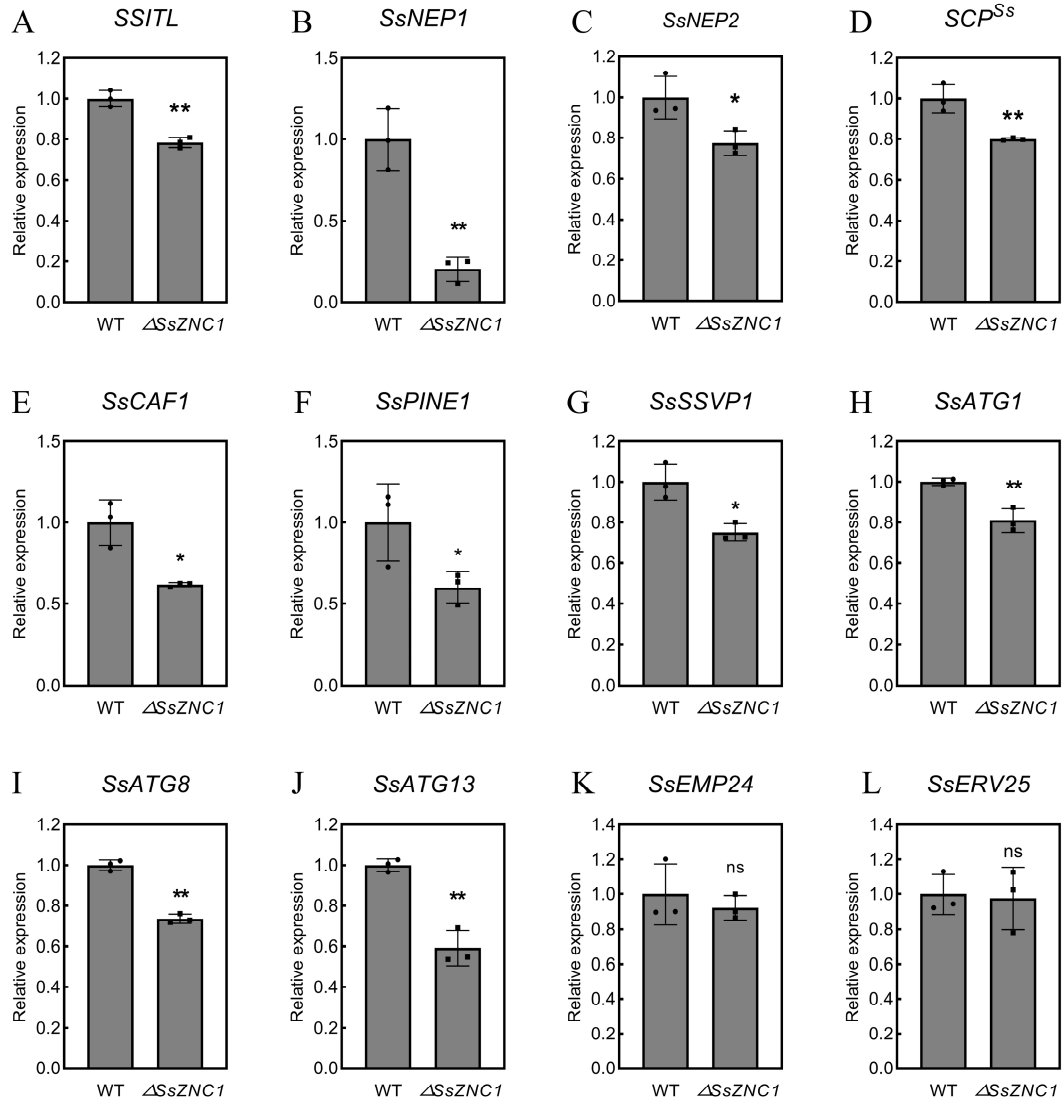


Figure S3. Validation of the RNA-seq data by RT-qPCR. **(A-G)** The relative expression levels of effectors were verified by RT-qPCR at 3 hpi. **(H-J)** The relative expression levels of autophagy related genes were verified by RT-qPCR at 3 hpi. **(K, L)** The relative expression levels of early secretory pathway related genes were verified by RT-qPCR at 3 hpi. The constitutively expressed *β -tubulin* gene was used as the reference gene to standardize data (*, $P < 0.05$; **, $P < 0.01$; ns, no significance).

Table S1. Primers used in this study.

Name	Fwd Primer	Rvs Primer	Description of primers
<i>SsZNC1</i>	atgcttaactgcaagtaagtcgatgc	tcaaggggatgacctaacaggc	Amplification of <i>SsZNC1</i> for sequencing
<i>SsZNC1</i> -promoter	tggaacaacaagtgaagaac	ctaatgagcgactgagaca	Amplification of <i>SsZNC1</i> promoter
<i>HYG</i>	cagaagatgatattgaaggagcac	aaagaaggattacctctaacaagtgt	Amplification of hygromycin-resistant gene
<i>SsZNC1</i> -upstream	ccaaaccgaacgacaatccg	ccggatcgacaccttggg	Amplification of <i>SsZNC1</i> upstream
<i>SsZNC1</i> -downstream	gctcgagcttgagcttgattg	agtgagtctgccagaagagg	Amplification of <i>SsZNC1</i> downstream
<i>SsZNC1</i> -up-verification	ataaacgacgctggtcacgc	cgccgccgctactgtacaagtg	Amplification of the upstream of <i>SsZNC1</i> overlapped PtpC for verification of deletion mutant
<i>SsZNC1</i> -down-verification	ctggaaagcaacaccgtgaact	agactgaggaaatccgctcttgg	Amplification of the downstream of <i>SsZNC1</i> overlapped TrpC for verification of deletion mutant
qPCR- <i>SsTubulin</i>	acctccatccaagaactc	gaactccatctcgtccat	<i>SS1G_04652</i> (β - <i>Tubulin</i>) for relative biomass
qPCR- <i>AtUBQ10</i>	agatccaggacaaggaaggtattc	cgcaggaccaagtgaagagtag	<i>AT4G05320</i> (<i>UBQ10</i>) for relative biomass
qPCR- <i>SsZNC1</i>	tggaacaacaagtgaagaac	ctaatgagcgactgagaca	<i>SsZNC1</i> expression assay
qPCR- <i>SS1G_09143</i>	cggattggtatcgtcagattgt	cgttaagaagtcgtgctaatgc	<i>SS1G_09143</i> expression assay
qPCR- <i>SS1G_04923</i>	gcggaagcgattattggtctg	ggttgagcaggcgaaggata	<i>SS1G_04923</i> expression assay
qPCR- <i>SS1G_01229</i>	tcggcactggagttgaacat	agcattggagcaggtgtag	<i>SS1G_01229</i> expression assay
qPCR- <i>SS1G_11895</i>	ctctcatctcccgtatggt	tgattcctccgtggtatctc	<i>SS1G_11895</i> expression assay
qPCR- <i>SS1G_10071</i>	cacatcggtcgtcaacacatt	caggtagcagagtaatcggaga	<i>SS1G_10071</i> expression assay
qPCR- <i>SS1G_12937</i>	gatggtggaatgctgcgaat	ccgtggcgttggtagaatc	<i>SS1G_12937</i> expression assay
qPCR- <i>SS1G_13036</i>	acctccacagccaactatga	ttactagcaccgtcttctcaa	<i>SS1G_13036</i> expression assay

Name	Fwd Primer	Rvs Primer	Description of primers
qPCR- <i>SSIG_02760</i>	cctccaccatctccaccatc	gccttcatagccgcaacac	<i>SSIG_02760</i> expression assay
qPCR- <i>SSIG_13736</i>	ttcatcggtcgcttcagttg	ctccagtagtcgtcggtgta	<i>SSIG_13736</i> expression assay
qPCR- <i>SSIG_00891</i>	ctcagttcaggcagtggttac	cggtagtagtggtgtcttcc	<i>SSIG_00891</i> expression assay
qPCR- <i>SSIG_02334</i>	ttgctgagatggatgctgatg	tgaccgttgatgaacttgatgt	<i>SSIG_02334</i> expression assay
qPCR- <i>SSIG_14362</i>	ggacacctgaagaataccaagt	ccatcggttacatccatatac	<i>SSIG_14362</i> expression assay
qPCR- <i>SCP^{Ss}</i>	aatctcctacgccatccaa	cgcagcacaggtataagc	<i>SCP^{Ss}</i> expression assay
qPCR- <i>SsCAF1</i>	tggcttgtagtgattgg	cgaagttgtctatgtgatgt	<i>SsCAF1</i> expression assay
qPCR- <i>SsITL</i>	ctcaggaagataacggaaca	catcaccatcatagtcatacac	<i>SsITL</i> expression assay
qPCR- <i>SsNEP1</i>	gtcaacctccataccaaca	acagttagcatcaccgaat	<i>SsNEP1</i> expression assay
qPCR- <i>SsNEP2</i>	cacactctatgaagcctaca	ccattgctactgccactt	<i>SsNEP2</i> expression assay
qPCR- <i>SsPINE1</i>	attctcgcagcatcaact	atccgtcaactaatccatca	<i>SsPINE1</i> expression assay
qPCR- <i>SsVPI</i>	atggcaatcctgtcaagtat	ggtcttcttatcgcacatatac	<i>SsVPI</i> expression assay
qPCR- <i>SsATG1</i>	tcatacactaccgccattag	taacctctccaccatcaca	<i>SsATG1</i> expression assay
qPCR- <i>SsATG13</i>	acactccagccatacctt	catcttctaacctgcctct	<i>SsATG13</i> expression assay
qPCR- <i>SsATG8</i>	ggtaattcgtctatgtcatc	ggcttcttctaaggcttca	<i>SsATG8</i> expression assay
qPCR- <i>SsEMP24</i>	ttcacggcattgtctatgt	cttcaccaaccagaactaac	<i>SsEMP24</i> expression assay
qPCR- <i>SsERV25</i>	cattgtaggcgagaagagaa	gttgtagaatacggcttggtg	<i>SsERV25</i> expression assay

Table S2. The information of genes used for RNA-Seq analysis.

Gene ID	Locus tag	Chromosomal location	SignalP4	TM	Gene function description
<i>SSIG_01229</i>	Sscl01g010410	Chromosome 1 (3541576..3544299)	YES	No TM	Glycoside hydrolase family 55 protein (FCW)
<i>SSIG_12937</i>	Sscl02g011730	Chromosome 2 (47473..48702)	YES	No TM	Glycosyl hydrolase 76 (mannans degradation)
<i>SSIG_10071</i>	Sscl16g107500	Chromosome 16 (46815..48014)	YES	No TM	Pectin lyase (pectin degradation)
<i>SSIG_02760</i>	Sscl04g036990	Chromosome 4 (1709458..1710439)	YES	TM	Carbohydrate esterase family 5 protein (hemicellulose degradation)
<i>SSIG_09143</i>	Sscl15g107260	Chromosome 15 (1740933..1742517)	YES	No TM	Amidohydrolase 2
<i>SSIG_13736</i>	Sscl10g079780	Chromosome 10 (1741791..1743368)	YES	No TM	Stress response protein rds1(ferritin 2)
<i>SSIG_13036</i>	Sscl02g021570	Chromosome 2 (3422968..3425247)	YES	No TM	Cu-oxidase 3
<i>SSIG_11895</i>	Sscl12g090620	Chromosome 12 (1405870..1406372)	YES	No TM	Hydrophobin class I
<i>SSIG_04923</i>	Sscl08g062810	Chromosome 8 (258861..260207)	YES	No TM	Hypothetical protein
<i>SSIG_00891</i>	Sscl03g023660	Chromosome 3 (604987..606652)	NO	No TM	Cellulose catabolic process and cellulose binding
<i>SSIG_02334</i>	Sscl04g033820	Chromosome 4 (604987..606652)	YES	No TM	Cellulose catabolic process and cellulose binding
<i>SSIG_14362</i>	Sscl16g110770	Chromosome 16(1227771..1230138)	NO	No TM	Methyltransferase activity