# Supporting Information

**Article title:** A virulence factor from Sclerotinia sclerotiorum targets the host chloroplast proteins to promote infection

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**Fig. S1**: Phylogenetic trees were constructed by using the Maximum Likelihood method based on full-length amino acid sequences of CPX amino acid sequences in different species.

**Fig. S2**: Phylogenetic trees were constructed by using the Maximum Likelihood method based on full-length amino acid sequences of SKL2 amino acid sequences in different species.

**Fig. S3**: Comparative transcriptome sequencing was analysis of Gm SKL2, including uninoculated WT (0h), WT inoculated with *S. sclerotiorum* for 24h and 48h (24h and 48h).

**Table S1**: Candidate interaction protein screening yeast two-hybrid library derived from soybeans infected with *S. sclerotiorum*.

**Table S2**: Primers used in this study.

**Fig. S1**

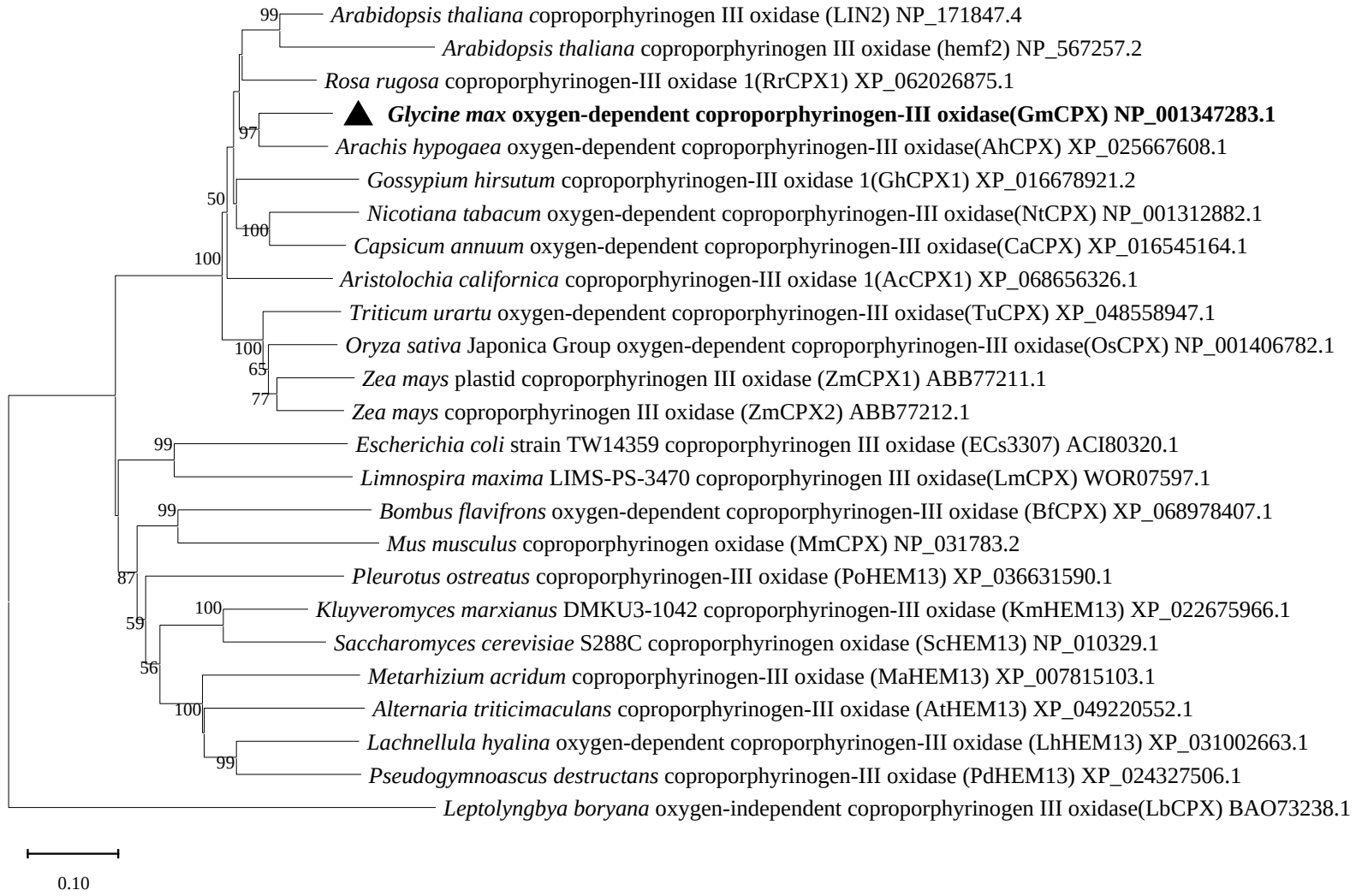

99
Arabidopsis thaliana coproporphyrinogen III oxidase (LIN2) NP_171847.4
Arabidopsis thaliana coproporphyrinogen III oxidase (hemf2) NP_567257.2
Rosa rugosa coproporphyrinogen-III oxidase 1(RrCPX1) XP_062026875.1
Glycine max oxygen-dependent coproporphyrinogen-III oxidase(GmCPX) NP_001347283.1
97
Arachis hypogaea oxygen-dependent coproporphyrinogen-III oxidase(AhCPX) XP_025667608.1
Gossypium hirsutum coproporphyrinogen-III oxidase 1(GhCPX1) XP_016678921.2
50
Nicotiana tabacum oxygen-dependent coproporphyrinogen-III oxidase(NtCPX) NP_001312882.1
100
Capsicum annuum oxygen-dependent coproporphyrinogen-III oxidase(CaCPX) XP_016545164.1
100
Aristolochia californica coproporphyrinogen-III oxidase 1(AcCPX1) XP_068656326.1
Triticum urartu oxygen-dependent coproporphyrinogen-III oxidase(TuCPX) XP_048558947.1
100
Oryza sativa Japonica Group oxygen-dependent coproporphyrinogen-III oxidase(OsCPX) NP_001406782.1
65
Zea mays plastid coproporphyrinogen III oxidase (ZmCPX1) ABB77211.1
77
Zea mays coproporphyrinogen III oxidase (ZmCPX2) ABB77212.1
99
Escherichia coli strain TW14359 coproporphyrinogen III oxidase (ECs3307) ACI80320.1
Limnospira maxima LIMS-PS-3470 coproporphyrinogen III oxidase(LmCPX) WOR07597.1
99
Bombus flavifrons oxygen-dependent coproporphyrinogen-III oxidase (BfCPX) XP_068978407.1
Mus musculus coproporphyrinogen oxidase (MmCPX) NP_031783.2
87
Pleurotus ostreatus coproporphyrinogen-III oxidase (PoHEM13) XP_036631590.1
100
Kluyveromyces marxianus DMKU3-1042 coproporphyrinogen-III oxidase (KmHEM13) XP_022675966.1
59
Saccharomyces cerevisiae S288C coproporphyrinogen oxidase (ScHEM13) NP_010329.1
56
Metarhizium acridum coproporphyrinogen-III oxidase (MaHEM13) XP_007815103.1
100
Alternaria triticimaculans coproporphyrinogen-III oxidase (AtHEM13) XP_049220552.1
Lachnellula hyalina oxygen-dependent coproporphyrinogen-III oxidase (LhHEM13) XP_031002663.1
99
Pseudogymnoascus destructans coproporphyrinogen-III oxidase (PdHEM13) XP_024327506.1
Leptolyngbya boryana oxygen-independent coproporphyrinogen III oxidase(LbCPX) BAO73238.1
0.10

**Fig. S2**

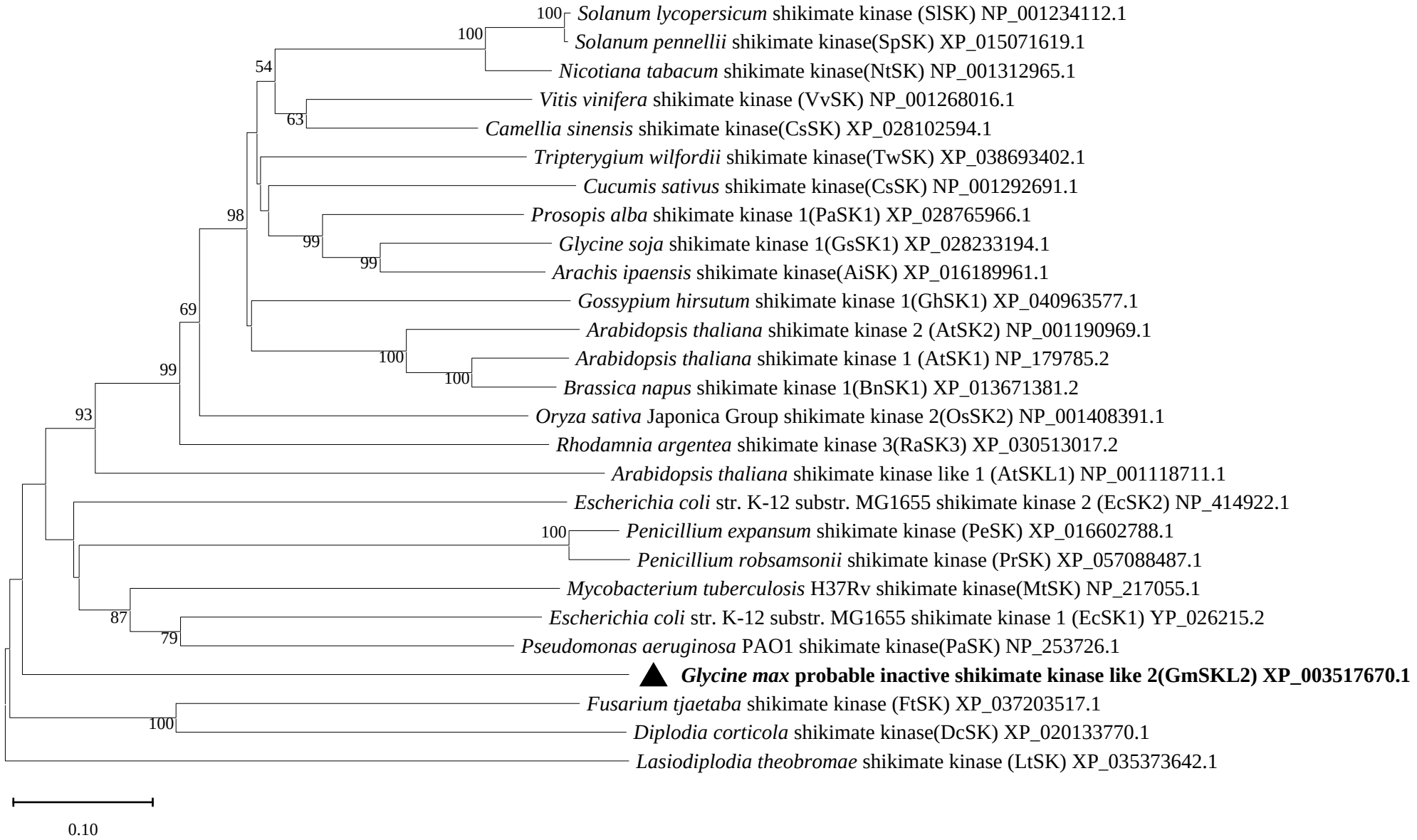

100 Solanum lycopersicum shikimate kinase (SlSK) NP_001234112.1
100 Solanum pennellii shikimate kinase(SpSK) XP_015071619.1
Nicotiana tabacum shikimate kinase(NtSK) NP_001312965.1
54
Vitis vinifera shikimate kinase (VvSK) NP_001268016.1
63
Camellia sinensis shikimate kinase(CsSK) XP_028102594.1
Tripterygium wilfordii shikimate kinase(TwSK) XP_038693402.1
Cucumis sativus shikimate kinase(CsSK) NP_001292691.1
98
Prosopis alba shikimate kinase 1(PaSK1) XP_028765966.1
99
Glycine soja shikimate kinase 1(GsSK1) XP_028233194.1
99
Arachis ipaensis shikimate kinase(AiSK) XP_016189961.1
69
Gossypium hirsutum shikimate kinase 1(GhSK1) XP_040963577.1
Arabidopsis thaliana shikimate kinase 2 (AtSK2) NP_001190969.1
100
Arabidopsis thaliana shikimate kinase 1 (AtSK1) NP_179785.2
99
100
Brassica napus shikimate kinase 1(BnSK1) XP_013671381.2
93
Oryza sativa Japonica Group shikimate kinase 2(OsSK2) NP_001408391.1
Rhodamnia argentea shikimate kinase 3(RaSK3) XP_030513017.2
Arabidopsis thaliana shikimate kinase like 1 (AtSKL1) NP_001118711.1
Escherichia coli str. K-12 substr. MG1655 shikimate kinase 2 (EcSK2) NP_414922.1
100
Penicillium expansum shikimate kinase (PeSK) XP_016602788.1
Penicillium robsamsonii shikimate kinase (PrSK) XP_057088487.1
Mycobacterium tuberculosis H37Rv shikimate kinase(MtSK) NP_217055.1
87
Escherichia coli str. K-12 substr. MG1655 shikimate kinase 1 (EcSK1) YP_026215.2
79
Pseudomonas aeruginosa PAO1 shikimate kinase(PaSK) NP_253726.1
Glycine max probable inactive shikimate kinase like 2(GmSKL2) XP_003517670.1
Fusarium tjaetaba shikimate kinase (FtSK) XP_037203517.1
100
Diplodia corticola shikimate kinase(DcSK) XP_020133770.1
Lasiodiplodia theobromae shikimate kinase (LtSK) XP_035373642.1
0.10

**Fig. S3**

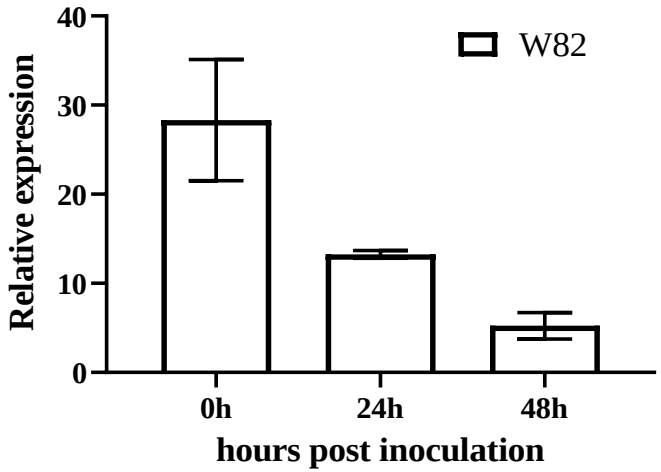

W82
Relative expression
40
30
20
10
0
0h
24h
48h
hours post inoculation

**Table S1**

| Protein name | Locus | Start to Stop (aa) | Frequency |
|---|---|---|---|
| **isoflavone reductase** | NP_001237637 | 128-terminate | 4/62 |
| **MYB transcription factor MYB145** | XP_006592208 | 54-terminate | 2/62 |
| **chlorophyll a-b binding protein 6A** | XP_006599410.2 | full-length | 1/62 |
| **eukaryotic translation initiation factor 3 subunit F** | XP_028198922 | full-length | 2/62 |
| **Phosphoribulo kinase** | XP_003534305 | 139-terminate | 2/62 |
| **glutamine synthetase precursor** | NP_001237784.2 | 87-323aa | 4/62 |
| **heat shock protein 90-5** | XP_003516650 | 72-303 | 5/62 |
| **shikimate kinase like 2, GmSKL2** | XP_003517670 | 81-terminate | 6/62 |
| **delta-aminolevulinic acid dehydratase** | NP_001238737.2 | 243-terminate | 5/62 |
| **coproporphyrinogen-III oxidase, GmCPX** | NP_001347283 | 226-terminate | 6/62 |

**Table S2**

| Primers name | Sequence 5'to 3' | Purpose |
|---|---|---|
| AD-F | CACTACAGGGATGTTTAA | yeast two-hybrid |
| AD-R | GGGCATTAATTCTAGTCA | |
| SsCTP1-BD-F | GAATTCATGTACTCTCCATTCGATAACAGTGGAT | |
| SsCTP1-BD-R | CTGCAGTTAGAAAGTGTAAACTGGTTGAGGA | |
| GmCPX-GFP-F | GGATCCATGATGCATTGTGCGAGCATTGTCT | Co-IP assay |
| GmCPX-GFP-R | TCTAGAGATCCATTCCTTGGGGTTGATGCAT | Subcellular localization of proteins |
| GmSKL2-GFP-F | GAGCTCATGGCAACTGTTCCTGCTCGTCTCT | |
| GmSKL2-GFP-R | TCTAGATAACTGTGTACCAAGAGTTGTGTTA | |
| cLUC-SsCTP1-F | GAGCTCATGGCACCAGCTTCTTTGGTAGCTAGAG | Spilt-LUC |
| cLUC-SsCTP1-R | GAGCTCTTAGAAAGTGTAAACTGGTTGAGGA | |
| GmCPX-nLUC-F | GGATCCATGATGCATTGTGCGAGCATTGTCT | |
| GmCPX-nLUC-R | TCTAGAGATCCATTCCTTGGGGTTGATGCAT | |
| GmSKL2-nLUC-F | GAGCTCATGGCAACTGTTCCTGCTCGTCTCT | |
| GmSKL2-nLUC-R | TCTAGATAACTGTGTACCAAGAGTTGTGTTA | |
| TRV2-NbCPX-F | CTGTGAGTAAGGTTACCGAAAGAGTGTGCAAATTCCGTCA | Virus-induced gene silencing |
| TRV2-NbCPX-R | GATCCATTCTTTAGGGTTGATACAATACCGGATCCCCATGGAGGC | |
| Q-NbCPX1-F | GTGCCTACAACACATGTCGC | quantitative real-time PCR |

| | | |
|---|---|---|
| Q-NBCPX1-R | CGCATTTGGAGCAGTTCGAC | |
| Q-NbEF1α-F | GGTTAAGATGATGCCGACCAAG | |
| Q-NbEF1α-R | CGCCAGTTGGGTCCTTCTTG | |
| Q-NbPR1a-F | CCGCCTTCCCTCAACTCAAC | |
| Q-NbPR1a-R | GCACAACCAAGACGTACTGAG | |
| Q-NbPR2-F | AGGTGTTTGCTATGGAATGC | |
| Q-NbPR2-R | TCTGTACCCACCATCTTGC | |