Supplementary files

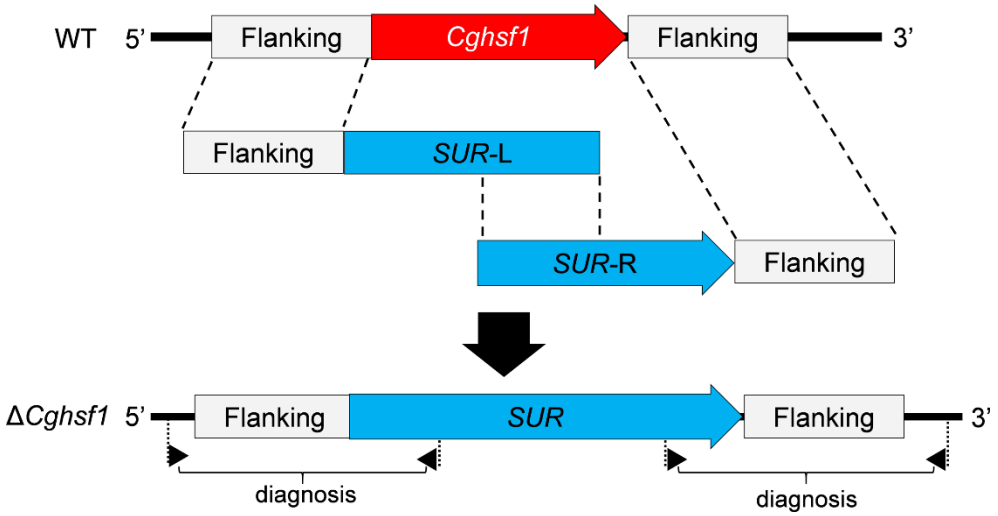

Figure S1. Split-Marker Strategy for construction of *Cghsf1* knock-out mutants. The acetolactate synthase gene (*SUR*) cassette from *Magnaporthe oryzae*, which confers resistance to chlorimuron ethyl, was used as selective marker. Diagnostic primers for integrations of the recombinant fragments are marked with black triangles. WT: wide type; ΔCgHSF1: the knock-out mutants.

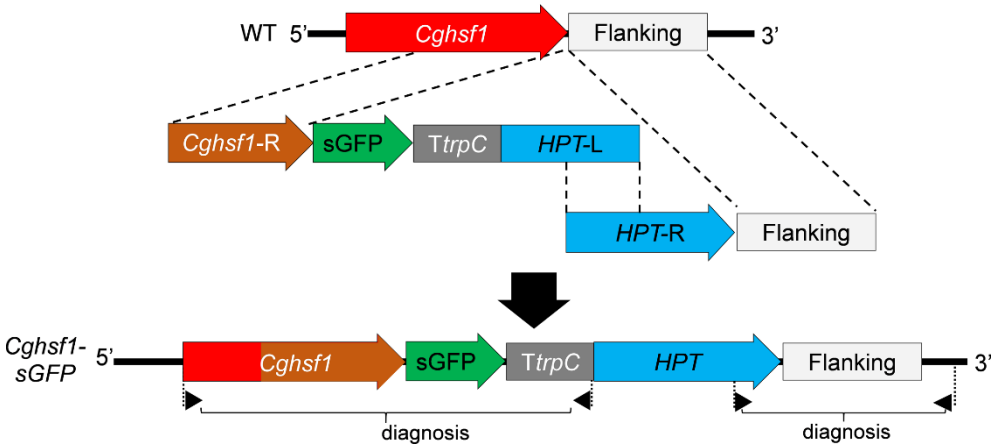

Figure S2. Strategy for construction of *CgHSF1-sGFP* mutant. The hygromycin B resistance cassette (*HPT*) was used as the selective marker. Diagnostic primers for integrations of the recombinant fragments are marked with black triangles. Cghsf1-R: The 700 bp nucleotides of 3′ part of *Cghsf1* without stop codon.

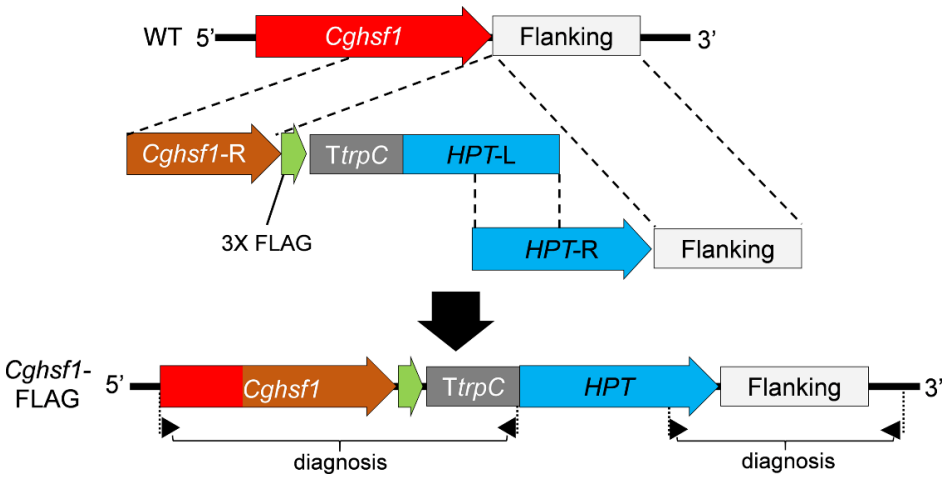

Figure S3. Strategy for construction of *CgHSF1*-FLAG mutant. The hygromycin B resistance cassette (*HPT*) was used as the selective marker. Diagnostic primers for integrations of the recombinant fragments are marked with black triangles. Cghsf1-R: The 700 bp nucleotides of 3′ part of *Cghsf1* without stop codon.

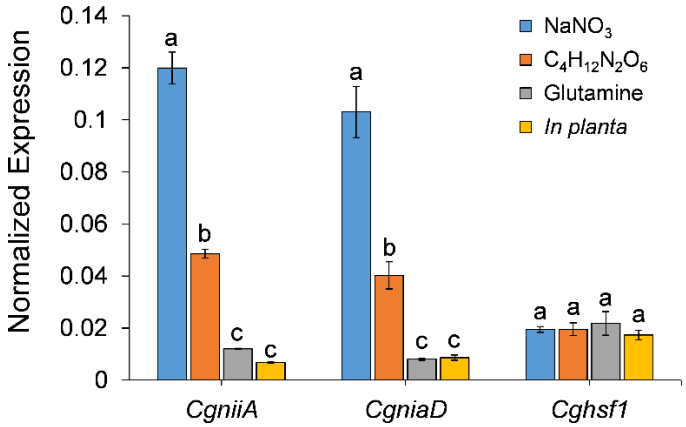

Figure S4. Relative expression levels of *CgniiA*, *CgniaD*, and *Cghsf1* of WT strain cultured *in vitro* on nitrogen sources of $NaNO_3$ (20 mmol L^{-1}), ammonium tartrate ($C_4H_{12}N_2O_6$) (10 mmol L^{-1}), and Glutamine (10 mmol L^{-1}) and during *in planta* stage. The β2-tubulin coding gene was used as an endogenous control for normalization. Columns with different letters indicate significant difference at $p < 0.05$.

Table S1. Nucleotide sequence of *Cghsf1* and the amino acid sequence of CgHSF1. The red letters indicate the intron.

>*CgHSF1* Nucleotide sequence
ATGCCGATGCCAGCAGTTCAGCAGTCTTTTCCCAGCCCGACGGGCGATCAGTTT
TTGCGATGGGGAGGAGCAGACGGGACCGCCCTTGTCGACGGAACCGCACCCC
CAGCCGTGAATTCGTATGGCATTGTCCCCGGCCAACAACAGCAATTCGTGCAG
CCCACGCCGAGCCCCAACAATGCTCTTGCACGAAGACAGATGAACAGAGCGC
TTGTGCCCACCGCTGCCAGGCCAAATTTCGATTCTGCCGCCGACCCCTGGTTCG
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CAACAACTACGCCTCATTTGTGCGACAACTCAACATGTACGGCTTCCACAAGC
GCGTTGGCTTGTCGGACAACTCCATGCGCGCGAGCGAGCGGAAGAACAAGAG
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GGGGGACATGCCCATCCAGAAGAAGGAGATGGCCCTCATTCGCGAAGAGTTG
GCCAAGCTGCGGGATCAGCAAAGGTTGATTATGTCGGCCATCCAGCGGATCCA
GCAAGATAACTCGGCACTATACAATCAGGCCGTCGTCTTCCAGAGCCAGCACG
ATCGTCACCAAAATTCTATCAACGCCATCCTCAACTTCCTGGCCAACGTCTTTA
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CTCGCGAAGCGTAGACAAGCGCTTCTGCCGCCAATTCCAAACGGCCGTGCCAA
CACGGTTTCTCCATCCCCAGCATCTAGCGCGCCCACGCCCCAGCCGTACAACA
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GCATCCTCCCCCAGCAACTACCTGGCTCAGGAGCTTGAGACCAACCCCCACGA
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TGACCAGCGCACCAAGATGCTCAACATCATGGCTGGCCGTTCCGCGACGCCCA
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GCTCCATCTGTCAGCGCTACCACCGACGCGCCTTCCATGCCCGCCACATCAGG
CCTTTCACTCTCGCCTATCATGGGTTCAGCCGAACCTCCGCCTTCCCTGCAGCA
TATCCAATACAACCAAGCCGACTTGGCCGCTCTTCAGCGGATGCAAGAAGAGC
AAGCTGCCAAGCTGGACCACCTTTCAAGCATGCTGGGCCCCCTGAGCCCCTCC
GGTCGGATTCCTGGCATTGACGAGAACGGCAACATCAATCACCAGAACGGCT
ACTTTGGGTCTGACCTTGACATTGACCAGTTCCTCAACCAAGATGCTTTCCAAG
GTGATGATGCCTTCCAAGGGGGCGTCTTCCCGGGAGATGGAACCGACTTCAAC
TTTTCCCTGGACGCTGCTACACCCAACGGCGGTGTTGCGGCTGCCAATGCAACC
AACACTCCTAGTGAGAGCAGTGGAACGGAAGAAATCGCACGCGACGGCTTTG
ACCCGTACACTGGCAGTCCTGATCGTGGCACTAAAAGGCGGCGCGTCGGCTGA

>CgHSF1 Amino acid sequence

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TPSPNNALARRQMNRALVPTAARPNFDSAADPWFVGDDNALLQQQQQQPNGN
MTATDNIEALEEMARKAMREAQQKRKQIPPFVQKLSSFLDDDKNSDLIRWSEKGDS
FIVLDEDEFAKKLIPDLFKHNNYASFVRQLNMYGFHKRVGLSDNSMRASERKNKSP
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PGDGTDFNFSLDAATPNGGVAAANATNTPSESSGTEEIARDGFDPYTGSPDRGTKR
RRVG