The *stuA* gene controls development, adaptation, stress tolerance, and virulence of the dermatophyte *Trichophyton rubrum*

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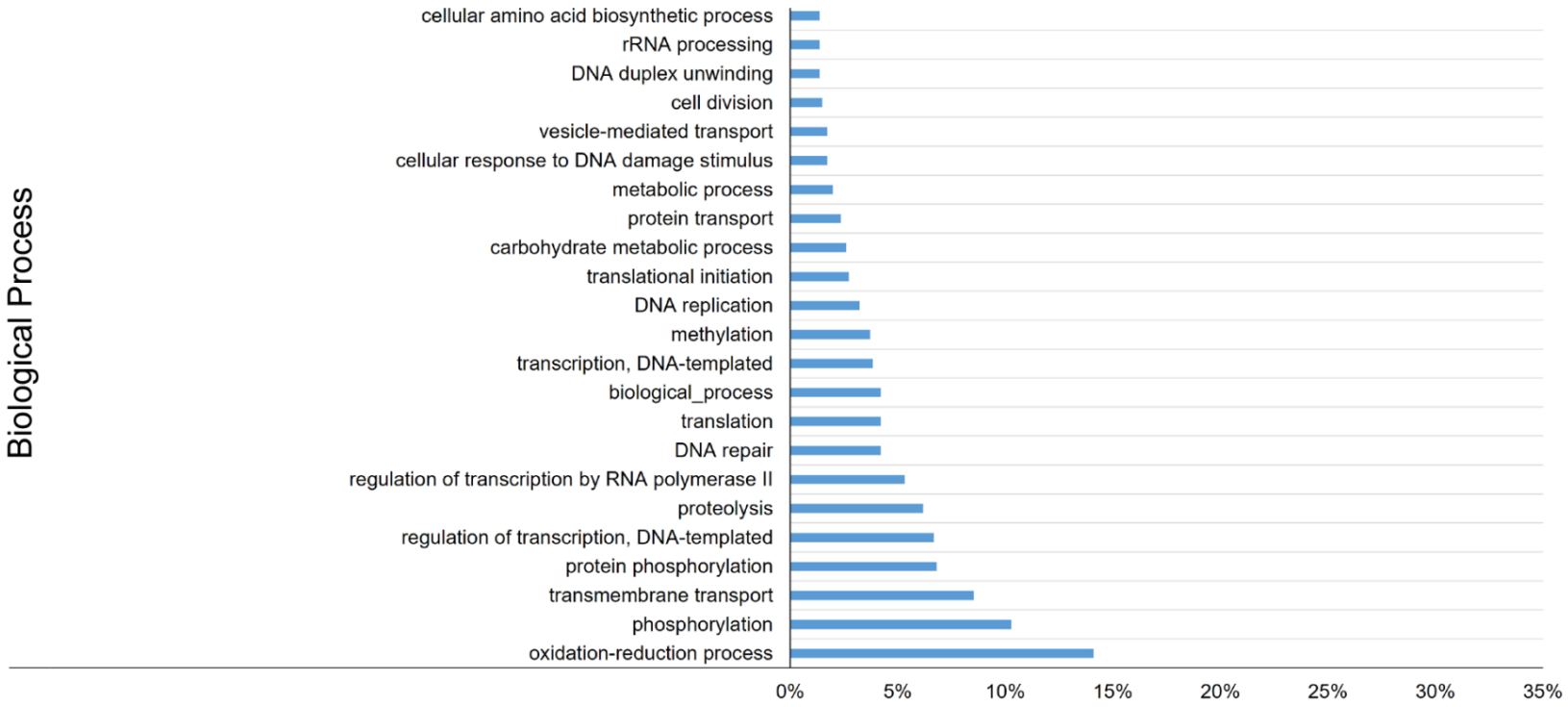
Supplementary Table 1. Primers used in this study

Primer name	Sequence (5'- 3')	Application
Primers used for gene targeting constructs		
M13_F	GTAAAACGACGGCCAGT	Amplification of *hph* cassete
M13_R	CAGGAAACAGCTATGAC	
P1	TGTCAGCGTCTCGTCTCTACC	Amplification of *stuA* 5' flanking sequence
P2	ACTGGCCGTCGTTTTACCATCCATGTACGGCTGTGTC[(a)]	
P3	GTCATAGCTGTTTCCTGAAACGCTCATCGACTCTGC[(b)]	Amplification of *stuA* 3' flanking sequence
P4	TGCTTCTTTTCTGCACGTTG	
P5	ATAGTGATCAACCAGACCAGCCAATCTGC	Generation of 5'split-marker fragment
H1	GATGTTGGCGACCTCGTATT	
P6	TAACAGGCCTGGATGGCGTGGTGAGTATCT	Generation of 3'split-marker fragment
H2	CTGCCTGAAACCGAACTGC	
Primers used for mutant screening		
S1	AGGCAGCCTCTGCTTCCA	Mutant screening
S2	TTTTGTACCGTTGATCATATGGTTGT	

P1	TGTCAGCGTCTCGTCTCTACC	Mutant screening
P4	TGCTTCTTTTCTGCACGTTG	
Primers used for qRT-PCR		
stuA_S1	AGGCAGCCTCTGCTTCCA	qRT-PCR
stuA_S2	TTTTGTACCGTTGATCATATGGTTGT	
rpb2_F	TGCAGGAGCTGGTGGAAGA	qRT-PCR
rpb2_R	GCTGGGAGGTACTGTTTGATCAA	
hypA_F	TCCTGCTGCAACACTGAGAC	qRT-PCR
hypA_R	AACCCTTGAGGAGGGAGAAG	

(*a*) The sequence with homology with M13_F sequence is underlined

(*b*) The sequence with homology with M13_R sequence is underlined



Supplementary Figure S1. *In silico* analysis of StuA target genes in *T. rubrum* genome. Gene ontology-based functional categorization of genes in the *T. rubrum* genome with a recognition site for the motif consensus (A/TCGCGT/ANA/C) in their promoter regions.