

Title page

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Supplementary Information

**The serine/threonine protein kinase MpSTE1 directly governs hyphal branching in *Monascus*
spp.**

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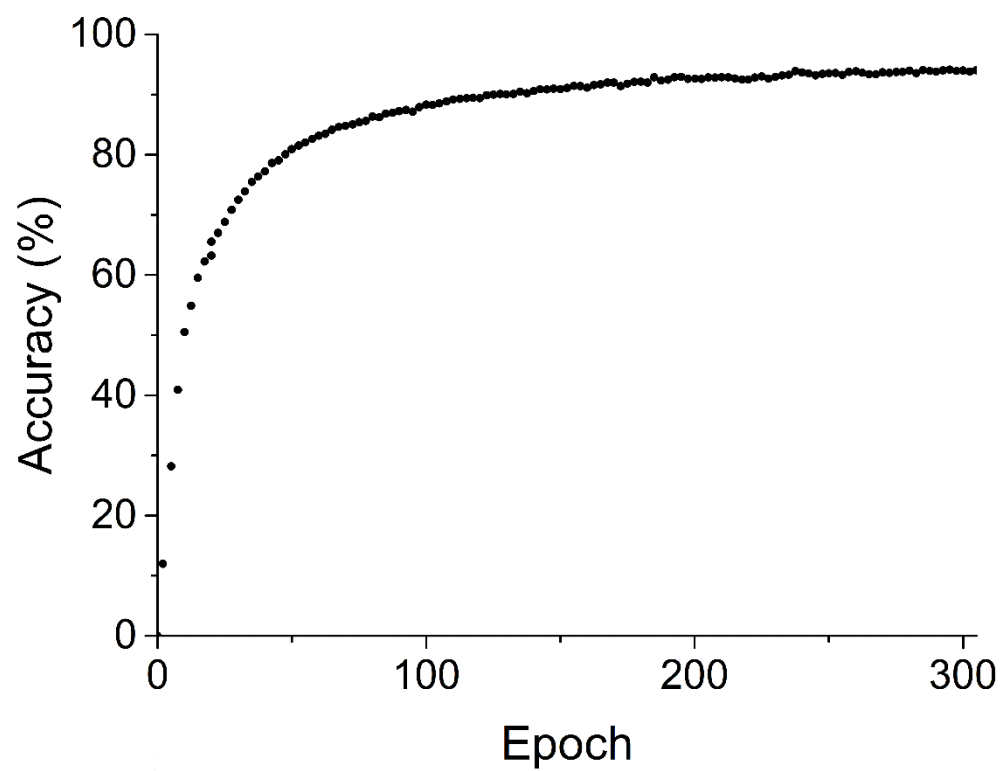


Fig. S1 Plot of accuracy on the training datasets over training epochs for quantification of hyphal branching in the micrograph by a deep learning model HBDL. The accuracy on the test set is close to 97%.

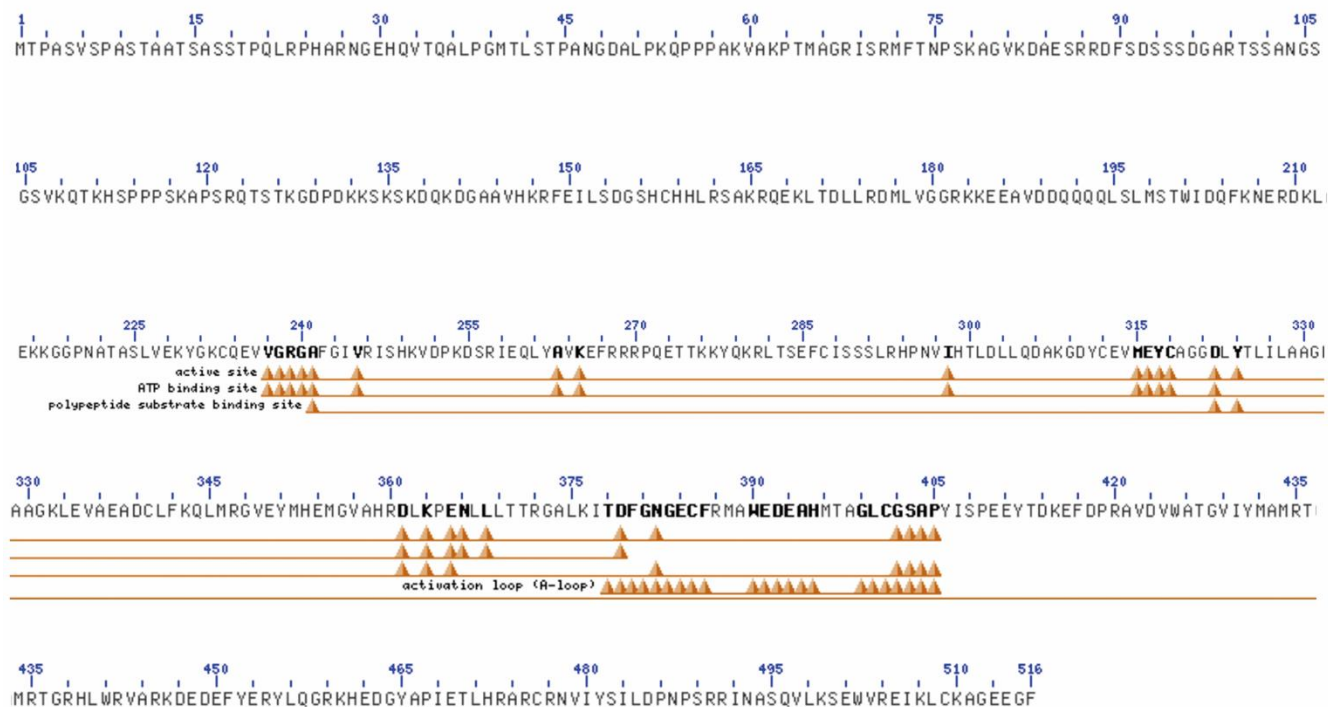


Fig. S2 Sequence and proposed active residues of MpSTE1. The conserved catalytic domain contained catalytic site, ATP binding site and polypeptide substrate binding site. The proposed site is indicated as bold letter.

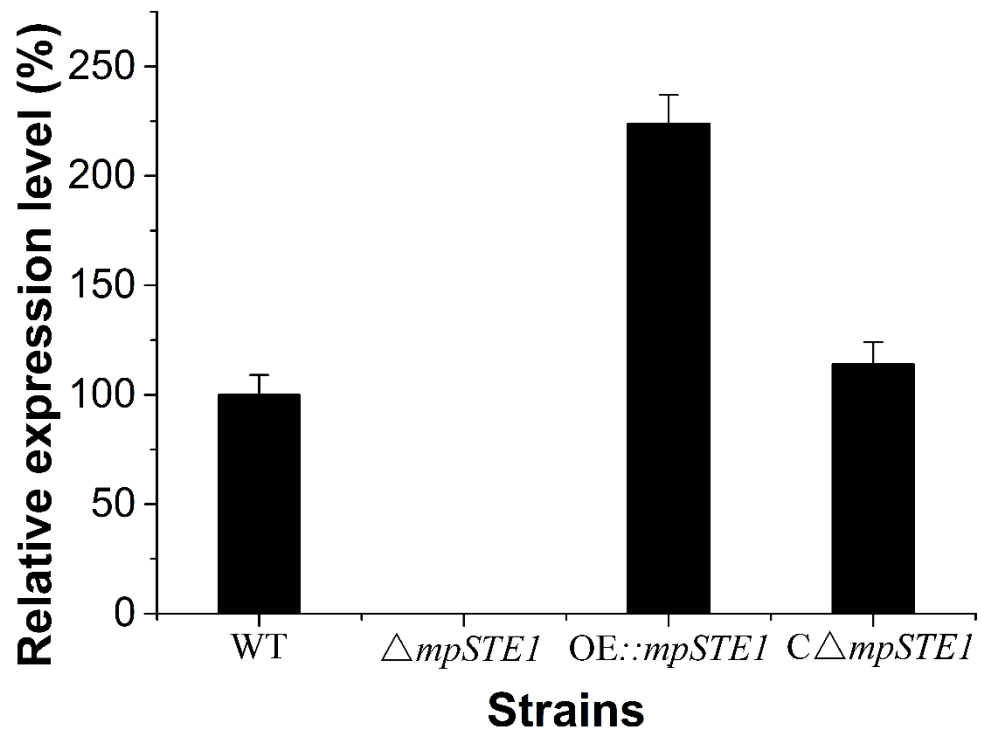


Fig. S3 The relative expression level of the wild-type strain, *mpSTE1* gene knockout ($\Delta mpSTE1$), complemented (C $\Delta mpSTE1$) and overexpression (OE::*mpSTE1*) mutants. The β -actin gene was used as an internal standard to normalize expression levels.