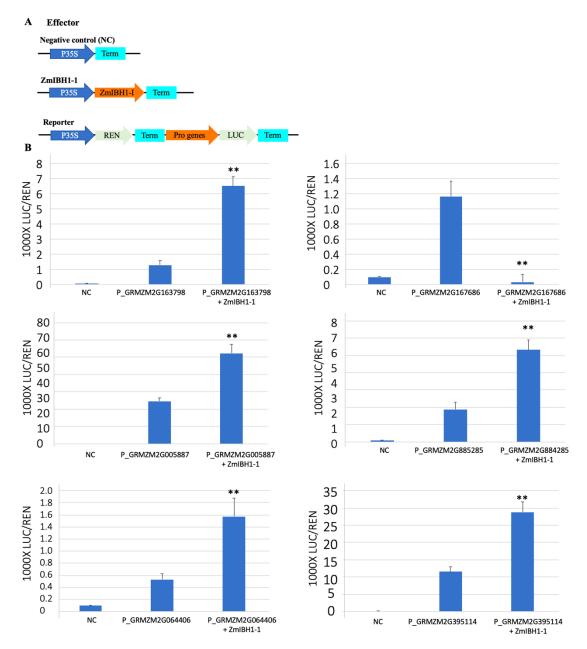


**Supplementary figure1.** Sequence alignment of Yu82 and Yu87-1. Polymorphisms are highlighted in cyan and the predicted translation start of ZmIBH1-1 is boxed in yellow and the predicted termination codon of ZmIBH1-1 is boxed in red.

GRMZM2G388823 Sevir.3G025700	MARKRTAARHQHQEPPPNPNPNLRRRAAASDPASDEPPPSSKRMLAFHFLRALAR MARKRTARPPPPPPPNPNPNPNRRAVASSAATAPDPASGSASPSKRMLAFHFLRALAR ****** **************************
GRMZM2G388823 Sevir.3G025700	IHSTTPAPRRPRTIRRAAYSSMARAASPRRAWTQALLRQARARRAAARSSRGAVLLRRRVIHSATPVPRRTRNIRRAAYSSMARAANPRRAWTQALLRQVRVCRAMRSRRAVLLRRRVSG***:**.*******************************
GRMZM2G388823 Sevir.3G025700	ASAAASPPPPLLRASAGESTSAPTPLAPAAVAARGPPPRQAGEPARADALRRLVPGGAEM APPAASPAPPLGAARSTVSAAGGTSAAAAALPRGGPPPRQAGEPARADALRRLVPGGSEM ****.*** * : *::. *. *.**:.
GRMZM2G388823 Sevir.3G025700	EYGSLLDETADYVRSLRAQVQLMQSLVDLFSAQ EYCSLLDETADYLRCLRAQVQLMQNLVDLFSGQ ** **********************************

**Supplementary figure 2. Protein sequence alignment of ZmIBH1-1 and SvIBH1-1.** Red squares indicate the conserved bHLH domain. '\*' indicates positions which have a single, fully conserved residue. ':' indicates that one of the following 'strong' groups is fully conserved: STA, NEQK, NHQK, NDEQ, QHRK, MILV, MILF, HY, and FYW. '.' indicates that one of the following 'weaker' groups is fully conserved: CSA, ATV, SAG, STNK, STPA, SGND, SNDEQK, NDEQHK, NEQHRK, FVLIM, and HFY.



Supplementary figure 3. Results of the dual-luciferase transient transcriptional activity assay. (A) The 35S:REN-Pro zein:LUC reporter constructs were transiently expressed in onion epidermal cells together with control vector or 35S:ZmIBH1-1effector, respectively. (B) The expression level of Renilla (REN) was used as an internal control. The LUC/REN ratio represents the relative activity of candidate gene promoters. Data are values of three independent experiments. Significant differences from the corresponding control values (using Student's t test [n=3]): \*P < 0.05, \*\*P < 0.01, and \*\*\*P < 0.001.