

Figure S1

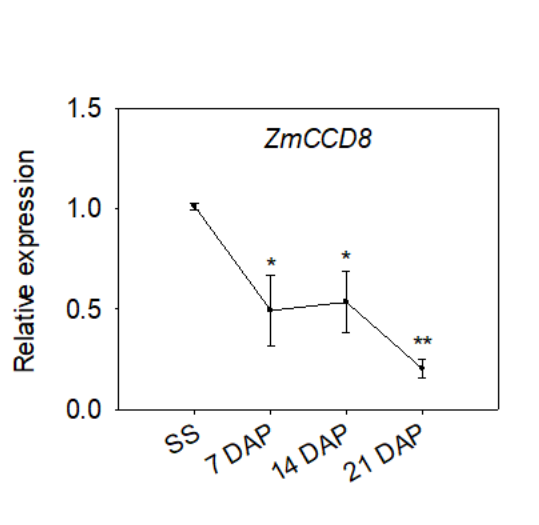


Figure S1 *ZmCCD8* expression in the maize ear. Relative expression of *ZmCCD8* in the maize ear at different developmental stages from silking (SS) to 21 days after pollination (21DAP). 7 DAP, 7 days after pollination. 14 DAP, days after pollination. The gene expression level at SS was normalized to 1 for comparison. Error bars represent the SD of three biological replicates. Asterisks indicate significant differences relative to SS as determined by the two-tailed Student's *t*-test (* $P < 0.05$; ** $P < 0.01$).

Figure S2

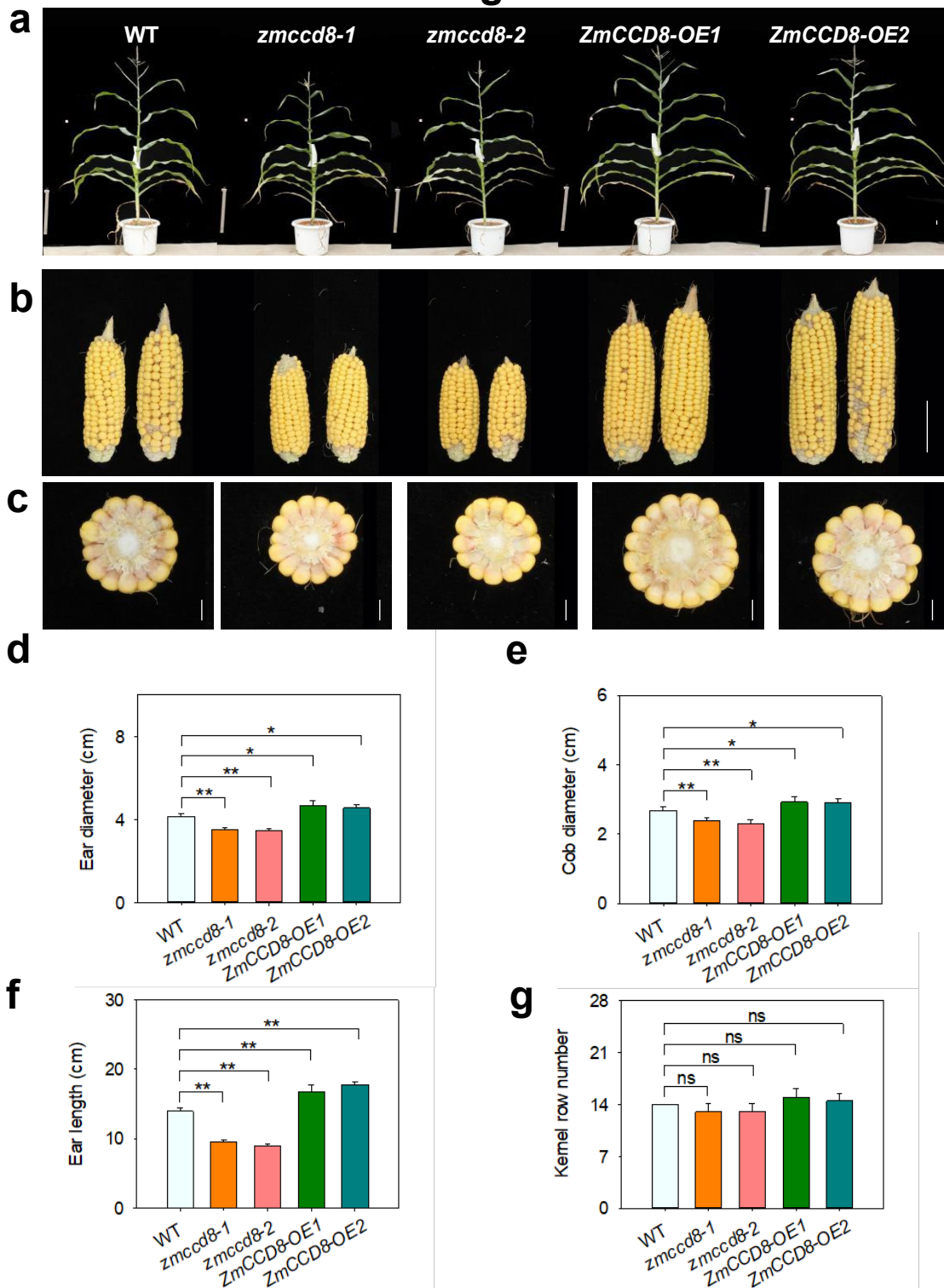


Figure S2 The phenotype of stable transgenic plants of *ZmCCD8* at 21 days after pollination (21 DAP). (a-c) The shoot and ear phenotype of two *ZmCCD8* knockout (*zmccd8-1*, *zmccd8-2*) and overexpression (*ZmCCD8-OE1*, *ZmCCD8-OE2*) lines. Scale bars = 50 cm. (d-g) Ear diameter (d), cob diameter (e), ear length (f), and kernel row number (g) of *ZmCCD8* knockout and overexpression lines. Scale bars = 5 cm. Error bars represent the SD of four (d-g) biological replicates. Asterisks indicate significant differences relative to WT as determined by the two-tailed Student's *t*-test (**P* < 0.05; ***P* < 0.01). ns, no significant difference.

Figure S3

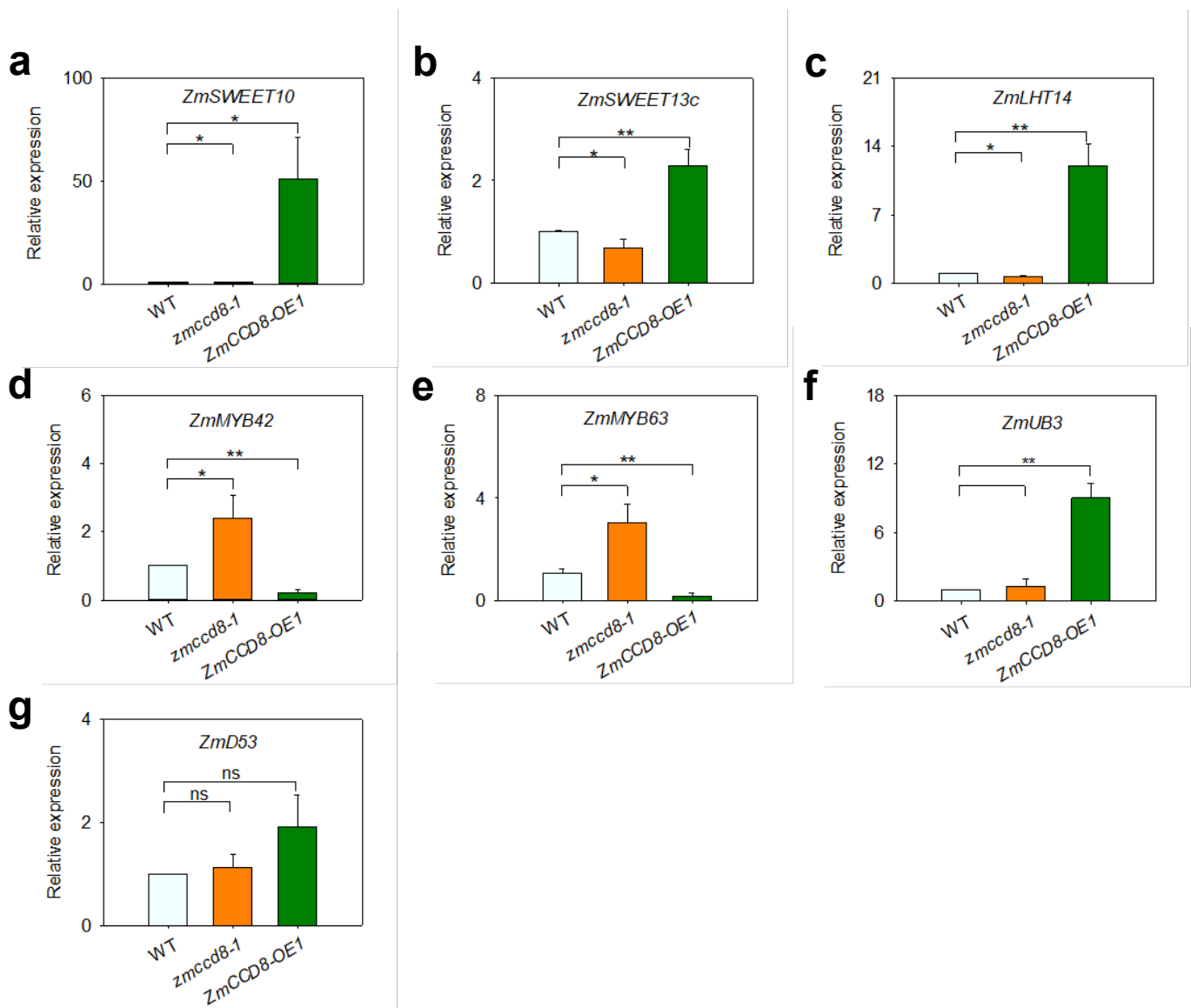


Figure S3 RT-qPCR analysis with kernel samples of *ZmCCD8* transgenic plants at 7 days after pollination (7 DAP). (a-g) Relative expression of *ZmSWEET10* (a), *ZmSWEET13c* (b), *ZmLHT14* (c), *ZmMYB42* (d), *ZmMYB63* (e), *ZmUB3* (f), and *ZmD53* (g) in kernels of *ZmCCD8* knockout (*zmccd8-1*) and overexpression (*ZmCCD8-OE1*) lines in comparison to wild type plants. Error bars represent the SD of three biological replicates. Asterisks indicate significant differences relative to WT as determined by the two-tailed Student's *t*-test (* $P < 0.05$; ** $P < 0.01$). ns, no significant difference.

Figure S4

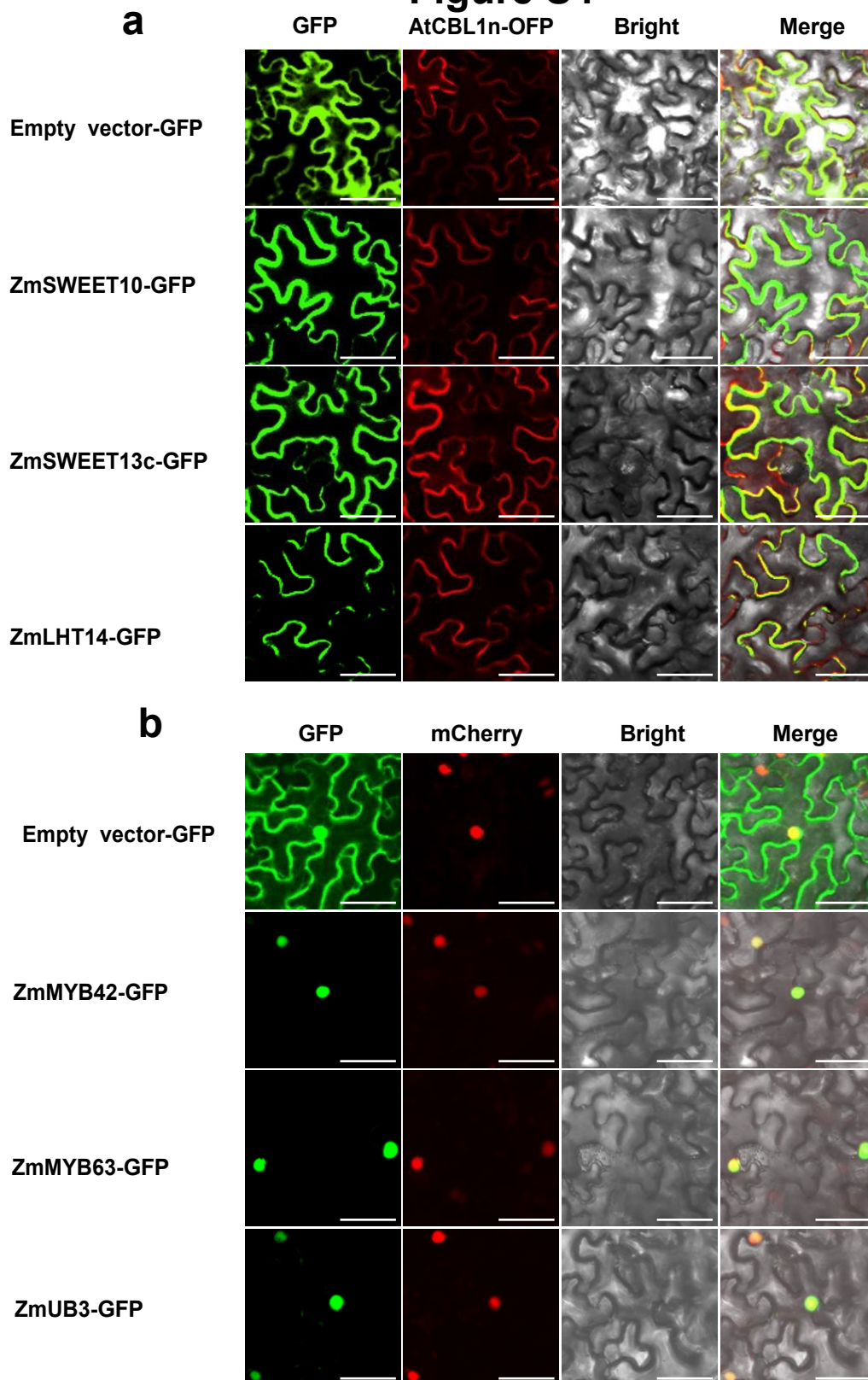
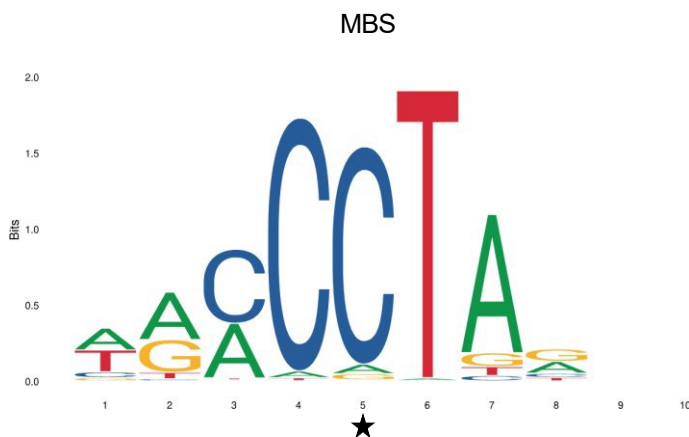


Figure S4 Subcellular localization of ZmSWEETs, ZmLHT14, ZmMYBs and ZmUB3. (a and b) Subcellular localization of GFP-tagged transporters ZmSWEET10, SWEET13c, ZmLHT14 (a), and transcription factors ZmMYB42, ZmMYB63, and ZmUB3 (b) in *N. benthamiana* leaves. The GFP protein itself is used as a control. AtCBL1n-OFP is a plasma membrane localized marker protein. The NF-YA4-mCherry is a nucleus marker. Scale bars = 50 μ m.

Figure S5

a



b

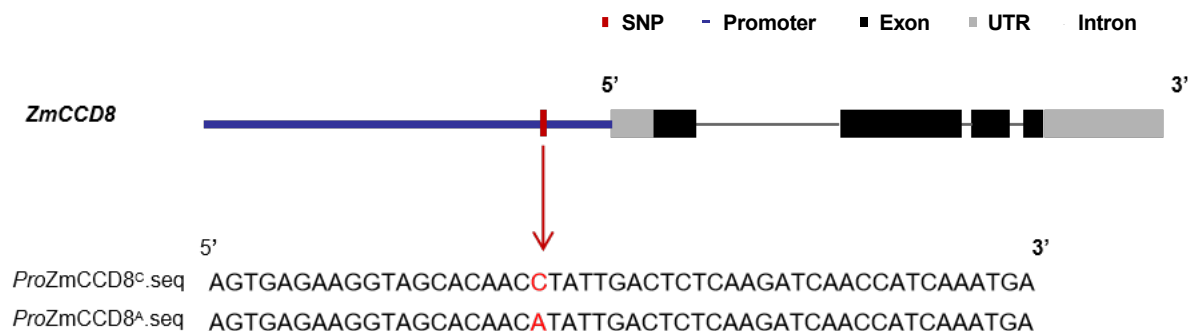
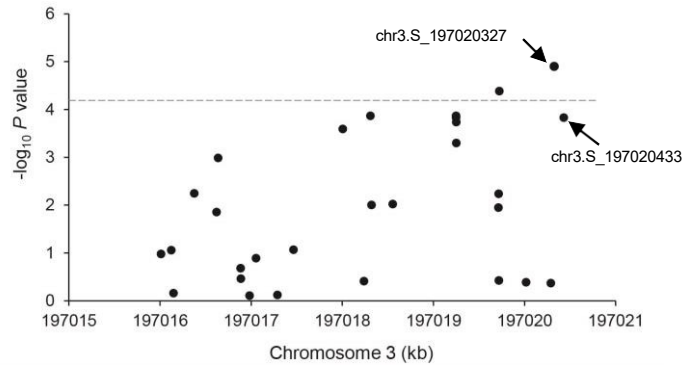


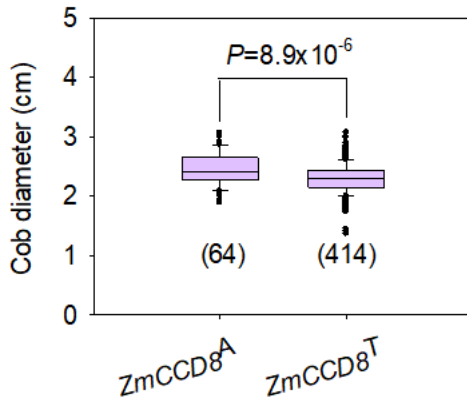
Figure S5 The SNP position in the *ZmCCD8* promoter. (a)The core binding sequence (MBS: CCTA) of MYB transcription factors and the position weight matrix. The black star indicates the SNP “C/A” in the promoter of *ZmCCD8*. (b) *ZmCCD8*’s gene structure and the SNP-containing 50-bp sequence alignment in the *ZmCCD8* promoter. The red arrow indicates the SNP, 1204 bp upstream of the start codon of *ZmCCD8*. The “C” to “A” change of MBS is highlighted in red.

Figure S6

a



b



c

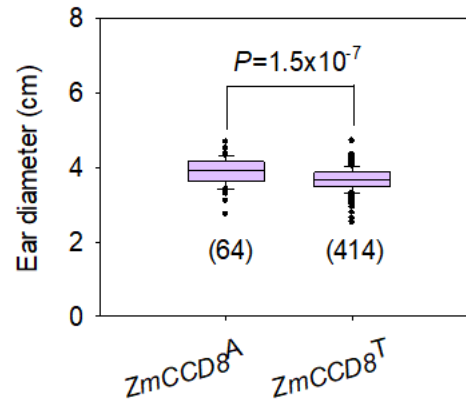


Figure S6 GWAS showing *ZmCCD8* variations associated with ears traits. (a) A partial Manhattan plot of ear diameter. (b and c) Boxplots of the cob diameter (b) and ear diameter (c) of different haplotypes. The *P* values in the box plots are derived from two-tailed Student's *t*-tests.