**Table S1.** RT-qPCR Primers used in this study

| Gene ID | Forward primer sequence (5'–3') | Reverse primer sequence (5'–3') |
|---|---|---|
| ZmCaM2 | TCGCCATGGCGGACCA | TCCGGCTCACAGGATCACG |
| pCAMBIA1 302-ZmCaM2 | TGACCATGGTAGATCTATGGCGGACCAGCTTAGC | CTTCTCCTTTACTAGTTGACAGGATCACGCATTTCTGG |
| PET-29b-ZmCaM2 | TTAGAAGGAGATATACATATGATGGCGGACCAGCTTAGC | ACGGAGCTCGAATTCGGATCCTGACAGGATCACGCATTTCTGGC |
| pCAMBIA3 301-UBI-ZmCaM2 | CGGGATCCATGGATTACAAGGATGACGACGATAAGATGGCGGACCAGCTTAGC | ACTAGTTCACAGGATCACGCATTTCTGG |
| M1830(493) | TTGAAGACTTATGGTCTGAAGC | ACGAACTCGTCGTAGTTGATG |
| pU6-T1 | CTCCGTTTTACCTGTGGAATCG | CATCACGGTTCCGAGCTCCTCGGCAGCCAAGCCAGCA |
| gRNA-T1 | CGGAGGAAAATTCCATCCAC | AGGAGCTCGGAACCGTGATGGTTTTAGAGCTAGAAAT |
| Pps | AGCGTGGGTCTCGCTCGACGCGTATCCATCCACTCCAAGCTC | TTCAGAGGTCTCTACCGACTAGTATGGAATCGGCAGCAAAGG |
| SP | GCGGTGTCATCTATGTTACTAG | TGCAATAACTTCGTATAGGC |
| ZmABF2-q | TTGTGCCTCCACTGCAATTCGG | TTACAAGTCGTCTCCCTCCATCTTCC |
| ZmRAB18-q | GTGGTGGGTTGAGGGGAAGGAAGC | ACGCCATCGCCGTTGAGCCT |
| ZmActin | CACTTCCTCATGCTATTCTCCG | GCTTCTCCTTTATGTCCCTGAC |

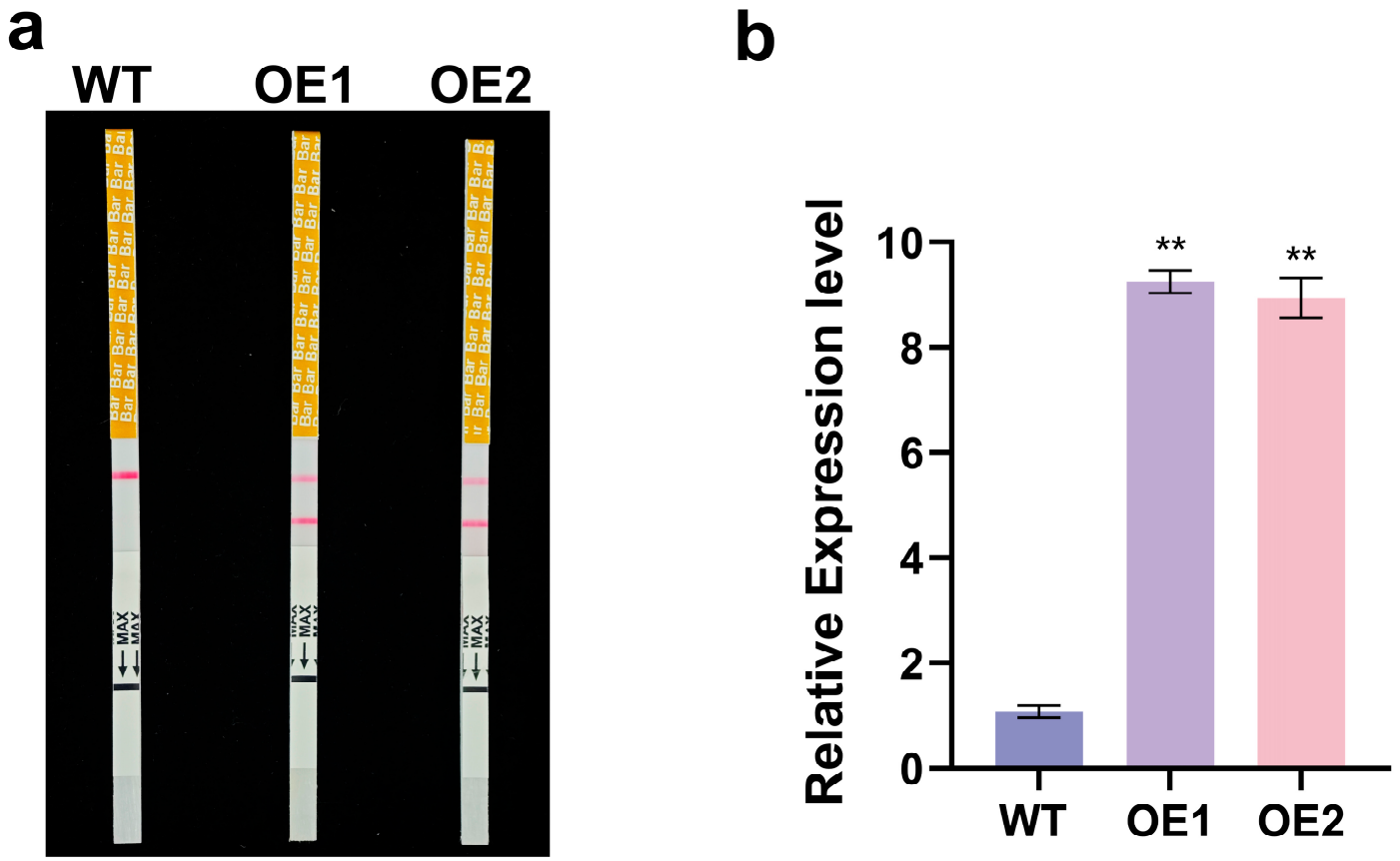


**Figure S1.** Detection of transgenic maize. (a) Bar test strip detection. (b) Expression detection of the *ZmCaM2* overexpressed B104 maize lines. The significance analysis compared with WT was performed using one-way ANOVA (**$P < 0.01$). Bars indicate standard error of the mean. The experiment was performed using three biological replicates.

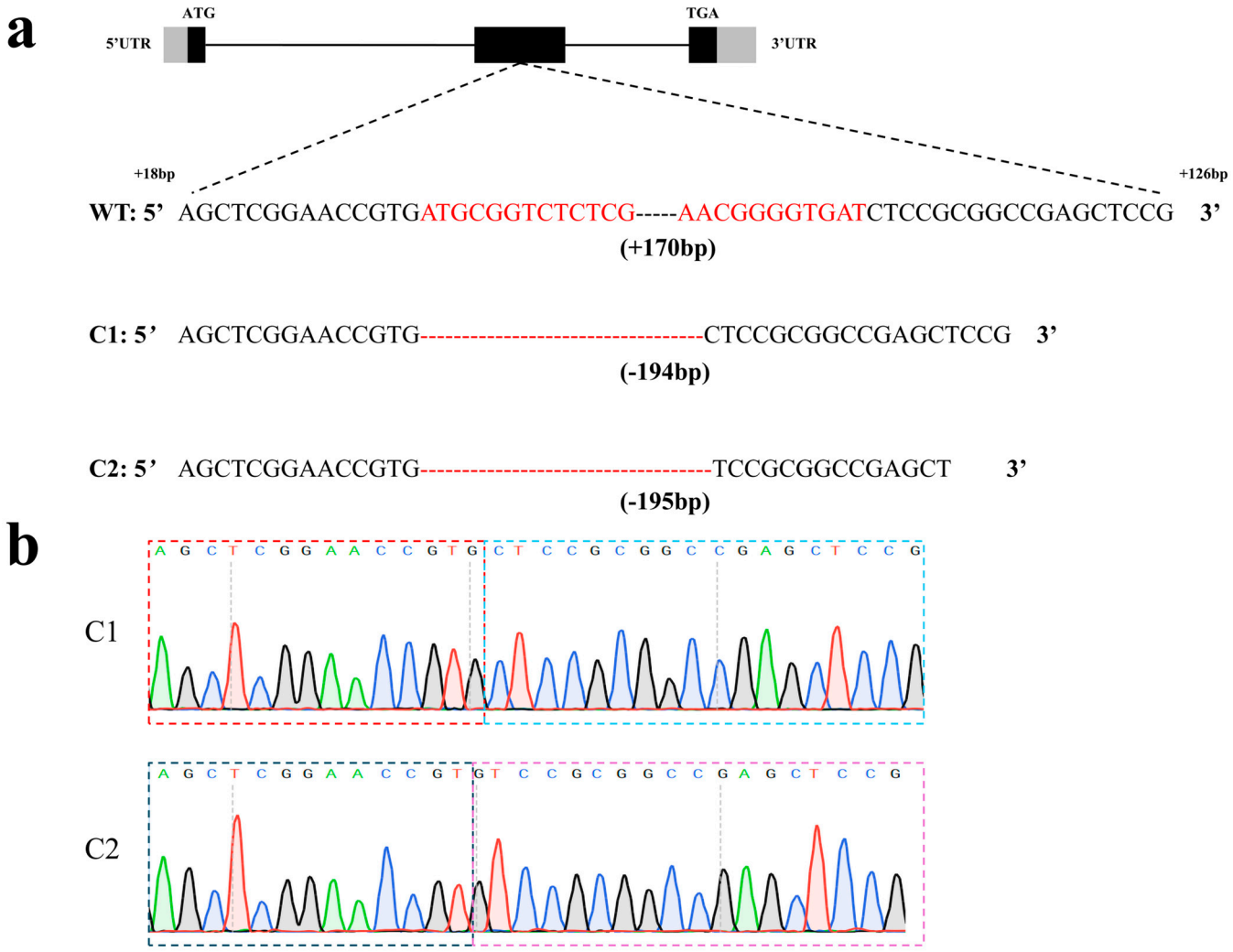



**Figure S2.** Detection of mutant maize. (a) Schematic diagrams of CRISPR/Cas9-*ZmCaM2* mutant lines generated using CRISPR/Cas9–mediated genome editing. (b) The CRISPR/Cas9-*ZmCaM2* mutant lines were identified using Sanger sequencing compared with WT.