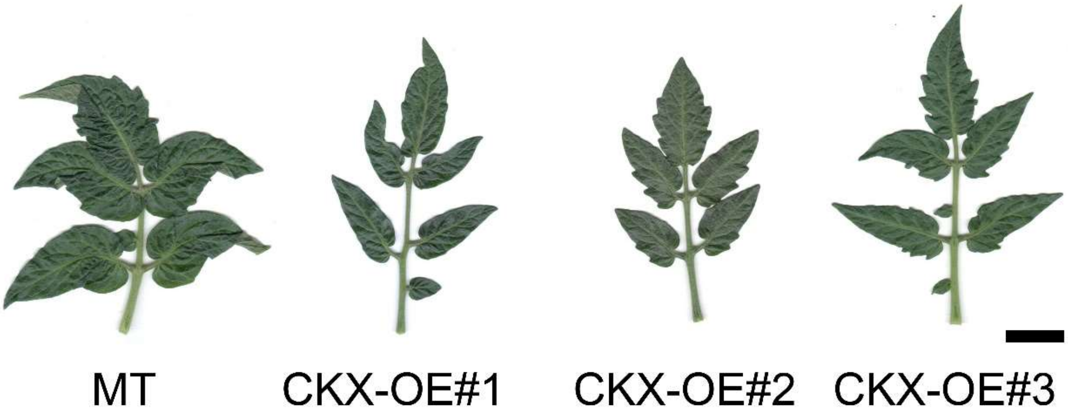

Figure S1. Compound leaf development is altered in CKX2-overexpressing tomato plants. Fully-expanded fifth leaf from each genotype at 45 DAE. Notice the smaller leaflets in the transgenic lines with smooth leaf margins.

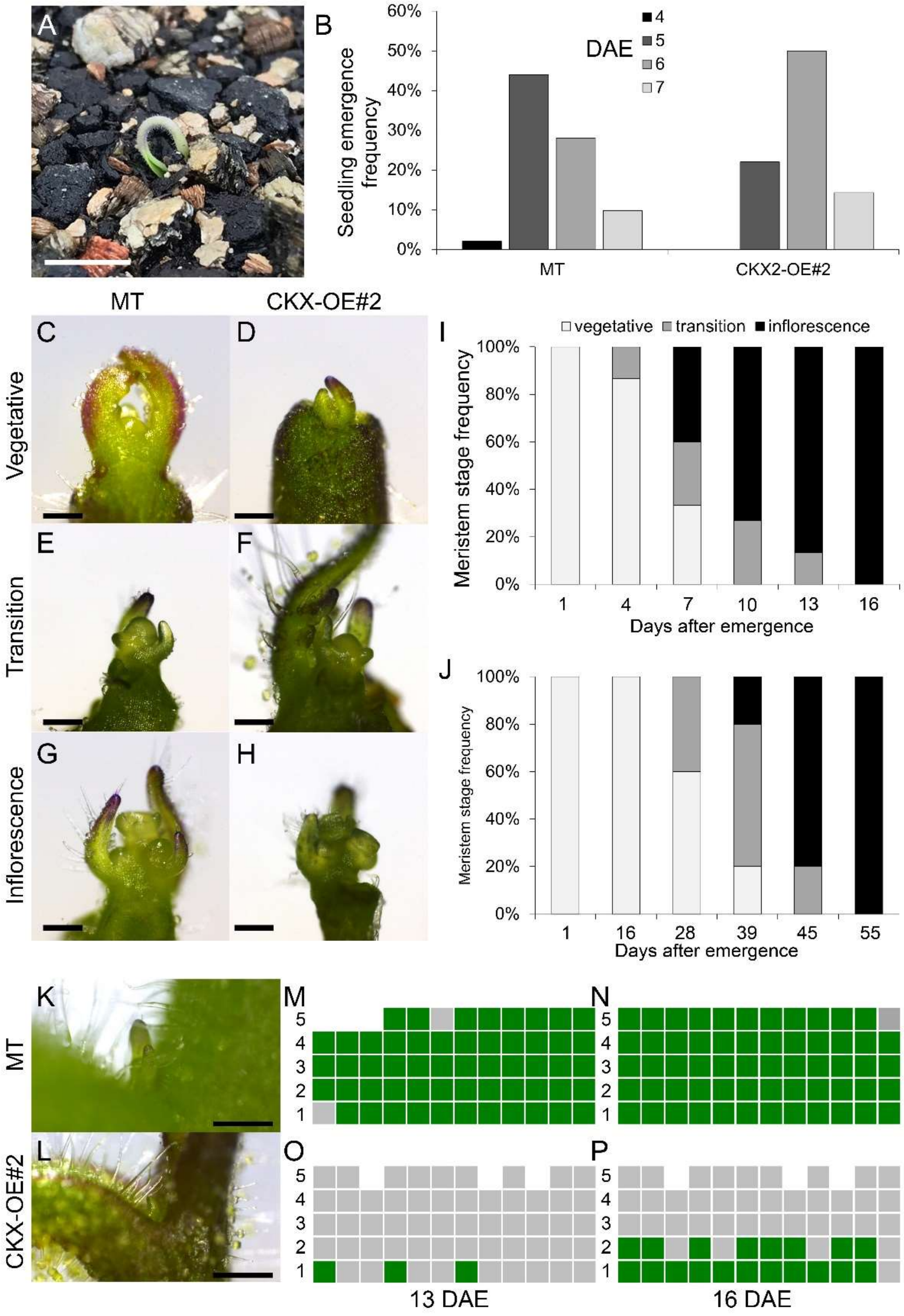

Figure S2. Tomato CKX2-overexpressing plants delay initial development and the transition to reproductive development. **A**. Seedlings considered as emerged from that stage; bar = 1cm. **B**. Seedling emergence frequency between 4 to 7 days after sowing (DAS). **C to H**. Representative images of meristem maturation of the primary shoot meristem of MT (C, E and

G) and CKX2-OE#2 (D, F and H) in the vegetative (C and D), transition (E and F) and reproductive (G and H) stages; bar = 200 µm. **I and J**. Vegetative to reproductive primary meristem transition evaluated by the seedling frequency in each developmental stage in MT (I) and CKX2-OE#2 (J), from the 1st to 55th DAE (days after emergence). **K and L**. Representative bud axil initiation in the 2nd leaf axil of MT (K) and CKX2-OE#2 (L); bar = 400 µm. **M to P**. Schematic representation of axillary bud formation in leaf axils at 13 and 16 DAE in MT (M and N) and in CKX2-OE#2 (O and P).

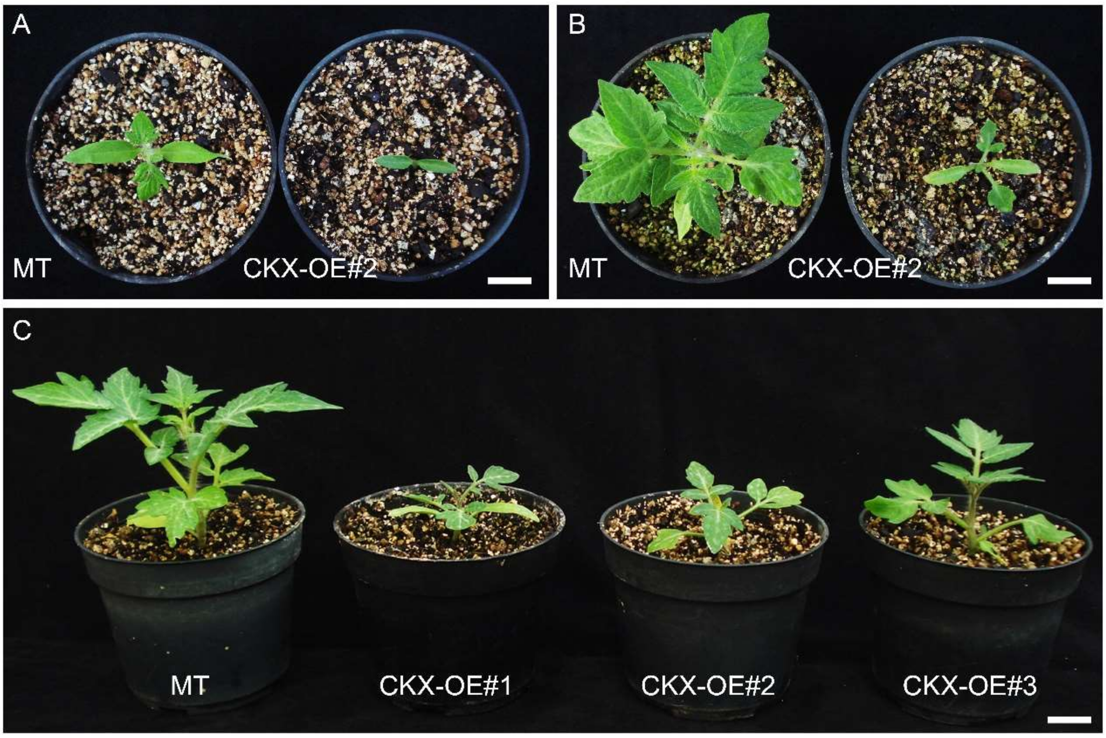

Figure S3. Shoot phenotype of CKX2-overexpressing tomato plants. The shoot development was registered in MT and CKX2-OE tomato plants at 14 DAE (**A**), 28 DAE (**B**) and 32 DAE (**C**). DAE, days after emergence.

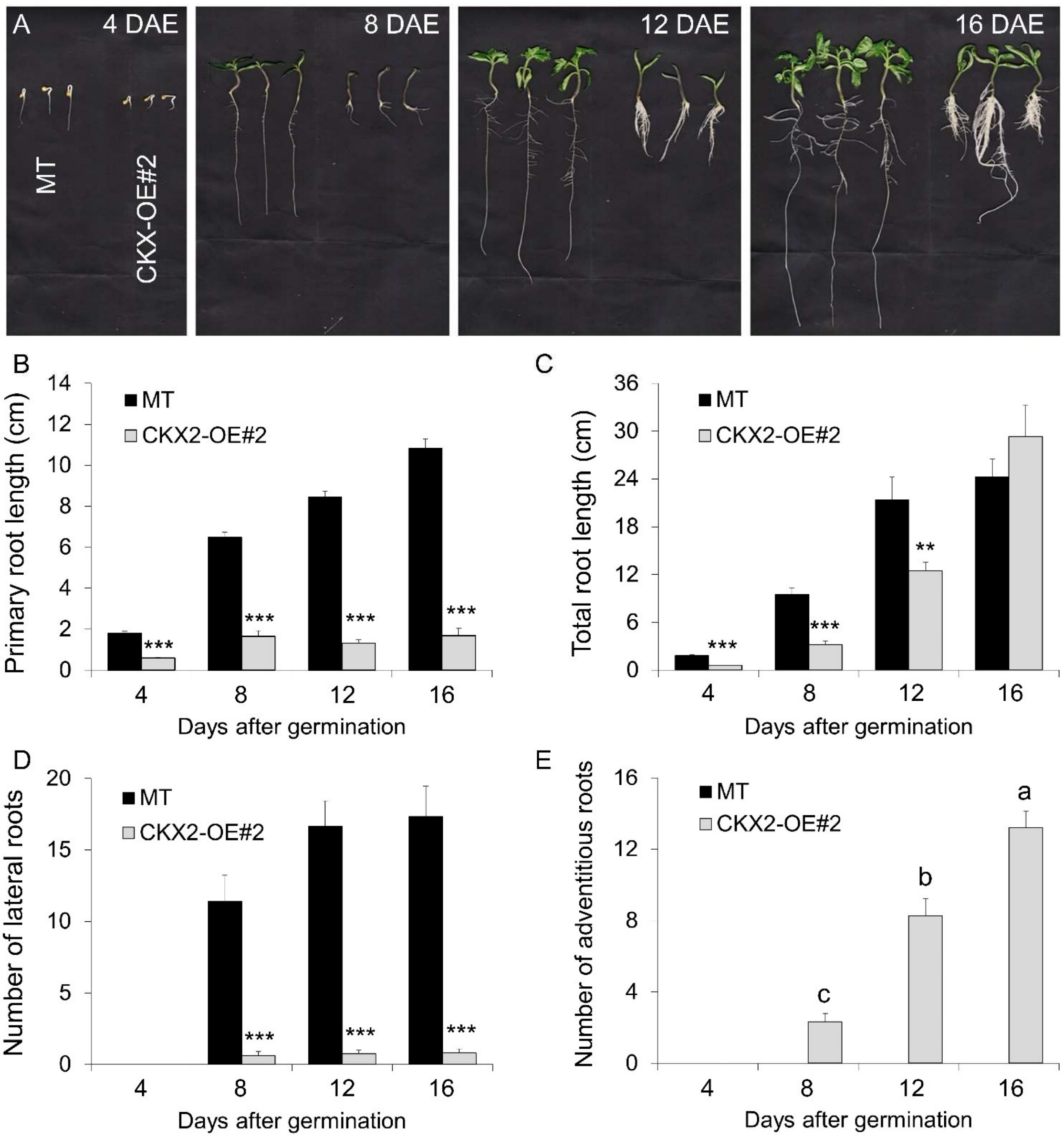

Figure S4. **Root development pattern is altered in tomato plants overexpressing *CKX2***. **A**. Comparison of root growth of MT and CKX2-OE#2 seedlings at 4, 8, 12 and 16 days after emergence (DAE). **B**. Primary root length. **C**. Total root length. **D**. Number of lateral roots. **E**. Number of adventitious roots. Data are means ± SE (n = 10). B-D: asterisks indicate significant differences between genotypes within a treatment (B and C: Student's *t*-test; D: Mann Whitney test; **$P < 0.01$, ***$P < 0.001$; E: letters indicate significant differences among treatments within the same genotype (Tukey test; $P < 0.05$).

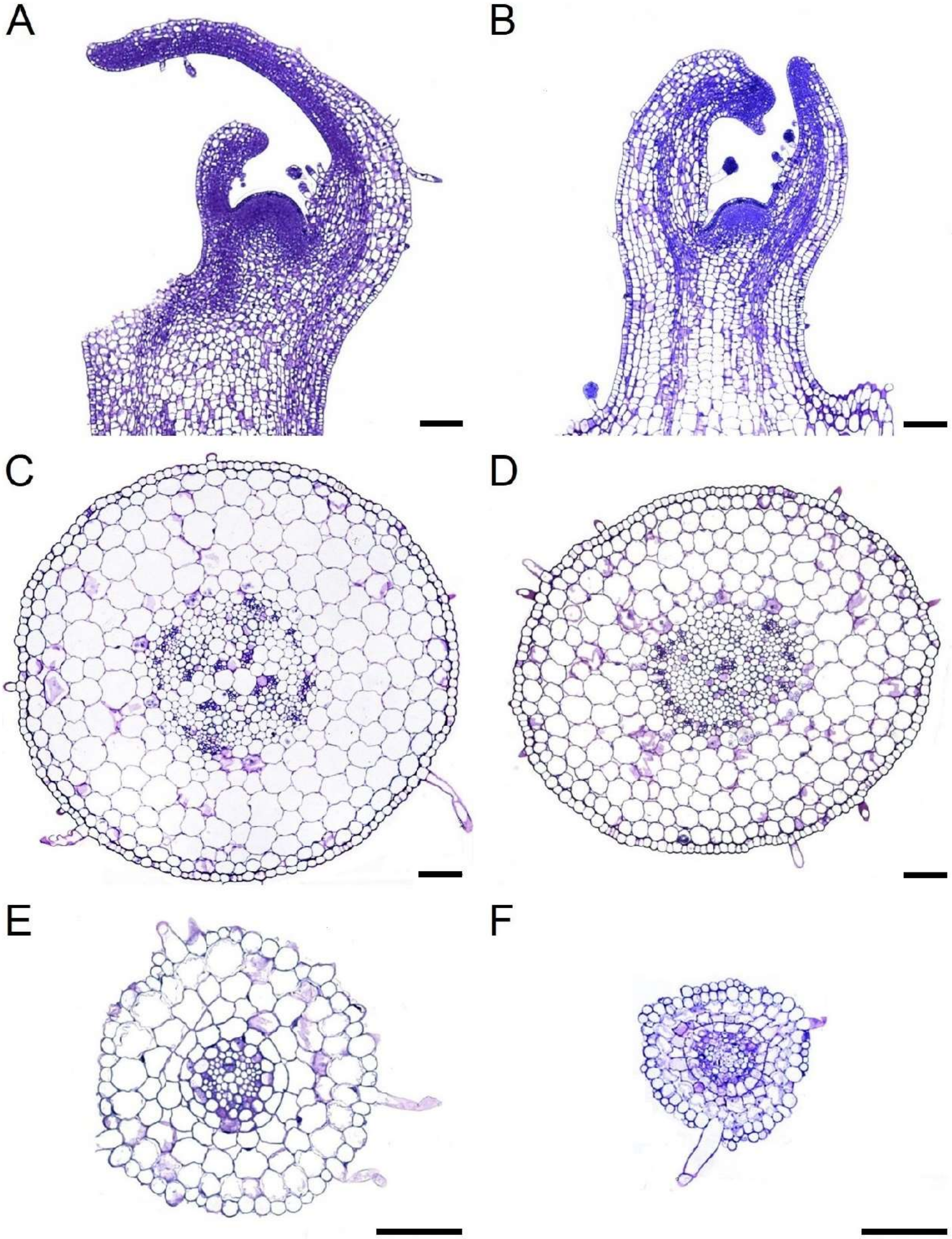

Figure S5. **Tomato CKX2-overexpressing plants alter SAM development, vessels organization and root development**. Apical shoot (**A** and **B**), hypocotyl (**C** and **D**) and primary root (**E** and **F**) were collected from MT (A, C and E) and CKX2-OE#2 (B, D and F) seedlings at

7 DAE. Apical shoots were longitudinally sectioned while hypocotyls and roots were cross-sectioned. Bar = 100 µm.

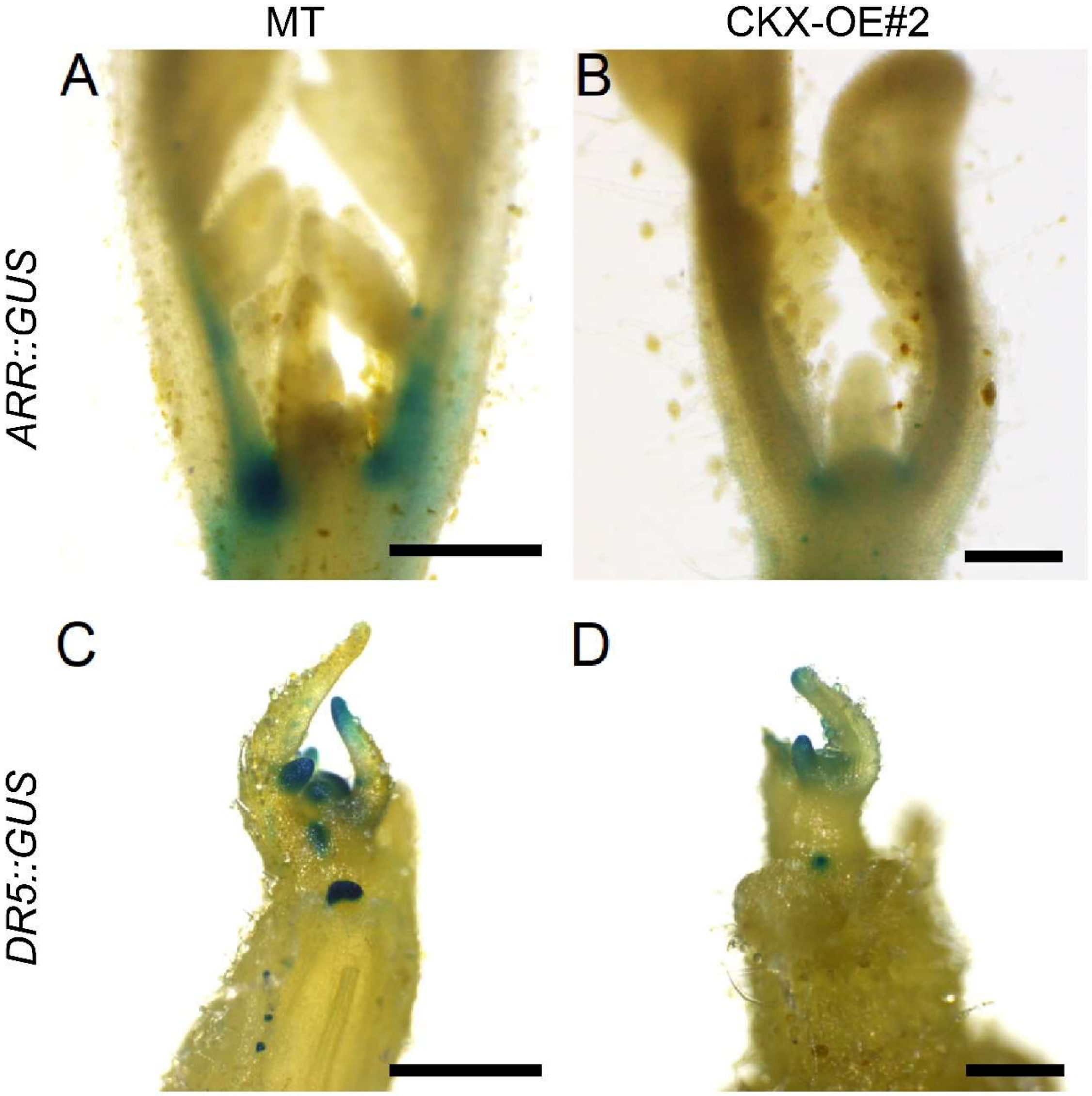

Figure S6. Reduced *ARR5::GUS* and *DR5::GUS* expression in the CKX2-overexpressing tomato plants. The *ARR5::GUS* (A and B) and DR5::GUS (C and D) expression was evaluated in apical shoots of MT (A and C) and CKX2-OE#2 (B and D) seedlings. Bars = 500 µm (A, C and D) and 200 µm (B).

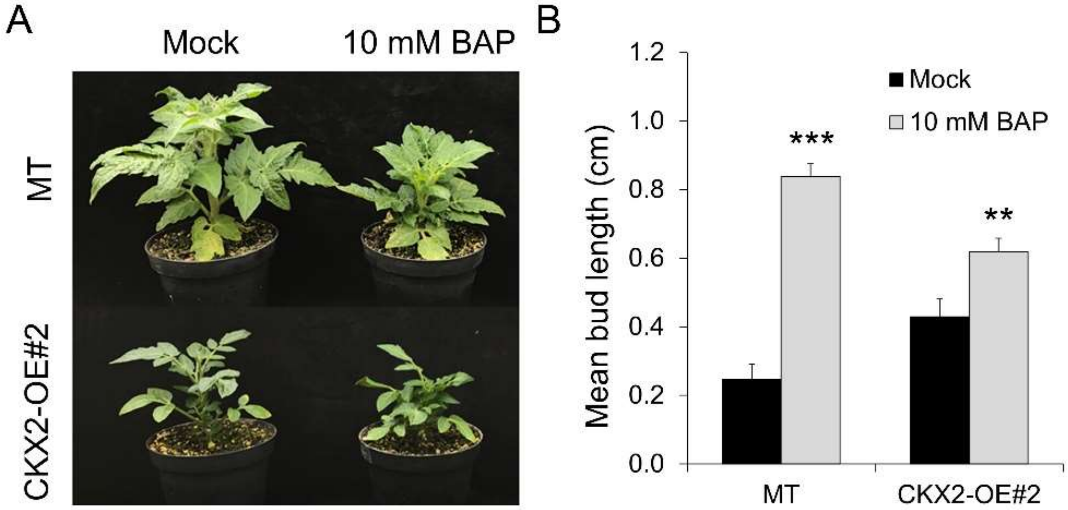

Figure S7. Bud length of tomato plants overexpressing *CKX2* upon application of BAP. Shoot phenotype (**A**) and mean bud length (**B**) of BAP-treated and non-treated CKX2-OE#2 compared to MT plants. BAP (10 mM) or mock (0 mM BAP) was applied in the leaf axil of MT and CKX2-OE#2 plants at the early vegetative (i.e., 20 DAE for MT and 38 DAE for CKX2-OE#2). The length of the bud in each axil were measured 13 days after treatment. Data are means ± SE (n =12). Asterisks indicate significant differences between treatments within the same genotype (Mann Whitney test; **P < 0.01, ***P < 0.001).

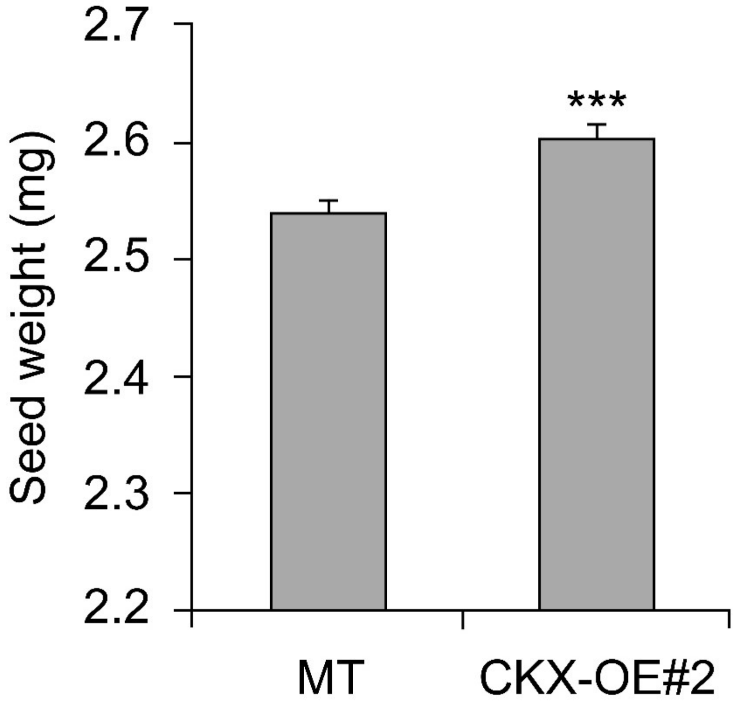

Figure S8. Increased seed weight of CKX2-overexpressing tomato plants. The weight of one seed was calculated from the weight of pools of 100 seeds. Data are means ± SE (n =12). Asterisk indicate significant difference between genotypes (Student's t-test; ***$P < 0.001$).