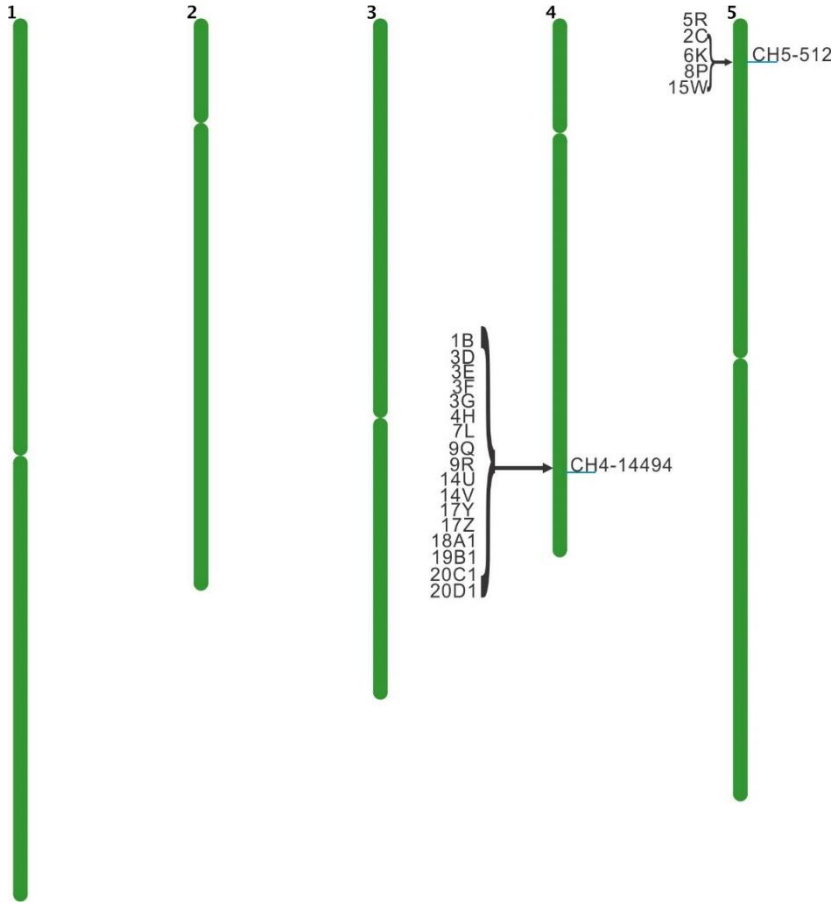
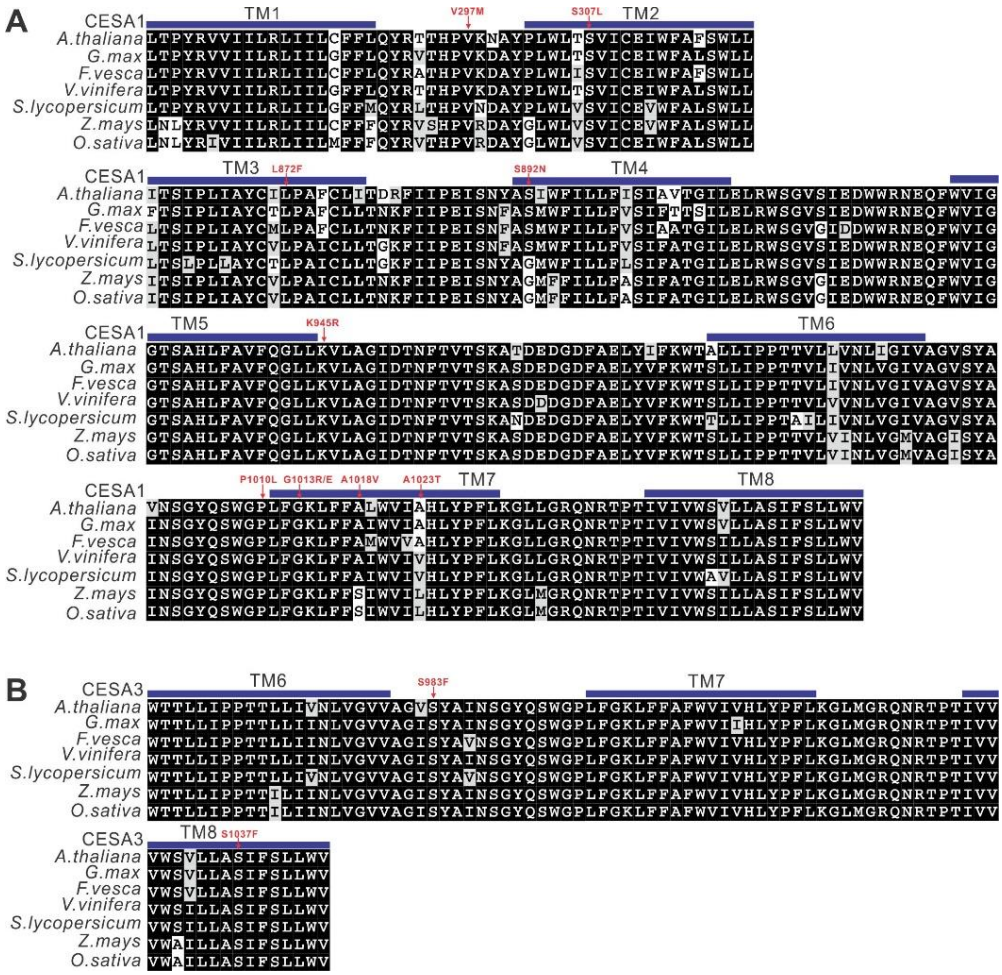
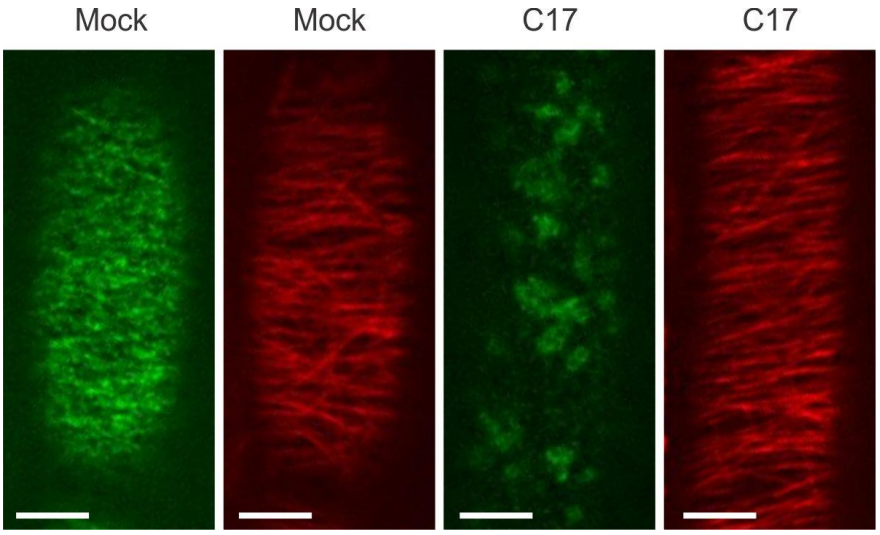


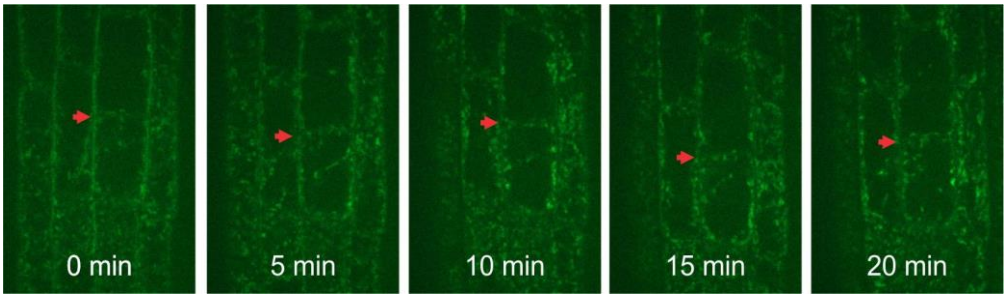
Supplemental Figure 1. Rough map position on the Arabidopsis genome of the mutated genes rendering C17 tolerance. Using 24 general simple sequence length polymorphism (SSLP) markers, the mutated genes in C17-tolerant mutants were mapped to Arabidopsis genome. The mutated genes are divided into two groups based on the linkage with SSLP markers, which were designated by corresponding markers, CH4-14494 and CH5-512, respectively.



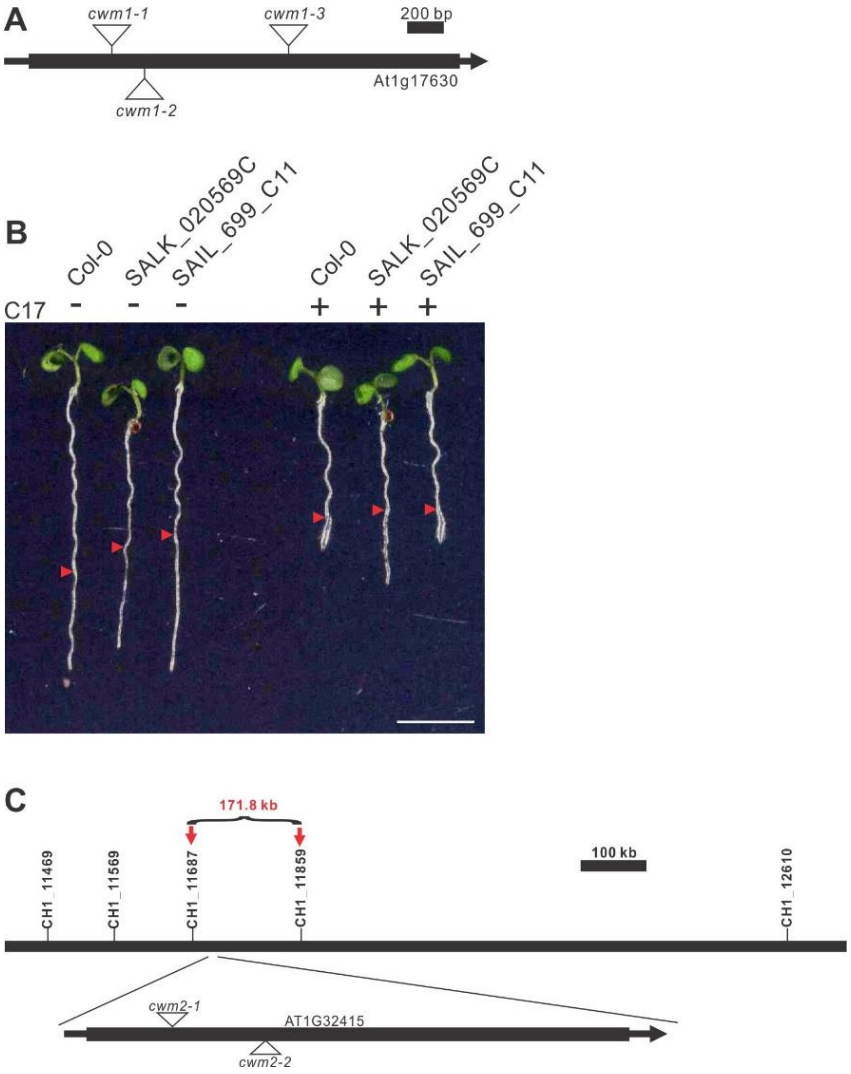
Supplemental Figure 2. Sequence alignment of *CESA1* (A) and *CESA3* (B) of several plant species. Sequences were aligned with a multiple sequence alignment programme (http://www.genome.jp/tools/clustalw/) using CLUSTALW algorithms. Protein database accession numbers are: CESA1$_{A.thaliana}$-NP_194967; CESA1$_{G.max}$-XP_003522623; CESA1$_{F.vesca}$-XP_004291468; CESA1$_{V.vinifera}$-XP_002282575; CESA1$_{S.lycopersicum}$-XP_004245031; CESA1$_{Z.mays}$-NP_001104954; CESA1$_{O.sativa}$-NP_001054788; CESA3$_{A.thaliana}$-NP_196136; CESA3$_{G.max}$-XP_003540527; CESA3$_{F.vesca}$-XP_004306536; CESA3$_{V.vinifera}$-XP_002278997; CESA3$_{S.lycopersicum}$-XP_004229630; CESA3$_{Z.mays}$-NP_001105621; CESA3$_{O.sativa}$-NP_001059162. The amino acid regions harbouring amino acid replacements in C17-tolerant mutants were selected. Arrowheads indicate the positions of the mutated amino acids. The blue lines indicate the predicted transmembrane domains (TM).



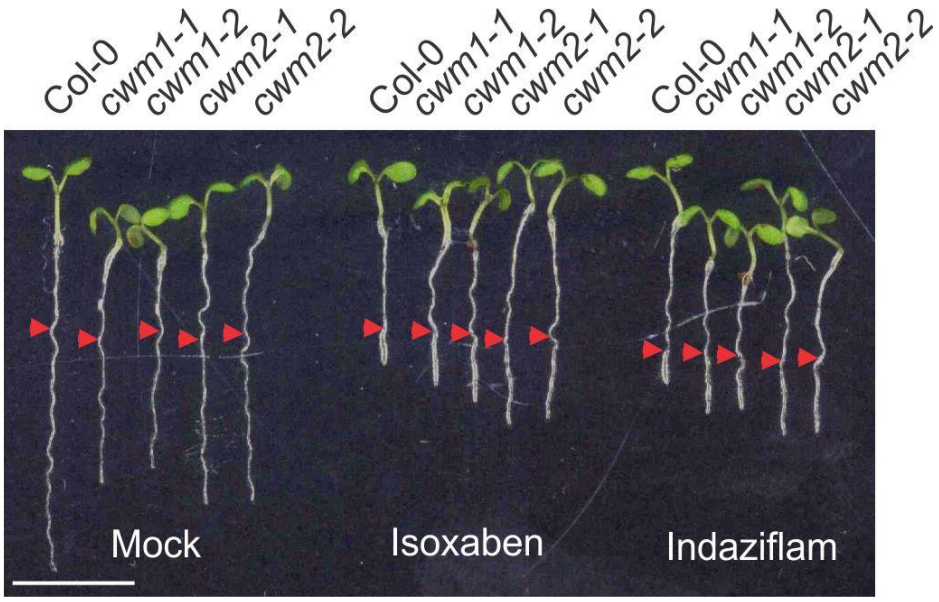
Supplemental Figure 3. C17 does not trigger microtubule polymerization. GFP-CESA3 localization at the plasma membrane and cortical microtubule arrays were observed in roots in absence (mock) or presence of C17 (200 nM) for 30 min. Transgenic plants harboring both GFP-CESA3 and Cherry-MBD were used. Scale bars＝5 μm.



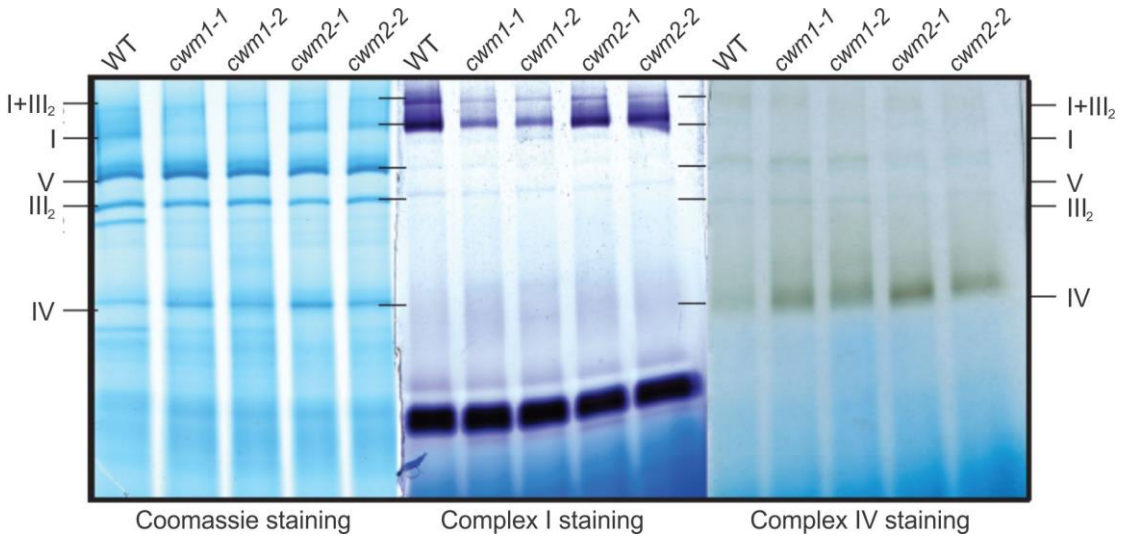
Supplemental Figure 4. C17 results in the depletion of CSCs from the root plasma membrane. Representative spinning confocal microscopy images of 4-day-old GFP-CESA3 roots treated with C17 (200 nM). The images were taken at indicated time points (0 min, 5 min, 10 min, 15 min and 20 min). Depletion of GFP-CESA3 is indicated by loss of GFP fluorescence from the plasma membrane (indicated by the arrows).



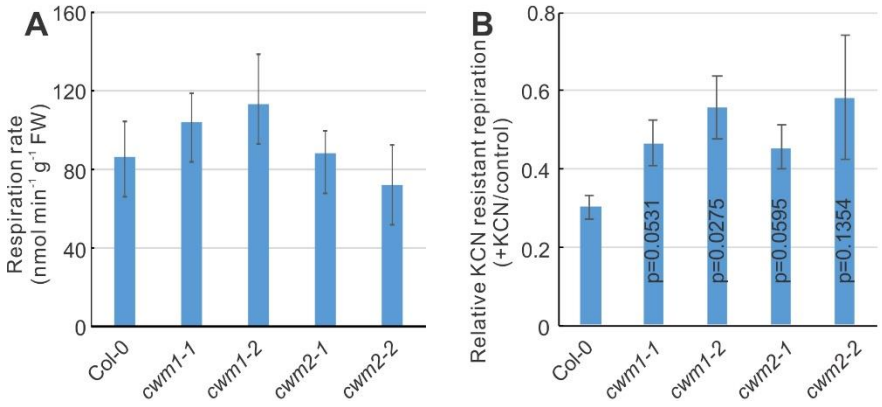
Supplemental Figure 5. Isolation of *cwm1* and *cwm2* mutants. (**A**) Intron-exon organization of the *CWM1* gene. The black box represents the exon. The position of T-DNA insertion sites (*cwm1-1, cwm1-2,* and *cwm1-3*) are indicated. Scale bar = 200 bp. (**B**) The C17 sensitivity of two independent *AT5G44570* knockout mutants lines (SALK_020569C and SAIL_699_C11). Three-day-old seedlings grown on half-strength MS medium were transferred to medium without (-) or with (+) 200 nM C17 for two days. Arrowheads indicate the root tip position at the moment of transfer. Scale bar = 5 mm. (**C**) Mapping and gene structure of *CWM2.* The *cwm2-1* locus was mapped into the 171.8-kb region between SSLP markers CH1_11687 and CH1_11589. Using PCR, a second T-DNA insert was found and positioned at the coding region of AT1G32415. The black box represents the exon. The position of the T-DNA insertion sites (*cwm2-1* and *cwm2-2*) are indicated.



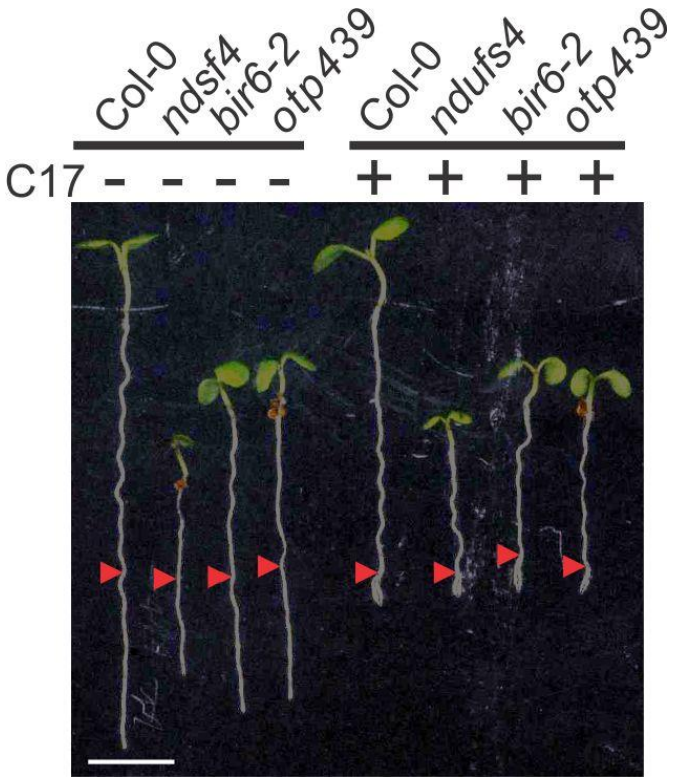
Supplemental Figure 6. Both *cwm1-1* and *cwm2-1* mutations counteract the growth inhibition induced by cellulose deficiency. Three-day-old seedlings grown on half-strength MS medium were transferred to medium without (mock, left panel) or with isoxaben (4 nM panel) or indaziflam (0.2 nM, right panel). Arrowheads indicate the root tip position at the moment of transfer. Scale bar = 5 mm.



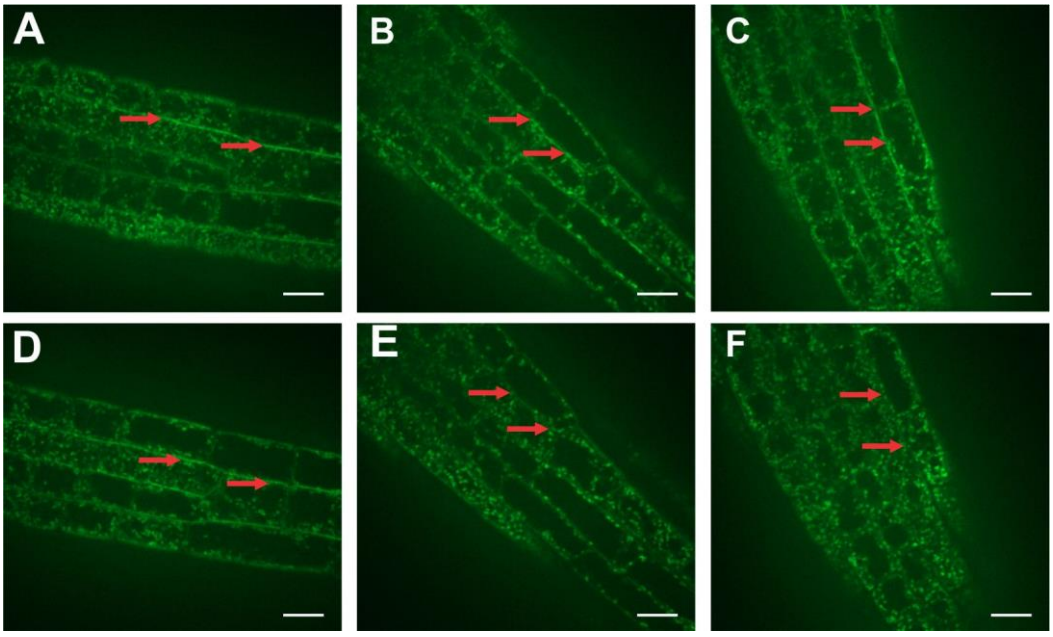
Supplemental Figure 7. Staining of respiratory protein complexes from wild type, *cwm1* and *cwm2*. Mitochondrial proteins were isolated from two-week old seedlings and solubilized by digitonin extraction buffer, separated by BN-PAGE and either visualized by Coomassie staining or by in-gel activity staining for complex I and complex IV. The identities of protein complexes are indicated on the left or right of the blots: I – complex I; IV – complex IV; V – complex V; III_2 – dimeric complex III; $I+III_2$ supercomplex composed of complex I and dimeric complex III; I_2+III_4 – a dimer of supercomplex $I+III_2$.



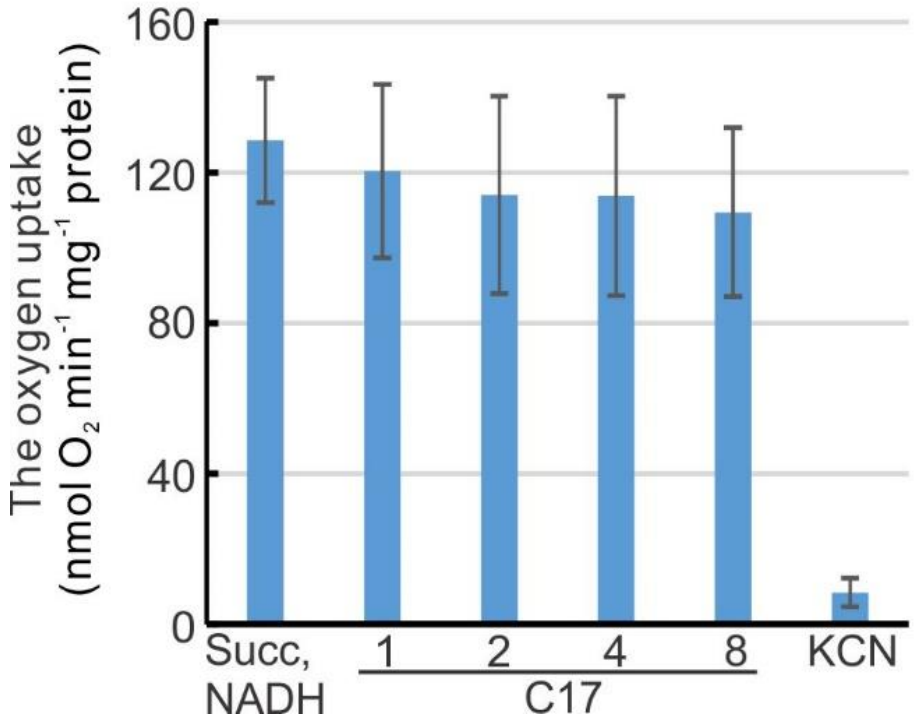
Supplemental Figure 8. Respiration rates of *cwm1* and *cwm2* mutants. (**A**) Oxygen consumption of whole seedlings of Col-0, *cwm1* and *cwm2* mutants. Data represent mean ± SE (n = 4). (**B**) Relative KCN-resistant respiration of whole seedlings of Col-0, *cwm1* and *cwm2*. Data represent mean ± SE (n = 4). Statistically significant differences compared with wild-type plants are indicated with P-value (two-tailed Student's *t*-test).



Supplemental Figure 9. C17 sensitivity of the mutants with defective mitochondrial complex I. Root growth of wild-type (Col-0) and mitochondrial complex I mutants (*ndsf4*, *bir6-2* and *otp439*). Three-day-old seedlings grown on half-strength MS medium were transferred to medium without (-) or with (+) of 200 nM C17 for two days. Arrowheads indicate the root tip position at the moment of transfer. Scale bar = 5 mm.



Supplemental Figure 10. Inhibition of mitochondrial activity did not restore CSC activity. (**A-F**) Representative spinning confocal microscopy images of 4-day-old GFP-CESA3 plants treated with 0.1% DMSO (A and D), 200 nM C17 (B and E), or a combination of 1 μM antimycin A with 200 nM C17 (C and F). The images were taken at 0 min (A, B and C) and 20 min (D, E and F). Depletion of GFP-CESA3 is indicated by loss of GFP fluorescence from the plasma membrane, such as the domains indicated by the arrows. Scale bars = 25 μm.



Supplemental Figure 11. C17 does not directly inhibit isolated mitochondrial respiration. The oxygen uptake of isolated mitochondria was measured to evaluate the effect of C17 on mitochondria. Data represent mean ± SE (n = 4). C17 concentrations ranging from 1 to 8 μM were added to mitochondria using succinate (succ) and NADH as substrates. A cytochrome pathway inhibitor, KCN (100 μM) was used as positive control.

Supplemental Table 1. Primer sequences used for mapping and cloning

Chr.	SSLP marker	Forward primer	Reverse primer
1	nga63	AACCAAGGCACAGAAGCG	ACCCAAGTGATCGCCACC
1	F8K7	GAACAATCAAGCCACCTCTAG	TCAGTGTCAGTTGAAAGTTTAAGC
1	F19K23	GAATTCTGTAACATCCCATTTCC	GGTCTAATTGCCGTTGTTGC
1	T17F3	GGACCGACGGTTACGAGAGT	TAACGGGCCGTTGCAAGA
2	T23K3	CGTGTTTACCGGGTCGGA	AAAACCCTTGAAGAATACG
2	F3P11	ATGTATTTGTTGCAAAATAA	TGCACAGAAGAAAAAACTA
2	T20P8	TCCGATTCGATTAAACTC	TTATTTCCTATTTCAAGACT
2	T16B24	ATGAACGGAGTAGCTATC	CGCGTAGAACATAATCTGTA
3	F20H23	CAATGGGAAGAAGGTGTGAG	CGCATTTCCATAAGTTTGTT
3	MGL6	ACCTGTTCAGTCTATGTTAC	GGGAATTATTAACATTATCA
3	T32N15	CAAAAGAAATGCAACGAGAC	TTTGATCATGAATGGTAGTG
3	F28P10	GAATAAACCATGTTGCCAAACATC	CATTTGATGCCCTGATAATTTCTC
4	T4I9	TTATAGCAAACGTACAAGTC	CTGCATACACGTCGTCTC
4	F17A8	CTGGACCCTAGTGGATGT	GACGGTTCTCCATTAATTAT
4	FCA8	TTCGGAGAAAGAAACGACAT	ATGGAACTATTCAGGCATTA
4	T15N24	GCAACCGCTGCTGCTTTA	AATATTTGGCTTTGCGTAGA
4	T4L20	ACCCTAAAACAATGTCTCTT	TGCTAACATGGAAATTTGTC
5	MBK20	CTCTGTTGGGGCAAAACC	GATGCTGGAGAGTAGCTTAG
5	nga139	AGAGCTACCAGATCCGATGG	GGTTTCGTTTCACTATCCAGG
5	T26D22	CACAGGCCATTGGATGTA	TGTTAGAACCCACCATTTG
5	K6M13	CCTGTTCCAATGAATATG	TGTAGCTGCTGAGTTGTC
5	MGI19	GCTTGACATGAAGTGCTAAAC	TCTGTGTGATTCTCTCCAAGG
5	CH5_512	GAATAAATGGGCCTTATAAC	TATTATTGTGCCAGATATTG
5	CH5_1037	GGCACAACTATATTTCCCTCCAT	TTGTTAGTGGTTGAATTGTGTCG
5	CH5_1316	ACCAGGTGAGAATAAAACTGCAA	ATAACATCCACCAATGCTACGTT
5	CH5_1531	AACACAACATGGTTTCAGT	GCCGTTTGTCTCTTCAC
5	CH5_1566	TGGTTAGATTTGCTGTT	ATTCTGCATTATTAGTTGTC
5	CH5_1779	CGCGATTAAAGATCCGGTA	TCGAGCAATAAGAGTGATTCC
5	CH5_2174	CATGATCCATCGTCTTAGT	AATATCGCTTGTTTTTGC
5	CH5_3177	AGGCACCAAAGAAACAAG	CGTTGTGTTCATTTATGAC
4	CH4_14494	TACCTTCATGCCAGGTGCT	GATGCTGAAATGGACAAGAT
4	CH4_15294	CATGGTGGTCTTGGAAGAT	GTACGTTAAATGGCAAAGAT
4	CH4_15593	GGCTGTGAATCTCACAAAC	CTTTGGATATCTATCTGTGTA
4	CH4_15659	CTGTTCCTCGTTTCGTGTTA	CAGGAAGGAGCACTCAATAG
4	CH4_15955	GTAATTGCTAGCGTCAAAC	AAGAAGCAAACCCCAAAAC
4	CH4_16853	AATTCAAGTTTGATGTTCTAC	AAAGTTCAAAGCATGCATTA
	Cloning primers		
	ANAC017_attB1	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCATGGCGGATTCTTCACCCGATTC	
	ANAC017_attB2	GGGGACCACTTTGTACAAGAAAGCTGGGTGCTAGTCTTTCAAGAGAAGACTTC	