# Supplementary data

## Arabidopsis membrane-associated acyl-CoA-binding protein ACBP1 is involved in stem cuticle formation

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**Supplementary Figure S1.**

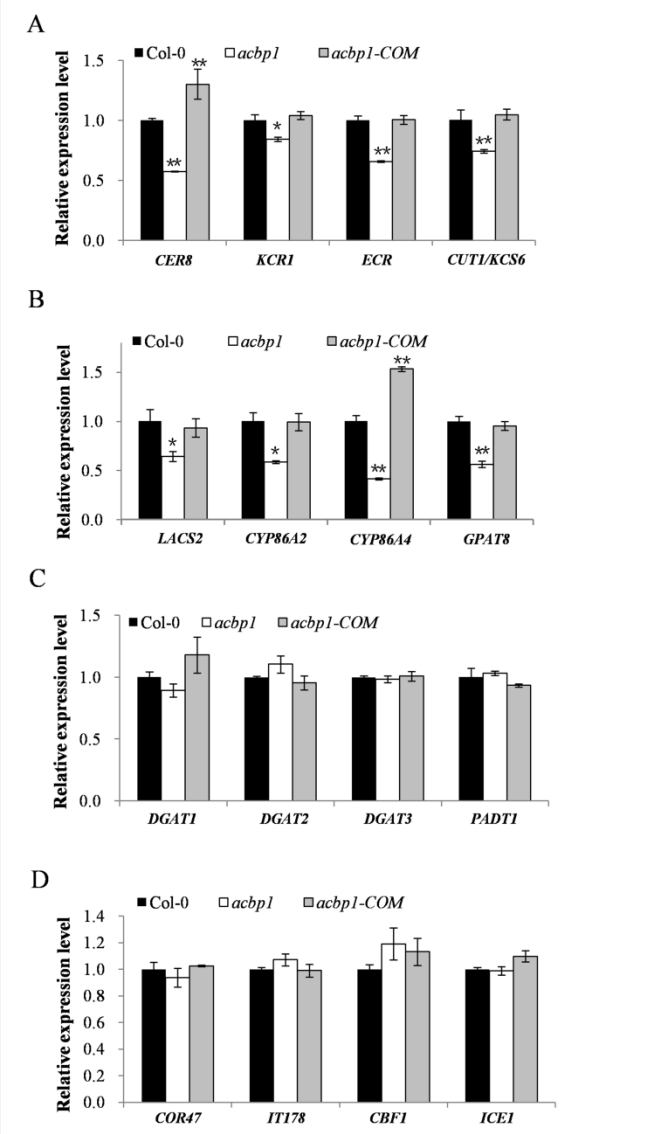


**Figure S1.** Expression analysis of wax biosynthetic genes (A), cutin biosynthetic genes (B), and genes with no implication on cuticle formation (triacylglycerol biosynthetic genes (C) and cold-related genes (D)) in stems of Col-0, the *acbp1* mutant and *acbp1-COM* line. Asterisks denote significant differences from the wild type (* $P < 0.05$, ** $P < 0.01$). Values are means ± SE (n = 3).

**Supplementary Figure S2.**

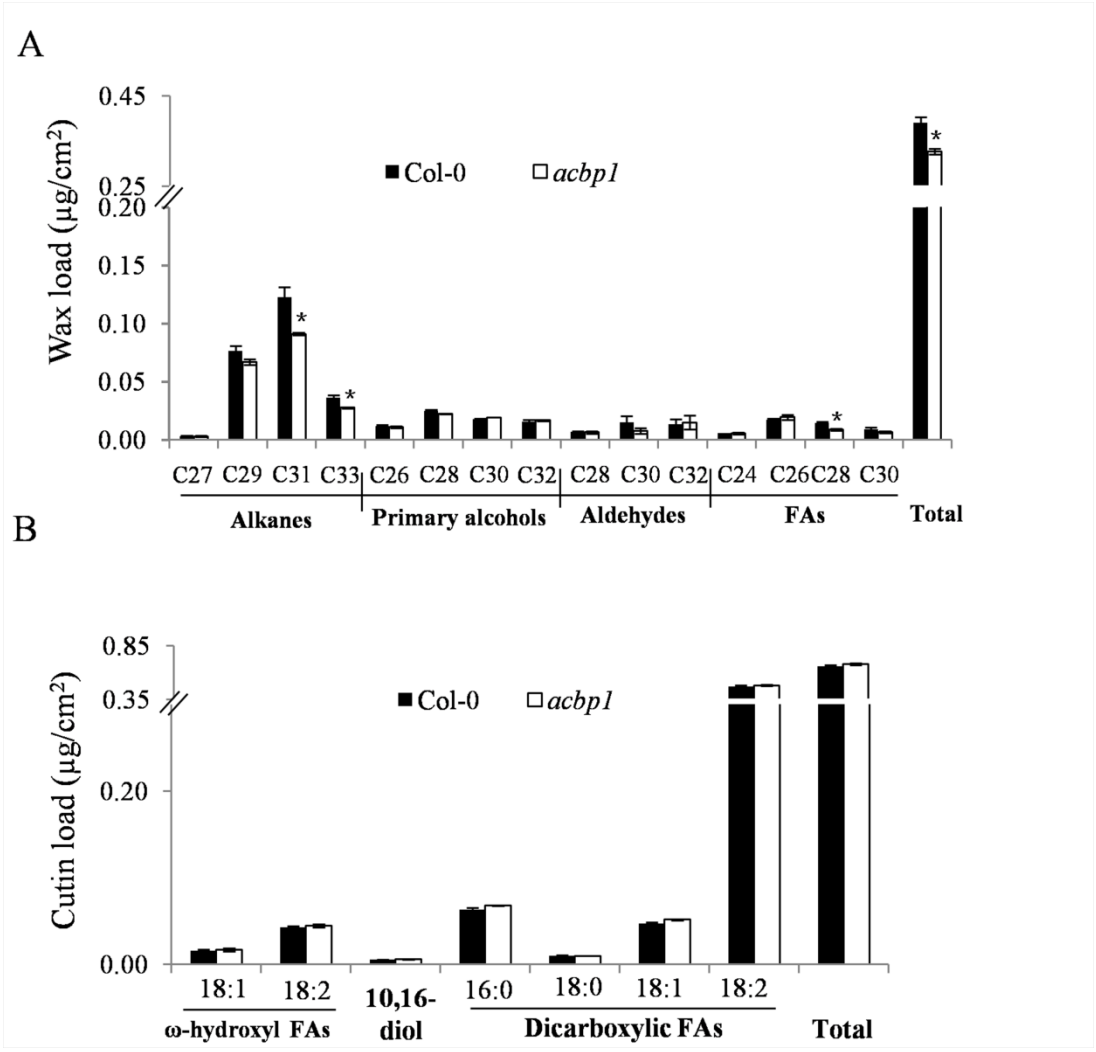


**Figure S2**. Cuticular wax (A) and cutin monomer (B) composition and amount in leaves of Col-0 and the *acbp1* mutant. Four-week-old leaves were used for wax and cutin analysis by gas chromatography (GC)-flame ionization detector and GC-mass spectrometry. FA, fatty acid; 10,16-diol, C16-10,16-dihydroxyl fatty acids. Asterisks denote significant differences from the wild type (* $P < 0.05$). Values are means ± SE (n = 3).

**Supplementary Table S1.** Sequences of gene-specific primers for qRT-PCR.

| Name | Sequence (5²→3') | Target gene |
|---|---|---|
| ML1124 | CCCGCTATGTATGTCGC | At3g18780 (*ACTIN2*) |
| ML1125 | AAGGTCAAGACGGAGGAT | |
| ML1824 | AGGCAAACATCACCACAATAGG | At1g68530 (*CUT1/KCS6*) |
| ML1825 | CTCGTCGATCACCGCTCTG | |
| ML1826 | AGCACCTTTGAGCCCTGAGA | At2g47240 ( *CER8*) |
| ML1827 | AACCGCTGGAATACCGACTG | |
| ML1828 | ATTCCACGCGGTTTCCTCTTC | At3g55360 (*ECR*) |
| ML1829 | GGCTTTCCATCTTTTCCATCAA | |
| ML1832 | ACCCACTTGGCTCCTCATTCTC | At1g67730 ( *KCR1*) |
| ML1833 | GCTTTACCGATTCCGTCTGTTG | |
| ML1917 | TAATACACGTAAGCAAGAAT | At4g00360 *(CYP86A2*) |
| ML1918 | GTCGTGATGAGCCAGAAAAACC | |
| ML1919 | GGCTCTTCCAACGCAAAACC | At1g01600 (*CYP86A4*) |
| ML1920 | CGAACGCCAATCCGCAAATG | |
| ML1933 | GATTGTGCCAGTAGCGATGAA | At4g00400 (*GPAT8*) |
| ML1934 | TCTTGCCACCACCGTTGAC | |
| ML1937 | AACGCAGCAATTTCGGTCCAG | At1g49430 (*LACS2*) |
| ML1938 | AATGTCGCCACGCCAGTATCC | |
| ML2026 | GGAGGGCGAGAGAGAGTCCACTT | At2g19450 (*DGAT1*) |
| ML2027 | CCAATCTCGCAGCGATCTTGAAC | |
| ML2028 | CCGAGCTGAGGAACATTCAAATCA | At3g51520 (*DGAT2*) |
| ML2029 | CGACCATATTTGCTACGATGATCGA | |
| ML2030 | GGTCTTGATCCTGAAGCTGGTTTG | At1g48300 (*DGAT3*) |
| ML2031 | TCAGTCATCTTCTTCATGGCTTTGG | |
| ML2032 | TGCTGAAGCAAAGGATGTTGCA | At5g13640 (*PDAT1*) |
| ML2033 | CCTTTCTCCGGTGACCAATCAAG | |
| ML1716 | GTCCACGCCGTTGGTTGT | At1g20440 (*COR47*) |
| ML1717 | AATCCCCTTCTTCTCCTCCG | |
| ML1718 | TTCCACCAGGGACAAAGG | At5g52310 (*LTI78*) |
| ML1719 | CATCGTGTCCGTAAGAGGC | |
| ML1785 | GGACTTTCCAAACCGCTGAG | At4g25490 (*CBF1*) |
| ML1786 | CAAGCCGAGTCAGCGAAGTT | |
| ML1901 | GATTTCTTGTCTGCTCGGTCACT | At3g26744 (*ICE1*) |
| ML1902 | CCATTAGCAGGACTACCAAAACC | |

The genes implicated in wax biosynthesis tested in qRT-PCR were *CUT1/KCS6*, *CER8*, *ECR* and *KCR1*. The genes implicated in cutin biosynthesis tested were

*CYP86A2*, *CYP86A4*, *GPAT8* and *LACS2*. The genes with no implication in cuticle formation tested included triacylglycerol biosynthetic genes (*DGAT1*, *DGAT2*, *DGAT3* and *PADT1*) and cold-related genes (*COR47*, *LTI78*, *CBF1* and *ICE1*).

**Supplementary Table S2.** Mass-to-charge ratios (m/z) of cutin compounds in mass spectrometry.

| Cutin compound | Mass-to-charge ratios (m/z) |
|---|---|
| C17:0-FA (internal standard) | 284 |
| C15:0 cycloketone (internal standard) | 282 |
| C18:1-FA | 296 |
| C18:2-FA | 294 |
| C10,16-dihydroxyl fatty acids | 343 |
| C16:0-DCA | 314 |
| C18:0-DCA | 342 |
| C18:1- DCA | 339 |
| C18:2-DCA | 337 |

FA, fatty acid; DCA, dicarboxylic fatty acid.