
Table S1. The primers used in this study.

Primer name	Primer sequences (5'-3')	Annotations
<i>AtEF1aA4</i>	CTGGAGGTTTTGAGGCTGGTA CCAAGGGTGAAAGCAAGAAGA	qRT-PCR
<i>LuAccD</i>	GAGCTTGATGCAAATGGCGAA CTCTTTTACCCGCAAACGCAA	qRT-PCR
<i>AtBCCP1</i>	TCACTCAAACCTCCTCGCAC TTGTGCTTTCACCACAGGGT	qRT-PCR
<i>AtBCCP2</i>	AACCCAATGGGATCTCCTTTCCCT ATAAATTCAGAGAGCTCGGCGGGT	qRT-PCR
<i>AtMCAT</i>	GATACTTGCACGCCAGGTGA CCTTTCCAGGTCCCAATTCGT	qRT-PCR
<i>AtKASI</i>	TCGATTTCAACTGCTTGTGC CCTCCCAACCCAATAGGAAT	qRT-PCR
<i>AtKASII</i>	TGCCTATCACATGACCGAGC CCAAAACAGTGAGCAAGGGC	qRT-PCR
<i>AtSSI2</i>	CGCTGTGCATAAGCATTCTC TTGGGGCCGGAGCTGAGAGC	qRT-PCR
<i>AtFAD2</i>	ATGGGTGCAGGTGGAAGAAT CCAGGAGAAGTAAGGGACGA	qRT-PCR
<i>AtFAD3</i>	CCACAGTACTCGGATGCTCAGA GCAATAAGCTTTCTCTCGCTTGGA	qRT-PCR
<i>AtPDAT2</i>	AGATGATGAGACGAGCCGAAGC TCTCTGGTGCCTCCGGTAATTTG	qRT-PCR

<i>AtNCED3</i>	GCTGCGGTTTCTGGGAGAT GTCGGAGCTTTGAGAAGACGAT	qRT-PCR
<i>AtAAO3</i>	GGAGTCAGCGAGGTGGAAGT TGCTCCTTCGGTCTGTCCTAA	qRT-PCR
<i>AtABI3</i>	GCGATGAAGCAGCTTTTAAAGCGAATT GTCGGAGCTTTGAGAAGACGAT	qRT-PCR
<i>AtEM1</i>	TAGGGCACGAGGGTTATCAG CGCTCTCCACCAGATTTTTC	qRT-PCR
<i>AtEM6</i>	GCAAACTCGAAAGGAGCAGT TAGGGCACGAGGGTTATCAG	qRT-PCR
35S: <i>LuAccD-6HA-EcoRI-F</i>	GATAAGCTTGATATCGAATTCATGACTAGTTCAGATAGAAT	35S: <i>LuAccD-6HA</i> Mutant genotyping
35S: <i>LuAccD-6HA-XmaI-R</i>	GTATGGGTAAGTAACTAGTATGAGTCAAAGCGTGGAGA	
35S_P	GACCCTTCCTCTATATAAGGAAGTTC	

Table S2. Comparison of percent identity between the amino acid sequences of AtAccD and LuAccD.

Protein domain	Protein name	AtAccD	LuAccD
Full-length protein	AtAccD	100.0%	
	LuAccD	58.4%	100.00%
Crotonase-like superfamily domain	AtAccD	100.00%	
	LuAccD	61.5%	100.00%

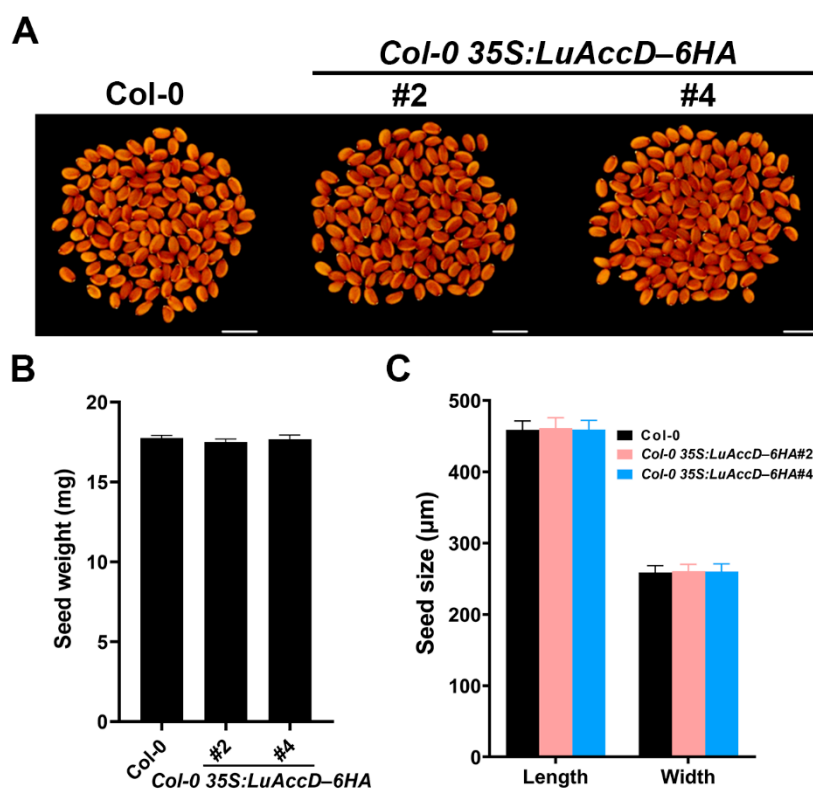


Figure S1. Morphological observation of mature *A. thaliana* seeds randomly selected from wild type (Col-0) and overexpression transgenic plants carrying *LuAccD* (*Col-0 35S: LuAccD-6HA#2* and *#4*). Comparison of seed coat color (A), 1000-seed weight (B), and seed size (C) between Col-0 and *Col-0 35S: LuAccD-6HA* transgenic plants. Bar: 2 mm. There was no significant difference at $P \leq 0.05$ based on the Student's *t*-test among Col-0 and *Col-0 35S: LuAccD-6HA* transgenic plants. Seeds were harvested from 12 individual plants grown in different pots arranged randomly within one of three blocks. Values are means \pm SD, and error bars denote SD. Three independent biological replicates and three technical replicates were performed for each experiment. For seed size measurement, each technical replicate contains 300 seeds.