Supplementary Material

Table S1. PCR oligonucleotides used in this study.

Primer	Sequence (5´- 3´)
LBb1.3	ATTTTGCCGATTTCGGAAC
AtLIP2p1-RP	ACTACCAAAGAGGCCCAAAAG
AtLIP2p2-RP	AAGATCCATTTTGTGATTCCG
AtLIP2p1-LP	TGAGGCATTTTAACGAACACC
AtLIP2p2-LP	TCAAAAGGTGGCTCAGAAGTG
AtLIP2p1-transcript-F	GGTCATGGCAGAAGAGCATTGTCG
AtLIP2p1-transcript-R	CACCTTCCTTTTAGCACTCCAATCG
AtLIP2p2-transcript-F	GTTGCAACAAGCTCTGTTACG
AtLIP2p2-transcript-R	TTGTTGCCAACCCAAACTCCA
At18S-F	GGTAGGCGATTGGCTAACATTGTCTGC
At18S-R	GAGACACCAACAGTCTTTCCTCTGCG

Figure S1

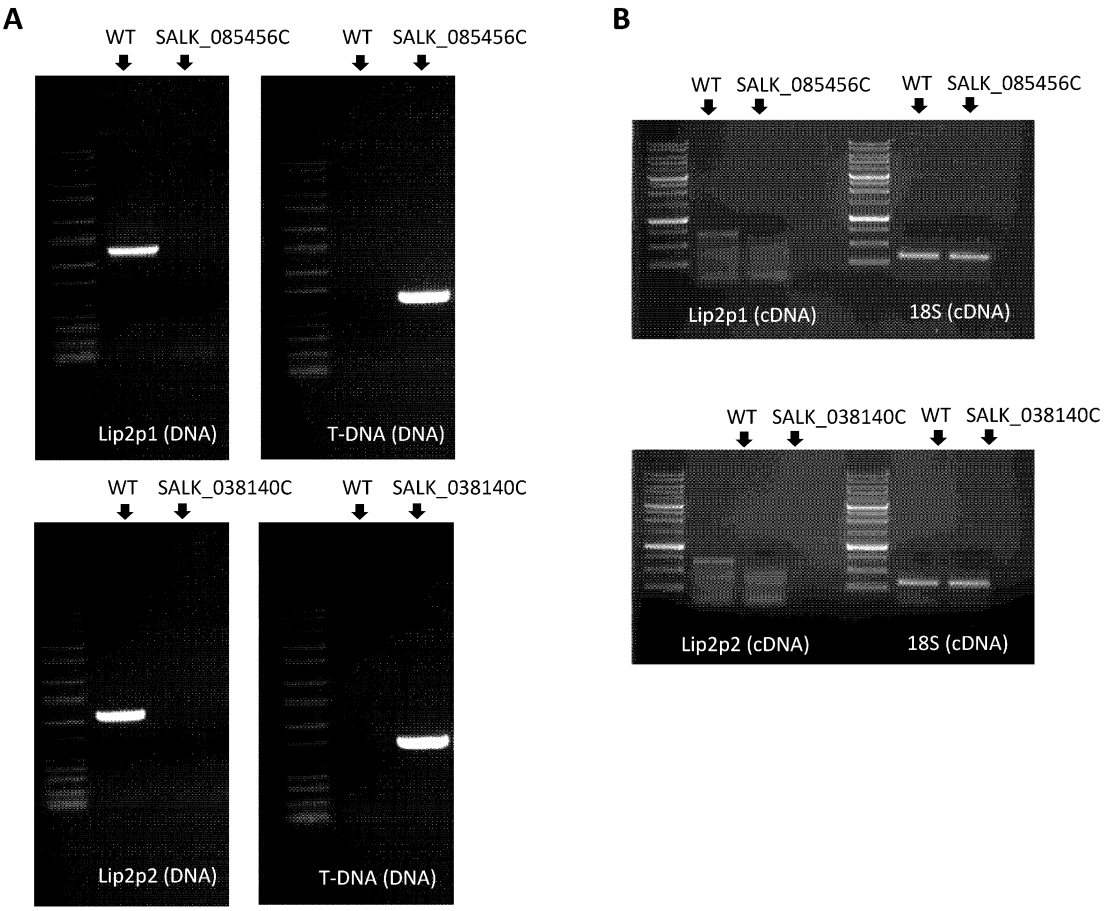

Figure S1. (A) Left panel, PCR with genomic DNA (gDNA) shows presence of intact LIP2p1 or LIP2p2 gene in the WT and absence of such genes in the *lip2p1* (SALK_085456C) and *lip2p2* (SALK_038140C) mutants. Right panel, PCR with gDNA shows presence of the T-DNA in the mutants and its absence in the WT. (B) RT-PCR shows absence of LIP2p1 and LIP2p2 transcripts in both mutants in comparison with control signals from the constitutively expressed 18S ribosomal gene.

Figure S2

Figure S2. Comparison of the deduced amino acid sequences and the predicted secondary structures of Arabidopsis octanoyltransferases LIP2P1 and LIP2P2. Structure: h, α-helix; s, β-sheet. Residues involved in forming the active site are highlighted in grey and the catalytic lysine and cysteine residues in bold [20].