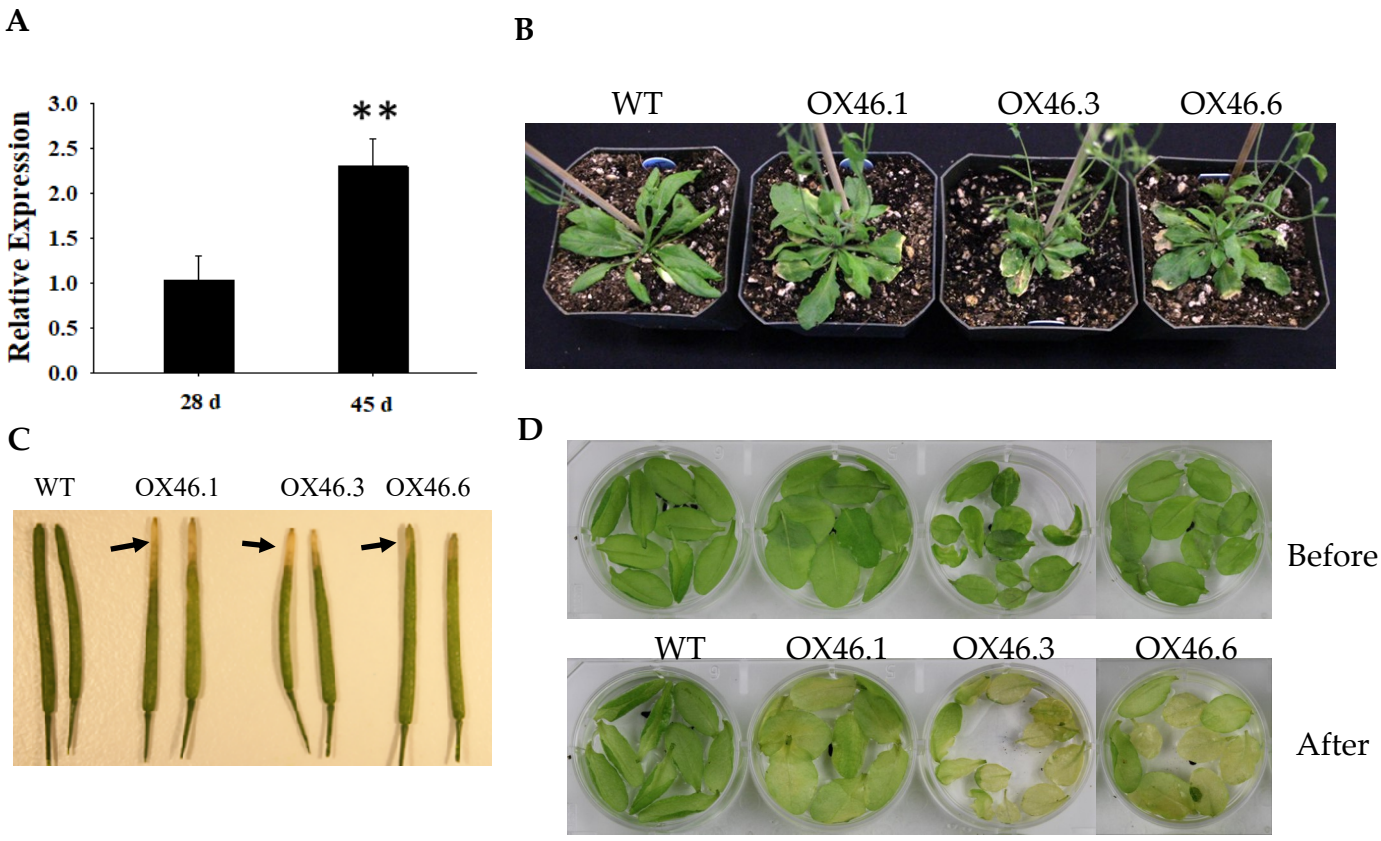

Figure S1: Senescence phenotype of ANAC046 Overexpression (OX46) lines. **(A)** Quantitative RT-PCR analysis of ANAC046 in the fifth leaf of Arabidopsis at 28 and 45 DAS. Values are the means (±SD) of two technical and three biological replicates. Data were analysed using Student's t-test (P**< 0.01). *ACT7* was used as an internal control. **(B)** Phenotype of WT and ANAC046 overexpression at 42 DAS (days after sowing). Overexpression lines clearly exhibit patches of wounds and premature senescence on their rosette leaves. Siliques of overexpression lines clearly exhibit symptoms of premature senescence on their apexes compared with WT. **(D)** Dark-induced leaf senescence in detached leaves of WT and ANAC046 overexpression lines. Three-week-old detached leaves were suspended in deionized water and incubated in dark for three-and-a-half days and then photographed.

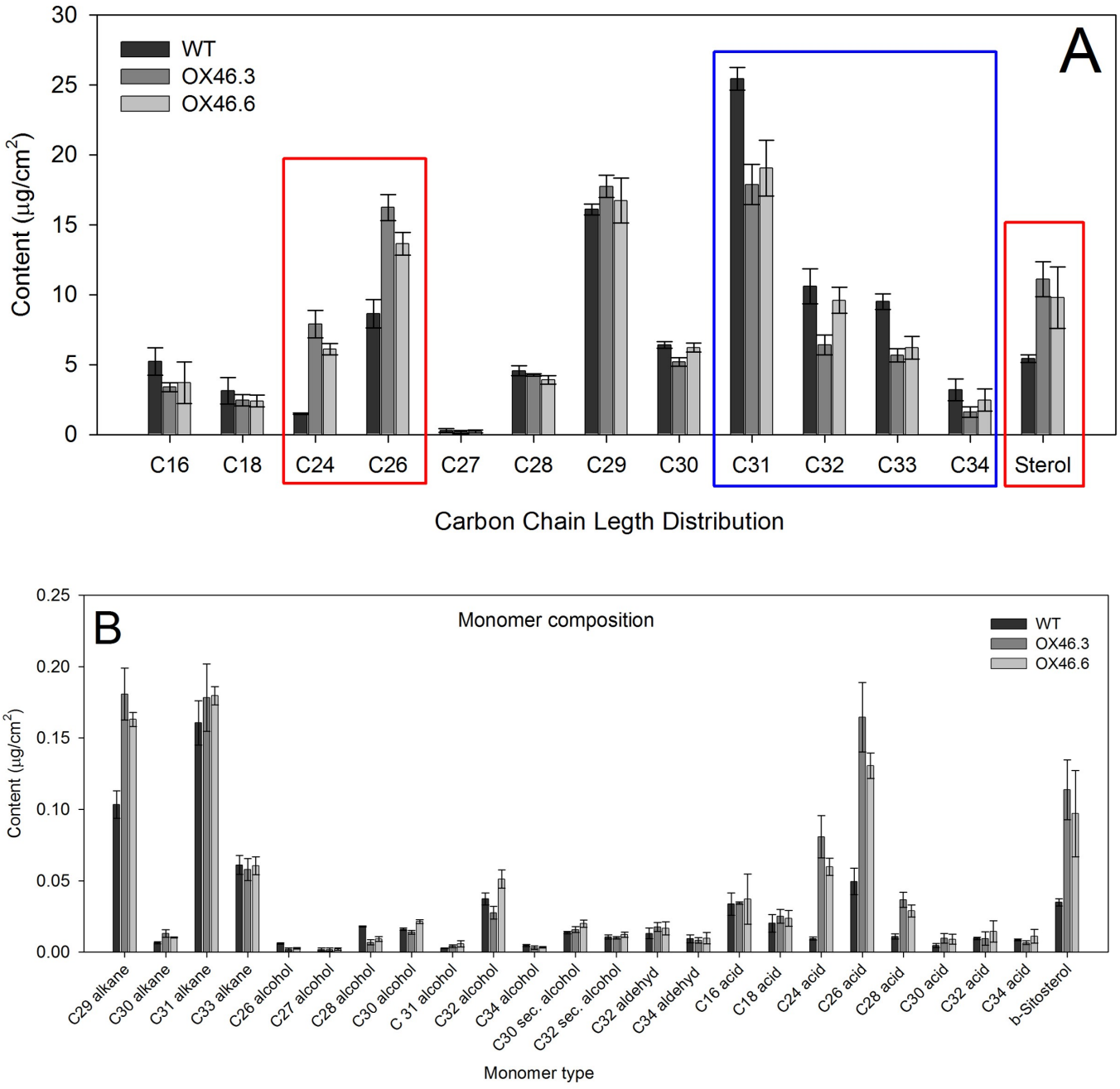

Figure S2: A) Carbon chain length distribution of leaf waxes. **B)** Monomer composition of leaf waxes. Total wax of the rosettes leaves of 21-day-old WT and ANAC046 transgenic lines were extracted by immersing leaves in $CHCl_3$ at 60° C for 20 s and analysed using GC and MS. The chain length distribution of waxes is given as means in µg per cm^2 ±SD for four leaves (n=4 leaves).

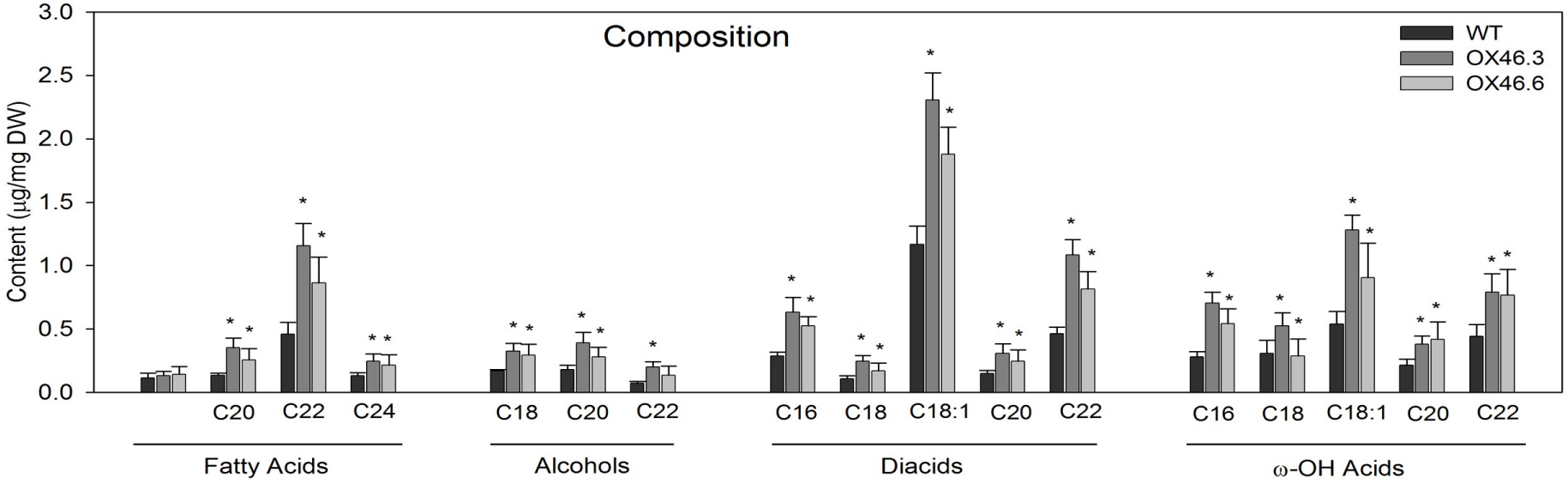

Figure S3: Monomer compositions of aliphatic suberin in the roots of 4-week-old Arabidopsis WT and ANAC046 transgenic plants. Enzymatically digested and solvent-extracted root cell walls were subjected to BF3/MeOH transesterification. Aliphatic monomers were analysed using gas chromatography and mass spectrometry. Absolute amounts of suberin monomers are given as means in µg per cm^2 ±SD for four roots (n=4). The statistical analysis was done for each group separately and compared with WT. The stars indicate significant differences at $P < 0.05$ level (one-way ANOVA, Tukey test).

Table S1. List of Primers used in the study

Oligo Name	Oligo Sequence
	5' → 3'
	Primers used in transcription activity assay
yNAC46-F	AGAATTCCATATGATGGTGGAAGAAGGCG
yNAC46-R	CGGGATCCTTAGCTAGTATATAAATCTTCCCAGAAGATC
yNAC46N-R	CGGGATCCTCAGTTCTTGTGAAAAACCCTAC
yNAC46C-F	AGAATTCCATATGGCTCCTAGTACTACAATCACTACTAC
	Primers used to generate transgenic lines (35S:ANAC046 and $P_{ANAC046}$:GUS)
DNAC46-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTTATGGTGGAAGAAGGCGG
DNAC46-R	GGGACCACTTTGTACAAGAAAGCTGGGTTTTAGCTAGTATATAAATCTTCCCAGAAGATC
PNAC46-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTTCCCAACTAGTAGTCATCATATCC
PNAC46-R	GGGACCACTTTGTACAAGAAAGCTGGGTTCTATATATATGTATGCTTGATCAAGA
AttB1	GGGGACAAGTTTGTACAAAAAAGCAGGCTTT
AttB2	GGGACCACTTTGTACAAGAAAGCTGGGTTT
	Primers used in quantitative RT-PCR analysis
qNAC46-F	AACCGCAACGCCAGAGATATC
qNAC46R	ACACGCTGACTTGCTACCATCC
	Cuticle Biosynthesis genes
CYP86A4 -F	TCGACCGTTTGGTTTACCTG
CYP86A4 -R	CCGATGGGTAAAGCCTGAG

CYP86A7 -F	CCACGTGTCTGGCCCTTA
CYP86A7 -R	CATGCGGTGAGCATTTGTTA
CYP86A8-F	ACCAGCCTAGAGCAGGAACA
CYP86A8-R	TAGGGTATGTGAAGCATGAGATG
CER1-F	CACCTCTTTCCTCCCCTCA
CER1-R	GTGGTGCAGCGAGTGGTAT
CER3-F	TTCTTGACTGGAGCCACTTCT
CER3-R	ACGGCGACAAAGGTAAAGAG
CER6-F	GACGTCGACATCCTTATCGTC
CER6-R	TAGCTGAGAGCGATGGTGTG
	Suberin Biosynthesis genes
CYP86A1-F	TTCTTCGGTGGCCTTGAG
CYP86A1-R	GTTTCCACCTCCCGGTTATT
CYP86B1-F	ATTCAACGCGGATGATGAA
CYP86B1-R	TGAAACTCAATGCTCGCTGT
FAR4-F	GGTTTCCTCGCCAAAGTGT
FAR4-R	TGCATGGCTGATTCATTGTC
FAR5-F	CATGAAAGAACTCGGAATGGA
FAR5-R	CAAGAAGCATTTCTCCCATTG
GPAT5-F	AGCTTCCTATGGAGGCAACA
GPAT5-R	GAACATAGTTCGCCACGTCA
GPAT7-F	GGATTCTCCAACTTTCCTATCTTTATG
GPAT7-F	TGGTTATGACCGTTGTAGTTCG
	Internal Control
ACT7-F	TGCACCGCCAGAGAGAAAAT
ACT7-R	TGAGGGATGCAAGGATTGATC
GAPDH-F	CTTGGAAGGAGCTAGGAATTGACA

GAPDH-R	ATGTGTTTCCCTGCACCTTCTC