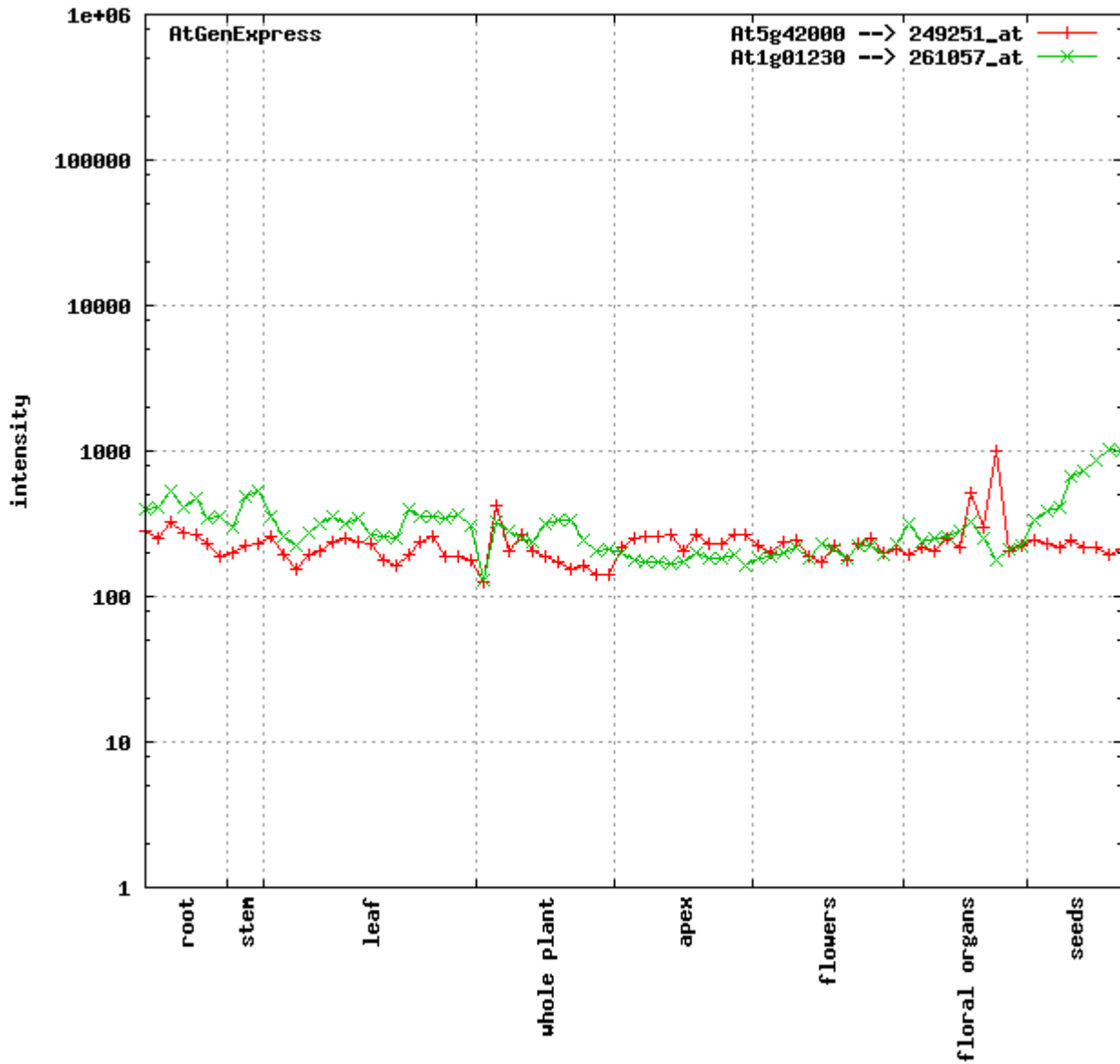
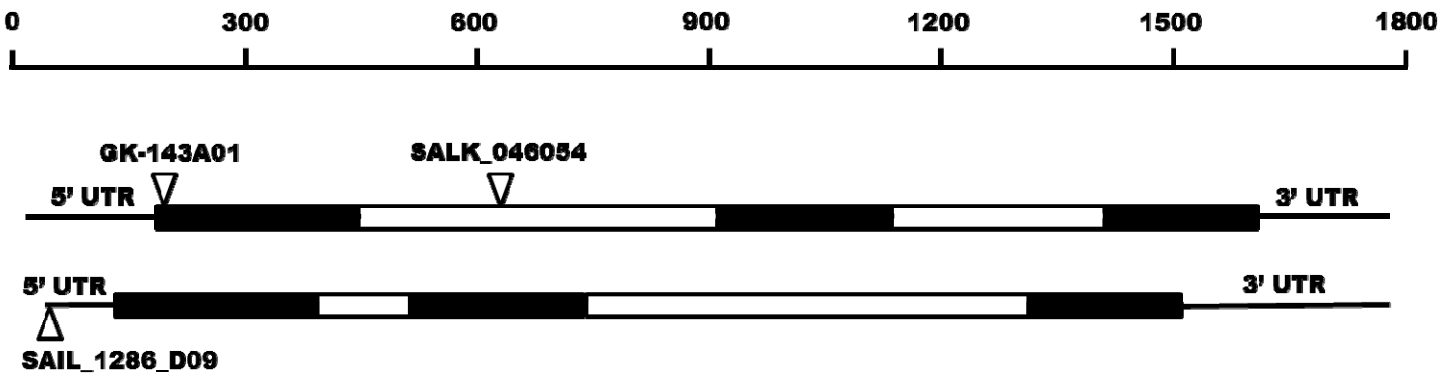
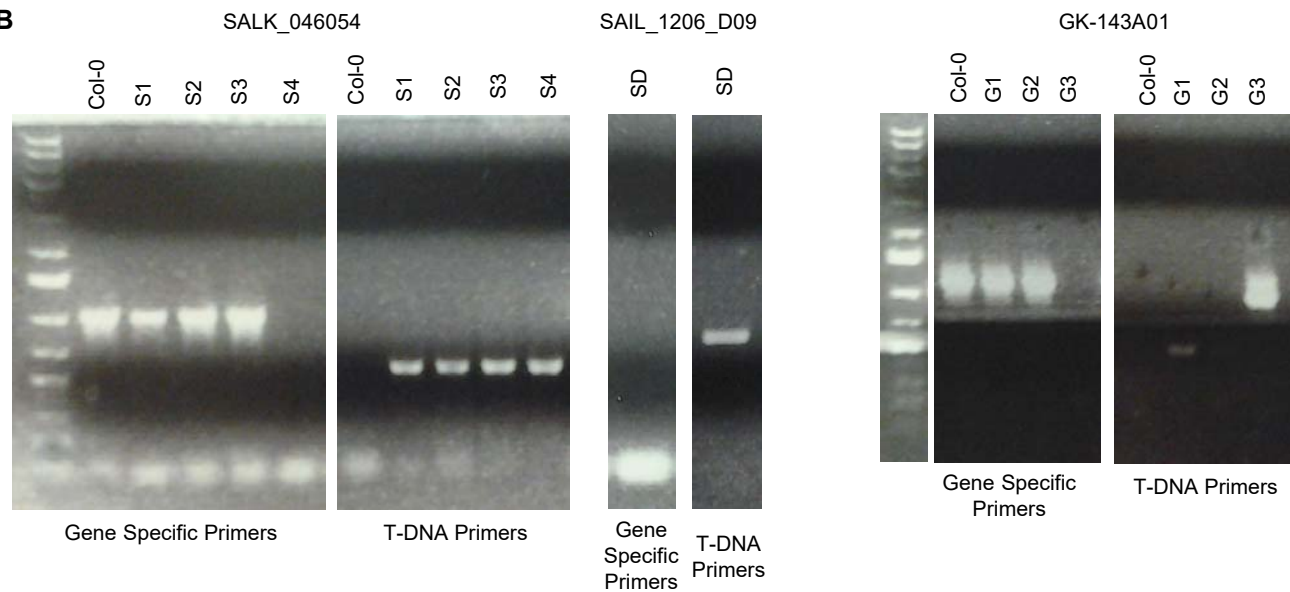
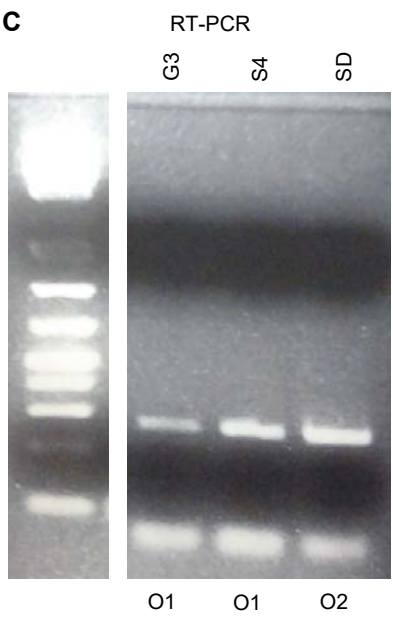


Table S1. Oligonucleotide primers used in the reported studies.

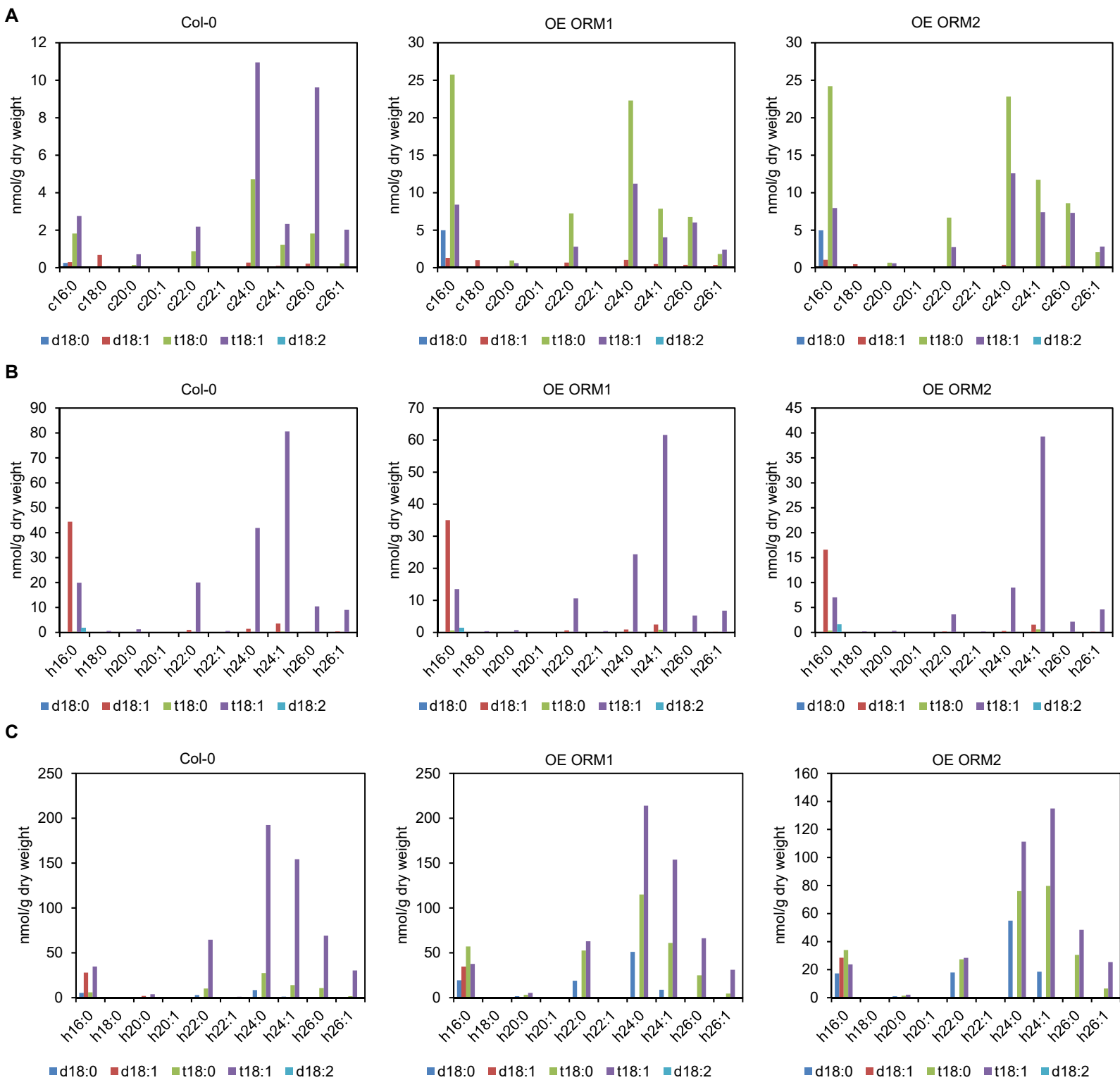
	Primer Name	Primer (5'-3')
P1	ORM1compF	ATGCCTGCAGATGGCGAATCTGTATGTGAAAGC
P2	ORM1compR	ATGCCTCGAGTTATTTATCACCATTGATACCAAAGATGCGTA
P3	ORM2compF	ATGCCTGCAGATGTACGTAAGAGCACTTCCGAC
P4	ORM2compR	ATGCCTCGAGTCATTGGTCTCCATTGATTCCAATAT
P5	AtORM1qPCRset (Qiagen)	Cat. No. QT00866887
P6	AtORM2qPCRset (Qiagen)	Cat. No. QT00736792
P7	AtPP2AA3qPCRset (Qiagen)	Cat. No. QT00857220
P8	ORM1cDNAF	CTGATTGAAGAAGAAATGGCGAATC
P9	ORM1cDNAR	TTATTTATCACCATTGATACC
P10	ORM2cDNAF	ATGTACGTAAGAGCACTTCC
P11	ORM2cDNAR	TCATTGGTCTCCATTGATTCC
P12	ORM1promoterF	ATGCGGATCCCTTTGGCTGCACTCCTCTCT
P13	ORM1promoterR	ATGCGAATTCTTCTTCTTCAATCAGATCGGATCG
P14	ORM2promoterF	ATGCGGATCCTGATGATCCACCATGATTTT
P15	ORM2promoterR	ATGCGAATTCGCTTTTTCCACGGAGGGA
P16	ORM1yfpF	ATGCGAGCTCATGGCGAATCTGTATGTGAA
P17	ORM1yfpR	ATGCGGTACCTTTATCACCATTGATACCAA
P18	ORM2yfpF	ATGCGAGCTCATGTACGTAAGAGCACTTCC
P19	ORM2yfpR	ATGCGGTACCTTGGTCTCCATTGATTCCAA
P20	SALK_046054L	TAGTCCGTTACACATCACCGG
P21	SALK_046054R	GTTGGCTCGTTGTTCTCTCTG
P22	GK_143A01L	TGCTTATTCCAAGTCCCATG
P23	GK_143A01R	TCCTAATTCGAAGCCTGATCC
P24	SAIL_1286_D09L	TCCTCAGAAATACGATGTTATTTCC
P25	SAIL_1286_D09R	GGATTTGGAAGAAGATCGGAG
P26	LBb1.3	ATTTTGCCGATTTCCGAAC
P27	SAIL T-DNA	GCTTCTATTATATCTTCCCAAATTACC
P28	GAB T-DNA	CCCATTTGGACGTGAATGTAGACAC
P29	ORM1OEF	ATGCGAATTCATGGCGAATCTGTATGTGA
P30	ORM1OER	ATGCTCTAGATTATTTATCACCATTG
P31	ORM2OEF	ATGCGAATTCATGTACGTAAGAGCACTTC
P32	ORM2OER	ATGCTCTAGATCATTGGTCTCCATTGA
P33	ORM1RNAiF	TAATTCTAGACTCGAGATGGCGAATCTGTATGTGAA
P34	ORM1RNAiR	TATAAAGCTTACTAGTGCGGGTAAGCTGTTGACCAT
P35	ORM2RNAiF	TAATTCTAGACTCGAGATGTACGTAAGAGCACTTCC
P36	ORM2RNAiR	TATAAAGCTTACTAGTCGGTGAGAAATTTGCGATTAC
P37	pINTF	GAATTCAATACGACTCACTATAGGGCGAA
P38	pINTR	TCTAGAAGCGCGCAATTAACCCCTCAC
P39	C144WF	TATGGGGTCGGTTCTTGGGGCCCTCGTGGATTC
P40	C144WR	GAATCCACGAGGCCCCCAAGAACCGACCCCAT



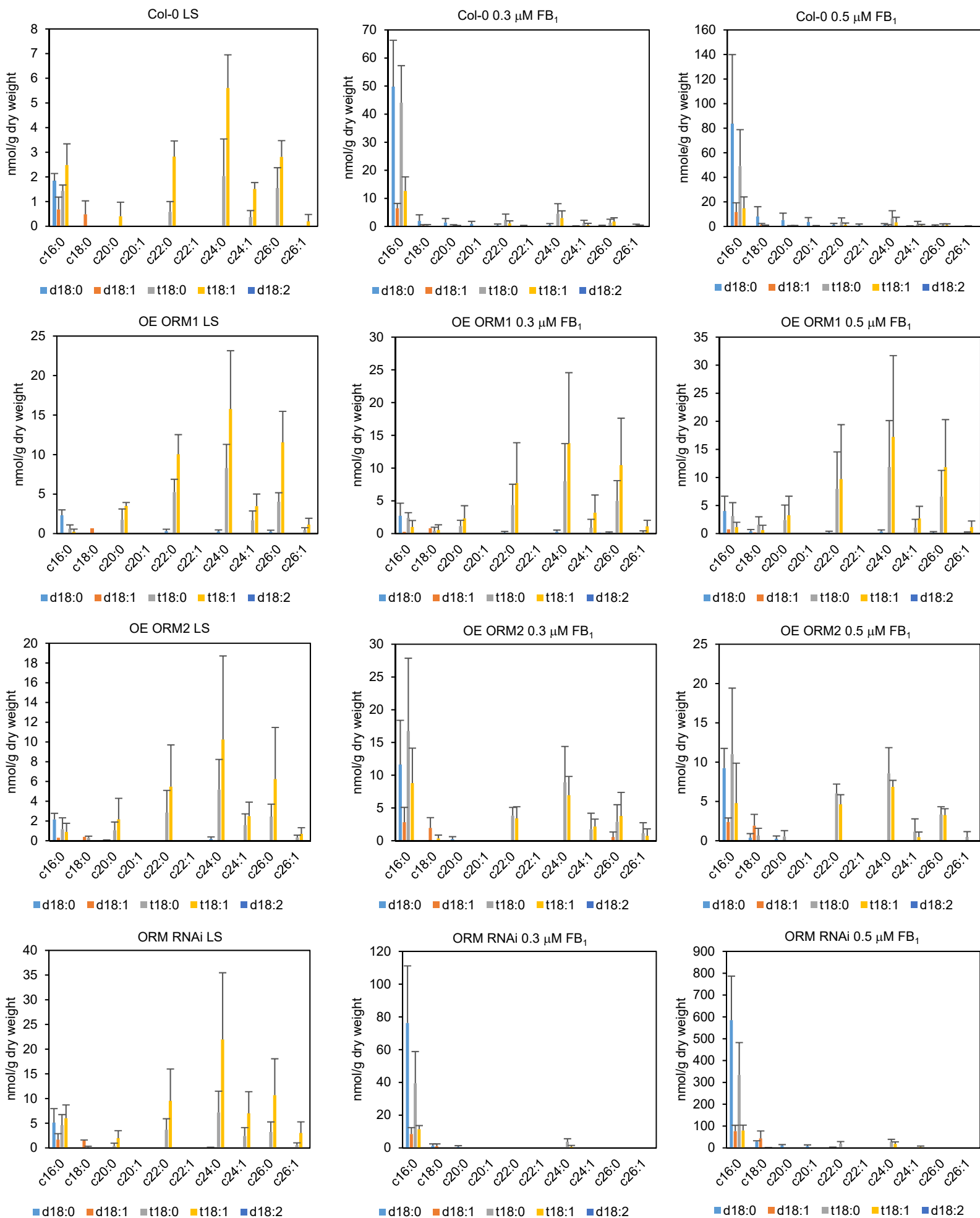
**Figure S1.** Gene expression levels for *AtORM1* (At1g01230) and *AtORM2* (At5g42000) in different tissue types. *AtORM1* is more highly expressed in tissues outside floral organs and seems predominately expressed in developing seed. *AtORM2* appears more highly expressed in floral tissues. Data shown are from: Schmid M, Davison TS, Henz SR, Pape UJ, Demar M, Vingron M, Scholkopf B, Weigel D, Lohmann JU (2005) A gene expression map of *Arabidopsis thaliana* development. *Nat Genet* 37: 501-506

**A****B****C**

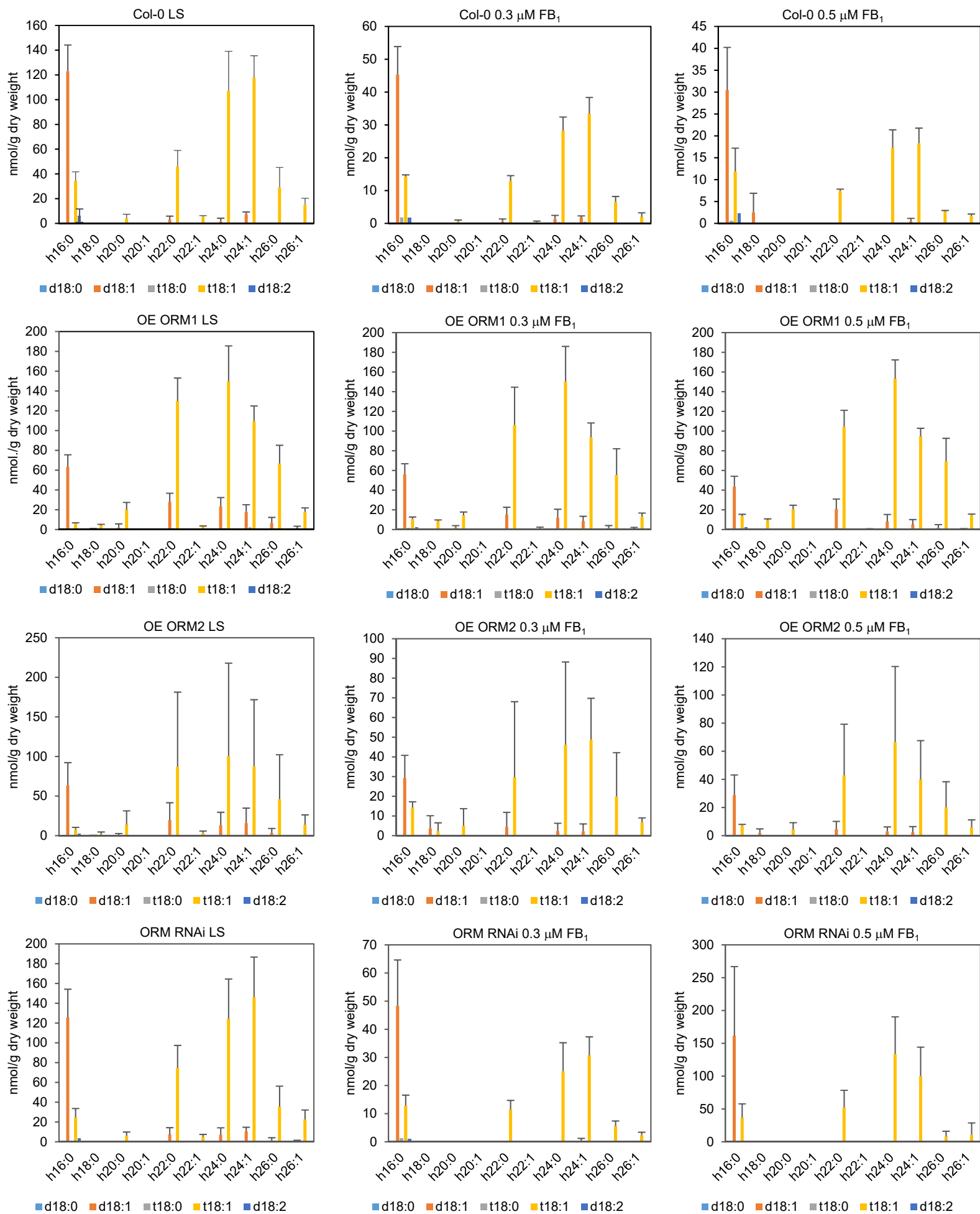
**Figure S2.** Genotyping of T-DNA mutants for *AtORM1* and *AtORM2*. The gene structures for three T-DNA mutant lines are displayed in **(A)**. Introns are shown as white boxes, exons are shown as black boxes, and the UTR regions are shown as black lines. Homozygous T-DNA mutants can be identified for SALK\_046054 and GK-143A01 lines for *AtORM1*, and SAIL\_1286\_D09 line for *AtORM2* **(B)**. T-DNA insertion mutant alleles were confirmed through PCR based genotyping. Genotyping was done using two primer pairs, one pair with two gene specific primers and another pair with one T-DNA specific primer and one gene specific primer, these primers can be found in Supplementary Table 1. These homozygous mutant lines still contain full length transcript as confirmed through RT-PCR using full length cDNA primer pairs found in Supplementary Table 1 **(C)**.



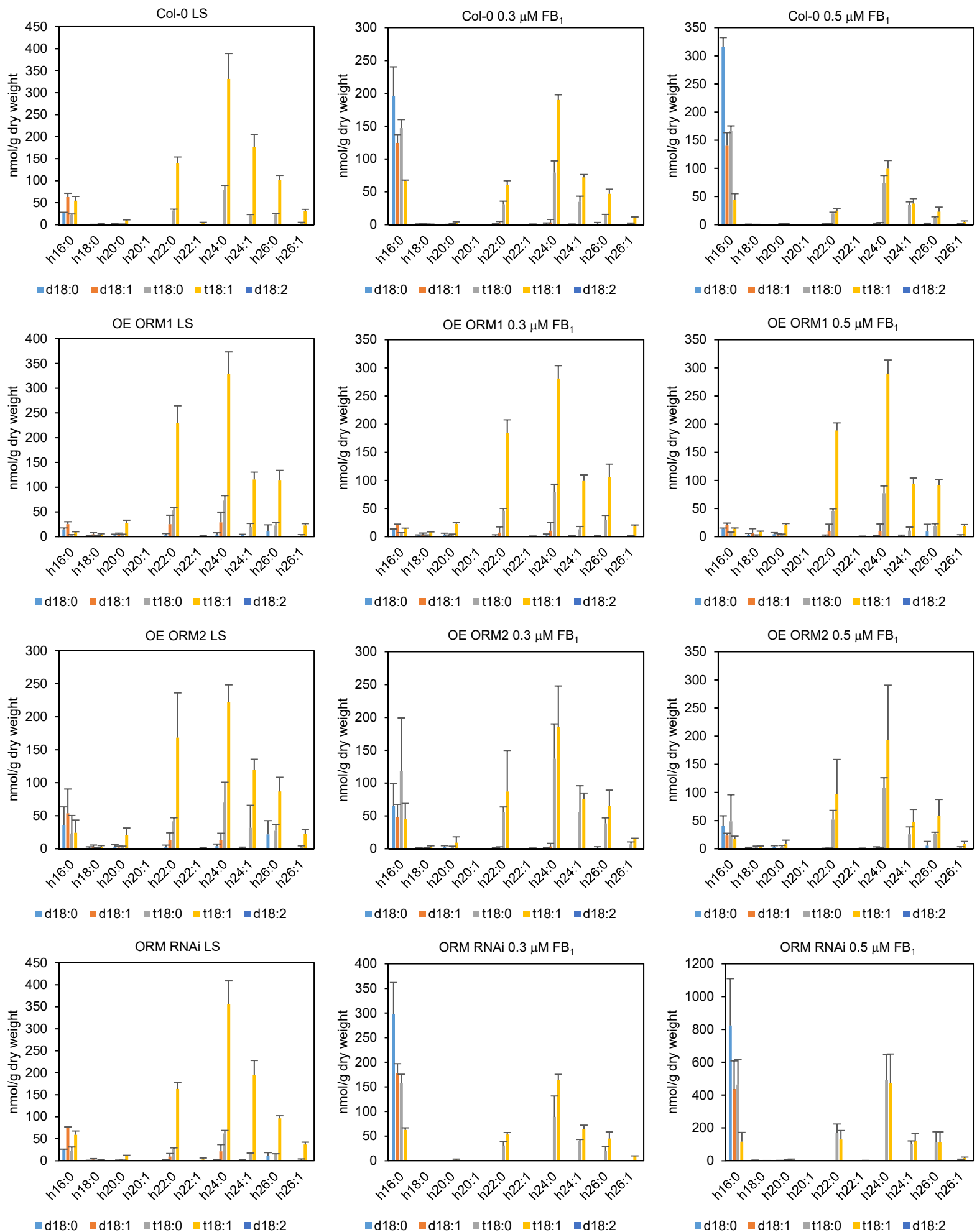
**Figure S3.** Spingolipid profile of *AtORM1* and *AtORM2* overexpression lines that display the dwarf phenotype. Ceramide profiles are shown in **(A)**, glucosylceramide profiles are shown in **(B)**, and GIPC profiles are shown in **(C)**.  $n=1$  sample of leaf tissue.



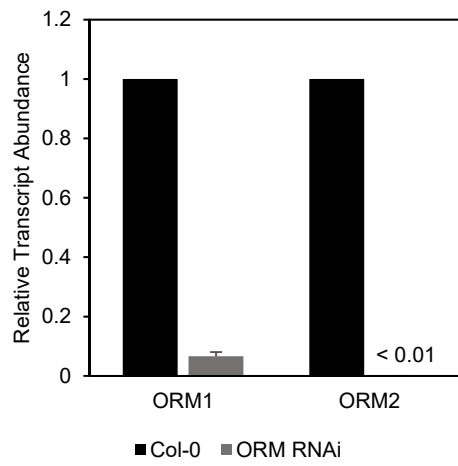
**Figure S4.** Ceramide profile for Col-0 and AtORM overexpression and RNAi lines grown on LS media  $\pm$ FB<sub>1</sub>. n=3 independent analyses of seedlings  $\pm$  SD.



**Figure S5.** Glucosylceramide (GlcCer) profile for Col-0 and *AtORM* overexpression and RNAi lines grown on LS ±FB<sub>1</sub>. n=3 independent analyses of seedlings ± SD.

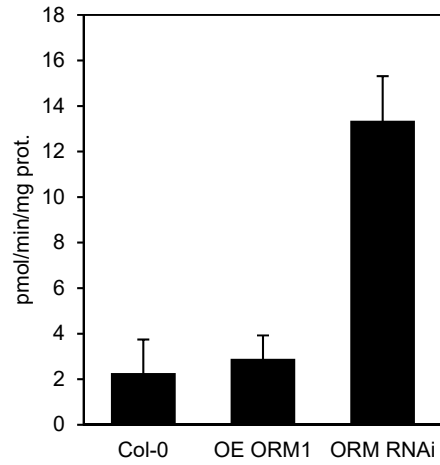


**Figure S6.** Glycosylinositolphosphorylceramide (GIPC) profile for Col-0 and AtORM overexpression and RNAi lines grown on LS  $\pm$  FB<sub>1</sub>. n=3 independent analyses of seedlings  $\pm$  SD.



**Figure S7.** qPCR analysis of ORM RNAi lines. RNA was extracted from leaf tissue of 3 week old plants. As shown, both *AtORM1* and *AtORM2* transcripts were suppressed.





**Figure S8.** SPT activity from root microsomes of wild-type and transgenic plants. ORM RNAi suppression lines show increased SPT activity when compared to wild type. ORM overexpression lines do not show significantly reduced SPT activity when compared to wild type.