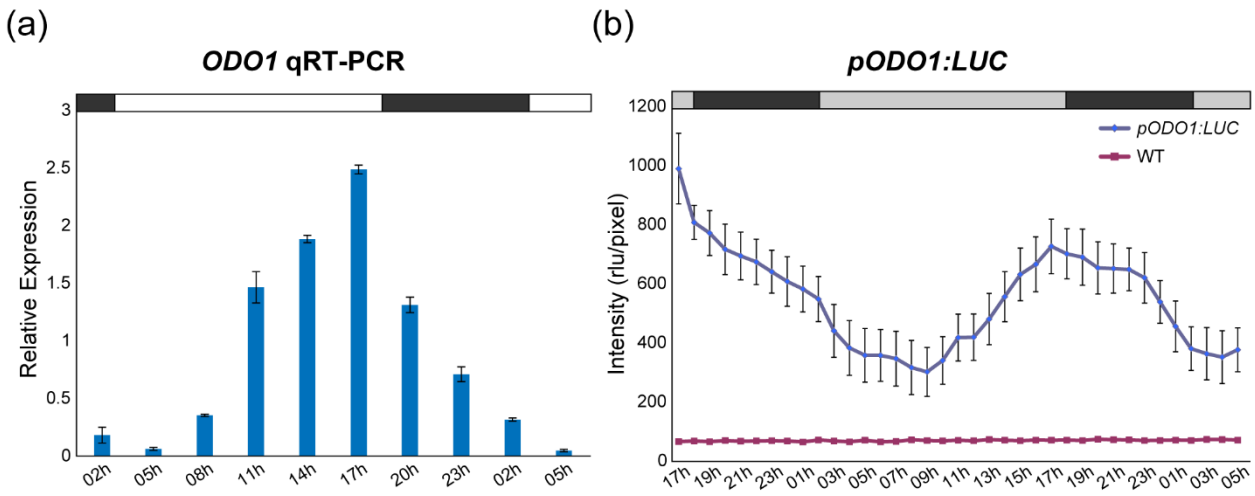


Figure S1. **Diurnal fluctuation of *ODO1* transcriptional activity.** (a) Corolla tissue from two-day-old W115 wild-type flowers was collected every three hours for RNA extraction and expression of *ODO1* was measured by qRT-PCR. Petunia housekeeping reference gene *FLORAL BINDING PROTEIN 1* (*FBP1*) was used for normalization (Angenent et al., 1992; Shaipulah et al., 2016). White and black bars represent periods of light and dark, respectively. Error bars represent standard error of the mean (n=3). Transcript levels were determined to have significantly rhythmic pattern at $p < 0.001$ (ANOVA followed by Tukey's post hoc analysis). (b) Measurement of *ODO1* promoter luciferase activity in *pODO1:LUC* petunia flowers (Movie 1). Pixel intensity was measured using the MetaVueTM Imaging System (Universal Imaging Corporation, USA). Luciferase activity was determined by collection at hourly intervals of luminescence counts per flower to determine intensity in relative light units per pixel (rlu/pixel). Image collection was performed in constant dark; grey and black bars represent light and dark periods respectively to which plants were acclimated. Diamond markers represent the mean intensity from *pODO1:LUC* flowers with error bars representing standard error of the mean (n=4), while square markers show background levels measured from a wild-type flower (n=1). Luciferase activity in *pODO1:LUC* flowers was determined to have a significantly rhythmic pattern at $p < 0.05$ (ANOVA followed by Tukey's post hoc analysis). The experiment was repeated twice with similar results.

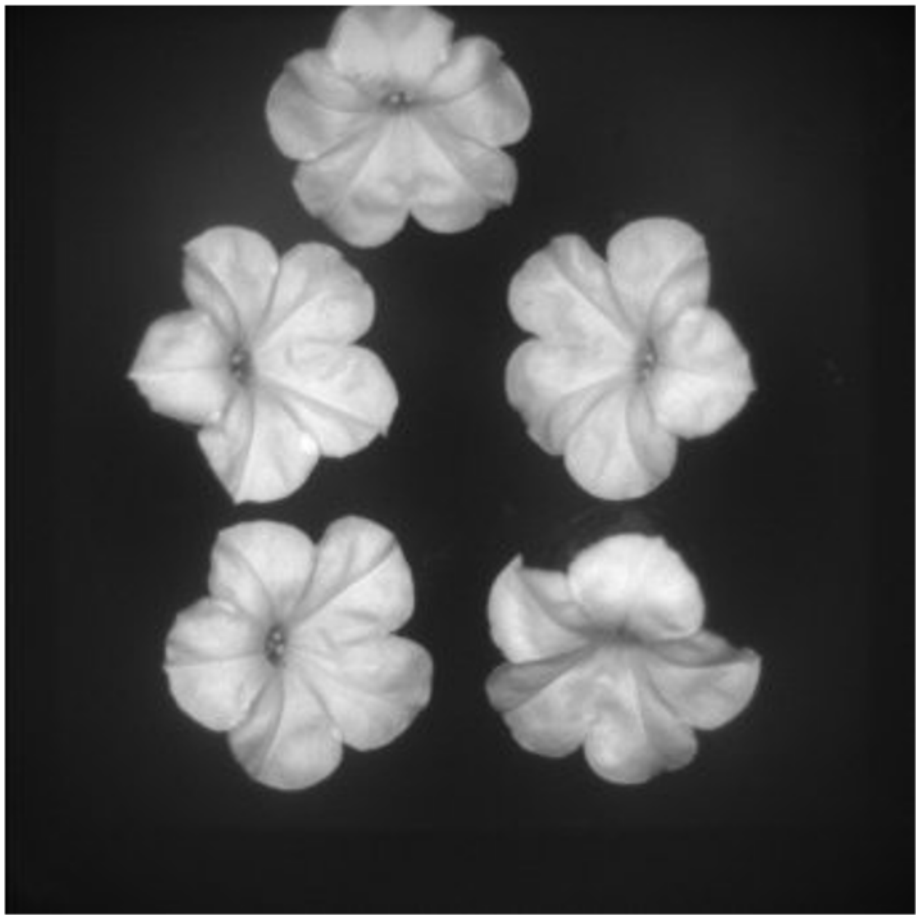


Figure S2. **Setup of detached flowers for luciferase imaging.** Depiction of the arrangement of four *pODO1:LUC* flowers (bottom) with one wild-type flower (top) for imaging in Movie 1.

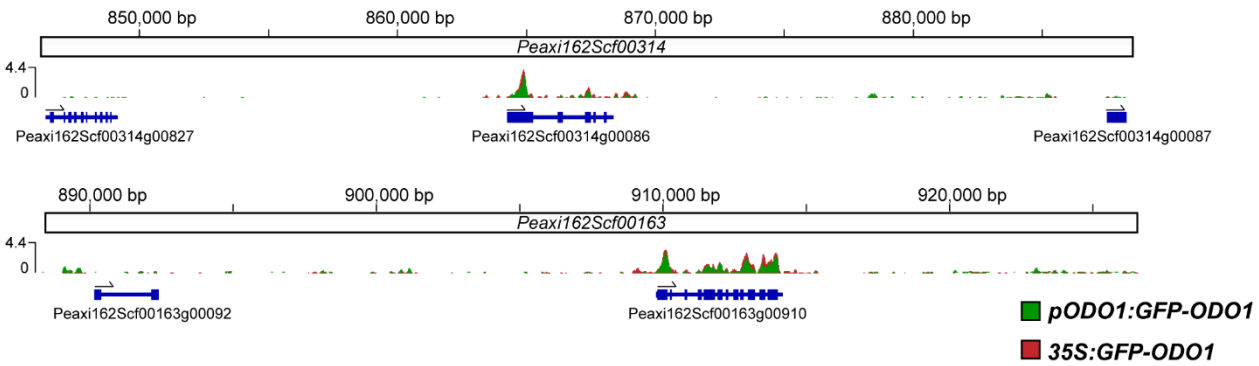


Figure S3. **ChIP-Seq signal in gene space surrounding example ODO1 targets.** ChIP-seq signals at *4CLa* (Peaxi162Scf00314g00086) and *CIMS1* (Peaxi162Scf00163g00910) with surrounding upstream and downstream regions. The Y axis represents the sequencing depth covered by ChIP-seq in fragments per million, after normalization to the total number of unique aligned fragments in each library. Ruler markings indicate location of ChIP signal along the corresponding petunia scaffolds, with annotated gene features below (thicker bar sections for coding regions, thinner sections for introns and untranslated regions).

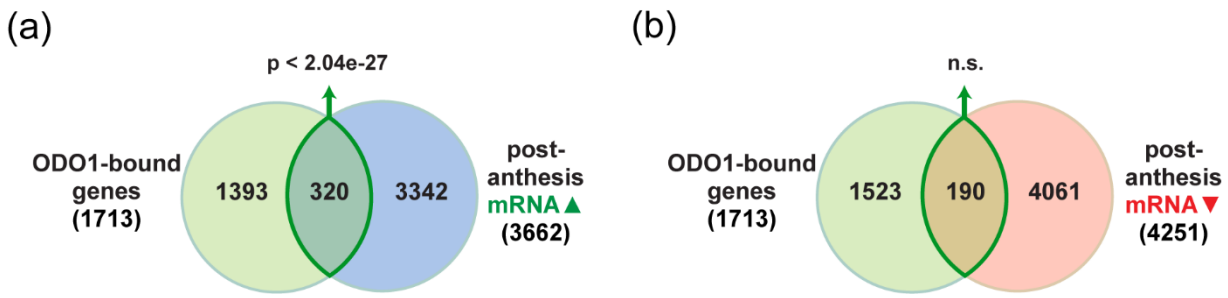
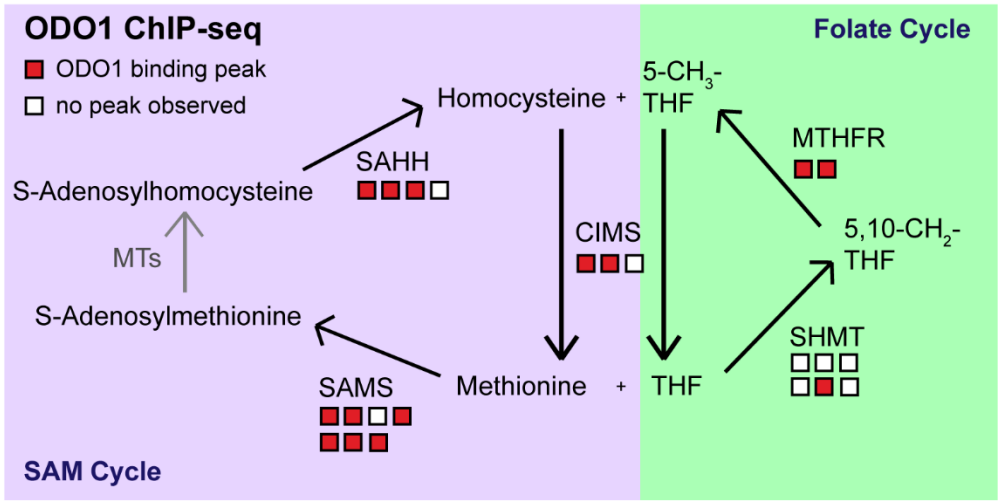


Figure S4. **Developmental regulation of ODO1-bound genes.** ODO1-bound genes are significantly overlapped with genes that are up-regulated (a) at day 2 relative to day 0 post-anthesis (Patrick et al., 2021), but not with genes that are down-regulated (b) at day 2 relative to day 0 post-anthesis (Patrick et al., 2021). The hypergeometric *p* value for the overlap between gene sets are shown. n.s.= not significant.

(a)



(b)

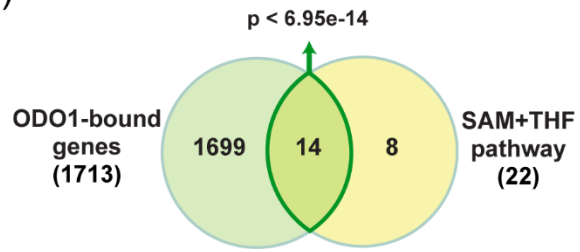


Figure S5. ODO1 binding of SAM cycle genes determined by ChIP-seq. (a) Methionine pathway with SAM and folate cycle genes identified in petunia (see also Table S2). The genes bound by ODO1 are indicated by red squares. (b) Overlap between ODO1-bound genes and SAM/THF genes with a *p* value representing the significance of the observed overlap determined by hypergeometric distribution against the whole genome as background. Abbreviations: CIMS, cobalamin-independent methionine synthase; MTHFR, methylenetetrahydrofolate reductase; MTs, methyltransferases; ODO1, ODORANT1; SAHH, S-adenosyl-L-homocysteine hydrolase; SAMS, S-adenosylmethionine synthetase; SHMT, serine hydroxymethyltransferase; THF, tetrahydrofolate

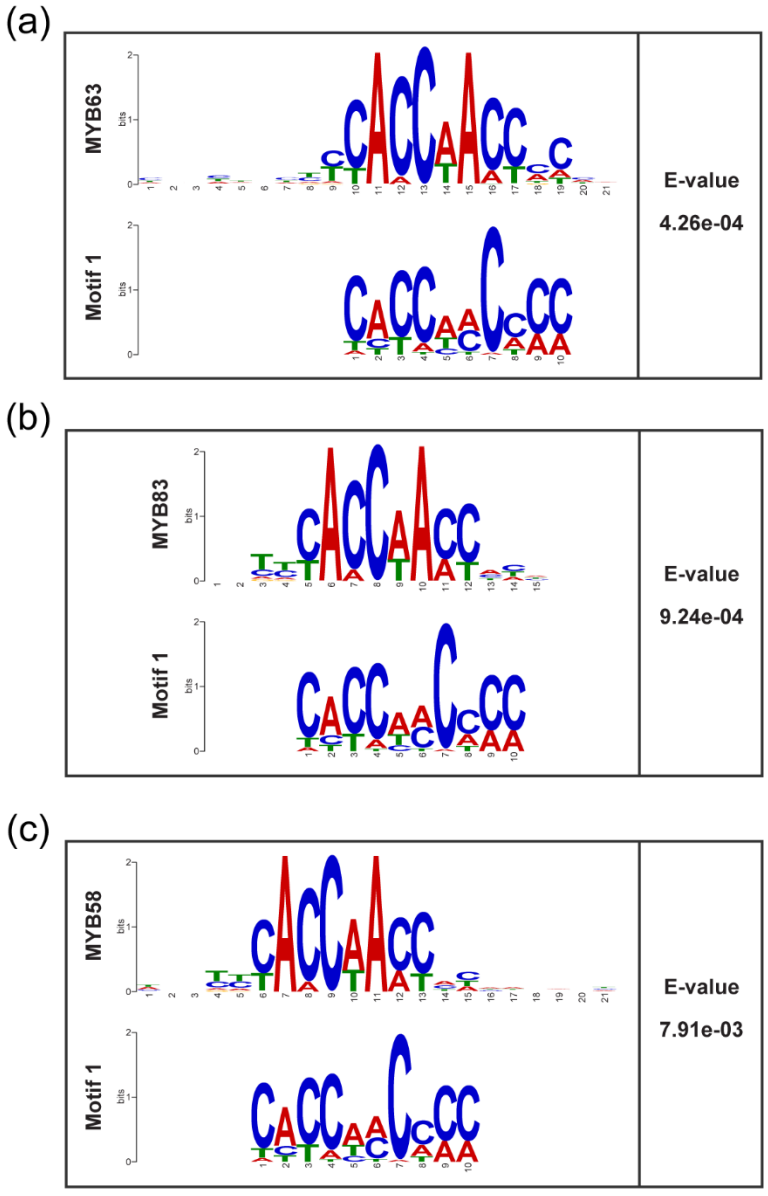


Figure S6. Comparison between the putative ODO1 binding motif with previously reported binding motifs of transcription factors in Arabidopsis. The putative binding motif of ODO1 (Motif 1, Figure 5a) was queried against the Arabidopsis DAP-Seq database (O'Malley et al., 2016) using Tomtom (Gupta et al., 2007). Top three matches by lowest E-value shown, all relating to MYB transcription factors.

Motif 1B in ODO1-bound FVBP pathway gene promoters

shikimate/phe biosynthesis	
gene	**motif**
DHD-SDH3	CACCAACCCC, CAACTACCCC, CCCCATCCAC, CAACTTCCTC
SK	CCCCCCCCCC, CCCCTACCTA
EPSPS1	CACCAACTAC, CACCAACAAC
DAHP1	CACCTACCTT
CS	CACCTACCCC, CCCCTCACCC
ADT1	CACCTACCCC, CCACCACCAC
ADT3	CACCTACCAC

general phenylpropanoid	
gene	**motif**
PALa	CCCCTCCCCC, CAACTACCAC, TACCAACCCT
PALb	CACCAACCCC (x2), CCCCACCCTC, CACCTACCAA, CACCTACCAT, CAACAACCCA (x2), CCCCTAGCCC, CACCAAACCT
PALc	CACCAACCCC, CAACAACCAC, CAACAACCCA
C4Ha	CACCAACTCC, TACCTACCCC, CACCTACCTA, CACCATCCTA
4CLa	CACCAACCAC, CCCCATCCCT
4CLd	CACCAACTCC
4CL-like	CAACTACTCC, CACCTTCCAT, CACCCACGCC

monolignol biosynthesis	
gene	**motif**
HCT1	CACCTACCAC, CACCTTACCC
HCT2	CACCTACCAC, CCCCTTCCAT
C3H	CACCAACTCC, CAACTACCAC, CACCAACCAA, CCCCAACTCT, CCCCTTCCAT
CCoAOMT1	CACCAACAAC
CCoAOMT3	CACCTACCAA
CAD	CCCCACCCCC, CACCAACCTC, CCCCCCCCCC

volatile benzenoid	
gene	**motif**
CNL3	CCACTTCCCC
CHD1	TCCCAACCCC, CCCCACACAC
BPBT2	CAACAACTAC

Figure S7. Motif 1B occurrences within promoters of ODO1-bound FVBP genes. Sequence matches to the predicted ODO1 binding motif within 500bp promoter of FVBP genes (Figure 5c) with *p* value < 1.0e-04 as determined by MEME (Bailey et al., 2009) are shown. Abbreviations: 4CL, 4-coumaryl-CoA ligase; ADT, arogenate dehydratase; BPBT, benzoyl-CoA:benzylalcohol/phenylethanol benzoyltransferase; C3H, coumarate 3-hydroxylase; C4H, cinnamate 4-hydroxylase; CAD, cinnamyl alcohol dehydrogenase; CCoAOMT, caffeoyl-CoA O-methyltransferase; CHD, cinnamoyl-CoA hydratase-dehydrogenase; CNL, cinnamoyl-CoA ligase; CS, chorismate synthase; DAHP, 3-deoxy-D-*arabino*-heptulosonate 7-phosphate synthase; DHD-SDH, 3-dehydroquinate dehydratase and shikimate dehydrogenase; EPSPS, 5-*enol*pyruvylshikimate 3-phosphate; HCT, hydroxycinnamoyl-CoA:shikimate/quinate hydroxycinnamoyl transferase; ODO1, ODORANT1; PAL, phenylalanine ammonia lyase; SK, shikimate kinase.

>pPALc
ccgagctcgcggccgcCTC**CAACAACCCA**AACAACTCACAAATCCCATCCCAATTC**CACCAACCCC**CAAAATATTGT
TTCTTTATTTTGTAAACAAAATAGATAAATAAACCCATGTTACATGGAATACCCACGTCATTCTCAAATCTCAACCG
TTTAATAAAATTAAAATCAAGGGACAAGATTTATTTTC**CAACAACCAC**CATTTAGCCCTCCCTATTATTCTTTACCT
ACCAACATTTGTGTTCCATCCCCTCTATTTATACACCACATCTCCTATCTACCACAtctagacc

>pEPSPS1
ccgagctcgcggccgcCGAATTAGTCGAGCCCCAAATAATATATACGTCGGGTGGAAAACTATAAAATGTTTGACAA
AAATGTCAAATTAATATATCAATCTGCAACAACCTTTTCACCTTGAGAACACAGCTGGAATTTTTTACAAAG**GTAGT**
TGGTGAAGCTAGTCAGCGAATCCCATTACCTTCCACTCTACCTAACCCCCTT**CACCAACAAC**AAATTTCTGTAATTT
AAAAACTAGCCAAAAAAGAACTCTCTTTTACAAAGAGCCAAAGACTCtctagacc

>mutpPALc
ccgagctcgcggccgcCTC**CAggAAggCA**AACAACTCACAAATCCCATCCCAATTC**CAggAAggCC**CAAAATATTGT
TTCTTTATTTTGTAAACAAAATAGATAAATAAACCCATGTTACATGGAATACCCACGTCATTCTCAAATCTCAACCG
TTTAATAAAATTAAAATCAAGGGACAAGATTTATTTTC**CAggAAggAC**CATTTAGCCCTCCCTATTATTCTTTACCT
ACCAACATTTGTGTTCCATCCCCTCTATTTATACACCACATCTCCTATCTACCACAtctagacc

>mutpEPSPS1
ccgagctcgcggccgcCGAATTAGTCGAGCCCCAAATAATATATACGTCGGGTGGAAAACTATAAAATGTTTGACAA
AAATGTCAAATTAATATATCAATCTGCAACAACCTTTTCACCTTGAGAACACAGCTGGAATTTTTTACAAAG**GTccT**
TccTGAAGCTAGTCAGCGAATCCCATTACCTTCCACTCTACCTAACCCCCTT**CAggAAggAC**AAATTTCTGTAATTT
AAAAACTAGCCAAAAAAGAACTCTCTTTTACAAAGAGCCAAAGACTCtctagacc

Figure S8. Synthetic promoter constructs. Restriction sites are underlined and ODO1 binding sites are bold. Mutated nucleotides are displayed in lower case and bold.

Table S1. Significantly enriched GO terms among ODO1-bound genes determined by ChIP-seq

GO term	description	fold enrichment	FDR corrected *p* value
GO:0006556	S-adenosylmethionine biosynthetic process	17.09	8.28E-06
GO:0015690	aluminum cation transport	14.24	0.000239
GO:0006730	one-carbon metabolic process	9.20	1.90E-07
GO:1901141	regulation of lignin biosynthetic process	9.20	0.000521
GO:0009423	chorismate biosynthetic process	9.06	0.001772
GO:2000762	regulation of phenylpropanoid metabolic process	8.55	0.00069
GO:0009086	methionine biosynthetic process	7.18	0.000101
GO:0016441	posttranscriptional gene silencing	6.65	0.000856
GO:0009073	aromatic amino acid family biosynthetic process	6.23	0.01131
GO:0009819	drought recovery	5.86	0.01317
GO:0009698	phenylpropanoid metabolic process	4.13	0.02411
GO:0019760	glucosinolate metabolic process	4.11	0.000378
GO:0006520	cellular amino acid metabolic process	3.40	0.02584
GO:0090351	seedling development	3.32	0.04717
GO:0009269	response to desiccation	3.32	0.04717
GO:0010218	response to far red light	2.74	0.01951
GO:0009646	response to absence of light	2.70	0.04841
GO:0007623	circadian rhythm	2.38	0.02412
GO:0009809	lignin biosynthetic process	2.35	0.01384
GO:0009740	gibberellic acid mediated signaling pathway	2.22	0.02412
GO:0010200	response to chitin	2.04	0.0154
GO:0080167	response to karrikin	1.93	0.02412
GO:0009611	response to wounding	1.90	0.002136
GO:0045892	negative regulation of transcription, DNA-templated	1.88	0.02439
GO:0009414	response to water deprivation	1.88	0.00069
GO:0006508	proteolysis	1.61	0.02536
GO:0009737	response to abscisic acid	1.57	0.012
GO:0046686	response to cadmium ion	1.56	0.02814
GO:0009651	response to salt stress	1.40	0.04055

Table S2. *P. axillaris* genes involved in SAM and folate cycle determined by BLAST against Arabidopsis whole gene set. E-Value: Expect value for sequence match relative to chance.

Gene ID	Name	*A. thaliana* BLAST Homology	E Value
Peaxi162Scf00163g00910	CIMS1	AT5G17920	0
Peaxi162Scf00163g01014	CIMS2	AT5G17920	0
Peaxi162Scf00342g00928	CIMS3	AT5G17920	0
Peaxi162Scf00668g00049	SAMS1a	AT1G02500	0
Peaxi162Scf00357g00318	SAMS1b	AT1G02500	0
Peaxi162Scf00164g00055	SAMS1c	AT1G02500	0
Peaxi162Scf01081g00002	SAMS3a	AT2G36880	0
Peaxi162Scf00578g00014	SAMS3b	AT2G36880	0
Peaxi162Scf00311g00131	SAMS3c	AT2G36880	0
Peaxi162Scf00071g00324	SAMS4	AT3G17390	0
Peaxi162Scf00047g00011	SAHH1	AT4G13940	0
Peaxi162Scf00423g00057	SAHH2	AT4G13940	0
Peaxi162Scf00652g00015	SAHH3	AT4G13940	0
Peaxi162Scf00089g00930	SAHH4	AT4G13940	0
Peaxi162Scf00943g00418	SHM1	AT4G37930	0
Peaxi162Scf00481g00018	SHM2	AT5G26780	0
Peaxi162Scf00436g00824	SHM3a	AT4G32520	0
Peaxi162Scf00064g01624	SHM3b	AT4G32520	0
Peaxi162Scf00423g00512	SHM4a	AT4G13930	0
Peaxi162Scf00652g00013	SHM4b	AT4G13930	0
Peaxi162Scf00344g00056	MTHFR1	AT2G44160	0
Peaxi162Scf00156g00015	MTHFR2	AT2G44160	0

Table S3. Significantly enriched GO terms for genes down-regulated in *odo1i*

GO term	**description**	**fold enrichment**	**FDR corrected *p* value**
GO:0046654	tetrahydrofolate biosynthetic process	13.76	0.01938
GO:0009645	response to low light intensity stimulus	11.47	0.00677
GO:0009769	photosynthesis, light harvesting in photosystem II	11.47	0.02416
GO:0009768	photosynthesis, light harvesting in photosystem I	9.70	1.60E-06
GO:0010417	glucuronoxylan biosynthetic process	8.60	0.03379
GO:0042761	very long-chain fatty acid biosynthetic process	7.65	0.02416
GO:0010192	mucilage biosynthetic process	7.65	0.04446
GO:0019853	L-ascorbic acid biosynthetic process	7.34	0.02416
GO:0018298	protein-chromophore linkage	6.80	7.62E-06
GO:0009698	phenylpropanoid metabolic process	6.33	0.02929
GO:2000022	regulation of jasmonic acid mediated signaling pathway	4.59	0.03379
GO:0009644	response to high light intensity	3.79	0.00677
GO:0009416	response to light stimulus	3.68	7.62E-06
GO:0009809	lignin biosynthetic process	3.04	0.02869
GO:0009753	response to jasmonic acid	2.87	0.005374
GO:0016042	lipid catabolic process	2.39	0.04446
GO:0009611	response to wounding	2.13	0.02416
GO:0055085	transmembrane transport	2.05	0.02416
GO:0009409	response to cold	1.89	0.02929
GO:0046686	response to cadmium ion	1.84	0.04472

Table S4. Significantly enriched GO terms for genes up-regulated in *odo1i*

GO term	description	fold enrichment	FDR corrected *p* value
GO:0051209	release of sequestered calcium ion into cytosol	28.71	0.002858
GO:0032959	inositol trisphosphate biosynthetic process	28.71	0.002858
GO:0010439	regulation of glucosinolate biosynthetic process	19.14	0.006935
GO:0048015	phosphatidylinositol-mediated signaling	14.35	0.002858
GO:0048437	floral organ development	14.35	0.0148
GO:0005986	sucrose biosynthetic process	13.25	0.01494
GO:0019344	cysteine biosynthetic process	10.77	0.01689
GO:0006865	amino acid transport	10.77	0.01689
GO:0009228	thiamine biosynthetic process	10.13	0.01898
GO:0007029	endoplasmic reticulum organization	9.07	0.02343
GO:0005983	starch catabolic process	8.51	0.0148
GO:0000103	sulfate assimilation	8.20	0.02686
GO:0016114	terpenoid biosynthetic process	8.20	0.02686
GO:0042594	response to starvation	6.89	0.03861
GO:0090351	seedling development	6.38	0.02067
GO:0048527	lateral root development	4.63	0.02414
GO:0010345	suberin biosynthetic process	4.59	0.04542
GO:0009926	auxin polar transport	4.47	0.01689
GO:0051603	proteolysis involved in cellular protein catabolic process	3.56	0.01689
GO:0010311	lateral root formation	3.52	0.03435
GO:0009553	embryo sac development	3.38	0.03861
GO:0009734	auxin-activated signaling pathway	3.24	0.002858
GO:0009723	response to ethylene	2.77	0.01689
GO:0055085	transmembrane transport	2.18	0.01689
GO:0055114	oxidation-reduction process	1.69	0.002858

Table S5. Transcription factor regulatory targets of ODO1

Gene ID	*odo1i* log2 FC	Family	Name	*A. thaliana* BLAST Homology	E Value
Peaxi162Scf00469g00624	-4.60547	WRKY	WRKY69	AT3G58710	6.88E-65
Peaxi162Scf00062g00421	-1.62916	bHLH	LRL1	AT2G24260	2.13E-91
Peaxi162Scf00235g00064	-1.02638	ERF	ERF3	AT1G50640	4.15E-52
Peaxi162Scf00362g00831	-0.94635	MYB	MYB4	AT4G38620	8.1E-107
Peaxi162Scf00052g01817	-0.94528	bHLH	PIL5	AT2G20180	2.42E-78
Peaxi162Scf00051g01410	-0.86999	NAC	ATAF1	AT1G01720	1.1E-140
Peaxi162Scf00002g00037	-0.82842	MYB	ODO1	AT4G12350	8.23E-56
Peaxi162Scf00102g00086	-0.77596	Trihelix	Myb/SANT-like	AT2G44730	4.92E-38
Peaxi162Scf00848g00031	0.650685	GRAS	SCL8	AT5G52510	4E-143
Peaxi162Scf02754g10013	0.99995	TALE	BLH2	AT4G36870	5E-134

Table S6. Primer sequences

gene	type	FW primer 5'-3'	RV primer 5'-3'
GFP-ODO1	transgene integration	TCACATGGTCCTGCTG	CCTGTTTCCAAGACGAGAATG
pODO1	cloning	CCCAAGCTTGAAGGGGGATCTCATG	GGGGTACCCACTACTGACTCTCAGCTACC
EPSPS1	qRT-PCR	GCCTGATGTTGCCATGACAC	TGCGCTCAGTTTCCTTGACT
4CLa	qRT-PCR	ACAGTACCCAAATCTCCATCGG	TGCCACCATCAGATTCCAAAC
PALb	qRT-PCR	AGTTAGCACTGCAGGCATCA	TGGGTGCCAATGGAGAACTT
PALc	qRT-PCR	GCAACCCAGCAATTCCGAAC	GACGCCTTCTCCTGTCAACA
CIMS	qRT-PCR	CATCCGTACTCAGCTTGCCA	TCAAGTTCAAAGAACACCGTCT
SAHH	qRT-PCR	CTGGCTTGTAAGGACCCTCA	AAAGCACCTCGACGAGAAGG
HCT2	qRT-PCR	GCTCTTGTTCGTGGTGCAC	TCGACCCCAGCCAAAATCTG
CS	qRT-PCR	AGCAAACTGTGACGAGAGACA	GGCTACCATTGCTTCAACCA
DHD-SDH3	qRT-PCR	TTCCTCCTTCTCCACTCGCT	AATCACGATTCGAGCTCCCC
CAD1	qRT-PCR	TGAAAATCTGCTCTGCCTTAGA	AATTGGGGACACTTGAGGAC
ODO1	qRT-PCR	GTGCCTTAGCTTGCTTCTTTAGAGG	CCTTTTCTTTGTGGACCTTTTTGG
PPA-AT	qRT-PCR	TTTGCCGATATTTGCTGGAT	TTGCAAGGTCGAGAGTGATG
CSE	qRT-PCR	GATACACTGGGAAGCCAAGG	TCCCATGCACTGTCAAAAAG
EGS	qRT-PCR	TGTTGTCTCCAATTCGCTCA	CCGATAAGCGCTAAAACAGG
EF1a	qRT-PCR	CCTGGTCAAATTGGAAACGG	CAGATCGCCTGTCAATCTTGG
FBP1	qRT-PCR	GACCTTGATCTACTTGGTGACGAC	GTCACTTAAACGATAAGGTACACGAG