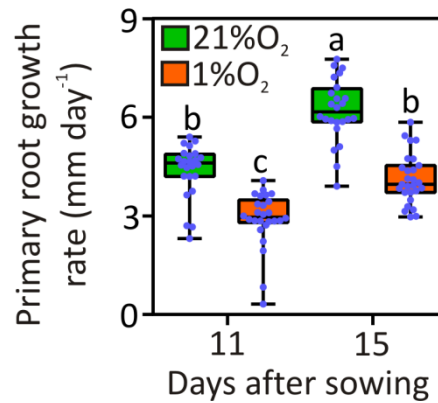
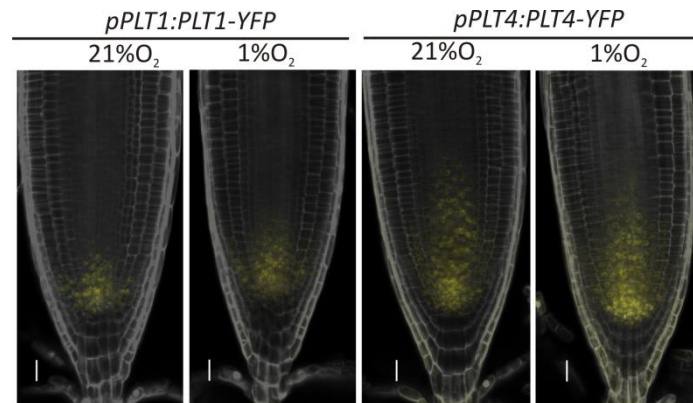


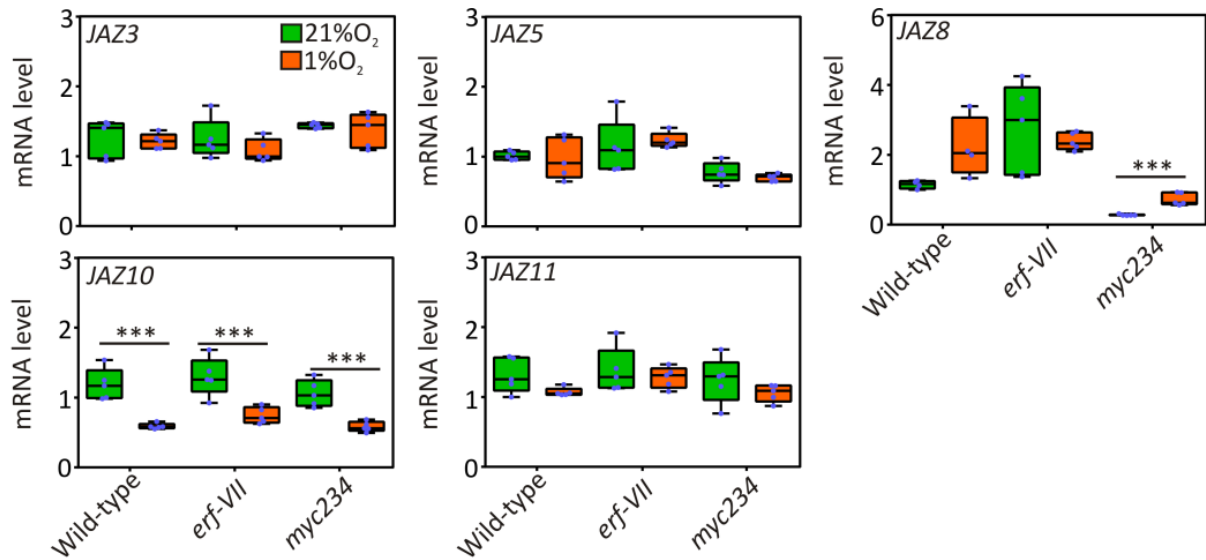
## Supplementary Figures and Tables



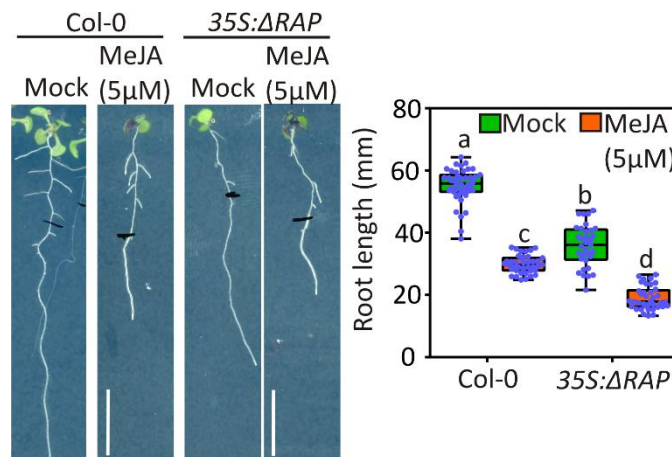
**Supplementary Figure S1.** Primary root growth rate in aerobic, hypoxic and post-hypoxic recovery conditions. Root elongation of 7 d old wild-type *Arabidopsis* plants grown under aerobic (green, 21% O<sub>2</sub>) and hypoxic (orange, 1% O<sub>2</sub>) conditions for four days and subsequently allowed to recover for four days under aerobic conditions. The growth rate is calculated as the difference between the root length measured for each plant at the time point shown on the x axis and four days before ( $n \geq 20$ ). Letters are used to distinguish statistically different groups (2-way ANOVA, Tukey post-hoc test,  $p \leq 0.05$ ).



**Supplementary Figure S2.** Effect of hypoxia on PLT1 and PLT4 protein level in the root apex. YFP signal in the root apex of *pPLT1:PLT1-YFP* and *pPLT4:PLT4-YFP* plants maintained 12 hours under aerobic (21% O<sub>2</sub>) and hypoxic (1% O<sub>2</sub>) conditions. Size bar = 20  $\mu$ m.



**Supplementary Figure S3.** Effect of hypoxia on the expression JAZ genes in the roots of wild-type and oxygen or jasmonate sensing mutants. Expression of five selected JAZ genes in wild-type, *erf-VII* and *myc234* mutants, under aerobic (green, 21% O<sub>2</sub>) and hypoxic (orange, 1% O<sub>2</sub>) conditions. mRNA level of each gene is normalized to the house-keeping gene (UBQ10-AT4G05320) to calculate  $\Delta\Delta Ct$ . Data shown in the graphs are the re-normalized  $\Delta\Delta Ct$  values to one of the biological replicate of Wild-type sample at 21% O<sub>2</sub>. Data are mean  $\pm$  SD of five biological replicates. Asterisks mark statistically significant differences in the indicated pairwise comparisons (\*\*\*) ( $p \leq 0.05$ , t-test).



**Supplementary Figure S4.** Effect of 5  $\mu$ M methyl-jasmonate (MeJA) on  $\Delta 13RAP$  root growth. (Left) Root phenotype of 11 d old  $\Delta 13RAP$  plants treated for four days with 5  $\mu$ M methyl jasmonate (Size bar = 10 mm). (Right) Root length of 11 d old  $\Delta 13RAP$  plants treated with 5  $\mu$ M methyl jasmonate ( $n \geq 30$ ). (2-way ANOVA, Tukey post-hoc test,  $p \leq 0.05$ ).



**Supplementary Table S1.** List of oligonucleotides used for realtime qPCR in this study.

qPCR primers		
Primer name	AGI code	Primer sequence (5'->3')
sgGRX480_fw	<i>AT1G28480</i>	ACGGAGAGGATGTTGCATGTGTC
sgGRX480_rv		AATCTCAAGGACCGCCGGATTC
sgAT2G47950_Fw	<i>AT2G47950</i>	AAATCTGGCTGTGGATTCTGCTG
sgAT2G47950_Rv		TGCGAGACAAGCTTCCCAGAAC
sgMAN7_fw	<i>AT5G66460</i>	AATCCTTGGAGATGGCAACAGC
sgMAN7_rv		TCTGAACCAGCACATAGCCTTGG
sgNIP1-2_fw	<i>AT4G18910</i>	GCCGTTTCCCTCTTAAACAGGTTC
sgNIP1-2_rv		CCGAACAAGAGCCGTAAAGTCG
sgPLT1_fw	<i>AT3G20840</i>	AGTTCGTGGCTGCCATTAGAAGG
sgPLT1_rv		ATCTTCCATGTTGGTGATGCCTTG
sgPLT2-F	<i>AT1G51190</i>	GAAGATGGCAAGCAAGGATCGG
sgPLT2-R		GCTTCTTCCCTCCGTGCTGAATG
sgPLT3-F	<i>AT5G10510</i>	GCTGTTGTGGCTGTGGAAACATC
sgPLT3-R		TCTTCCCGTCCATCTATGTCGAG
sgPLT4-F	<i>AT5G17430</i>	ACCCTCGAAGCTTTCACCAGAG
sgPLT4-R		ACCACCATTGATGTCCCAATCTCG
sgWOX5_fw	<i>At3g11260</i>	CGTGAAAGGTCGAAGCTTACGTG
sgWOX5_rv		ATTCCATCTCCCGCACTTCGTC
sgJAZ1_Fw	<i>AT1G19180</i>	AGCTTCACTTCACCGGTTCTTGGA
sgJAZ1_rv		TCTTGTCTTGAAGCAACGTCGTCA
sgJAZ3_Fw	<i>AT3G17860</i>	CTGCCCAGTACCAGTTTCTTGTTT
sgJAZ3_rv		AGCCAGAGGTAATGCCACTGTTG
sgJAZ5_Fw	<i>AT1G17380</i>	TTCCAAAGGCGAACCCTCTACC
sgJAZ5_rv		TCCTGGCTGTGATTCACTGAGG
sgJAZ8_Fw	<i>AT1G30135</i>	GGTCGGATCCTCCAAACAAGTC
sgJAZ8_rv		TCGTCGTGAATGGTACGGTGAAG
sgJAZ10_fw	<i>At5g13220</i>	TCGAGAAGCGCAAGGAGAGATTAG
sgJAZ10_rv		TCGTTTAGGCCGATGTCGGATAG
sgJAZ11_fw	<i>At3g43440</i>	TGCCAATTGCTAGGAGACGTTTAC
sgJAZ11_rv		GTAAGGCTTCGTGTGGACAAATCG

**Supplementary Table S4.** Presence of HRPE motif in the promoter of JA-regulated genes shown in Fig. 4. The 5'-AAACCA(G/C)(G/C)(G/C)GC-3' element was searched in 1 kb upstream of the translation start site (ATG) of each gene. Sequences that displayed such feature are highlighted in bold. The position of the identified element is relative to the ATG site.

	Gene Symbol	AGI code	HRPE element			score	p-value
			start	stop	strand		
Up-regulated genes		<i>AT5G14730</i>	NA	NA	NA	NA	NA
		<i>AT1G76600</i>	NA	NA	NA	NA	NA
	<i>GRXC9</i>	<i>AT1G28480</i>	NA	NA	NA	NA	NA
	<i>WRKY40</i>	<i>AT1G80840</i>	NA	NA	NA	NA	NA
	<i>BCB</i>	<i>AT5G20230</i>	NA	NA	NA	NA	NA
	<i>NAC102</i>	<i>AT5G63790</i>	NA	NA	NA	NA	NA
		<i>AT2G47950</i>	NA	NA	NA	NA	NA
		<b><i>AT5G12340</i></b>	185	196	+	14.2727	6.11E-06
		<b><i>AT5G19110</i></b>	32	43	+	10.2222	8.88E-05
	<i>TIFY10A</i>	<i>AT1G19180</i>	NA	NA	NA	NA	NA
Down-regulated genes	<i>UGT73B4</i>	<i>AT2G15490</i>	NA	NA	NA	NA	NA
	<i>BRL2</i>	<i>AT2G01950</i>	NA	NA	NA	NA	NA
	<i>MAN7</i>	<i>AT5G66460</i>	NA	NA	NA	NA	NA
	<i>CEL1</i>	<i>AT1G70710</i>	NA	NA	NA	NA	NA
	<i>NIP1-2</i>	<i>AT4G18910</i>	NA	NA	NA	NA	NA
	<i>SMO1-1</i>	<i>AT4G12110</i>	NA	NA	NA	NA	NA
	<i>LAX2</i>	<i>AT2G21050</i>	NA	NA	NA	NA	NA
		<i>AT4G09890</i>	NA	NA	NA	NA	NA
		<i>AT4G39320</i>	NA	NA	NA	NA	NA
	<i>CYP90B1</i>	<i>AT3G50660</i>	NA	NA	NA	NA	NA
		<i>AT3G10080</i>	NA	NA	NA	NA	NA
		<b><i>AT1G04680</i></b>	130	141	+	10.2727	8.63E-05
		<i>AT5G51560</i>	NA	NA	NA	NA	NA
		<i>AT4G35720</i>	NA	NA	NA	NA	NA