

Supplementary Table 1. Absolute and relative expression level of 49 core hypoxia induced genes, as defined by Mustroph et al. (2008)¹, in shoot apical meristem (SAM) and juvenile leaves belonging to the datasets AT-00048, AT-00050, AT-00080, AT-00087, AT-00088, AT-00123, AT-00151, AT-00245, AT-00307, AT-00322, AT-00325, AT-00330, AT-00363, AT-00382, AT-00396, AT-00654 and AT-00685. Statistical difference was calculated applying a Bonferroni correction to a t-test performed on each gene. Data were retrieved by the Genevestigator database².

Gene	Expression Level		Standard Error		Ratio SAM/Leaf	<i>p</i> -value <0.05
	SAM n=71	Juvenile leaf n=192	SAM	Juvenile leaf		
<i>AT1G43800</i>	304	10471	22.08	1563.48	34.44	yes
<i>AT4G10270</i>	529	6165	27.73	683.32	11.65	yes
<i>AT4G33560</i>	243	2585	3.83	556.48	10.64	yes
<i>AT1G77120</i>	915	8413	68.26	801.38	9.19	yes
<i>AT3G27220</i>	417	2744	10.18	329.33	6.58	yes
<i>AT2G16060</i>	1017	6484	36.44	693.91	6.38	yes
<i>AT5G15120</i>	879	4583	47.87	423.73	5.21	yes
<i>AT3G02550</i>	2457	12382	130.03	1308.56	5.04	yes
<i>AT2G17850</i>	419	1542	14.56	264.17	3.68	yes
<i>AT5G44730</i>	1785	5688	75.05	383.08	3.19	yes
<i>AT3G10040</i>	351	1111	10.47	100.84	3.17	yes
<i>AT5G39890</i>	639	1825	15.98	196.53	2.86	yes
<i>AT4G24110</i>	368	1040	17.50	128.76	2.83	yes
<i>AT4G27450</i>	4968	13927	476.26	1371.41	2.80	yes
<i>AT1G33055</i>	741	1997	27.02	216.14	2.70	yes
<i>AT2G19590</i>	893	2303	29.96	334.33	2.58	yes
<i>AT5G61440</i>	1447	3696	86.26	227.68	2.55	yes
<i>AT4G32840</i>	1385	3004	36.53	116.22	2.17	yes
<i>AT5G47060</i>	1348	2823	54.79	120.04	2.09	yes
<i>AT5G66985</i>	160	315	1.47	42.46	1.97	yes
<i>AT1G19530</i>	143	269	4.38	27.97	1.88	yes
<i>AT3G23150</i>	578	1049	32.86	82.26	1.81	yes
<i>AT1G55810</i>	2271	3899	79.54	142.16	1.72	yes
<i>AT1G74940</i>	2010	3365	112.42	95.25	1.67	yes
<i>AT4G39675</i>	180	290	1.93	46.86	1.61	yes
<i>AT5G45340</i>	1925	2609	203.54	381.59	1.36	yes
<i>AT2G47520</i>	469	613	11.70	34.81	1.31	yes
<i>AT5G58070</i>	19967	23785	1176.05	2436.23	1.19	no
<i>AT5G10040</i>	140	164	1.57	7.47	1.17	no
<i>AT3G43190</i>	350	394	4.57	24.04	1.13	no
<i>AT5G42200</i>	1161	1245	45.46	32.72	1.07	no
<i>AT3G61060</i>	1944	1987	162.48	181.06	1.02	no

<i>AT5G47910</i>	6010	6067	368.87	351.84	1.01	no
<i>AT1G26270</i>	3003	2887	125.87	144.08	0.96	no
<i>AT3G17860</i>	3499	3323	163.03	138.73	0.95	no
<i>AT4G17670</i>	2087	1763	129.12	57.35	0.84	no
<i>AT4G22780</i>	800	651	53.49	27.33	0.81	no
<i>AT5G26200</i>	701	548	39.10	22.67	0.78	yes
<i>AT1G17290</i>	16856	13052	824.84	524.24	0.77	yes
<i>AT1G72940</i>	1949	1504	143.88	134.39	0.77	yes
<i>AT5G54960</i>	5781	4446	506.66	303.72	0.77	yes
<i>AT1G76650</i>	843	563	94.71	36.71	0.67	yes
<i>AT1G35140</i>	1812	1156	322.91	170.30	0.64	yes
<i>AT5G02200</i>	429	259	18.78	5.90	0.60	yes
<i>AT5G62520</i>	614	345	71.35	12.22	0.56	yes
<i>AT1G63090</i>	2384	1304	143.12	50.06	0.55	yes
<i>AT2G34390</i>	385	198	5.08	4.55	0.51	yes
<i>AT3G23170</i>	1030	468	63.95	30.94	0.45	yes
<i>AT4G33070</i>	1059	253	402.54	17.86	0.24	yes

Supplementary Table 2. Absolute and relative expression level of 49 core hypoxia induced genes, as defined by Mustroph et al. (2008)¹, in root tip meristem (RM), elongation zone (EZ) and maturation zone (MZ) belonging to the datasets AT-00191, AT-00286, AT-00437, AT-00485, AT-00489, AT-00526, AT-00546, AT-00652, AT-00694. Statistical differences were calculated applying a Bonferroni correction to a one-way ANOVA followed by a Holm-Sidak post-hoc test performed on each gene. Data were retrieved by the Genevestigator database².

Gene	Expression Level			Standard Error			Ratio		p-value<0.05	
	RM n=17	EZ n=66	MZ n=33	RM	EZ	MZ	RM/EZ	RM/MZ	RMvsEZ	RMvsMZ
AT1G55810	6074	2716	2598	596.22	227.95	176.67	2.24	2.34	yes	yes
AT2G19590	5105	2298	4624	1213.70	326.36	456.84	2.22	1.10	yes	no
AT4G32840	3245	2011	1228	392.99	172.02	85.98	1.61	2.64	yes	yes
AT4G10270	448	308	263	111.05	15.80	13.67	1.45	1.70	no	no
AT5G39890	1047	768	823	120.69	26.73	64.23	1.36	1.27	no	no
AT1G33055	598	466	814	65.21	15.66	103.80	1.28	0.73	no	no
AT3G23150	1780	1390	1032	366.21	91.96	61.73	1.28	1.72	no	no
AT5G26200	437	358	418	42.16	16.91	23.12	1.22	1.05	no	no
AT1G26270	7666	6389	5093	871.13	404.08	438.67	1.20	1.51	no	no
AT2G16060	5388	4514	2923	746.24	394.30	387.93	1.19	1.84	no	no
AT3G02550	876	734	851	104.32	34.31	123.30	1.19	1.03	no	no
AT4G27450	2714	2276	2802	518.73	197.15	268.42	1.19	0.97	no	no
AT5G61440	4461	3880	3311	622.59	341.62	376.44	1.15	1.35	no	no
AT5G47060	2573	2250	2374	196.50	187.90	167.65	1.14	1.08	no	no
AT3G27220	780	704	664	76.36	45.98	30.26	1.11	1.17	no	no
AT5G02200	658	609	572	103.51	36.15	71.03	1.08	1.15	no	no
AT4G17670	1306	1309	1323	150.37	79.25	93.46	1.00	0.99	no	no
AT5G15120	403	411	385	37.89	16.62	26.23	0.98	1.05	no	no
AT4G33560	299	310	275	17.16	16.26	13.23	0.96	1.09	no	no
AT5G44730	1511	1588	2464	184.91	89.05	277.35	0.95	0.61	no	no
AT3G17860	3800	4002	2373	318.99	272.26	150.09	0.95	1.60	no	no
AT1G19530	259	276	223	15.33	17.07	9.91	0.94	1.16	no	no
AT3G10040	320	343	270	19.86	16.68	8.62	0.93	1.19	no	no
AT2G17850	309	354	320	20.42	17.85	16.77	0.87	0.97	no	no
AT3G61060	2381	2771	4191	482.57	391.70	550.70	0.86	0.57	no	no
AT1G17290	10416	12309	11785	1918.85	857.75	782.82	0.85	0.88	no	no
AT5G45340	1826	2191	4415	401.30	424.31	689.69	0.83	0.41	no	no
AT1G43800	225	270	247	14.00	16.29	14.68	0.83	0.91	no	no
AT2G34390	486	585	606	34.23	26.46	44.62	0.83	0.80	no	no
AT5G10040	220	273	232	7.75	16.35	13.86	0.81	0.95	no	no
AT4G24110	1924	2918	2864	443.78	701.92	663.51	0.66	0.67	no	no
AT5G62520	870	1341	2273	127.07	243.97	447.26	0.65	0.38	no	no
AT5G42200	707	1108	1503	68.18	86.11	146.48	0.64	0.47	no	yes
AT3G23170	868	1395	1384	240.44	295.49	251.67	0.62	0.63	no	no
AT4G22780	256	416	702	10.96	24.69	78.66	0.62	0.36	no	yes
AT5G54960	1666	2993	9753	106.18	250.43	1074.29	0.56	0.17	no	yes

<i>AT1G63090</i>	594	1082	1655	56.51	74.28	204.43	0.55	0.36	no	yes
<i>AT1G72940</i>	667	1258	1021	111.31	100.01	130.40	0.53	0.65	no	no
<i>AT1G74940</i>	1788	3457	5020	211.53	329.73	578.87	0.52	0.36	no	yes
<i>AT3G43190</i>	654	1539	2449	54.43	264.52	305.17	0.42	0.27	no	no
<i>AT5G58070</i>	6583	16906	31702	1096.43	2909.53	5435.53	0.39	0.21	no	yes
<i>AT5G47910</i>	698	2253	12569	131.11	357.70	1539.17	0.31	0.06	no	yes
<i>AT1G76650</i>	635	2096	1758	70.59	567.71	415.30	0.30	0.36	no	no
<i>AT1G77120</i>	647	2209	2279	50.87	615.07	464.57	0.29	0.28	no	no
<i>AT5G66985</i>	645	2988	9271	98.56	634.87	1737.40	0.22	0.07	no	yes
<i>AT2G47520</i>	831	4202	1127	100.79	845.34	160.69	0.20	0.74	no	no
<i>AT4G39675</i>	476	3082	3906	64.99	1002.59	905.50	0.15	0.12	no	no
<i>AT1G35140</i>	319	4729	4215	35.08	1348.96	1252.00	0.07	0.08	no	no
<i>AT4G33070</i>	317	4710	11647	32.70	1374.72	2361.30	0.07	0.03	no	yes

Supplementary Table 3. MAS5-normalized absolute expression level of core-hypoxia inducible genes in the SAM and RM cell types belonging to the datasets. Absolute levels were retrieved from the Arabidopsis EFP browser⁵⁴ considering the datasets Root Cell Types^{4,5} and Shoot Apical Meristem⁶.

Gene	PZ	CZ	OC	LRC	Stele	C+En	En	Ep	QC
<i>AT3G02550</i>	3233	2566	5435	91.62	29.81	174.79	274.80	28.33	541.36
<i>AT5G47910</i>	2447.19	1928.18	2863.42	260.80	42.60	172.10	148.00	16.80	117.60
<i>AT4G22780</i>	1078.46	1029.27	3169.33	40.40	33.30	41.90	42.20	8.90	148.19
<i>AT5G15120</i>	1484	1289	2184	40.70	8.70	66.10	129.00	11.00	448.41
<i>AT5G58070</i>	1162.78	1325.78	1942.21	193.20	163.90	213.70	812.80	73.60	1719.35
<i>AT1G76650</i>	550.9	1457.05	1935.25	1404.40	590.90	849.10	1189.50	893.60	365.71
<i>AT4G10270</i>	1094.69	1315.12	1457.92	88.80	17.20	193.10	637.30	26.20	219.70
<i>AT5G54960</i>	1121.35	948.04	1458.61	11.60	21.60	46.10	140.80	6.50	339.49
<i>AT4G24110</i>	848.98	488.37	1955.69	164.30	65.10	181.40	195.10	72.90	239.17
<i>AT1G17290</i>	724.64	742.64	1706.42	978.80	404.00	652.50	725.20	678.20	1243.88
<i>AT5G44730</i>	1003.9	852.52	1193.87	270.20	62.50	332.50	322.70	86.80	710.16
<i>AT1G63090</i>	452.79	707.53	1671.13	119.00	192.40	176.40	87.30	73.40	292.39
<i>AT1G77120</i>	974	609	1195	532.10	12.20	499.50	865.10	87.80	653.76
<i>AT4G27450</i>	1420.55	273.03	1049.24	685.30	76.70	687.10	1354.70	107.80	815.61
<i>AT5G39890</i>	494	1212	974	80.60	16.00	187.10	220.50	36.80	227.32
<i>AT5G20830</i>	563	389	1672	114.30	53.60	104.00	538.40	87.20	289.79
<i>AT1G26270</i>	676.64	569.3	980.68	389.30	153.30	301.20	414.40	318.20	542.40
<i>AT5G62520</i>	318.17	754.87	1073.75	868.90	572.40	801.20	602.10	350.90	1363.59
<i>AT3G10040</i>	732	417	960	32.20	5.10	55.90	81.40	10.40	127.18
<i>AT5G47060</i>	647.81	574.54	580.04	113.70	124.90	165.90	196.70	55.00	281.84
<i>AT4G32840</i>	561.43	474.71	553.19	133.00	127.80	175.60	141.40	125.80	161.85
<i>AT5G61440</i>	317.02	218.21	935.42	25.90	48.90	35.70	57.60	52.90	227.46
<i>AT3G27220</i>	560.72	286.94	582.26	72.00	18.30	148.90	163.70	25.90	184.81
<i>AT1G43800</i>	661	307	438	440.90	0.20	560.50	535.50	39.60	13.10
<i>AT1G35140</i>	291	402	329	48.90	12.10	104.50	25.20	12.30	39.09
<i>AT1G55810</i>	228.52	190.08	494.48	85.90	79.20	86.70	85.20	102.90	203.36
<i>AT3G17860</i>	154.26	205.48	528.97	709.10	333.00	437.10	376.10	303.10	666.52
<i>AT5G45340</i>	191.24	402.53	262.47	400.50	86.80	254.60	122.90	180.80	313.05
<i>AT3G61060</i>	151.08	166.51	436.57	32.40	44.20	50.60	48.00	26.40	124.47
<i>AT1G72940</i>	271.16	193.13	242.87	29.20	23.30	41.10	51.40	19.90	358.63
<i>AT1G74940</i>	208.24	88.82	269.15	5.10	8.60	10.40	11.60	4.20	102.28
<i>AT4G17670</i>	80.73	107.8	81.14	35.60	55.00	40.20	70.80	29.60	64.74
<i>AT4G33560</i>	93.12	68.33	89.56	141.10	5.90	226.40	309.70	15.60	12.32
<i>AT3G23150</i>	77.74	62.72	99.36	47.60	22.50	56.90	90.40	35.20	159.95
<i>AT5G26200</i>	71.52	40.67	123.5	44.80	2.70	61.40	280.90	4.40	74.26
<i>AT2G47520</i>	62.64	79.43	91.81	50.60	24.60	47.60	133.30	32.20	75.36
<i>AT3G23170</i>	80.36	45.55	82.97	112.00	95.20	133.10	181.30	90.20	54.44
<i>AT1G33055</i>	78.5	39.32	64.76	19.70	5.10	13.50	459.50	10.10	69.86
<i>AT2G16060</i>	48	63	60	1772.90	271.00	926.50	2285.30	389.80	106.62
<i>AT5G02200</i>	26.69	48.21	90.52	31.60	20.20	40.70	27.80	15.40	40.83
<i>AT5G42200</i>	54.85	26.9	74.55	8.20	50.90	20.60	24.90	10.00	20.96

<i>AT3G43190</i>	17	37	59	375.20	21.70	235.80	700.80	18.60	78.64
<i>AT4G33070</i>	44	23	23	15.70	5.90	136.40	622.80	4.40	1594.17
<i>AT2G17850</i>	28.86	22.32	36.04	148.00	28.70	40.40	225.90	24.80	41.50
<i>AT2G34390</i>	24.24	21.86	23.55	53.50	16.00	30.90	98.20	10.70	44.71
<i>AT2G19590</i>	34.5	13.13	15.82	911.90	58.30	676.30	905.50	160.00	137.96
<i>AT5G10040</i>	13	17	19	65.30	17.40	112.50	228.30	8.20	36.86
<i>AT5G66985</i>	1.81	12.8	8.18	134.90	13.10	171.10	111.50	8.50	96.25
<i>AT4G39675</i>	4.45	4.2	6.98	157.80	26.70	39.30	80.80	0.80	3.75
<i>AT1G19530</i>	2.28	2.07	6.84	52.00	4.50	42.40	144.60	14.90	54.46

Supplementary Table 4. List of ZPR sequences used to build up the phylogenetic tree shown in Extended Data Fig. 6b.

Species	Identifier	Name in Figure 6b
<i>Oryza sativa</i>	LOC_Os09g34890.1	OsZPR2-like 1
	LOC_Os04g33560.1	OsZPR3-like 1
	LOC_Os02g32850.1	OsZPR3-like 2
<i>Solanum lycopersicum</i>	Solyc08g079690.2.1	SlZPR2-like 2
	Solyc08g007570.2.1	SlZPR2-like 1
	Solyc01g091490.2.1	SlZPR2-like 3
	Solyc01g005180.1.1	SlZPR3-like 1
<i>Amborella trichopoda</i>	evm_27.model.AmTr_v1.0_scaffold00040.112	AtZPR3-like
	evm_27.model.AmTr_v1.0_scaffold00041.3	AtZPR2-like
<i>Sorghum bicolor</i>	Sobic.006G068200.1	SbZPR3-like 2
	Sobic.004G164700.2	SbZPR3-like 3
	Sobic.002G267800.1	SbZPR2-like 1
	Sobic.005G038000.1	SbZPR3-like 1
<i>Aquilegia coerulea</i>	Aqcoe7G064000.1	AcZPR2-like 1
	Aqcoe2G139400.1	AcZPR3-like 1
<i>Populus trichocarpa</i>	Potri.003G117200.1	PtZPR2-like 2
	Potri.001G114900.1	PtZPR2-like 1
	Potri.014G071200.1	PtZPR2-like 3
	Potri.006G083200.1	PtZPR3-like 1
	Potri.010G237600.1	PtZPR3-like 2
<i>Medicago truncatula</i>	Medtr7g075120.1	MtZPR2-like 1
	Medtr2g439220.1	MtZPR3-like 1
<i>Arabidopsis thaliana</i>	At3g52770	AtZPR3
	At2g36307	AtZPR4
	At3g60890	AtZPR2
	At2g45450	AtZPR1
<i>Daucus carota</i>	DCAR_008443	DcZPR2-like 1
	DCAR_013380	DcZPR3-like 1

Supplementary Table 5. Comparison of the mRNA levels of HD-ZIP III target genes in estradiol-inducible *ZPR2* overexpressors, treated with hypoxia, or normoxia as control. Estradiol induction was carried out for 4 hours prior to harvest. Data are represented as means relative to the ethanol treated samples at normoxia $\pm$ s.d. for n=4. *p*-values calculated using one-way ANOVA and Holm-Sidak post-hoc test.

Gene	Ethanol		Estradiol		<i>p</i> -value	Estradiol		
	Normoxia		Normoxia			Hypoxia		
	Fold change		Fold change			Fold change		
	(log2)	st.Dev	(log2)	st.Dev		(log2)	st.Dev	<i>p</i> -value
<i>ZPR2</i>	0.00	1.02	9.00	1.21	0.04	2.42	5.06	0.37
<i>ATH1</i>	0.00	0.58	-0.76	1.80	0.49	-3.45	1.09	0.01
<i>HEC1</i>	0.00	0.15	0.08	0.59	0.80	-3.28	0.04	<0.01
<i>FAF1</i>	0.00	0.20	-0.35	0.80	0.55	-2.29	0.84	0.02
<i>ZPR1</i>	0.00	0.38	-0.50	0.73	0.32	-2.47	0.56	0.01
<i>POL</i>	0.00	0.06	-0.05	0.34	0.86	-1.42	0.41	0.04
<i>AMP</i>	0.00	0.86	0.24	0.22	0.67	-1.72	0.73	0.04
<i>HAT2</i>	0.00	0.48	0.08	0.41	0.82	-1.48	0.21	0.01
<i>MAX2</i>	0.00	0.72	-0.07	0.54	0.88	-1.77	0.36	0.02

<i>TAA1</i>	0.00	0.46	-0.35	0.20	ns	-0.92	0.40	ns
<i>KNAT6</i>	0.00	0.64	0.13	0.55	ns	-0.68	0.28	ns
<i>PSK5</i>	0.00	0.79	0.01	0.46	ns	-0.56	0.29	ns

Supplementary Table 6. Full list of the primers used in this study. (F = forward primer; R = reverse primer)

Primer name:	5'-3' sequence
isZPR2F	ATGCATATCTCTGGCCCCTC
isZPR2R	TCTCTATCACGGATCGGCAT
Sail_lb1	GCCTTTTCAGAAATGGATAAATAGCCTTGCTTCC
GK_lb1	ATATTGACCATCATACTCATTGC
gwpZPR1F	CACCTTTGAAAGATTAAGATGTGTC
gwpZPR1R	TATTCGTTTAAAGAGAGGAGAGAG
gwpZPR2F	CACCTTATCGTAACTACAATTTCTGG
gwpZPR2R	CTTCTTGTGGTTTTATCACACA
gwpMAX2F	CACCATCCATTGTTTCACGTT
gwpMAX2R	GAGAAGCGGCAAATCTACAAGAG
gwpTAA1F	CACCTTTTGTGAGTGCCTCATTGT
gwpTAA1R	TCCTCGAGTTCTCCAGTTTC
gwpPSK5_F	CACCACGTATATGAAACGGCTTGG
gwpPSK5_R	GGAAAGTTGTGAACTTAACCA
pZPR2ZPR2MAC F	CCACAAGAAGATGGCTTGTCTGACAACTTC
pZPR2ZPR2MAC R	GAAGTTGTCAGACAAGCCATCTTCTTGTGG
pZPR2ZPR2MALF	GATAAAACCACAAGAAGATGGCTCTGACAACTTCAGAGCCAC
pZPR2ZPR2MALR	GTGGCTCTGAAGTTGTCAGAGCCATCTTCTTGTGGTTTTATC
gwZPR2F	CACCATGTGTCTGACAACTTCAGAG
gwMACZPR2 F	CACCATGGCTTGTCTGACAACTTCAGA
gwZPR2nostop R	CTGAAGCAAGGAGGTTGAAAC
gwZPR2R	CTGAAGCAAGGAGGTTGAACTAA
gwCORF	CACCATGGCAATGTCTTGCAAGGA
gwCORR	TCACACAAAGGACCAATTGATG
gwREVF	CACCATGGAGATGGCGGTGGCTAA
gwREVR	CACAAAAGACCAGTTTACAAAG
gwPHVF	CACCATGATGGCTCATCACTCCAT
gwPHVR	TCAAACAAACGACCAACTAA

sgAt5G15120_F	ATTGGGTGGTTGATGCTCCAATG
sgAt5g15120_R	ATGCATGTTCCCGCCATCTTC
sgAt4g05320 F	GGCCTTGTATAATCCCTGATGAATAAG
sgAt4g05320 R	AAAGAGATAACAGGAACGGAACATAGT
sgAt4g33070 F	CACAGAATCTTCAATGTTCTTACC
sgAt4g33070 R	CCATGATAAAGCGTACATGGAA
sgAt3g10040 F	ACAACCACCGCAACAGAATCC
sgAt3g10040 R	TCTCCGCAATTCTCGCCAT
At5g39890_F	CTTCGAGCCGTTTTGGATGA
At5g39890_R	ACGTCACTAACGGAGATCGTCC
At1g77120 F	TATTCGATGCAAAGCTGCTGTG
At1g77120 R	CGAACTTCGTGTTTCTGCGGT
At2g16060_F	TTTGAGGTGGCCAAGTATGCA
At2g16060_R	TGATCATAAGCCTGACCCCAA
At4g10270_F	ATGGACAGTGGCAGTGAGCATC
At4g10270_R	GTTCCACCGACAAAGACCTAGTTG
sgAt4g32980 F	ACCTCAACGAGGTTTGCCTGAG
sgAt4g32980 R	TCTCCGAATCTTTCGGGTAAGGG
sgAt4g02810 F	TGGCCAAGCTTACCAACATCTTCC
sgAt4g02810 R	AGAAACTCCATCCACCCACGTC
sgAt2g46920 F	ACCGGTAAAGATGAGAGCAGTTC
sgAt2g46920 R	ATCCGCCAAATTTCTTCTTCCAC
sgAt3g60890 F	TGACAACTTCAGAGCCACCATTC
sgAt3g60891 R	ACGAAGCAGATCTCATAGTTGGTG
sgAt2g45450 F	CATTTTCAGACACACCCACGA
sgAt2g45450 R	CTTTTCTCTTCCCGCCACA
sgAt5g67060 F	GGGAGTCGTTATGAAAGGGTGTGG
sgAt5g67060 R	ATCTGTGCATTGCCCACCATCTG
sgAt2g42620 F	CCGGAGACGATAATGAGCACAAGAG
sgAt2g42620 R	TTGGTCCTCGAATCGGCTACAC
sgAt1g70560 F	TTCGTGGTCAATCTGGATCATGG
sgAt1g70560 R	TACACCTGTCACCCATCTTCCTC

sgAt1g23380 F	GTGGAGGTGATCATGAGGTAGCAG
sgAt1g23380 R	TTGAGGTCCCGGTCTTCACATC
sgAt5g47370 F	ACACTCTCAATCCCAAACAGAAGC
sgAt5g47370 R	TGTCTTGCCGTCAAGTTCAGC
sgAt5g65870 F	ACAACTTTCCTCTGCATCATCGC
sgAt5g65870 R	GATGTTGGATTGAGCCGAGCTG
sgAt3g54720 F	AGCCGCAGATGAAGCAAAGAAG
sgAt3g54720 R	ACCCTCTTTCTACAAGCATCAACC
sgSl06g059740 F	CTTCTGGGAAGCTAAGGGTCAA
sgSl06g059740 R	ATGGTCTCCTGGTGCAAGGT
sgSlHK SIEF1a F	GCTGCTGTAACAAGATGGATGC
sgSlHK SIEF1a R	GGGGATTTTGTGAGGGTTGTAA
sgSl07g008240 F	TGGAAAGGTTGTGGTGAGGGATTG
sgSl07g008240 R	TCAAAGTGCTCATCAACCACACC
sgSl02g067440 F	CCTGCTGACGGAGGTAATATGCAC
sgSl02g067440 R	ATCTAGTACGGCGCAAGCTGTC
sgSl02g087740 F	GGTGGCTATGCATGGCTGAAAG
sgSl02g087740 R	GGTCCCTTGTACAATGCTCCAACC

Supplementary Table 7. Full list of the vectors used with their references.

Final construct	Original vector	Reference
iOX ZPR2	pMDC7	7
pZPR2:GFP-GUS	pKGWFS7	43
pHRPEX5:GFP-GUS	pKGWFS7	43
35S:MAC ZPR2	p2GW7	43
35S:REV	p2GW7	43
35S:ATHB8	p2GW7	43
35S:CNA	p2GW7	43
35S:PHV	p2GW7	43
35S:PHB	p2GW7	43
35S:Renilla	p2GW7	43
pZPR1:FLUC	pGWL7	43
35S:MC ZPR2-GFP	PH7FWG2	43
35S:MAC ZPR2-GFP	PH7FWG2	43
pTAA1:GFP-GUS	pHGWFS7	43
pPSK5:GFP-GUS	pHGWFS7	43
pMAX2:GFP-GUS	pHGWFS7	43
pZPR2:ZPR2-GUS	pGWB203	10
pZPR2:ZPR2-FLAG	pGWB510	11
YFPc-ZPR2	pSPYCE-GW	12
YFPn-REV	pSPYNE-GW	12
YFPn-ATHB8	pSPYNE-GW	12
ZPR2-cYFP	pUBN-cYFP-GW	13
PHB-nYFP	pUBN-nYFP-GW	13

Supplementary Table 8. List of author contribution to each experiment reported in the figures.

Figure	Panel	Experiment	Contributing author
Figure 1	a	Oxygen concentration measurements in meristems in the apical-basal direction	D.A.W., O.P.
	b	HRPEX5 GFP imaging in inflorescence meristems	D.A.W.
	c	Plant growth in hyperoxia	D.A.W.
	d	Leaf initiation rate in hyperoxia	D.A.W.
Figure 2	b	Conserved N-terminal domain of ZPR2 and ZPR3-like proteins	F.L.
	c	Quantification of ZPR2-GFP using western blotting	D.A.W.
Figure 3	d	Confocal microscopy analysis of ZPR2-GFP subcellular localisation	D.A.W.
	a	Tissue specific expression of <i>ZPR2</i>	D.A.W.
	b	Meristem specific stability of <i>pZPR2:ZPR2-GUS</i>	N.C.W.K., D.A.W.
	c	Rosette phenotype of wild type, <i>zpr2-2</i> and <i>zpr2-3</i> T-DNA insertion lines	D.A.W., F.L.
Figure 4	d	Leaf initiation rate of wild type, <i>zpr2-2</i> and <i>zpr2-3</i>	D.A.W., F.L.
	a	Transactivation assay showing the effect of ZPR2 on HD-ZIP III activity	A.B.K, Z.N.V., D.A.W.
	b	BiFC assays of ZPR2 and HD-ZIP III	D.A.W.
	c	qRT-PCR analysis of HD-ZIP III target genes in inducible <i>ZPR2</i> overexpressors	D.A.W., N.C.W.K., N.K.P.
Extended data Fig. 1		Benchmarking of the microsensor used in this study against a commercially available OX10 sensor	
	a		O.P.
	c	Oxygen profile in the apical-basal direction of a 4-day seedling	D.A.W.
	d	Tracking of the sensor insertion pattern of oxygen profile (c)	D.A.W.
	e	Lateral oxygen profiles at different positions in the apex region	D.A.W., O.P.
	f	Position of lateral insertion positions of the profiles shown in (e)	D.A.W.
Extended data Fig. 2	a	Differential expression of core hypoxia-inducible genes in SAM, RM, leaf and root tissue	F.L.
	b	Schematic representation of SAM and RM cell types	F.L., D.A.W.
	c	Expression levels of core-hypoxia inducible genes in SAM and RM cell types depicted in (b)	F.L.
Extended data Fig. 3	a	HRPEX5 GUS staining after treatment with different oxygen concentrations	K.M.S.P., D.A.W.
	b	Relative staining intensity of HRPEX5 at 21, 10 and 5% oxygen	K.M.S.P., D.A.W.
	c	Relative staining intensity of HRPEX5 at 21 and 80% oxygen	K.M.S.P., D.A.W.

Extended data Fig. 4	d	Expression of Hypoxia-inducible genes in SAM and leaves after 21 and 80% oxygen treatment	D.A.W.
	a	Oxygen profile in <i>Arabidopsis thaliana</i> inflorescence meristems	D.A.W.
	b	<i>pPCO1:GFP-GUS</i> and <i>pPCO2:GFP-GUS</i> imaging in the SAM	D.A.W.
Extended data Fig. 5	a	Oxygen profiling in tomato micro-tom meristems in the apical-basal direction	D.A.W.
	b	Photo showing the insertion of a microsensor inside a Tomato SAM	D.A.W.
	c	Overlay of an oxygen profile and the microsensor penetration site in a Tomato SAM	D.A.W.
	d	Replicate of (c)	D.A.W.
	e	Expression of Hypoxia-inducible genes in tomato shoot meristems	N.K.P., F.L.
Extended data Fig. 6	a	Multi-alignment of ZPR-type sequences from angiosperm species	F.L.
	b	Phylogenetic tree of ZPR	F.L.
Extended data Fig. 7	a	Relative luciferase activity of a ZPR2-PpLUC fusion	F.L., D.A.W.
	b	Relative GUS activity of ZPR2-GUS fusions	F.L., D.A.W.
	c	Relative staining intensity of GUS stained plants expressing a <i>pZPR2:ZPR2-GUS</i> reporter	D.A.W., N.C.W.K.
	d	Relative mRNA level of the genotypes used for immune-detection of GFP in Fig. 2d under 21 and 2% O ₂	F.L.
	e	Effect of ZPR2 and ZPR2-GUS on the transactivation activity of REVOLUTA	F.L.
Extended data Fig. 8	a	Schematic depiction of <i>zpr2-2</i> and <i>zpr2-3</i> T-DNA insertion sites and the primers used for their detection	Z.N.V., F.L.
	b	Genotyping of <i>zpr2-2</i> and <i>zpr2-3</i> T-DNA insertion lines	Z.N.V., F.L.
	c	Amplification of the ZPR2 coding sequence in the wild type, <i>zpr2-2</i> and <i>zpr2-3</i> genotypes	Z.N.V., F.L.
	d	Relative mRNA levels of ZPR2 in wild type, <i>zpr2-2</i> and <i>zpr2-3</i>	Z.N.V., F.L.
	e	Progression of leaf production in wild type, <i>zpr2-2</i> and <i>zpr2-3</i>	D.A.W., F.L.
	f	Phenotypes of wild type, <i>zpr2-3</i> and <i>pZPR2:ZPR2-FLAG</i> in <i>zpr2-3</i> genotypes	D.A.W., A.B.K
	g	Leaf initiation rate of wild type, <i>zpr2-3</i> and <i>pZPR2:ZPR2-FLAG</i> in <i>zpr2-3</i> genotypes	D.A.W., A.B.K
	h	Phenotypes of wild type and ZPR2 overexpressors on agarized MS under 21 and 2% oxygen	D.A.W.
	i	Percentage of meristem termination in wild type and ZPR2 overexpressors under 21 and 2% oxygen	D.A.W., F.L.

Extended data Fig. 9	a	Schematic representation of the experimental setup of <i>ZPR2</i> inducible overexpression	D.A.W., F.L.
	b	Combined effect of <i>ZPR2</i> induction and hypoxia treatment on <i>pHEC1</i> and <i>pPSK5:GUS</i> reporters	D.A.W., F.L.
	c	<i>pTAA1:GUS</i> activity in wild type and <i>ZPR2</i> inducible overexpressors	D.A.W., F.L.
Extended data Fig. 10	a	Expression of HD-ZIP III target genes in wild type <i>zpr2-3</i> shoot apices	D.A.W.
	b	<i>pMAX2:GUS</i> activity in wild type <i>zpr2-3</i> genotypes	D.A.W., F.L.

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