

Supplemental Figure 1. Scheme for laser microdissection of leaf primordial domains.

(A) Lateral section of maize shoot apex processed for LCM. Boxes indicate regions selected for microdissection. Pre-ligule tissue (red box) was microdissected from 100 µm high rectangles, centred on the PLB. Pre-blade (green) and pre-sheath (blue) tissue was taken from 100 µm rectangles 50µm above and below the preligule selection respectively. For the comparison of wild-type and *Ig1-R* transcriptomes, tissue between 400-900 µm from the base of P6 leaf primordia was microdissected from lateral sections (purple dashed line). Numbers in white boxes are automated annotations inserted by the P.A.L.M. laser-microdissection system. (B) Cartoon illustrating plane of lateral section through shoot apex (green dashed line). Red circle = midrib, red arrowhead indicates margins of grey leaf primordium. (C) Preligule region of P7 primordium before microdissection. Arrowhead indicates position of PLB. (D) Red outline indicates region selected for microdissection. (E) Primordium after microdissection of preligule region. The circles in (E) indicate locations of laser pulses during microdissection. SAM = shoot apical meristem. P indicates plastochron number. Scale bar in (A) = 300 µm.

Supplemental Data. Johnston et al. (2014). Plant Cell 10.1105/tpc.114.132688

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	2 > >	CDMZM # Nama
Α	* *	2G036297 ZIII Lg1
	·····	
	* *	2G101511 Zm Iga1
	^ ^ ^	2G067624 Zm Sbp29
		2G168229 Zm Sbp26
	* *	2G169270 Zm Sbp16
	* *	2G148467 Zm Sbp21
	<u>о п о</u>	Homeobox TF (adaxial epidermis)
	دَ دَ هَ	Name
В	* *	GRMZM # Zm Ns1
-	* * *	2G069028 Zm Hb82
	* *	2G122537 At HB9
	* *	2G029692 Zm Hb11
	* *	2G127537 Zm Hb69/ At REV
	* *	2G469551 Zm Bel14
	* *	2G125976 Zm Bel12
	* *	2G154641 At PHB
	*	2G423337 Zm Ocl5a
	* *	2G130442 Zm Hb91/At ATML 1
	* *	2G122807 Zm Ool1
	* *	20122097 ZIII 0017 20026643 Zm 00/2
	*	20020043 ZIII 003
	*	2G110058 ZIII HD/5/ ALPDF2
	*	2G001289 Zm Hb54
	* *	2G041127 Zm Hb5
	* *	2G132367 <i>Os HDZipI-1</i>
	* *	2G127776 Zm Hb83
	* *	2G126646 Zm Hb102
	* *	2G139963 Zm Hb49
	*	2G097349 Zm Hb4
		2G106276
	<u>о п о</u>	ARF TF (adaxial epidermis)
	دَ دَ هُ	GRMZM # Name
С	* *	2G034840 At ARF5/MP
Ŭ	* * *	2G441325 At ARF3
	* *	2G030710 Zm ARF3a/ At ARF3
	* *	2G378580 At ARF2
	* *	2G035405 At ARF6
	* *	2G086949 At ABE5/MP
	*	2G352159 At ARF2
	* *	2G102845 At ABE19
	*	2G475882 At ARF6
	*	2G159399 At ABE16
	*	2G338259 At ARE2
	* *	2G078274 At ARE8
	<u>о Ш о</u>	Gibberellin (all cell layers)
	دَ دَ هَ	♀ GRMZM # Name
D	* *	2G093195 Zm Dwarf plant3
-	* *	2G152354 At GA2ox1
	* * *	2G031724 At GA20x1
	* *	2G006964 At $GA20x8$
	* *	$2G060940 \Omega_{c} GA20ax^{2}$
	* *	20000940 03 0A200A2
	* *	2G150088 US GASH2
	* *	2010/003 US 0A3H4
	*	2G001426 Zm Gras46
	* *	2G036340 At GA30X1
		2G022679AtGA2ox1
	sυ	Cutokinin (adavial anidarmia)
	~ ~ ~	GRM7M # Name
-		
E	* *	20024470 ZM 0K040/AI UKX5
	* *	20129904 ALAMMY
	*	
	*	20348452 At UKX5
	*	2G1/3/10 At HP4
		2G4/1529 Zm HK2/At HK3
	log fold	hange
		-

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Supplemental Figure 2. Expression profiles for DE genes.

(A) Expression profiles for DE Sbp family genes (all-cell-layers LM). (B) Expression profiles for DE homeobox transcription factor family genes (epidermis-only LM). (C) Expression profiles for DE ARF transcription factor genes (epidermis-only LM). (D) Expression profiles for DE gibberellinrelated genes (all-cell-layers LM). (E) Expression profiles for DE cytokinin-related genes (epidermisonly LM). (F) In situ hybridisation of Zm sbp3 in longitudinal section through leaf primordium with developing liqule. BvS= blade relative to sheath. LvB=ligule relative to blade, LvS=ligule relative to sheath, *Ig1=Ig1-R* mutant relative to wild-type sibling. * indicates P<0.05. "*Zm*" indicates maize gene name, "At" indicates name of closest Arabidopsis gene, "Os" indicates name of closest rice gene. Scale bar in (F) =100 µm



Supplemental Figure 3. In situ hybridisation of the ZmPHB gene.

(A) Longitudinal section through shoot apex shows transcript accumulation on the adaxial side of young leaf primordia, in vasculature and in the PLB of P8 leaf primordium. (B) Longitudinal section through leaf primordium at midrib. (C) Longitudinal section through PLB near margins of P8 primordium. Arrow indicates transcript accumulation in provascular strand. Arrowheads indicate PLB at margins. Asterisk indicates preligule region at midrib. P indicates plastochron number. Scale bar in (A) = 500 μ m. Scale bars in (B-C) = 100 μ m.



Supplemental Figure 4. Ligule genes overlap with genes implicated in regulation of branching.

(A) Overlap between genes that are DE (up- or down-regulated) in the ligule region (blue), DE in *ra1*1-mm ears (yellow) and DE in *ra1*2-mm ears (green). (B) Overlap between genes that are DE in the ligule region (blue), DE between tassel primordia and 1-mm ears (yellow) and DE between tassel primordia and 2-mm ears. (C) Overlap between genes that are DE in *lg1-R* mutants (blue), DE in *ra1*1-mm ears (yellow) and DE in *ra1* 2-mm ears (green). (D) Overlap between genes that are DE in *lg1-R* mutants (blue), DE in *ra1*1-mm ears (yellow) and DE in *ra1* 2-mm ears (green). (D) Overlap between genes that are DE in *lg1-R* mutants (blue), DE between tassel primordia and 2-mm ears.

Supplemental Table 1. Primer sequences used for synthesis of *in situ* hybridisation probes.

Gene ID	Primer name	Primer sequence
GRMZM2G036297	Lg1-F7	GTCCCCTACGCATCCATTT
	Lg1-R6	CCGTACGTGTAGCCTCCTCT
GRMZM2G393433	Cuc2-F1	TACCATTTCCTCCCCAGCTC
	Cuc2-R1	GAACGACGACCCAGTCACTT
GRMZM2G101682	UN1-F1	ATCATCACACCCAACGCAAC
	UN1-R1	CACACAAGCCCTAACGTGAC
GRMZM2G039867	BOP-like-F1	CACGTGGAGCCCAACAAG
	BOP-like-R1	GCCGCATGCTACAACAACT
GRMZM2G087741	Lg3-F1	TCCTACGGAGGAAGACAAGG
	Lg3-R1	AAGCCCTTCAGCCTATCTAACA
GRMZM2G154641	BEL12-F1	GTAGCAGTGTGGGTGCCTTC
	BEL12-R1	ATTTGATAGCACGCCTGGAC
GRMZM2G125976	BEL14-F2	CAGCAGCAGAACCACCACT
	BEL14-R2	ACATGTGTTAACGCCACACC
GRMZM2G103773	BR6Ox2-F1	ACCACTCTTCCCCTCTCCTC
	BR6Ox2-R1	TGGAGCCCTTTGCTGTAGTT
GRMZM2G107199	DWF4-F1	TCCCCTGCCTTCTGCTACTA
	DWF4-R1	ACACAGGGGCCCTTCTTTT
GRMZM2G152354	GA2Ox-F1	CGGGTGTCCATGGTCTTCTT
	GA2Ox-R1	CATTGGTGGCTGTGCGTAAT
GRMZM2G101499	SBP3-F1	ATCATCCTGTCGTGCTCCTC
	SBP3-R1	TTGTCGCTGGATAATGCAAA