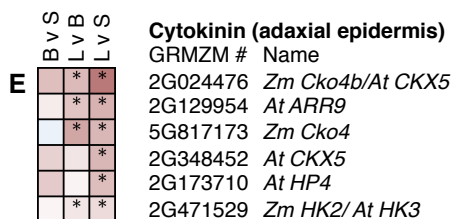
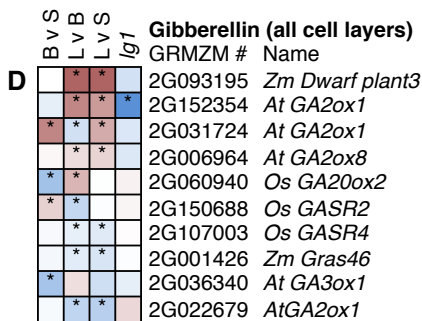
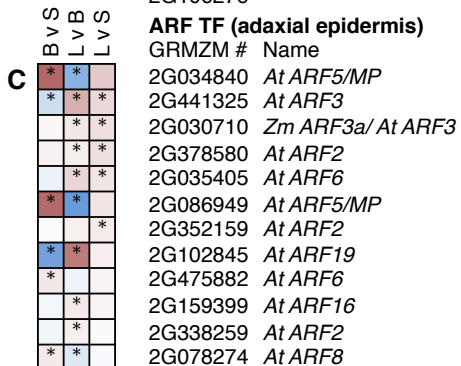
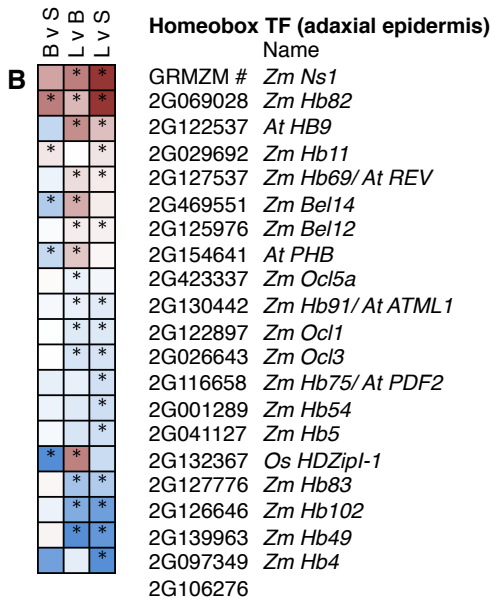
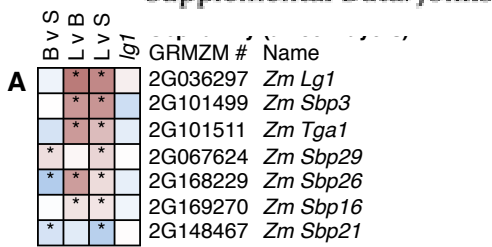
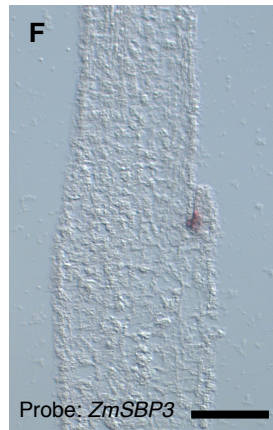
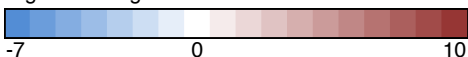


Supplemental Figure 1. Scheme for laser microdissection of leaf primordial domains.

(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.

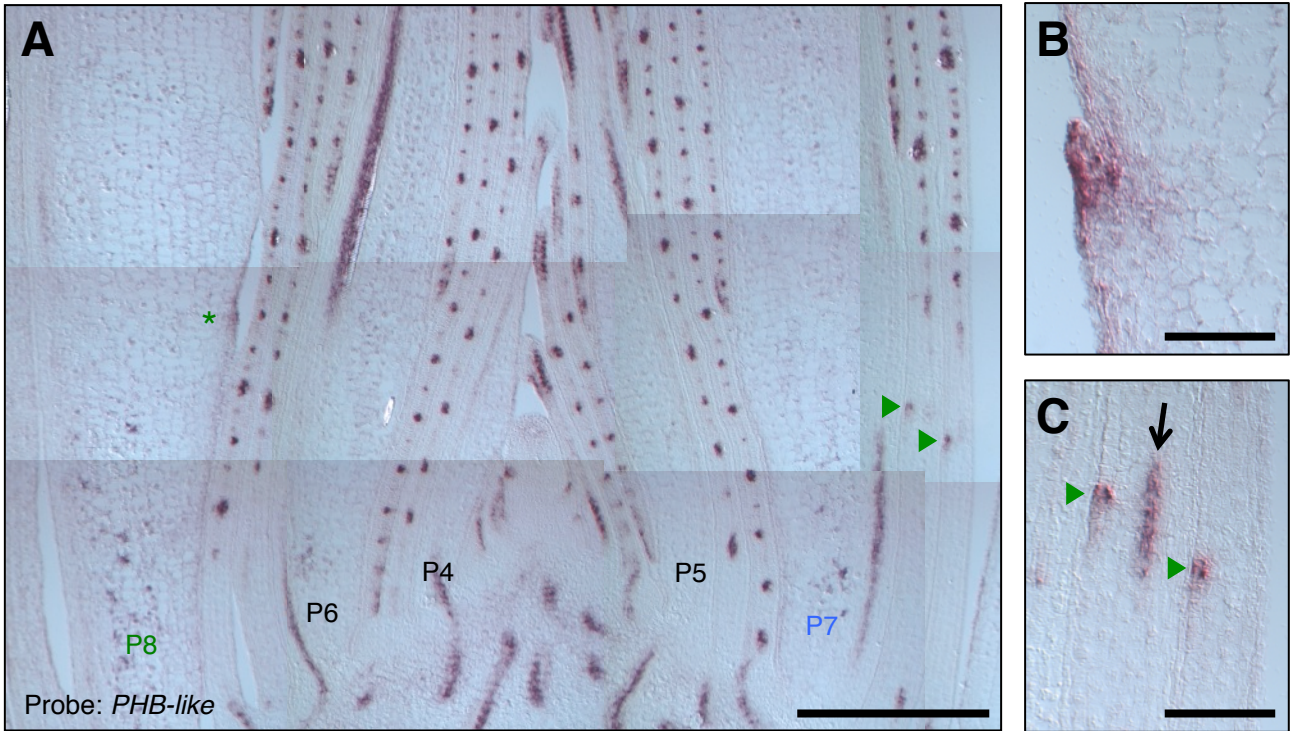


log fold change



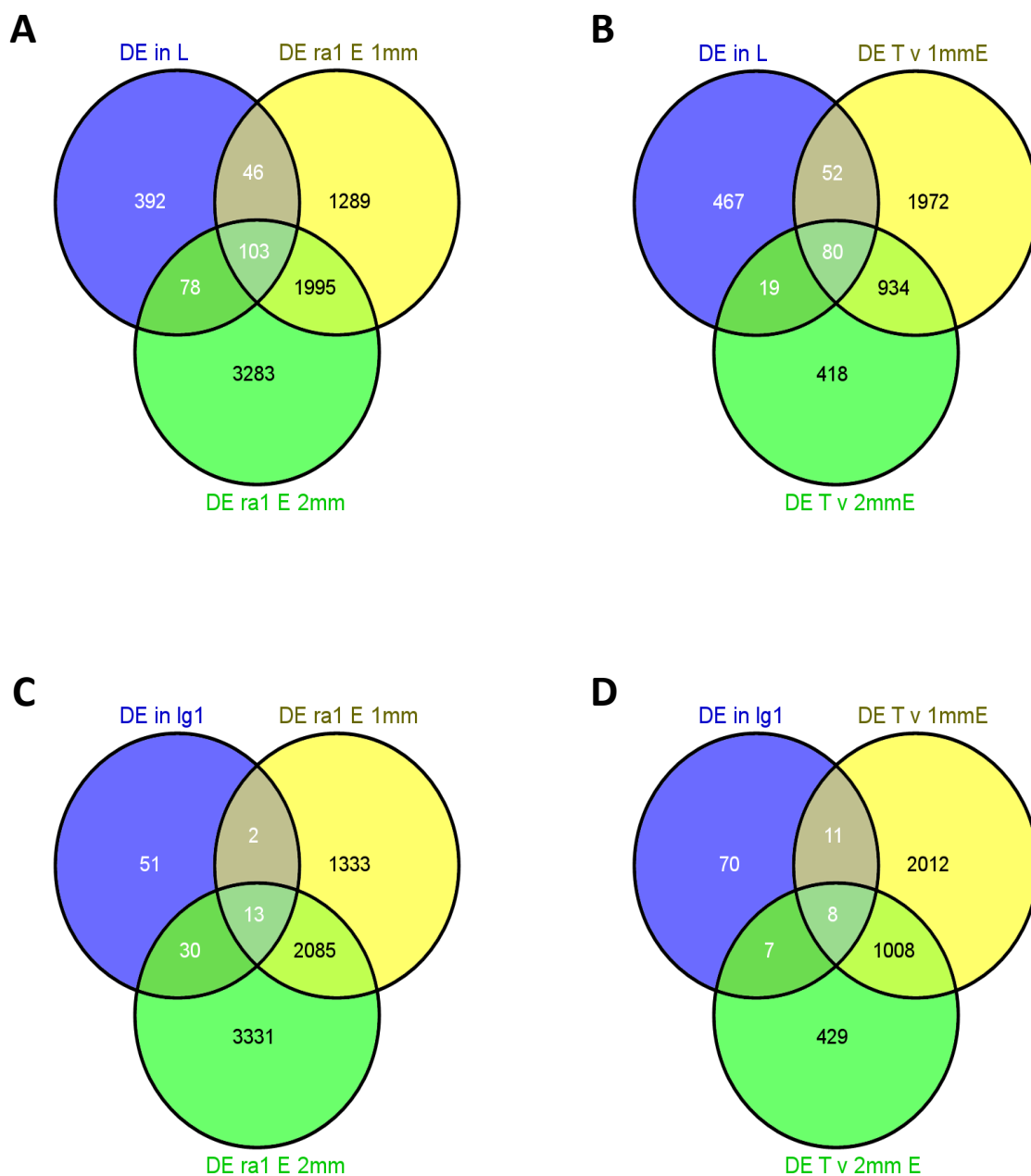
Supplemental Figure 2. Expression profiles for DE genes.

(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 gibberellin-related genes (all-cell-layers LM). (E) Expression profiles for DE cytokinin-related genes (epidermis-only LM). (F) In situ hybridisation of *Zm sbp3* in longitudinal section through leaf primordium with developing ligule. BvS= blade relative to sheath, LvB=ligule relative to blade, LvS=ligule relative to sheath, *lg1=lg1-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 μ m



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*-1mm 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*-1mm 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 1-mm ears (yellow) and 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	TACCATTTCTCCCCAGCTC
	Cuc2-R1	GAACGACGACCCAGTCACTT
GRMZM2G101682	UN1-F1	ATCATCACACCCAACGCAAC
	UN1-R1	CACACAAGCCCTAACGTGAC
GRMZM2G039867	BOP-like-F1	CACGTGGAGCCCAACAAG
	BOP-like-R1	GCCGCATGCTACAACAAC
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	ACACAGGGGCCCTTCTTTTT
GRMZM2G152354	GA2Ox-F1	CGGGTGTCCATGGTCTTCTT
	GA2Ox-R1	CATTGGTGGCTGTGCGTAAT
GRMZM2G101499	SBP3-F1	ATCATCCTGTCGTGCTCCTC
	SBP3-R1	TTGTCGCTGGATAATGCAAA