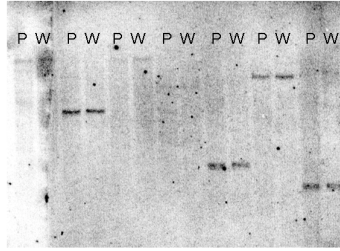


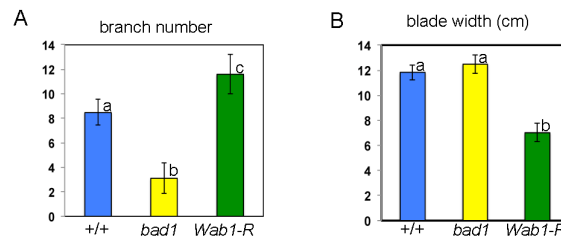
**Figure S1. Phenotype and LG1 accumulation in *lg2-R* leaves.**

A) Leaves of *lg2-R* plants develop ligule and auricle only at the margin (right).  
B) Accumulation of LG1 is only detected in the narrow marginal domains of *lg2* leaves. C, D) In transverse sections, LG1 accumulation typically appears in one side of a leaf at a time. This accumulation pattern reflects the phenotype of *lg2* mutant plants in which the marginal ligule has displaced symmetry across the midrib, with ligule higher on one side than the other.



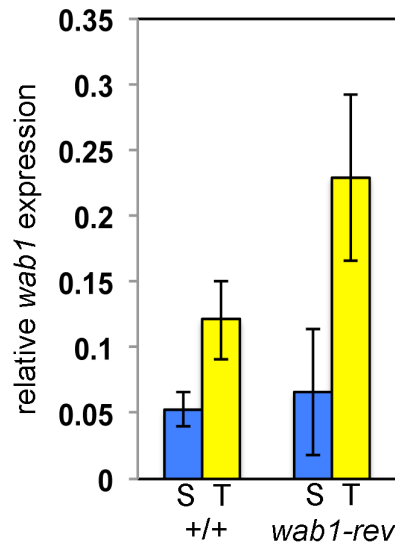
**Figure S2. Southern blot analysis of *wab1* mapping interval.**

DNA from *Wab1-R* homozygotes and their progenitor, PF4902, was digested with 7 enzymes (from left to right: *Bste II*, *EcoRI*, *EcoRV*, *HindIII*, *NcoI*, *SstI* and *Xba*) electrophoresed, blotted and hybridized with a 5' fragment of *wab1*. No differences were detected.



**Figure S3. Quantification of tassel branch number and blade width.**

Maize plants from family 1013, segregating *A619/wab1-bad1* (+), *wab1-bad1/wab1-bad1* (*bad*), *Wab1-R/A619* or *Wab1-R/wab1-bad1* (*Wab1-R*), were scored for tassel branch number and mid-blade width. Tassel branch number is significantly different between each genotype (A) while significant differences in leaf width at mid-blade can be seen when comparing *A619/wab1-bad1* or *wab1-bad1* to *Wab1-R/wab1-bad1* (B). Standard deviation is shown. Significance is indicated by letter (A, B or C): each letter is significantly different from another letter (i.e. B is similar to B but significantly different from A or C at  $p < 0.001$ ).



**Figure S4. *wab1* expression in *wab1-rev* shoots and tassels.**

Quantitative real time PCR analysis of *wab1* in *wab1-rev* seedlings (S) or tassels (T) compared to normal siblings shows that ectopic expression caused by the *Wab1-R* mutation remains in the tassel but not seedlings. This suggests that in the leaf, an active DNA binding domain is required to keep *wab1* levels high. Standard deviations are shown in graphs.



**Figure S5. LG1 accumulates in *wab1-rev* leaves.**

Wild-type (A, +/+) and *wab1-rev* (B) leaves both accumulate LG1 at the blade sheath boundary. Longitudinal sections off-centered from the SAM reveal the earliest signs of LG1 accumulation. Figure 5 J,K are a zoom in taken from these images.

**Table S1. Oligonucleotides used in this study.**

Primer	Sequence
P1	GTGTGGGAGTTCTTGGGAGA
P2	TGCACGACCCAGTGTATTGT
P3	CACCATGTTGCCGTACCCTAACAACCC
P4	CCAACTTCTCGGCAACTCCTC
P5	ACATAAAACGCTCCCCACTG
P6	TGGCAGTACGACGACACCTA
P7	GGGGAGGCAAAGTAGATCC
P8	GCTCGATAAAAAGGCACCAC
P9	CTCTCACATCTTTCTGCTTCCTG
P10	CGGCAGGCAGACTACCGTT
P11	GAGCGACGACGCAGCTTT
P12	AGTAACGTCAAAGCACAAGATCAG
P13	TCCAGGAAATCACCGTCTTC
P14	AGCGACGACGCAGCTTTCTCA
P15	GCTAAAGACAAAGCAGAGAG
P16	CTAGTGATCGAAGTCGAGATC
P17	CCTGCTTCTCATGGATGGTT
P18	TGGTAGCAGGAAGGGAAACA
P19	CACCATGATGAACCTATCGGCTGCCG
P20	CTAGTGATCGAAGTCGAGATCAAAC