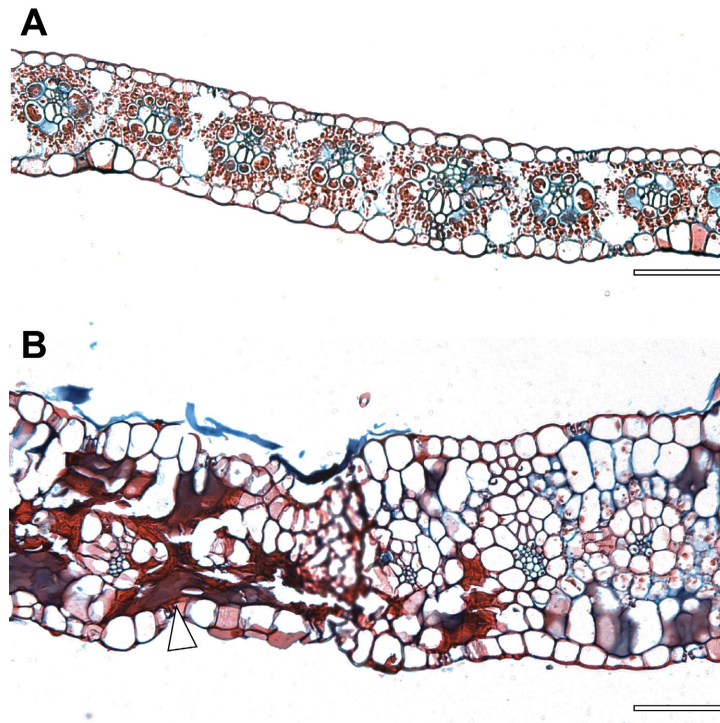


**Supplemental Figure 1.** Additional Phenotypes of *rte-1* and *rte-2* Mutants.

(A) Tassel of wild-type sibling and (B) *rte-2* mutant.

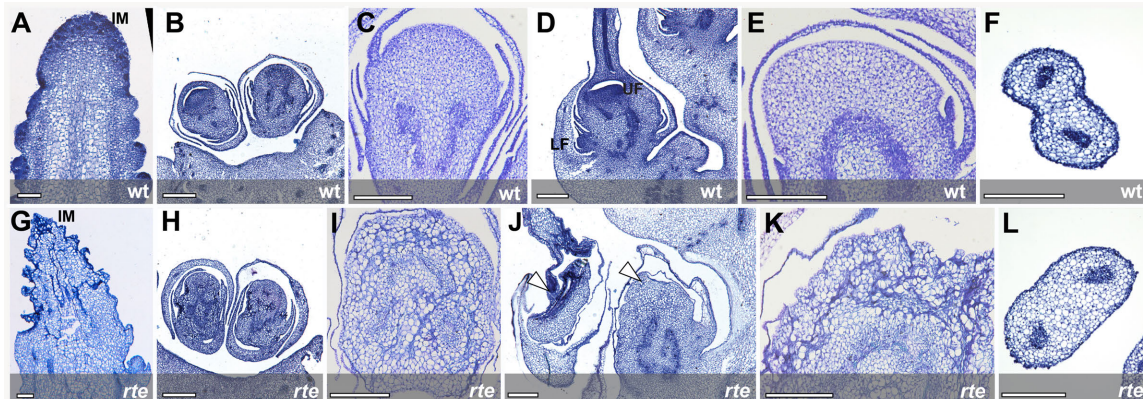
(C) and (D) Wild-type and *rte-2* spikelets showing two florets with stamens. Gl: glume; st: stamens.

(E) and (F) Wild-type ears are borne at the tip of a primary lateral branch (E). In *rte* mutants, several ears (arrowheads) are borne on the primary lateral branch, due to activation of secondary axillary buds (F).



**Supplemental Figure 2.** *rte* Leaf Sections.

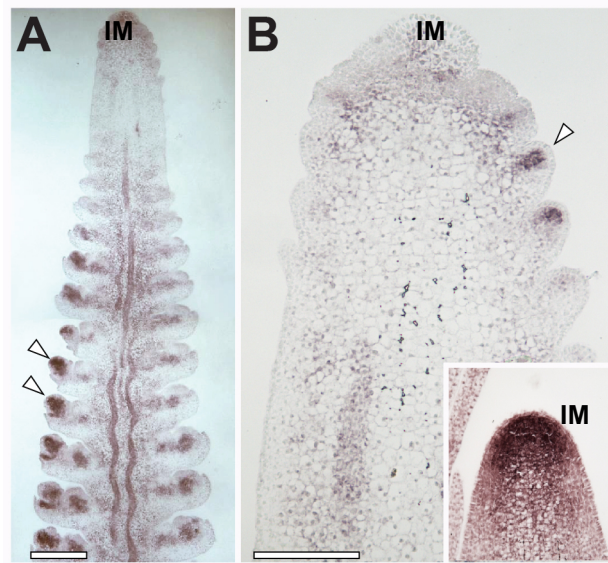
(A) and (B) Cross sections of leaves stained with Safranin O/Alcian Blue. Lignified red patches (arrowhead) are observed in *rte* mutant leaves. Scale bars: 100 $\mu$ m



**Supplemental Figure 3.** Histological Analysis of *rte* Reproductive Development.

(A) and (E) Sections of ear tips in wild-type and *rte* mutants stained with Toluidine blue, showing the collapse of the inflorescence meristem (IM) and axillary meristems in *rte*. Scale bars: 100  $\mu$ m.

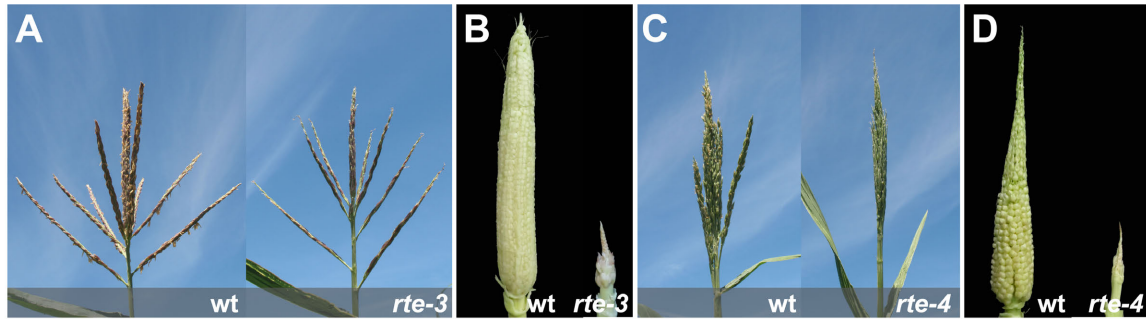
(B-F) and (G-L) Sections of developing spikelets and florets from wild-type and *rte-1* stained with Toluidine blue. (B,C) and (F,I) Cross sections of paired spikelets. The sections are taken from the middle of developing spikelets. Note that in (H) the spikelets have begun to shrink at the margins, and in (I) the internal tissue organization is disrupted when compared to wild type (C). (D,E) and (J,K) Longitudinal sections of developing florets (D,J) and floral meristems (E,K). In the *rte* mutant (J) the meristems and developing floral organs have collapsed (arrowheads) and the tip of the meristems is wrinkly and its structure disrupted (K). UF: upper floret; LF: lower floret. (F) and (L) Cross sections of silks from wild-type and *rte* appear morphologically similar. Scale bars: 200 $\mu$ m.



**Supplemental Figure 4.** In Situ Hybridizations of *rte-1* Ears Probed With the Meristem Marker *knotted1* (*kn1*).

**(A)** Immature ears showing *kn1* expression in spikelet meristems (arrowheads) and vasculature.

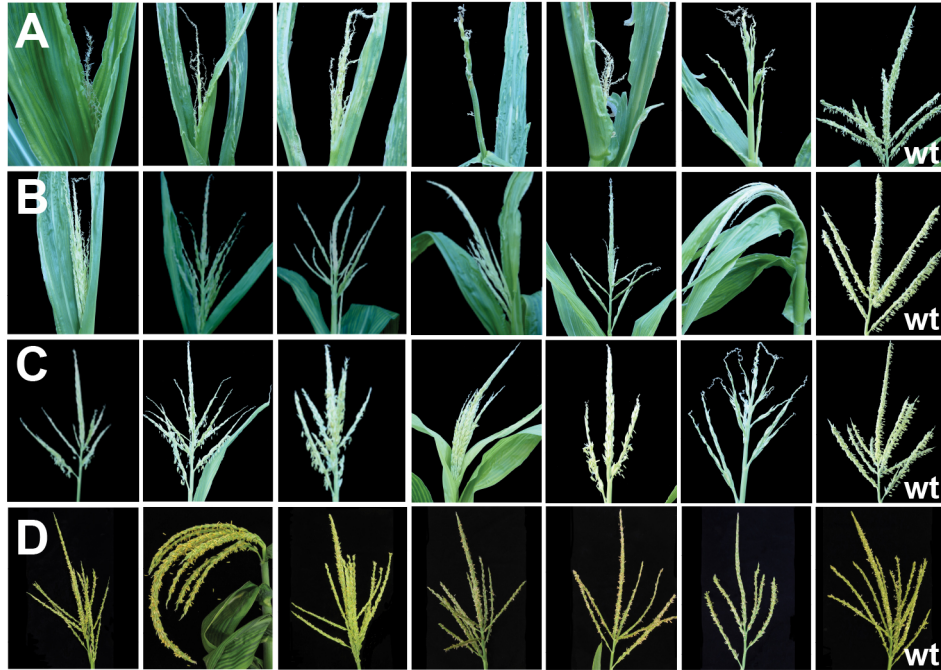
**(B)** Close-up view of a mutant *rte-1* inflorescence meristem. Strong *kn1* expression is only observed in SPMs (arrowhead) of the mutant but not in the inflorescence meristem where *kn1* expression is normally strong. The IM in this ear sample (~1cm stage) has already started to collapse. Inset: *kn1* in wild type inflorescence meristem (IM). Scale bars 200 $\mu$ m.



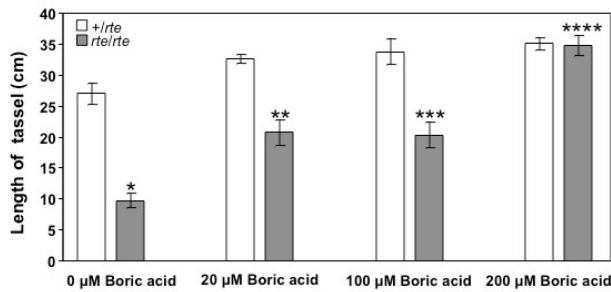
**Supplemental Figure 5.** The Tassel and Ear Phenotype of *rte-3* and *rte-4*.  
(A) Wild type (left) and *rte-3* (right) tassels in an A632 background.  
(B) Corresponding wild-type (left) and *rte-3* (right) unfertilized ears.  
(C) Wild type (left) and *rte-4* (right) tassels in an A619 *ramosa2-R* background.  
(D) Corresponding wild-type (left) and *rte-4* (right) unfertilized ears.

GRMZM2G166159_RTE	1	MEESFVPLRGIKNDLHGRACYKQDWTGGFRAGIRILAPTTYIFFASAIPVISFGEQLER
GRMZM2G082203	1	MEESFVPLRGIKNDLHGRACYKQDWTGGFRAGIRILAPTTYIFFASAIPVISFGEQLER
Sb08g018440	1	MEESFVPLRGIKNDLHGRACYKQDWTGGFRAGIRILAPTTYIFFASAIPVISFGEQLER
Os12g37840	1	MEESFVPLRGIKNDLHGRACYKQDWTGGFRAGIRILAPTTYIFFASAIPVISFGEQLER
AT2G47160_BOR1	1	MEETFVPEFEGIKNDLHGRACYKQDWTGGFRAGIRILAPTTYIFFASAIPVISFGEQLER
GRMZM2G166159_RTE	61	NTDGVLTAVQTLASTALCGIHSIVGGOPLLILGVAEPTVLMYTFMNFPAKDRPDLGRNL
GRMZM2G082203	61	NTDGVLTAVQTLASTALCGIHSIVGGOPLLILGVAEPTVLMYTFMNFPAKDRPDLGRSL
Sb08g018440	61	NTDGVLTAVQTLASTALCGIHSIVGGOPLLILGVAEPTVLMYTFMNFPAKDRPDLGRNL
Os12g37840	61	NTDGVLTAVQTLASTALCGIHSIVGGOPLLILGVAEPTVLMYTFMNFPAKDRPDLGRNL
AT2G47160_BOR1	61	STDGVLTAVQTLASTALCGIHSIVGGOPLLILGVAEPTVLMYTFMNFPAKDRPDLGRNL
		<i>rte-1</i> frameshift
GRMZM2G166159_RTE	121	FLAWTGWVCVWTAILLFLLAAILGACSIINRFTRVAGELFGLLIAMLFMQQAIKGLVDFER
GRMZM2G082203	121	FLAWTGWVCVWTAILLFLLAAILGACSIINRFTRVAGELFGLLIAMLFMQQAIKGLVDFER
Sb08g018440	121	FLAWTGWVCVWTAILLFLLAAILGACSIINRFTRVAGELFGLLIAMLFMQQAIKGLVDFER
Os12g37840	121	FLAWTGWVCVWTAILLFLLAAILGACSIINRFTRVAGELFGLLIAMLFMQQAIKGLVDFER
AT2G47160_BOR1	121	FLAWSGWVCVWTAILLFLLAAILGACSIINRFTRVAGELFGLLIAMLFMQQAIKGLVDFER
GRMZM2G166159_RTE	181	VPERENRKALEFVPSWRFANGMFAIVLSFGLLLTALRSRKARSWRYGTGWLRFIADYGV
GRMZM2G082203	181	IPERENRKALEFVPSWRFANGMFAIVLSFGLLLTALRSRKARSWRYGTGWLRFIADYGV
Sb08g018440	181	IPERENRKALEFVPSWRFANGMFAIVLSFGLLLTALRSRKARSWRYGTGWLRFIADYGV
Os12g37840	181	IPERENRKALEFVPSWRFANGMFAIVLSFGLLLTALRSRKARSWRYGTGWLRFIADYGV
AT2G47160_BOR1	181	IPERENRKALEFVPSWRFANGMFAIVLSFGLLLTALRSRKARSWRYGTGWLRFIADYGV
GRMZM2G166159_RTE	241	PLMVLVWCGVSYIPYGNVPGKIPRRLFSPNPWSPGAYDNWTVIKDMTQVPLLYITIGAFIP
GRMZM2G082203	241	PLMVLVWCGVSYIPYGNVPGKIPRRLFSPNPWSPGAYDNWTVIKDMTQVPLLYITIGAFIP
Sb08g018440	241	PLMVLVWCGVSYIPYGNVPGKIPRRLFSPNPWSPGAYDNWTVIKDMTQVPLLYITIGAFIP
Os12g37840	241	PLMVLVWCGVSYIPYGNVPGKIPRRLFSPNPWSPGAYDNWTVIKDMTQVPLLYITIGAFIP
AT2G47160_BOR1	241	PLMVLVWCGVSYIPYGNVPGKIPRRLFSPNPWSPGAYDNWTVIKDMTQVPLLYITIGAFIP
		<i>rte-3</i> W to stop
GRMZM2G166159_RTE	301	ATMIAVLVYFDHVSASQLAQQEFNLRKPPSFHYDLLLLGFLTLMCGLIGIPPSNGVIIQ
GRMZM2G082203	301	ATMIAVLVYFDHVSASQLAQQEFNLRKPPSFHYDLLLLGFLTLMCGLIGIPPSNGVIIQ
Sb08g018440	301	ATMIAVLVYFDHVSASQLAQQEFNLRKPPSFHYDLLLLGFLTLMCGLIGIPPSNGVIIQ
Os12g37840	301	ATMIAVLVYFDHVSASQLAQQEFNLRKPPSFHYDLLLLGFLTLMCGLIGIPPSNGVIIQ
AT2G47160_BOR1	301	ASMIAVLVYFDHVSASQLAQQEFNLRKPPSFHYDLLLLGFLTLMCGLIGIPPSNGVIIQ
		<i>rte-2</i> Q to stop
GRMZM2G166159_RTE	361	SPMHTKSLATLKHQLLRNRLVATARKMSQNASLSQLYGSMQDAYQQMOTPLVYQQQSVR
GRMZM2G082203	361	SPMHTKSLATLKHQLLRNRLVATARKMSQNASLSQLYGSMQDAYQQMOTPLVYQQQSVR
Sb08g018440	361	SPMHTKSLATLKHQLLRNRLVATARKMSQNASLSQLYGSMQDAYQQMOTPLVYQQQSVR
Os12g37840	361	SPMHTKSLATLKHQLLRNRLVATARKMSQNASLSQLYGSMQDAYQQMOTPLVYQQQSVR
AT2G47160_BOR1	361	SPMHTKSLATLKHQLLRNRLVATARKMSQNASLSQLYGSMQDAYQQMOTPLVYQQQSVR
		<i>rte-4</i> S to L
GRMZM2G166159_RTE	421	RGLNELKDSTVOLASSMGNIDAPVDETVDFIEKEIDDLLPIEVKEQRLSNLLOASMVGGC
GRMZM2G082203	421	RGLNELKDSTVOLASSMGNIDAPVDETVDFIEKEIDDLLPIEVKEQRLSNLLOASMVGGC
Sb08g018440	421	RGLNELKDSTVOLASSMGNIDAPVDETVDFIEKEIDDLLPIEVKEQRLSNLLOASMVGGC
Os12g37840	421	RGLNELKDSTVOLASSMGNIDAPVDETVDFIEKEIDDLLPIEVKEQRLSNLLOASMVGGC
AT2G47160_BOR1	418	QGLNELKDSTVOLASSMGNIDAPVDETVDFIEKEIDDLLPIEVKEQRLSNLLOASMVGGC
GRMZM2G166159_RTE	481	VAAMPLKKIPTSVLWGYFAPMAIESLPGNQFWERILLFTAPSRRYKVLEBYHTTFVET
GRMZM2G082203	481	VAAMPLKKIPTSVLWGYFAPMAIESLPGNQFWERILLFTAPSRRYKVLEBYHTTFVET
Sb08g018440	481	VAAMPLKKIPTSVLWGYFAPMAIESLPGNQFWERILLFTAPSRRYKVLEBYHTTFVET
Os12g37840	480	VAAMPLKKIPTSVLWGYFAPMAIESLPGNQFWERILLFTAPSRRYKVLEBYHTTFVET
AT2G47160_BOR1	478	VAAMPLKMIPTSVLWGYFAPMAIESLPGNQFWERILLFTAPSRRYKVLEBYHTTFVET
GRMZM2G166159_RTE	541	VPFKTIAMFTVFQTAVLLVCFGITWPIAGVLFPLMIMLLVVPVROYILPKLFKGAHLTDL
GRMZM2G082203	541	VPFKTIAMFTVFQTAVLLVCFGITWPIAGVLFPLMIMLLVVPVROYILPKLFKGAHLTDL
Sb08g018440	541	VPFKTIAMFTVFQTAVLLVCFGITWPIAGVLFPLMIMLLVVPVROYILPKLFKGAHLTDL
Os12g37840	540	VPFKTIAMFTVFQTAVLLVCFGITWPIAGVLFPLMIMLLVVPVROYILPKLFKGAHLTDL
AT2G47160_BOR1	538	VPFKTIAMFTVFQTAVLLVCFGITWPIAGVLFPLMIMLLVVPVROYILPKLFKGAHLTDL
GRMZM2G166159_RTE	601	DAAEYEESPAIPFSLAAQDIDVALGRSQ-SAEILDDMVTRSRGEIKRLNSPKITSSGGTP
GRMZM2G082203	601	DAAEYEESPAIPFSLAAQDIDVALGRSQ-SAEILDDMVTRSRGEIKRLNSPKITSSGGTP
Sb08g018440	601	DAAEYEESPAIPFSLAAQDIDVALGRSQ-SAEILDDMVTRSRGEIKRLNSPKITSSGGTP
Os12g37840	600	DAAEYEESPAIPFSLAAQDIDVALGRSQ-SAEILDDMVTRSRGEIKRLNSPKITSSGGTP
AT2G47160_BOR1	598	DAAEYEESPAIPFSLAAQDIDVALGRSQ-SAEILDDMVTRSRGEIKRLNSPKITSSGGTP
GRMZM2G166159_RTE	660	VAEKLGIRSPSTSEKAYSPRLTEIHERSPLGGRSPRT----PSKLGEGSAPK
GRMZM2G082203	660	VAEKLGIRSPSTSEKAYSPRVTEIHERSPLGGRSPRT----PSKLGEGSAPK
Sb08g018440	660	VAEKLGIRSPSTSEKAYSPRLTEIHERSPLGGRSPRT----PSKLGEGSAPK
Os12g37840	658	VAEKLGIRSPSTSEKAYSPRTEIHERSPLGGRSPRTGETRSKLGEGSAPK
AT2G47160_BOR1	658	VNNRS--LSQVFSRVSIGIRLGGQSPRVVG----NSPKPASCGRSPLNQSSEN-

**Supplemental Figure 6.** Protein sequence alignment of BOR1 homologs in different species. The lesions of all four *rte* alleles are indicated in red. In green are marked the putative transmembrane domains. Sb, *Sorghum*; Os, *Oryza*; AT, *Arabidopsis thaliana*.

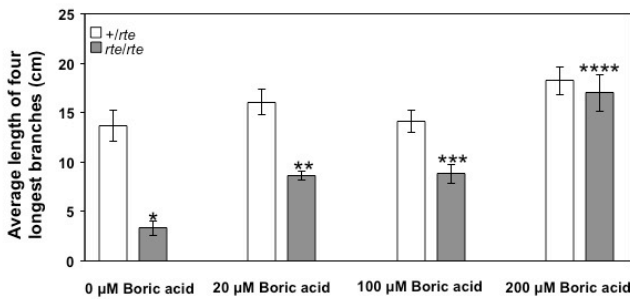
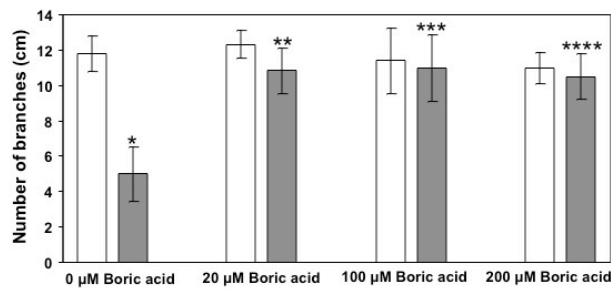


**Supplemental Figure 7.** Rescue of the *rte-1* Tassel Phenotype. (A) to (D) Six representative *rte-1* tassels from plants grown at different concentration of boric acid: (A) 0 $\mu$ M; (B) 20 $\mu$ M; (C) 100 $\mu$ M; (D) 200 $\mu$ M. A wild type tassel grown under same conditions is shown in the far right panel.

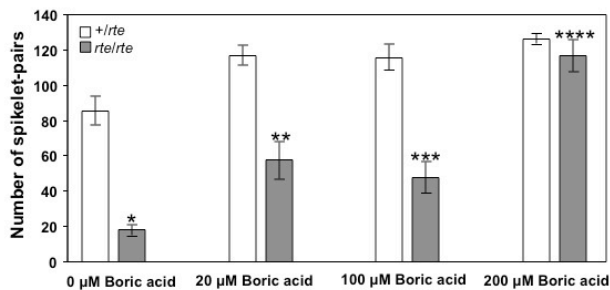


**Supplemental Figure 8. Rescue of the *rte-1* Tassel Phenotype.** Quantification of tassel length, number of primary branches, length of primary branches and number of spikelet-pairs. Error bars, standard error.

\*ttest, P=0.00001168; \*\*ttest, P=0.0002171; \*\*\*ttest, P= 0.001377, \*\*\*\*ttest, P= 0.8905144

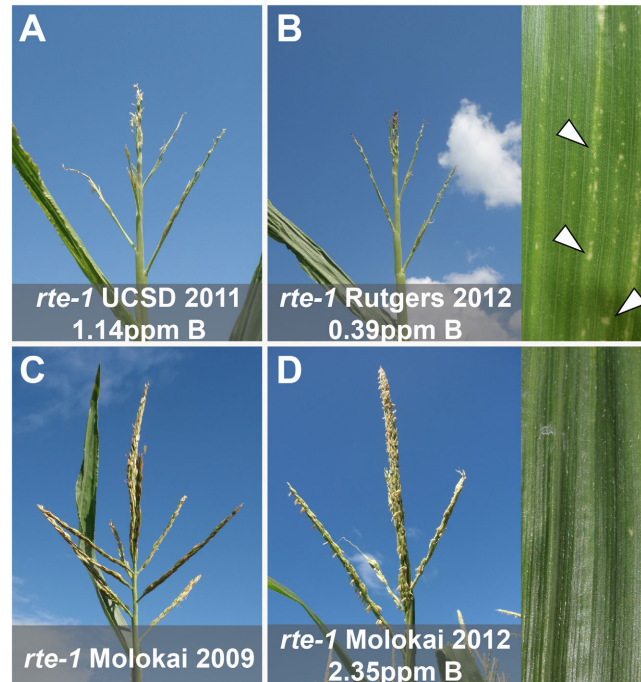


\*ttest, P=0.000134; \*\*ttest, P=0.000222; \*\*\*ttest, P= 0.006231;\*\*\*\*ttest, P=0.578323



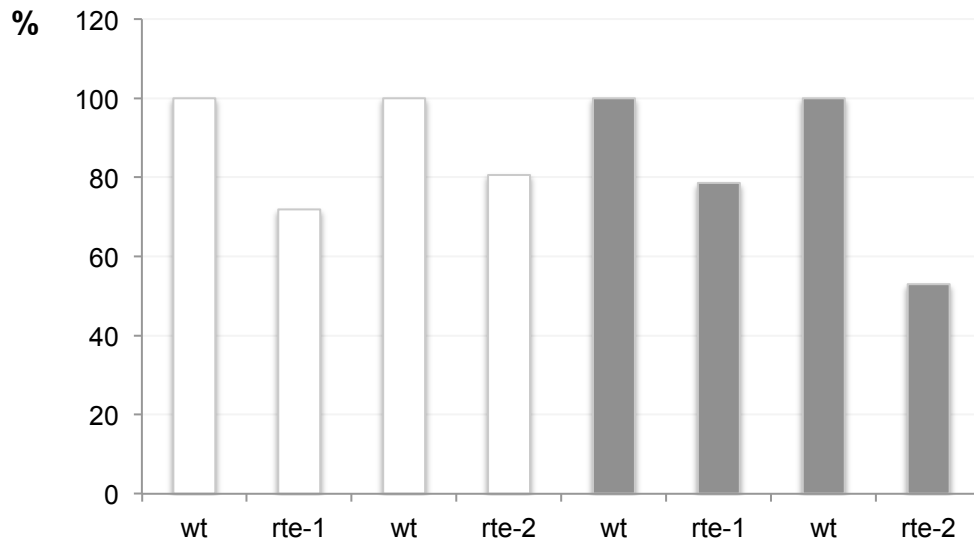
ttest, P= 2.17851E-06; \*\*ttest, P=0.0004116; \*\*\*ttest, P= 0.00021280; \*\*\*\*ttest, P=0.283702175



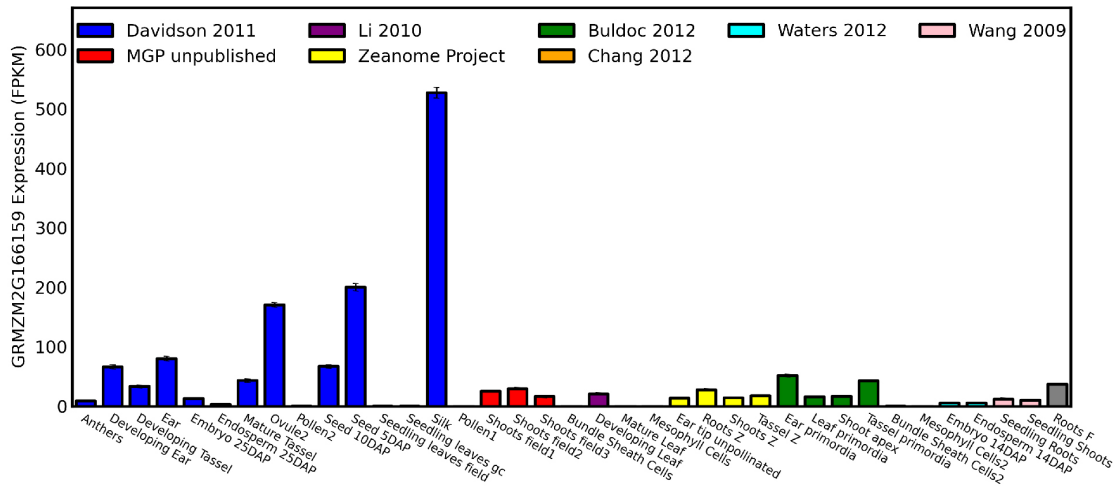


**Supplemental Figure 9.** The *rte* Phenotype is Influenced by the Boron Concentration in the Soil.

(A) to (D) Effects of different soil boron concentrations on the *rte* tassel phenotype. Representative tassels and leaves from *rte-1* mutant plants grown at three different locations where soil boron concentrations ranged from low (B; 0.39ppm) to moderate (A; 1.14ppm), and high (D; 2.35ppm). The comparatively boron-rich soil of Molokai consistently resulted in a relatively less severe phenotype (C, D). In (B) and (D) a close-up of a leaf is provided. Note the lesions apparent in (B) (arrowheads) that are not present in (D).



**Supplemental Figure 10.** Boron Measurements in *rte* Mutants. Boron measurements expressed as percentage (Y axis) relative to wild type in leaf (white) and immature ear (grey) samples. Each sample is bulked tissue from at least three different plants.



**Supplemental Figure 11.** Tissue-specific expression data of *rte* derived from multiple RNAseq datasets, available at [www.qsteller.com](http://www.qsteller.com). Error bars represent the upper and lower FPKM limits.

**Supplemental Table 1**

List of primers used.

	<b>PRIMERS 5'-3'</b>	<b>PURPOSE</b>
MAGIv4_1364	For: GTTGACATCTCTACTACTAAGGTC Rev: AGCCTGGAGAAGATATGGACGACT	Indel marker
MAGIv4_55889	For: AGCAGCCTGCCTTATCTTCACAGC Rev: CTGATGTCAGGCTTGACGCTACAC	dCAPS marker-digest with AluI
RTE-F1 RTE-R1	CCGACTGGCCATCCAGAATATAACC GCACATGCCTTTGAGCAACCTACT	<i>rte</i> gene
RTE-F2 RTE-R2	CTCTGTGGCCATCTGGATGTGCGA TGCCATGTGAGTGAGAAATCAGATG	<i>rte</i> gene
RTE-F3 RTE-R3	CATCTGATTTCTCACTCACATGGCA GGAGTGCTATACCTGTAATCTCTG	<i>rte</i> gene
RTE-cds-F1 RTE-cds-R3	ATGGAGGAGAGCTTCGTGCCCTTG CACCATCGAAGCCTGTAGAAGGTTG	<i>rte</i> cds
RTE-cds-F3 RTE-cds-R2	ACAGGCTTCGATGGTGGTGGGCTGT TCACTTTGGTGCCGAGCCTTCACC	<i>rte</i> cds
<i>rte-1</i>	For: TACTTGTGCAGATGGAGTCCTCAC Rev: CTGCACGCAAACATGACAACAAAC	CAPS marker-digest with Styl
<i>rte-2</i>	For: CCTCCATCAAATGGTGTCAATTGTA Rev: GAAAATGTTATGTAAACAAATTGTCTG	dCAPS marker-digest with RsaI
BOR1-037312-F	ATGCTTGATGTTCCAATCGTC	<i>bor1</i> genotyping
BOR1-037312-R	ATCCATGTGAGACCAAAGCAG	<i>bor1</i> genotyping
Lb1.3	ATTTTGCCGATTTTCGGAAC	<i>bor1</i> genotyping
RTE793-Nco-F	CGCCTTTTTAGCCCTAATCCATGG	RTE-L361 cloning
RTE1195-Leu-R	CGTATGCATGGGTAATTGTGGAATGACACCATTGA	RTE-L361 cloning
RTE1069-Leu-F	GTCATTCCACAATTACCCATGCATACGAAGAGTTTG	RTE-L361 cloning
RTE2103-Stu-R	CTTGATGGCGTCCTAGGCCTGCT	RTE-L361 cloning
RTE-pENTR-SFI-F	GAATTCGGCCGTCAAGGCCAATGGAGGAGAGCTTCGTGCCCT	35S: <i>RTE:YFP</i> transient assay
RTE-pENTR-SFI-R	AGTCGACGGCCCATGAGGCCCTTTGGTGCCGAGCCTTCACC	35S: <i>RTE:YFP</i> transient assay
RTE-35s/pBJ36-XhoI-F1	GTCGACCTGCAGACGCGTCTCGAGATGGAGGAGAGCTTCGTGCC	35S: <i>RTE</i> complementation
RTE-35s/pBJ36-XhoI-R1	ACCCGGGGTACCGAATTCCTCGAGTCACTTTGGTGCCGAGCTT	