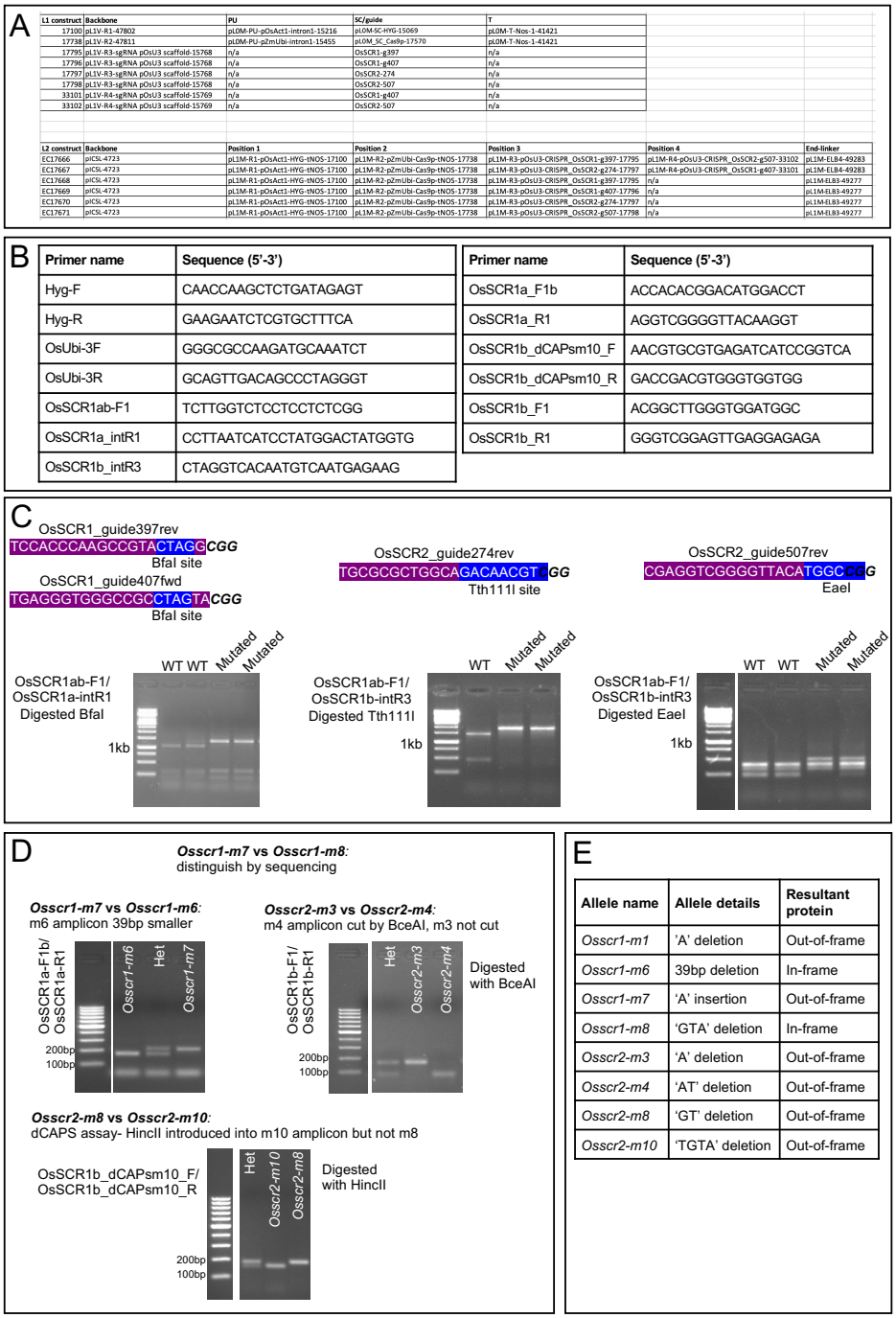
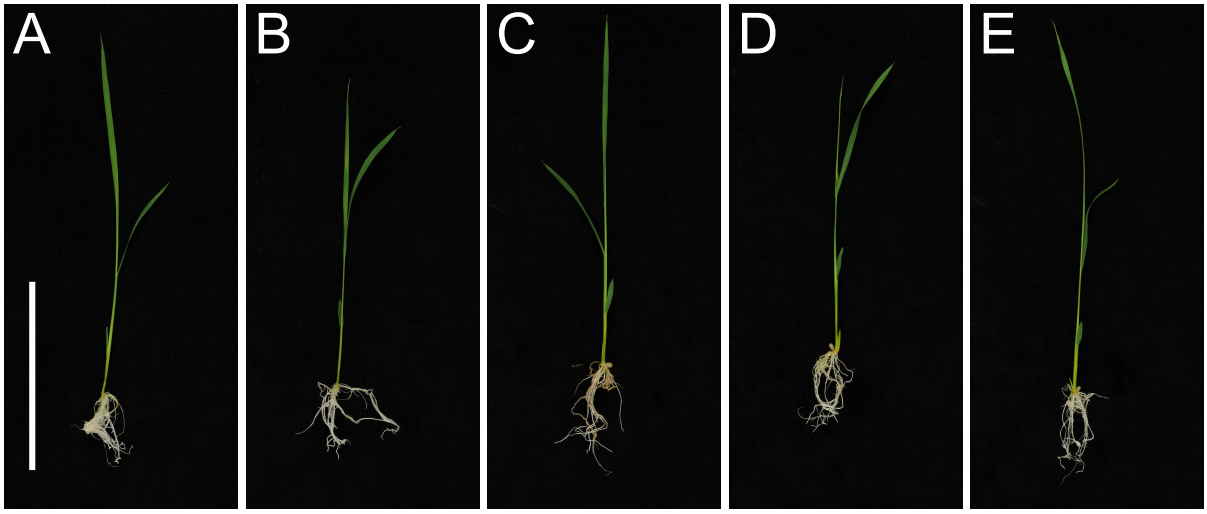


Fig. S1. Generation of CRISPR mutants. A) Golden gate modules and cloning used in this study. **B)** Genotyping primers used in this study. **C)** Restriction digest assays used to identify mutant alleles for each CRISPR guide. Guide sequence is depicted with purple highlighting and white lettering, the protospacer adjacent motif (PAM) sequence is depicted in black italic text, and the restriction enzyme site is depicted with blue highlighting. **D)** Distinguishing pairs of known alleles identified in Fig. 2C using different restriction enzyme assays. **E)** Summary of all alleles used for phenotyping in this study.



Kitaake WT	*Osscr1-m7* 17668-1a-19-8	*Osscr1-m1* 17668-4a-6-12	*Osscr2-m3* 17671-6b-21-8	*Osscr1a-m8; Osscr2-m3* 17666-13a-2-5-5-5-10

Fig. S2. *Osscr1* and *Osscr2* single mutants grow normally. A-E) Photographs of WT (A), *Osscr1-m7* (B), *Osscr1-m1* (C), *Osscr2-m3* (D) and *Osscr1-m8;Osscr2-m3* (E) plants taken 13 days after sowing. Orange alleles indicate out-of-frame mutations whereas blue alleles indicate an in-frame mutation not predicted to alter protein function. All mutants were obtained from independent lines or constructs, as indicated underneath the allele names. Scalebar in A is 10 cm and all images are at the same magnification.

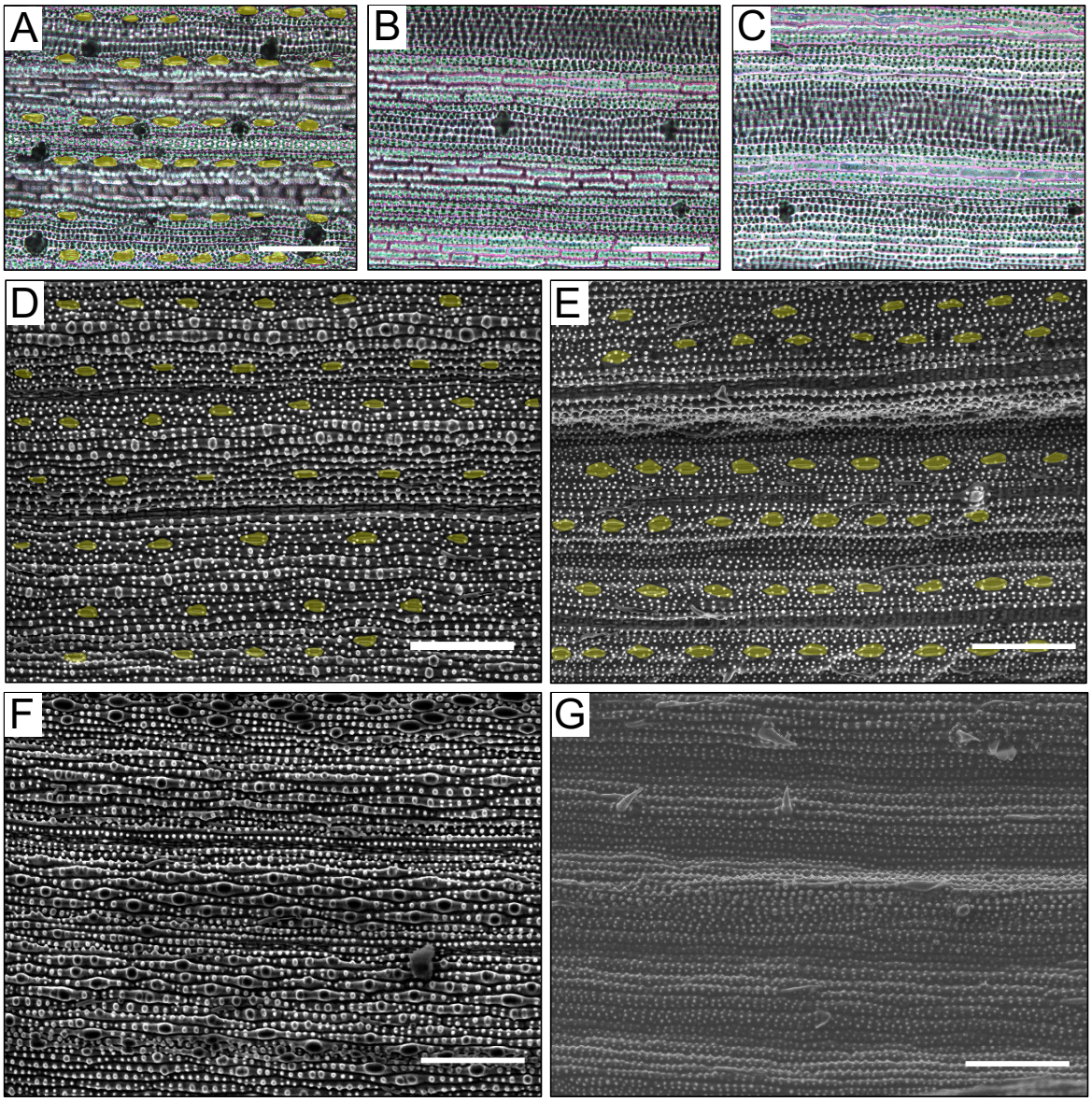


Fig. S3. Stomatal phenotypes are consistent on both sides of the leaf and not an artefact caused by taking impressions. A-C) Adaxial impressions of WT (A), *Osscr1-m7;Osscr2-m3* (B) and *Osscr1-m7;Osscr2-m10* (C) leaf 5. Scalebars are 100μm. **D-G)** Scanning electron microscope images of leaf 5 for kitaake WT (D and E) or *Osscr1-m7;Osscr2-m3* (F and G) abaxial (D and F) and adaxial (E and G) surfaces. Scalebars are 100μm. Stomata are false coloured yellow.

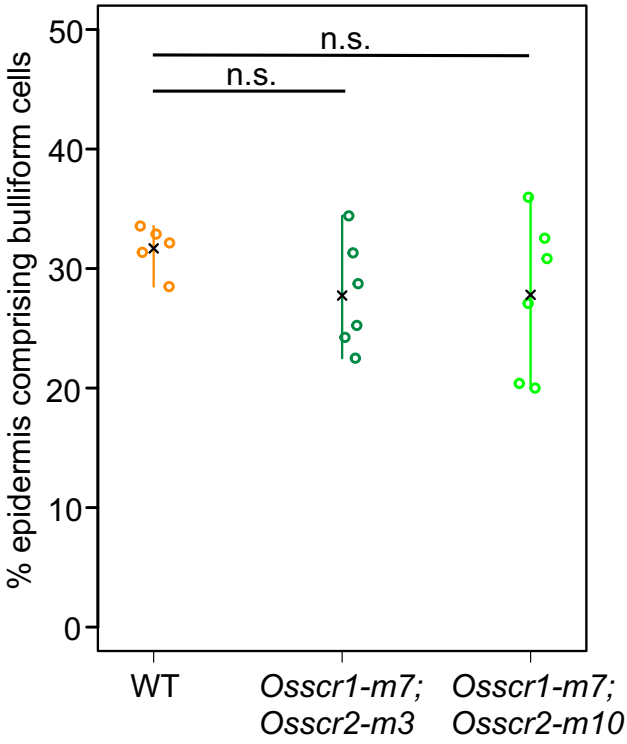


Fig. S4. % of the epidermis comprising bulliform cells is unchanged in *Osscr1;Osscr2* mutants. Quantification of the number of bulliform cells on the adaxial surface of fully expanded leaf 5 expressed as a percentage of the total number of epidermal cells. Each datapoint is a biological replicate, and the mean values for each genotype are indicated by a black cross. Samples sizes are WT, n=5; *Osscr1-m7;Osscr2-m3*, n=6; *Osscr1-m7;Osscr2-m10*, n=6. Statistical significance between each genotype was assessed using one-way ANOVA: n.s. $P>0.05$.

A

Gene	Accession/ ref	Forward primer (5'-3')	Reverse primer (5'-3')	Product size (bp)
OsACTIN	Wang *et al.* (2017)	GGCACCACACCTTCTACAAT	CTCACACCATCACCAGAGT	223
OsUBQ5	Jain *et al.* (2006)	ACCACTTCGACCGCCACTACT	ACGCCTAAGCCTGCTGGTT	69
OsROC5	LOC_Os02g45250	ATACCCAGCACCAGATCCAA	CATCTGTGTGCGCTTGTTCT	146
OsMUTE	LOC_Os05g51820	TCAACATCACCACCATGGAC	CATGAAGGACTGGTGGACCT	113
OsFAMA	LOC_Os05g50900	GAGATGGCGGAGAACAAGTC	CATGTGCATCTCCTCCAGTG	138

B

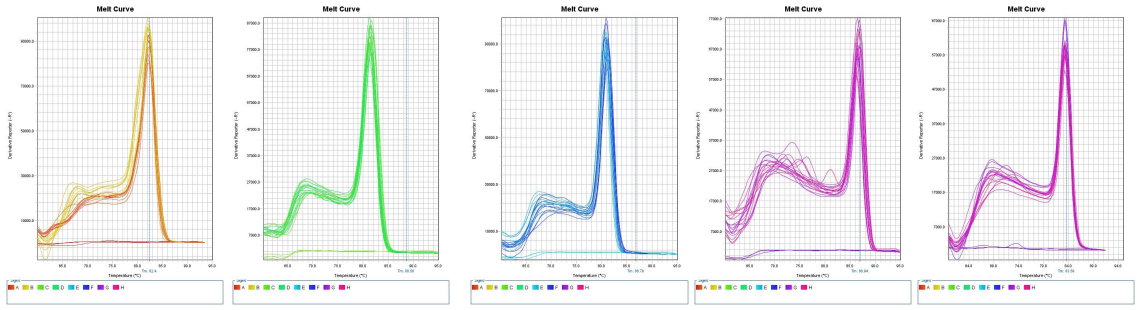


Fig. S5. Quantitative RT-PCR primer design and validation. A) Primer sequences and product sizes. **B)** Melt-curves for each primer pair used in the study.