

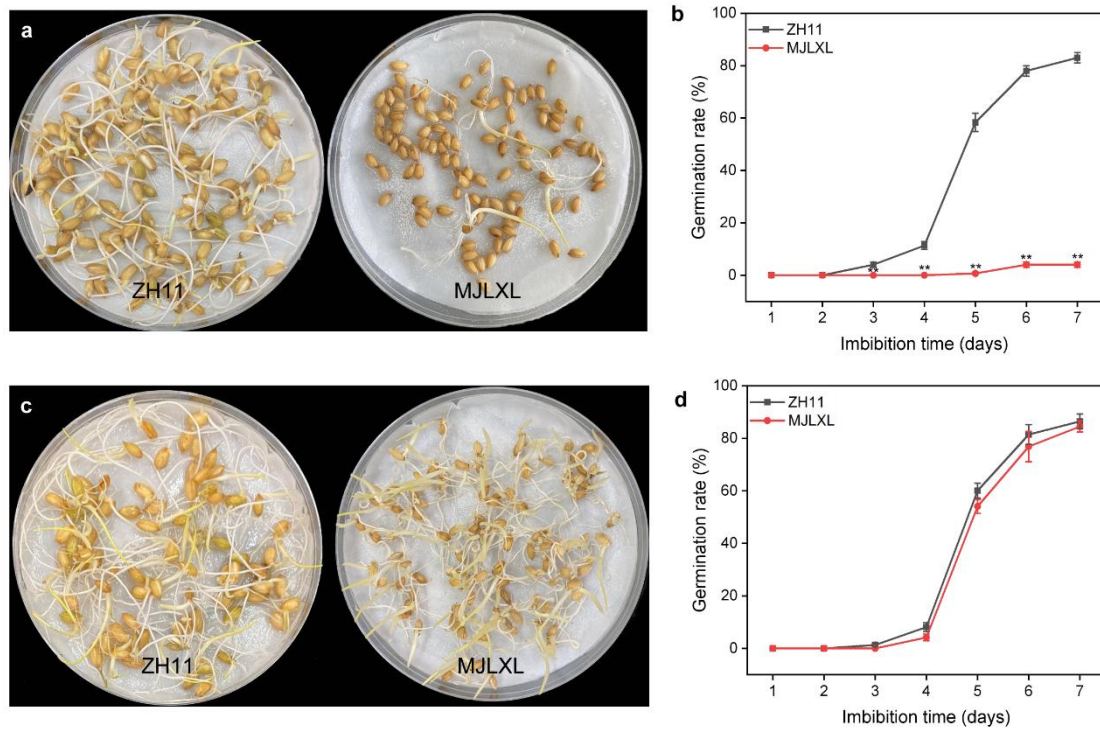


Figure S1 Parental phenotypic identification. **a** Parental 35 DAH, seven-day germination phenotypes. **b** Parental germination rate 35 DAH (n = 3). **c** Three months after harvest, seven-day germination phenotype of both parents. **d** Parental germination rate three months after harvest (n = 3). The data are mean values $\pm$ SD, **P < 0.01.

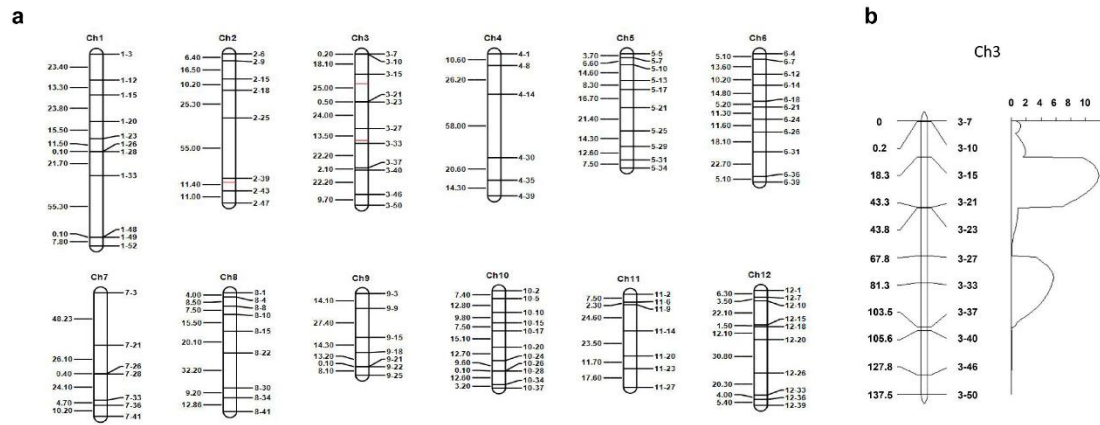


Figure S2 Chromosomal locations of QTLs for seed dormancy. **a** There are three rice dormancy QTLs on chromosome 2 and 3. The red line indicates the mapped seed dormancy QTLs site. **b** The LOD for chromosome 3.

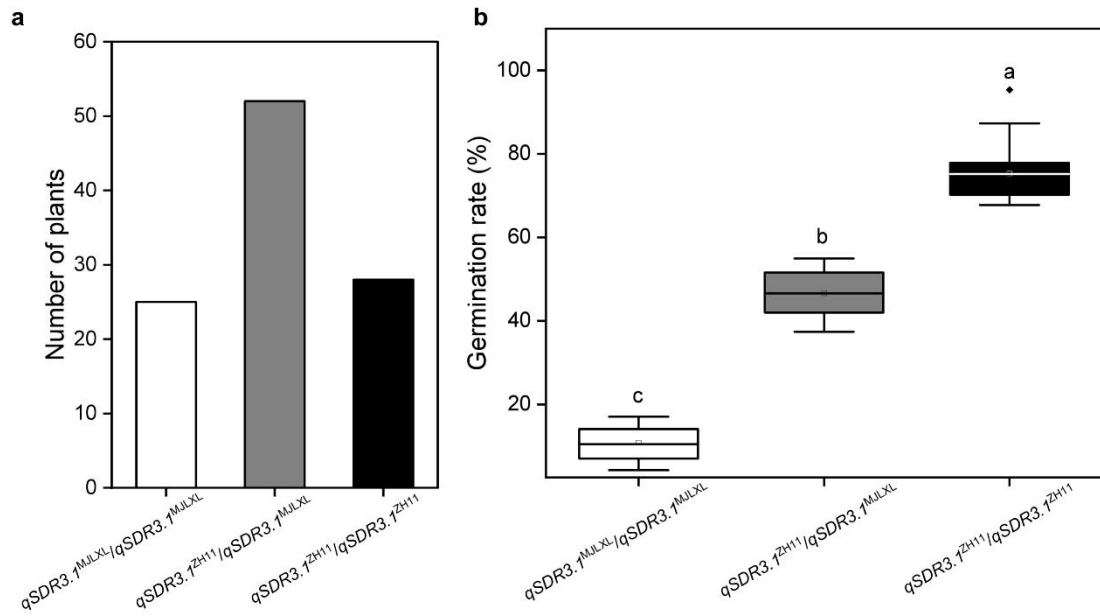


Figure S3 The recessive *qSDR3.1* allele from MJLXL is correlated with seed dormancy. **a** Segregation of the BC₃F₂ population derived from ZH11 and MJLXL. **b** Box plots for germination rate among homozygotes for the MJLXL *qSDR3.1* allele, heterozygotes for the MJLXL *qSDR3.1* allele and the ZH11 *qSDR3.1* allele, and homozygotes for the ZH11 *qSDR3.1* allele. The data are mean values $\pm$ SD, and the letters above the bars indicate significant differences based on ANOVA analysis ($P < 0.05$).

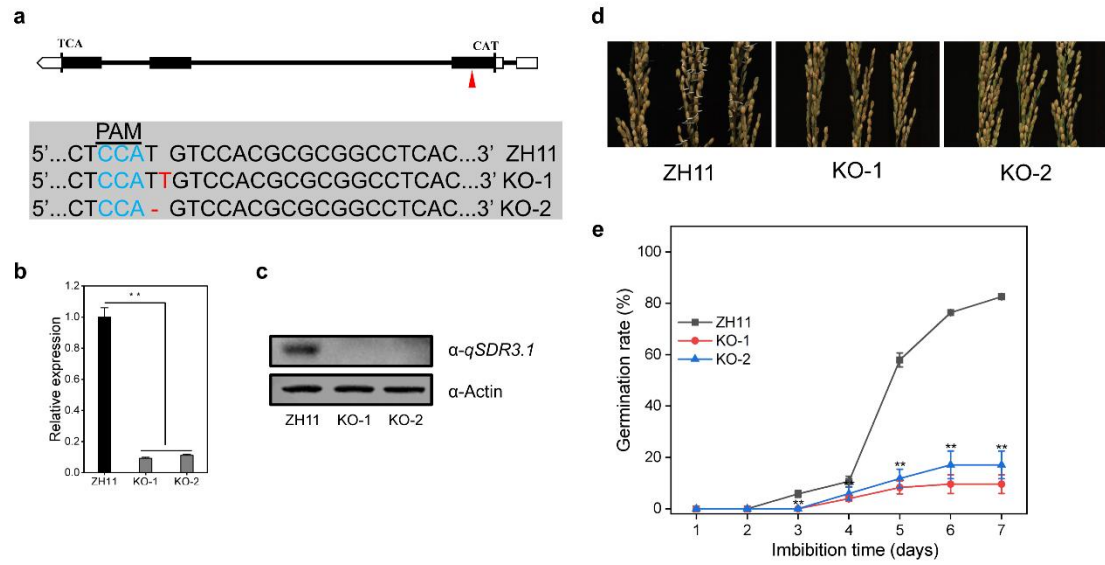


Figure S4 Phenotype of *qSDR3.1* knockout lines. **a** *qSDR3.1* mutant sites of two knockout lines; red arrows indicated knockout sites. **b** Relative expression levels of *qSDR3.1* in two knockout lines and wild-type ZH11 (n = 3). **c** Proteins levels of *qSDR3.1* in two knockout lines and wild-type ZH11 (n = 3). **d** 35 DAH, germination phenotypes of two mutant lines and ZH11 for seven days. **e** Germination rates of two mutant lines and ZH11 35 DAH (n = 3). The data are mean values $\pm$ SD, **P < 0.01.

ZH11	MEGFSRDLLC	GIGKGGDGPR	GEVRPRVDME	AEEVELNLGL	SLGGRFGLDR
KO-1	MEGFSRDLLC	GIGKGGDGPR	GEVRPRVDNG	G-----	-----
KO-2	MEGFSRDLLC	GIGKGGDGPR	GEVRPRVDWR	LRRWSSTSGC	RSAAGSGWTG
	RG-EKLARSS	SVAAILAAPT	EPSAPPSGLF	RTSSLPTVAA	AEAARKQGVD
	-----	-----	-----	-----	-----
	EGRSSPGRRR	SRPSWRRRRS	RRRRRPGSSG	RARCRPWPPR	RRKRSRVWMN
	ELNCRRPSSG	AEAEPAAARL	PASGSPSSGS	SDGEGRRLEV	NMTDTLMRTS
	-----	-----	-----	-----	-----
	SLPAGIEDEW	RKRKEAQLK	RLEVKRKRIE	RRNSLTSNIS	KEAVGQILEE
	-----	-----	-----	-----	-----
	MNAGAEKVES	CDDVATGNKK	TGGNVNHSSD	RNRCTGLPPV	HRATYTQQRG
	-----	-----	-----	-----	-----
	SLSGIPTKHI	PAMKGSADAE	EHNVPASAATE	HRNGAAIATP	PFSALAVRAV
	-----	-----	-----	-----	-----
	ALASRGEQLR	ATGRVAARAK	SMGDVERIMM	QEMPCVCTKG	LPNGKRVEGF
	-----	-----	-----	-----	-----
	LYKYRKGEV	RIVCVCHGSF	LTPAEFVKHA	GGGDVANPLR	HIVVNPIPPS
	-----	-----	-----	-----	-----
	LY				
	--				
	--				

Figure S5 Protein sequence of *qSDR3.1* in ZH11, KO-1, and KO-2.

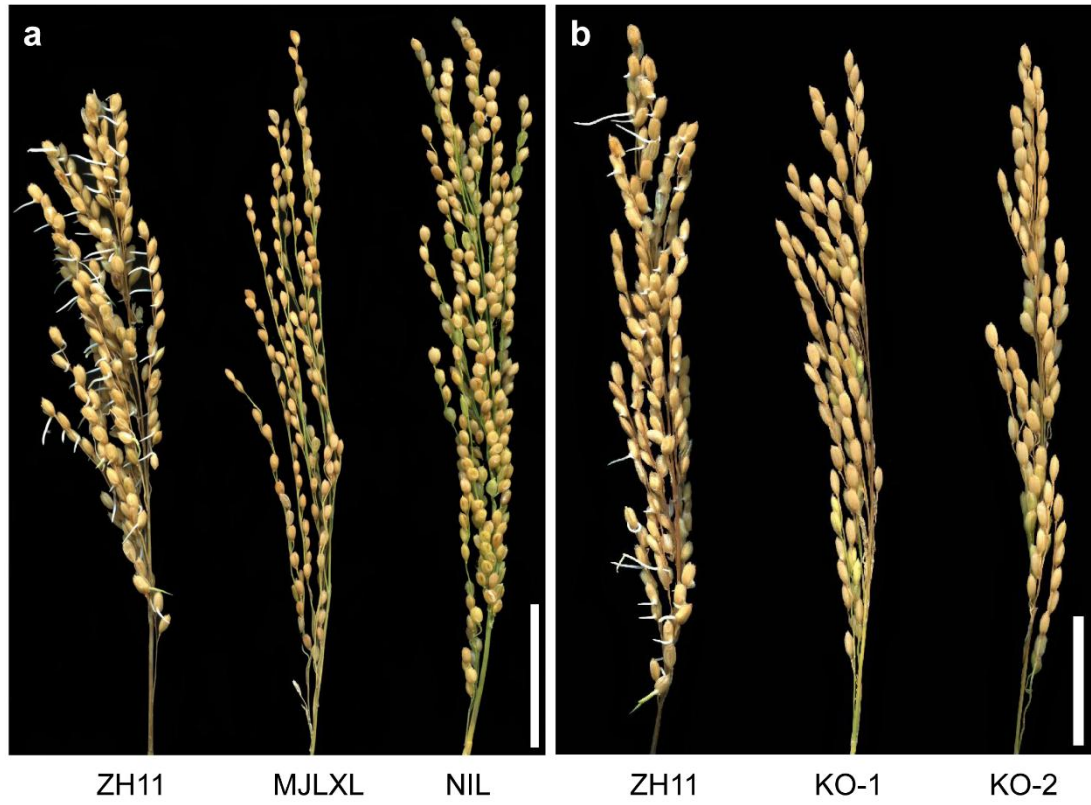


Figure S6 Pre-harvest sprouting of ZH11, MJLXL, and NIL (**a**) and ZH11, KO-1, and KO-2 (**b**). Bar = 10 cm.

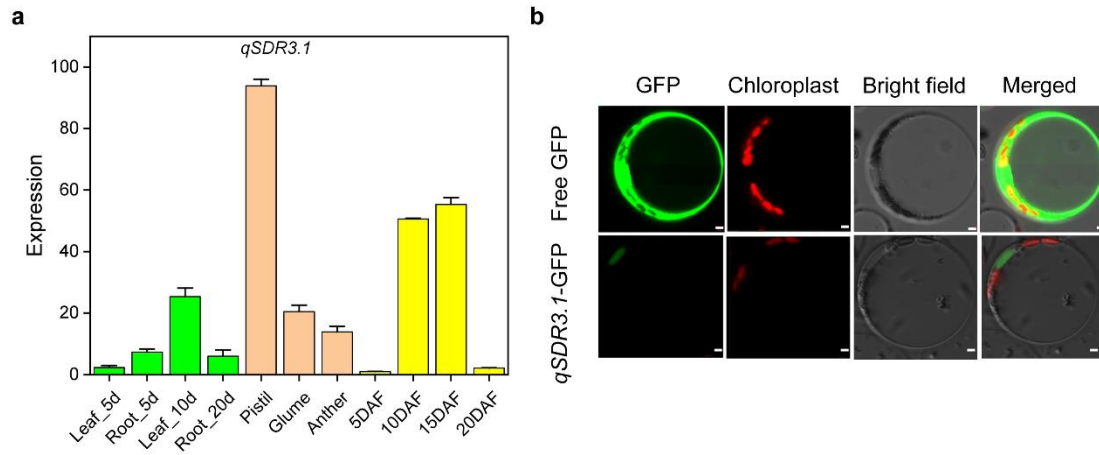


Figure S7 Expression pattern and subcellular localization of *qSDR3.1*. **a** Relative expression levels of *qSDR3.1* in the different tissues. **b** Subcellular localization of *qSDR3.1* in rice protoplasts. Shown are signals from GFP fluorescence, chlorophyll autofluorescence, bright field, and merged images. The data are mean values $\pm$ SD ($n = 3$), bar = 2 μ m.

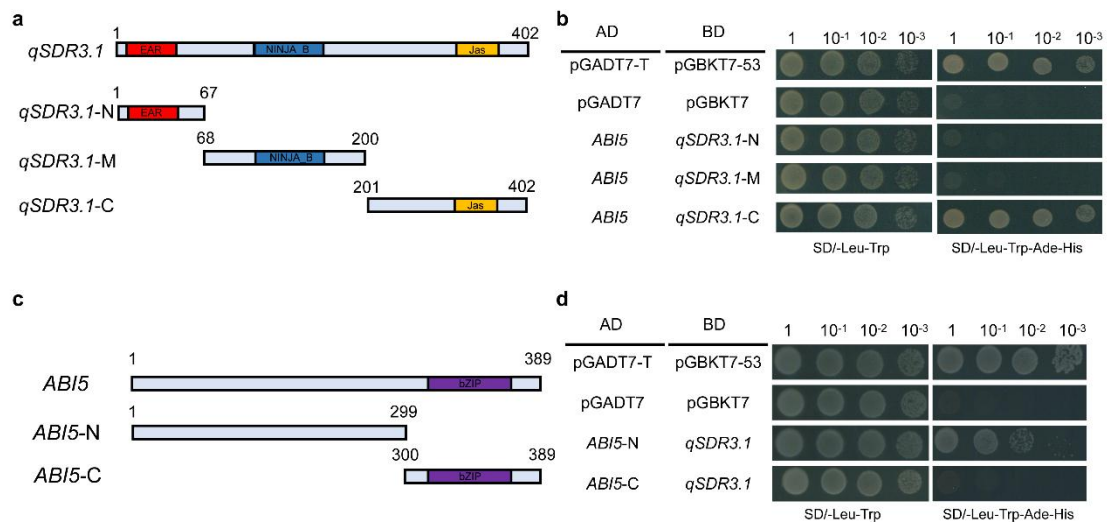


Figure S8 Yeast two-hybrid screening assays to identify *ABI5* and *qSDR3.1* regions for their interaction. **a** Diagrams showing the conserved EAR domain, NINJA_B domain, and Jas domain of *qSDR3.1* and the truncated versions of *qSDR3.1* in the assays. *qSDR3.1-N* represents amino acids 1-67; *qSDR3.1-M* is 68-200, and *qSDR3.1-C* is amino acids 201-402. **b** The yeast two-hybrid assay showed interaction of truncated versions of *qSDR3.1* with full-length *ABI5* protein. **c** Diagrams showing the conserved bZIP domain of *ABI5* and the truncated versions of *ABI5* in the assays. *ABI5-N* represents amino acids 1-299, *ABI5-C* represents amino acids 300-389. **d** The yeast two-hybrid assay showed the interaction of truncated versions of *ABI5* with the full-length *qSDR3.1* protein.

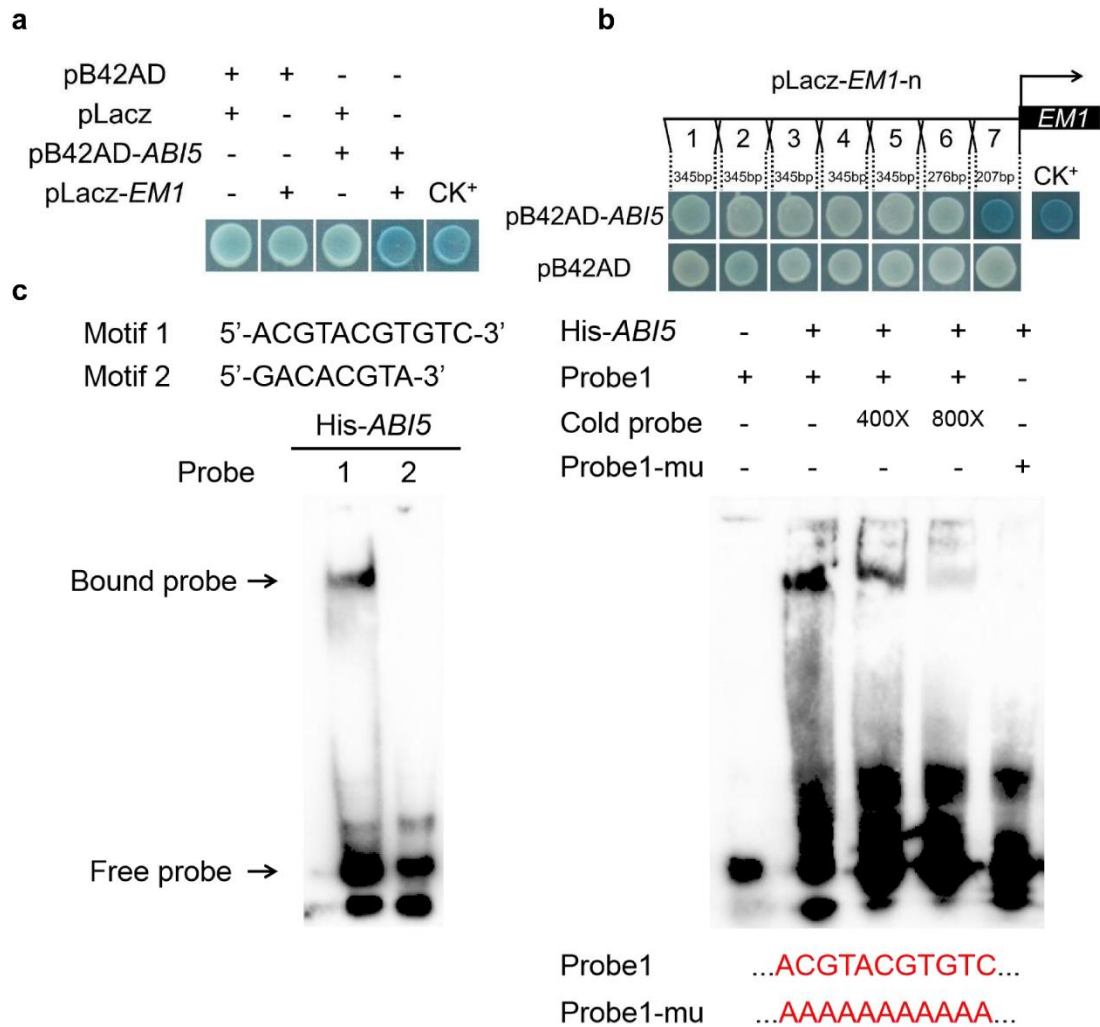


Figure S9 *ABI5* activates the expression of *EMI*. **a** Yeast one-hybrid assay showed that *ABI5* bound to the *EMI* promoter (2000 bp upstream of ATG). **b** Yeast one-hybrid assay showed that *ABI5* bound to the *EMI* promoter (207 bp upstream of ATG). **c** Electromobility shift assay showed that *ABI5* bound to the biotin probe on the promoter of *EMI*. Probe 1 contained motif 1, and the probe 2 contained motif 2.

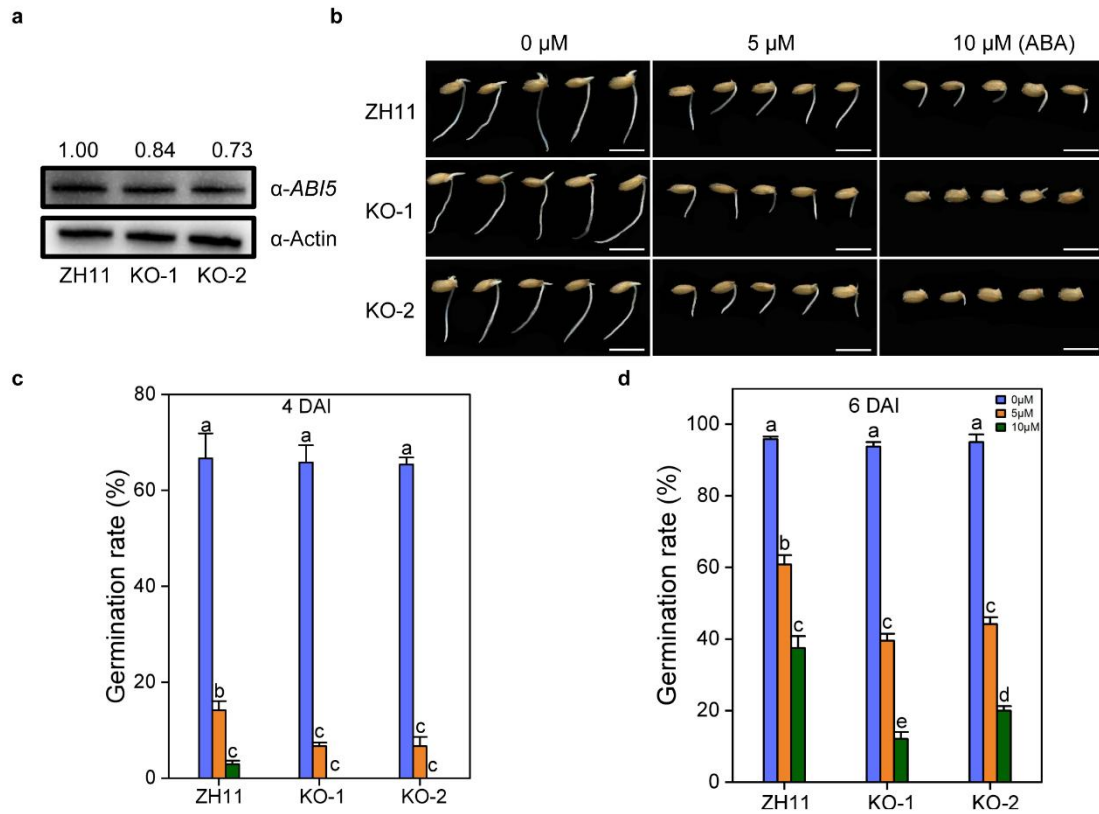


Figure S10 ABA sensitivity experiments. **a** Proteins expression levels of *ABI5* in two knockout lines and the wild-type ZH11 ($n = 3$). **b** Germination performance of two knockout lines and the wild-type ZH11 seeds with 0, 5, or 10 μM ABA treatment at 4 days after imbibition (DAI). Bar = 1 cm. **(c)** and **(d)** Germination rate of seeds in **(b)** at 4 DAI **(c)** and 6 DAI **(d)** ($n = 3$). The data are mean values $\pm$ SD, and the letters above the bars indicate significant differences based on ANOVA analysis ($P < 0.05$).

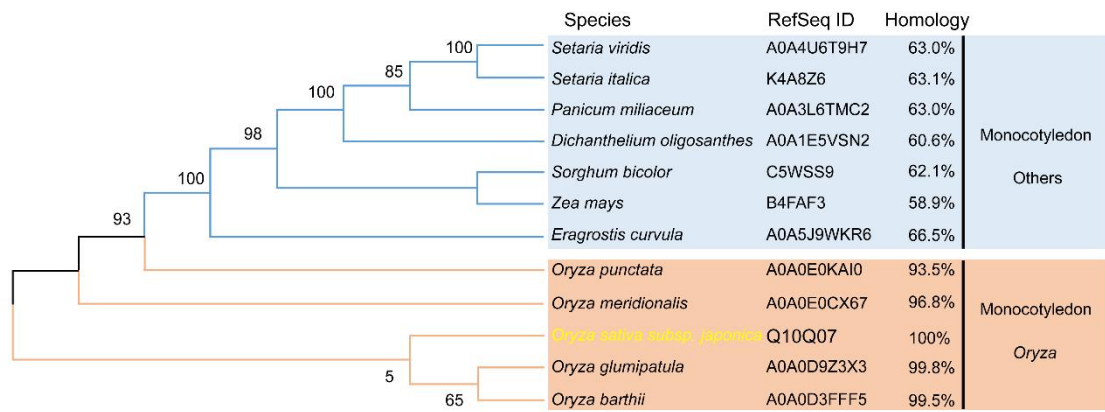


Figure S11 Phylogenetic analysis of *qSDR3.1* protein with homologous protein.

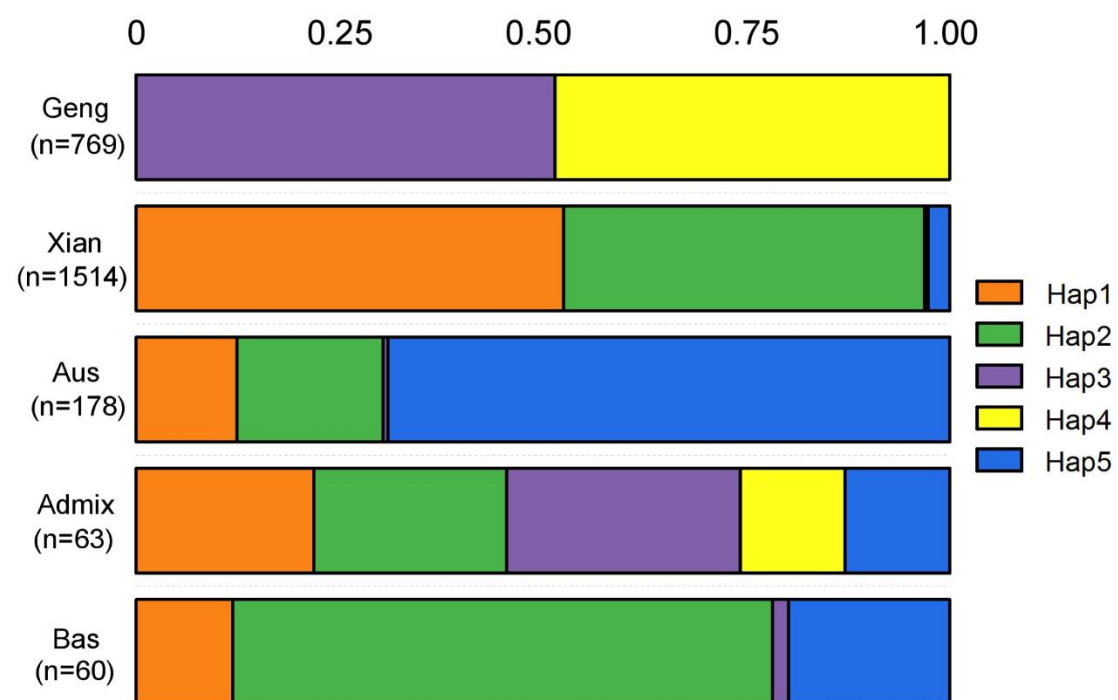


Figure S12 Haplotype frequency of *qSDR3.1* in subpopulations of 3K RG.

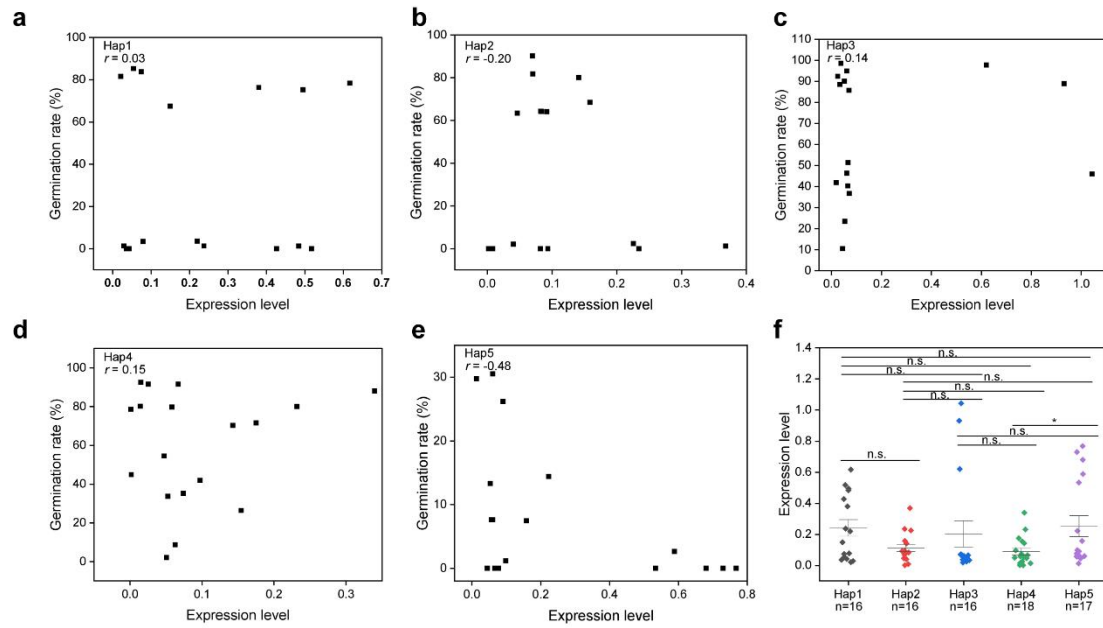


Figure S13 Relationship between *qSDR3.1* expression and dormancy. **a** *qSDR3.1* expression levels of 16 varieties randomly selected from the haplotype1 accessions. **b** *qSDR3.1* expression levels of 16 varieties randomly selected from the haplotype2 accessions. **c** *qSDR3.1* expression levels of 16 varieties randomly selected from the haplotype3 accessions. **d** *qSDR3.1* expression levels of 18 varieties randomly selected from the haplotype4 accessions. **e** *qSDR3.1* expression levels of 17 varieties randomly selected from the haplotype5 accessions. **f** *qSDR3.1* expression levels with the five haplotypes. The “r” is the correlation coefficient between germination rate and *qSDR3.1* expression level. *P < 0.05.

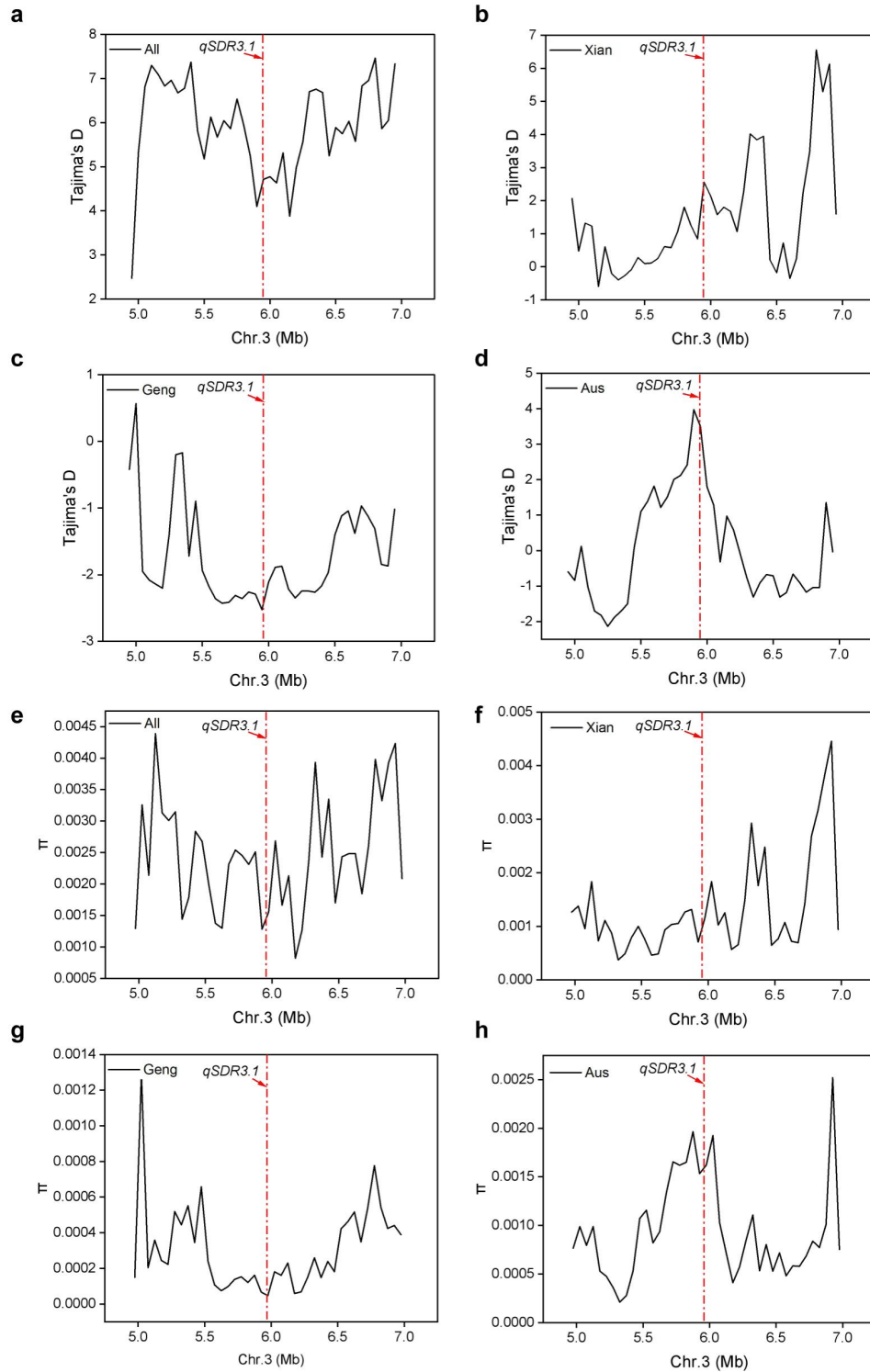


Figure S14 Tajima's D for 2-Mb genomic region flanking *qSDR3.1* of All (a), Xian (b), Geng (c), Aus (d) in 3K RG. Nucleotide diversity (π) for 2-Mb genomic region flanking *qSDR3.1* of All (e), Xian (f), Geng (g), Aus (h) in 3K RG. The *qSDR3.1* gene is indicated by a red dashed line.

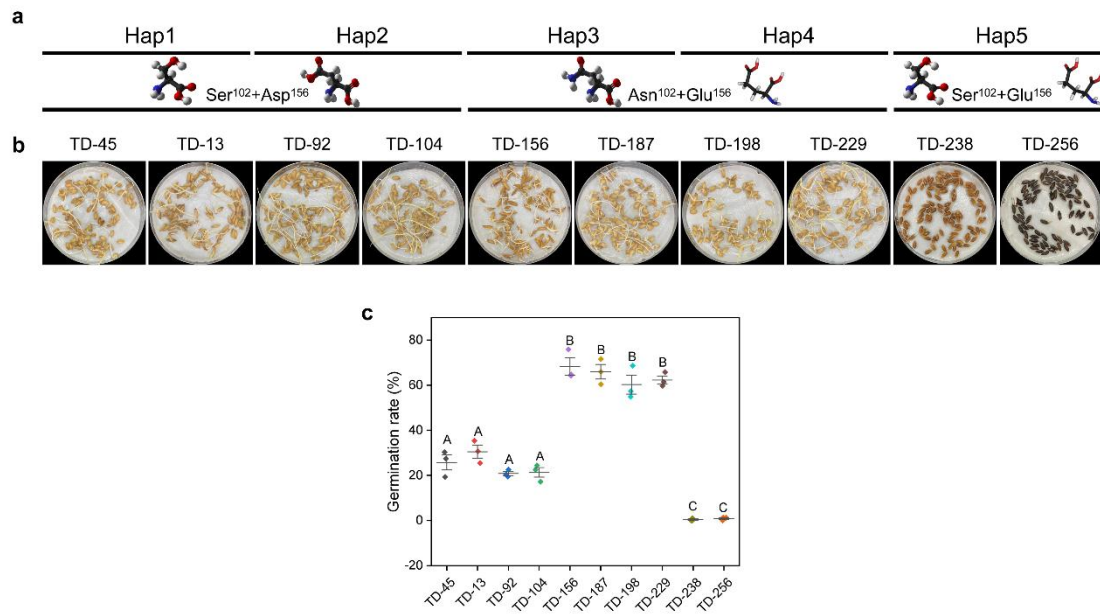


Figure S15 Germination rate of varieties with different amino acid combinations. **a** Amino acid composition of five haplotypes. **b** The seven-day germination phenotype for each haplotype. **c** The seven-day germination rate for each haplotype. The data are mean values $\pm$ SD ($n = 3$), and the letters above the bars indicate significant differences based on ANOVA analysis ($P < 0.01$).

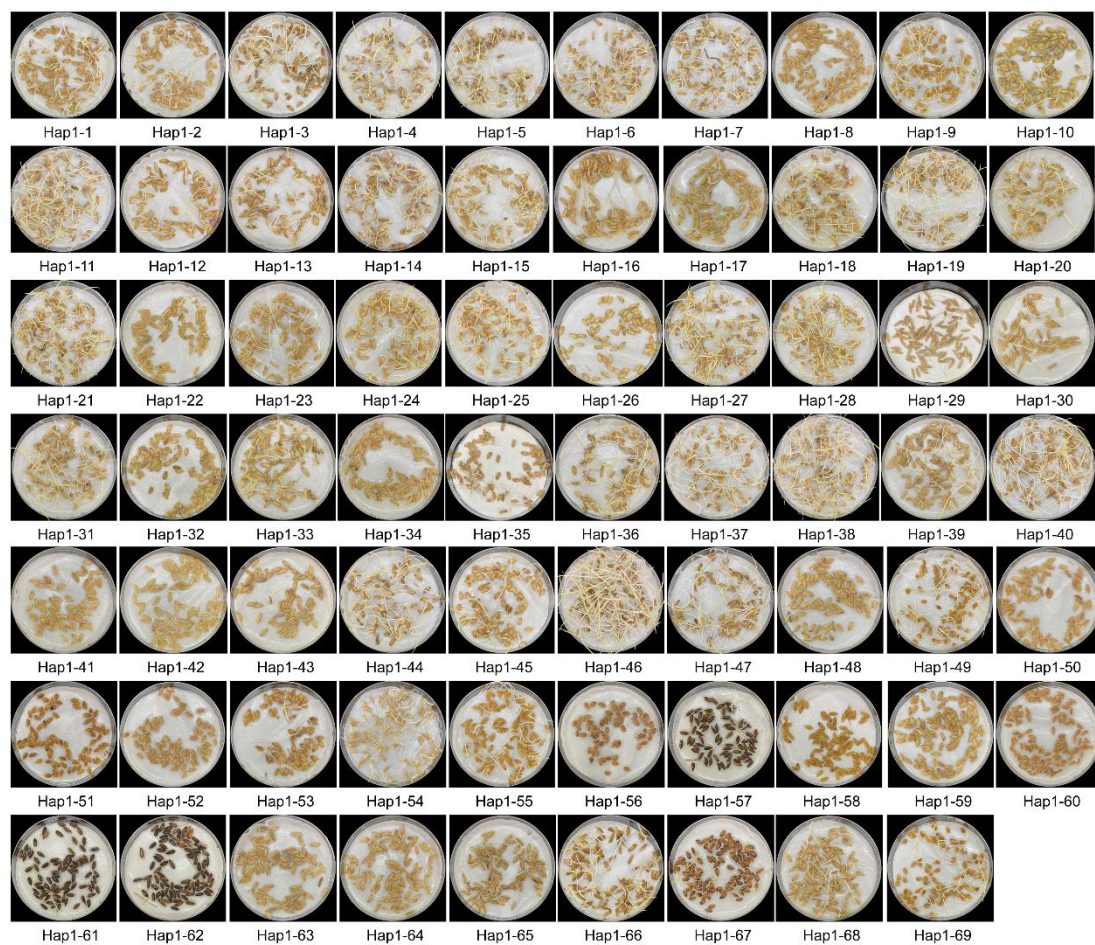


Figure S16 Seven-day germination phenotype of haplotype1.

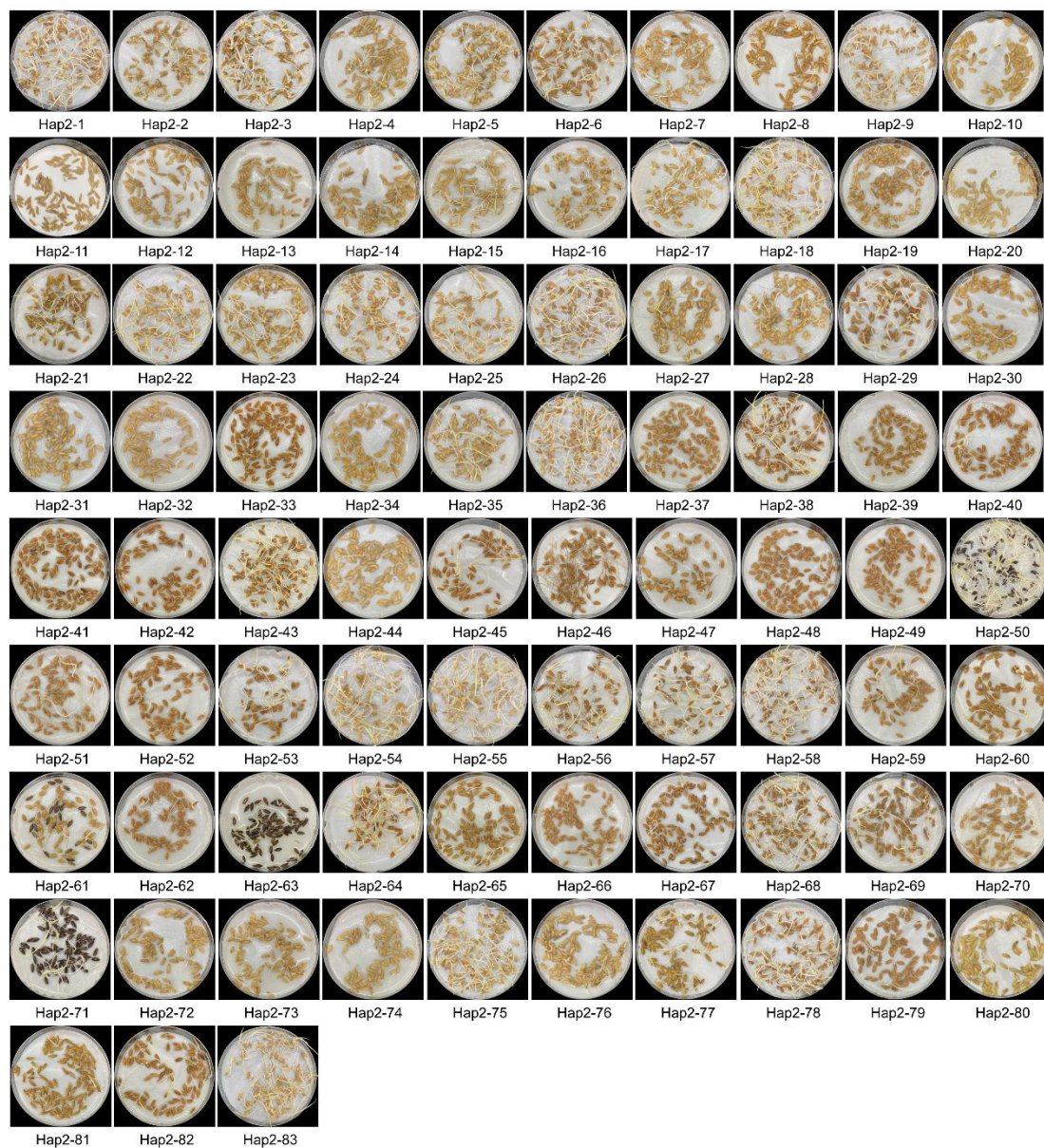


Figure S17 Seven-day germination phenotype of haplotype2.

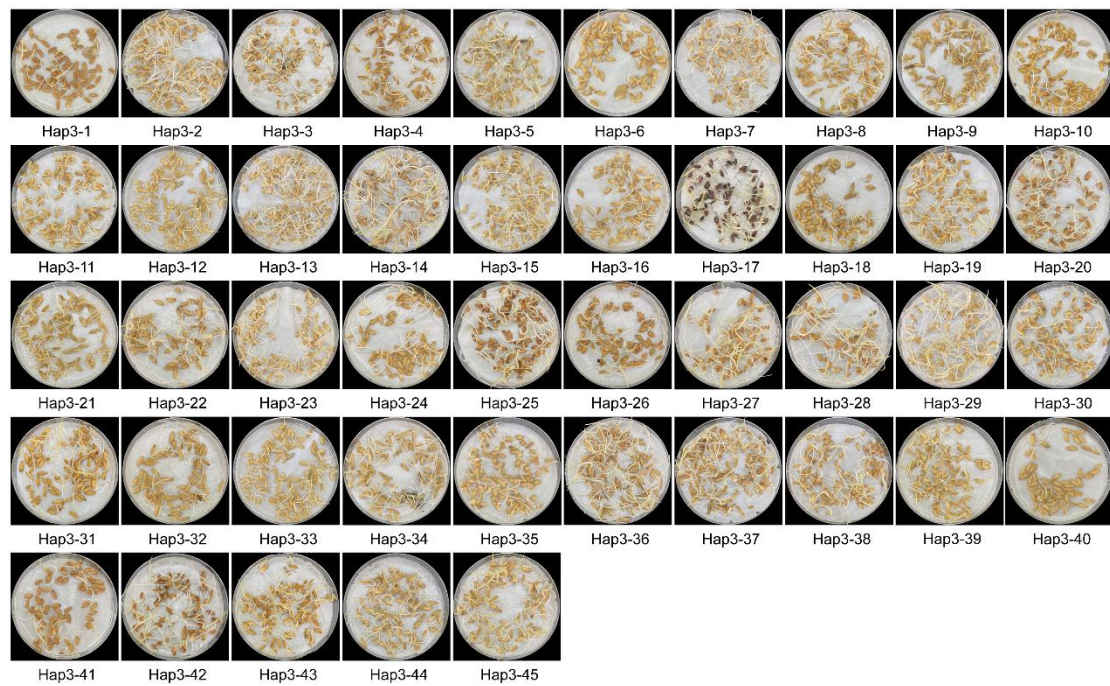


Figure S18 Seven-day germination phenotype of haplotype3.

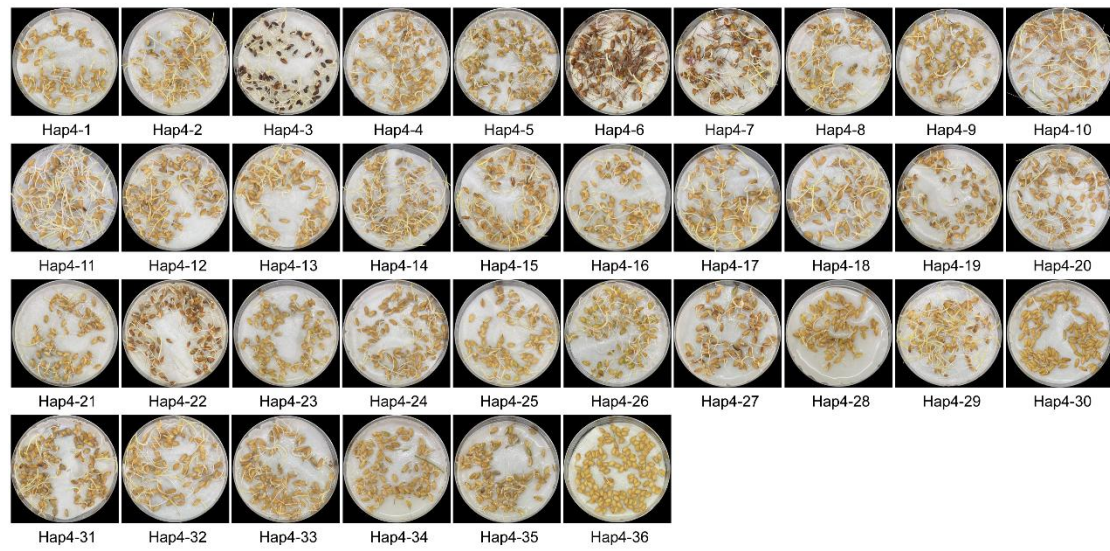


Figure S19 Seven-day germination phenotype of haplotype4.

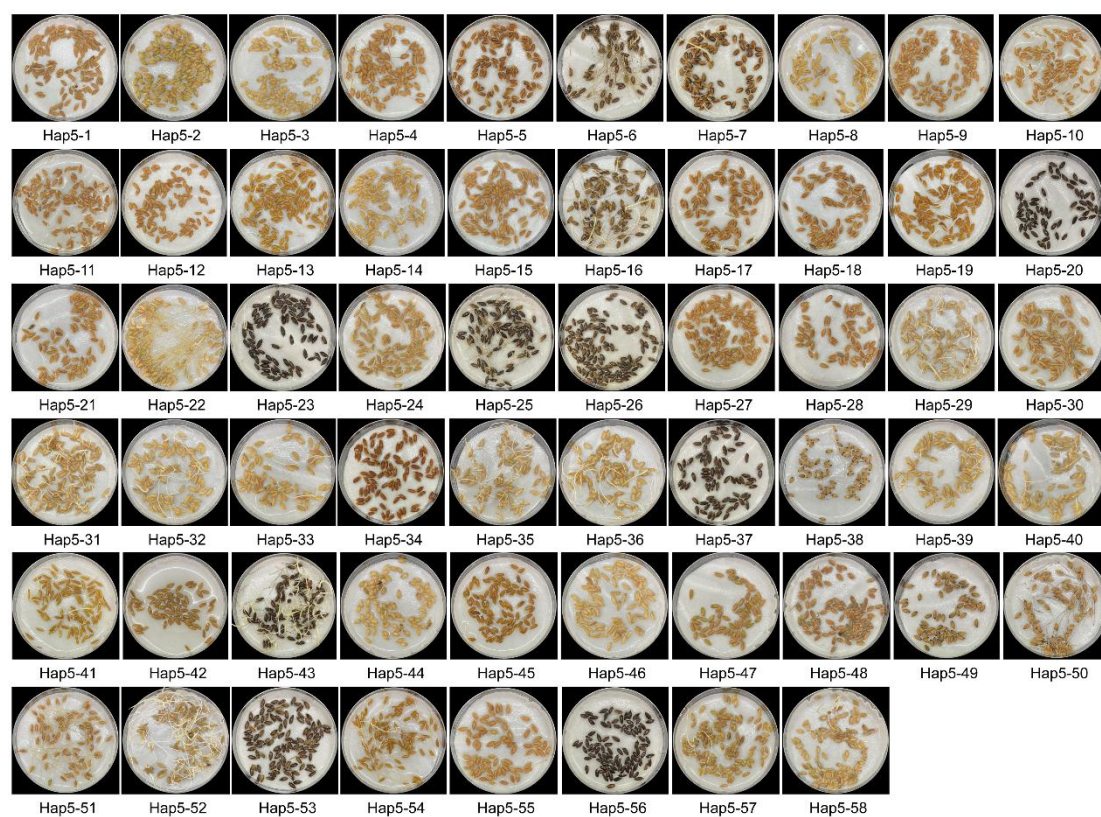


Figure S20 Seven-day germination phenotype of haplotype5.

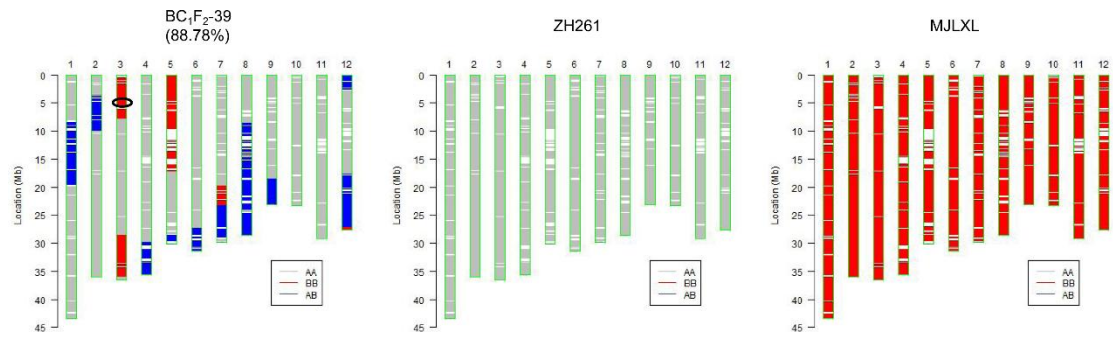


Figure S21 The genetic background similarity of BC₁F₂-39. The black circle indicates the location of *qSDR3.1*.