

Table S1. Primers used in this study for qRT-PCR.

Primers	Forward primers (5'-3')	Reverse primers (5'-3')
<i>Ubiquitin</i>	CCCTCCACCTCGTCCTCAG	AGATAACAACGGAAGCATAAAAGTC
<i>SGR</i>	AGGGGTGGTACAACAAGCTG	GTCCTTGCGGAAGATGTAG
<i>RCCR1</i>	CGCATTTCTCATGGAATTT	CTTCTCACGCTGTTTGTCCA
<i>Osh36</i>	AACGCATTTGTGGTTGGCTC	TCAACTTTGGCCGGTGTCTT
<i>OsI57</i>	ACCCTAAAGTAAATGAAGTC	CCTGCTCTTGTCTTGTTA
<i>OsNCED1</i>	ACCATGAAGTCCATGAGGCT	TCTCGTAGTCTTGGTCTTGG
<i>OsNCED3</i>	CAAGTTCGAGTACGGCGAGG	GACAGGATGTAGCCGTCGTC
<i>OsNCED4</i>	TCGGGAGGTACGACTTCCAT	TTGAGGTACGGCTTGGACAC
<i>OsZEP</i>	GGATGCCATTGAGTTTGGTT	TGGCTGACTGAAGTCTCTCG
<i>OsABA8ox1</i>	CAAGCCCAACACGTTTCATGC	TGTACTIONGGTTGCGAGGTGG
<i>OsABA8ox2</i>	CTACTGCTGATGGTGGCTGA	CCCATGGCCTTTGCTTTAT
<i>OsABA8ox3</i>	AGTACAGCCCATTCCTGTG	ACGCCTAATCAAACCATTGC
<i>CAO</i>	TTGGCACAAATGGAGACCC	GCTGCACTGGACCAGACAC
<i>rbcS</i>	CCGTGAGAACCACAGATCCC	ACGTTGTCTGAAGCCGATGAT
<i>rbcL</i>	ATCGTGCTCGCGGTATCTTT	ACCAGGTGCATTACCCCAAG
<i>HEMA1</i>	ACACGCCATCTGTTTGAGGT	CAAGCCTCCACTGTTTTGCC
<i>psbA</i>	TGTAGCTGGTGTATTCGGCG	ATAACCATGAGCGGCCACAA
<i>porA</i>	ATCACCAAGGGCTACGTCTC	GAGTTGTTGTTCCAGCTCCA
<i>NPH1a</i>	CACTTGCAACCAATGCGTGA	ATCCGGGAGTTCCTTTGCAG
<i>CHLI</i>	CGGAGTAACCTTGGTGCTGT	CTTGGCAGCCCTGTTAGTCA
<i>psbS1</i>	CTGAGCCGAAGCCAAAGTTC	ATCCCCGTCTCCAGGTTTCAG
<i>CHLH</i>	TGACTCAGACCCGACAAAGC	TCCCCTCGTACCACTTAGGG
<i>CHLD</i>	GGAAAGAGAGGGCATTAG	CAATACGATCAAGTAAGTGTT
<i>cab2R</i>	GTTCTCCATGTTCCGGCTTCT	GACGAAGTTGGTGGCGTAG

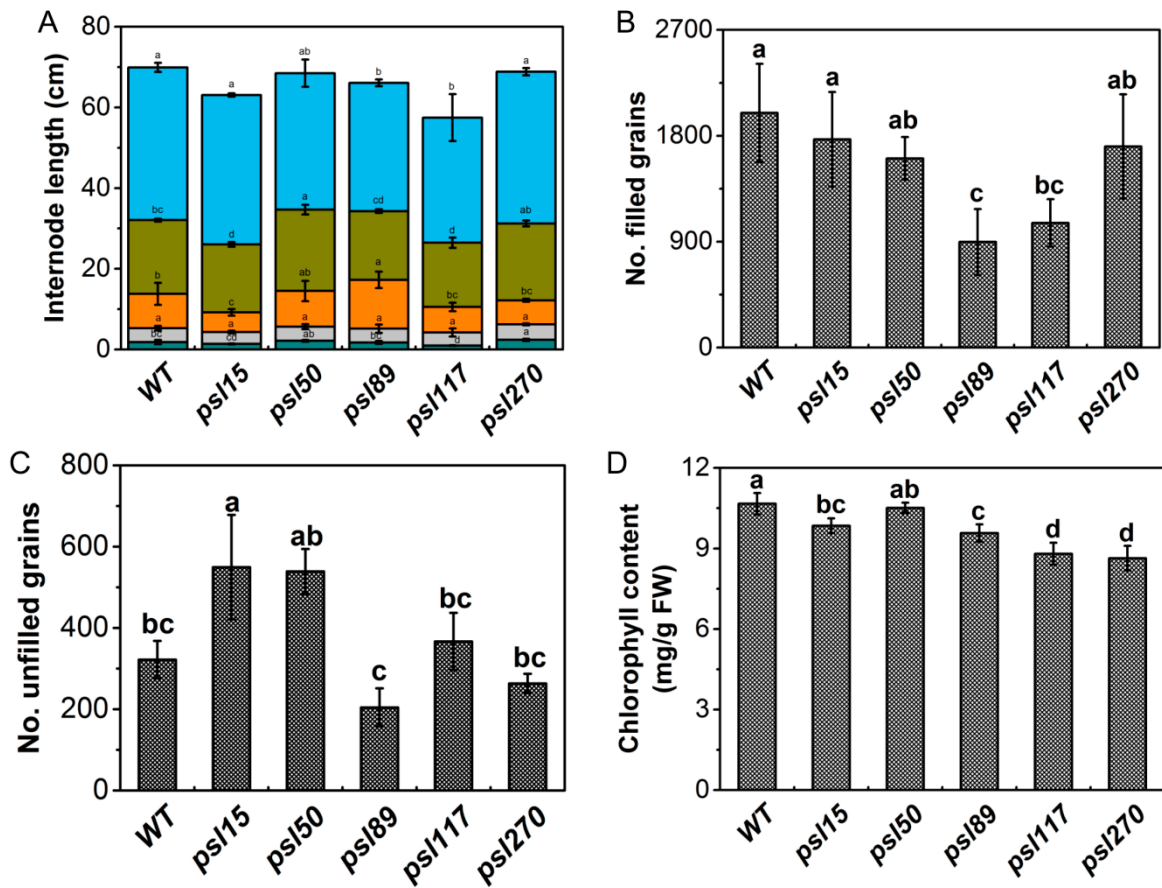


Figure S1. Agronomic traits and chlorophyll contents in WT and mutants. (A) internode length of WT and mutants; Columns from bottom to top represent internode I , internode II , internodeIII, internodeIV and internode V , respectively. (B) number of filled grain in WT and mutants. (C) number of unfilled grain in WT and mutants. (D) chlorophyll contents of WT and mutants at the seedling stage. Error bars indicate \pm SD (n=3). Different letters above the columns indicate a statistical difference at $P \leq 0.05$ by Duncan's test.

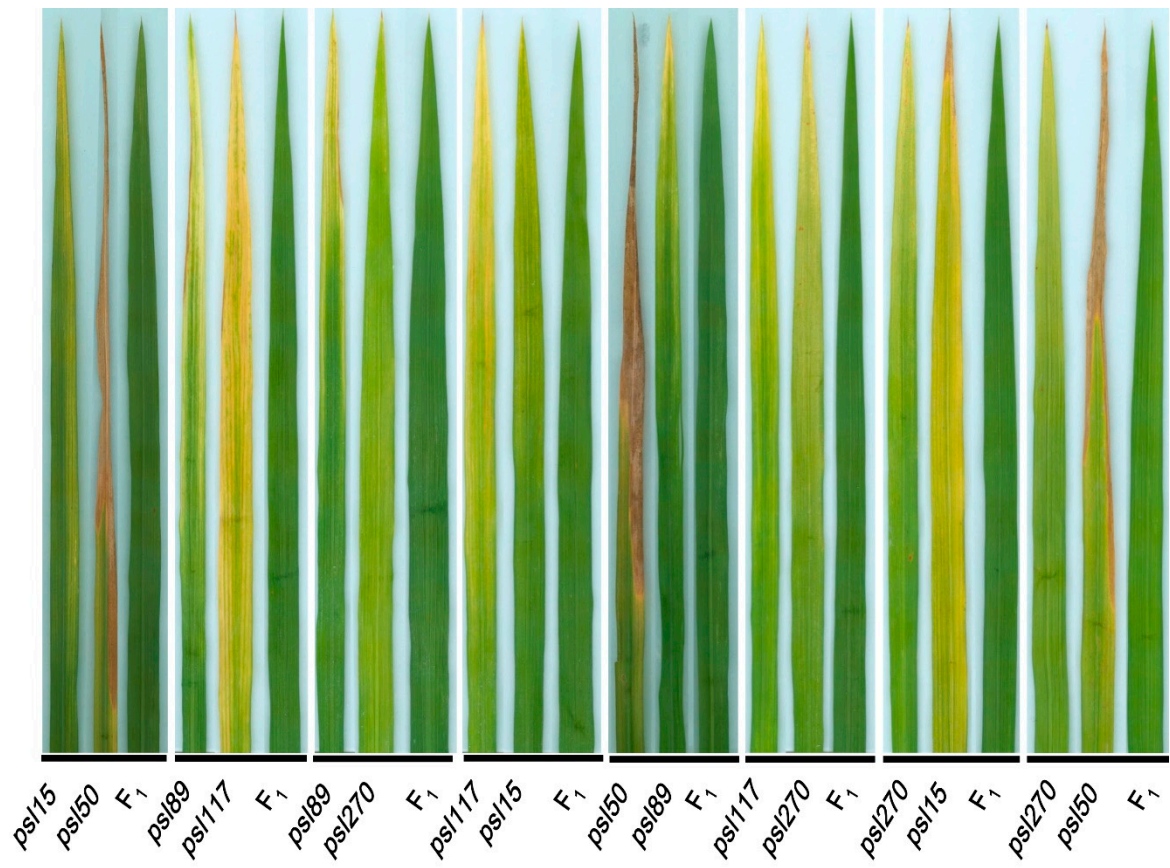


Figure S2. Bottom second leaf phenotypes of parental mutant lines and F₁ plants at the tillering stage.