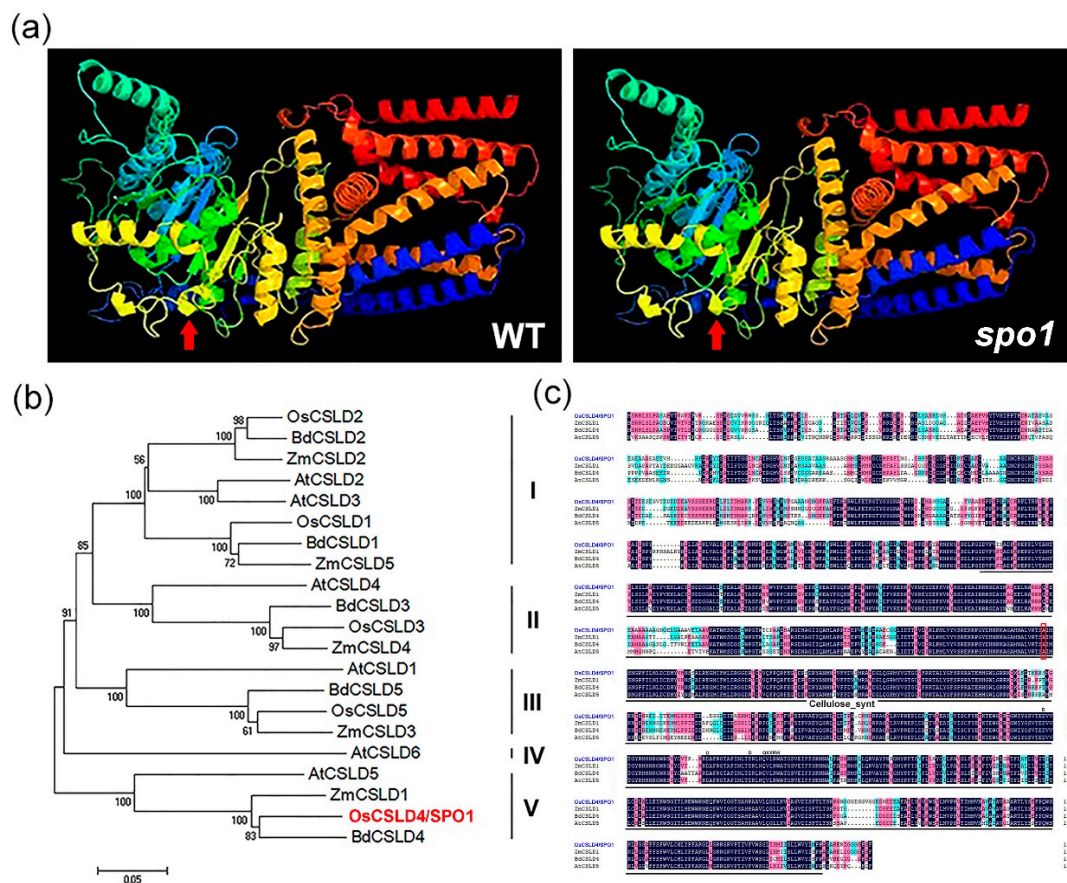
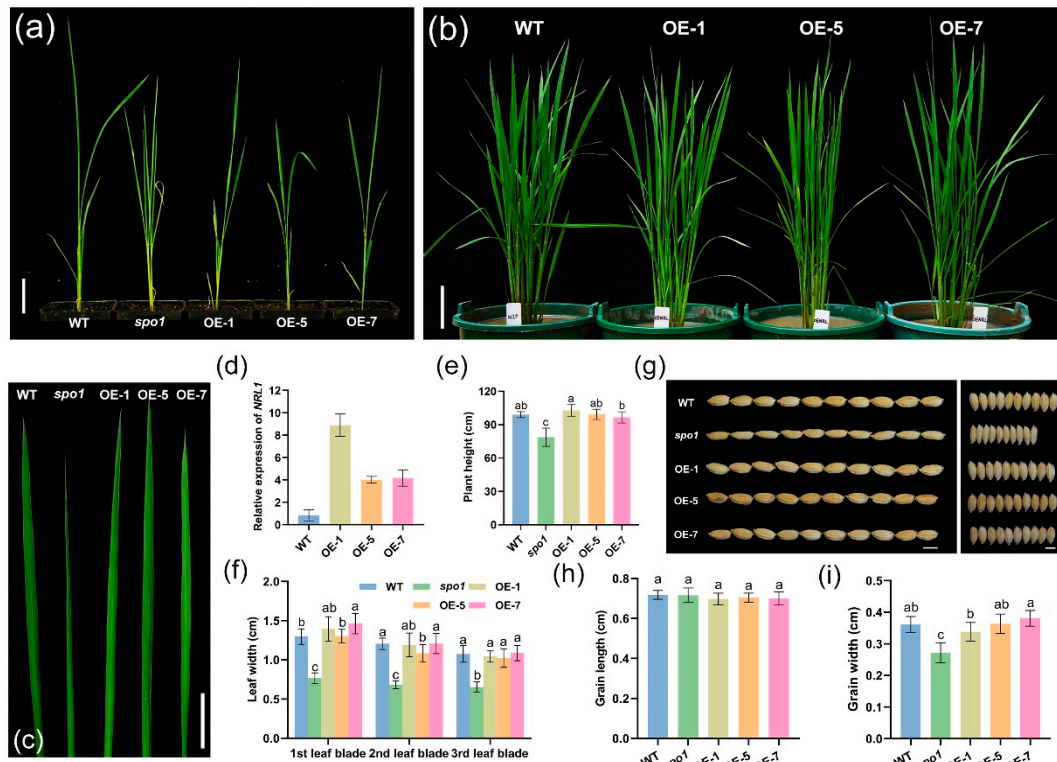


**Figure S1.** Characterization of pigment content of *spo1* mutant. The pigment contents of second leaf from the top at tillering stage. Pigment contents data are mean  $\pm$  SD (n = 4), asterisks indicate significant differences according to Student's t-test (\*P < 0.05).

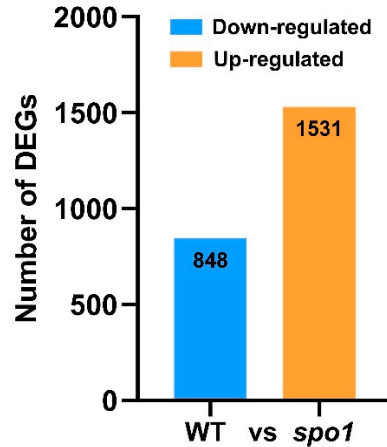


**Figure S2.** *SPO1* encodes a cellulose synthase-like protein D4. (a) The three-level structure prediction model of WT and *spo1* protein. The arrow is the position of the structural change. (b) Phylogenetic tree of *SPO1* and its highly similar proteins of CSLD family members among other species. Numbers at each node represent bootstrap support. The scale bar indicates the genetic distance based on branch length.

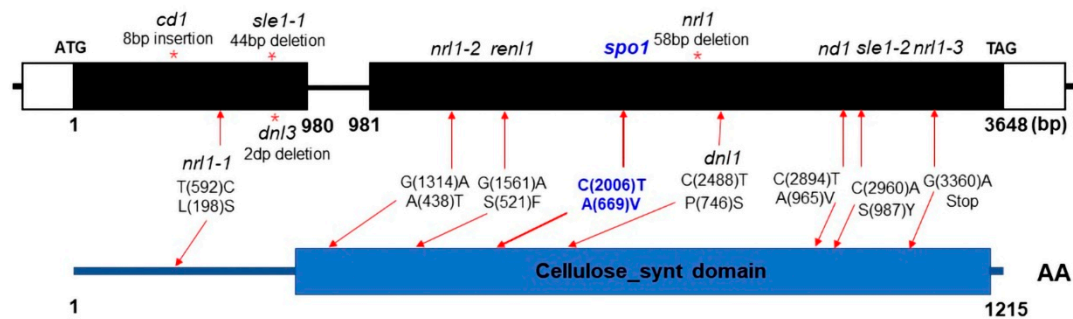
(c) Multiple sequences alignment of *Oryza sativa* Japonica Group SPO1/OsCSLD4 (Os12g0555600), BdCSLD4 (XP\_003575482.1), AtCSLD5 (NP\_171773.1), ZmCSLD1 (GRMZM2G015886). The amino acids showing identity are shaded dark blue, whereas similar amino acids are pink and light blue. The conserved D, D, D, QXXRW motifs are labelled. The black horizontal line marked the Cellulose\_synt domain. The red box is marked with the *spo1* mutation site. The accession numbers of the CSLDs used in this study are AtCSLD1 (NP\_001324935.1), AtCSLD2 (NP\_197193.1), AtCSLD3 (NP\_186955.1), AtCSLD4 (NP\_195532.1), AtCSLD5 (NP\_171773.1), AtCSLD6 (NP\_174497.1), OsCSLD1 (XP\_015614304.1), OsCSLD2 (XP\_015643356.1), OsCSLD3 (XP\_015649263.1), SPO1/OsCSLD4 (Os12g0555600), OsCSLD5 (XP\_015642593.1), BdCSLD1 (XP\_024317796.1), BdCSLD2 (XP\_003557145.1), BdCSLD3 (XP\_003573792.1), BdCSLD4 (XP\_003575482.1), BdCSLD5 (XP\_003568676.1), ZmCSLD1 (GRMZM2G015886), ZmCSLD2 (GRMZM5G870176), ZmCSLD3 (GRMZM2G061764), ZmCSLD4 (GRMZM2G044269), ZmCSLD5 (GRMZM2G436299).



**Figure S3.** Characterization of overexpression (OE) plant morphology. (a) The seedlings of WT, *spo1*, OE-1, OE-5 and OE-7 plant. (b) Gross morphology of WT, OE-1, OE-5 and OE-7 plants at the tillering stage. (c) Morphology of the second leaf blades from top of WT, *spo1*, OE-1, OE-5 and OE-7 plants. (d) qRT-PCR analysis of the expression of *SPO1* in *spo1*. (e, f) Statistical analysis of plant height (e), the top three leaf blades width (f) among WT, *spo1*, OE-1, OE-5 and OE-7 plant at the mature stage. (g) Paddy rice grains of WT, *spo1*, OE-1, OE-5 and OE-7 plant. (h, i) Statistical analysis of seed length (h), seed width (i). Data presented are means ± SD; different letters indicate significant differences according to Duncan's multiple range test (5% α). Scale bars: (a) 5 cm; (b) 20 cm; (c) 5 cm; (d) 0.45cm (left) and 0.25cm (right).



**Figure S4.** RNA-seq detected 2379 differentially expressed genes, of which 848 genes were downregulated, 1531 genes were significantly upregulated, fold change > 2, FDR < 0.05.



**Figure S5.** Comparative analysis of identified *OsCSLD4* allele mutation sites. The *OsCSLD4* gene structure and protein domain are shown above and below, respectively. The black box, black line, white box, and blue box represent exon, intron, UTR, and protein domain, respectively. Italics indicate *OsCSLD4* mutant alleles in previously studies. The blue font is a *spo1* mutant for this study. Asterisks represent the bases deletion or insertion and arrows represent single base substitution.

**Table S1.** The analysis of the potentially cis-elements in the promoter sequence

Motif	Distance	Sequence	Function
ABRE	-1215(+)	CACGTG	cis-acting element involved in the
	-312(-)	ACGTG	abscisic acid responsiveness
CGTCA-motif	-315(+)	CGTCA	cis-acting regulatory element
			involved in the MeJA responsiveness
TGACG-motif	-1392(-)	TGACG	cis-acting regulatory element
	-311(-)	TGACG	involved in the MeJA responsiveness
LTR	-63(-)	CCGAAA	cis-acting element involved in
			low-temperature responsiveness
MBS	-1072(-)	CAACTG	MYB binding site involved in
			drought inducibility
TATC-box	-1647(+)	TATCCCA	cis-acting element involved in
			gibberellin responsiveness
TGA-element	-1496(+)	AACGAC	auxin-responsive element
MSA-like	-478(+)	CCAAACGGCT	cis-acting element involved in cell
		ACTTCCATCT	cycle regulation
		TCCACCC	

**Table S2.** Summary of the primers used in this study.

Primer name	Forward primer (5'→3')	Reverse primer (5'→3')	Purpose
R12M10	ATCATTTTCAGCCTGTGC C	AGCTTAATAGGGGGG ACG	Gene mapping
RM101	GTGAATGGTCAAGTGAC TTAGGTGGC	ACACAACATGTTCCCT CCCATGC	
RM277	CGGTCAAATCATCACCT GAC	CAAGGCTTGCAAGGG AAG	
RM17	TGCCCTGTTATTTTCTTC TCTC	GGTGATCCTTTCCCATT TCA	
RM519	AGAGAGCCCCTAAATTT CCG	AGGTACGCTCACCTGT GGAC	
RM463	TTCCCCTCCTTTTATGGT GC	TGTTCTCCTCAGTCACT GCG	
RM28433	AATAGCTGCATATACCC GGTTGG	TGTGTCTCTGATGATC CGTTTCG	
RM28449	CACCCATTGATGTGAAA CTCTGG	GGATTCATGATACAGT GTGCAACG	
RM28460	ACCGCACCACTACCTC TGG	TGCACAGCCCTATATA GCAACTCC	
RM28465	GCCTCGTAGAGACTCAA ACTAAACG	GTAGCTAGCCACCAAT AGCATGG	
RM3726	TACACCCACCCACATAC GTCAGC	GTCGTACTCCCGGATC TTCTTCC	
RM6410	GGAAGAAGCATCTGCA GTAGTAGACG	GAATTAGCCGACAGC GTCTTGG	
RM5479	CTCACCATAGCAATCTC CTGTGC	ACTTCGTTCACTTGCA TCATGG	
RM28637	TCACATGTCATACGGCT ACAGACC	CACAATCACAGTGTGT GCAAAGG	
RM6411	GTGAAGGCTGTACCATC CAACG	CGGGTATTGTCGGTGT TCAGG	
R12M43	CCGCCGAGAAGAAACA AAG	CCCAAGAACAGGATT ACA	
RM235	AGAAGCTAGGGCTAAC GAAC	TCACCTGGTCAGCCTC TTTC	
RM28428	AACTCCTCGACTTTCGC GATATGACC	GCGGATGATTTCTCCG GTAAATTGG	
RM6217	CGCAGATGGAGATTCTT GAAGG	ACAGCAGCAAGAGCA AGAAATCC	
RM28457	TTAGCTAGCCACTACCA AGAGAGG	GTCCTTTCGACAGTAC ATCTGG	
RM28451	TGAGTTCGAGTTCGATT TCTCG	TCCTTCAAGAATCTCC ATCTGC	
RM28456	TGTACACTCACCTTCGC TTCTCC	CCTCTCTTCGTTCTGGA GTCTGG	
RM28621	GTGTCAACTGTCAACAA ACACC	AAGGTCAGGGTTACAT GATAGG	
RM28610	GAGTAAGTTCCTGCTTC TGTTTGC	GTCGAAGCTTTCATCT CTATCTCC	

Pun- <i>SPO1</i>	CGGGATCCATGTCGCGG CGGCTGTCGT	CGAGCTCCTATGGGAA GCTGAATCCGC	Transformation construct
P35s- <i>SPO1</i> - GFP	GCTCTAGAATGTCGCGG CGGCTGTCGT	CGGGATCCTGGGAAG CTGAATCCGCCG	
q <i>OsActin1</i>	GTGGTCGCCCCCTCCTGA AAG	GGCTTAGCATTCTTGG GTCCG	qRT-PCR
q <i>SPO1</i>	CAGCGTCTCCCAAGCCA TTC	CCACCGACATCGCCCA CAG	
q <i>NAL1</i>	ACATTGGGGATGTCAAG GTTAT	ACATTGGGGATGTCAA GGTTAT	
q <i>NAL7</i>	ATCGTAGAGTTCTTCAC CAT	CCAGATAAGCAGGCA GTA	
q <i>NRL2</i>	TCCCTTTCTTTTGATGAG GA	GCTACATGTAACGCCG ATTC	
q <i>ACL1</i>	CTGAAGCTGAACCTCTC GCTG	GGAGCATGACGTAGA TGAAGCAG	
q <i>ACL2</i>	CTCGTGCCTGTCGTCGG AG	TCGGCGAGCATGACGT AGAG	
q <i>RL14</i>	GAGGATGAACTACTATC CACCG	GTGCTCAACACTTCTG AACTTT	
q <i>OsZHD1</i>	CAGGAGCAGAAGGACA AGATG	CGACGATGAGATCAA ATGCATT	
q <i>NAL9</i>	TTTATGATTGCATGTCCT GGAT	TCTCACCGCCAGCAAG TAT	
q <i>SLL1</i>	CAGCTCGCAGGTGTCCA A	CCTCCCTAGAGTGAAC TCGAGACT	
q <i>Roc5</i>	CGCAAGAGGAAGAAGC GATAC	GCTCCAGTTGCGTCTT CATC	
q <i>RL9</i>	ATTCTTGCAACATGGAC GCC	CATTAGCCTCTGTGAT TGCC	