

Supplementary Material

Supplementary Table 1 Primers used for qRT-PCR

Primer name	Forward primer (5'→3')	Reverse primer (5'→3')
<i>OsActin</i>	TGGCATCTCTCAGCACATTCC	TGCACAATGGATGGGTCAGA
<i>MPK12</i> -qRT	TGACCAAGAGAGGAGTGCAG	CGTCATCGTTGTGCACTAGG
<i>AOS2</i> -qRT	GAGAGACGGAGAACCCTAGC	GAAGTGATGGCCGGCTTAAG
<i>LYP6</i> -qRT	AACTGCTGGAAATGTGTGC	TTGAAGACCAGAGGAGAGACG
<i>PR2</i> -qRT	CGGTACAAGTAGGAGGAGCT	GCTCGACGTTGAACCTGATC
<i>ASP90</i> -qRT	CCTTCCAAC TGAGGTCGAGT	AGACTGCAGGCTGTGTAAGA
<i>PR1a</i> -qRT	TCTCACCAGCATACGTCGT	ATCCCAAGTCCTGCGTACAA

Supplementary Table 2 Primers used for mapping

Primer name	Forward primer (5'→3')	Reverse primer (5'→3')
M1	CGCTGCTCACCGTCACTG	GCAAAGCAATCGCAGAATTT
M2	CCTCTTCCTCCCACTCTCCT	GTCGTCGTCGTACTCCTCGT
M3	GCCATGTCATATTCCTATGCAA	GGGTGAATTAGACATAACCATAGG
M4	ACTCCCTCCGTTTCATAATGT	TGTGTATGATAGGTGGGACCAG
M5	TCGTGGTTAGTAAGCTTCCATGT	CGAACCAATGGCTTCTTGAC
M6	TTTTTCGTCACGTCAAATGTT	CCTGTAAACAGCGAGACGAA
M7	TGGAGAGTAAATGGGGGAAT	CCGCTGGTTCATCAAGTCTA
M8	CTGATGGGCGAACAACCT	CTTGGTCGTCGTCACCTGTTG
M9	GCATGCCACAAATCGTTGTA	TCGCCATTCGTGTGACTACT
M10	GGCATAAATTAGGCGCAAAG	TTTTACCGTGTGGTGCAAA

Supplementary Table 3 Primers used for vector construction

Primer name	Primer sequence (5'→3')
<i>SPL88-1300-F</i>	CATGATTACGAATTCGCTGCACATGGTCAAAGTGA
<i>SPL88-1300-R</i>	GCCAGTGCCAAGCTTGGCTGTGAATTTGACGATCCAT
<i>SPL881305.1-F</i>	CATGATTACGAATTCGCTGCACATGGTCAAAGTGA
<i>SPL88-1305.1-R</i>	TCAGATCTACCATGGCGCCGCCGCCGGTGAGGTC
<i>SPL88-1132-F</i>	TTCGATATCAAGCTTATGAGCGGGGGCGGG
<i>SPL88-1132-R</i>	GCTCACCATGGTACCTGCAAGATAGCGATATAACTTCC

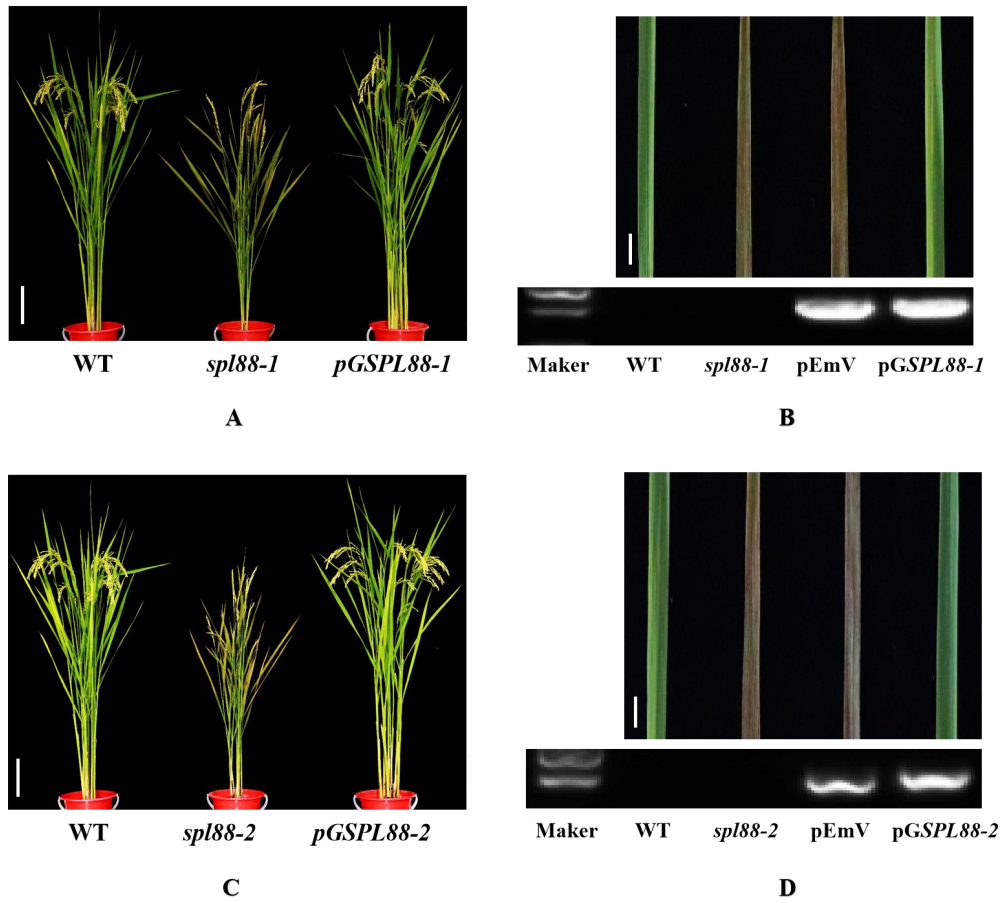
Supplementary Table 4 *spl88-1* genetic analysis

Cross	F ₁ phenotype	F ₂ phenotype			χ^2 (3; 1)
		Normal	Lesion mimics	Total	
<i>spl88-1/NJ06</i>	normal	681	231	912	0.0526
<i>NJ06/spl88-1</i>	normal	594	193	787	0.0953

Supplementary Table 5 *spl88-2* genetic analysis

Cross	F ₁ phenotype	F ₂ phenotype			χ^2 (3; 1)
		Normal	Lesion mimics	Total	
<i>spl88-2/NJ06</i>	normal	573	154	627	0.0643
<i>NJ06/spl88-2</i>	normal	659	215	874	0.0748

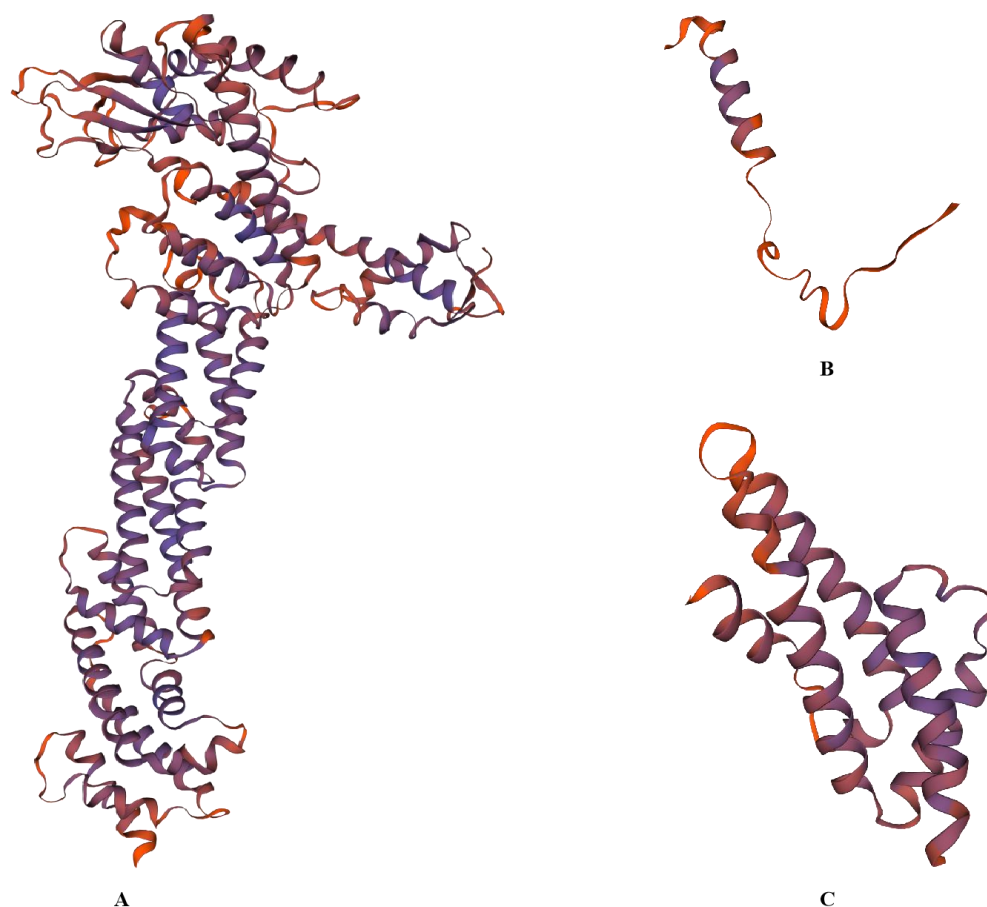
Supplementary Figure 1 Functional Complementation of the *spl88-1* and *spl88-2* Mutants with *LOC_Os02g51180*



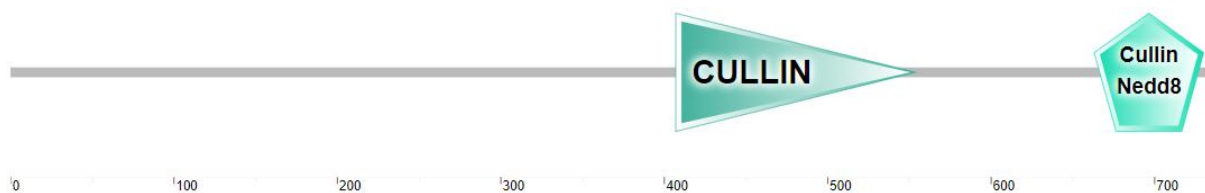
A, C: the phenotype of the *spl88-1* and *spl88-2* transformed with the genomic sequence of *SPL88* (pGSPL88) was completely recovered to that of the wild type; Bar=15 cm.

B, D: hygromycin selection of transgenic plants. pEmV: empty vector; Bar=3 cm.

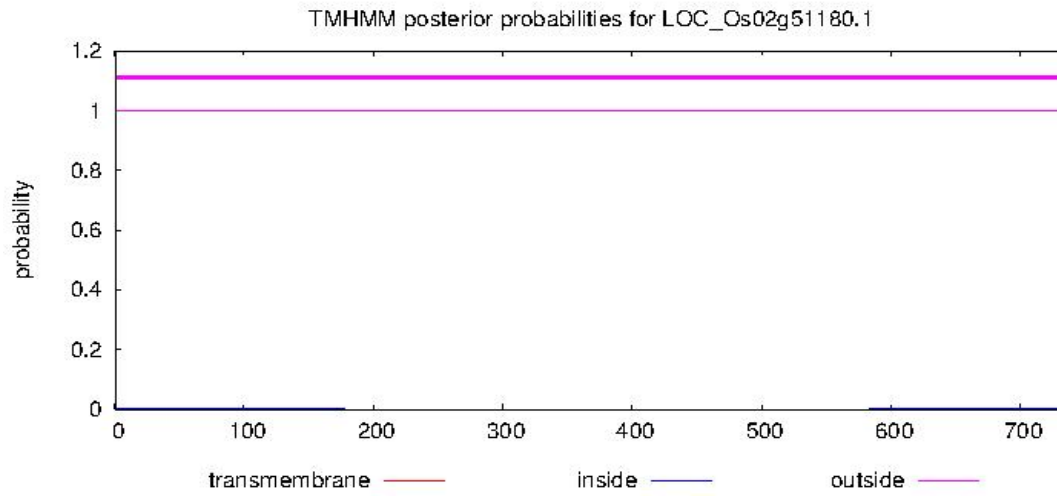
Supplementary Figure 2 Three-dimensional structure of SPL88, SPL88-1 and SPL88-2



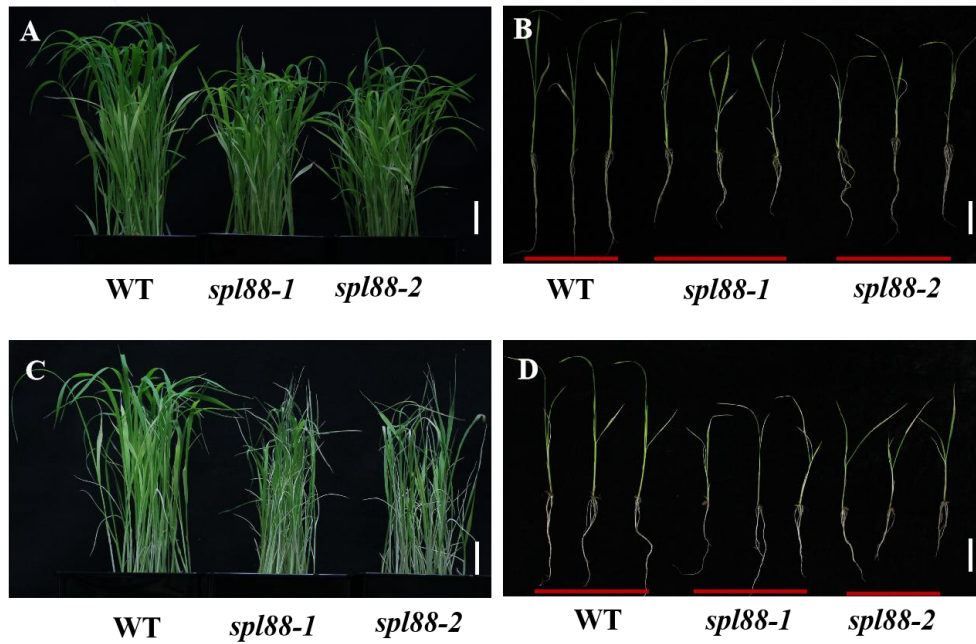
Supplementary Figure 3 Structural prediction of the protein encoded by *SPL88*



Supplementary Figure 4 *SPL88* transmembrane domain analysis



Supplementary Figure 5 Analysis of salt stress in wild type, *spl88-1* and *spl88-2*



A, B: Wild-type and mutant plants on 0 mM NaCl at 4 days of culture.
 C, D: Wild-type and mutant plants on 150 mM NaCl at 4 days of culture.