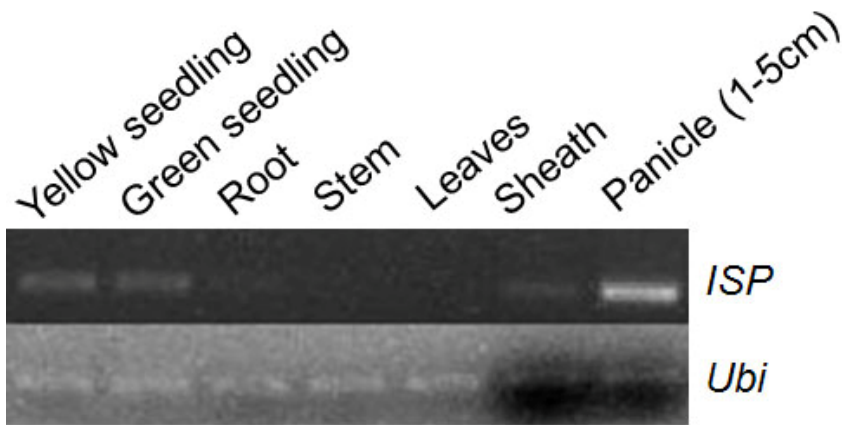


Supplementary Information

Table S1. The rice varieties used in this study.

No.	Varieties	Subspecies	No.	Varieties	Subspecies
1	Zhefu 802	<i>indica</i>	11	Zhonghua 11	<i>japonica</i>
2	93-11	<i>indica</i>	12	Xiangnuo 8333	<i>japonica</i>
3	Nanjing 6	<i>indica</i>	13	Nipponbare	<i>japonica</i>
4	Nanjing 11	<i>indica</i>	14	Nanjing 46	<i>japonica</i>
5	Guichao 2	<i>indica</i>	15	Shennong 1033	<i>japonica</i>
6	Xieqingzao	<i>indica</i>	16	Wyunjing 8	<i>japonica</i>
7	Zhenshan 97B	<i>indica</i>	17	Wuyujing 3	<i>japonica</i>
8	Longtepu	<i>indica</i>	18	Balilla	<i>japonica</i>
9	Teqing	<i>indica</i>	19	Taibei 309	<i>japonica</i>
10	Minghui63	<i>indica</i>	20	Yandao 8	<i>japonica</i>

Figure S1. Relative expression of *ISP* by RT-PCR analysis. Amplification of the rice *Ubiquitin* gene (*Ubi*) was used as a control. Total RNA was extracted from various tissues (roots, stems, leaves, sheath, and panicles) of 93-11 at the heading stage, and seedlings of 93-11.



The 3.1 kb sequence of *ISP* gene region from 93-11. The red upper letters show the exon

cagggtgctgctcaaaacaacgggtaagcagatccgtcaattagataggttacatccgtcttaggctgggtgtataattagtttgcctgctatccatcaagatctgtaacgcgt
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 GTCCATGGGGTGGGGGCGAAGGCACCTCTACAGaggttaatttactgcttaattaagggttaagcacttaatttacaagggtattcctataatag
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The *ISP* gene region sequence from Nipponbare. The red upper letters show the exon

cagggtgctgctcaaaaacagggttaagcagatatccgtcaatttgatagtaagatctgtaacgcgtggtctttcagctgaaaactatggactctttgaaacaaagataatatta
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