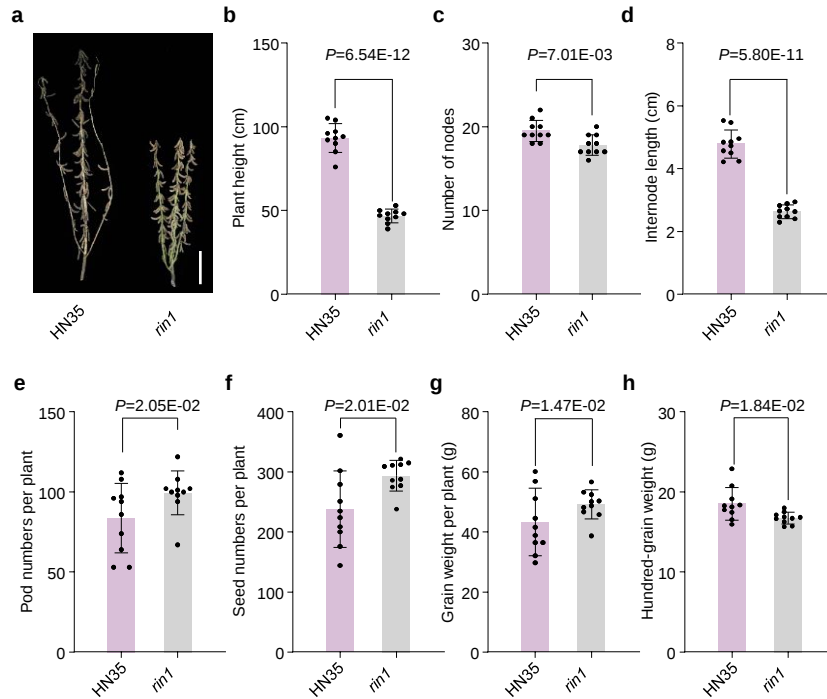
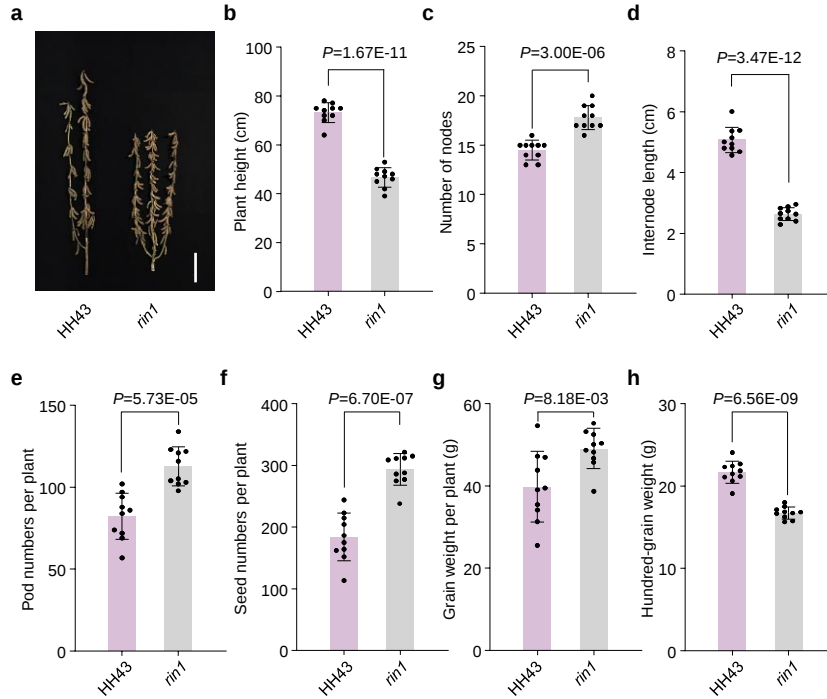




Supplementary Fig. 1 Phenotypic differences between wild-type HN35 and its mutant *rin1* in the field in Harbin, 2017.

a Phenotype of HN35 and *rin1* at maturity. Scale bar = 10 cm. **b** Plant height (cm). **c** Number of nodes. **d** Internode length (cm). **e** Pod numbers per plant. **f** Seed numbers per plant. **g** Grain weight per plant (g). **h** Hundred-grain-weight per plant (g). All plants were planted in a nature field of Harbin, China (45°75'N, 126°63'E) and the phenotypes were scored after maturity. All data of (b)–(h) are means $\pm$ SEM ($n = 10$ plants). A student's *t*-test (two-sided) was used to generate the *P* values.



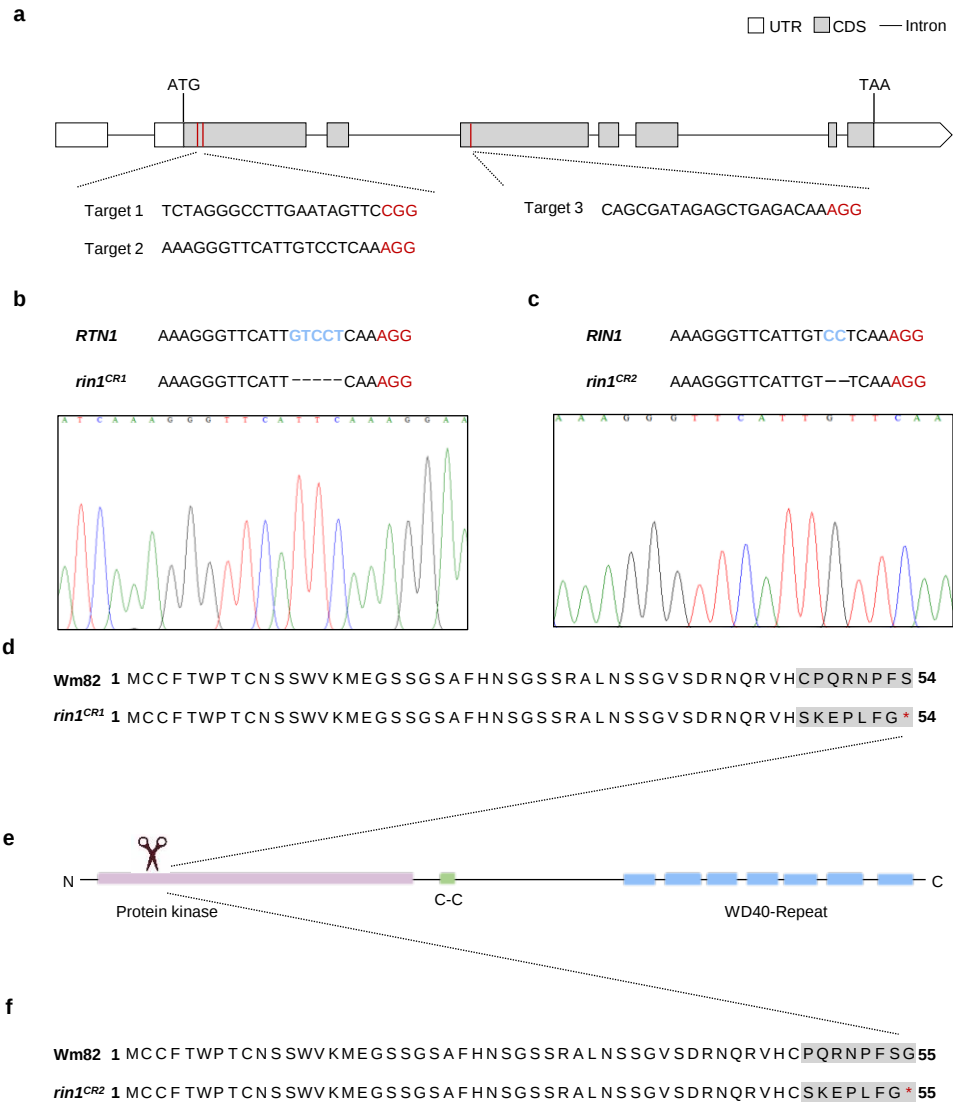
Supplementary Fig. 2 Phenotypic differences between HH43 and *rin1* in the field in Harbin, 2017.

a Phenotype of HH43 and *rin1* at maturity. Scale bar = 10 cm. **b** Plant height (cm). **c** Number of nodes. **d** Internode length (cm). **e** Pod numbers per plant. **f** Seed numbers per plant. **g** Grain weight per plant (g). **h** Hundred-grain-weight per plant (g). All plants were planted in a nature field of Harbin, China (45°75'N, 126°63'E) and the phenotypes were scored after maturity. All data of (b)–(h) are means $\pm$ SEM ($n = 10$ plants). A student's *t*-test (two-sided) was used to generate the *P* values.

				Kinase domain	
Wm82	MCCFTWPTCNSSWVKMEGSSGSAFHNSGSSRALNSSGVSDRNQVRVHCPQRNPFSGEASQDSGFRKERDRVLLAQGGQPKNLGGGFSGLCEDEVEVDPPFC	100			
HH43	MCCFTWPTCNSSWVKMEGSSGSAFHNSGSSRALNSSGVSDRNQVRVHCPQRNPFSGEASQDSGFRKERDRVLLAQGGQPKNLGGGFSGLCEDEVEVDPPFC	100			
HN35	MCCFTWPTCNSSWVKMEGSSGSAFHNSGSSRALNSSGVSDRNQVRVHCPQRNPFSGEASQDSGFRKERDRVLLAQGGQPKNLGGGFSGLCEDEVEVDPPFC	100			
rin1	MCCFTWPTCNSSWVKMEGSSGSAFHNSGSSRALNSSGVSDRNQVRVHCPQRNPFSGEASQDSGFRKERDRVLLAQGGQPKNLGGGFSGLCEDEVEVDPPFC	100			
	<u>mccftwptcnsswvkmegegssgafhnsgssralnssgvsdnrqvrhchpqrnpfsgsasqdsgrfkerdrvllaq gqpknlgggfsglcedevevdppfc</u>				
Wm82	AVEWGDISLRQWLDKPFERSVDAFECLHIFRQIVEIVSVAHSQGQVVVHNVRPSCFVMSSFNHISFIESASCSDTGSDSLDGMNNQGGVEKTPTSLCPHDM	200			
HH43	AVEWGDISLRQWLDKPFERSVDAFECLHIFRQIVEIVSVAHSQGQVVVHNVRPSCFVMSSFNHISFIESASCSDTGSDSLDGMNNQGGVEKTPTSLCPHDM	200			
HN35	AVEWGDISLRQWLDKPFERSVDAFECLHIFRQIVEIVSVAHSQGQVVVHNVRPSCFVMSSFNHISFIESASCSDTGSDSLDGMNNQGGVEKTPTSLCPHDM	200			
rin1	AVEWGDISLRQWLDKPFERSVDAFECLHIFRQIVEIVSVAHSQGQVVVHNVRPSCFVMSSFNHISFIESASCSDTGSDSLDGMNNQGGVEKTPTSLCPHDM	200			
	<u>awewgdslsrqlwdkpersvdafeclhifrqiveivsahsqgvvvhnrpscfvmsfnhifiesascsdtgdsldgmnngqgevktptslcphdm</u>				
Wm82	HQQSLGSEDFMPIKTSTTPARSDSSCMLSSAVYAARASLIETEENKMKDRRKDEEVEGKKQSFPMKQILLMEMSWYTSPEEGAGESSSCASDVYRLGVL	300			
HH43	HQQSLGSEDFMPIKTSTTPARSDSSCMLSSAVYAARASLIETEENKMKDRRKDEEVEGKKQSFPMKQILLMEMSWYTSPEEGAGESSSCASDVYRLGVL	300			
HN35	HQQSLGSEDFMPIKTSTTPARSDSSCMLSSAVYAARASLIETEENKMKDRRKDEEVEGKKQSFPMKQILLMEMSWYTSPEEGAGESSSCASDVYRLGVL	300			
rin1	HQQSLGSEDFMPIKTSTTPARSDSSCMLSSAVYAARASLIETEENKMKDRRKDEEVEGKKQSFPMKQILLMEMSWYTSPEEGAGESSSCASDVYRLGVL	300			
	<u>hqqslgsedfmpiktsttparsdsscmllssavyaaraslieteenkmkdrkdeevegkkqsfpmkqillmemswytspeegagegssscasdvyrllgvl</u>				
Wm82	LFELFCPLSSREEKSRMTSSLRHRLVLPQQLLLKWPKEASFCLWLLHDPKSRPTLGELLQSEFLNEQRDDTEERAAIELRQRIEDQELLLEFLLLLQQR	400			
HH43	LFELFCPLSSREEKSRMTSSLRHRLVLPQQLLLKWPKEASFCLWLLHDPKSRPTLGELLQSEFLNEQRDDTEERAAIELRQRIEDQELLLEFLLLLQQR	400			
HN35	LFELFCPLSSREEKSRMTSSLRHRLVLPQQLLLKWPKEASFCLWLLHDPKSRPTLGELLQSEFLNEQRDDTEERAAIELRQRIEDQELLLEFLLLLQQR	400			
rin1	LFELFCPLSSREEKSRMTSSLRHRLVLPQQLLLKWPKEASFCLWLLHDPKSRPTLGELLQSEFLNEQRDDTEERAAIELRQRIEDQELLLEFLLLLQQR	400			
	<u>lfelfcplssreeksrmtsslrhrlvlpqlllkwpkeasfclwllhdpkrsrptlgellqseflneqrddteereaaielrqriedqelllefilllqqr</u>				
Wm82	KQVEAEKLQHTVSFLCSDIEEVTQKHVRFEKITGAELGSDERSASSFFSMTFVDSSEDSAFGLTRKRVRVRLGMDVKNIEECDDVGDQKNSGFSLSKSSRL	500			
HH43	KQVEAEKLQHTVSFLCSDIEEVTQKHVRFEKITGAELGSDERSASSFFSMTFVDSSEDSAFGLTRKRVRVRLGMDVKNIEECDDVGDQKNSGFSLSKSSRL	500			
HN35	KQVEAEKLQHTVSFLCSDIEEVTQKHVRFEKITGAELGSDERSASSFFSMTFVDSSEDSAFGLTRKRVRVRLGMDVKNIEECDDVGDQKNSGFSLSKSSRL	500			
rin1	KQVEAEKLQHTVSFLCSDIEEVTQKHVRFEKITGAELGSDERSASSFFSMTFVDSSEDSAFGLTRKRVRVRLGMDVKNIEECDDVGDQKNSGFSLSKSSRL	500			
	<u>kqveaeklqhtvsfclsdieevtkqhvrfekitgaelgsdersassffsmtfvdsedsafgltrkrvrvgmdvkniececddvgdqkngsflskssrl</u>				
Wm82	MKNFKKLESAYFLTRCRPAYSSGKLAVRHPPVTS DGRGSSVVVTERSCINDLSKEQCREGASAWINPFLEGLCKYLSFSKLVKADLKQGDLLHSSNLVC	600			
HH43	MKNFKKLESAYFLTRCRPAYSSGKLAVRHPPVTS DGRGSSVVVTERSCINDLSKEQCREGASAWINPFLEGLCKYLSFSKLVKADLKQGDLLHSSNLVC	600			
HN35	MKNFKKLESAYFLTRCRPAYSSGKLAVRHPPVTS DGRGSSVVVTERSCINDLSKEQCREGASAWINPFLEGLCKYLSFSKLVKADLKQGDLLHSSNLVC	600			
rin1	MKNFKKLESAYFLTRCRPAYSSGKLAVRHPPVTS DGRGSSVVVTERSCINDLSKEQCREGASAWINPFLEGLCKYLSFSKLVKADLKQGDLLHSSNLVC	600			
	<u>mknfkkllesayfltrcrpayssgklavrhppvtsdgrgssvvvterscindlskeqcregasawinpfleglckylsfsklvkadtqgdllhssnlvc</u>				
Wm82	SLSFDRDGEFFATAGVNNKKIKVFECDISIINEDRDIHYPPVEMASRSKLSSICWNNTYIKSQIASSNFEGVVQLWDVTRSQVISEMREHERRVWSIDFSSAD	700			
HH43	SLSFDRDGEFFATAGVNNKKIKVFECDISIINEDRDIHYPPVEMASRSKLSSICWNNTYIKSQIASSNFEGVVQLWDVTRSQVISEMREHERRVWSIDFSSAD	700			
HN35	SLSFDRDGEFFATAGVNNKKIKVFECDISIINEDRDIHYPPVEMASRSKLSSICWNNTYIKSQIASSNFEGVVQLWDVTRSQVISEMREHERRVWSIDFSSAD	700			
rin1	SLSFDRDGEFFATAGVNNKKIKVFECDISIINEDRDIHYPPVEMASRSKLSSICWNNTYIKSQIASSNFEGVVQLWDVTRSQVISEMREHERRVWSIDFSSAD	700			
	<u>slsfdrdgeffatagvnnkikvfecdssiinedrdihypvemasrsklssicwnntyiksqiassnfegvvqlwdvtrsqvise mreher rvwsidfssad</u>				
Wm82	PTMLASGSDDGSVKLWSINQGVSVGTIKTKANVCCVQFPDLSARFLAFGSADHRIYYYDLRNLKMFCLTLVGHNKTVSYIKFVDTVNLVSASTDNTLKLW	800			
HH43	PTMLASGSDDGSVKLWSINQGVSVGTIKTKANVCCVQFPDLSARFLAFGSADHRIYYYDLRNLKMFCLTLVGHNKTVSYIKFVDTVNLVSASTDNTLKLW	800			
HN35	PTMLASGSDDGSVKLWSINQGVSVGTIKTKANVCCVQFPDLSARFLAFGSADHRIYYYDLRNLKMFCLTLVGHNKTVSYIKFVDTVNLVSASTDNTLKLW	800			
rin1	PTMLASGSDDGSVKLWSINQGVSVGTIKTKANVCCVQFPDLSARFLAFGSADHRIYYYDLRNLKMFCLTLVGHNKTVSYIKFVDTVNLVSASTDNTLKLW	800			
	<u>ptmlasgsddgsvklwsinqgvsvgtiktkanvccvqfpdlsarflafgsadhriyydlrnlkmpcltlvgnhktvsyikfvdtnlvsaastdntklw</u>				
Wm82	DLSTCASRVIDSPIQSFTGHANVKNFVGLSVSDGYIATGSEINEVFIYHKAFMPALSFQNTDPLSGNEVDDAVQFVSSVCWBGQSSSTLLAANSTGN	900			
HH43	DLSTCASRVIDSPIQSFTGHANVKNFVGLSVSDGYIATGSEINEVFIYHKAFMPALSFQNTDPLSGNEVDDAVQFVSSVCWBGQSSSTLLAANSTGN	900			
HN35	DLSTCASRVIDSPIQSFTGHANVKNFVGLSVSDGYIATGSEINEVFIYHKAFMPALSFQNTDPLSGNEVDDAVQFVSSVCWBGQSSSTLLAANSTGN	900			
rin1	DLSTCASRVIDSPIQSFTGHANVKNFVGLSVSDGYIATGSEINEVFIYHKAFMPALSFQNTDPLSGNEVDDAVQFVSSVCWBGQSSSTLLAANSTGN	840			
	<u>dlstcasrvidspiqsftghanvknfvglsvsdgyiatgseinevfiyhkafmpalsfqn</u>				
Wm82	VKILEM	906			
HH43	VKILEM	906			
HN35	VKILEM	906			
rin1					
	Stop gain	WD40-Repeat			

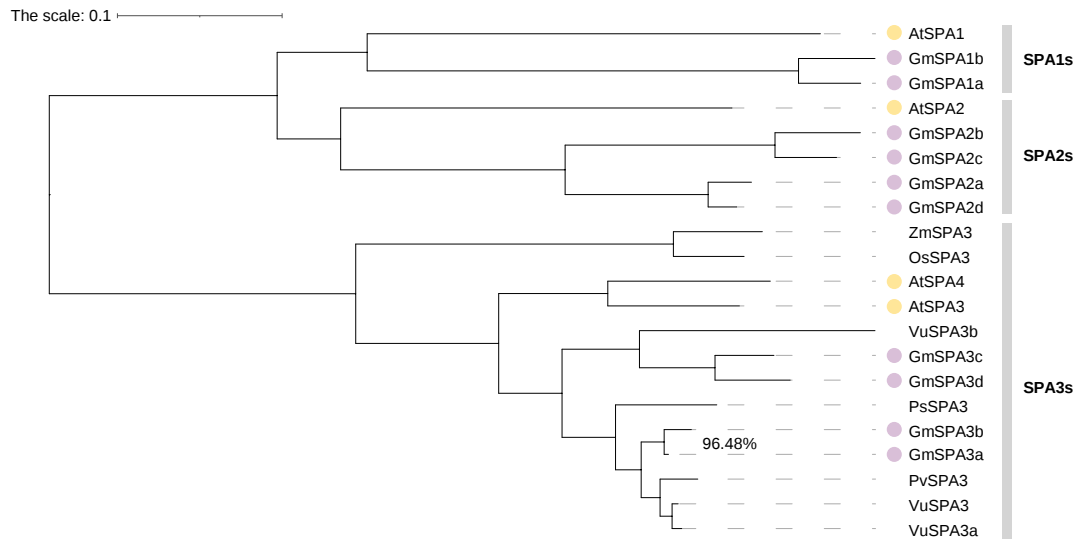
Supplementary Fig. 3 Alignment of soybean RIN1 sequences between the reference accession Wm82, HH43, HN35, and *rin1*.

Amino-acid sequences were aligned by ClustalW Multiple alignment in DNAMAN. Three amino-acid differences were detected in the kinase domain and WD40-repeat domain, respectively. The red line represents kinase domain and blue line represents WD40-repeat domain. The pink box represents the amino acid variant position. The asterisk indicates stop-codon gain.



Supplementary Fig. 4 CRISPR/Cas9 targets and proteins of RIN1 in *rin1^{CR}* mutants.

a The position of three editing targets in *RIN1*. The red lines indicate the CRISPR/Cas9 targets. **b,c** Sanger sequencing reveals a 5-bp deletion at target site 2, designated as *rin1^{CR1}* (**b**) and a 2-bp deletion at target site 2 is designated as *rin1^{CR2}* (**c**). The picture of (**b**) and (**c**) were generated by BioEdit. **d** Protein sequence of RIN1 in Wm82 and *rin1^{CR1}*. **e** Schematic of functional domains of RIN1. The scissor represents the protein termination position. **f** Protein sequence of RIN1 in Wm82 and *rin1^{CR2}*. The gray highlighting in (**d**) and (**f**) depicts the amino acids in *rin1^{CR}* mutants that differ from wild-type Wm82. The asterisk indicates stop codon.



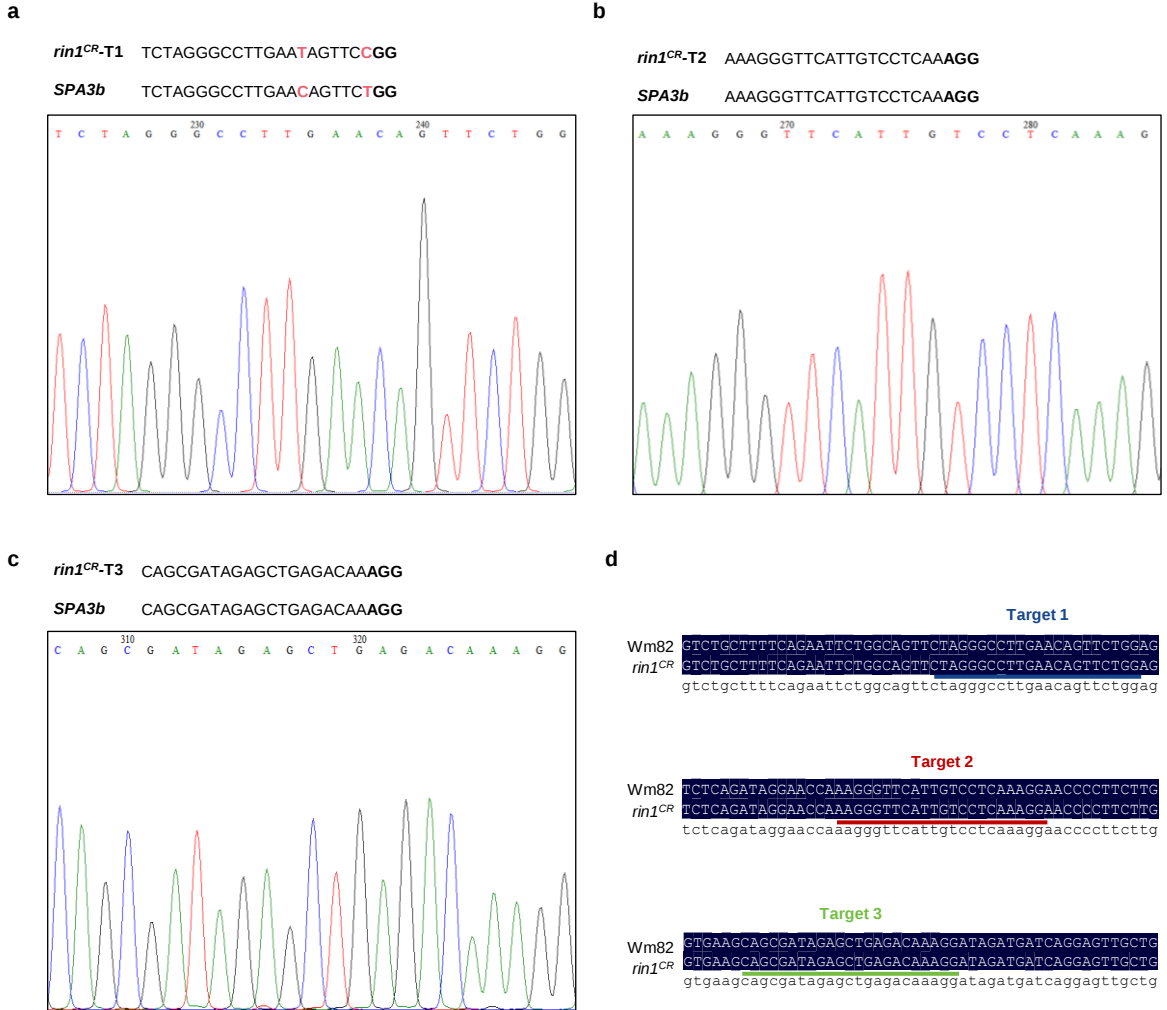
Supplementary Fig. 5 Phylogenetic tree of the SPA proteins from Arabidopsis, soybean, rice, maize and certain leguminous crops.

There are 10 SPA genes in soybean, including SPA1a (*Glyma.07G058200*), GmSPA1b (*Glyma.16G027200*), GmSPA2a (*Glyma.08G021200*), GmSPA2b (*Glyma.05G214900*), GmSPA2c (*Glyma.11G018700*), GmSPA2d (*Glyma.01G224200*), GmSPA3a (*Glyma.12G224600*), GmSPA3b (*Glyma.13G276700*), GmSPA3c (*Glyma.06G242100*) and GmSPA3d (*Glyma.12G155700*), which cluster into three clades that we designate SPA1s, SPA2s and SPA3s. Phylogenetic tree of SPA proteins from *Arabidopsis* (At), *Glycine max* (Gm), *Pisum sativum* (Ps), *Phaseolus vulgaris* (Pv), *Vigna unguiculata* (Vu), *Oryza sativa* (Os), *Zea mays* (Zm) using the Neighbor-Joining Method by MEGA6 software. The protein homology between GmSPA3a and GmSPA3b is 96.48%. The purple circles represent the SPA in soybeans and the yellow circles represent the SPA in Arabidopsis. All amino-acid sequences are listed in Source Data file.

	Target 1	Target 2	
Glyma.12G224600	GGTGAAGATGGAGGGTTCTTCTGGGTCTGCTTTTCACAATTCTGGCAGTTCTAGGGCCTTGAATAGTTCCGGAGTCTCAGATAGGAATCAAAGGGTTCAT	GGTGAAGATGGAGGGTTCTTCTGGGTCTGCTTTTCACAATTCTGGCAGTTCTAGGGCCTTGAACAGTTCTGGAGTCTCAGATAGGAATCAAAGGGTTCAT	138
Glyma.13G276700	GATGAAGATGGAG...CCTTCTGGGTCTGCTTTTCAGAAATCTGGCAGTTCTAGGGCCTTGAACAGTTCTGGAGTCTCAGATAGGAATCAAAGGGTTCAT	GATGAAGATGGAG...CCTTCTGGGTCTGCTTTTCAGAAATCTGGCAGTTCTAGGGCCTTGAACAGTTCTGGAGTCTCAGATAGGAATCAAAGGGTTCAT	135
Glyma.06G242100			0
Glyma.12G155700			0
Glyma.16G027200	AATGCACATCTAATTAGCAGTATAACTCAGAGTA.CTTCATCTGCATATAATTATCCTCAATTGATTGTAAAGCAAACAAGGAAGGGAAGGGGATTATT	AATGCACATCTAATTAGCAGTATAACTCAGAGTA.CTTCATCTGCATATAATTATCCTCAATTGATTGTAAAGCAAACAAGGAAGGGAAGGGGATTATT	609
Glyma.07G058200	AATGCACATCTTATTAGCAGTATAACTCAGAGTA.CTTCATCTGCATATAATTATCCTCAATTGATTGTAAAGCAAACAAGGAAGGGAAGGGGATTATT	AATGCACATCTTATTAGCAGTATAACTCAGAGTA.CTTCATCTGCATATAATTATCCTCAATTGATTGTAAAGCAAACAAGGAAGGGAAGGGGATTATT	642
Glyma.01G224200	GTCATTGATGCGGATCAGAATCAGCTAAAGACTGGCATTG.ATGCGGATCAGAATCGGCTAAAGACTGGCATTGATGCAGACCAGAATCAGATGAAGGCT	GTCATTGATGCGGATCAGAATCAGCTAAAGACTGGCATTG.ATGCGGATCAGAATCGGCTAAAGACTGGCATTGATGCAGACCAGAATCAGATGAAGGCT	894
Glyma.05G214900	ATGACG	ATGACG	6
Glyma.11G018700	GTCATTGATGTGATTTCAGAAATCGGCTGAAGACTGGCATTG.ATGCAGATCAGAATCCGATGAAGACTGGCATTGAT.....CAGAGTCGGATGAAGACC	GTCATTGATGTGATTTCAGAAATCGGCTGAAGACTGGCATTG.ATGCAGATCAGAATCCGATGAAGACTGGCATTGAT.....CAGAGTCGGATGAAGACC	876
Glyma.08G021200	GATGAAGGTCATGCTCACGAAGGAATACAAACAAAAGTTATACACAAATCAGGATTTCGACAGTATTCTGGTAGAAGTACATTGAAGGGAAGGGTGTG	GATGAAGGTCATGCTCACGAAGGAATACAAACAAAAGTTATACACAAATCAGGATTTCGACAGTATTCTGGTAGAAGTACATTGAAGGGAAGGGTGTG	622
Consensus			
	Target 2		
Glyma.12G224600	TGTCCTCAAAGGAACCCCTTTTCGGGTGAGGCATCACAGGATTCGGGGTTTAGAAAGGAAAGGGATAGGGTTCTGTTGGCTCAAGGTGGTCAGCCTAAAA	TGTCCTCAAAGGAACCCCTTTTCGGGTGAGGCATCACAGGATTCGGGGTTTAGAAAGGAAAGGGATAGGGTTCTGTTGGCTCAAGGTGGTCAGCCTAAAA	238
Glyma.13G276700	TGTCCTCAAAGGAACCCCTTTTCGGGTGAGGCATCCAGGATTTCGGGGTTTCAGAAAGGAAAGGGATAGGTTTCTGTTGGCTCAAGGTGGTCAGCCTAAGA	TGTCCTCAAAGGAACCCCTTTTCGGGTGAGGCATCCAGGATTTCGGGGTTTCAGAAAGGAAAGGGATAGGTTTCTGTTGGCTCAAGGTGGTCAGCCTAAGA	235
Glyma.06G242100			0
Glyma.12G155700			0
Glyma.16G027200	TGTGAAGATTTAAACCAAGCTTCAGTACTGGAGGAGCACTTAACAG..CCAAGAGGATGAGAAACCTGCTTTTGCAGCTAAGTTTCAATCCGAGACACT	TGTGAAGATTTAAACCAAGCTTCAGTACTGGAGGAGCACTTAACAG..CCAAGAGGATGAGAAACCTGCTTTTGCAGCTAAGTTTCAATCCGAGACACT	707
Glyma.07G058200	TGTGAAGATTTAAACCAAGCTTCAGTATTGGAGGAGCACTTAAGAG..TCAAGAGGATGAGAAACCTGGTTTTCGCGCTAAGTTTCAATCCGAGACACT	TGTGAAGATTTAAACCAAGCTTCAGTATTGGAGGAGCACTTAAGAG..TCAAGAGGATGAGAAACCTGGTTTTCGCGCTAAGTTTCAATCCGAGACACT	740
Glyma.01G224200	AGCATTGGCACAGATCAGAATCAGATGAAGAATCAGATGGTACTGA..TCAGAAACAGATGAAGACTGGCATTGTTACTCATTGAACCTCTAATCAATC	AGCATTGGCACAGATCAGAATCAGATGAAGAATCAGATGGTACTGA..TCAGAAACAGATGAAGACTGGCATTGTTACTCATTGAACCTCTAATCAATC	992
Glyma.05G214900	TCTCTAACAAAGTTATGAAGTAGTAGTTTATTATCCGGTG.TGCGG...TGGAACCTGATAAAGTCTGGCATTGACACTCAGATGGATTCTAAGGCATT	TCTCTAACAAAGTTATGAAGTAGTAGTTTATTATCCGGTG.TGCGG...TGGAACCTGATAAAGTCTGGCATTGACACTCAGATGGATTCTAAGGCATT	101
Glyma.11G018700	GGCATTGATACAGATCAGAATCAGATGAAAACCTGGCATTGGTACTGA..TCAGAAACAGATGAAGACCAGCATTGGTACTCATTGAACCTCTAATCAATC	GGCATTGATACAGATCAGAATCAGATGAAAACCTGGCATTGGTACTGA..TCAGAAACAGATGAAGACCAGCATTGGTACTCATTGAACCTCTAATCAATC	974
Glyma.08G021200	TATGTAAAGGTCATCTTCTAATGGCTTATATATTGAGTC.TAGAGA..TCAGAAACCCGATAAAGTCTGGTATTGACACTCAGATGGATTCTAATGCATT	TATGTAAAGGTCATCTTCTAATGGCTTATATATTGAGTC.TAGAGA..TCAGAAACCCGATAAAGTCTGGTATTGACACTCAGATGGATTCTAATGCATT	719
	Target 3		
Glyma.12G224600	AACAGAGAGATGATACGGAAGAAGCTGAAGCAGCGATAGAGCTGAGACAAAGGATA.GAGGATCAGGAGTTGTTGTTAGAGTTCCTTTTGTACTTCAAC	AACAGAGAGATGATACGGAAGAAGCTGAAGCAGCGATAGAGCTGAGACAAAGGATA.GAGGATCAGGAGTTGTTGTTAGAGTTCCTTTTGTACTTCAAC	1195
Glyma.13G276700	AACAGAGAGATGATATGGAAGAAGCTGAAGCAGCGATAGAGCTGAGACAAAGGATA.GATGATCAGGAGTTGCTGTTAGAAATTCCTTTTATTACTTCAAC	AACAGAGAGATGATATGGAAGAAGCTGAAGCAGCGATAGAGCTGAGACAAAGGATA.GATGATCAGGAGTTGCTGTTAGAAATTCCTTTTATTACTTCAAC	1195
Glyma.06G242100	AACCAAGAGATGATATAGAAAAGTGTGAAGCAGTGGTAGAAATTTGGAGAAAGGATA.GATGACCAGGAGTTGTTGCTAGAAATTCCTTTTCGTTAATCAAC	AACCAAGAGATGATATAGAAAAGTGTGAAGCAGTGGTAGAAATTTGGAGAAAGGATA.GATGACCAGGAGTTGTTGCTAGAAATTCCTTTTCGTTAATCAAC	874
Glyma.12G155700	AACCAAGAGATGATATAGAAAAGTGTGAGGCAGCGGTAGAAGTTAGAGAAAGGATA.GATGATCAGGAGTTGTTGCAAGAATTCCTTTTCATTAAATCAAC	AACCAAGAGATGATATAGAAAAGTGTGAGGCAGCGGTAGAAGTTAGAGAAAGGATA.GATGATCAGGAGTTGTTGCAAGAATTCCTTTTCATTAAATCAAC	871
Glyma.16G027200	AATCAGAGGA...ATCAAATTCGTAGA.TGATGTTGGAATATC..TGATGACGAGGCTGAACACAGAGCAATTACTAGATTTTCTAATTTTAAATCAAAG	AATCAGAGGA...ATCAAATTCGTAGA.TGATGTTGGAATATC..TGATGACGAGGCTGAACACAGAGCAATTACTAGATTTTCTAATTTTAAATCAAAG	1630
Glyma.07G058200	AATCAAAGGA...ATCAAATTCGTAGA.TGATGTTGGAATATC..TGATGATGAGGCTGAACACAGAGCAATTACTAGATTTTCTAATTTTATTCAAAG	AATCAAAGGA...ATCAAATTCGTAGA.TGATGTTGGAATATC..TGATGATGAGGCTGAACACAGAGCAATTACTAGATTTTCTAATTTTATTCAAAG	1666
Glyma.01G224200	GATTGCAAGA...GTTGTTTAGTGAGGAATTGTCATCAAGTATTGACCAAGAAGATGCAGAATCTGAATTGTTATTGCATTTCCCTCGTTTTGTAAAAAG	GATTGCAAGA...GTTGTTTAGTGAGGAATTGTCATCAAGTATTGACCAAGAAGATGCAGAATCTGAATTGTTATTGCATTTCCCTCGTTTTGTAAAAAG	1963
Glyma.05G214900	GAATGCGGGA...GGTGACTTTGAGGAATTATCATTAAGTCTTAATCAAGATGATGCAGAATCAGAATTGCTATTGCATTTCCCTCATCTCACTAGAAG	GAATGCGGGA...GGTGACTTTGAGGAATTATCATTAAGTCTTAATCAAGATGATGCAGAATCAGAATTGCTATTGCATTTCCCTCATCTCACTAGAAG	1090
Glyma.11G018700	GATTGCAAGA...GTTGTTTAGTGAGGAATTGTCATCAAGTATTGACCAAGAAGATGCAGAATCAGAATTGTTATTGCATTTCCCTCGTTTTGTAAAAAG	GATTGCAAGA...GTTGTTTAGTGAGGAATTGTCATCAAGTATTGACCAAGAAGATGCAGAATCAGAATTGTTATTGCATTTCCCTCGTTTTGTAAAAAG	1945
Glyma.08G021200	GAATCCATGA...GGTGACTGTGAGGAATTATCATCAAGTCTCAATCAAGATGATGCAGAATCAGAATTGCTATTGCATTTCCCTCATCTCACTAGAAAAAG	GAATCCATGA...GGTGACTGTGAGGAATTATCATCAAGTCTCAATCAAGATGATGCAGAATCAGAATTGCTATTGCATTTCCCTCATCTCACTAGAAAAAG	1708

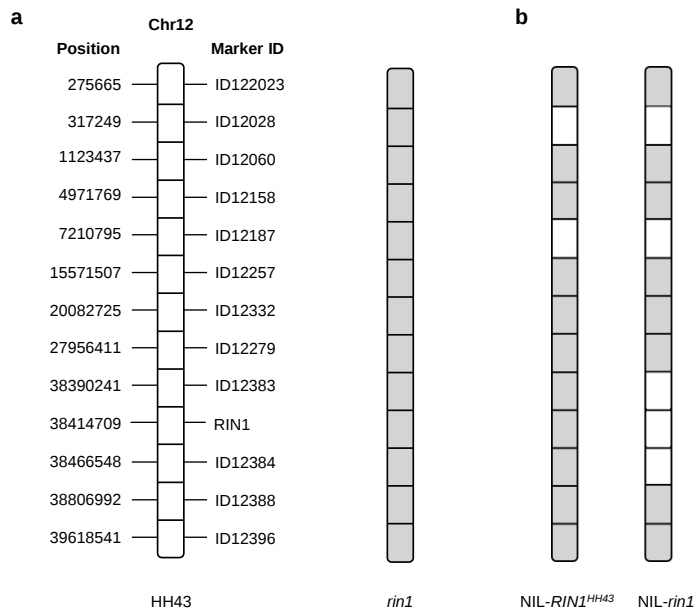
Supplementary Fig. 6 The similarity comparison between 10 *RIN1* homologous genes in soybean for *RIN1* CRISPR/Cas9 targets.

The blue line, red line and green line represents the Target 1, Target 2 and Target 3, respectively. *SPA3b* (*Glyma.13G276700*) gene shares the same sequences with the Target 2 and Target 3 of *rin1^{CR}*. In the Target 1, *SPA3b* differs from *rin1^{CR}* with a SNP. Nucleic acid sequences were aligned by DNAMAN.



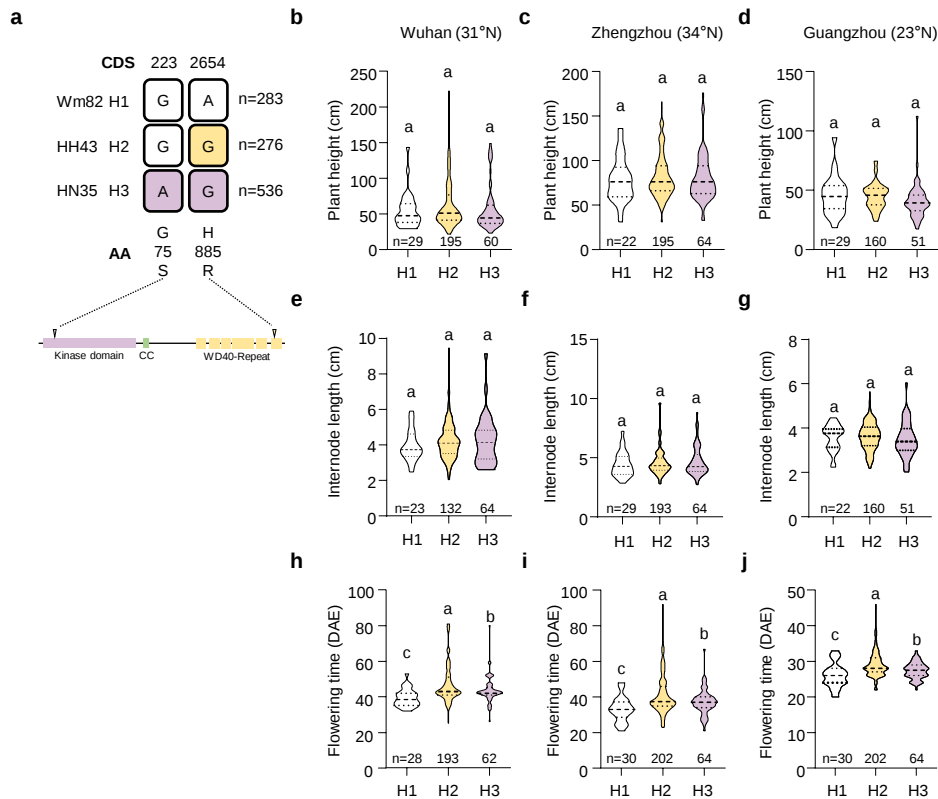
Supplementary Fig. 7 The nucleic acid sequences of *SPA3b* gene in the position of *rin1^{CR}* targets in Wm82 and *rin1^{CR}*.

a The nucleic acid sequence of *SPA3b* gene in the position of *rin1^{CR}* Target 1 (*rin1^{CR}-T1*). **b** The nucleic acid sequence of *SPA3b* gene in the position of *rin1^{CR}* Target 2 (*rin1^{CR}-T2*). **c** The nucleic acid sequence of *SPA3b* gene in the position of *rin1^{CR}* Target 3 (*rin1^{CR}-T3*). The picture of **(a)**, **(b)** and **(c)** were generated by BioEdit. **d** The nucleic acid sequences of *SPA3b* gene in the position of *rin1^{CR}* targets in Wm82 and *rin1^{CR}*. The nucleic acid sequences were aligned by DNAMAN. The blue line, red line and green line represents the Target 1, Target 2 and Target 3, respectively.



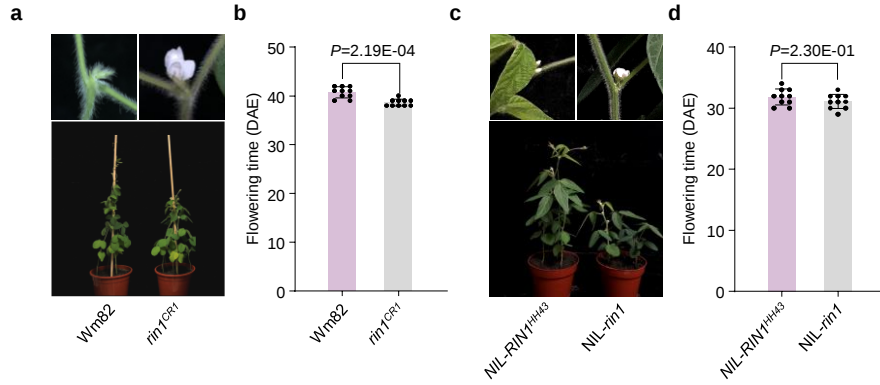
Supplementary Fig. 8 The construction of *RIN1* NILs derived from the cross between HH43 and *rin1*.

a Molecular markers and their genomic positions in HH43 (left) and *rin1* (right) on chromosome 12. **b** Introgression segments of *RIN1* in NIL-*RIN1*^{HH43} (left) and NIL-*rin1* (right). White represents the segments derived from HH43, and gray represents the segments derived from *rin1*. Marker sequences are listed in Supplementary Table 4.



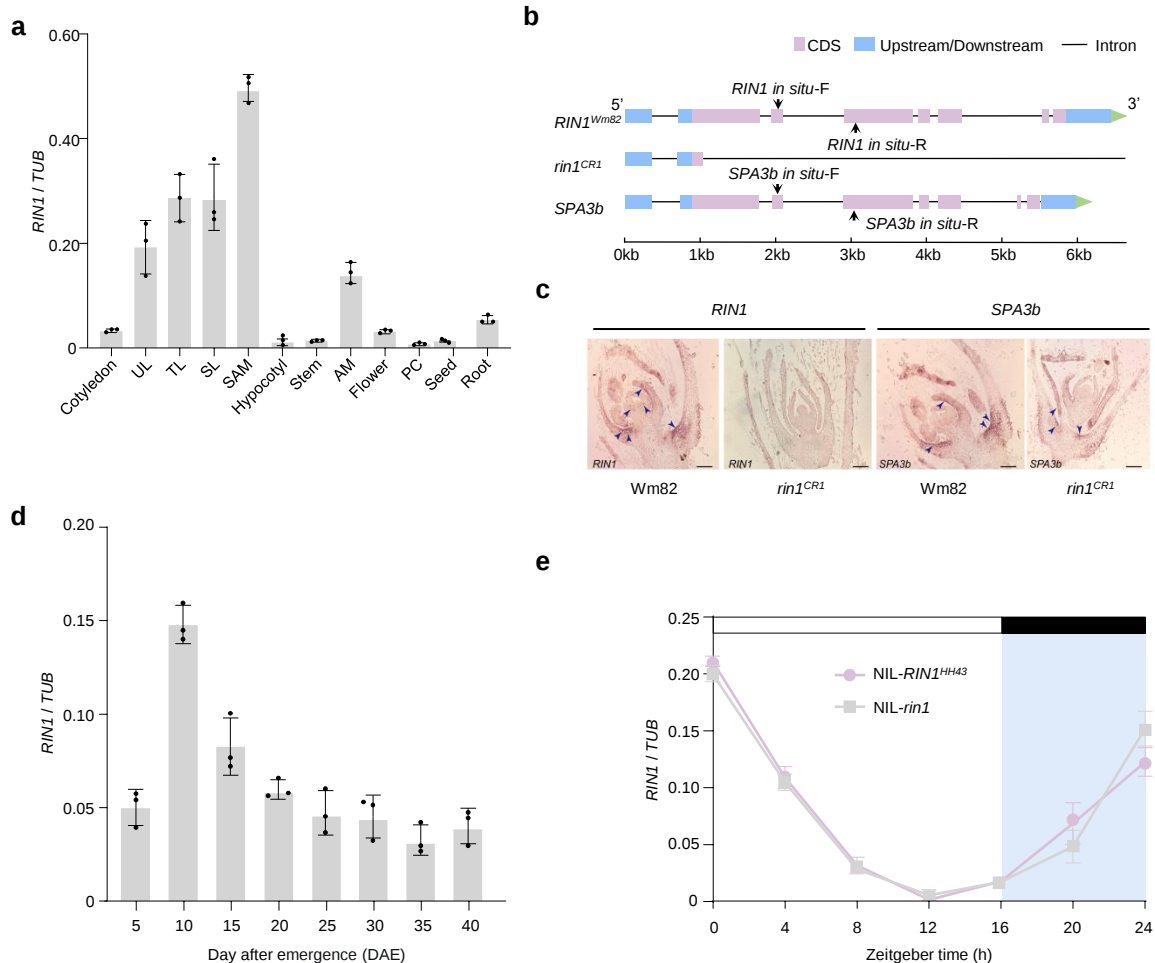
Supplementary Fig. 9 Haplotypes and phenotype correlation analysis of *RIN1*.

a Haplotypes of *RIN1*. CDS, coding region. AA, amino acid. n, the number of accessions with each haplotype. Haplotypes were extracted from the panel of 1,295 of sequenced accessions comprising 146 wild soybeans, 575 landraces and 574 improved cultivars as previously described²⁸. The total number of accessions of three haplotypes are 1,095 due to the filtering of some poorly sequenced data. **b–d** Plant height (cm) of different haplotypes in *RIN1* in different regions in 2019, including Wuhan (**b**), Zhengzhou (**c**) and Guangzhou (**d**), China. **e–g** Internode length per plant (cm) of different haplotypes in *RIN1* in different regions in 2019, including Wuhan (**e**), Zhengzhou (**f**) and Guangzhou (**g**), China. **h–j** Flowering time (DAE) of different haplotypes in *RIN1* in different regions in 2019, including Wuhan (**h**), Zhengzhou (**i**) and Guangzhou (**j**), China. 297 accessions, including 137 landraces and 160 improved cultivars were used for correlation analysis in (**b**)–(**j**). The 297 accessions are listed in the Supplementary table 5 and phenotypes of 297 accessions are listed in the Source Data file. One-way ANOVA with Tukey's post-test was performed to determine statistically significant differences in (**b**)–(**j**), $P < 0.05$. a, b and c letters indicate statistically significant differences.



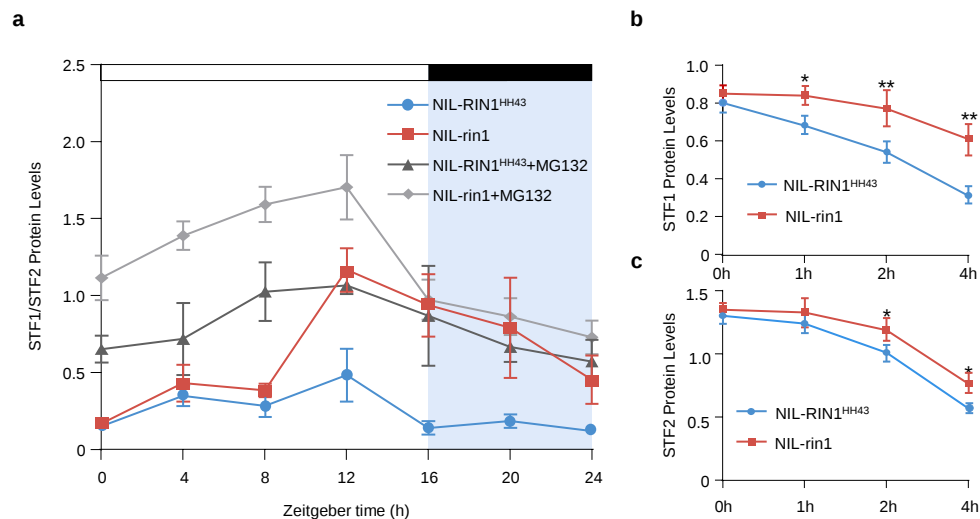
Supplementary Fig. 10 Flowering time of *Wm82*, *rin1^{CR1}* mutants and *RIN1*-NILs.

a Phenotypes of *Wm82* and *rin1^{CR1}* at 38 DAE. **b** Flowering time (DAE) of *Wm82* and *rin1^{CR1}*. **c** Phenotypes of NIL-*RIN1^{HH43}* and NIL-*rin1* at 30 DAE. **d** Flowering time (DAE) of NIL-*RIN1^{HH43}* and NIL-*rin1*. Plants in all panels were grown in growth chambers under long-day photoperiods (16 h light/8 h dark). All data are means $\pm$ SEM ($n = 10$ plants). A student's *t*-test (two-sided) was used to generate the *P* values in **(a)** and **(d)**.



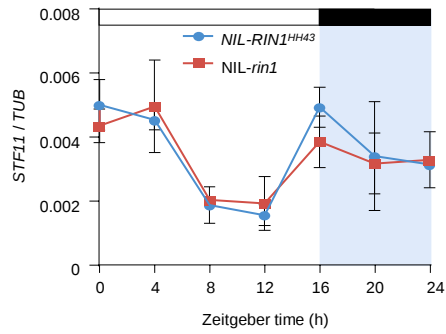
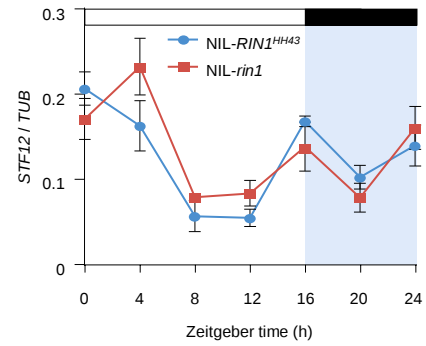
Supplementary Fig. 11 Expression pattern of *RIN1* in long-day photoperiods.

a Expression of *RIN1* in different tissues in Wm82. UL: Unifoliate leaf; TL: First trifoliate leaf; SL: Second trifoliate leaf; SAM: Shoot apical meristem; AM: Axillary meristem; PC: Pod coat. Data shown are relative to the control gene *Tubulin* (*TUB*). Data shown are means $\pm$ SD from three independent biological replicates. **b** Schematic representation of the positions of the *RIN1* and *SPA3b* probes used for *in situ* hybridization in (c). **c** *In situ* hybridization to determine the spatial expression pattern of *RIN1* and *SPA3b* in the stem tips of Wm82 and *rin1*^{CR1}. Arrows represent the expression positions of *RIN1* and *SPA3b*. Scale bars = 100 μ m. **d** *RIN1* dynamics in the shoot apex at different stages in Wm82. Data shown are relative to the control gene *Tubulin* (*TUB*). Data shown are means $\pm$ SD from three independent biological replicates. **e** Relative expression levels of *RIN1* in NIL-*RIN1*^{HH43} and NIL-*rin1*. Data shown are relative to the control gene *Tubulin* (*TUB*). Data shown are means $\pm$ SD from three independent biological replicates. All plants used in (a)–(e) were grown in growth chambers under long-day photoperiods (16 h light/8 h dark).



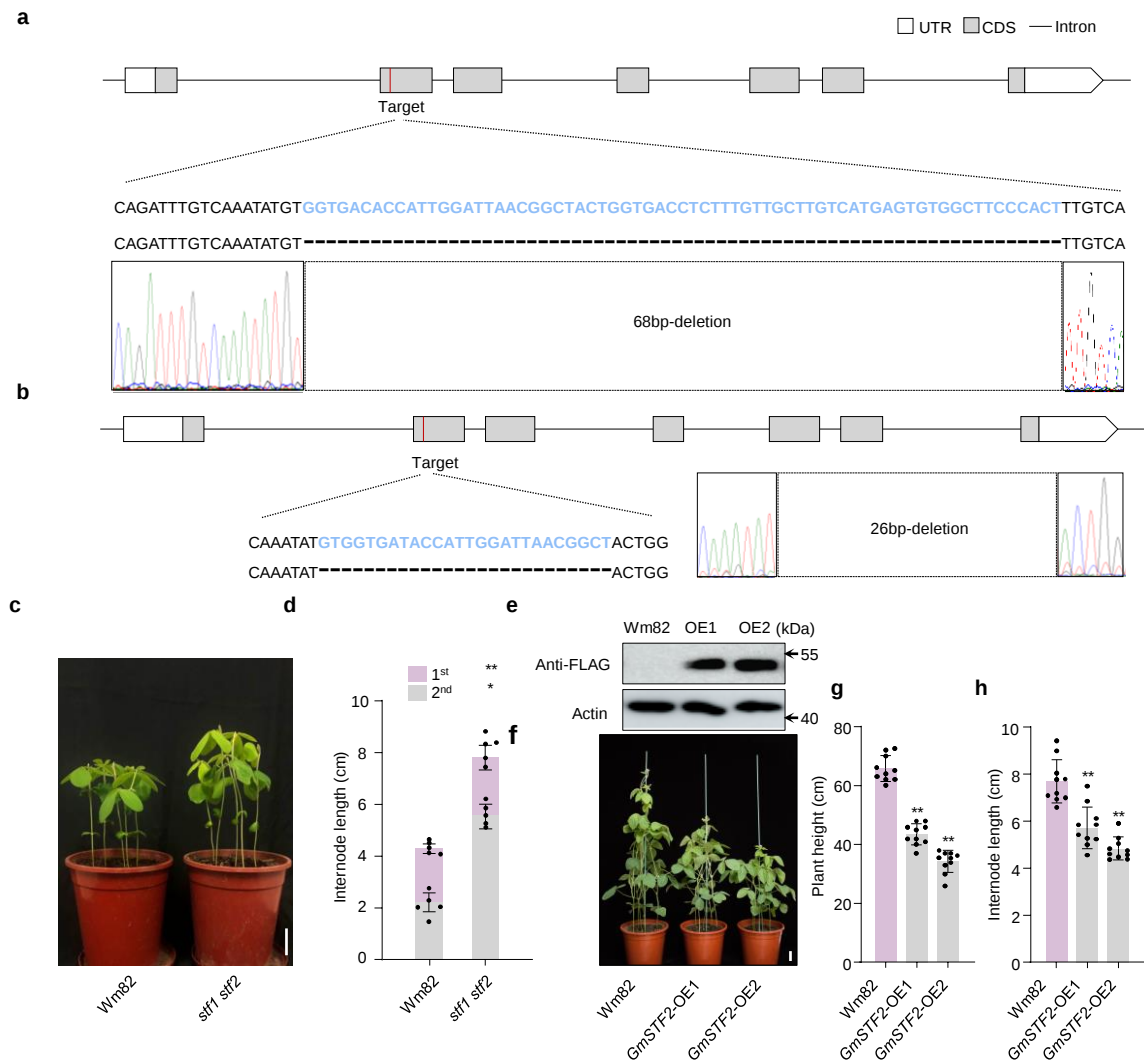
Supplementary Fig. 12 Quantitative analysis of relative STF protein abundance by ImageJ software.

a Quantitative analysis of relative STF1 and STF2 protein from **Fig. 3e**. **b,c** Quantitative analysis of relative STF1 (**b**) and STF2 protein (**c**) from **Fig. 3f**. Data shown in (**b**) and (**c**) are means $\pm$ SD from three independent biological replicates. A student's *t*-test (two-sided) was used to generate the *P* values of (**b**) and (**c**), **P* < 0.05, ***P* < 0.01.

a**b**

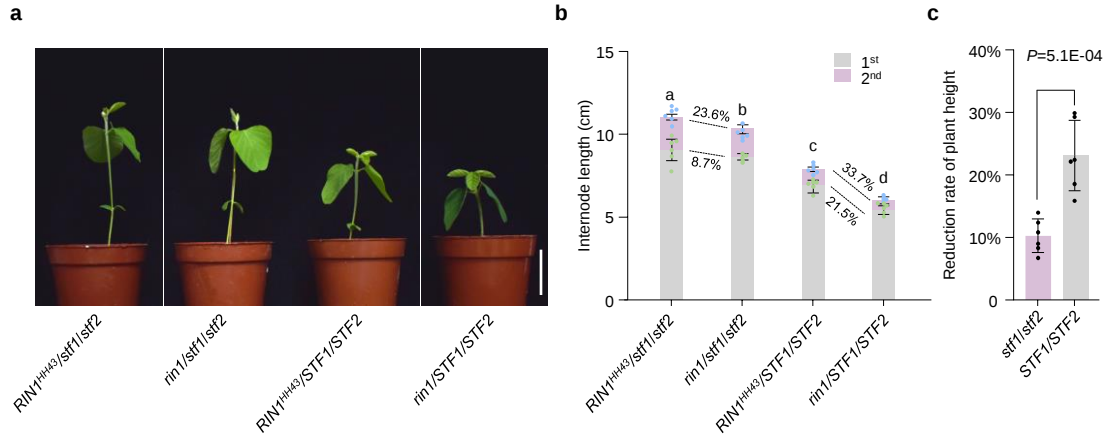
Supplementary Fig. 13 The *rin1* mutation does not lead to differential expression of *STF1* and *STF2*.

a–b Relative expression of *STF1* (a) and *STF2* (b) in the SAM of NILs-*RIN1* plants. Samples were harvested from ZT0 to ZT24 at 10 DAE. Data shown are relative to the control gene *Tubulin* (*TUB*). Data shown are means $\pm$ SD from three independent biological replicates. All plants in (a) and (b) were grown in growth chambers under long-day photoperiods (16 h light/8 h dark).



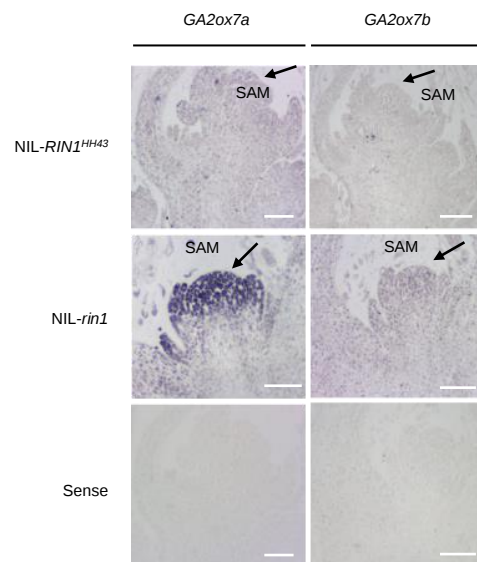
Supplementary Fig. 14 *STF1* and *STF2* genes regulate soybean internode length in long-day photoperiods.

a CRISPR/Cas9 induced a 68-bp deletion in *STF1* used to generate the *stf1 stf2* double mutant. The red lines indicate the CRISPR/Cas9 target that shares homology with *STF2*. **b** CRISPR/Cas9 induced a 26-bp deletion in *STF2* used to generate the *stf1 stf2* double mutant. The red lines indicate the CRISPR/Cas9 target that shares homology with *STF1*. The picture of **(a)** and **(b)** were generated by BioEdit. **c** Phenotypes of Wm82 and *stf1 stf2* double mutants under long-day photoperiods (16 h light/8 h dark). Scale bar = 5 cm. **d** Internode length of Wm82 and *stf1 stf2* double mutants under long-day photoperiods (16 h light/8 h dark). 1st, the first internode; 2nd, the second internode. Data are means $\pm$ SEM (n = 5 plants). A student's *t*-test (two-sided) was used to generate the *P* values, **P* < 0.05, ***P* < 0.01. **e** Western blot against the FLAG epitope in two genetically independent transgenic lines constitutively expressing p35S-STF2-3FLAG. Black arrows represent the positions of protein ladder. **f-h** Phenotypic differences between Wm82 and *STF2* overexpression lines. **f** Phenotypes of Wm82 and transgenic *STF2* overexpression lines at 30 DAE under long-day photoperiods (16 h light/8 h darkness). **g** Plant height (cm). **h** Internode length per plant (cm). All data in **(g)** and **(h)** are means $\pm$ SEM (n = 10 plants). A student's *t*-test (two-sided) was used to generate the *P* values, **P* < 0.05, ***P* < 0.01.



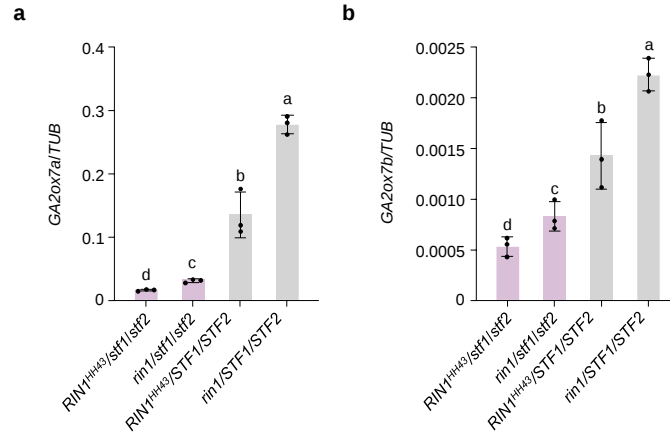
Supplementary Fig. 15 *RIN1* is partially dependent on *STF1* and *STF2* for internode-length regulation.

a Phenotypes of *RIN1^{HH43}/STF1/STF2*, *rin1/STF1/STF2*, *RIN1^{HH43}/stf1/stf2*, and *rin1/stf1/stf2* under long-day photoperiods (16 h light/8 h dark). Scale bar = 5 cm. **b** Internode length (cm) of *RIN1^{HH43}/STF1/STF2*, *rin1/STF1/STF2*, *RIN1^{HH43}/stf1/stf2*, and *rin1/stf1/stf2* under long-day photoperiods (16 h light/8 h dark). All data are means $\pm$ SEM (n = 6 plants). One-way ANOVA with Tukey's post-test was performed to determine statistically significant differences, $P < 0.05$. a, b, c and d letters indicate statistically significant differences. The green dots for 1st internode length and blue dots for 2nd internode length. **c** Significant differences analysis of the rate of plant height reduction in *rin1* under *STF1/STF2* and *stf1/stf2* backgrounds, respectively, in (b). All data are means $\pm$ SEM (n = 6 plants). A student's *t*-test (two-sided) was used to generate the *P* values.



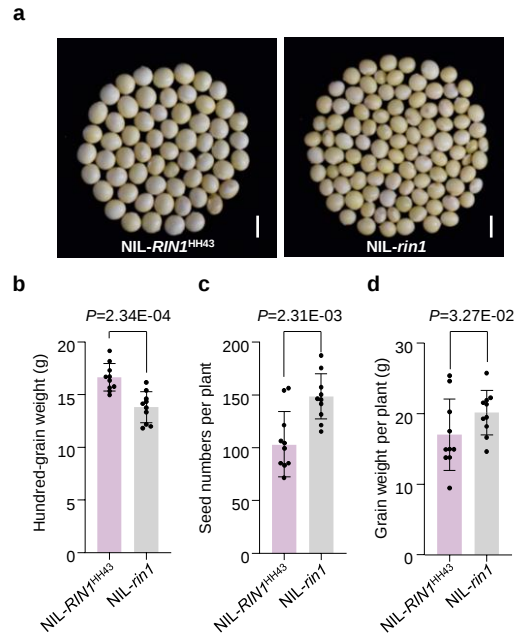
Supplementary Fig. 16 *In situ* hybridization of *GA2ox7a* and *GA2ox7b* in NIL-*RIN1*^{HH43} and NIL-*rin1*.

Spatial expression pattern of *GA2ox7a* and *GA2ox7b* in the stem tips of NIL-*RIN1*^{HH43} and NIL-*rin1* at 10 DAE under long-day photoperiods (16 h light/8 h dark) detected by *in situ* hybridization. Black arrows point to shoot apical meristems (SAMs). Scale bars = 100 μ m. Three independent biological replicates were performed.



Supplementary Fig. 17 RT-qPCR further confirms that *RIN1* is partially dependent on *STF1* and *STF2* for internode-length regulation.

a,b Relative expression of *GA2ox7a* (d) and *GA2ox7b* (e) in the SAM of *RIN1^{HH43}/STF1/STF2*, *rin1/STF1/STF2*, *RIN1^{HH43}/stf1/stf2*, and *rin1/stf1/stf2* under long-day photoperiods (16 h light/8 h dark). Samples were harvested at ZT0 of 10 DAE. Data shown are relative to the control gene *Tubulin* (*TUB*). Data shown are means $\pm$ SD from three independent biological replicates. One-way ANOVA with Tukey's post-test was performed to determine statistically significant differences, $P < 0.05$. a, b, c and d letters indicate statistically significant differences. Plants were grown in growth chambers under long-day photoperiods (16 h light/8 h dark).



Supplementary Fig. 18 *RIN1* contributes to grain yield in field conditions.

a–d Yield traits of NIL-RIN1^{HH43} and NIL-rin1 plants cultivated in a field in Shijiazhuang, China (37°27'N, 113°30'E) at a normal density under long-day natural photoperiods. **a** Representative images of whole seeds from NIL-RIN1^{HH43} (left) and NIL-rin1 (right). Scale bar = 1 cm. **b** Hundred-grain weight (g); **c** Seed number per plant (g); **d** Grain weight per plant (g). All data of (**b**)–(**d**) are means $\pm$ SEM (n = 10 plants). A student's *t*-test (two-sided) was used to generate the *P* values.

Supplementary Table 1 QTLs for plant height detected in the HNH population.

QTL-LG	Year	Chr.	Detection method	Physical length (Wm82)	Max LOD	PVE%	ADD
<i>RIN1</i>	2017-F ₂	12	Map-QTL	26,744,935-38,784,872	20.43	37.40	-13.53
<i>RIN1</i>	2018-F ₃	12	Map-QTL	26,744,935-38,784,872	10.48	43.20	-12.68

PVE (%), percentage of phenotypic variance explained by the QTL.
ADD, The additive effects contributed by QTLs. Positive value (+) of the additive effect indicates the allele from *rin1* phenotype, negative value (-) of the additive effect indicates the allele originating from HH43 reduced phenotype.
Max LOD, maximum logarithm-of-odds (LOD) scores.

Supplementary Table 2 QTLs for internode length detected in the HNH population.

QTL-LG	Year	Chr.	Detection method	Physical length (Wm82)	Max LOD	PVE%	ADD
<i>RIN1</i>	2017-F ₂	12	Map-QTL	26,744,935-38,784,872	13.83	27.20	-0.51
<i>RIN1</i>	2018-F ₃	12	Map-QTL	26,744,935-38,784,872	11.10	43.30	-0.58

PVE (%), percentage of phenotypic variance explained by the QTL.
ADD, The additive effects contributed by QTLs. Positive value (+) of the additive effect indicates the allele from *rin1* phenotype, negative value (-) of the additive effect indicates the allele originating from HH43 reduced phenotype.
Max LOD, maximum logarithm-of-odds (LOD) scores.

Supplementary Table 3 Polymorphic variations of the predicted genes between parents within CDS in the interval of RIN1 locus.

Gene ID	Gene Name	Position (Wm82 reference)	Changes of codon ^a	Changes of amino acid ^b	Mutation type	<i>rin1</i> -type	HH43-type	HN35-type
<i>Glyma.12G224500</i>	Protein kinase superfamily protein	38388858..38396091	-	-	-	-	-	-
<i>Glyma.12G224600</i>	SPA1-related 3	38408929..38415581	G223A	G75S	nonsynonymous SNV	1/1	0/0	1/1
			G2521T	E841X	stop gain	1/1	0/0	0/0
			A2654G	H885R	nonsynonymous SNV	1/1	1/1	1/1
<i>Glyma.12G224700</i>	Core-2/1-branching beta-1,6-N-acetylglucosaminyltransferase family protein	38418438..38422071	-	-	-	-	-	-
<i>Glyma.12G224800</i>	Proton pump interactor 1	38431962..38436035	G1381C	E461Q	nonsynonymous SNV	1/1	1/1	1/1
			T1643C	V548A	nonsynonymous SNV	1/1	1/1	1/1
<i>Glyma.12G224900</i>	RNA-binding S4 domain-containing protein	38438727..38445151	T8C	V3A	nonsynonymous SNV	1/1	1/1	1/1
<i>Glyma.12G225000</i>	Ribosomal protein L3 plastid	38447980..38452353	-	-	-	-	-	-
<i>Glyma.12G225100</i>	Stigma-specific Stig1 family protein	38454691..38456172	-	-	-	-	-	-

Changes of codon^a, number represents the SNP position in the CDS.
Changes of amino acid^b, number represents the amino acid position in protein.
type, 0/0 and 1/1 represented bases type same to reference (Glycine max Wm82.a2.v1) and mutation type, respectively.

Supplementary Table 4 Indel and single-nucleotide polymorphism (SNP) markers used to map-based cloning and NILs construction.

Primer ID	Position (Wm82)	Type	Primer Sequences (F/R)
ID122023	275665	Indel	TGCATGCAAAAAATAACACGA AAAGGGTGGAGTGGGCAT CAGCAAGGGGGAACAGAA
ID12028	317249	Indel	GTTTGTGGCGGAGCAGT GGGTGGTTGGAGAAGCCT
ID12060	1123437	Indel	TCATCTACGTTTGGCGCT CCTGCATCCGCAAGATTC
ID12158	4971769	Indel	CCGGAGACGGAGAAGGAT TCATCTTTGAGGCCTTCTCA
ID12187	7210795	Indel	CATGGGTTTGATGGAGTGC GAAACGGTGCCGTATTGG
ID12257	15571507	Indel	ATCTCCACACCACACGC GCGAAGCCGTTGAGAGAA
ID12332	20082725	Indel	ACTCCAAGCCTCCCATC CACTAATCAGGTGCTGCATC
M1(ID12279)	27956411	Indel	CCCTTTATTCTACTCTACCAG TCCAAAATCTACTCTATGCG
M2(ID12383)	38390241	Indel	GGTGATTTGTTGTTTGC CTTTGTGGGGTTATCAGTATCTGATGGTTACATTGCCACTGGTTTC
RIN1	38414709	SNP	CTGCACAGCATCGTCCACTTCGTTGC GCACCCCAGGTTTATCATTG
M3(ID12384)	38466548	Indel	CTATAGGTCTCTAGTGTGCCTC ACAAACCCAGCATTTCGTG
M4 (ID12385)	38528916	Indel	GAGATGACATAATTATGTTTATCGTG AGAATGTGGGCGTAGCTAG
M5 (ID12386)	38666649	Indel	GTTAGATCCCGGGAGTTC TTATCTTTTGGGAAAATGAC
M6 (ID12388)	38806992	Indel	GTCCTATATACTCTTGTC CCTTTTGATATATTCTTAC
M7 (ID12390)	39038815	Indel	TTGAAGTTAAGAAACCTGAG AAAGCTCTCTCCCTGGGGC
M8 (ID12396)	39618541	Indel	TTACCTCTAATTATCCCTC

Supplementary Table 5 The 297 resequenced aceessions used for correlation analysis.

Haplotype	Accessions	Type
H1	GDC004	Improved cultivar
H1	GDC021	Landrace
H1	GDC034	Improved cultivar
H1	GDC037	Landrace
H1	GDC038	Improved cultivar
H1	GDC042	Improved cultivar
H1	GDC048	Improved cultivar
H1	GDC073	Improved cultivar
H1	GDC121	Improved cultivar
H1	GDC140	Improved cultivar
H1	GDC152	Improved cultivar
H1	GDC164	Improved cultivar
H1	GDC170	Improved cultivar
H1	GDC175	Improved cultivar
H1	GDC191	Improved cultivar
H1	GDC196	Improved cultivar
H1	GDC197	Improved cultivar
H1	GDC204	Improved cultivar
H1	GDC209	Improved cultivar
H1	GDC213	Improved cultivar
H1	GDC217	Improved cultivar
H1	GDC229	Improved cultivar
H1	GDL001	Landrace
H1	GDL104	Landrace
H1	GDL117	Landrace
H1	GDL127	Landrace
H1	GDL139	Landrace
H1	GDL140	Landrace
H1	GDL153	Landrace
H1	GDL180	Improved cultivar
H2	GDC003	Landrace
H2	GDC005	Landrace
H2	GDC008	Landrace
H2	GDC013	Improved cultivar
H2	GDC014	Improved cultivar
H2	GDC015	Landrace
H2	GDC017	Landrace
H2	GDC018	Landrace
H2	GDC019	Landrace
H2	GDC023	Landrace
H2	GDC024	Landrace
H2	GDC025	Landrace
H2	GDC026	Landrace
H2	GDC036	Landrace
H2	GDC039	Improved cultivar
H2	GDC040	Landrace
H2	GDC041	Landrace

Supplementary Table 5 The 297 resequenced aceessions used for correlation analysis.

Haplotype	Accessions	Type
H2	GDC044	Landrace
H2	GDC047	Landrace
H2	GDC050	Improved cultivar
H2	GDC051	Improved cultivar
H2	GDC053	Improved cultivar
H2	GDC054	Landrace
H2	GDC055	Landrace
H2	GDC058	Landrace
H2	GDC061	Landrace
H2	GDC066	Improved cultivar
H2	GDC067	Improved cultivar
H2	GDC068	Improved cultivar
H2	GDC071	Improved cultivar
H2	GDC074	Improved cultivar
H2	GDC075	Improved cultivar
H2	GDC078	Improved cultivar
H2	GDC079	Improved cultivar
H2	GDC081	Improved cultivar
H2	GDC082	Improved cultivar
H2	GDC083	Improved cultivar
H2	GDC084	Improved cultivar
H2	GDC085	Improved cultivar
H2	GDC086	Improved cultivar
H2	GDC088	Improved cultivar
H2	GDC090	Improved cultivar
H2	GDC091	Improved cultivar
H2	GDC092	Improved cultivar
H2	GDC094	Improved cultivar
H2	GDC096	Improved cultivar
H2	GDC097	Improved cultivar
H2	GDC098	Improved cultivar
H2	GDC101	Improved cultivar
H2	GDC102	Improved cultivar
H2	GDC104	Improved cultivar
H2	GDC105	Improved cultivar
H2	GDC106	Improved cultivar
H2	GDC107	Improved cultivar
H2	GDC108	Improved cultivar
H2	GDC110	Improved cultivar
H2	GDC111	Improved cultivar
H2	GDC113	Improved cultivar
H2	GDC114	Improved cultivar
H2	GDC118	Improved cultivar
H2	GDC119	Improved cultivar
H2	GDC120	Improved cultivar
H2	GDC122	Improved cultivar
H2	GDC123	Improved cultivar
H2	GDC124	Improved cultivar
H2	GDC125	Improved cultivar

Supplementary Table 5 The 297 resequenced aceessions used for correlation analysis.

Haplotype	Accessions	Type
H2	GDC127	Improved cultivar
H2	GDC130	Improved cultivar
H2	GDC131	Improved cultivar
H2	GDC132	Improved cultivar
H2	GDC134	Improved cultivar
H2	GDC137	Improved cultivar
H2	GDC138	Improved cultivar
H2	GDC139	Improved cultivar
H2	GDC141	Improved cultivar
H2	GDC142	Improved cultivar
H2	GDC145	Improved cultivar
H2	GDC146	Improved cultivar
H2	GDC147	Improved cultivar
H2	GDC150	Improved cultivar
H2	GDC153	Improved cultivar
H2	GDC154	Improved cultivar
H2	GDC155	Improved cultivar
H2	GDC156	Improved cultivar
H2	GDC158	Improved cultivar
H2	GDC160	Improved cultivar
H2	GDC161	Improved cultivar
H2	GDC162	Landrace
H2	GDC163	Improved cultivar
H2	GDC165	Improved cultivar
H2	GDC168	Improved cultivar
H2	GDC173	Improved cultivar
H2	GDC174	Improved cultivar
H2	GDC176	Improved cultivar
H2	GDC178	Improved cultivar
H2	GDC182	Improved cultivar
H2	GDC183	Improved cultivar
H2	GDC184	Improved cultivar
H2	GDC185	Improved cultivar
H2	GDC187	Improved cultivar
H2	GDC189	Improved cultivar
H2	GDC190	Improved cultivar
H2	GDC194	Improved cultivar
H2	GDC195	Improved cultivar
H2	GDC201	Improved cultivar
H2	GDC202	Improved cultivar
H2	GDC206	Improved cultivar
H2	GDC211	Improved cultivar
H2	GDC214	Improved cultivar
H2	GDC215	Improved cultivar
H2	GDC216	Improved cultivar
H2	GDC218	Improved cultivar
H2	GDC220	Landrace
H2	GDC221	Improved cultivar
H2	GDC226	Landrace

Supplementary Table 5 The 297 resequenced aceessions used for correlation analysis.

Haplotype	Accessions	Type
H2	GDC227	Landrace
H2	GDC228	Improved cultivar
H2	GDC230	Improved cultivar
H2	GDC231	Improved cultivar
H2	GDL002	Landrace
H2	GDL003	Landrace
H2	GDL006	Landrace
H2	GDL008	Landrace
H2	GDL014	Landrace
H2	GDL016	Landrace
H2	GDL019	Landrace
H2	GDL020	Landrace
H2	GDL024	Landrace
H2	GDL026	Landrace
H2	GDL029	Landrace
H2	GDL030	Landrace
H2	GDL034	Landrace
H2	GDL035	Landrace
H2	GDL040	Landrace
H2	GDL041	Landrace
H2	GDL042	Landrace
H2	GDL048	Landrace
H2	GDL049	Landrace
H2	GDL054	Landrace
H2	GDL055	Landrace
H2	GDL056	Landrace
H2	GDL057	Landrace
H2	GDL059	Landrace
H2	GDL063	Landrace
H2	GDL065	Landrace
H2	GDL067	Landrace
H2	GDL069	Landrace
H2	GDL070	Landrace
H2	GDL071	Landrace
H2	GDL073	Landrace
H2	GDL074	Landrace
H2	GDL076	Landrace
H2	GDL079	Landrace
H2	GDL080	Landrace
H2	GDL082	Landrace
H2	GDL083	Landrace
H2	GDL084	Landrace
H2	GDL088	Landrace
H2	GDL089	Landrace
H2	GDL091	Landrace
H2	GDL092	Improved cultivar
H2	GDL094	Landrace
H2	GDL099	Landrace
H2	GDL108	Landrace

Supplementary Table 5 The 297 resequenced aceessions used for correlation analysis.

Haplotype	Accessions	Type
H2	GDL110	Landrace
H2	GDL111	Landrace
H2	GDL120	Landrace
H2	GDL121	Landrace
H2	GDL125	Landrace
H2	GDL129	Landrace
H2	GDL133	Landrace
H2	GDL136	Landrace
H2	GDL138	Landrace
H2	GDL142	Landrace
H2	GDL143	Landrace
H2	GDL144	Landrace
H2	GDL145	Landrace
H2	GDL147	Landrace
H2	GDL151	Landrace
H2	GDL154	Landrace
H2	GDL156	Landrace
H2	GDL158	Landrace
H2	GDL159	Landrace
H2	GDL161	Landrace
H2	GDL165	Improved cultivar
H2	GDL166	Landrace
H2	GDL169	Landrace
H2	GDL170	Landrace
H2	GDL173	Landrace
H2	GDL175	Landrace
H2	GDL177	Landrace
H2	GDL181	Landrace
H2	GDL182	Landrace
H2	GDL183	Improved cultivar
H2	GDL184	Landrace
H2	GDL185	Landrace
H2	GDL186	Landrace
H2	GDL188	Landrace
H2	GDL190	Landrace
H2	GDL192	Landrace
H2	GDL197	Landrace
H2	GDL202	Landrace
H2	GDL204	Landrace
H3	GDC006	Improved cultivar
H3	GDC010	Landrace
H3	GDC012	Landrace
H3	GDC020	Improved cultivar
H3	GDC032	Landrace
H3	GDC043	Improved cultivar
H3	GDC046	Landrace
H3	GDC049	Improved cultivar
H3	GDC057	Improved cultivar
H3	GDC059	Improved cultivar

Supplementary Table 5 The 297 resequenced aceessions used for correlation analysis.

Haplotype	Accessions	Type
H3	GDC062	Improved cultivar
H3	GDC063	Improved cultivar
H3	GDC064	Improved cultivar
H3	GDC065	Improved cultivar
H3	GDC069	Improved cultivar
H3	GDC070	Improved cultivar
H3	GDC072	Improved cultivar
H3	GDC077	Improved cultivar
H3	GDC080	Improved cultivar
H3	GDC089	Improved cultivar
H3	GDC100	Improved cultivar
H3	GDC103	Improved cultivar
H3	GDC116	Improved cultivar
H3	GDC117	Improved cultivar
H3	GDC126	Improved cultivar
H3	GDC128	Improved cultivar
H3	GDC129	Improved cultivar
H3	GDC133	Improved cultivar
H3	GDC159	Improved cultivar
H3	GDC166	Improved cultivar
H3	GDC167	Improved cultivar
H3	GDC169	Improved cultivar
H3	GDC171	Improved cultivar
H3	GDC172	Improved cultivar
H3	GDC179	Improved cultivar
H3	GDC180	Improved cultivar
H3	GDC181	Improved cultivar
H3	GDC186	Improved cultivar
H3	GDC188	Improved cultivar
H3	GDC200	Improved cultivar
H3	GDC210	Improved cultivar
H3	GDC212	Improved cultivar
H3	GDC219	Improved cultivar
H3	GDC222	Landrace
H3	GDC225	Improved cultivar
H3	GDL004	Landrace
H3	GDL015	Landrace
H3	GDL033	Landrace
H3	GDL043	Landrace
H3	GDL058	Landrace
H3	GDL062	Landrace
H3	GDL064	Landrace
H3	GDL096	Landrace
H3	GDL102	Landrace
H3	GDL105	Improved cultivar
H3	GDL112	Landrace
H3	GDL124	Landrace
H3	GDL126	Landrace
H3	GDL131	Landrace
H3	GDL132	Landrace
H3	GDL155	Landrace
H3	GDL160	Landrace
H3	GDL176	Landrace
H3	GDL195	Landrace

Supplementary Table 6 Primers used in the study.

Gene cloning 5'-3'	
<i>RIN1</i> -Outside-F	CTGTTGTGAGGTTGGCCTAGC
<i>RIN1</i> -Outside-R	GGTTCGTGCACCTCATGCTC
<i>RIN1</i> -F	ATGTGTTGTTTACTTGGCC
<i>RIN1</i> -R	TTAAACCATCTCCAGAATTTTGAC
<i>STF1</i> -F	ATGGAACGAAGTGGCGGAATG
<i>STF1</i> -R	CTCAGCATTATTGGTACCAT
<i>STF2</i> -F	ATGGAACGAAGTGGCGGAATG
<i>STF2</i> -R	CTCAGCATTATTGGTACCAC
CRISPR/Cas9 construction 5'-3'	
<i>RIN1</i> -At3d-T1F1	gtcaTCTAGGGCCTTGAATAGTTC
<i>RIN1</i> -At3d-T1R1	aaacGAACTATTCAAGGCCCTAGA
<i>RIN1</i> -At3b-T2F2	gtcaAAGGGTTCATTGTCCTCAA
<i>RIN1</i> -At3b-T2R2	aaacTTGAGGACAATGAACCCTT
<i>RIN1</i> -At6-1-T3F3	attgCAGCGATAGAGCTGAGACAA
<i>RIN1</i> -At6-1-T3R3	aaacTTGTCTCAGCTCTATCGCTG
Mutants sequencing primers 5'-3'	
<i>RIN1</i> -cas9test-F1	CTGAAGAGTTTGTGAATCCATGG
<i>RIN1</i> -cas9test-R1	GATGACATGACGAAGCAGGAAGG
<i>RIN1</i> -cas9test-F2	CAAGTGCCTGACTGATCAAACC
<i>RIN1</i> -cas9test-R2	AGCTGACTCAAGTTTCTTAA
<i>STF1</i> -cas9test-F	TGAGTGATTTTCTGATCGTGATGC
<i>STF1</i> -cas9test-R	TCCGATGAGGGAAGACCAA
<i>STF2</i> -cas9test-F	AAGAGATTGAACTGCATAGGCT
<i>STF2</i> -cas9test-R	CTTGCACTGGGGACAAGACT
qRT-PCR 5'-3'	
<i>RIN1</i> -RT-F	GGAGTTGTTGCAGAGCGAG
<i>RIN1</i> -RT-R	GAAACTTGATGCTGAACGCT
<i>STF1</i> -RT-F	ACACGGTTCGACAGTGGGTCTAAA
<i>STF1</i> -RT-R	AAGCCACACTCATGACAAGCAACAA
<i>STF2</i> -RT-F	ACATAATGTCAAAGATGGCAGAG
<i>STF2</i> -RT-R	CATTGTATTCCAAACGCACACCTA
<i>GA2ox7a</i> -qF	TGTAACCAACCAACCTGAT
<i>GA2ox7a</i> -qR	AACTCTATGCTCCACACTCTT
<i>GA2ox7b</i> -qF	ACGGTCTCATGCCACATACT
<i>GA2ox7b</i> -qR	TTAACTGCGATCCATTGCT
<i>TUB</i> -F	CTACACCGTTGGCAAAGAGA
<i>TUB</i> -R	GAAGACGAGGAAGCCTTGTA
In situ hybridization probe 5'-3'	
<i>RIN1</i> -positive-F	GATTTAGGTGACACTATAGAATGCTCTGGGGAGTTGTTGCAGAGCGAG
<i>RIN1</i> -positive-R	TGTAATACGACTCACTATAGGGGAAACTTGATGCTGAACGCT
<i>SPA3b</i> -positive-F	GATTTAGGTGACACTATAGAATGCTCGGCAGGGAGTTGTTGCAGAGCGAC
<i>SPA3b</i> -positive-R	TGTAATACGACTCACTATAGGGGAAACTTGATGCTGAATG
<i>GA2ox7a</i> -positive-F	GATTTAGGTGACACTATAGAATGCTTGTAACCAACCAACCTGAT
<i>GA2ox7a</i> -positive-R	TGTAATACGACTCACTATAGGGAACCTATGCTCCACACTCTT
<i>GA2ox7b</i> -positive-F	GATTTAGGTGACACTATAGAATGCTACGGTCTCATGCCACATACT
<i>GA2ox7b</i> -positive-R	TGTAATACGACTCACTATAGGGTTAACTGCGATCCATTGCT

Supplementary Table 6 Primers used in the study.

Y2H vector construction 5'-3'	
RIN1-AD-ECOR1-F	GCCATGGAGGCCAGTGAATTCATGTGTTGTTTACTTGGCCTAC
RIN1-AD-BamH1-R	CAGCTCGAGCTCGATGGATCCTTAACCATCTCCAGAATTTGAC
STF1-BD-ECOR1-F	ATGGCCATGGAGGCCGAATTCATGGAACGAAGTGGCGGAATG
STF1-BD-BamH1-R	CAGCTCGAGCTCGATGGATCCTTACTCAGCATTATTGGTACCAT
STF2-BD-ECOR1-F	ATGGCCATGGAGGCCGAATTCATGGAACGAAGTGGCGGAATG
STF2-BD-BamH1-R	CAGCTCGAGCTCGATGGATCCTTACTCAGCATTATTGGTACCAT
Pull down assay and Cell free assay 5'-3'	
RIN1-GST-F	CGCGGATCCATGTGTTGTTTACTTGGCCTAC
RIN1-GST-R	AACCATCTCCAGAATTTGACGAATTCGGG
STF1-MBP-F	TCCATGGGCGGCCGCGATATCATGGAACGAAGTGGCGGAATG
STF1-MBP-R	ACCTGCAGGGAATTCGGATCCTTACTCAGCATTATTGGTACCAT
STF2-MBP-F	TCCATGGGCGGCCGCGATATCATGGAACGAAGTGGCGGAATG
STF2-MBP-R	ACCTGCAGGGAATTCGGATCCTTACTCAGCATTATTGGTACCAC
BIFC assay 5'-3'	
RIN1-YCE-F	CCTGGCGCGCCACTAGTGGATCCATGTGTTGTTTACTTGGCCTAC
RIN1-YCE-R	CATCCCGGGAGCGGTACCAACCATCTCCAGAATTTGAC
STF1-YNE-F	ACGGGGGACTCTAGAATGGAACGAAGTGGCGGAATG
STF1-YNE-R	AGCGGTACCCTCGAGCTCAGCATTATTGGTACCAT
STF2-YNE-F	ACGGGGGACTCTAGAATGGAACGAAGTGGCGGAATG
STF2-YNE-R	AGCGGTACCCTCGAGCTCAGCATTATTGGTACCAC
PRR5a-YCE-F	CCTGGCGCGCCACTAGTGGATCCATGCCAGAGGTGGTGAT
PRR5a-YCE-R	CATCCCGGGAGCGGTACCTGCTCTCCTCTCCAG
PRR5a-YNE-F	ACGGGGGACTCTAGAATGCCAGAGGTGGTGAT
PRR5s-YNE-R	AGCGGTACCCTCGAGTGCTCTCCTCTCCAG
Transient expression assay	
pGA2ox7a-F	GTCGACGGTATCGATAAGCTTGGTAGCCGACATGGATCGA
pGA2ox7a-R	CGCTCTAGAACTAGTGGATCCAGAAGGAGACTAGCCACCGAGT
pGA2ox7b-F	GTCGACGGTATCGATAAGCTTCAAATTGCTAGCCAGTAGCCAGC
pGA2ox7b-R	CGCTCTAGAACTAGTGGATCCTCTATCTTCTGTGATAGAAATTAGAAAAAGC