

Supplementary Table S1
Primers used in this study

Gene	Forward (5'-3')	Reverse (5'-3')	Purpose
<i>CHS1-Glyma.08G109400</i> cds	ATGGTGAGTGTTGAAGAGATTC	TCAGAGAGTGACACTGCGGAGC	gene cloning
<i>CHS3-Glyma.08G109300</i> cds	ATGGTCAGTGTTGAAGAGATCCGTA	TTAGACAGTGACACTGCGGAGCACA	gene cloning
<i>CHS4-Glyma.08G110700</i> cds	ATGGTGAGTGTTGAAGAGATTCGTA	TTAGACAGTGACACTGCGGAGTACA	gene cloning
<i>Glyma.08g122400</i> cds	ATGAATGCTAGAAAGCTGGCA	CTAGATGTAATTTGCTAGTTGA	gene cloning
<i>Glyma.08g125100</i> cds	ATGGAGGTGACCAACCTTGT	CTAGAAATGGGAAGGATGGA	gene cloning
<i>Glyma.08G137600</i> cds	ATGGGAAGTCTATAGACATGT	TCATATAGCTTCCCAATCAATC	gene cloning
<i>Glyma.08g145300</i> cds	ATGATGAAGAACGATAGAGA	TCAGGCAGAAGAAGAGGAGC	gene cloning
<i>Glyma.08G149200</i> cds	ATGGCAGAGTCTCAGAAACAAC	TTAGGCATAATGTATATTGAGGGG	gene cloning
qPCR- <i>Glyma.08g125600</i>	CGCATGCAAGAAATAGGTTC	TGTAATTGACTGCACACATT	qRT-PCR expression analysis
qPCR- <i>Glyma.08g119500</i>	TGGTGCATTTTCAGAACTCA	TCACGTTTATCTGATACCCT	qRT-PCR expression analysis
qPCR- <i>Glyma.08g119600</i>	AACTTAACTCACAGCTCGTA	GGGTATCAAAGTTTGAGATT	qRT-PCR expression analysis
qPCR- <i>Glyma.08g122400</i>	ATAATCCGAACACTGTCCGC	GTTGGTGGTGGCTGATTAGT	qRT-PCR expression analysis
qPCR- <i>Glyma.08g125000</i>	TTCCTGGAACAAGGTTTCAT	CATTTTCGGTCATAAACCTTC	qRT-PCR expression analysis
qPCR- <i>Glyma.08g125100</i>	CTCAGAACTACTTGCCAAA	AAATTTTAAGGAAAGCTTTG	qRT-PCR expression analysis
qPCR- <i>Glyma.08g128600</i>	CAGAAAGTTTGAGGACTTGT	ATTGGCATGTGGCTGAAATT	qRT-PCR expression analysis
qPCR- <i>Glyma.08g145300</i>	TCATGGTGGCAACTCTGTTCTC	CTCCTCGCTTCTTCTCCTCCT	qRT-PCR expression analysis
qPCR- <i>Glyma.08G137600</i>	TCTAAGACACCACGAGCCTTC	TTTGCCACGTCAGACTCGACCT	qRT-PCR expression analysis
qPCR- <i>Glyma.08G149200</i>	TTGGAGAGGATTGAGAACCCGA	CCCATTTTCTCTGCCTAACACC	qRT-PCR expression analysis
qRT- <i>Actin11</i>	ATGACCCAAATCATGTTTGAGACC	TCAGTTAGATCACGACCAGCGA	qRT-PCR expression analysis
<i>GmSFT1(Glyma.08G137600)</i>	AGCCACCATGCTCGAGATGGGAAC TGCTATAGACATGTAC	TGCTCACCATCTCGAGTATAGCTTC CCAATCAATCTCCAC	vector construction

Table S2

ANOVA of GR, NSR and EC in two RIL populations.

Population	Trait	Source	DF ^a	MS ^b	F ^c
NJRINP	GR	Genotype	280	0.37	2.43***
		Env	1	1.87	12.32***
		Block	1	0.00	0.00
		Gen × Env	265	0.17	1.09**
		Error	485	0.15	
	NSR	Genotype	280	0.17	12.05***
		Env	1	46.23	3300.74***
		Block	1	0.07	4.83
		Gen × Env	264	0.13	9.29***
		Error	482	0.01	
	EC	Genotype	280	131017.63	23.36***
		Env	1	139454.82	24.87***
		Block	1	23624.23	4.21
		Gen × Env	269	13471.06	2.4**
		Error	541	5607.53	
NJRI4P	GR	Genotype	160	0.43	9.08***
		Env	1	0.64	13.34***
		Block	1	0.00	0.00
		Gen × Env	159	0.10	2.01**
		Error	302	0.05	
	NSR	Genotype	160	0.44	11.23***
		Env	1	0.29	7.26**
		Block	1	0.00	0.01
		Gen × Env	158	0.09	2.37**
		Error	282	0.04	
	EC	Genotype	160	185786.52	8.69***
		Env	1	137737.31	6.44**
		Block	1	15016.54	0.70
		Gen × Env	159	37284.26	1.74**
		Error	312	21388.16	

*** $p < 0.001$; ** $p < 0.01$. ^a Degrees of freedom. ^b Mean square. ^c F value is for determining significance.

Table S3

Analysis of nucleotide mutation position of *CHS1*, *CHS3* and *CHS4*.

Gene	Position(bp)	Nucleotide variation	Amino acid variation	
			Variation way	Variation type
<i>CHS1</i>	396	T/C	-	S
	498	C/T		
	531	C/T		
<i>CHS3</i>	219	T/C		
	225	A/G		
	243	G/C		
	255	T/A		
	258	C/T		
<i>CHS4</i>	531	C/T		

x/y = x nucleotide change into y nucleotide, - = No variation, S = Synonymous mutations, N = Non-synonymous mutations.

Table S4

Functional annotation of 10 candidate genes associated with seed-flooding tolerance located in the QTL hotspots on Chr.08.

Gene	Function annotation
<i>Glyma.08g119500</i>	FASCICLIN-like arabinogalactan-protein 12
<i>Glyma.08g119600</i>	FASCICLIN-like arabinogalactan-protein 11
<i>Glyma.08g122400</i>	Carbohydrate-binding X8 domain superfamily protein
<i>Glyma.08g125000</i>	Cytochrome P450, family 716, subfamily A, polypeptide 1
<i>Glyma.08g125100</i>	Cytochrome P450, family 716, subfamily A, polypeptide 1
<i>Glyma.08g125600</i>	UDP-glycosyltransferase 74 F1
<i>Glyma.08g128600</i>	Cytochrome P450, family 716, subfamily A, polypeptide 1
<i>Glyma.08G137600</i>	Ethylene response factor/AP2 domain
<i>Glyma.08g145300</i>	Integrase-type DNA-binding superfamily protein/AP2 domain
<i>Glyma.08G149200</i>	Integrase-type DNA-binding superfamily protein/AP2 domain

A

P1-CHS1	ATGGTGAGTGTGAAGAGATTGTAAGCGCAACGTCAGAAAGGCCCTGCCACTGTCATGGCTATTGGCACGCGCACTCTCCCAACTGGGTGGATCAGAGTAACCTATCTGACTATTATTCCCGATCACCACACGGA	140
P2-CHS1	ATGGTGAGTGTGAAGAGATTGTAAGCGCAACGTCAGAAAGGCCCTGCCACTGTCATGGCTATTGGCACGCGCACTCTCCCAACTGGGTGGATCAGAGTAACCTATCTGACTATTATTCCCGATCACCACACGGA	140
P3-CHS1	ATGGTGAGTGTGAAGAGATTGTAAGCGCAACGTCAGAAAGGCCCTGCCACTGTCATGGCTATTGGCACGCGCACTCTCCCAACTGGGTGGATCAGAGTAACCTATCTGACTATTATTCCCGATCACCACACGGA	140
P1-CHS1	GCACATGACCGAGCTCAAAGAAAAATTCAAGCGCATGTGTGATAAGTCAGTAAAGAGCGATACATGACTTAAAGAGAGATCCTGAAAGAGAAATCCGAGTGTGTTGCTGTACATGGCACCTTCGTTGGATGCAA	280
P2-CHS1	GCACATGACCGAGCTCAAAGAAAAATTCAAGCGCATGTGTGATAAGTCAGTAAAGAGCGATACATGACTTAAAGAGAGATCCTGAAAGAGAAATCCGAGTGTGTTGCTGTACATGGCACCTTCGTTGGATGCAA	280
P3-CHS1	GCACATGACCGAGCTCAAAGAAAAATTCAAGCGCATGTGTGATAAGTCAGTAAAGAGCGATACATGACTTAAAGAGAGATCCTGAAAGAGAAATCCGAGTGTGTTGCTGTACATGGCACCTTCGTTGGATGCAA	280
P1-CHS1	GGCAAGACATGGTGTGTGGAGGTACCAAGTTGGGAAAAGAGGCTGCAACTAAGGCAATCAAGGAATGGGGTCAACCAAGTCCAAGATTACCATCTCATCTTTGACCACTAGTGGTGTGACATGCGTGGTGT	420
P2-CHS1	GGCAAGACATGGTGTGTGGAGGTACCAAGTTGGGAAAAGAGGCTGCAACTAAGGCAATCAAGGAATGGGGTCAACCAAGTCCAAGATTACCATCTCATCTTTGACCACTAGTGGTGTGACATGCGTGGTGT	420
P3-CHS1	GGCAAGACATGGTGTGTGGAGGTACCAAGTTGGGAAAAGAGGCTGCAACTAAGGCAATCAAGGAATGGGGTCAACCAAGTCCAAGATTACCATCTCATCTTTGACCACTAGTGGTGTGACATGCGTGGTGT	420
P1-CHS1	GATTATCAGCTCACTAAACTATTAGGCTTCGCCCTCCGTCAGGCTTACATGATGTACCAACAAGGCTGCTTTGGTGTGGCACGGTCTCGTTTGGCCAAAGACCTCTCTGAAAACAACAGGGTGTCTCGGTGT	560
P2-CHS1	GATTATCAGCTCACTAAACTATTAGGCTTCGCCCTCCGTCAGGCTTACATGATGTACCAACAAGGCTGCTTTGGTGTGGCACGGTCTCGTTTGGCCAAAGACCTCTCTGAAAACAACAGGGTGTCTCGGTGT	560
P3-CHS1	GATTATCAGCTCACTAAACTATTAGGCTTCGCCCTCCGTCAGGCTTACATGATGTACCAACAAGGCTGCTTTGGTGTGGCACGGTCTCGTTTGGCCAAAGACCTCTCTGAAAACAACAGGGTGTCTCGGTGT	560
P1-CHS1	TGCTGTTGTTCTGAGATCACCAGTACACATTTCGGGCCCCAAGTACACCCATCTGATAGCTTTGGGTCAAGCTTTGTTGGAGATGTTGACAGCGCTGTCTATTGATGATCAGACCCCTTACCAGTTGAAAAG	700
P2-CHS1	TGCTGTTGTTCTGAGATCACCAGTACACATTTCGGGCCCCAAGTACACCCATCTGATAGCTTTGGGTCAAGCTTTGTTGGAGATGTTGACAGCGCTGTCTATTGATGATCAGACCCCTTACCAGTTGAAAAG	700
P3-CHS1	TGCTGTTGTTCTGAGATCACCAGTACACATTTCGGGCCCCAAGTACACCCATCTGATAGCTTTGGGTCAAGCTTTGTTGGAGATGTTGACAGCGCTGTCTATTGATGATCAGACCCCTTACCAGTTGAAAAG	700
P1-CHS1	CTTTGTTTTCAGCTGTCTGGACTGCCAGACATCTTCCAGACAGTGAAGGGCTATTGATGACACCTTCGCGAAGTTGGTCTCATTTCATCTCCTCAAGGATGTTCTGGACTCATCTCCAAGAAATATTGAGAAG	840
P2-CHS1	CTTTGTTTTCAGCTGTCTGGACTGCCAGACATCTTCCAGACAGTGAAGGGCTATTGATGACACCTTCGCGAAGTTGGTCTCATTTCATCTCCTCAAGGATGTTCTGGACTCATCTCCAAGAAATATTGAGAAG	840
P3-CHS1	CTTTGTTTTCAGCTGTCTGGACTGCCAGACATCTTCCAGACAGTGAAGGGCTATTGATGACACCTTCGCGAAGTTGGTCTCATTTCATCTCCTCAAGGATGTTCTGGACTCATCTCCAAGAAATATTGAGAAG	840
P1-CHS1	GCCTTGGTTGAAGCTTCCAAACCTTGGGAATCTCGGATTAACAATCTATCTTGGATTGCAACCCCTGGTGGACCCCAATTTGGACCAAGTTGAGGCTAAGTTAGGCTGAAGCTGAAAAATGGAAGTACTAG	980
P2-CHS1	GCCTTGGTTGAAGCTTCCAAACCTTGGGAATCTCGGATTAACAATCTATCTTGGATTGCAACCCCTGGTGGACCCCAATTTGGACCAAGTTGAGGCTAAGTTAGGCTGAAGCTGAAAAATGGAAGTACTAG	980
P3-CHS1	GCCTTGGTTGAAGCTTCCAAACCTTGGGAATCTCGGATTAACAATCTATCTTGGATTGCAACCCCTGGTGGACCCCAATTTGGACCAAGTTGAGGCTAAGTTAGGCTGAAGCTGAAAAATGGAAGTACTAG	980
P1-CHS1	ACATGTGCTCAGCGAGTATGTAACATGTCAAGTGCATGGCTGCTATTATCTTGGATCAAAATGAGGAAGAAATCAATAGAAAATGGACTTGGCACAACCGGTGAAGGCTTGTGCTGGGTGTGCTATTGGTTTGGGCT	1120
P2-CHS1	ACATGTGCTCAGCGAGTATGTAACATGTCAAGTGCATGGCTGCTATTATCTTGGATCAAAATGAGGAAGAAATCAATAGAAAATGGACTTGGCACAACCGGTGAAGGCTTGTGCTGGGTGTGCTATTGGTTTGGGCT	1120
P3-CHS1	ACATGTGCTCAGCGAGTATGTAACATGTCAAGTGCATGGCTGCTATTATCTTGGATCAAAATGAGGAAGAAATCAATAGAAAATGGACTTGGCACAACCGGTGAAGGCTTGTGCTGGGTGTGCTATTGGTTTGGGCT	1120
P1-CHS1	CTGGACTCACCGTTGAGACTGTGTGCTCCGAGTGTCACTCTCTGA	1167
P2-CHS1	CTGGACTCACCGTTGAGACTGTGTGCTCCGAGTGTCACTCTCTGA	1167
P3-CHS1	CTGGACTCACCGTTGAGACTGTGTGCTCCGAGTGTCACTCTCTGA	1167

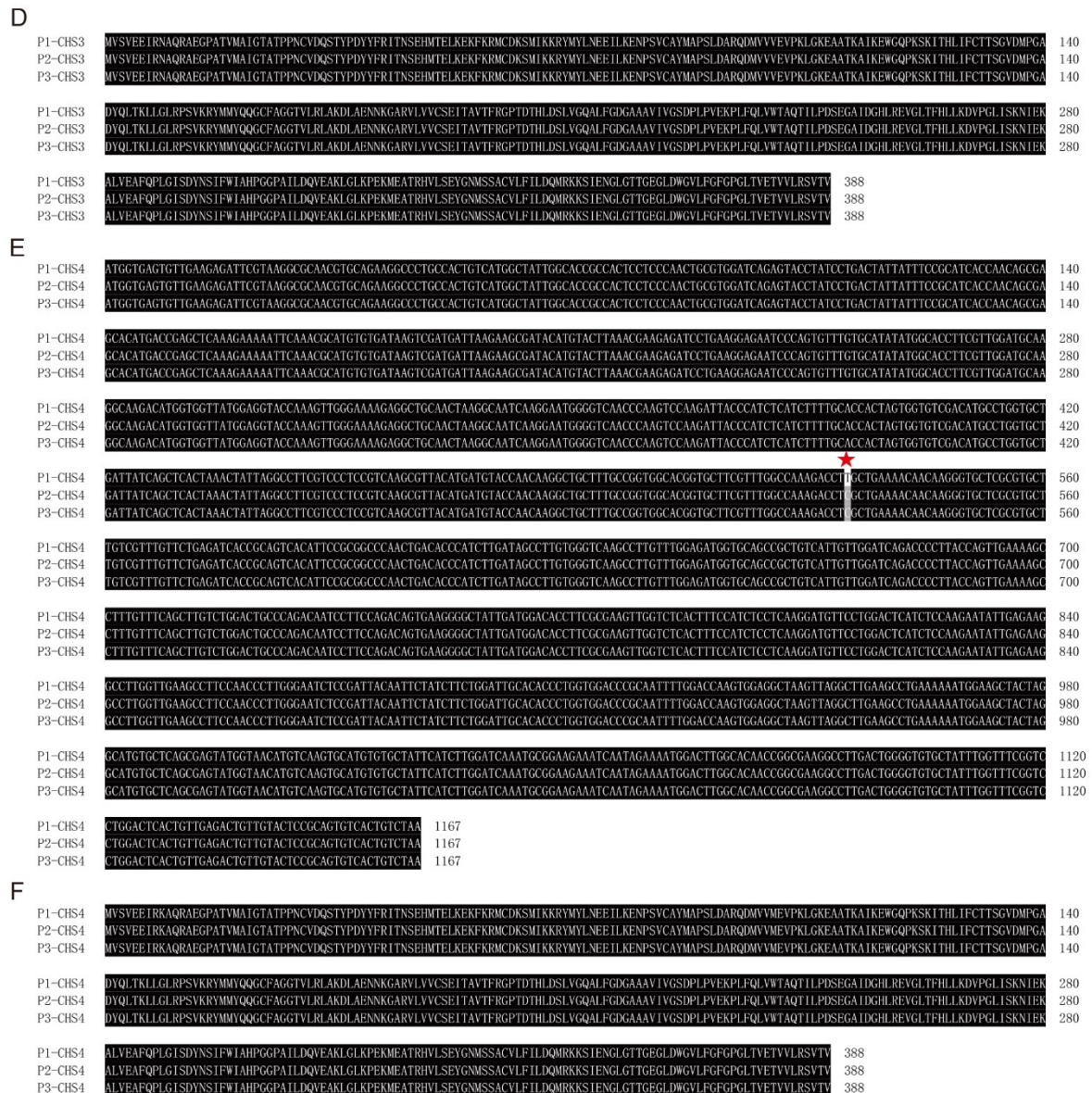
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P1-CHS1	MVSEIRKAQRAEGPATVMAIGTATPPNCVDQSTYPDYFRITNSEHMTLKEKFKRMCDKSMIKRMYLNEEILKENPVCAYMAPSLDARQDMVVEVPKLGKEAATKAKEWGQPKSKIHLIFCTTSGVDMPGA	140
P2-CHS1	MVSEIRKAQRAEGPATVMAIGTATPPNCVDQSTYPDYFRITNSEHMTLKEKFKRMCDKSMIKRMYLNEEILKENPVCAYMAPSLDARQDMVVEVPKLGKEAATKAKEWGQPKSKIHLIFCTTSGVDMPGA	140
P3-CHS1	MVSEIRKAQRAEGPATVMAIGTATPPNCVDQSTYPDYFRITNSEHMTLKEKFKRMCDKSMIKRMYLNEEILKENPVCAYMAPSLDARQDMVVEVPKLGKEAATKAKEWGQPKSKIHLIFCTTSGVDMPGA	140
P1-CHS1	DYQLTKLLGLRPSVKRYMMQGGCFAGTVLRLAKDLAENKAGARVLVVCSEITAVTFRPTDTHLDSLVQALFGDGAAGVIVGSDPLPVEKPLFQLVWTAQTLIPDSEAGIDGHLREVGLTHLLKDVPLISKNIEX	280
P2-CHS1	DYQLTKLLGLRPSVKRYMMQGGCFAGTVLRLAKDLAENKAGARVLVVCSEITAVTFRPTDTHLDSLVQALFGDGAAGVIVGSDPLPVEKPLFQLVWTAQTLIPDSEAGIDGHLREVGLTHLLKDVPLISKNIEX	280
P3-CHS1	DYQLTKLLGLRPSVKRYMMQGGCFAGTVLRLAKDLAENKAGARVLVVCSEITAVTFRPTDTHLDSLVQALFGDGAAGVIVGSDPLPVEKPLFQLVWTAQTLIPDSEAGIDGHLREVGLTHLLKDVPLISKNIEX	280
P1-CHS1	ALVEAFQPLGIDSYNSIFWIAHPGGPAILDQVEARKLGLPEKMEATRHVLSEYGMSSACVFLILDQMRKKSIEGLGTTGEGLDWGLFQFGPGLTVETVLRSVTL	388
P2-CHS1	ALVEAFQPLGIDSYNSIFWIAHPGGPAILDQVEARKLGLPEKMEATRHVLSEYGMSSACVFLILDQMRKKSIEGLGTTGEGLDWGLFQFGPGLTVETVLRSVTL	388
P3-CHS1	ALVEAFQPLGIDSYNSIFWIAHPGGPAILDQVEARKLGLPEKMEATRHVLSEYGMSSACVFLILDQMRKKSIEGLGTTGEGLDWGLFQFGPGLTVETVLRSVTL	388

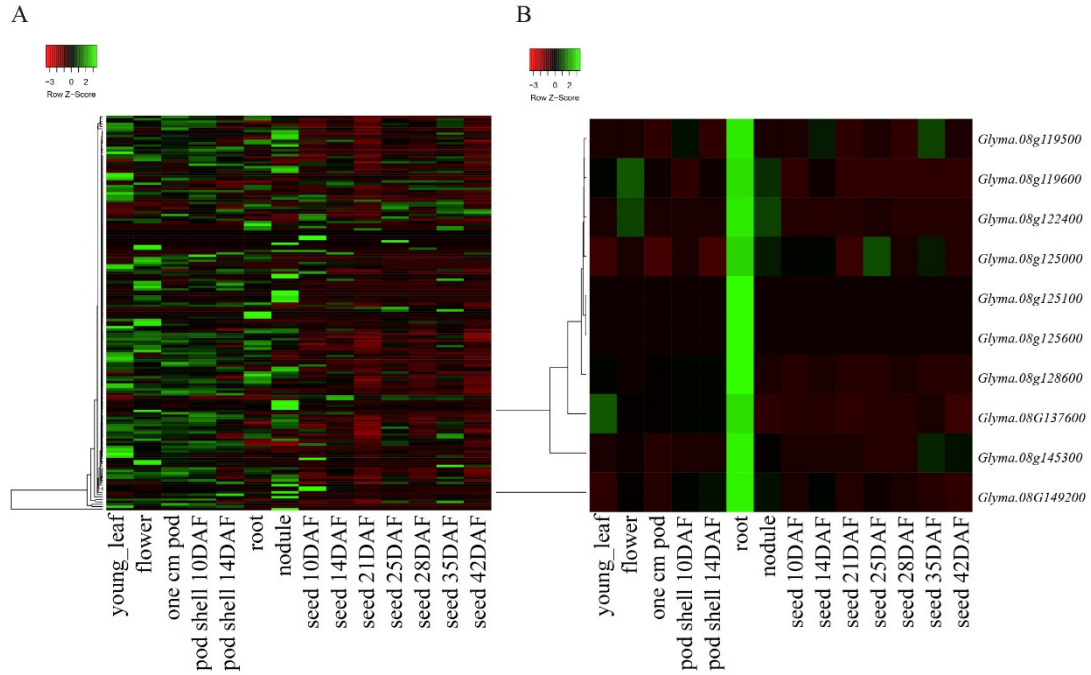
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P1-CHS3	ATGGTCAGTGTGAAGAGATCCGTAATGCACAACGTCAGAGGGCCCTGCCACTGTCATGGCTATTGGCACGCGCACTCTCCAAACTGTGTCGATCAGAGTAACCTATCTGACTATTATTCCCGATCACCACACGGA	140
P2-CHS3	ATGGTCAGTGTGAAGAGATCCGTAATGCACAACGTCAGAGGGCCCTGCCACTGTCATGGCTATTGGCACGCGCACTCTCCAAACTGTGTCGATCAGAGTAACCTATCTGACTATTATTCCCGATCACCACACGGA	140
P3-CHS3	ATGGTCAGTGTGAAGAGATCCGTAATGCACAACGTCAGAGGGCCCTGCCACTGTCATGGCTATTGGCACGCGCACTCTCCAAACTGTGTCGATCAGAGTAACCTATCTGACTATTATTCCCGATCACCACACGGA	140
P1-CHS3	GCACATGACCGAGCTCAAAGAAAAATTCAAGCGCATGTGTGATAAGTCAATGATTAAAGAGCGATACATGACTTAAAGAGAGATCCTGAAAGAGAAATCCGAGTGTGTTGCTGTACATGGCACCTTCGTTGGATGCAA	280
P2-CHS3	GCACATGACCGAGCTCAAAGAAAAATTCAAGCGCATGTGTGATAAGTCAATGATTAAAGAGCGATACATGACTTAAAGAGAGATCCTGAAAGAGAAATCCGAGTGTGTTGCTGTACATGGCACCTTCGTTGGATGCAA	280
P3-CHS3	GCACATGACCGAGCTCAAAGAAAAATTCAAGCGCATGTGTGATAAGTCAATGATTAAAGAGCGATACATGACTTAAAGAGAGATCCTGAAAGAGAAATCCGAGTGTGTTGCTGTACATGGCACCTTCGTTGGATGCAA	280
P1-CHS3	GGCAAGACATGGTGTGTGGAGGTACCAAGTTGGGAAAAGAGGCTGCAACTAAGGCAATCAAGGAATGGGGTCAACCAAGTCCAAGATTACCATCTCATCTTTGACCACTAGTGGTGTGACATGCGTGGTGT	420
P2-CHS3	GGCAAGACATGGTGTGTGGAGGTACCAAGTTGGGAAAAGAGGCTGCAACTAAGGCAATCAAGGAATGGGGTCAACCAAGTCCAAGATTACCATCTCATCTTTGACCACTAGTGGTGTGACATGCGTGGTGT	420
P3-CHS3	GGCAAGACATGGTGTGTGGAGGTACCAAGTTGGGAAAAGAGGCTGCAACTAAGGCAATCAAGGAATGGGGTCAACCAAGTCCAAGATTACCATCTCATCTTTGACCACTAGTGGTGTGACATGCGTGGTGT	420
P1-CHS3	GATTATCAGCTCACTAAACTATTAGGCTTCGCCCTCCGTCAGGCTTACATGATGTACCAACAAGGCTGCTTTGGTGTGGCACGGTCTCGTTTGGCCAAAGACCTCTCTGAAAACAACAGGGTGTCTCGGTGT	560
P2-CHS3	GATTATCAGCTCACTAAACTATTAGGCTTCGCCCTCCGTCAGGCTTACATGATGTACCAACAAGGCTGCTTTGGTGTGGCACGGTCTCGTTTGGCCAAAGACCTCTCTGAAAACAACAGGGTGTCTCGGTGT	560

Supplementary Fig. S1. Multiple sequence alignment describing the base sequence and amino acids sequence of *CHS1*, *CHS3* and *CHS4* in P1(P1342618B), P2(NN86-4) and P3(NN493-1). (A),(C),(E) represent multiple base sequence alignment of *CHS1*, *CHS3* and *CHS4*. (B),(D),(F) represent multiple amino acids sequence alignment of *CHS1*, *CHS3* and *CHS4*.



Supplementary Fig. S1. Multiple sequence alignment describing the base sequence and amino acids sequence of *CHS1*, *CHS3* and *CHS4* in P1(PI342618B), P2(NN86-4) and P3(NN493-1). (A),(C),(E) represent multiple base sequence alignment of *CHS1*, *CHS3* and *CHS4*. (B),(D),(F) represent multiple amino acids sequence alignment of *CHS1*, *CHS3* and *CHS4*.



Supplementary Fig. S2. Expression analysis of candidate genes in the QTL hotspot(8-2) region related to seed-flooding tolerance. (A) Heat maps of expression levels for 164 candidate genes in different soybean tissues. (B) Heat maps of expression levels for 10 screened candidate genes associated with seed-flooding tolerance in different tissues. The RNA-seq data were obtained from Soybase (<https://www.soybase.org/soyseq/>).

P1-Glyma. 08g122400	ATGAATCTACAGACCTGGACCTGATATATCTCTTATGTCTTTCTTTGGTTCAGGCTTGGAAACACCAAAATATTAAATAATGGCAAAAACAGGAATCTCTCATATGGGAATTTGGGTACTCAATTACATAT	139
P2-Glyma. 08g122400	ATGAATGCTAGAGACCTGGACCTGATATATCTCTTATGTCTTTCTTTGGTTCAGGCTTGGAAACACCAAAATATTAAATAATGGCAAAAACAGGAATCTCTCATATGGGAATTTGGGTACTCAATTACATAT	140
P3-Glyma. 08g122400	ATGAATGCTAGAGACCTGGACCTGATATATCTCTTATGTCTTTCTTTGGTTCAGGCTTGGAAACACCAAAATATTAAATAATGGCAAAAACAGGAATCTCTCATATGGGAATTTGGGTACTCAATTACATAT	140
P1-Glyma. 08g122400	TGTTCTCTATGCTCAATCCCAACACTCTCTGACACAGGAAATCCATATATGGGAAACCTAACATTTCTCTAAACACCTTGACACATTCAGGCGCAAGCCCAACACCAACCAATCCAAACACCCCAACCAAGGCCA	279
P2-Glyma. 08g122400	TGTTCTCTATGCTCAATCCCAACACTCTCTGACACAGGAAATCCATATATGGGAAACCTAACATTTCTCTAAACACCTTGACACATTCAGGCGCAAGCCCAACACCAACCAATCCAAACACCCCAACCAAGGCCA	280
P3-Glyma. 08g122400	TGTTCTCTATGCTCAATCCCAACACTCTCTGACACAGGAAATCCATATATGGGAAACCTAACATTTCTCTAAACACCTTGACACATTCAGGCGCAAGCCCAACACCAACCAATCCAAACACCCCAACCAAGGCCA	280
P1-Glyma. 08g122400	CACCCCAACTACACACCAACACCCCACTACTACATCTCCAGTATGCTCAATGTGTGTTGCTTAACCGAGAGCTTGACACATGCTCTACAGGTTGCTCTTGACTATGCTTGTGGGTTGGAGGTGCAGACTGCTCA	419
P2-Glyma. 08g122400	CACCCCAACTACACACCAACACCCCACTACTACATCTCCAGTATGCTCAATGTGTGTTGCTTAACCGAGAGCTTGACACATGCTCTACAGGTTGCTCTTGACTATGCTTGTGGGTTGGAGGTGCAGACTGCTCA	420
P3-Glyma. 08g122400	CACCCCAACTACACACCAACACCCCACTACTACATCTCCAGTATGCTCAATGTGTGTTGCTTAACCGAGAGCTTGACACATGCTCTACAGGTTGCTCTTGACTATGCTTGTGGGTTGGAGGTGCAGACTGCTCA	420
P1-Glyma. 08g122400	GCAATACAAACAGGAGCAAGCTGTTATATCTCAACACTGTCGGCAGATGCTCTTATGCAATCAATGACTACTACCAAGAAATCCAGACCTACACGCTTGATATTGGAGGAACAGCATCTCTTACAAGCAATGA	559
P2-Glyma. 08g122400	GCAATACAAACAGGAGCAAGCTGTTATATCTCAACACTGTCGGCAGATGCTCTTATGCAATCAATGACTACTACCAAGAAATCCAGACCTACACGCTTGATATTGGAGGAACAGCATCTCTTACAAGCAATGA	560
P3-Glyma. 08g122400	GCAATACAAACAGGAGCAAGCTGTTATATCTCAACACTGTCGGCAGATGCTCTTATGCAATCAATGACTACTACCAAGAAATCCAGACCTACACGCTTGATATTGGAGGAACAGCATCTCTTACAAGCAATGA	560
P1-Glyma. 08g122400	TCCAAGTAGTGGGATTTGCAAAATACGATACCCAGTACCAAGCAATCAAGCCACCAACACCAAAATTTGTACGCCACCAAGTCCACAACTCCAGTAGTATGCCCACTTCCACAGCAATGCTAAATCTCTG	699
P2-Glyma. 08g122400	TCCAAGTAGTGGGATTTGCAAAATACGATACCCAGTACCAAGCAATCAAGCCACCAACACCAAAATTTGTACGCCACCAAGTCCACAACTCCAGTAGTATGCCCACTTCCACAGCAATGCTAAATCTCTG	700
P3-Glyma. 08g122400	TCCAAGTAGTGGGATTTGCAAAATACGATACCCAGTACCAAGCAATCAAGCCACCAACACCAAAATTTGTACGCCACCAAGTCCACAACTCCAGTAGTATGCCCACTTCCACAGCAATGCTAAATCTCTG	700
P1-Glyma. 08g122400	GTGGCGGATCAACTGTTTGTGTCAGAACCAACAGGAGGCCAACACAGCCATTTGCAATTAATTCCTGCTGATGTGTGTACATGTGGTCTGTGGCTTCCTTCAACTAGCAAAATACACTAG	830
P2-Glyma. 08g122400	GTGGCGGATCAACTGTTTGTGTCAGAACCAACAGGAGGCCAACACAGCCATTTGCAATTAATTCCTGCTGATGTGTGTACATGTGGTCTGTGGCTTCCTTCAACTAGCAAAATACACTAG	831
P3-Glyma. 08g122400	GTGGCGGATCAACTGTTTGTGTCAGAACCAACAGGAGGCCAACACAGCCATTTGCAATTAATTCCTGCTGATGTGTGTACATGTGGTCTGTGGCTTCCTTCAACTAGCAAAATACACTAG	831

P1-Glyma. 08612240	MNARSWHVLFSLCLFFSGSLGKTKILLKNGKKEIFSSSELGTQLDVPINVTPTDGNVGNPNAPQPTDSGNPTPTTNNPTPTPTPTPTPTPTPTSSGGQWCVANGASDIALQVADYACGFGGADS	140
P2-Glyma. 08612240	MNARSWHVLFSLCLFFSGSLGKTKILLKNGKKEIFSSSELGTQLDVPINVTPTDGNVGNPNAPQPTDSGNPTPTTNNPTPTPTPTPTPTPTPTSSGGQWCVANGASDIALQVADYACGFGGADS	140
P3-Glyma. 08612240	MNARSWHVLFSLCLFFSGSLGKTKILLKNGKKEIFSSSELGTQLDVPINVTPTDGNVGNPNAPQPTDSGNPTPTTNNPTPTPTPTPTPTPTPTSSGGQWCVANGASDIALQVADYACGFGGADS	140
P1-Glyma. 08612240	AIQPGASCYNPTVRDHASAFYNDYQKNPAPTSVCFGGTASLTNSDPSSGSKYASPKSTNGNMPNPTFVSPSPPTVMITPTPDLMLNGGGSVTFGSEPTGSPNTATFANSLMLFTGGLASLQIANT	276
P2-Glyma. 08612240	AIQPGASCYNPTVRDHASAFYNDYQKNPAPTSVCFGGTASLTNSDPSSGSKYASPKSTNGNMPNPTFVSPSPPTVMITPTPDLMLNGGGSVTFGSEPTGSPNTATFANSLMLFTGGLASLQIANT	276
P3-Glyma. 08612240	AIQPGASCYNPTVRDHASAFYNDYQKNPAPTSVCFGGTASLTNSDPSSGSKYASPKSTNGNMPNPTFVSPSPPTVMITPTPDLMLNGGGSVTFGSEPTGSPNTATFANSLMLFTGGLASLQIANT	276

Supplementary Fig. S3. Multiple sequence alignment describing the base sequence and amino acids sequence of *Glyma.08G122400* in P1(PI342618B), P2(NN86-4) and P3(NN493-1). (A) represent multiple base sequence alignment of *Glyma.08G124400*. (B) represent multiple amino acids sequence alignment of *Glyma.08G124400*.