

Supplementary Table S1. Source of material for testing.

Area	Quantity	Area	Quantity
Heilongjiang	180	United States	8
Jilin	33	Canada	3
Liaoning	18	Germany	1
Beijing	19	Italy	1
Inner Mongolia	20	Russia	1
Hebei	4	Ukraine	1
Shanxi	2	Japan	3
Gansu	1	Unknown	10
Xinjiang	1		

Supplementary Table S2. Primers sequence information.

Primer Name	Primer Sequence(5'-3')	Restriction Sites	Target Fragment Size /bp	Functions
<i>OXGmRF2</i> -like-F	<u>TCGAGCTCCGTCGACAAGCTTATGGAGTTGATGCAACAAGT</u>	<i>Hind</i> III	1236bp	Clone
<i>OXGmRF2</i> -like-R	<u>GCCCTTGCTCACCATAAAGCTTTCAGTGGCGATGATACTGCA</u>			
<i>subGmRF2</i> -like-F	<u>ACGGGGGACTCTTGACCATGGATGGAGTTGATGCAACAAGT</u>	<i>Nco</i> I	1236bp	subcellular
<i>subGmRF2</i> -like-R	<u>TACTAGTCAGATCTACCATGGGTGGCGATGATACTGCAAAAG</u>			
<i>Actin 4</i> -F	GTTTCAAGCTCTTGCTCGTAATCA		104bp	housekeeping

<i>Actin 4-R</i>	GTGTCAGCCATACTGTCCCCATTT		primer
<i>qGmRF2-like-F</i>	GGCTCCATTCTTCTCACATCA	106 bp	quantitative primer
<i>qGmRF2-like-R</i>	CTCATCGGAAGTAGGCACATTAG		

The underlined part is the vector sequence, the italicized part is the restriction enzyme site, and the double-underlined part is the cloned gene primer sequence.

Supplementary Table S3. 30× The acid fuchsine solution stock solution.

Main Components of the Medium	Content
Fuchsine (C ₂₀ H ₂₀ ClN ₃)	3.5 g
CH ₃ COOH	250 mL
ddH ₂ O	750 mL

Supplementary Table S4. MS medium formulations.

Main Components of the Medium	Component	Content
Major element	NH ₄ NO ₃	1650 mg/L
	CaCl ₂	332.2 mg/L
	MgSO ₄	180.7 mg/L
	KNO ₃	1900 mg/L
	KH ₂ PO ₄	170 mg/L
Trace element	H ₃ BO ₃	6.2 mg/L
	CoCl ₂ .6H ₂ O	0.025 mg/L
	CuSO ₄ .5H ₂ O	0.025 mg/L
	FeNa EDTA	36.7 mg/L
	MnSO ₄ .H ₂ O	16.9 mg/L
	Na ₂ MoO ₄ .2H ₂ O	0.25 mg/L
	KI	0.83 mg/L
	ZnSO ₄ .7H ₂ O	8.6 mg/L
carbon source	Sucrose	30 g/L

Agar	Agar	8 g/L
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Supplementary Table S5. Number of soil cysts in the nursery.

Place	Number of Air Dried Soil Cysts per 100g (Unit :number)				
	1	2	3	4	5
Field disease nurseries	53	45	50	44	43

Supplementary Table S6. Information on medium resistance material.

No.	Materials	Area	Female Index
1	HH45	Heilongjiang, China	MR
2	HJ03-286	Inner Mongolia, China	MR
3	HN69	Heilongjiang, China	MR
4	HJ1H	Heilongjiang, China	MR
5	H115	Inner Mongolia, China	MR
6	HH50	Heilongjiang, China	MR
7	HH38H	Heilongjiang, China	MR
8	Domaca Tolisa	Hubei, China	MR
9	DD1	Heilongjiang, China	MR
10	NF20	Heilongjiang, China	MR
11	HF70	Heilongjiang, China	MR
12	JL27	Jilin, China	MR
13	HJ11-359	Inner Mongolia, China	MR

14	S09-3690	Heilongjiang, China	MR
15	BJ9H	Heilongjiang, China	MR
16	JY94H	Jilin, China	MR
17	L-114	Hubei, China	MR
18	HHXHD	Heilongjiang, China	MR
19	TF3	Liaoning, China	MR
20	HN64	Heilongjiang, China	MR
21	KF14	Heilongjiang, China	MR
22	HH51H	Heilongjiang, China	MR
23	HF66	Heilongjiang, China	MR
24	HF25	Heilongjiang, China	MR
25	HH33H	Heilongjiang, China	MR
26	HH35H	Heilongjiang, China	MR
27	HH43H	Heilongjiang, China	MR
28	SN35	Heilongjiang, China	MR
29	QAHD	Heilongjiang, China	MR
30	S03-3046	Heilongjiang, China	MR
31	JY55H	Heilongjiang, China	MR
32	HHSD	Jilin, China	MR
33	JMD1H	Inner Mongolia, China	MR
34	JY204	Jilin, China	MR
35	KX3H	Beijing, China	MR
36	KJ4430-20	Heilongjiang, China	MR
37	JF6	Heilongjiang, China	MR
38	JY1H	Jilin, China	MR
39	L-58Keburi	Japan	MR

40	Charleston	America	MR
41	KD5H	Inner Mongolia, China	MR
42	HN37	Heilongjiang, China	MR
43	KY3	Liaoning, China	MR
44	HJ423	Inner Mongolia, China	MR
45	DK09-1230	Inner Mongolia, China	MR
46	ZD32	Beijing, China	MR
47	HH4	Heilongjiang, China	MR
48	H05-991	Heilongjiang, China	MR
49	TJSLH	Jilin, China	MR
50	L-59Peking	Japan	MR
51	HH19	Heilongjiang, China	MR
52	century lx13	America	MR
53	HF37	Heilongjiang, China	MR
54	SN8	Heilongjiang, China	MR
55	FS22	Heilongjiang, China	MR
56	BF14	Heilongjiang, China	MR
57	XBM	Jilin, China	MR
58	FDH	Jilin, China	MR
59	JSP	Heilongjiang, China	MR
60	SDD1H	Hebei, China	MR
61	SN25	Heilongjiang, China	MR
62	HH23H	Heilongjiang, China	MR
63	MD11	Inner Mongolia, China	MR
64	KSSLJ	Heilongjiang, China	MR
65	BCMSD	Jilin, China	MR

66	MD9H	Inner Mongolia, China	MR
67	MCJ	Liaoning, China	MR
68	ZZ GHJ14215	Beijing, China	MR
69	HH5	Heilongjiang, China	MR
70	HF35	Heilongjiang, China	MR
71	HF11	Heilongjiang, China	MR
72	KJD27	Heilongjiang, China	MR
73	ZH 901	Beijing, China	MR
74	DN49	Heilongjiang, China	MR
75	BF 9	Heilongjiang, China	MR
76	L-234	Hubei, China	MR
77	KF 16	Heilongjiang, China	MR
78	JL 20	Jilin, China	MR
79	S05-7304	Heilongjiang, China	MR
80	CD1H	Heilongjiang, China	MR
81	DN42	Heilongjiang, China	MR
82	HN68	Heilongjiang, China	MR
83	HN38	Heilongjiang, China	MR
84	HF31	Heilongjiang, China	MR
85	S03-3952	Heilongjiang, China	MR

Supplementary Table S7. SNPs that significantly associated with SCN resistance of soybean.

SNP Site	Chr	Physical Position	<i>p</i> (Value)	-Log10(<i>p</i>)
Chr.6:28161491	6	28161491	2.37E-08	7.63
Chr.19:8334736	19	8334736	2.68E-08	7.57
Chr.19:8507367	19	8507367	2.93E-08	7.53
Chr.6:29475879	6	29475879	3.73E-08	7.43
Chr.19:8220770	19	8220770	3.83E-08	7.42
Chr.19:8394130	19	8394130	3.99E-08	7.40
Chr.19:8446190	19	8446190	4.44E-08	7.35
Chr.19:8250257	19	8250257	4.9E-08	7.31
Chr.19:8354294	19	8354294	4.95E-08	7.31
Chr.19:8264253	19	8264253	5.25E-08	7.28
Chr.6:28632077	6	28632077	5.56E-08	7.25
Chr.19:8190889	19	8190889	6.78E-08	7.17
Chr.19:8339229	19	8339229	1.5 E-07	6.82
Chr.19:8250339	19	8250339	1.67E-07	6.78
Chr.5:28410730	5	28410730	1.70E-07	6.77
Chr.19:8246191	19	8246191	1.75E-07	6.76
Chr.19:8232498	19	8232498	2.04E-07	6.69
Chr.19:8147431	19	8147431	2.09E-07	6.68
Chr.19:8232497	19	8232497	2.19E-07	6.66
Chr.6:28550270	6	28550270	2.26E-07	6.65
Chr.19:8504682	19	8504682	2.28E-07	6.64
Chr.19:8460234	19	8460234	2.59E-07	6.59
Chr.18:33817618	18	33817618	2.60E-07	6.59
Chr.19:8400085	19	8400085	2.62E-07	6.58

Chr.19:8326038	19	8326038	3.17E-07	6.50
Chr.19:8243373	19	8243373	3.23E-07	6.49
Chr.19:8331466	19	8331466	3.38E-07	6.47
Chr.19:8158114	19	8158114	3.44E-07	6.46
Chr.19:8382716	19	8382716	3.46E-07	6.46
Chr.19:8237731	19	8237731	3.59E-07	6.44
Chr.19:8250409	19	8250409	4.03E-07	6.39
Chr.19:8231287	19	8231287	5.26E-07	6.28
Chr.19:8413952	19	8413952	5.35E-07	6.27
Chr.19:8237692	19	8237692	5.83E-07	6.23
Chr.19:8237693	19	8237693	5.83E-07	6.23
Chr.19:8223440	19	8223440	5.94E-07	6.23
Chr.15:40736992	15	40736992	6.01E-07	6.22
Chr.6:24653717	6	24653717	6.17E-07	6.21
Chr.19:8244536	19	8244536	6.50E-07	6.19
Chr.6:23536393	6	23536393	6.70E-07	6.17
Chr.18:33817617	18	33817617	7.51E-07	6.12
Chr.14:17149994	14	17149994	7.87E-07	6.10
Chr.19:8255556	19	8255556	8.23E-07	6.08
Chr.3:40069320	3	40069320	8.28E-07	6.08
Chr.19:8246258	19	8246258	8.36E-07	6.08
Chr.19:8393977	19	8393977	8.58E-07	6.07
Chr.19:8353287	19	8353287	8.60E-07	6.07
Chr.19:8388219	19	8388219	8.62E-07	6.06
Chr.19:8331883	19	8331883	8.75E-07	6.06
Chr.19:8203555	19	8203555	8.79E-07	6.06

Chr.19:8354196	19	8354196	9.25E-07	6.03
Chr.6:28786190	6	28786190	9.26E-07	6.03
Chr.19:8213785	19	8213785	9.92E-07	6.00
Chr.19:8203590	19	8203590	1.02E-06	5.99
Chr.19:8395877	19	8395877	1.07E-06	5.97
Chr.18:9411325	18	9411325	1.08E-06	5.97
Chr.19:8304063	19	8304063	1.08E-06	5.97
Chr.15:24463600	15	24463600	1.13E-06	5.95
Chr.15:24463614	15	24463614	1.13E-06	5.95
Chr.6:27580765	6	27580765	1.16E-06	5.94
Chr.19:8329545	19	8329545	1.19E-06	5.92
Chr.19:8243093	19	8243093	1.20E-06	5.92
Chr.19:8505580	19	8505580	1.26E-06	5.90
Chr.19:8345725	19	8345725	1.28E-06	5.89
Chr.19:8241570	19	8241570	1.30E-06	5.89
Chr.15:40694427	15	40694427	1.36E-06	5.87
Chr.19:8443693	19	8443693	1.36E-06	5.87
Chr.19:8400146	19	8400146	1.37E-06	5.86
Chr.19:8504899	19	8504899	1.37E-06	5.86
Chr.3:40069325	3	40069325	1.38E-06	5.86
Chr.18:25012412	18	25012412	1.41E-06	5.85
Chr.19:8165092	19	8165092	1.41E-06	5.85
Chr.19:8347013	19	8347013	1.42E-06	5.85
Chr.19:8384176	19	8384176	1.43E-06	5.84
Chr.19:8328444	19	8328444	1.44E-06	5.84
Chr.6:24176736	6	24176736	1.44E-06	5.84

Chr.19:8346639	19	8346639	1.48E-06	5.83
Chr.19:8345576	19	8345576	1.50E-06	5.82
Chr.19:8317275	19	8317275	1.51E-06	5.82
Chr.19:8498013	19	8498013	1.52E-06	5.82
Chr.19:8387234	19	8387234	1.53E-06	5.82
Chr.19:8245129	19	8245129	1.56E-06	5.81
Chr.19:8484132	19	8484132	1.56E-06	5.81
Chr.19:8246586	19	8246586	1.61E-06	5.79
Chr.19:8253482	19	8253482	1.67E-06	5.78
Chr.19:8253486	19	8253486	1.67E-06	5.78
Chr.19:8248234	19	8248234	1.70E-06	5.77
Chr.6:27732903	6	27732903	1.72E-06	5.76
Chr.20:14533642	20	14533642	1.75E-06	5.76
Chr.19:8312146	19	8312146	1.78E-06	5.75
Chr.4:49244968	4	49244968	1.79E-06	5.75
Chr.19:8245387	19	8245387	1.83E-06	5.74
Chr.19:8523596	19	8523596	1.85E-06	5.73
Chr.19:8246075	19	8246075	1.86E-06	5.73
Chr.19:8224582	19	8224582	1.88E-06	5.73
Chr.19:8495538	19	8495538	1.95E-06	5.71
Chr.19:8415918	19	8415918	1.96E-06	5.71
Chr.19:8256792	19	8256792	1.97E-06	5.71
Chr.19:8345858	19	8345858	1.97E-06	5.71
Chr.19:8248161	19	8248161	1.98E-06	5.70
Chr.19:8306161	19	8306161	2.02E-06	5.69
Chr.19:8231372	19	8231372	2.06E-06	5.69

Chr.19:8400866	19	8400866	2.09E-06	5.68
Chr.19:8434413	19	8434413	2.09E-06	5.68
Chr.19:8246024	19	8246024	2.10E-06	5.68
Chr.19:47885693	19	47885693	2.11E-06	5.68
Chr.15:40447401	15	40447401	2.14E-06	5.67
Chr.19:8255527	19	8255527	2.17E-06	5.66
Chr.6:22970716	6	22970716	2.18E-06	5.66
Chr.19:8448359	19	8448359	2.20E-06	5.66
Chr.19:8243445	19	8243445	2.24E-06	5.65
Chr.3:15293419	3	15293419	2.28E-06	5.64
Chr.6:23903813	6	23903813	2.30E-06	5.64
Chr.19:8255225	19	8255225	2.31E-06	5.64
Chr.19:8243138	19	8243138	2.32E-06	5.63
Chr.19:8512902	19	8512902	2.33E-06	5.63
Chr.19:8231383	19	8231383	2.35E-06	5.63
Chr.19:8257083	19	8257083	2.35E-06	5.63
Chr.19:8224421	19	8224421	2.44E-06	5.61
Chr.19:8241538	19	8241538	2.45E-06	5.61
Chr.15:39978332	15	39978332	2.48E-06	5.61
Chr.3:13484208	3	13484208	2.50E-06	5.60
Chr.19:8431596	19	8431596	2.51E-06	5.60
Chr.19:8261571	19	8261571	2.54E-06	5.60
Chr.19:8318739	19	8318739	2.56E-06	5.59
Chr.6:27014431	6	27014431	2.64E-06	5.58
Chr.19:8257071	19	8257071	2.65E-06	5.58
Chr.19:8306294	19	8306294	2.66E-06	5.58

Chr.8:25698364	8	25698364	2.79E-06	5.55
Chr.14:39307738	14	39307738	3.09E-06	5.51

Supplementary Table S8. Candidate gene information.

Candidate Gene	CHR	Positive and Negative Chains	Arabidopsis Homologous Gene	Functional Annotation
<i>Glyma.14G120600</i>	14	+	AT2G38090.1	Duplicated homeodomain-like superfamily protein
<i>Glyma.14G120700</i>	14	-	AT1G21480.1	Exostosin family protein
<i>Glyma.15G223600</i>	15	+	AT2G07050.1	cycloartenol synthase 1
<i>Glyma.15G223700</i>	15	+	AT1G04400.1	cryptochrome 2
<i>Glyma.15G223800</i>	15	-	AT3G10710.1	root hair specific 12
<i>Glyma.18G155300</i>	15	-	ATCG01060.1	iron-sulfur cluster binding;electron carriers;4 iron, 4 sulfur cluster binding
<i>Glyma.18G155400</i>	18	-	ATCG01070.1	NADH-ubiquinone/plastoquinone oxidoreductase chain 4L
<i>Glyma.18G155500</i>	18	-	ATCG01090.1	NADPH dehydrogenases
<i>Glyma.18G155600</i>	18	-	ATCG01100.1	NADH dehydrogenase family

00				protein
<i>Glyma.18G1557</i> 00	18	-	ATCG01110.1	NAD(P)H dehydrogenase subunit H
<i>Glyma.18G1558</i> 00	18	-	ATCG01130.1	Ycf1 protein
<i>Glyma.18G1559</i> 00	18	-	AT3G53110.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
<i>Glyma.19G0505</i> 00	19	+	AT3G02580.1	sterol 1
<i>Glyma.19G0506</i> 00	19	-	AT5G38220.1	alpha/beta-Hydrolases superfamily protein
<i>Glyma.19G0508</i> 00	19	+	AT5G33370.1	GDSL-like Lipase/Acylhydrolase superfamily protein
<i>Glyma.19G0509</i> 00	19	-	AT5G33370.1	GDSL-like Lipase/Acylhydrolase superfamily protein
<i>Glyma.19G0510</i> 00	19	-	AT5G33370.1	GDSL-like Lipase/Acylhydrolase superfamily protein
<i>Glyma.19G0511</i> 00	19	-	AT5G33370.1	GDSL-like Lipase/Acylhydrolase superfamily protein
<i>Glyma.19G0512</i> 00	19	-	AT3G27440.1	uridine kinase-like 5
<i>Glyma.19G0513</i> 00	19	-	AT3G51700.1	PIF1 helicase
<i>Glyma.19G0514</i> 00	19	+	AT3G09640.1	ascorbate peroxidase 2

<i>Glyma.19G051500</i>	19	+	AT3G01650.1	RING domain ligase1
<i>Glyma.19G051700</i>	19	-	AT5G55690.1	MADS-box transcription factor family protein
<i>Glyma.19G051800</i>	19	+	AT3G16857.2	response regulator 1
<i>Glyma.19G051900</i>	19	+	ATCG00830.1	ribosomal protein L2
<i>Glyma.19G052000</i>	19	+	AT4G16110.1	response regulator 2
<i>Glyma.19G052100</i>	19	+	AT4G35850.1	Pentatricopeptide repeat (PPR) superfamily protein
<i>Glyma.19G052200</i>	19	+	AT3G56510.1	RNA-binding (RRM/RBD/RNP motifs) family protein
<i>Glyma.19G052300</i>	19	-	AT4G35860.1	GTP-binding 2
<i>Glyma.19G052400</i>	19	+	AT1G07930.1	GTP binding Elongation factor Tu family protein
<i>Glyma.03G189300</i>	3	+	AT2G36620.1	ribosomal protein L24
<i>Glyma.03G189400</i>	3	-	AT5G03790.1	homeobox 51
<i>Glyma.03G189500</i>	3	-	AT3G53000.1	phloem protein 2-A15
<i>Glyma.03G189600</i>	3	+	AT1G21200.1	sequence-specific DNA binding transcription factors

<i>Glyma.03G189700</i>	3	-	AT3G52990.1	Pyruvate kinase family protein
<i>Glyma.03G189800</i>	3	-	AT2G36570.1	Leucine-rich repeat protein kinase family protein
<i>Glyma.03G189900</i>	3	+	AT3G52970.1	cytochrome P450, family 76, subfamily G, polypeptide 1
<i>Glyma.03G190000</i>	3	-	AT5G04550.1	Protein of unknown function (DUF668)
<i>Glyma.03G190200</i>	3	+	AT5G03760.1	Nucleotide-diphospho-sugar transferases superfamily protein
<i>Glyma.03G190300</i>	3	+	AT5G12100.1	pentatricopeptide (PPR) repeat-containing protein
<i>Glyma.03G190400</i>	3	-	AT3G52960.1	Thioredoxin superfamily protein
<i>Glyma.05G106800</i>	5	+	AT1G70210.1	CYCLIN D1;1
<i>Glyma.05G106900</i>	5	+	AT4G37690.1	Galactosyl transferase GMA12/MNN10 family protein
<i>Glyma.06G219400</i>	6	-	AT5G57950.1	26S proteasome regulatory subunit, putative
<i>Glyma.06G219500</i>	6	+	AT5G33406.1	hAT dimerisation domain-containing protein / transposase-related
<i>Glyma.06G221700</i>	6	-	AT2G41480.1	Peroxidase superfamily protein
<i>Glyma.18G0931</i>	18	+	AT5G15280.1	Pentatricopeptide repeat (PPR)

00				superfamily protein
<i>Glyma.18G0930</i> 00	18	+	AT1G50650.1	Stigma-specific Stig1 family protein
<i>Glyma.06G2232</i> 00	6	-	AT3G16840.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein
<i>Glyma.18G0932</i> 00	18	+	AT4G26900.1	HIS HF
<i>Glyma.18G0933</i> 00	18	+	AT3G07040.1	NB-ARC domain-containing disease resistance protein
<i>Glyma.18G0934</i> 00	18	+	AT3G07040.1	NB-ARC domain-containing disease resistance protein
<i>Glyma.03G0668</i> 00	3	-	AT2G37770.2	NAD(P)-linked oxidoreductase superfamily protein
<i>Glyma.03G1893</i> 00	3	+	AT2G36620.1	ribosomal protein L24
<i>Glyma.03G1894</i> 00	3	-	AT5G03790.1	homeobox 51
<i>Glyma.03G1895</i> 00	3	-	AT3G53000.1	phloem protein 2-A15
<i>Glyma.03G1896</i> 00	3	+	AT1G21200.1	sequence-specific DNA binding transcription factors
<i>Glyma.03G1897</i> 00	3	-	AT3G52990.1	Pyruvate kinase family protein
<i>Glyma.03G1898</i> 00	3	-	AT2G36570.1	Leucine-rich repeat protein kinase family protein

<i>Glyma.03G1899</i> 00	3	+	AT3G52970.1	cytochrome P450, family 76, subfamily G, polypeptide 1
<i>Glyma.03G1900</i> 00	3	-	AT5G04550.1	Protein of unknown function (DUF668)
<i>Glyma.03G1902</i> 00	3	+	AT5G03760.1	Nucleotide-diphospho-sugar transferases superfamily protein
<i>Glyma.03G1903</i> 00	3	+	AT5G12100.1	pentatricopeptide (PPR) repeat-containing protein
<i>Glyma.03G1904</i> 00	3	-	AT3G52960.1	Thioredoxin superfamily protein
<i>Glyma.04G2212</i> 00	4	+	AT1G06890.1	nodulin MtN21 /EamA-like transporter family protein
<i>Glyma.04G2213</i> 00	4	+	AT3G10920.1	manganese superoxide dismutase 1
<i>Glyma.04G2214</i> 00	4	+	AT2G40510.1	Ribosomal protein S26e family protein
<i>Glyma.04G2216</i> 00	4	+	AT2G40540.1	potassium transporter 2
<i>Glyma.04G2218</i> 00	4	-	AT5G58900.1	Homeodomain-like transcriptional regulator
<i>Glyma.04G2219</i> 00	4	-	AT2G17510.1	ribonuclease II family protein
<i>Glyma.04G2220</i> 00	4	+	AT2G40550.1	E2F target gene 1
<i>Glyma.04G2221</i> 00	4	-	AT2G40610.1	expansin A8

<i>Glyma.04G222200</i>	4	-	AT2G40620.1	Basic-leucine zipper (bZIP) transcription factor family protein
<i>Glyma.08G261400</i>	8	+	AT5G03450.1	Transducin/WD40 repeat-like superfamily protein
<i>Glyma.08G261500</i>	8	+	AT1G68550.1	Integrase-type DNA-binding superfamily protein
<i>Glyma.14G162400</i>	14	+	AT5G53050.2	alpha/beta-Hydrolases superfamily protein
<i>Glyma.14G162500</i>	14	+	AT1G62850.2	Class I peptide chain release factor
<i>Glyma.15G200400</i>	15	+	AT5G60570.1	Galactose oxidase/kelch repeat superfamily protein
<i>Glyma.15G200500</i>	15	+	AT3G47700.1	RINT-1 / TIP-1 family
<i>Glyma.15G200600</i>	15	-	AT1G19250.1	flavin-dependent monooxygenase 1
<i>Glyma.15G219900</i>	15	-	AT4G30160.1	villin 4
<i>Glyma.15G220200</i>	15	+	AT1G05230.1	homeodomain GLABROUS 2
<i>Glyma.15G220700</i>	15	+	AT1G51990.2	O-methyltransferase family protein
<i>Glyma.15G220800</i>	15	+	AT5G17770.1	NADH:cytochrome B5 reductase 1
<i>Glyma.15G220900</i>	15	+	AT5G27600.1	long-chain acyl-CoA synthetase 7

<i>Glyma.15G221000</i>	15	-	AT5G04920.1	EAP30/Vps36 family protein
<i>Glyma.15G221100</i>	15	-	AT5G62890.1	Xanthine/uracil permease family protein
<i>Glyma.15G221200</i>	15	-	AT3G45310.1	Cysteine proteinases superfamily protein
<i>Glyma.15G221300</i>	15	+	AT4G34131.1	UDP-glucosyl transferase 73B3
<i>Glyma.15G222500</i>	15	+	AT5G61750.1	RmlC-like cupins superfamily protein
<i>Glyma.15G222700</i>	15	-	AT3G52590.1	ubiquitin extension protein 1
<i>Glyma.15G223600</i>	15	+	AT2G07050.1	cycloartenol synthase 1
<i>Glyma.18G147300</i>	18	+	AT2G22560.1	Kinase interacting (KIP1-like) family protein

Supplementary Table S9. Statistics Table of Sample Sequencing Data.

Sample ID	Clean_Total_Bases	Clean_Q20_Rate(%)	Clean_Q30_Rate(%)	Clean_GC_Content(%)
L10-T ₁	9,988,274,324	97.68	94.38	41.98
L10-T ₂	13,076,458,401	97.77	94.57	41.76
L10-T ₃	13,716,935,012	97.91	94.87	41.75
L10-W ₁	13,203,902,091	97.95	94.97	42.49
L10-W ₂	8,099,583,312	98.11	95.28	42.64
L10-W ₃	13,880,086,424	98.14	95.32	41.82
HN37-T ₁	14,126,216,065	97.83	94.67	42.17

HN37-T ₂	13,029,105,033	97.88	94.77	43.19
HN37-T ₃	15,391,586,517	97.84	94.72	42.32
HN37-W ₁	16,777,498,963	97.74	94.48	44.15
HN37-W ₂	16,730,021,211	97.87	94.73	42.13
HN37-W ₃	11,974,571,901	98.03	95.05	42.40

L10-T₁-T₃: Soybean variety DN L10 treated with SCN race 3; L10-W₁-W₃: Untreated soybean variety DN L10; HN37-T₁-T₃: Soybean variety HN 37 treated with SCN3 race 3; HN37-W₁-W₃: Untreated soybean variety HN 37.

Supplementary Table S10. Statistics of sequencing data aligned with reference genome sequence.

Sample ID	Input Reads	Mapped Reads	unique	Mapped Rate(%)
L10-T ₁	94391250	85241022	82304195	90.31 %
L10-T ₂	87044958	77867660	74674158	89.46 %
L10-T ₃	102807512	92802027	88886363	90.27 %
L10-W ₁	112088924	102557942	87443571	91.50 %
L10-W ₂	111864356	102713687	95739112	91.82 %
L10-W ₃	80049000	73906646	69167932	92.33 %
HN37-T ₁	66798468	55095406	51361495	82.48 %
HN37-T ₂	66798468	55095406	67300880	83.02 %
HN37-T ₃	91698542	76533564	71452819	83.46 %
HN37-W ₁	88454734	74809791	72043626	84.57 %
HN37-W ₂	54166110	45712281	43868062	84.39 %
HN37-W ₃	92758260	79558047	76790886	85.77 %

L10-T₁-T₃: Soybean variety DN L10 treated with SCN race 3; L10-W₁-W₃: Untreated soybean variety DN L10; HN37-T₁-T₃: Soybean variety HN 37 treated with SCN3 race 3; HN37-W₁-W₃: Untreated soybean variety HN 37.

Supplementary Table S11. Design of PCR-related procedures, restriction enzyme digestion and ligation procedures.

Procedures	Temperature/time
qRT-PCR Systems (step 2-4 35 cycles)	
pre-denaturation step 1	95°C for 30 s
Denaturation step 2	95°C for 3 s
Annealing step 3	60°C for 30 s
Extension step 4	72°C for 30 s
Cloning of the <i>GmRF2-like</i> Systems (step 2-4 38 cycles)	
pre-denaturation step 1	98 °C for 3 min
denaturation step 2	98 °C for 10 s
annealing step 3	58 °C for 5 s
extension step 4	68 °C for 5 s
final extension step 5	68 °C for 10 min
holding step 6	12 °C ∞
pCAMBIA3300 /pCAMBIA1302 vector was linearized Systems	
incubation	37°C for 5 h
denaturation	65 °C for 25 min
storage	12 °C ∞

Supplementary Table S12. Composition of restriction enzyme digestion, linearization and ligation-cloning systems.

Drug Name	Content
qRT-PCR Systems(20 µL)	
<i>GmRF2-like</i> -F primers	1 µL
<i>GmRF2-like</i> -R primers	1 µL
SYBR Green (TaKaRa, Japan)	10 µL
cDNA template	1 µL

nuclease-free water	7 μ L
Cloning of the <i>GmRF2-like</i> (20 μ L)	
Dongnong L-10 cDNA	2 μ L(200ng/ μ L)
KOD One™ PCR Master Mix	10 μ L
-Blue(TOYOBO, Japan)	
<i>OXGmRF2</i> -like-F primers	1 μ L
<i>OXGmRF2</i> -like-R primers	1 μ L
ddH ₂ O	6 μ L
pCAMBIA3300 vector was linearized (20 μ L)	
<i>Hind</i> III	2 μ L
<i>Hind</i> III Buffer	4 μ L
pCAMBIA3300 plasmid	10 μ L (150 ng/ μ L)
ddH ₂ O	4 μ L
pCAMBIA1302 vector was linearized (20 μ L)	
<i>Nco</i> I	2 μ L
<i>Nco</i> I Buffer	4 μ L
pCAMBIA1302 plasmid	10 μ L (150 ng/ μ L)
ddH ₂ O	4 μ L
Homologous recombination ligation with linearized pCAMBIA3300/pCAMBIA1302(20 μ L)	
homologous recombinase	2 μ L
homologous recombinase Buffer	4 μ L
Linearized pCAMBIA3300 vector	3.5 μ L
Target DNA fragment	1.5 μ L
ddH ₂ O	9 μ L