

Table S1 Sequence information of 210 TNL-like proteins.

Number	Gene ID	Length (aa)	Primary accession	Type
1	GLYMA_01G032400	1453 aa	K7K1I4	TNLX
2	GLYMA_01G032900	956 aa	K7K1J3	TNL
3	GLYMA_01G033200	1417 aa	A0A0R0LCQ5	TNL
4	GLYMA_01G033300	1201 aa	A0A0R0L5W8	TNL
5	GLYMA_01G039000	1379 aa	I1J5H4	TNL
6	GLYMA_01G046900	1036 aa	A0A0R0L6J4	TNL
7	GLYMA_01G112200	1227 aa	K7K360	TNLX
8	GLYMA_01G112300	1258 aa	K7K361	TNL
9	GLYMA_01G119800	175 aa	K7K3C5	T
10	GLYMA_01G125300	1063 aa	K7K3H1	TNL
11	GLYMA_01G125400	1156 aa	K7K3H2	TNL
12	GLYMA_01G220900	999 aa	K7K584	T
13	GLYMA_02G023600	169 aa	A0A0R0KQA9	T
14	GLYMA_02G023700	263 aa	K7K612	T
15	GLYMA_02G023800	257 aa	C6ZS34	T
16	GLYMA_02G023900	263 aa	C6ZS33	T
17	GLYMA_02G024000	257 aa	C6THX9	TX
18	GLYMA_02G033000	787 aa	A0A0R0KY80	TNL
19	GLYMA_02G041800	784 aa	K7K6E2	TNX
20	GLYMA_02G077000	426 aa	A0A0R0LOH1	TNX
21	GLYMA_02G193400	427 aa	K7K9I6	T
22	GLYMA_02G222500	745 aa	A0A0R0KZP3	TNLX
23	GLYMA_02G268900	1177 aa	K7KB13	TNL
24	GLYMA_02G284000	101 aa	K7KBB1	T
25	GLYMA_02G284100	1548 aa	K7KBB2	TNL
26	GLYMA_02G284200	1683 aa	A0A0R0L2V4	TNL
27	GLYMA_02G290300	380 aa	I1JJ81	TTX
28	GLYMA_02G290400	375 aa	C6TIX3	TTX
29	GLYMA_03G047700	829 aa	A0A0R0KP92	TNLX
30	GLYMA_03G047900	1049 aa	A0A0R0KES8	TNL
31	GLYMA_03G048500	1012 aa	A0A0R0KET5	TNL
32	GLYMA_03G048700	531aa	A0A0R0KEW1	TN
33	GLYMA_03G048800	185 aa	K7KCX0	T
34	GLYMA_03G052800	1444 aa	K7KCZ9	TNLX
35	GLYMA_03G053300	191 aa	K7KD03	T
36	GLYMA_03G053500	758 aa	A0A0R0KF26	TN
37	GLYMA_03G054100	887 aa	A0A0R0KLY1	TNL
38	GLYMA_03G054600	316 aa	A0A0R0KFL6	TX
39	GLYMA_03G075300	1128 aa	K7KDI2	TNL
40	GLYMA_03G077400	1127 aa	K7KDG9	TNLX
41	GLYMA_03G087500	1084 aa	I1JM77	TNLX
42	GLYMA_03G087600	772 aa	A0A0R0KGG0	TNL

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Number	Gene ID	Length (aa)	Primary accession	Type
43	GLYMA_03G088000	905 aa	K7KDW3	TNL
44	GLYMA_03G088100	1081 aa	K7KDW5	TNL
45	GLYMA_04G219600	464 aa	A0A0R0KB65	TNL
46	GLYMA_05G165800	1355 aa	K7KQM9	TNLX
47	GLYMA_06G146200	222 aa	K7KV37	TX
48	GLYMA_06G205100	397 aa	A0A0R0JJM6	TN
49	GLYMA_06G216900	112 aa	A0A0R0JKE6	T
50	GLYMA_06G248700	204 aa	I1KDX9	T
51	GLYMA_06G256000	1158 aa	A0A0R0JTT7	TNL
52	GLYMA_06G256100	180 aa	K7KXC7	T
53	GLYMA_06G259100	1091 aa	I1KE91	TNL
54	GLYMA_06G259400	1099 aa	I1KE93	TNL
55	GLYMA_06G259800	1202 aa	A0A0R0JLQ6	TNL
56	GLYMA_06G260100	1098 aa	I1KE99	TNL
57	GLYMA_06G260500	572 aa	A0A0R0JLQ8	TL
58	GLYMA_06G261400	1523 aa	A0A0R0JT19	XTNL
59	GLYMA_06G261500	1110 aa	I1KEB4	TNLX
60	GLYMA_06G263500	1143 aa	K7KXJ1	TNL
61	GLYMA_06G263700	380 aa	K7KXJ4	TT
62	GLYMA_06G263900	1322 aa	A0A0R0JM06	TNL
63	GLYMA_06G264100	336 aa	A0A0R0JXY0	TT
64	GLYMA_06G264300	522 aa	A0A0R0JLW9	TNX
65	GLYMA_06G265000	1310 aa	A0A0R0JS96	TNL
66	GLYMA_06G265200	266 aa	K7KXK7	TT
67	GLYMA_06G265400	1296 aa	A0A0R0JM20	TNLX
68	GLYMA_06G267300	636 aa	Q8H6S7	TNX
69	GLYMA_06G267400	1238 aa	K7KXM9	TNTT
70	GLYMA_06G268500	412 aa	A0A0R0JT99	TTX
71	GLYMA_06G268600	641 aa	I1KEG1	TNX
72	GLYMA_06G268700	1387 aa	A0A0R0JM07	TTTNL
73	GLYMA_06G285500	1084 aa	I1KEV5	TNL
74	GLYMA_06G310000	1464 aa	K7KYE4	TNLX
75	GLYMA_07G007900	110 aa	A0A0R0J4I4	T
76	GLYMA_07G037000	1090 aa	K7KZI3	TNLX
77	GLYMA_07G067900	905 aa	A0A0R0J6E0	TNL
78	GLYMA_07G123000	1171 aa	K7L0Z9	TNL
79	GLYMA_07G193000	185 aa	I1KLG4	T
80	GLYMA_08G159200	125 aa	A0A0R0IMV1	T
81	GLYMA_08G192900	1137 aa	K7L7M1	TNL
82	GLYMA_08G293600	1430 aa	K7L9P4	TNL
83	GLYMA_08G295000	265 aa	K7L9Q3	T
84	GLYMA_08G295100	150 aa	A0A0R0J0J4	T

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Number	Gene ID	Length (aa)	Primary accession	Type
85	GLYMA_08G295400	128 aa	A0A0R0J042	TX
86	GLYMA_08G301200	1231 aa	K7L9U4	TNLX
87	GLYMA_08G303600	362 aa	K7L9W1	TN
88	GLYMA_08G303700	882 aa	K7L9W3	TNL
89	GLYMA_09G056400	1072 aa	I1L1A5	TNLD
90	GLYMA_09G056500	67 aa	K7LBZ9	T
91	GLYMA_09G057000	1036 aa	K7LC01	TNL
92	GLYMA_09G075500	1055 aa	A0A0R0IEZ9	TNL
93	GLYMA_09G134400	441 aa	A0A0R0IDT0	TLT
94	GLYMA_09G161400	1390 aa	K7LE88	TNXLD
95	GLYMA_09G164800	459 aa	A0A0R0IFK2	TND
96	GLYMA_09G202800	1008 aa	A0A0R0IAY8	TNL
97	GLYMA_10G184300	1220 aa	A0A0R0HV98	TNL
98	GLYMA_10G184400	1030 aa	A0A0R0HVF4	TNX
99	GLYMA_11G022700	1008 aa	K7LMN0	T
100	GLYMA_11G153000	1085 aa	K7LQJ9	TNL
101	GLYMA_11G160500	636 aa	K7KPR3	TTNL
102	GLYMA_12G027100	1163 aa	K7LSQ4	TNL
103	GLYMA_12G132000	1076 aa	K7LU16	TNL
104	GLYMA_12G132200	1087 aa	K7LUI7	TNL
105	GLYMA_12G132400	411 aa	A0A0R0H572	TN
106	GLYMA_12G133000	620 aa	K7LUJ2	TL
107	GLYMA_12G135600	1141 aa	I1LSM9	TNL
108	GLYMA_12G137900	902 aa	A0A0R0HDM9	TNL
109	GLYMA_12G138400	685 aa	A0A0R0HEA3	TNL
110	GLYMA_12G138500	234 aa	A0A0R0H5P2	TND
111	GLYMA_12G163000	522 aa	A0A0R0HG01	TNL
112	GLYMA_12G212500	1190 aa	K7LW75	TNL
113	GLYMA_12G221600	200 aa	I1LUY0	T
114	GLYMA_12G239200	919 aa	K7LWN3	TNL
115	GLYMA_12G239700	1481 aa	K7LWN5	TNL
116	GLYMA_12G239800	1368 aa	A0A0R0HAA3	TNL
117	GLYMA_12G240100	1014 aa	K7LWN7	TNL
118	GLYMA_13G028100	1036 aa	K7LYT2	TNL
119	GLYMA_13G076200	979 aa	I1LWA0	TNL
120	GLYMA_13G078200	576 aa	A0A0R0GJV2	TNL
121	GLYMA_13G194700	1095 aa	I1M0P9	TNL
122	GLYMA_13G194800	490 aa	I1M0Q0	TND
123	GLYMA_13G194900	530 aa	I1M0S0	TNX
124	GLYMA_13G195100	1095 aa	A0A0R0GQV9	TNL
125	GLYMA_13G242900	106 aa	K7M1M8	T
126	GLYMA_13G243000	193 aa	I1M289	T

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Number	Gene ID	Length (aa)	Primary accession	Type
127	GLYMA_13G279700	200 aa	A0A0R0GW30	T
128	GLYMA_14G024400	337 aa	C6ZS32	TT
129	GLYMA_14G024500	370 aa	A0A0R4J566	TT
130	GLYMA_14G048600	1127 aa	K7M4Z6	TNL
131	GLYMA_14G151100	1167 aa	K7M6W8	TNL
132	GLYMA_14G152600	128 aa	A0A0R0GKC9	T
133	GLYMA_15G024800	1158 aa	I1MD01	TNL
134	GLYMA_15G070400	182 aa	I1MEE1	T
135	GLYMA_15G070500	181 aa	K7MA27	T
136	GLYMA_15G152200	1161 aa	A0A0R0G1P5	TNLX
137	GLYMA_15G152300	87 aa	A0A0R0G9S6	T
138	GLYMA_15G152400	1149 aa	A0A0R0G9U0	TNL
139	GLYMA_15G160900	1106 aa	K7MBP2	TNL
140	GLYMA_15G162700	929 aa	A0A0R0G1P9	TNL
141	GLYMA_15G232400	498 aa	K7MDC7	TND
142	GLYMA_15G232600	494 aa	A0A0R0G4X0	TN
143	GLYMA_15G232700	522 aa	K7MDD3	TN
144	GLYMA_16G006400	1054 aa	K7MEG0	TNLX
145	GLYMA_16G033900	1162 aa	A0A0R0FKV4	TNL
146	GLYMA_16G085400	981 aa	A0A0R0FN48	TNL
147	GLYMA_16G085700	1059 aa	I1MM77	TNLX
148	GLYMA_16G085900	1113 aa	I1MM78	TNL
149	GLYMA_16G086500	987 aa	K7MG05	TNL
150	GLYMA_16G086700	1036 aa	A0A0R0FN84	TNL
151	GLYMA_16G087100	1041 aa	K7MG09	TNLX
152	GLYMA_16G118600	797 aa	I1MMX8	TN
153	GLYMA_16G127900	1422 aa	A0A0R0G1J4	TNLX
154	GLYMA_16G128000	997 aa	A0A0R0FQ34	TNL
155	GLYMA_16G135200	1058 aa	K7MH68	TNL
156	GLYMA_16G135500	1047 aa	I1MNC5	TNL
157	GLYMA_16G135900	376 aa	I1MNC7	TNX
158	GLYMA_16G136000	1055 aa	A0A0R0FQC6	TNL
159	GLYMA_16G136200	956 aa	A0A0R0FQD0	TNL
160	GLYMA_16G136600	1403 aa	K7MH77	TNL
161	GLYMA_16G136900	907 aa	A0A0R0FQD6	TNL
162	GLYMA_16G137200	423 aa	I1MND4	TN
163	GLYMA_16G137300	1029 aa	I1MND5	TNL
164	GLYMA_16G137600	1079 aa	A0A0R0FZ27	TNL
165	GLYMA_16G147000	709 aa	A0A0R0G2F8	TNL
166	GLYMA_16G147400	732 aa	A0A0R0FZL1	TNL
167	GLYMA_16G159100	1149 aa	K7MHM2	TNL
168	GLYMA_16G159200	272 aa	A0A0R0G0Q0	TN

(continued table)

Number	Gene ID	Length (aa)	Primary accession	Type
169	GLYMA_16G159400	176 aa	K7MHM5	T
170	GLYMA_16G159600	1079 aa	A0A0R0G1Y1	TNL
171	GLYMA_16G159700	1040 aa	K7MHM7	TNL
172	GLYMA_16G198900	1087 aa	A0A0R0FT41	TNL
173	GLYMA_16G209000	164 aa	A0A0R0G203	T
174	GLYMA_16G210600	1420 aa	I1MQE7	TNLX
175	GLYMA_16G210800	1432 aa	K7MIT8	TNLX
176	GLYMA_16G211400	1288 aa	A0A0R0G194	TNL
177	GLYMA_16G212300	1051 aa	D6PT14	TNL
178	GLYMA_16G213700	1088 aa	A0A0R0FTG2	TNL
179	GLYMA_16G213800	1098 aa	A0A0R0FTF9	TNL
180	GLYMA_16G213900	1097 aa	A0A0R0FTC3	TNL
181	GLYMA_16G214000	966 aa	A0A0R0FT79	TNL
182	GLYMA_16G214100	1103 aa	I1MQI3	TNL
183	GLYMA_16G214200	641 aa	Q84ZU9	TNX
184	GLYMA_16G214300	670 aa	A0A0R0FTY7	TNX
185	GLYMA_16G214500	264 aa	Q84ZV1	TX
186	GLYMA_16G214600	1044 aa	A0A0R0FTH7	TNL
187	GLYMA_16G214700	77 aa	Q84ZV4	T
188	GLYMA_16G214800	305 aa	K7MIY3	TX
189	GLYMA_16G214900	923 aa	A0A0R0FTD8	TNL
190	GLYMA_16G215000	1105 aa	A0A0R0G4T7	TNL
191	GLYMA_16G215100	353 aa	K7MIY7	TN
192	GLYMA_16G215200	68 aa	K7MIY8	T
193	GLYMA_16G215400	393 aa	K7MIZ0	TN
194	GLYMA_17G197100	211 aa	K7MMQ0	T
195	GLYMA_18G127800	136 aa	A0A0R0F079	T
196	GLYMA_18G127900	299 aa	C6ZS22	T
197	GLYMA_18G128000	171 aa	K7MRQ4	T
198	GLYMA_19G022700	1073 aa	I1N650	TNL
199	GLYMA_19G054700	1080 aa	I1N6X6	TNL
200	GLYMA_19G054800	723 aa	A0A0R0EJF1	TNL
201	GLYMA_19G054900	1124 aa	K7MWR8	TNL
202	GLYMA_19G055000	1119 aa	K7MWR9	TNL
203	GLYMA_20G020200	1344 aa	K7N0U7	TNL
204	GLYMA_20G020500	214 aa	A0A0R0E5K4	T
205	GLYMA_20G048800	1114 aa	A0A0R0E807	TNL
206	GLYMA_20G061300	1033 aa	K7N1C6	TNL
207	GLYMA_U005000	199 aa	K7KCX9	T
208	GLYMA_U008300	1070 aa	A0A0R0E307	TNL
209	GLYMA_U035400	825 aa	A0A0R0EE48	TNL
210	GLYMA_U035700	1043 aa	A0A0R0E2U1	TNL

Table S2 Soybean *Gm-TNL-ID* genes information.

Gene names	Gene ID	Gene Description	Integrated domain
<i>Gm-TNL-ID1</i>	GLYMA_13G194700	TMV resistance protein N like	DUF4571
<i>Gm-TNL-ID2</i>	GLYMA_06G265000	disease resistance protein RPV1 like	DUF4277
<i>Gm-TNL-ID3</i>	GLYMA_03G087500		DUF2207
<i>Gm-TNL-ID4</i>	GLYMA_12G240100	disease resistance protein RUN1 like	AAA22
<i>Gm-TNL-ID5</i>	GLYMA_15G152400		AAA22
<i>Gm-TNL-ID6</i>	GLYMA_06G265400	LRR domain-containing protein	DUF3760
<i>Gm-TNL-ID7</i>	GLYMA_16G087100	disease resistance protein RUN1 like	ATPase2
<i>Gm-TNL-ID8</i>	GLYMA_13G078200		FBD
<i>Gm-TNL-ID9</i>	GLYMA_06G310000	TMV resistance protein N like	AnfG_VnfG
<i>Gm-TNL-ID10</i>	GLYMA_09G056400	disease resistance protein RPV1 like	DUF3557
<i>Gm-TNL-ID11</i>	GLYMA_16G210800	candidate disease-resistance protein	zf-RVT, RVT3
<i>Gm-TNL-ID12</i>	GLYMA_16G127900		zf-RVT, RVT3
<i>Gm-TNL-ID13</i>	GLYMA_09G161400	TMV resistance protein N like	zf-RVT, RVT3
<i>Gm-TNL-ID14</i>	GLYMA_16G210600	TMV resistance protein N like	zf-RVT, RVT3
<i>Gm-TNL-ID15</i>	GLYMA_08G301200	TMV resistance protein N like	zf-RVT
<i>Gm-TNL-ID16</i>	GLYMA_06G285500	disease resistance protein RUN1 like	Zinc_ribbon 13
<i>Gm-TNL-ID17</i>	GLYMA_05G165800		WRKY
<i>Gm-TNL-ID18</i>	GLYMA_03G075300	disease resistance protein RPV1 like	RNA_helicase
<i>Gm-TNL-ID19</i>	GLYMA_03G077400	disease resistance protein RPV1 like	NfeD
<i>Gm-TNL-ID20</i>	GLYMA_07G123000	disease resistance protein RPV1 like	RICTOR_M
<i>Gm-TNL-ID21</i>	GLYMA_16G085700	disease resistance protein RUN1 like	Pox_RNA_Pol_19
<i>Gm-TNL-ID22</i>	GLYMA_03G047900		Phage_rep_org_N
<i>Gm-TNL-ID23</i>	GLYMA_16G006400	disease resistance protein RPV1 like	NTPase1
<i>Gm-TNL-ID24</i>	GLYMA_07G037000	disease resistance protein RPV1 lke	NTPase1
<i>Gm-TNL-ID25</i>	GLYMA_06G267300	KR3 disease resistance protein KR3	MotA_activ
<i>Gm-TNL-ID26</i>	GLYMA_16G213700		MotA_activ
<i>Gm-TNL-ID27</i>	GLYMA_19G022700	TMV resistance protein N like	MotA_activ
<i>Gm-TNL-ID28</i>	GLYMA_16G159600		MotA_activ
<i>Gm-TNL-ID29</i>	GLYMA_19G054900	KR1 resistance protein KR1	MotA_activ
<i>Gm-TNL-ID30</i>	GLYMA_19G054700	disease resistance protein RPV1 like	MotA_activ
<i>Gm-TNL-ID31</i>	GLYMA_16G147400		MotA_activ
<i>Gm-TNL-ID32</i>	GLYMA_16G137300	disease resistance protein RUN1 like	MotA_activ
<i>Gm-TNL-ID33</i>	GLYMA_16G136000		MotA_activ
<i>Gm-TNL-ID34</i>	GLYMA_16G136200		MotA_activ
<i>Gm-TNL-ID35</i>	GLYMA_16G135500	TMV resistance protein N ilke	MotA_activ
<i>Gm-TNL-ID36</i>	GLYMA_16G135200	Disease resistance protein RUN1 like	MotA_activ
<i>Gm-TNL-ID37</i>	GLYMA_03G052800	Disease resistance protein RUN1 like	Hirudin
<i>Gm-TNL-ID38</i>	GLYMA_01G032400	TMV resistance protein N like	HAUS_augmin3
<i>Gm-TNL-ID39</i>	GLYMA_14G151100	Disease resistance protein RPV1 like	NACHT
<i>Gm-TNL-ID40</i>	GLYMA_16G085400		NACHT
<i>Gm-TNL-ID41</i>	GLYMA_15G152200	disease resistance-like protein DSC1 like	FNIP

Table S3 Identification of proteins interacting with SRZ4.

Gene ID	Annotations
GLYMA_06G029400	<i>Glycine max</i> 26S proteasome regulatory subunit 10B homolog A, mRNA
GLYMA_11G021400	<i>Glycine max</i> 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase, chloroplastic-like
GLYMA_10G078400	<i>Glycine max</i> 2-cys peroxiredoxin, mRNA
GLYMA_20G082800	<i>Glycine max</i> 31 kDa ribonucleoprotein, chloroplastic-like, mRNA
GLYMA_11G078700	<i>Glycine max</i> 3-dehydroquinate synthase, transcript variant X1, mRNA
GLYMA_19G254600	<i>Glycine max</i> anthocyanidin reductase, mRNA
GLYMA_08G036400	<i>Glycine max</i> auxin-responsive protein IAA27-like , transcript variant X1, mRNA
GLYMA_04G082900	<i>Glycine max</i> casein kinase 1-like protein 4
GLYMA_05G128000	<i>Glycine max</i> chlorophyll a-b-binding protein (CAB3), mRNA
GLYMA_09G154700	<i>Glycine max</i> chlorophyll a-b binding protein CP26
GLYMA_06G194900	<i>Glycine max</i> chlorophyll a-b binding protein P4, chloroplastic, mRNA
GLYMA_05G059200	<i>Glycine max</i> Cwf15/Cwc15 cell cycle control family protein, mRNA
GLYMA_08G241600	<i>Glycine max</i> cyclic nucleotide-gated ion channel 2, transcript variant X2, mRNA
GLYMA_11G113500	<i>Glycine max</i> cysteine protease RD19A, mRNA
GLYMA_18G154900	<i>Glycine max</i> cytochrome b5, mRNA
GLYMA_11G213600	<i>Glycine max</i> cytochrome c oxidase assembly protein COX11, mitochondrial-like, mRNA
GLYMA_13G237000	<i>Glycine max</i> dormancy-associated protein 1-like, transcript variant 1, mRNA
GLYMA_11G110000	<i>Glycine max</i> epimerase family protein slr1223-like, mRNA; nuclear gene for chloroplast product
GLYMA_01G028800	<i>Glycine max</i> F-box/kelch-repeat protein At1g23390, mRNA
GLYMA_11G111400	<i>Glycine max</i> fructose-bisphosphate aldolase 1, chloroplastic, mRNA
GLYMA_17G100700	<i>Glycine max</i> geranylgeranyl diphosphate reductase, chloroplastic, mRNA
GLYMA_06G015900	<i>Glycine max</i> glyceraldehyde-3-phosphate dehydrogenase B subunit, transcript variant 2, mRNA
GLYMA_05G180600	<i>Glycine max</i> inositol-3-phosphate synthase , mRNA
GLYMA_07G185400	<i>Glycine max</i> malate dehydrogenase, glyoxysomal-like, mRNA
GLYMA_17G063000	<i>Glycine max</i> NADPH--cytochrome P450 reductase 2, mRNA
GLYMA_11G061300	<i>Glycine max</i> oxygen-evolving enhancer protein 1, chloroplastic-like
GLYMA_08G124900	<i>Glycine max</i> PDZ and TPR domain-containing protein, mRNA
GLYMA_01G214300	<i>Glycine max</i> PGR5-like protein 1A, chloroplastic, transcript variant X2, misc_RNA
GLYMA_10G222600	<i>Glycine max</i> phytosulfokine receptor 2, mRNA
GLYMA_04G020300	<i>Glycine max</i> plastocyanin, mRNA
GLYMA_11G014900	<i>Glycine max</i> probable acyl-activating enzyme 1, peroxisomal, mRNA
GLYMA_10G212200	<i>Glycine max</i> probable ubiquitin-conjugating enzyme E2 C, mRNA
GLYMA_01G077600	<i>Glycine max</i> protease Do-like 9, transcript variant X2, mRNA
GLYMA_19G260600	<i>Glycine max</i> protein curvature thylakoid 1B-like, mRNA
GLYMA_18G213500	<i>Glycine max</i> protein fatty acid export 3, chloroplastic, transcript variant X2, mRNA
GLYMA_09G043800	<i>Glycine max</i> protein pleiotropic regulatory locus 1, transcript variant X2, mRNA
GLYMA_09G227100	<i>Glycine max</i> protein reticulata-related 4, chloroplastic, mRNA
GLYMA_08G309300	<i>Glycine max</i> ribose-phosphate pyrophosphokinase 4
GLYMA_16G089000	<i>Glycine max</i> putative 1-deoxy-D-xylulose 5-phosphate reductoisomerase (DXR2)
GLYMA_03G202900	<i>Glycine max</i> putative chloroplast RNA-binding protein 33, mRNA; nuclear gene for chloroplast product
GLYMA_17G073300	<i>Glycine max</i> signal recognition particle receptor subunit alpha, mRNA

(continued table)

Accession number	Annotations
GLYMA_02G195400	<i>Glycine max</i> syntaxin-121, mRNA
GLYMA_20G001600	<i>Glycine max</i> transcription factor TCP7, mRNA
GLYMA_08G206000	<i>Glycine max</i> translation machinery associated TMA7 superfamily protein, mRNA
GLYMA_19G127700	<i>Glycine max</i> tubulin beta-4 chain, mRNA
GLYMA_16G037700	<i>Glycine max</i> U5 small nuclear ribonucleoprotein 40 kDa protein-like, mRNA
GLYMA_09G023700	<i>Glycine max</i> ubiquitin-40S ribosomal protein S27a
GLYMA_08G112000	<i>Glycine max</i> UBX domain-containing protein 1, transcript variant X2, mRNA

Table S4 Primers used in this study.

Primer name	Sequence (5'-3')	Purpose
Gm-TNL-ID1-F	ATGTCGAAGGCAGTTTCAGAATC	ORF sequence cloned in pCE2
Gm-TNL-ID1-R	TTATAAGATGGTGGGTTTATAAGGATC	
Gm-TNL-ID2-F	ATGGCTTCTAAGGCCATCATCC	
Gm-TNL-ID2-R	CTACTGCTGCTTCCACTGT	
Gm-TNL-ID3-F	ATGGAATTAGAGTCTTCTTC	
Gm-TNL-ID3-R	TTACAATTCTTCTCTGCGTGGAATAC	
Gm-TNL-ID5-F	ATGTTGTATTTTTTGTCTA	
Gm-TNL-ID5-R	TTAAACATGGAGCGAGTCATG	
Gm-TNL-ID7-F	ATGTCATCTTCTTCATTCTCAAC	
Gm-TNL-ID7-R	CTACTGCTCTTCATTTTACTTGATA	
Gm-TNL-ID8-F	ATGGAATGCAAGAAACAAGGAG	
Gm-TNL-ID8-R	TCAATCGTTGAACCTTACTTAACACTG	
Gm-TNL-ID9-F	ATGGCTGTGATGCTGTGTGGAG	
Gm-TNL-ID9-R	TTAATCAAACCCTTCATGCCTTAAG	
Gm-TNL-ID10-F	ATGTCCAACAAAGCTGCTCC	
Gm-TNL-ID10-R	TCAGTCACTGTCATGCAATTC	
Gm-TNL-ID11-F	ATGGCTTGGGGATCACG	
Gm-TNL-ID11-R	TTATATGTATTCATAACAAAAGGTTGG	
Gm-TNL-ID12-F	ATGGCTACGGGATCACCT	
Gm-TNL-ID12-R	TTACGTAAACATGTAACATGTATCTCTC	
Gm-TNL-ID14-F	ATGGCTTGGGGATCAAGTTC	
Gm-TNL-ID14-R	TTATCTGTATTCTGAAATATAAGGTTGGC	
Gm-TNL-ID15-F	ATGACACAGCAATCATGTTCC	
Gm-TNL-ID15-R	TTACCTTAAATCAATGGATTGACAG	
Gm-TNL-ID16-F	ATGGCTTCCAACAACAACAG	
Gm-TNL-ID16-R	CTAGTTCCATCTTCCAAGAAAGG	
Gm-TNL-ID17-F	ATGGCTTCCTCGGCCTT	
Gm-TNL-ID17-R	TTATAACTTGCAGGATTGACTTGC	
Gm-TNL-ID18-F	ATGCCAACAGAGATTGCAATG	
Gm-TNL-ID18-R	TCAAGTTTGACCTAACATTCTTTTAC	
Gm-TNL-ID19-F	ATGCCTCCGATCGTGAAAT	
Gm-TNL-ID19-R	TCATTCAATTTTCTTCTTTTCTGTTTTT	
Gm-TNL-ID21-F	ATGGAATTCGTGGCTTCTTC	
Gm-TNL-ID21-R	CTACTGCTCTTGAATCTTGCTCG	
Gm-TNL-ID23-F	ATGGCTTTCCAAGTTTCTCATA	
Gm-TNL-ID23-R	TCACCCATTCCACACGGA	
Gm-TNL-ID24-F	ATGCCATATTCTTATTCGTCCG	
Gm-TNL-ID24-R	TTATTCTACTAACCTTCTAAATAAATCCTAGA	
Gm-TNL-ID25-F	ATGAAGTTGGTTCTATATCCAACAG	
Gm-TNL-ID25-R	CTATTCCAAGTCGCGTATGGC	

(continued table)

Primer name	Sequence (5'-3')	Purpose
Gm-TNL-ID26-F	ATGGCTGCGACAACACG	
Gm-TNL-ID26-R	CTATGGTTTGTAGTCTGATGCAG	
Gm-TNL-ID28-F	ATGTCCTCCTCCTCCATTAGCT	
Gm-TNL-ID28-R	CTAAAAATAACCAAATGATGACTTATTGG	
Gm-TNL-ID29-F	ATGGCTAAGCAATCATCCTCAT	
Gm-TNL-ID29-R	TCATTGATTGTTGCGGCG	
Gm-TNL-ID30-F	ATGGCTATGCAATCATCCTCA	
Gm-TNL-ID30-R	TTATGATTCTGAACTATTGAAATCATCA	
Gm-TNL-ID35-F	ATGGCTGTGCGATCATTCTC	
Gm-TNL-ID35-R	TTATGAACTAATGAGATCATCATTTAATTTTT	
Gm-TNL-ID36-F	ATGGCTCTGCGATCATTCT	
Gm-TNL-ID36-R	CTACAAATTGTGTCACAACACTTC	
Gm-TNL-ID39-F	ATGCCCTCACTATTGCGAG	
Gm-TNL-ID39-R	TTACCAGAAGTCACACATTACAAT	
BD-ID1 ^X -F	CatatggccatggaggccgaattcTACCTCGAGAAGGAGGTTTTTC	ID ^X sequence cloned
BD-ID1 ^X -R	tagttatgcgccgctgcaggtcgacTTATAAGATGGTGGGTTATAAGGATC	in pGBK17
BD-ID2 ^X -F	catatggccatggaggccgaattcAATGACAGGAAATATTTTAGATATTGC	
BD-ID2 ^X -R	tagttatgcgccgctgcaggtcgacCTACTGCTGCTTCCACTGT	
BD-ID3 ^X -F	catatggccatggaggccgaattcAAGGATATATTCCTTGATGTGTG	
BD-ID3 ^X -R	tagttatgcgccgctgcaggtcgacTTACAATTCTTCTGCGTGGAAATAC	
BD-ID4 ^X -F	catatggccatggaggccgaattcGAAGATGAAAAGGGAATTTTCCTTG	
BD-ID4 ^X -R	tagttatgcgccgctgcaggtcgacTTATACAATTGATAATACAAGCAACC	
BD-ID5 ^X -F	catatggccatggaggccgaattcCAGATTTTTCTAGATTGGCATGTTT	
BD-ID5 ^X -R	tagttatgcgccgctgcaggtcgacTTAAACATGGAGCGAGTCATG	
BD-ID7 ^X -F	catatggccatggaggccgaattcGAAAAGGATATTTTCTGATATATGTTGTT	
BD-ID7 ^X -R	tagttatgcgccgctgcaggtcgacCTACTGCTCTTCATTTTACTTGATA	
BD-ID8 ^X -F	catatggccatggaggccgaattcTTTTCTGCAGATATAGGACAAGAAG	
BD-ID8 ^X -R	tagttatgcgccgctgcaggtcgacTCAATCGTGAACCTACTTAACACTG	
BD-ID9 ^X -F	catatggccatggaggccgaattcATTCCCAACAAAGAGGTCAGAA	
BD-ID9 ^X -R	tagttatgcgccgctgcaggtcgacTTAATCAAACCTTCATGCCTTAAG	
BD-ID10 ^X -F	catatggccatggaggccgaattcGATCGTAAAGAGCAACAAATTTTCT	
BD-ID10 ^X -R	tagttatgcgccgctgcaggtcgacTCAGTCACTGTCATGCAATTC	
BD-ID11 ^X -F	catatggccatggaggccgaattcGAAGAAGAGAAGAAAGTTTTCTTGAC	
BD-ID11 ^X -R	tagttatgcgccgctgcaggtcgacTTATATGATTCACTAACAAAAGGTTGG	
BD-ID12 ^X -F	catatggccatggaggccgaattcATGGCTACGGGATCACCT	
BD-ID12 ^X -R	tagttatgcgccgctgcaggtcgacTTACGTAAACATGTATCTCTC	
BD-ID13 ^X -F	catatggccatggaggccgaattcGAAGAGAAAAGTGTTTTCTTGACC	
BD-ID13 ^X -R	tagttatgcgccgctgcaggtcgacTCAAACATCTACAAAAGGTGCAC	
BD-ID14 ^X -F	catatggccatggaggccgaattcAAGGAAATTCTAGATGTACTTACAGTA	
BD-ID14 ^X -R	tagttatgcgccgctgcaggtcgacTTATCTGTATTCTGAAATATAAGGTTGGC	
BD-ID15 ^X -F	catatggccatggaggccgaattcAATGAGAAGGAAGTTTTCCTTGAC	
BD-ID15 ^X -R	tagttatgcgccgctgcaggtcgacTTACCTTAAATCAATGGATTGACAG	

(continued table)

Primer name	Sequence (5'-3')	Purpose
BD-ID16 ⁺ -F	catatggccatggagccgaattcAACAAAGATATTCTGGATGTGCTTC	
BD-ID16 ⁺ -R	tagttatgcggccgctgcaggtcgacCTAGTTCCATCTCCAAAAGAAAGG	
BD-ID17 ⁺ -F	catatggccatggagccgaattcGTCAATGCATTCTGTAATATTATCTGG	
BD-ID17 ⁺ -R	tagttatgcggccgctgcaggtcgacTTATAACTTGCAGGATTGACTTGC	
BD-ID18 ⁺ -F	catatggccatggagccgaattcGATACAGAGAGACATATTCCTTGA	
BD-ID18 ⁺ -R	tagttatgcggccgctgcaggtcgacTCAAGTTTGACCTAACATTCTTTCAC	
BD-ID19 ⁺ -F	catatggccatggagccgaattcGATACAGAGAGAAATATTCCTTGAT	
BD-ID19 ⁺ -R	tagttatgcggccgctgcaggtcgacTCAITCAATTTTCTTCTTTTCTGTTTT	
BD-ID21 ⁺ -F	catatggccatggagccgaattcCCCTTGAAAAGGATATATTCCTTG	
BD-ID21 ⁺ -R	tagttatgcggccgctgcaggtcgacCTACTGCTCTTGAATCTTGCTCG	
BD-ID22 ⁺ -F	catatggccatggagccgaattcGAGAAAAATATTTCTTAGATATTGCATGT	
BD-ID22 ⁺ -R	tagttatgcggccgctgcaggtcgacTTAATCGAAGAATTCATTGTGTAATG	
BD-ID23 ⁺ -F	catatggccatggagccgaattcGAAAAGAAGATACTTATGGATATTGCATG	
BD-ID23 ⁺ -R	tagttatgcggccgctgcaggtcgacTCACCCATTCCACACGGA	
BD-ID24 ⁺ -F	catatggccatggagccgaattcGAAAAGAAGATATTTTGGATATTGCATG	
BD-ID24 ⁺ -R	tagttatgcggccgctgcaggtcgacTTATICTACTAACCTTCTAAAATAAATCCTAGA	
BD-ID25 ⁺ -F	catatggccatggagccgaattcAAGGAAATCTTGAAGATACTTAAAGTAAGC	
BD-ID25 ⁺ -R	tagttatgcggccgctgcaggtcgacCTATTCCAAGTCGCGTATGGC	
BD-ID26 ⁺ -F	catatggccatggagccgaattcGATGAAATCCAAGAGATTCTAAAAGTAAG	
BD-ID26 ⁺ -R	tagttatgcggccgctgcaggtcgacCTATGTTTGTAGTCTGATGCAG	
BD-ID28 ⁺ -F	catatggccatggagccgaattcAAAAAGATTCAAGACGTACTCAAAGT	
BD-ID28 ⁺ -R	tagttatgcggccgctgcaggtcgacCTAAAAATAACCAATGATGACTTATTTGG	
BD-ID29 ⁺ -F	catatggccatggagccgaattcAAGAGATCCAAGAGATACTTAAAGTG	
BD-ID29 ⁺ -R	tagttatgcggccgctgcaggtcgacTCATTGATTGTTGCGGCC	
BD-ID30 ⁺ -F	catatggccatggagccgaattcAAGAGATCCAAGAGATACTTAAAGTG	
BD-ID30 ⁺ -R	tagttatgcggccgctgcaggtcgacTTATGATTCTGAATATTGAAATCATCAA	
BD-ID35 ⁺ -F	catatggccatggagccgaattcGATAAAAGTATCTATATGATACTTAAAGTAAGCT	
BD-ID35 ⁺ -R	tagttatgcggccgctgcaggtcgacTTATGAACATAAGATCATCATTTAATTTTT	
BD-ID36 ⁺ -F	catatggccatggagccgaattcAAAAAGATCTATGACATACTTAAAGTAAGC	
BD-ID36 ⁺ -R	tagttatgcggccgctgcaggtcgacCTACAAATTGTGTCACAACCTTC	
BD-ID37 ⁺ -F	catatggccatggagccgaattcGATACAGAGAAAGGAATATTCCTTGAT	
BD-ID37 ⁺ -R	tagttatgcggccgctgcaggtcgacTTAACCTTGATTTTCTTATTTTCTGAG	
BD-ID38 ⁺ -F	catatggccatggagccgaattcACTGAGCAGGAAATATTTCTAGACAT	
BD-ID38 ⁺ -R	tagttatgcggccgctgcaggtcgacCTAAATGTCAAATATGCATAAGCTGG	
BD-ID39 ⁺ -F	catatggccatggagccgaattcGATGATGAGAAAACATTTTCTTGAC	
BD-ID39 ⁺ -R	tagttatgcggccgctgcaggtcgacTTACCAGAAGTCACACATTACAAT	
qRT-PCR-SMV-F	CCGCTGAAACCCATTGTTGA	qRT-PCR for virus
qRT-PCR-SMV-R	GCGGGCCAGTTCTCTATCTC	titer detection
qRT-PCR-TMV-F	CACGACTGCCGAAACGTTAG	
qRT-PCR-TMV-R	TCAAGTTGCAGGACCAGAGG	
qRT-PCR-PPV-F	GAGAAGGCGAGGAGGAAGTT	
qRT-PCR-PPV-R	TGCAGGCTGTATGACTGGAG	

(continued table)

Primer name	Sequence (5'-3')	Purpose	
qRT-PCR-PCV-F	CAGTCTTACGAGCAGCGACA		
qRT-PCR-PCV-R	TGTCACGCACCAACCAAAAC		
qRT-PCR-BSMV-F	GAAAGTGTGCTGGCCTTTCG		
qRT-PCR-BSMV-R	CATCTGAGCGCTGACTCGTA		
qRT-PCR-TRV2-F	ACTACCAAGCGAACAACCTGG		
qRT-PCR-TRV2-R	GAGGCGGTGCAGATGAACTA		
pCambia1300-ID1-F	gagaacacgggggacgagctcATGTCGAAGGCAGTTTCAGAATC	ORF	sequence
pCambia1300-ID1-R	atttgttgatccgggtaccTTATAAGATGGTGGTTTATAAGGATC	cloned	in
pCambia1300-ID2-F	gagaacacgggggacgagctcATGGCTTCTAAGGCCATCATCC	pCambia1300	
pCambia1300-ID2-R	atttgttgatccgggtaccCTACTGCTGCTTCCACTGT		
pCambia1300-ID3-F	gagaacacgggggacgagctcATGGAATTAGAGTCTTCTTC		
pCambia1300-ID3-R	atttgttgatccgggtaccTTACAATTCTTCTGCGTGGAAATAC		
pCambia1300-ID5-F	gagaacacgggggacgagctcATGTTGTAATTTTTTGCTA		
pCambia1300-ID5-R	atttgttgatccgggtaccTTAAACATGGAGCGAGTCATG		
pCambia1300-ID7-F	gagaacacgggggacgagctcATGCATCTTCTTCATCTCAAC		
pCambia1300-ID7-R	atttgttgatccgggtaccCTACTGCTCTTCATTTTACTTGATA		
pCambia1300-ID8-F	gagaacacgggggacgagctcATGGAATGCAAGAAACAAGGAG		
pCambia1300-ID8-R	atttgttgatccgggtaccTCAATCGTTGAACCTACTTAACACTG		
pCambia1300-ID9-F	gagaacacgggggacgagctcATGGCTGTGATGCTGTGTGGAG		
pCambia1300-ID9-R	atttgttgatccgggtaccTTAATCAAACCTTCATGCCTTAAG		
pCambia1300-ID10-F	gagaacacgggggacgagctcATGTCCAACAAGCTGTCTC		
pCambia1300-ID10-R	atttgttgatccgggtaccTCAGTCACTGTCATGCAATTC		
pCambia1300-ID11-F	gagaacacgggggacgagctcATGGCTTGGGGATCACG		
pCambia1300-ID11-R	atttgttgatccgggtaccTTATATGTAATCACTAACAAGGTTGG		
pCambia1300-ID12-F	gagaacacgggggacgagctcATGGCTACGGGATCACCT		
pCambia1300-ID12-R	atttgttgatccgggtaccTTACGTAAACATGTAACATGTATCTCTC		
pCambia1300-ID14-F	gagaacacgggggacgagctcATGGCTTGGGGATCAAGTTC		
pCambia1300-ID14-R	atttgttgatccgggtaccTTATCTGTATTCTGAAATATAAGGTTGGC		
pCambia1300-ID15-F	gagaacacgggggacgagctcATGACACAGCAATCATGTTC		
pCambia1300-ID15-R	atttgttgatccgggtaccTTACCTTAAATCAATGGATTGACAG		
pCambia1300-ID16-F	gagaacacgggggacgagctcATGGCTTCCAACAACAACAG		
pCambia1300-ID16-R	atttgttgatccgggtaccTAGTTTCCATCTTCCAAGAAAGG		
pCambia1300-ID17-F	gagaacacgggggacgagctcATGGCTTCCTCGCCTT		
pCambia1300-ID17-R	atttgttgatccgggtaccTTATAACTTGACGATTGACTTGC		
pCambia1300-ID18-F	gagaacacgggggacgagctcATGCCAACAGAGATTGCAATG		
pCambia1300-ID18-R	atttgttgatccgggtaccTCAAGTTGACCTAACATCTTTACAC		
pCambia1300-ID19-F	gagaacacgggggacgagctcATGCCCTCCGATCGTGAAAT		
pCambia1300-ID19-R	atttgttgatccgggtaccTCATCAATTTTCTTCTTTCTGTTTT		
pCambia1300-ID21-F	gagaacacgggggacgagctcATGGAATTCGTGGCTTCTTC		
pCambia1300-ID21-R	atttgttgatccgggtaccCTACTGCTCTTGAATCTTGCTCG		
pCambia1300-ID23-F	gagaacacgggggacgagctcATGGCTTCCAAGTTTCTCATA		
pCambia1300-ID23-R	atttgttgatccgggtaccTCACCATTCACACGGA		

(continued table)

Primer name	Sequence (5'-3')	Purpose
pCambia1300-ID24-F	gagaacacgggggacgagctcATGCCATATTCTTATTCGTTCCG	
pCambia1300-ID24-R	atttggtggatccgggtaccTTATTCTACTAACCTTCTAAATAAATCCTAGA	
pCambia1300-ID25-F	gagaacacgggggacgagctcATGAAGTTTGGTTCTATATTCCAACAG	
pCambia1300-ID25-R	atttggtggatccgggtaccCTATTCCAAGTCGCGTATGGC	
pCambia1300-ID26-F	gagaacacgggggacgagctcATGGCTGCGACAACACG	
pCambia1300-ID26-R	atttggtggatccgggtaccCTATGGTTTGTAGTCTGATGCAG	
pCambia1300-ID28-F	gagaacacgggggacgagctcATGTCCTCTCTCCATTAGCT	
pCambia1300-ID28-R	atttggtggatccgggtaccCTAAAAATAACCAAATGATGACTTAATTGG	
pCambia1300-ID29-F	gagaacacgggggacgagctcATGGCTAAGCAATCATCCTCAT	
pCambia1300-ID29-R	atttggtggatccgggtaccTCATTGATTGTTGCGGCG	
pCambia1300-ID30-F	gagaacacgggggacgagctcATGGCTATGCAATCATCCTCA	
pCambia1300-ID30-R	atttggtggatccgggtaccTTATGATTCTGAACATTGAAATCATCAA	
pCambia1300-ID35-F	gagaacacgggggacgagctcATGGCTGTGCGATCATTCTC	
pCambia1300-ID35-R	atttggtggatccgggtaccTTATGAATAATGAGATCATCATTTAATTTTTT	
pCambia1300-ID36-F	gagaacacgggggacgagctcATGGCTCTGCGATCATCTCT	
pCambia1300-ID36-R	atttggtggatccgggtaccCTACAAATTGTGTCTCAACAACCTC	
pCambia1300-ID39-F	gagaacacgggggacgagctcATGCCCTCACTATTGCGAG	
pCambia1300-ID39-R	atttggtggatccgggtaccTTACCAGAAGTCACACATTACAAT	
pC-SRC7 ^{TN} -F	gagaacacgggggacgagctcATGGCTGCAACGAAACGTTCCCTTGC	SRC7 ^{TN} cloned in
pC-SRC7 ^{TN} -R	TGTTTCCTGCTTTGTAGCATCA	pCambia1300
pC-SRC7 ^{TN} -ID1 ^X -F	tgatgctacaaagcaggaacaTACCTCGAGAAGGAGGTTTTTC	ID ^X sequence cloned
pC-SRC7 ^{TN} -ID1 ^X -R	atttggtggatccgggtaccTTATAAGATGGTGGGTTTATAAGGATC	after SRC7 ^{TN} in
pC-SRC7 ^{TN} -ID2 ^X -F	tgatgctacaaagcaggaacaAATGACAGGAAATATTTTATGATATTGC	pCambia1300
pC-SRC7 ^{TN} -ID2 ^X -R	atttggtggatccgggtaccCTACTGCTGCTTCCACTGT	
pC-SRC7 ^{TN} -ID3 ^X -F	tgatgctacaaagcaggaacaAAGGATATATTCCTTGATGTGTGT	
pC-SRC7 ^{TN} -ID3 ^X -R	atttggtggatccgggtaccTTACAATTCTTCTGCTGGGAAATAC	
pC-SRC7 ^{TN} -ID4 ^X -F	tgatgctacaaagcaggaacaGAAGATGAAAAGGGAATTTTCCTTG	
pC-SRC7 ^{TN} -ID4 ^X -R	atttggtggatccgggtaccTTATACAACCTTGATAATACAAGCAACC	
pC-SRC7 ^{TN} -ID5 ^X -F	tgatgctacaaagcaggaacaCAGATTTTCTAGATTGGCATGTTT	
pC-SRC7 ^{TN} -ID5 ^X -R	atttggtggatccgggtaccTTAAACATGGAGCGAGTCATG	
pC-SRC7 ^{TN} -ID7 ^X -F	tgatgctacaaagcaggaacaGAAAAGGATATATTTCTTGATATGTGTT	
pC-SRC7 ^{TN} -ID7 ^X -R	atttggtggatccgggtaccCTACTGCTCTTCATTTTACTTGATA	
pC-SRC7 ^{TN} -ID8 ^X -F	tgatgctacaaagcaggaacaTTTTCTGCAGATATAGGGACAAGAAG	
pC-SRC7 ^{TN} -ID8 ^X -R	atttggtggatccgggtaccTCAATCGTTGAACCTTAAACACTG	
pC-SRC7 ^{TN} -ID9 ^X -F	tgatgctacaaagcaggaacaATTCCCAACAAGAGGTTTCAGAA	
pC-SRC7 ^{TN} -ID9 ^X -R	atttggtggatccgggtaccTTAATCAAACCCTTCATGCCTTAAAG	
pC-SRC7 ^{TN} -ID10 ^X -F	tgatgctacaaagcaggaacaGATCGTAAAGAGCAACAAATTTTCT	
pC-SRC7 ^{TN} -ID10 ^X -R	atttggtggatccgggtaccTCAGTCACTGTCATGCAATTC	
pC-SRC7 ^{TN} -ID11 ^X -F	tgatgctacaaagcaggaacaGAAGAAGAGAAGAAAGTTTTTCTTGAC	
pC-SRC7 ^{TN} -ID11 ^X -R	atttggtggatccgggtaccTTATATGTATTTACTAACAAAAGTTGG	

(continued table)

Primer name	Sequence (5'-3')	Purpose
pC-SRC7 ^{TN} -ID12 ^X -F	tgatgctacaagcaggaaacaATGGCTACGGGATCACCT	
pC-SRC7 ^{TN} -ID12 ^X -R	atttgttggatccgggtaccTTACGTAAACATGTAACATGTATCTCTC	
pC-SRC7 ^{TN} -ID13 ^X -F	tgatgctacaagcaggaaacaGAAGAGAAAAGTGTTTTCTTGACC	
pC-SRC7 ^{TN} -ID13 ^X -R	atttgttggatccgggtaccTCAAACATCTACAAAAGGTGCAC	
pC-SRC7 ^{TN} -ID14 ^X -F	tgatgctacaagcaggaaacaAAGGAAATTCTAGATGTACTTACAGTA	
pC-SRC7 ^{TN} -ID14 ^X -R	atttgttggatccgggtaccTTATCTGTATTCTGAAATATAAGGTGGC	
pC-SRC7 ^{TN} -ID15 ^X -F	tgatgctacaagcaggaaacaAATGAGAAGGAAGTTTTCCTTGAC	
pC-SRC7 ^{TN} -ID15 ^X -R	atttgttggatccgggtaccTTACCTTAAATCAATGGATTGACAG	
pC-SRC7 ^{TN} -ID16 ^X -F	tgatgctacaagcaggaaacaAACAAGATATTCTGGATGTGCTTC	
pC-SRC7 ^{TN} -ID16 ^X -R	atttgttggatccgggtaccCTAGTTCCATCTTCCAAAGAAAGG	
pC-SRC7 ^{TN} -ID17 ^X -F	tgatgctacaagcaggaaacaGTCAATGCATTCGTAAATATTACTGG	
pC-SRC7 ^{TN} -ID17 ^X -R	atttgttggatccgggtaccTTATACTTGACGATTGACTTGC	
pC-SRC7 ^{TN} -ID18 ^X -F	tgatgctacaagcaggaaacaGATACAGAGAGACATATTCCTTGA	
pC-SRC7 ^{TN} -ID18 ^X -R	atttgttggatccgggtaccTCAAGTTTGACCTAACATCTTTCAC	
pC-SRC7 ^{TN} -ID19 ^X -F	tgatgctacaagcaggaaacaGATACAGAGAGAAATATTCCTTGAT	
pC-SRC7 ^{TN} -ID19 ^X -R	atttgttggatccgggtaccTCATTC AATTTTCTTCTTTCTGTTTT	
pC-SRC7 ^{TN} -ID21 ^X -F	tgatgctacaagcaggaaacaCCCTTGGAAAAGGATATATTCCTTG	
pC-SRC7 ^{TN} -ID21 ^X -R	atttgttggatccgggtaccCTACTGCTCTTGAATCTTGCTCG	
pC-SRC7 ^{TN} -ID22 ^X -F	tgatgctacaagcaggaaacaGAGAAAAATATTTCTTAGATATTGCATG	
pC-SRC7 ^{TN} -ID22 ^X -R	atttgttggatccgggtaccTTAATCGAAGAATTCATTGTTGAATG	
pC-SRC7 ^{TN} -ID23 ^X -F	tgatgctacaagcaggaaacaGAAAAGAAGATACTTATGGATATTCATG	
pC-SRC7 ^{TN} -ID23 ^X -R	atttgttggatccgggtaccTCACCCATTCCACACGGA	
pC-SRC7 ^{TN} -ID24 ^X -F	tgatgctacaagcaggaaacaGAAAAGAAGATATTTTGGATATTGCATG	
pC-SRC7 ^{TN} -ID24 ^X -R	atttgttggatccgggtaccTTATTCTACTAACCTTCTAAAATAATCCTAGA	
pC-SRC7 ^{TN} -ID25 ^X -F	tgatgctacaagcaggaaacaAAGGAAATCTTGAAGATACTTAAAGTAAGC	
pC-SRC7 ^{TN} -ID25 ^X -R	atttgttggatccgggtaccCTATTCCAAGTCGCGTATGGC	
pC-SRC7 ^{TN} -ID26 ^X -F	tgatgctacaagcaggaaacaGATGAAATCCAAGAGATTCTAAAAGTAAG	
pC-SRC7 ^{TN} -ID26 ^X -R	atttgttggatccgggtaccCTATGGTTTGTAGTCTGATGCAG	
pC-SRC7 ^{TN} -ID28 ^X -F	tgatgctacaagcaggaaacaAAAAAGATTCAAGACGTA CTCAAAGT	
pC-SRC7 ^{TN} -ID28 ^X -R	atttgttggatccgggtaccCTAAAAATAACCAAATGATGACTTATTTGG	
pC-SRC7 ^{TN} -ID29 ^X -F	tgatgctacaagcaggaaacaAAAGAGATCCAAGAGATACTTAAAGTG	
pC-SRC7 ^{TN} -ID29 ^X -R	atttgttggatccgggtaccTCATTGATTGTTGCGGCG	
pC-SRC7 ^{TN} -ID30 ^X -F	tgatgctacaagcaggaaacaAAAGAGATCCAAGAGATACTTAAAGTG	
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pC-SRC7 ^{TN} -ID35 ^X -F	tgatgctacaagcaggaaacaGATAAAAGTATCTATATGATACTTAAAGTAAGCT	
pC-SRC7 ^{TN} -ID35 ^X -R	atttgttggatccgggtaccTTATGAACTAATGAGATCATCAITTAATTTTT	
pC-SRC7 ^{TN} -ID36 ^X -F	tgatgctacaagcaggaaacaAAAAAGATCTATGACATACTTAAAGTAAGC	
pC-SRC7 ^{TN} -ID36 ^X -R	atttgttggatccgggtaccCTACAAATTGTCTCAACAACCTC	
pC-SRC7 ^{TN} -ID37 ^X -F	tgatgctacaagcaggaaacaGATACAGAGAAAGGAATATTCCTTGAT	
pC-SRC7 ^{TN} -ID37 ^X -R	atttgttggatccgggtaccTTAACCTTGATTTTCTTATTTTCTGAG	
pC-SRC7 ^{TN} -ID38 ^X -F	tgatgctacaagcaggaaacaACTGAGCAGGAAATATTCTAGACAT	
pC-SRC7 ^{TN} -ID38 ^X -R	atttgttggatccgggtaccCTAAATGTCAAAATATGCATAAGCTGG	

(continued table)

Primer name	Sequence (5'-3')	Purpose
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pC-SRC7 ^{TN} -ID39 ^κ -R	atttgttggatccgggtaccTTACCAGAAGTCACACATTACAAT	
BD-SRZ4-F	catatggccatggaggccgaattcATGGCTTGGGGATCAAGTTC	
BD-SRZ4-R	tagttatgcggcgcgtgcaggtcgacTTATCTGTATTCTGAAATATAAGGTGGC	
pCambia1300-SRZ4 ^{TIR} -F	gagaacacgggggacgagctcATGGCTTGGGGATCAAGTTC	SRZ4 truncated
pCambia1300-SRZ4 ^{TIR} -R	atttgttggatccgggtaccTTATGGGTAATCCGCAACATGTA	sequence cloned in
pCambia1300-SRZ4 ^{NBS} -F	gagaacacgggggacgagctcATGGACTAGAGTCACGAGTGCTAGA	pCambia1300
pCambia1300-SRZ4 ^{NBS} -R	atttgttggatccgggtaccTTACTCCAAAGCATCAAAGCTTAC	
pCambia1300-SRZ4 ^{TN} -F	gagaacacgggggacgagctcATGGCTTGGGGATCAAGTTC	
pCambia1300-SRZ4 ^{TN} -R	atttgttggatccgggtaccTTACTCCAAAGCATCAAAGCTTAC	
pCambia1300-SRZ4 ^{TNL} -F	gagaacacgggggacgagctcATGGCTTGGGGATCAAGTTC	
pCambia1300-SRZ4 ^{TNL} -R	atttgttggatccgggtaccTTAACGCAAGCAGCCACTC	
pCambia1300-SRZ4 ^{TNLZ} -F	gagaacacgggggacgagctcATGGCTTGGGGATCAAGTTC	
pCambia1300-SRZ4 ^{TNLZ} -R	gagaacacgggggacgagctcTTAACTTCTCCAAAATGCAGCCA	
pCambia1300-SRZ4 ^{NLZ3} -F	gagaacacgggggacgagctcATGGACTAGAGTCACGAGTGCTAGA	
pCambia1300-SRZ4 ^{NLZ3} -R	gagaacacgggggacgagctcTTATAAACCGAATTGGCAA	
pCambia1300-SRZ4 ^{Z3} -F	gagaacacgggggacgagctcATGAATGTGAGTGGTGCCATG	
pCambia1300-SRZ4 ^{Z3} -R	gagaacacgggggacgagctcTTATAAACCGAATTGGCAA	
pQBV3-ID3 ^κ -F	AAAGCAGGCTCAGGGgatacATGAAGGATATATTCCTTGATGTGTG	ID ^κ sequence cloned
pQBV3-ID3 ^κ -R	AGCTGGGTGCAGGGCgatacCAATCTCTCTCGCTGGAATAC	in entry vector
pQBV3-ID13 ^κ -F	AAAGCAGGCTCAGGGgatacATGGAAGAGAAAAGTGTTTTCTTGACC	pQBV3
pQBV3-ID13 ^κ -R	AGCTGGGTGCAGGGCgatacAACATCTACAAAAGGTGCAC	
pQBV3-ID16 ^κ -F	AAAGCAGGCTCAGGGgatacATGAACAAGATATTCTGGATGTGCTTC	
pQBV3-ID16 ^κ -R	AGCTGGGTGCAGGGCgatacGTTTCATCTTCCAAAGAAAGG	
pQBV3-ID25 ^κ -F	AAAGCAGGCTCAGGGgatacATGAAGGAAATCTTGAAGATACTTAAAG	
pQBV3-ID25 ^κ -R	AGCTGGGTGCAGGGCgatacTTCCAAGTCGCGTATGGC	
pQBV3-ID29 ^κ -F	AAAGCAGGCTCAGGGgatacATGAAAGAGATCCAAGAGATACTTAAAG	
pQBV3-ID29 ^κ -R	AGCTGGGTGCAGGGCgatacTTGATTGTTGCGGCG	
pQBV3-ID30 ^κ -F	AAAGCAGGCTCAGGGgatacATGAAAGAGATCCAAGAGATACTTAAAG	
pQBV3-ID30 ^κ -R	AGCTGGGTGCAGGGCgatacTGATTCTGAATATTGAAATCATCAA	
pQBV3-ID35 ^κ -F	AAAGCAGGCTCAGGGgatacATGGATAAAGTATCTATGATACTTA	
pQBV3-ID35 ^κ -R	AGCTGGGTGCAGGGCgatacTGAACATAAGATCATCATTTAATTTT	
pQBV3-CP-F	AAAGCAGGCTCAGGGgatacATGTCAGGCAAGGAGAAAGAAGG	
pQBV3-CP-R	AGCTGGGTGCAGGGCgatacCTGCTGTGGGCCCATGCCAG	
pQBV3-P3-F	AAAGCAGGCTCAGGGgatacATGGGTGATGCGCAACAAAGGATG	
pQBV3-P3-R	AGCTGGGTGCAGGGCgatacCTGTGCGGAAACATCTCTG	
pQBV3-6K2-F	AAAGCAGGCTCAGGGgatacATGAGCAAACATGAGGTGAGCA	
pQBV3-6K2-R	AGCTGGGTGCAGGGCgatacTTGAGTTGATACTGGTTCACG	
pQBV3-P1-F	AAAGCAGGCTCAGGGgatacATGGCAACAATCATGATCGGAAG	
pQBV3-P1-R	AGCTGGGTGCAGGGCgatacGTAATGTTGAATATCCTCTATG	
pQBV3-NIb-F	AAAGCAGGCTCAGGGgatacATGGGAAAAAGGAAAGATGGGTT	
pQBV3-NIb-R	AGCTGGGTGCAGGGCgatacTTGCAAAGAACTGATTAC	

(continued table)

Primer name	Sequence (5'-3')	Purpose
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pQBV3-HC-Pro-R	AGCTGGGTGCAGGGgata ^c ACCAACTCTATAAAATTTCATC	
pQBV3-SRZ4-F	AAAGCAGGCTCAGGgata ^c ATGGCTTGGGGATCAAGTTC	
pQBV3-SRZ4-R	AGCTGGGTGCAGGGgata ^c TCTGTATTCTGAAATATAAGGTGGC	
T7	TAATACGACTCACTATAGG	AD universal primers for screening
3'AD	AGATGGTGCACGATGCACAG	candidate proteins

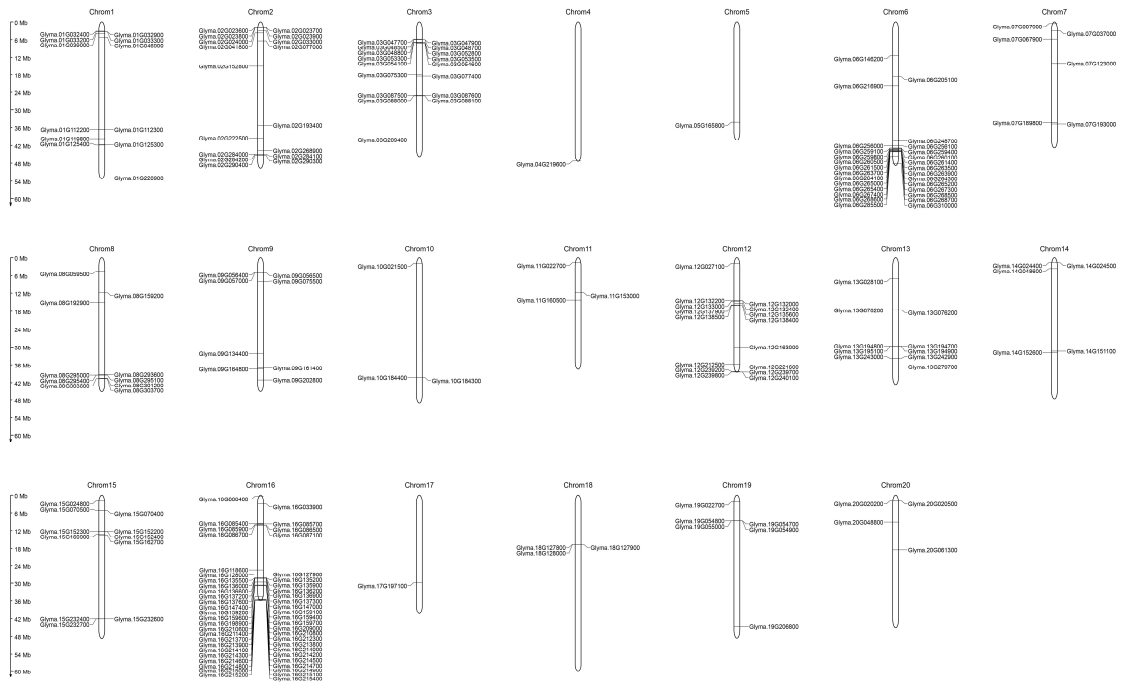


Figure S1. Chromosomal distribution of 210 *TNL-like* genes in soybean. The soybean genome consists of 20 pairs of chromosomes, and these 210 *TNL-like* genes are distributed on all 20 pairs of chromosomes in soybean. The left y-axis represents chromosome length, a cylindrical shape represents a chromosome, and the short lines connected to it represent the coding position of the gene. This image was drawn by the Mapgene2chrom website (http://mg2c.iask.in/mg2c_v2.0/) (accessed on 18 December 2020).

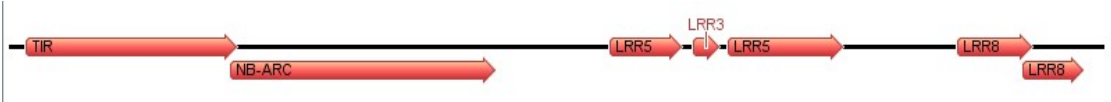


Figure S2. Structural domain prediction analysis of 210 TNL-like proteins in soybean. FASTA format corresponding to candidate genes was obtained from the NCBI database through gene number, and BATCH SMART in TBtools was used for domain predictions.

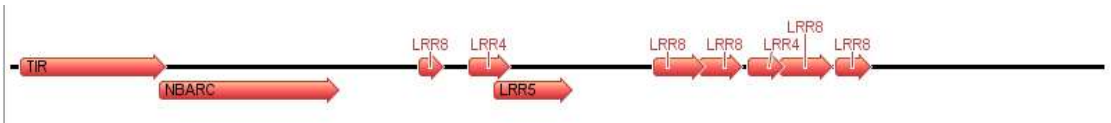
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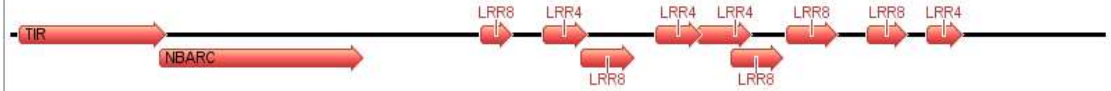
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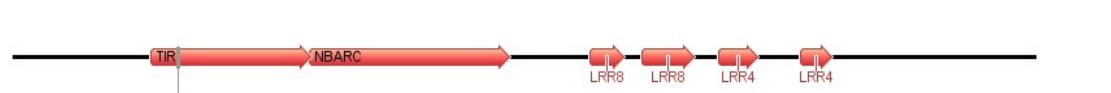
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GLYMA_01G112300



GLYMA_01G119800



A schematic representation of the domain organization of the protein. A horizontal line represents the protein sequence, with three red arrows indicating domains: TIR, AAA 16, and AAA 22.

MSGLCAAATHTLSSQSLSTLT
 TIR

The diagram illustrates a timeline with two main phases: TIR (Tumor Infiltration Response) and PRD (Post-Resection Disease). The TIR phase is represented by a red arrow pointing right, followed by a blue dashed line, and then a red arrow pointing right. The PRD phase is represented by a red arrow pointing right. The timeline is marked with a vertical line at the start of the TIR phase and another vertical line at the start of the PRD phase.

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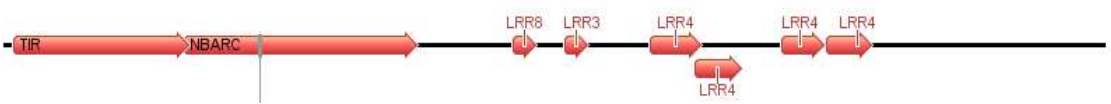
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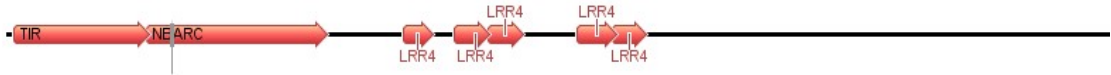
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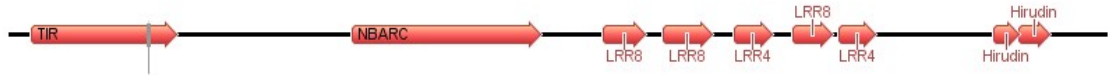
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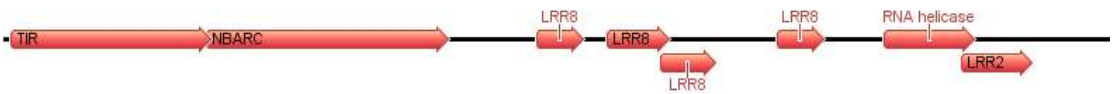
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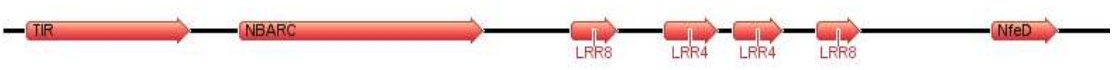
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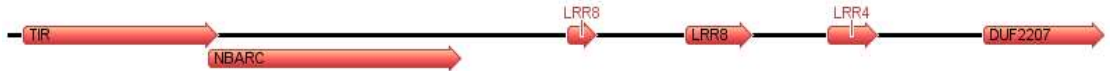
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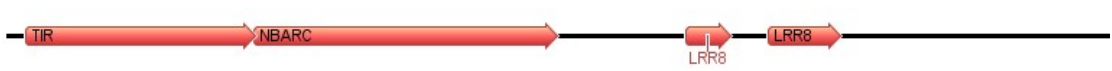
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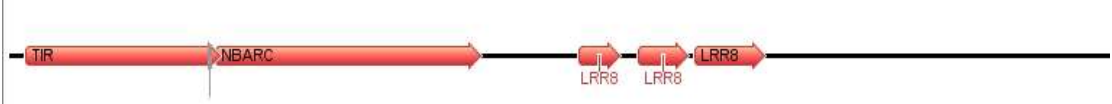
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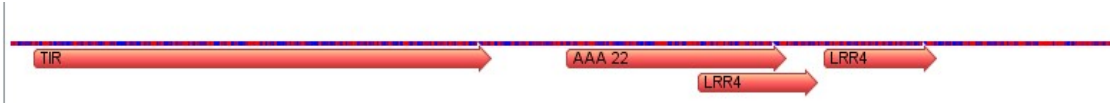
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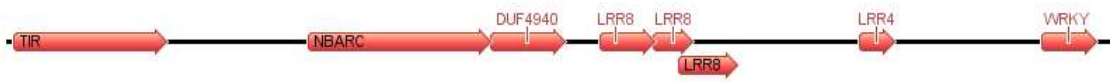
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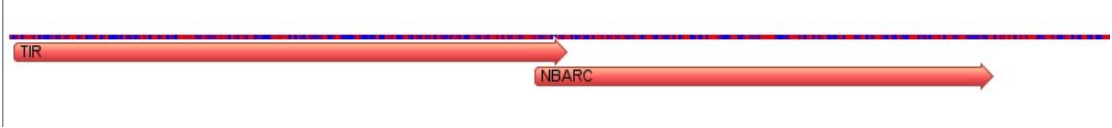
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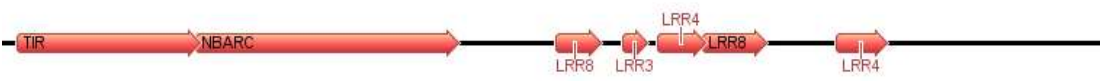
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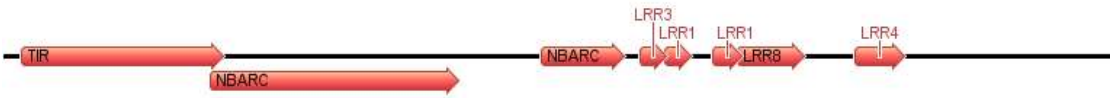
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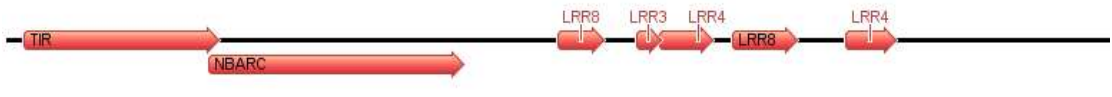
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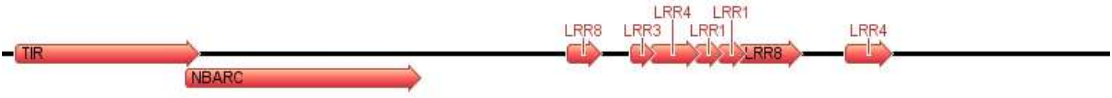
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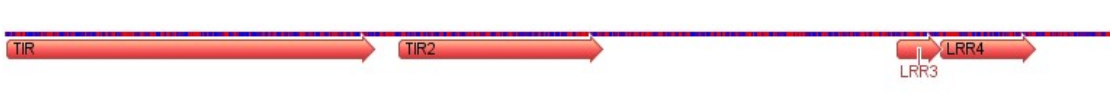
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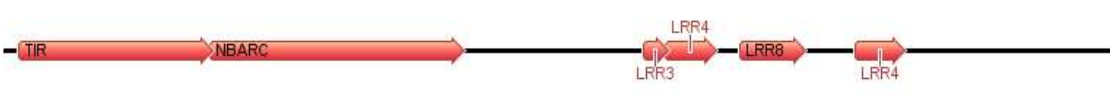
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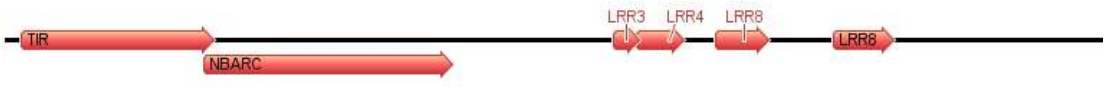
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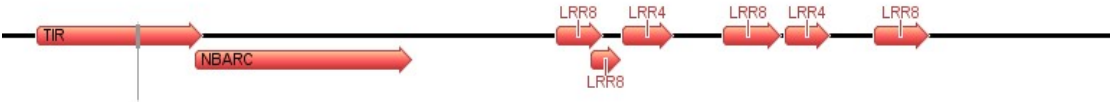
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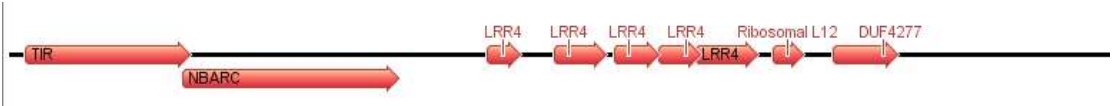
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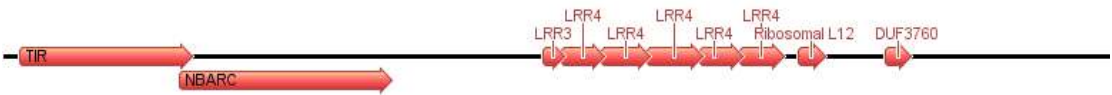
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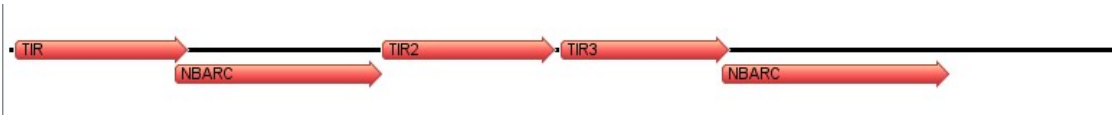
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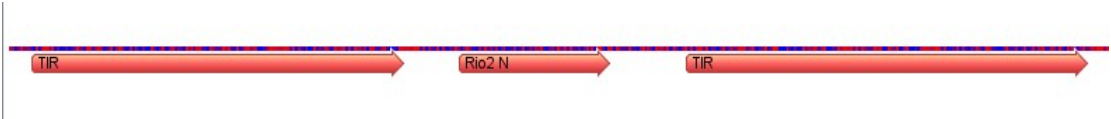
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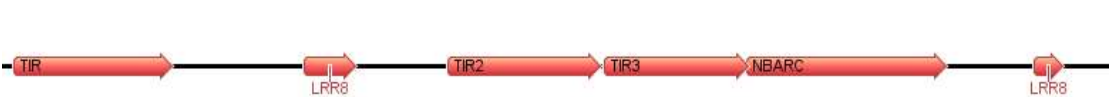
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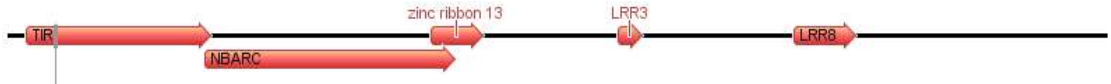
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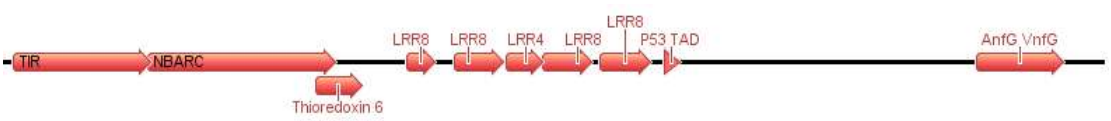
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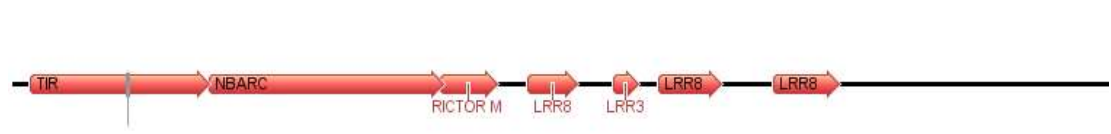
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GLYMA_08G293600



GLYMA_08G295000



GLYMA_08G295100



GLYMA_08G295400



GLYMA_08G301200



GLYMA_08G303600



The diagram illustrates the domain architecture of the AtNLR1 gene. It features a TIR domain (Transmembrane Invariant Region) at the N-terminus, followed by an NB-ARC domain (Nucleotide-Binding and Arabinosyl-Cyclase domain). The LRR domain (Leucine-Rich Repeat domain) is located at the C-terminus and is composed of five LRRs: LRR8, LRR4, LRR3, LRR4, and LRR8. The LRR3 domain is highlighted in red, indicating its role in the study.

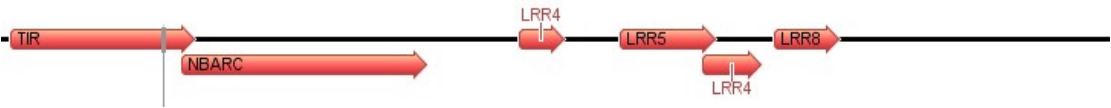
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The schematic diagram illustrates the domain architecture of the protein. It begins with a TIR domain, followed by an NB-ARC domain. The protein then contains a series of LRR domains: LRR8, LRR3, LRR8, LRR8, and LRR4. The LRR3 domain is shown with a mutation symbol (a vertical line with a horizontal bar) indicating a specific site of interest.

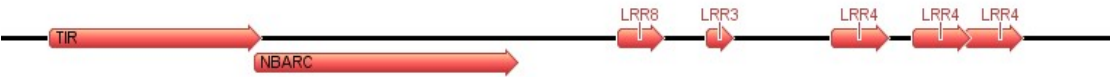
Schematic diagram of the LRR domain organization of the RVT-3 protein. The protein structure is shown as a linear sequence of domains: TIR, NBARC, LRR8, LRR4, DUF4435, LRR4, LRR4, ATPase 2, zf-RVT, and RVT-3. The LRR4 domain is highlighted in blue.

A horizontal timeline diagram with a red background. It features two red arrows pointing to the right. The first arrow is labeled 'TIR' and the second arrow is labeled 'NBARC'. A vertical line segment connects the end of the 'TIR' arrow to the start of the 'NBARC' arrow, indicating a transition or continuation of the process.

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GLYMA_10G184400



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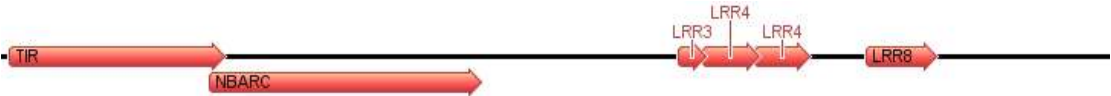
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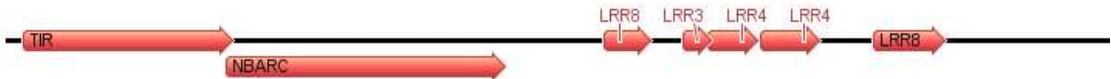
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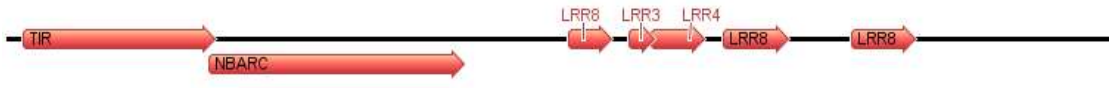
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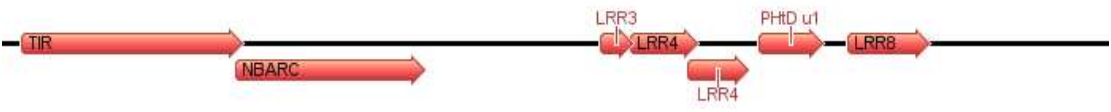
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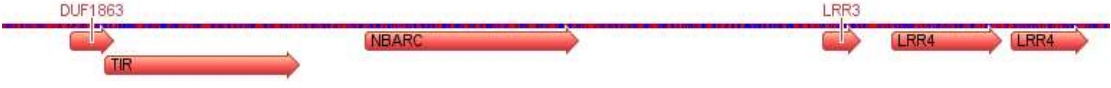
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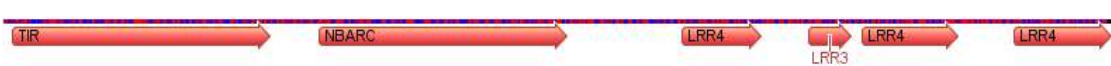
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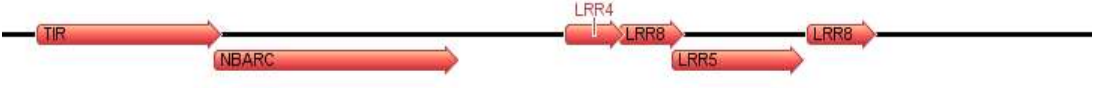
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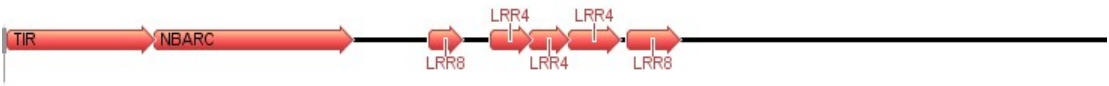
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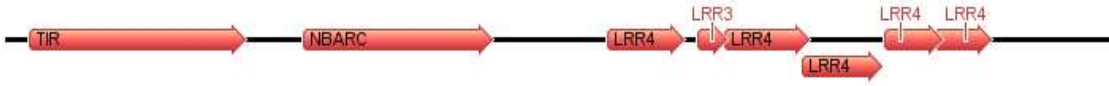
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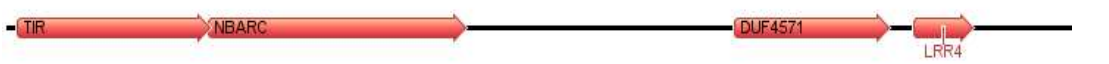
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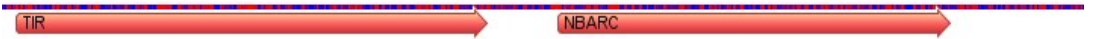
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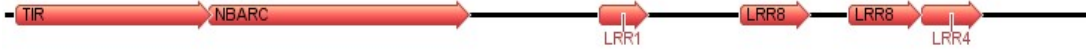
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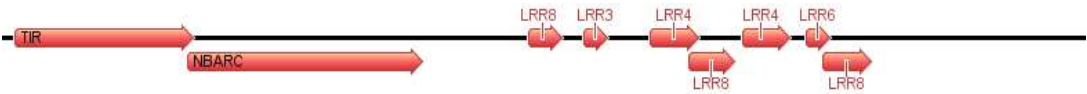
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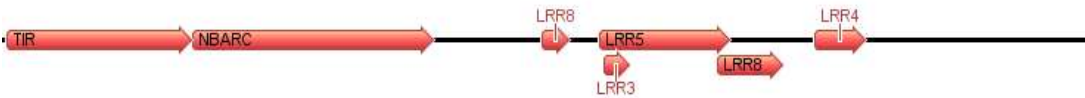
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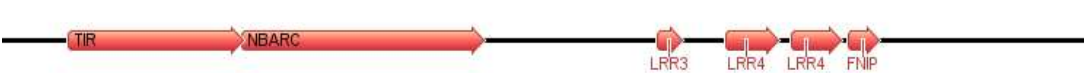
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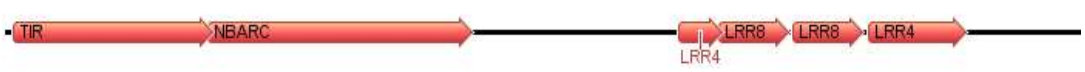
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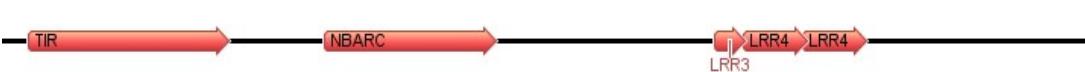
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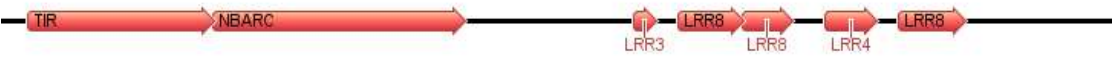
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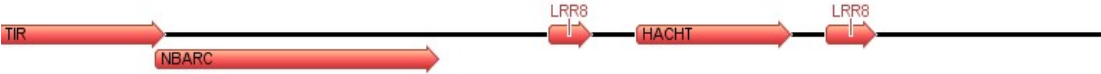
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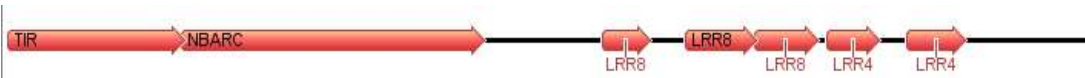
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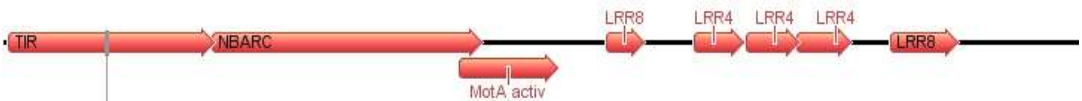
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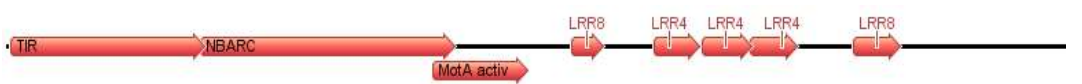
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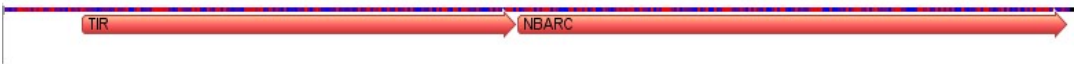
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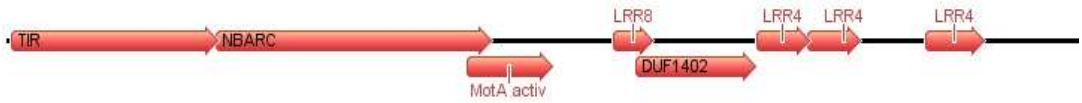
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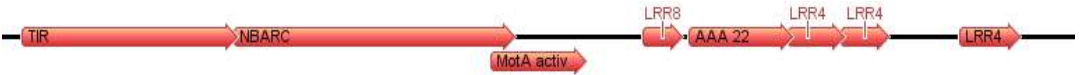
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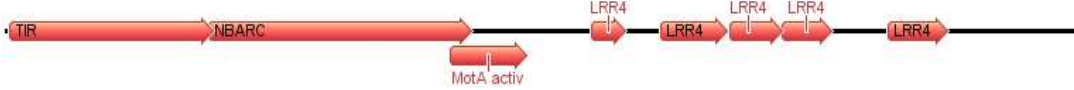
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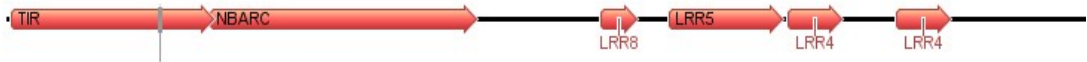
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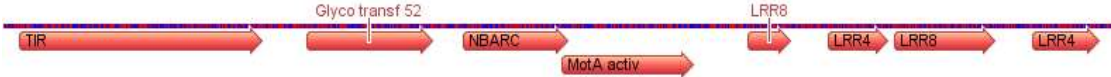
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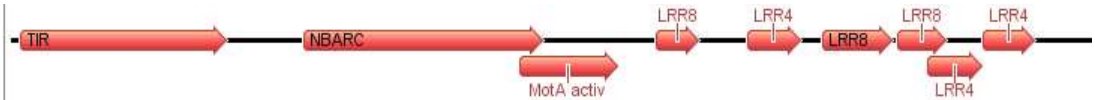
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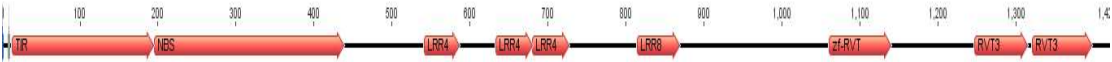
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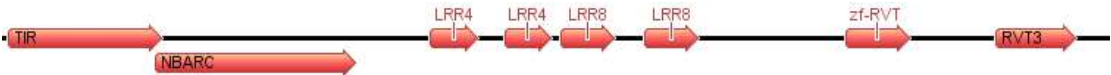
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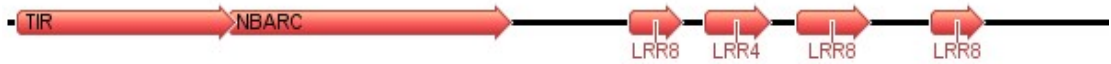
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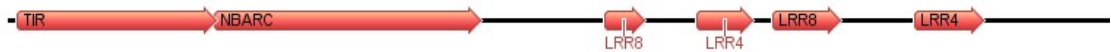
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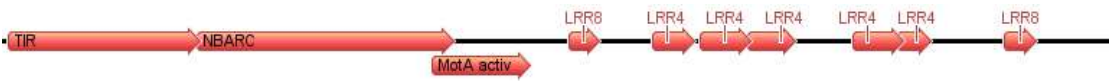
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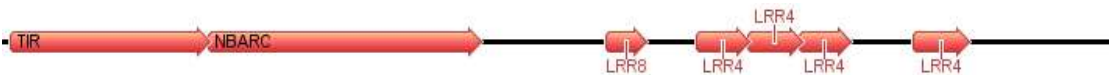
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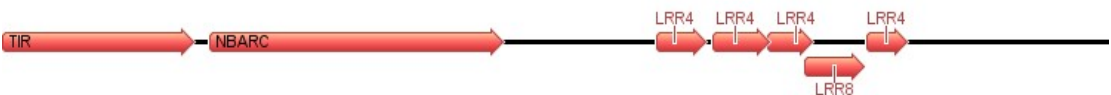
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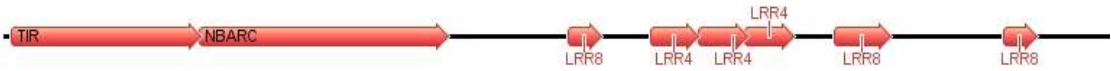
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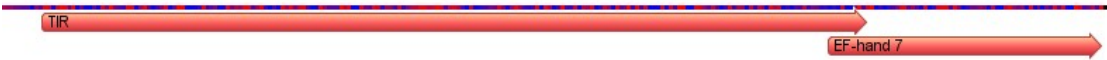
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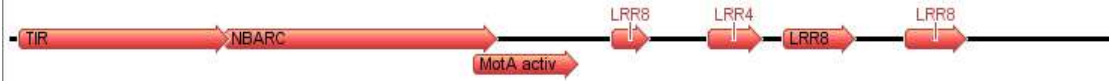
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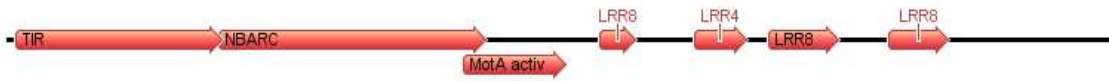
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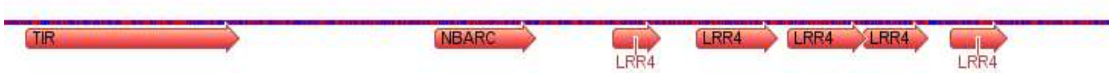
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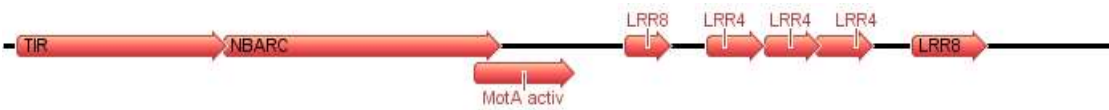
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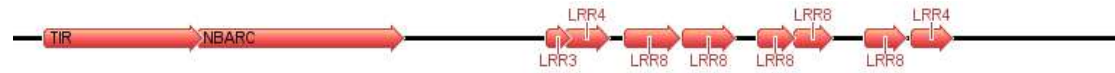
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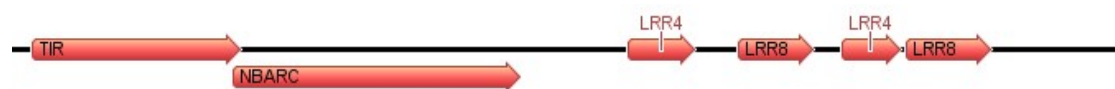
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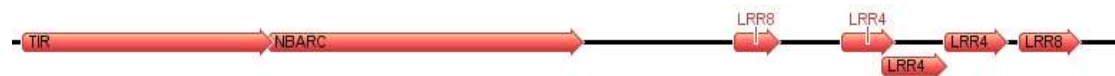
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GLYMA_U035400



GLYMA_U035700



Figure S3. Domain diagram of 210 TNL-like proteins. Structural domain prediction and position calibration of the 210 TNL-like proteins using GENEIOUS v4.8.4 software based on PFAM database (<http://pfam-legacy.xfam.org/>) (accessed on 18 December 2020).

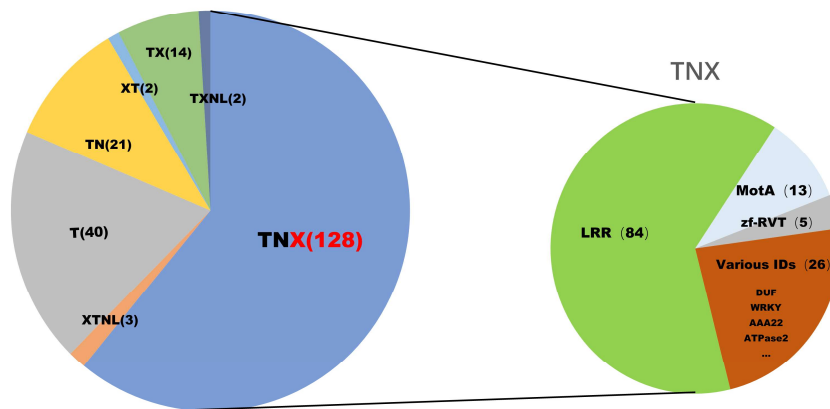


Figure S4. Classification of 210 soybean TNL-like proteins. The 210 soybean TNL-like proteins were grouped by domain type.

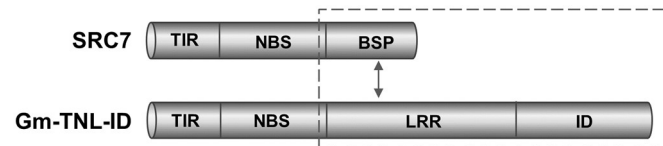


Figure S5. Domain architecture of SRC7 and soybean Gm-TNL-ID proteins. The above diagram shows the basic structural domains of SRC7 and the Gm-TNL-ID proteins we had screened.

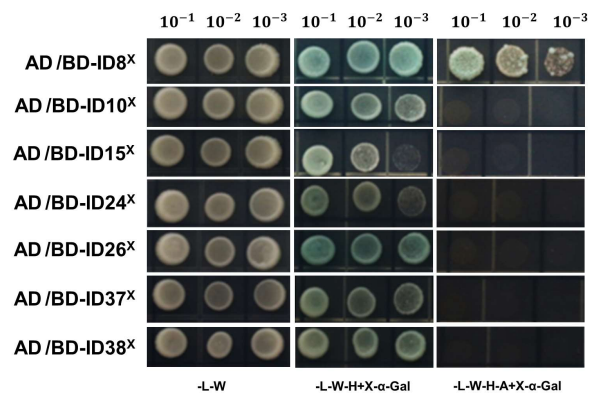


Figure S6. Evaluation of these BD-Gm-TNL-ID^x bait vectors. The auto-activation activity of these BD-Gm-TNL-ID^x were tested. The yeast cells containing indicated constructs were grown on different selective media, and 100 µl of X-α-Gal was added visualized the reporter expression. The yeast concentration gradients were 10⁻¹, 10⁻² and 10⁻³, respectively.



Figure S7. Domain architecture of SRZ4. Domain architecture of SRZ4. These grey boxes indicate TIR, NBS, LRR4, LRR4, LRR4, LRR8, zf-RVT, RVT3 and RVT3 domains, respectively.

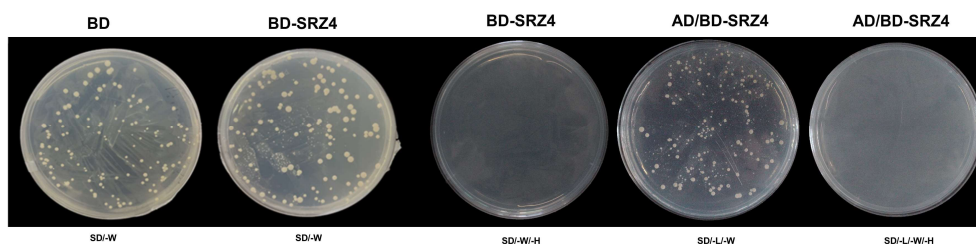


Figure S8. Testing the toxicity and auto-activation of SRZ4. For toxicity validation, the yeast cells containing BD-SRZ4 was grown on minimal media (SD/-W). For auto-activation activity validation, the yeast cells containing BD-SRZ4 and AD were grown on minimal media (SD/-L/-W) and stringent selective media (SD/-L/-W/-H).

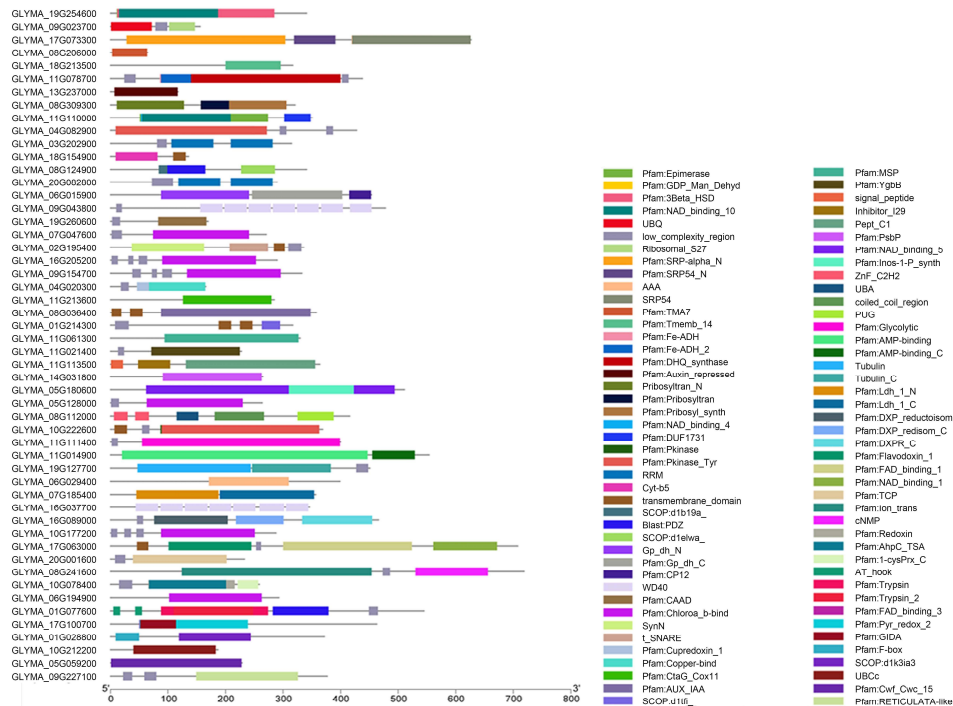


Figure S9. Structural domain prediction analysis of the soybean protein interacting with SRZ4. Schematic diagram of domain prediction for 48 soybean proteins interacting with SRZ4 using BATCH SMART in TBtools.

