

Supplemental Table 1 Sequence variation of *Glyma10g02140* (*Glyma.10g017100*) and *Glyma10g02160* (*Glyma.10g017200*), two candidate genes responsible for SRKN resistance, among 13 soybean lines

Soybean line	Reaction to SRKN	<i>Glyma10g02140</i> (<i>Glyma.10g017100</i>)																																											
		First exon								Intron		2nd exon		Intron																															
		Gm 10: 1,506,154 (1,510,762)	Gm 10: 1,506,012 (1,510,620)	Gm 10: 1,505,931 (1,510,539)	Gm 10: 1,505,848 (1,510,456)	Gm 10: 1,505,843 (1,510,451)	Gm 10: 1,505,839 (1,510,447)	Gm 10: 1,505,789 (1,510,397)	Gm 10: 1,505,647 (1,510,255)	Gm 10: 1,505,584 (1,510,192)	Gm 10: 1,505,565 (1,510,175)	Gm 10: 1,505,401 (1,510,009)	Gm 10: 1,505,246 (1,509,854)	Gm 10: 1,505,086 (1,509,694)	Gm 10: 1,504,939 (1,509,694)	Gm 10: 1,504,848 (1,509,456)	Gm 10: 1,504,598 (1,509,206)	Gm 10: 1,504,384 (1,508,992)	Gm 10: 1,504,257 (1,508,865)	Gm 10: 1,504,216 (1,508,824)	Gm 10: 1,504,209 (1,508,817)	Gm 10: 1,504,159 (1,508,767)	Gm 10: 1,504,125 (1,508,733)	Gm 10: 1,504,086 (1,508,694)	Gm 10: 1,504,012 (1,508,620)	Gm 10: 1,503,953 (1,508,561)	Gm 10: 1,503,941 (1,508,549)	Gm 10: 1,503,791 (1,508,399)	Gm 10: 1,503,777 (1,508,385)	Gm 10: 1,503,774 (1,508,382)	Gm 10: 1,503,762 (1,508,370)	Gm 10: 1,503,728 (1,508,336)	Gm 10: 1,503,636 (1,508,244)	Gm 10: 1,503,606 (1,508,214)	Gm 10: 1,503,567 (1,508,175)	Gm 10: 1,503,372 (1,507,980)	Gm 10: 1,503,353 (1,507,961)	Gm 10: 1,503,326 (1,507,934)	Gm 10: 1,503,311 (1,507,919)	Gm 10: 1,503,099 (1,507,707)	Gm 10: 1,503,016 (1,507,624)	Gm 10: 1,502,971 (1,507,579)	Gm 10: 1,502,926 (1,507,534)		
Williams 82	s	G	C	C	A	A	G	C	T	A	A	A	A	G	CTGTTG AAAATA GTCCTA CATTGG ATGTTT ACGAAA	TCT	T	A	GTG	AC	A	A	A	A	ATCTTT TTTCA GCATT ATGTT CAATC ACCGA	C	G	C	TC	G	T	C	C	C	C	T	C	C	C	C	A	G	ATAA	G	G
PI 437654	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
Magellan	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
PI 424298	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
Hutcheson	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
Essex	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
PI 438489B	R	A	T* (V ⁹³ I)	A* (D ¹²⁰ Y)	C	C* (L ¹⁴⁹ R)	A	T* (C ¹⁶⁷ Y)	A* (E ²¹⁴ D)	G	A* (Stop)	A	AAAAA	G	C	T	C	T	A	G	G	A	A	C	G	A	T	C	A	T	A	C	G	T	A	T	G	CCTCTGCC	G	A	A	A	A		
PI 567516C	R	A	T* (V ⁹³ I)	A* (D ¹²⁰ Y)	C	C* (L ¹⁴⁹ R)	A	T* (C ¹⁶⁷ Y)	A* (E ²¹⁴ D)	G	A* (Stop)	A	AAAAA	G	-	T	C	T	A	G	G	A	A	C	G	A	T	C	A	T	A	C	G	T	A	T	G	CCTCTGCC	G	A	A	A	A		
PI 567387	R	A	T* (V ⁹³ I)	A* (D ¹²⁰ Y)	C	C* (L ¹⁴⁹ R)	A	T* (C ¹⁶⁷ Y)	A* (E ²¹⁴ D)	G	A* (Stop)	A	AAAAA	G	-	T	C	T	A	G	G	A	A	C	G	A	T	C	A	T	A	C	G	T	A	T	G	CCTCTGCC	G	A	A	A	A		
PI 209332	R	A	T* (V ⁹³ I)	A* (D ¹²⁰ Y)	C	C* (L ¹⁴⁹ R)	A	T* (C ¹⁶⁷ Y)	A* (E ²¹⁴ D)	G	A* (Stop)	A	AAAAA	G	-	T	C	T	A	G	G	A	A	C	G	A	T	C	A	T	A	C	G	T	A	T	G	CCTCTGCC	G	A	A	A	A		
PI88788	R	A	T* (V ⁹³ I)	A* (D ¹²⁰ Y)	C	C* (L ¹⁴⁹ R)	A	T* (C ¹⁶⁷ Y)	A* (E ²¹⁴ D)	G	A* (Stop)	A	AAAAA	G	C	T	C	T	A	G	G	A	A	C	G	A	T	C	A	T	A	C	G	T	A	T	G	CCTCTGCC	G	A	A	A	A		
PI 567305	R	A	T* (V ⁹³ I)	A* (D ¹²⁰ Y)	C	C* (L ¹⁴⁹ R)	A	T* (C ¹⁶⁷ Y)	A* (E ²¹⁴ D)	G	A* (Stop)	A	AA	G	-	T	C	T	A	G	-	A	A	C	-	A	T	C	A	T	A	C	G	T	A	T	G	CCTCTGCC	G	A	A	A	A		
PI 404198B	R	A	T* (V ⁹³ I)	A* (D ¹²⁰ Y)	C	C* (L ¹⁴⁹ R)	A	T* (C ¹⁶⁷ Y)	A* (E ²¹⁴ D)	G	A* (Stop)	A	AA	G	-	T	C	T	A	G	-	A	A	C	-	A	T	C	A	T	A	C	G	T	A	T	G	CCTCTGCC	G	A	A	A	A		

Note:

1. Evaluation of Mi resistance for the above soybean lines were conducted for at least two replicates. S, susceptible; R, resistant.
2. - represent that the position is identical to Williams 82 sequence.
3. The positions highlighted with red color represent the exon.
4. The SNP/Indels highlighted with yellow color represent the sequence variation common in all resistant lines but different from all susceptible lines.
5. The SNPs marked with * in the exon regions represent nonsynonymous mutation. For other SNPs without * represent synonymous mutation.

