

Supplemental Table 1.
Identification of *RsRBCS* genes

Genome source	Contig	Blast hit region	Direction	Sequence of forward primer (5'-3') ^a Sequence of reverse primer (5'-3')	PCR amplification ^b	Functional / Pseudo	Gene Name	TILLING Length (bp)
Kazusa ^c	Rsa1.0_00756.1	56975-57776	+	GGACCTTTTGTTCACTAGGGCTTTTGGC GCAGGAACAGTGCAATTCCTGTTTTGAG	+	Functional	<i>RsRBCS1A</i>	1224
Kazusa	Rsa1.0_01047.1	7699-8498	+	CCACGTGGCATTATTTTAGTGGTTAAAACCGATA GGATAAAGTTTTGTTGTTTACACAAAGCAATGAAGCTG	+	Functional	<i>RsRBCS2B</i>	1105
Kazusa	Rsa1.0_01369.1	9382-8570	-	GTGGTCAAGTATCGATAAGGGTATCAACACCG TGAATGTTTTCTTATCCCAATAAATTGAGAACCCTAATAGC	+	Functional	<i>RsRBCS3A</i>	1180
Kazusa	Rsa1.0_01446.1	39634-40486	+	AAAAGCCCAATCTAAGTTTCAATTTGGGCC CCATCATAGATTTTTCAGTGGTCCATCTTTTACTTC	+	Pseudo	<i>RsRBCS1B</i>	-
Kazusa	Rsa1.0_04010.1	1683-1050	-	GTGGCAGGTAACGACGTTATCATCAGCC TATGTCCATAAATCAGACATTGACAATCGG	-	-	-	-
Kazusa	Rsa1.0_06054.1	10467-11271	+	CCTTTGATCATTAGGGATTATACCTCTTGCGG CCCATCGCGTTACCTATTCCGTTTTGTAA	+	Functional	<i>RsRBCS4A</i>	1172
Kazusa	Rsa1.0_06054.1	794-1589	+	GGAGGCCAGCAGTAAATCAGTAAGTCAGTAACCA TGAAAACCTAATAGCCATCAGAAAGTAACCAAGACG	+	Functional	<i>RsRBCS5A</i>	1166
MSU ^d	RrC23820	1288-487	-	CGCACTCTTTGATCATTAGGGCTTTATGCC CGAAAAATAACCAAGAAAAAGAAGCGATGCAG	+	Functional	<i>RsRBCS2A</i>	1082
MSU	RrC6617	8265-7495	-	ATCACAGTGGCCTGTATTGATAAGGGTGCC CGATAGAAAATGTCTCTGAAACGTAAACCC	-	-	-	-
MSU	RrC9110	1285-2093	+	ATTAGGGATTATACCTCTTGCGGTTCTCAC GTTCTAACGAATATGGCTATTTCATTAG	-	-	-	-

^a The primer sequences were used for both of gene identification and TILLING. ^b "+" indicates that the region was amplified by PCR, "-" was not. ^c Kazusa (Kazusa DNA Research Institute; <http://radish.kazusa.or.jp/>). ^d MSU (Michigan State University; <http://radish.plantbiology.msu.edu>).

Supplemental Table 2.**Putative chromosome positioning in seven *RBCS*s in Radish**

Gene ID	Similar gene in <i>B. rapa</i>	Homology (%)	Chromosome (<i>B. rapa</i>)	Putative Chromosome Position in <i>R. sativus</i>
<i>RsRBCS1A</i>	LOC103850112	85	A02	LG1 /LG4
<i>RsRBCS2A</i>	LOC103864160	93	A04	LG3
<i>RsRBCS4A</i>	LOC103863779	92	A04	LG3
<i>RsRBCS5A</i>	LOC103863779	92	A04	LG3
<i>RsRBCS3A</i>	LOC103863779	88	A04	LG3
<i>RsRBCS2B</i>	LOC103852369	90	A02	LG1/LG4
	LOC103852368	90	A02	LG1/LG4
<i>RsRBCS1B</i>	LOC103852372	87	A02	LG1 /LG4

Supplemental Table 3.
Mutations and amino acid substitutions of *RBCS*
genes in the Radish mutant population

Gene ID	Position from ATG	Amino acid change	Concentration of EMS (%)
<i>RsRBCS2A</i>	G310A	G104R	0.25
<i>RsRBCS5A</i>	C-83T	-	0.25
<i>RsRBCS5A</i>	G-9A	-	0.25
<i>RsRBCS2B</i>	C11T	S4F	0.50
<i>RsRBCS2B</i>	C134T	S45F	0.50
<i>RsRBCS2B</i>	G352A	D118N	0.50