Supplementary Table S1. Sanger sequencing analysis of the PCR amplicons of the DNA from *GST1* genome-edited lines and the WT control

Line no.	Allele	Number of sequenced clones			Target1	In/Del	Target2	In/Del
WT	1, 2	Total	Number		GGGTATACCCACCGATTCTTCGG		GCTGATATGTGCCACCTGCCGGG	
#1	1	3	2	2	GGGTATACC-----||------	-24	GCTGATATGTGCCACCTGCCGGG	0
	2		1	1	GGGTATACCCACCGATTCTTCGG	0	GCTGATATGTGCCACCTGCCGGGG	+1
#3	1	5	0	0	No detection			
	2		5	4	GGGTATAC---------CTTCGG	-9	GCTGATATGTGCCACCTGCCGGG	0
				1	GGGTATAC---------CTTCGG	-9	GCTGATATGTGCCACCTGCCGGGG	+1
#8	1	5	9	9	GGGTATACC------||-----	-15	GCTGATATGTGCCAC--GCCGGG	-2
	2		2	1	GGGTATACCCACCGATTCTTCGG	0	GCTGATATGTGC-----GCCGGGG	-5, +1
				1	GGGTATACCCACCGATTCTTCGG	0	GCTGATATGTGC-----GCCGGGGG	-5, +2
#12	1	7	5	1	--------||-------TTCGG	-19	GCTGATAT-------CTGCCGGG	-7
				1	--------||-------TTCGG	-19	GCTGATATGTGCC-------GGGGGG	-7,+3
				3	--------||-------TTCGG	-19	GCTGATATGT-------GCCGGG	-7
	2		2	2	GGTATACCCACCGA--CTTCGG	-2	GCTGATATGTGCCAC--GCCGGG	-2
#13	1	7	7	7	GGGTATACCCACCGA-TCTTCGG	-1	GCTGATATGTGC-----GCCGGG	-5
	2		0	0				
#23	1	5	5	5	GGGTATACCCACCGATTCTTCGG	0	GCTGATATGTGCCAC--GCCGGG	-2
	2		0	0				
#29	1	9	0	0	No detection			
	2		9	9	GGGTATACCCA------CTTCGG	-6	GCTGATATGTGC-----GCCGGG	-5

Supplementary Table S2. Next-generation sequencing analysis of the PCR amplicons of the DNA and RNA from *GST1* genome-edited lines and the WT control

Line no.	Allele	Number of fragments (DNA)	Number of fragments (RNA)	Target1	In/Del	Target2	In/Del	Flower color phenotype
WT	1	9,782	20,438	GGGTATACCCACCGATTCTTCGG	0	GCTGATATGTGCCACCTGCCGGG	0	Blue
	2	10,199	3,992	GGGTATACCCACCGATTCTTCGG	0	GCTGATATGTGCCACCTGCCGGG	0	
#3	1	-	-	Large insertion			-	Bale blue
	2	25,763	31,764	GGGTATAC---------CTTCGG	-9	GCTGATATGTGCCACCTGCCGGG	0	
#12	1	27,408	17,831	-------------------TCGG	-19	GCTGATATGT-------GCCGGG	-7	Almost white color
	2	26,029	3,222	GGGTATACCCACCGA--CTTCGG	-2	GCTGATATGTGCCAC--GCCGGG	-2	
#13	1	12,587	18,989	GGGTATACCCACCGA-TCTTCGG	-1	GCTGATATGTGC-----GCCGGG	-5	Almost white color
	2	13,805	1,728	GGGTATACCCAC-----CTTCGG	-5	GCTGATATGTGCCACCTGCCGGG	0	
#23	1	19,080	29,053	GGGTATACCCACCGATTCTTCGG	0	GCTGATATGTGCCAC--GCCGGG	-2	Almost white color
	2	27,740	12,542	GGGTATACC-------------------||--------------------GCCGGG			-129	
#29	1	-	-	Large insertion			-	Almost white color
	2	24,369	18,889	GGGTATACCCA------CTTCGG	-6	GCTGATATGTGC-----GCCGGG	-5	

Supplementary Table S3. Primers used in this study

#	Primer name	Sequence (5'-3')	Index
	Isolation of GST1		
	3' RACE PCR		
#276	GST1-1_3race_first	GTCGATCAATGGCTGGAAGT	
#277	GST1-1_3race_nested	AACAAGCTCCAAAACGTGCT	
	Full-length amplification		
#325	Alb.GST1_5'UTR_F1	TAAAGGTTTAGCAGAAGAAAAATAGCA	
#326	Alb.GST1_3'UTR_R1	CCGTATTAAACATTTCTACTACCACT	
	Genome sequence for 2_{nd} intron		
#98	GST1_exon2_Fw	TTCCTGTCATTGAAGATGGTGA	
#99	GST1_exon3_Rv	AAGTGGTTCCGAGGAGGTTT	
	Direct sequence		
#154	GST1_U238	GACAAGGGACCAAACCTCCT	
#155	GST1_L639	TTTCATCAAATCGAGCACTTTC	
	Selection of genome-edited transformants		
#61	Cas9U1898	AAGAAAGGCTCAAGACCTACGCTCAT	
#62	Cas9L2260	TCGATCACGATGTTCTCAGGCTTATG	
	Amplicon sequence		
	1st PCR primer sets		
#404	Alb.GST1tar1,2_D50X-2	ACACTCTTTCCCTACACGACGCTCTTCCGATCtGACAAGGGACCAAACCTCCT	
#365	Alb.GST2tar1,2_D70X	TGACTGGAGTTCAGACGTGTGCTCTTCCGATCtCCTTAATCAAATCCCCAACG	
	2nd PCR forward primers		
	D503	AATGATACGGCGACCACCGAGATCTACACCCTATCCTACACTCTTTCCCTACACGACG	CCTATCCT
	D504	AATGATACGGCGACCACCGAGATCTACACGGCTCTGAACACTCTTTCCCTACACGACG	GGCTCTGA
	D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTTCCCTACACGACG	AGGCGAAG
	D506	AATGATACGGCGACCACCGAGATCTACACTAATCTTAACACTCTTTCCCTACACGACG	TAATCTTA
	D507	AATGATACGGCGACCACCGAGATCTACACCAGGACGTACACTCTTTCCCTACACGACG	CAGGACGT
	D508	AATGATACGGCGACCACCGAGATCTACACGTACTGACACACTCTTTCCCTACACGACG	GTACTGAC
	2nd PCR reverse primers		
	D710	CAAGCAGAAGACGGCATACGAGATTTCGCGGAGTGACTGGAGTTCAGACGTGT	TCCGCGAA
	D711	CAAGCAGAAGACGGCATACGAGATGCGCGAGAGTGACTGGAGTTCAGACGTGT	TCTCGCGC
	D712	CAAGCAGAAGACGGCATACGAGATCTATCGCTGTGACTGGAGTTCAGACGTGT	AGCGATAG
	Real Time PCR		
#5	GST1-RT-F	GCGTTGGGGATTTGATTAAG	
#6	GST1-RT-R	TCGAGCACTTTCTTCCAAGC	
#19	CHS-RT-F	ATGGTTGAAGTCCCAAAACTTG	
#20	CHS-RT-R	CCCCATTCTTTAATTGCCTTCT	
#7	CHI-RT-F	TGGAGCTATTCCTGAAGTAAGCA	
#8	CHI-RT-R	TGCAGCTGGTGAAACACCTT	
#21	F3′5′H-RT-F	GCTTAAAGCCATGTTTGAATCG	
#22	F3′5′H-RT-R	CGTTAGCATCTCCGAAATCATC	
#13	DFR-RT-F	CACGAATTTGACGTTGTTGAAG	
#14	DFR-RT-R	AAACACCATGACAGCCATGAAT	
#15	ANS-RT-F	ACCCAGATAGTACCAACCATCG	
#16	ANS-RT-R	GTTCTTTAATTCGCCGTGACAT	
#17	5/3′AT-RT-F	GCAGTCCCTTCTGTTTTACGAC	
#18	5/3′AT-RT-R	AGAGTGAGAGACAAAGAGGCCTTA	
#11	MYB3-RT-F	CACCGGATGAAGAAGATTTGAT	
#12	MYB3-RT-R	ATCAGTCCTTCCTGGGATTCTC	
#9	UBQ-RT-F	GGGAAGCAGTTGGAAGATGG	
#10	UBQ-RT-R	TTCAGAAACCACCACGGAGA	

Supplementary Table S4. Glutathione *S*-transferase proteins used for constructing the phylogenetic tree in Figure 1A

Gene name	**GST class**	**Database**	**Accession Number**	**Plant species**
BZ2	*Tau*	NCBI	NP_001183661.1	*Zea may*
GmHSP26-A	*Tau*	NCBI	NP_001238439.1	*Glycine max*
VvGST1	*Tau*	NCBI	NP_001268177.1	*Vitis vinifera*
CsGSTb	*Tau*	GeneBank	MK431868	*Camellia sinensis*
CsGSTc	*Tau*	GeneBank	MK431869	*Camellia sinensis*
AtGSTU1	*Tau*	NCBI	XP_020885836.1	*Arabidopsis thaliana*
AtGSTU10	*Tau*	NCBI	NP_177598.1	*Arabidopsis thaliana*
AtGSTU11	*Tau*	NCBI	NP_177151.1	*Arabidopsis thaliana*
AtGSTU17	*Tau*	GeneBank	OAP15816.1	*Arabidopsis thaliana*
AtGSTL1	*Lambda*	NCBI	NP_001119157.1	*Arabidopsis thaliana*
AtGSTL2	*Lambda*	NCBI	NP_191064.1	*Arabidopsis thaliana*
AtGSTL3	*Lambda*	NCBI	NP_195899.1	*Arabidopsis thaliana*
GmGSTL3	*Lambda*	NCBI	NP_001304515	*Glycine max*
GST1	*Phi*	This study	LC536038	*Gentiana triflora* x *G. scabra*
AN9	*Phi*	GeneBank	CAA68993.1	*Petunia* x hybrida
RAP	*Phi*	NCBI	XP_004288578	*Fragaria vesca* subsp. *vesca*
VvGST4	*Phi*	NCBI	NP_001267869.1	*Vitis vinifera*
DcGSTF2	*Phi*	GeneBank	BAM21533.1	*Dianthus caryophyllus*
CkmGST3	*Phi*	GeneBank	AB682678.1	*Cyclamen persicum* x *C. purpurascens*
MdGSTF6	*Phi*	NCBI	NP_001315851.1	*Malus domestica*
DcGSTF1	*Phi*	GeneBank	BAM21532.1	*Dianthus caryophyllus*
AcGST1	*Phi*	GeneBank	MK238757.1	*Actinidia chinensis*
CsGSTa	*Phi*	GeneBank	QCQ77495.1	*Camellia sinensis*
AtGSTF2	*Phi*	NCBI	NP_192161.1	*Arabidopsis thaliana*
AtGSTF3	*Phi*	NCBI	NP_178394.1	*Arabidopsis thaliana*
AtGSTF4	*Phi*	NCBI	NP_849581.1	*Arabidopsis thaliana*
AtGSTF5	*Phi*	NCBI	NP_001322019.1	*Arabidopsis thaliana*
AtGSTF6	*Phi*	NCBI	NP_171792.1	*Arabidopsis thaliana*
AtGSTF7	*Phi*	NCBI	NP_171791.1	*Arabidopsis thaliana*
AtGSTF8	*Phi*	NCBI	NP_850479.1	*Arabidopsis thaliana*
AtGSTF9	*Phi*	NCBI	NP_180643.1	*Arabidopsis thaliana*
AtGSTF10	*Phi*	NCBI	NP_180644.1	*Arabidopsis thaliana*
AtGSTF11	*Phi*	NCBI	NP_186969.1	*Arabidopsis thaliana*
AtGSTF12 / TT19	*Phi*	NCBI	NP_197224.1	*Arabidopsis thaliana*
AtGSTF13	*Phi*	NCBI	NP_191835.1	*Arabidopsis thaliana*
AtGSTF14	*Phi*	NCBI	NP_175408.1	*Arabidopsis thaliana*
AtGSTT1	*Theta*	NCBI	NP_198937.1	*Arabidopsis thaliana*
AtGSTT2	*Theta*	NCBI	NP_198940.3	*Arabidopsis thaliana*
AtGSTT3	*Theta*	NCBI	NP_198938.1	*Arabidopsis thaliana*
HsGSTZ1	*Zeta*	NCBI	AAC33591.1	*Homo sapiens*