

Figure S1. Effects of N6022 on *SIGSNOR* gene expression and *SIGSNOR* enzyme activity. (A) Expression of *SIGSNOR*; (B) *SIGSNOR* activity. Error bars represent standard deviations (n=3). Different lowercase letters denote statistically significant distinctions within different treatments according to Duncan's test ($p < 0.05$).

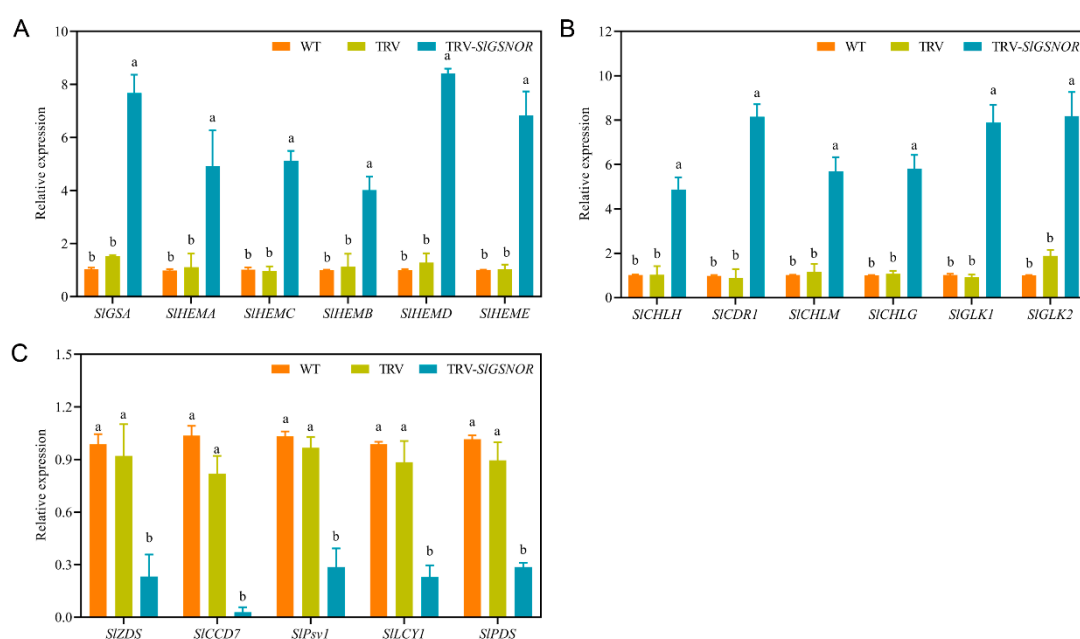


Figure S2. Effect of *SIGSNOR* silencing on pigment metabolism-related gene expressions. (A) Expressions of *SIGSA*, *SIHEMA*, *SIHEMC*, *SIHEMB*, *SIHEMD*, and *SIHEME*; (B) Expressions of *SICHLH*, *SICDR1*, *SICHLM*, *SICHLG*, *SIGLK1*, and *SIGLK2*; (C) Expressions of *SIZDS*, *SICCD7*, *SIPsy1*, *SILCY1*, and *SIPDS*. Error bars represent standard deviations (n=3). Different lowercase letters denote statistically significant distinctions within different treatments according to Duncan's test ($p < 0.05$).

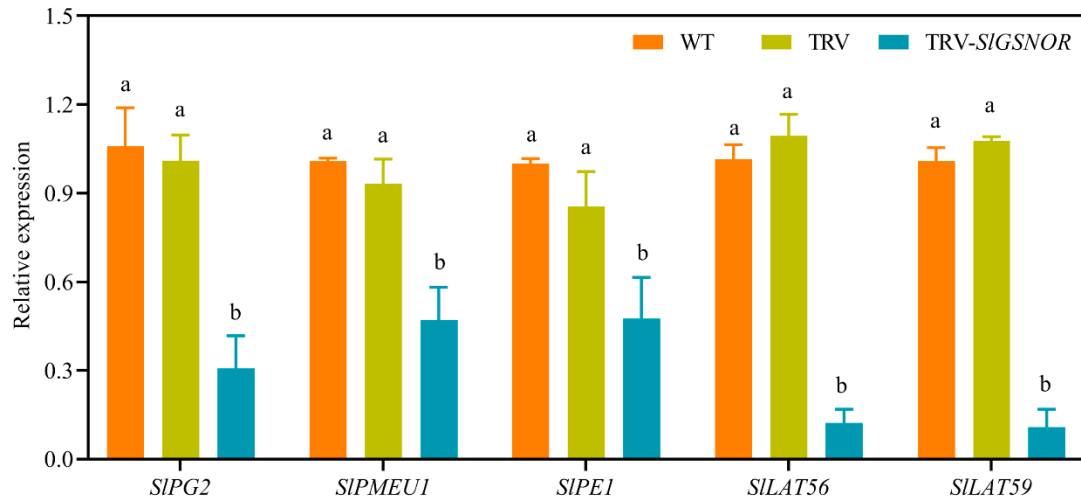


Figure S3. Effect of *SIGSNOR* silencing on hardness and texture related gene expressions. Expressions of *SIPG2*, *SIPMEU1*, *SIPE1*, *SILAT56*, and *SILAT59*. Error bars represent standard deviations (n=3). Different lowercase letters denote statistically significant distinctions within different treatments according to Duncan's test ($p < 0.05$).

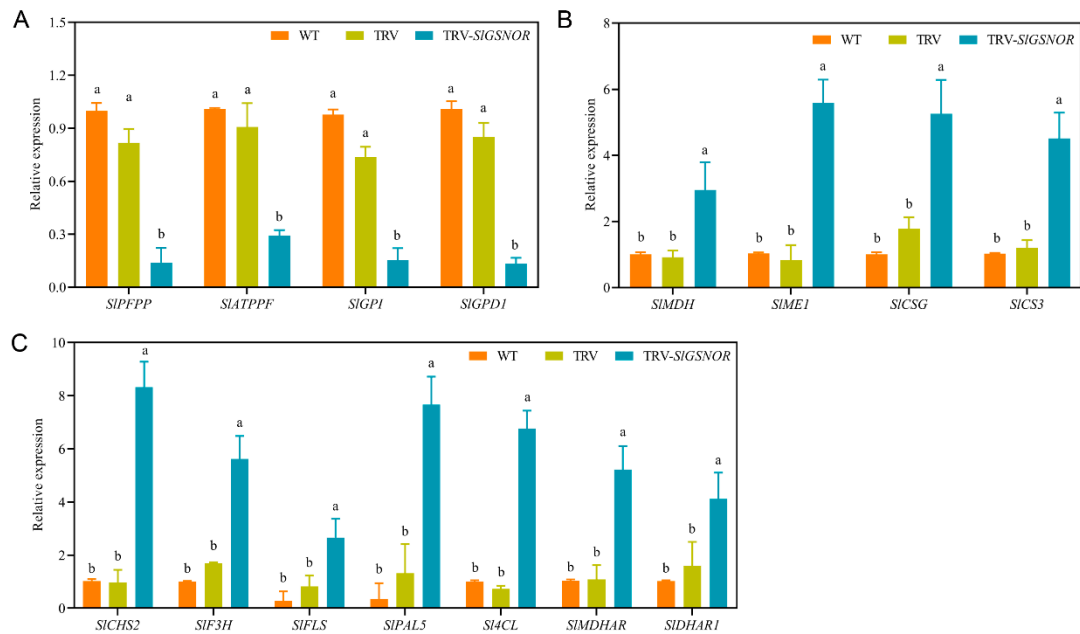


Figure S4. Effect of *SIGSNOR* silencing on nutrient related gene expressions. (A) Expressions of *SIPFPP*, *SIATPPF*, *SIGPI*, and *SIGPD1*; (B) Expressions of *SIMDH*, *SIME1*, *SICSG*, and *SICS3*; (C) Expressions of *SICH2*, *SIF3H*, *SIFLS*, *SIPAL5*, *SI4CL*, *SIMDHAR*, and *SIDHAR1*. Error bars represent standard deviations (n=3). Different lowercase letters denote statistically significant distinctions within different treatments according to Duncan's test ($p < 0.05$).

Table S1. Primers used for qRT-PCR analysis.

Gene name	Gene ID	Primer sequence (5' to 3')	
<i>SIACTIN</i>	Solyc10g080500.2.1	F: AATGAACTTCGTGTGGCTCCAGAG	R: ATGGCAGGGGTGTTGAAGGTTTC
<i>SIGSA</i>	Solyc04g009200.3.1	F: CCATCTCACCGTCGATGCAA	R: TGGCATCAACTCCTTGGCTT
<i>SIHEMA</i>	Solyc04g076870.4.1	F: AACTTCTGCTGCTGATCGATATAC	R: CGACTGGTGCTGTGTGAATG
<i>SIHEMC</i>	Solyc03g098795.1.1	F: ACCTGCAGATCCGTTTCCTG	R: GGCAGCGGCAAGAATAATGG
<i>SIHEMB</i>	Solyc08g069030.4.1	F: ATGGTCTTGTGAAGAGGTC	R: TATCAGTCCTTCAGACTCA
<i>SIHEMD</i>	Solyc04g079320.4.1	F: TACTCGGCTGAACACTTACACAACG	R: TGCTACAGTAACAACGGGAACAGAG
<i>SIHEME</i>	Solyc10g007320.3.1	F: GCTTGTGTTGTGGAATTAGGG	R: AAAATTGCAGCTTGTCTCC
<i>SICHLH</i>	Solyc04g015750.3.1	F: GCTTTGGACCCACAGGCTAT	R: CTGTGCCAACGACTCTCCAT
<i>SICDR1</i>	Solyc08g005830.1.1	F: CCATCGTGATTCTCCTCTTT	R: ACATTACCACCACCTAAACC
<i>SICHLM</i>	Solyc03g118240.4.1	F: ACCTTAAACCCTAATCCCCAAC	R: TGCCGCCACTGAACTACCT
<i>SICHLG</i>	Solyc09g014760.4.1	F: TTCAACTACAACAACCCACTTCG	R: CGTTTCTTGCTTGGCTCCTTT
<i>SIGLK1</i>	Solyc07g053630.4.1	F: GAGAAGTGGAGGCAGCGAGTTG	R: GAGAAGTGGAGGCAGCGAGTTG
<i>SIGLK2</i>	Solyc10g008160.3.1	F: AGCTTATGGCAACTCATGGTCTCAC	R: CGATTGTGGTGGCTCCGCTATAC
<i>SIZDS</i>	Solyc01g097810.3.1	F: CGGTTATTCGGGCTGATTG	R: CCAAATCAGCCCCGAATAACC
<i>SICCD7</i>	Solyc01g090660.3.1	F: CCACGTCCCCAACTCATGAA	R: CTTCCACGACCCGAAGTGAA
<i>SIPsy1</i>	Solyc03g031860.3.1	F: TTATGTTGCTGGTACGGTTGGGTTG	R: CGCTCTCTGTTGTTGCCTTTGATTC
<i>SILCY1</i>	Solyc04g040190.1.1	F: GTTGTGTGGATCTTGCTGTGGTTG	R: AGAGAGTCCTGCTTCAGAACTTGC
<i>SIPDS</i>	Solyc03g123760.3.1	F: TTATCTCGCAAGTGTGGCTATGGTG	R: GAAGATGCCTGCTTTCGGTGATTG
<i>SIPG2</i>	Solyc10g080210.2.1	F: TGGAGGAGGAGGAACATCAATGGC	R: GTTAAGGCCGTTGGTGCATCCC
<i>SIPMEU1</i>	Solyc03g123620.4.1	F: AAGCCGTTTCGACGCAACTACTATG	R: AGTGTCTCGTCCATCGTCTCCAG
<i>SIPe1</i>	Solyc07g064190.2.1	F: CCCGCTAAAGCTATGCCGTTTAC	R: CACATACGCCACGCCAGTAGAC
<i>SILAT56</i>	Solyc03g058910.3.1	F: GCACTCGGGACAGCAATAAA	R: GTCACATCTCCAGCACTTGTC
<i>SILAT59</i>	Solyc03g058890.4.1	F: ATTAGGTTGCACCAGGAGATG	R: GAGGGTTATACCAGCACCTTTAG
<i>SIPFPP</i>	Solyc02g081160.3.1	F: GAGATCCACACGGCAATGTCCAG	R: CCTTCTGCTTCCTCTGATCCAATC
<i>SIATPPF</i>	Solyc08g066100.3.1	F: CACGGCTTCTTGCTTCAACCAATC	R: CTTTGTGAGTGCTGTGCTTATGC
<i>SIGPI</i>	Solyc12g014380.3.1	F: CATTCGCTTCTTGGACTGGGTAG	R: ATGGTGCTGAGAGGAAATGCTGATC
<i>SIGPD1</i>	Solyc02g093830.4.1	F: GCCGTATTCGTGGGTATCTTTCTCG	R: TTCGTGCTCAGATATTGCCTTGTC
<i>SIMDH</i>	Solyc11g007990.2.1	F: ATGAGGTGTTCCAGGATGCAGAATG	R: TCCAATAAGCCAGCTCGTTCCATAC
<i>SIME1</i>	Solyc12g044600.3.1	F: TCCCTCCTCTCATCCTCCCTCTC	R: CCCAGCTCCAGAAGATCCAATCAAG
<i>SICSG</i>	Solyc12g011000.2.1	F: ACAGCATTACAGCAGTTCCACAAGG	R: AAGCATTAGCGGGTGACGAATCTG
<i>SICS3</i>	Solyc01g073740.4.1	F: GTCTTTCTCCGCCTCTGTCTGTTTG	R: GCTCGGCAATATGGGATCGTGAC
<i>SICH52</i>	Solyc05g053550.3.1	F: GCCGACTACCAACTACCAAGC	R: TCCCACCAGCAAAGCAACCTTG
<i>SIF3H</i>	Solyc02g083860.3.1	F: GAGGCAATGGGCTTAGAGAAAGAGG	R: GGTAATGGTTCCTGGATCGGTGTG
<i>SIFLS</i>	Solyc11g013110.2.1	F: ACCTTGAATGAGTCGGTGCTTGTTG	R: GAGCCAGATTGTGGTCAGGTGTTT
<i>SIPAL5</i>	Solyc09g007910.2.1	F: GCCATCTAATCTCACAGCAGGAAGG	R: AAGTTCCGAGCAGTAAGAAGCCATC
<i>SI4CL</i>	Solyc03g117870.3.1	F: ACCGCCTATTGTTCTCGCCATTG	R: GCTCGGACGGCATCTTCAAGTTC
<i>SIMDHAR</i>	Solyc08g081530.3.1	F: TGCTTCTCCACCATAACCCATTGC	R: GCGCGAAAGTTCAACAAGATCAGTG
<i>SIDHAR1</i>	Solyc05g054760.4.1	F: AAGAAGTGGAGTGTGCCTGAAAGC	R: CACGCATACAAGGACACGGTGAG
<i>SIGSNOR</i>	Solyc09g064370.4.1	F: ATGGCTACACAAGGTCAA	R: GTCCTGGATATGTTTGTATGA

Table S2. The complete name, function, pathway, and classification of the detected genes.

Gene name	Complete name	Function	Pathway	Gene classification
<i>SIGSA</i>	glutamate 1-semialdehyde 2,1-aminomutase	enables glutamate-1-semialdehyde 2,1-aminomutase activity	involved_in tetrapyrrole biosynthetic process that related to chlorophyll biosynthesis	chlorophyll biosynthesis-related genes
<i>SIHEMA</i>	glutamyl-tRNA reductase	enables glutamyl-tRNA reductase activity	involved_in tetrapyrrole biosynthetic process that related to chlorophyll biosynthesis	
<i>SIHEMC</i>	hydroxymethylbilane synthase	enables hydroxymethylbilane synthase activity	involved_in chlorophyll biosynthetic process	
<i>SIHEMB</i>	δ -aminolevulinic acid dehydratase	enables porphobilinogen synthase activity	involved_in heme biosynthetic process that related to chlorophyll biosynthesis	
<i>SIHEMD</i>	uroporphyrinogen-III synthase	enables uroporphyrinogen-III synthase activity	involved_in uroporphyrinogen III biosynthetic process that related to chlorophyll biosynthesis	
<i>SIHEME</i>	uroporphyrinogen decarboxylase	enables uroporphyrinogen decarboxylase activity	involved_in porphyrin-containing compound biosynthetic process that related to chlorophyll biosynthesis	
<i>SICHLH</i>	magnesium-chelatase H subunit	enables magnesium chelatase activity	involved_in chlorophyll biosynthetic process	
<i>SICDR1</i>	aspartic proteinase	enables aspartic-type endopeptidase activity	involved_in proteolysis process that related chlorophyll biosynthetic process	
<i>SICHLM</i>	magnesium protoporphyrin IX methyltransferase	enables magnesium protoporphyrin IX methyltransferase activity	involved_in chlorophyll biosynthetic process	
<i>SICHLG</i>	chlorophyll synthase	enables chlorophyll synthetase activity	involved_in chlorophyll biosynthetic process	
<i>SIGLK1</i>	golden1-like protein 1	enables DNA-binding transcription factor activity	involved_in positive regulation of DNA-templated transcription that related to chlorophyll biosynthesis	
<i>SIGLK2</i>	golden1-like protein 2	enables DNA-binding transcription factor activity	involved_in positive regulation of DNA-templated transcription that related to chlorophyll biosynthesis	
<i>SIZDS</i>	ζ -carotene desaturase	enables 9,9'-di-cis- ζ -carotene desaturase activity	involved_in carotenoid biosynthetic process	
<i>SICCD7</i>	carotenoid cleavage dioxygenase 7	enables 9-cis-epoxycarotenoid dioxygenase activity	involved_in carotene catabolic process	
<i>SIPsy1</i>	phytoene synthase 1	enables phytoene synthase activity	involved_in carotenoid biosynthetic process	
<i>SILCY1</i>	lycopene β -cyclase 1	enables oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	involved_in carotenoid biosynthetic process	
<i>SIPDS</i>	phytoene dehydrogenase	enables phytoene dehydrogenase activity	involved_in carotenoid biosynthetic process	

<i>SIPG2</i>	polygalacturonase-2a	enables polygalacturonase activity	involved_in pectin catabolic process	fruit softening-related genes
<i>SIPMEU1</i>	pectin methylesterase	enables pectinesterase activity	involved_in cell wall modification	
<i>SIPE1</i>	pectinesterase 1	enables pectinesterase activity	involved_in cell wall modification	
<i>SILAT56</i>	pectate lyase P56	enables pectate lyase activity	involved_in cell wall degradation and fruit softening	
<i>SILAT59</i>	pectate lyase P59	enables pectate lyase activity	involved_in cell wall degradation and fruit softening	
<i>SIPFPP</i>	pyrophosphate-fructose 6-phosphate 1-phosphotransferase subunit β -like	enables diphosphate-fructose-6-phosphate 1-phosphotransferase activity	involved_in fructose 6-phosphate metabolic process	glucose and fructose metabolism-related genes
<i>SIATPPF</i>	ATP-dependent 6-phosphofructokinase 6	enables 6-phosphofructokinase activity	involved_in fructose 6-phosphate metabolic process	
<i>SIGPI</i>	glucose-6-phosphate isomerase	enables glucose-6-phosphate isomerase activity	involved_in glucose 6-phosphate metabolic process	
<i>SIGPD1</i>	glucose-6-phosphate 1-dehydrogenase 1	enables glucose-6-phosphate dehydrogenase activity	involved_in glucose metabolic process	
<i>SIMDH</i>	malate dehydrogenase	enables L-malate dehydrogenase activity	involved_in malate metabolic process	
<i>SIME1</i>	NADP-malic enzyme	enables malate dehydrogenase (decarboxylating) (NAD ⁺) activity	involved_in malate metabolic process	
<i>SICSG</i>	citrate synthase, glyoxysomal	enables citrate (Si)-synthase activity	involved_in carbohydrate metabolic process	
<i>SICS3</i>	citrate synthase 3	enables citrate (Si)-synthase activity	involved_in carbohydrate metabolic process	
<i>SICHS2</i>	chalcone synthase	enables chalcone synthase activity	involved_in flavonoid metabolism process	flavonoid metabolism-related genes
<i>SIF3H</i>	flavanone 3-hydroxylase	enables flavanone 3-hydroxylase activity	involved_in flavonoid metabolism process	
<i>SIFLS</i>	flavonol synthase	enables flavonol synthase activity	involved_in flavonoid metabolism process	
<i>SIPAL5</i>	phenylalanine ammonia-lyase 5	enables ammonia-lyase activity	involved_in phenol metabolism process	phenol metabolism-related genes
<i>SI4CL</i>	4-coumarate-CoA ligase	enables CoA-ligase activity	involved_in phenol metabolism process	
<i>SIMDHAR</i>	monodehydroascorbate reductase	enables oxidoreductase activity, acting on NAD(P)H	involved_in ascorbic acid metabolism process	ascorbic acid metabolism-related genes
<i>SIDHAR1</i>	dehydroascorbate reductase 1	enables glutathione dehydrogenase (ascorbate) activity	involved_in ascorbate glutathione cycle	
<i>SIGSNOR</i>	S-nitrosoglutathione reductase	enables S-nitrosoglutathione reductase activity	involved_in reduction of protein S-nitrosylation	protein S-nitrosylation reduction-related gene

