

## SUPPLEMENTARY MATERIAL

**Supplementary Table S1.** Transcription data of *SIMS1* and *SIMS2* gene under 0, 1, 3 days of hydrogen sulfide (H<sub>2</sub>S) treatment (0.6 mM NaHS as H<sub>2</sub>S donor).

Gene	CK 0 d	H <sub>2</sub> S 1 d	CK 1 d	H <sub>2</sub> S 3 d	CK 3d
SIMS1	321.64	247.5	328.28	129.3	323.67
SIMS2	21.68	20.37	17.06	14.88	20.85

**Supplementary Table S2.** Primers for VIGS-*SIMSI* and *SIMSI*-pSAK277 vectors.

Gene	Primers	Sequences	Amplicon size (bp)
Solyc10g081510.1.1	<i>SIMSI</i> -277-F	ACTAGTGGATCCAAAGAATTCATGGC ATCTCATGTTGTTGGATAT	2298
	<i>SIMSI</i> -277-R	TCATTAAAGCAGGACTCTAGATCACTT GGCGCTGGCGAG	
	VIGS- <i>SIMSI</i> - F	GTGAGTAAGGTTACCGAATTCATGTG TGAAGCCACCAATCATCT	400
	VIGS- <i>SIMSI</i> - R	CGTGAGCTCGGTACCGGATCCGTTGA AGTTGGAGTAGCACATGTGA	
	GFP- <i>SIMSI</i> -F	GAGAACACGGGGGACTCTAGAATGG CATCTCATGTTGTTGG	2298
	GFP- <i>SIMSI</i> -R	GCCCTTGCTCACCATGGATCCCTTGGC GCTGGCGAGC	

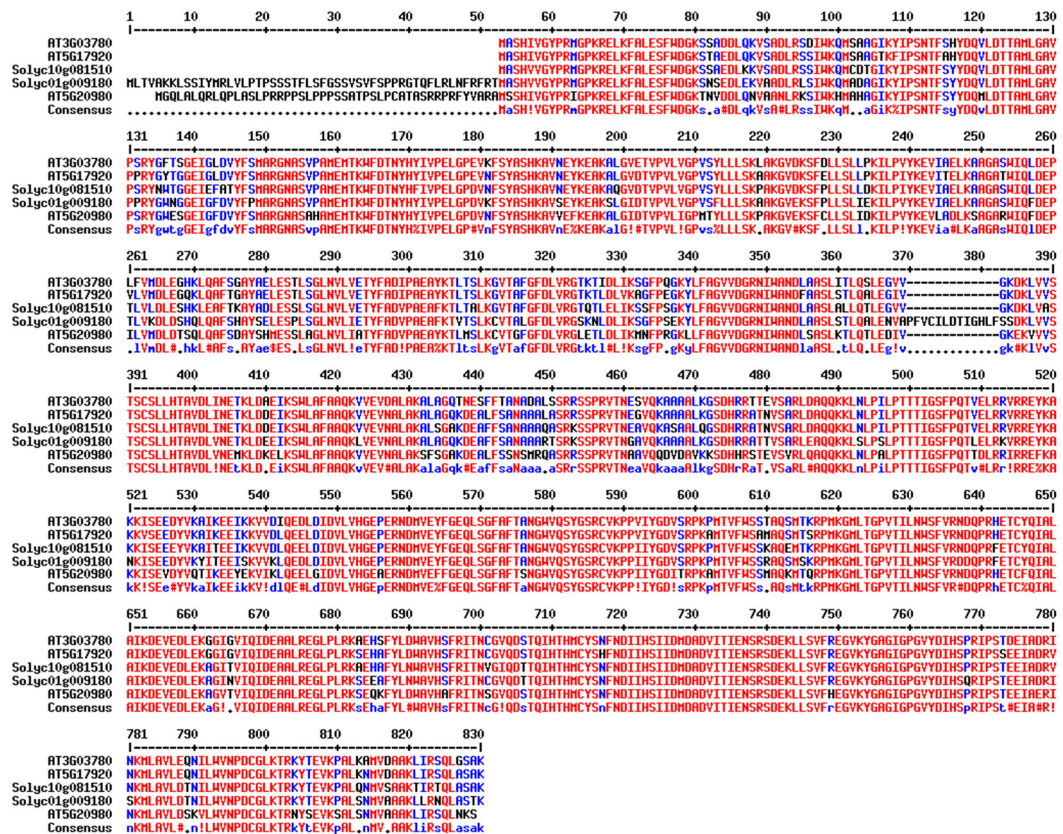
**Supplementary Table S3.** Primers used for quantitative RT-PCR.

Primers	Sequence	Gene ID	Amplicon size (bp)
<i>SISGR1</i> (forward)	GGCTATCTCCCAAACCATCAA	Solyc08g080090	80
<i>SISGR1</i> (reverse)	ACTCTGCAACAACCTTCATCTCT		
<i>SIPPH</i> (forward)	CAGATGTCGTGGATGGGAAA	Solyc01g088090	101
<i>SIPPH</i> (reverse)	GCCTTTAGCTTCACTTGGTAAAC		
<i>SIPAO</i> (forward)	CCTCATCGTCTTGCTCCTTTAT	Solyc11g066440	119
<i>SIPAO</i> (reverse)	GCAGCTTGAGGTATCCTTGT		
<i>SINYC1</i> (forward)	GATCAGGGAAGAGCACTGTATG	Solyc07g024000	128
<i>SINYC1</i> (reverse)	GAGAACACAGACACCCAAGTAT		
<i>SIPSY1</i> (forward)	GAAGATGCCAGAAGAGGAAGAG	Solyc03g031860	93
<i>SIPSY1</i> (reverse)	GGTCACCCTTCCAGCAAATA		
<i>SIPDS</i> (forward)	CAAGACCAGAGCTGGACAATAC	Solyc03g123760	119
<i>SIPDS</i> (reverse)	CAAACCTGCACCAGCAATAAC		
<i>SIZDS</i> (forward)	GATTGGTTCCTCAGAAGTGGAG	Solyc01g097810	101
<i>SIZDS</i> (reverse)	CCAGCCATTGTAGCGTAGTT		
<i>SLACO1</i> (forward)	CCATGTCCTAAGCCCGATT	NM_001247095. 2	94
<i>SLACO1</i> (reverse)	GGCCACTCACTTTGTCATCT		
<i>SLACO3</i> (forward)	GCGCCATCTTCCTACTTCTAAT	Solyc07g049550	103
<i>SLACO3</i> (reverse)	CTCAGCCAACTTCTCCAATCT		

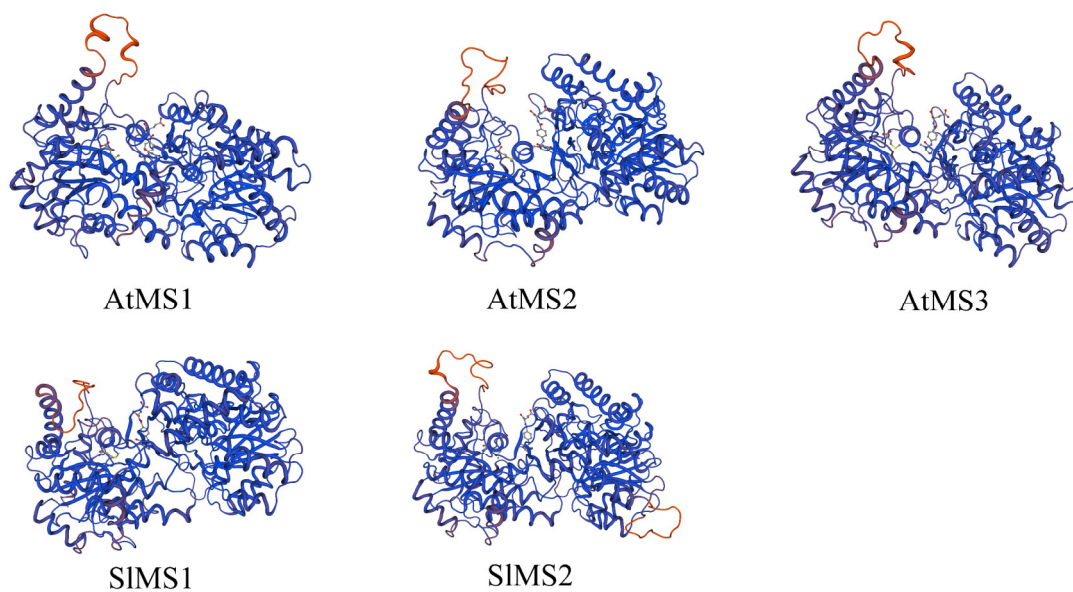
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<i>SLACS2</i> (forward)	GAGGTTCGTAGGTGTTGAGAAA	Solyc01g095080	147
<i>SLACS2</i> (reverse)	GGAGGAATAGGTGACGAAAGTG		
<i>SLPG</i> (forward)	TTGGAGGAGGAGGAACTATCA	Solyc10g080210	83
<i>SLPG</i> (reverse)	CCTGCATGGCAGTGATTTATTT		
<i>SICEL2</i> (forward)	CTGCTGTTTGGCCTTTCTATTG	Solyc09g010210	94
<i>SICEL2</i> (reverse)	TGCCTTCTTCTTGTTGCTTTATG		
<i>SLEXP</i> (forward)	CCGACGATTGGACACCTAAA GGTCCTCCTTAATCAAAGGACAT	Solyc06g051800	105
<i>SLEXP</i> (reverse)	A		
<i>SITBG4</i> (forward)	GCCATTGGCCTGGATACATA	Solyc12g008840	101
<i>SITBG4</i> (reverse)	AGAAGGTTGTCCGCAGTTAG		
<i>SIXTH5</i> (forward)	AGGATTCAGCCATCTCTTTGG	Solyc01g081060	101
<i>SIXTH5</i> (reverse)	ACTTGAACCCTGAACCTGTG		
<i>SlTubulin</i> (forward)	TAGAGCCTGGTACGATGGATAG	Solyc08g006890	134
<i>SlTubulin</i> (reverse)	CAACTCAGCGCCTTCAGTATAA		

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**Supplementary Figure S1.** Amino acid sequence alignment of methionine synthases in Arabidopsis and tomato.



**Supplementary Figure S2.** Tertiary structures of methionine synthases in Arabidopsis and tomato.