Gene	Homology											
Yeast	100%											
Human	47.5%	100%										
Chlamy	39.2%	46.5%	100%									
OsSQS1	41.7%	48.1%	54.8%	100%								
AtSQS1	41.7%	45.9%	54.8%	72.6%	100%							
GmSQS	43.0%	48.1%	56.7%	79.0%	81.8%	100%						
MtSQS	42.0%	48.4%	56.7%	77.1%	79.0%	91.4%	100%					
MsSQS	41.4%	48.7%	57.0%	76.8%	79.0%	92.0%	97.8%	100%				

Table S1. Sequence homology of SQS proteins in the indicated species.

Primer name	Sequence	Application					
MsSQS-f	5'-ATGGGAAGywTrArwrCGATTTTG-3'	ORF					
MsSQS-r	5'- TTAkywmTTryrwyGATTkGCwkwGAGA -3'	amplification					
SQS-PE-f	5'-ATGGGAAGTATAAAAGCGATTTTG-3'	Prokomuotia					
SQS-PE-r	5'-GTTATTGTAACGGTTGGCAGAGAG-3'						
SQS-PE- Δ C30-r	5'-CCTCAAAACGTAAGATTTCCTTTTGG-3'	expression					
SQS-pA7-f	5'-CC <u>CTCGAG</u> ATGGGAAGTATAAAAGCGATTTTGA-3'	subcellular					
SQS-pA7-r	5'-GC <u>GTCGAC</u> GTTATTGTAACGGTTGGCAGAGAGA-3'	localization					
SQS-QPCR-f	5'-CTTCGGTCTTGTTATTCAGCAGC-3'	PCR/aRT PCR					
SQS-QPCR-r	5'-CTTGTATCATCCTCAACGGTGTC-3'	I CMQKI-I CK					
Actin-f	5'-CAAAAGATGGCAGATGCTGAGGAT-3'	house-keeping					
Actin-r	5'-CATGACACCAGTATGACGAGGTCG-3'	gene					
SQS-f	5'-GC <u>TCTAGA</u> ATGGGAAGTATAAAAGCGATTTTGA-3'	overexpression					
SQS-r	5'-CG <u>GGATCC</u> TTAGTTATTGTAACGGTTGGCAGAG-3'	overexpression					
35S-f	5'-ACTATCCTTCGCAAGACCCTTCCTC-3'	Identification of					
SQS-r	5'-CG <u>GGATCC</u> TTAGTTATTGTAACGGTTGGCAGAG-3'	transgenic lines					
gSQS-f1	5'-CTGAAAATCGCGGCGAGAAA-3'						
gSQS-r1	5'-AGCTTTGATAAACCCAGCCCA-3'	Amplification of					
gSQS-f2	5'-GGACTTGTTGGGCTGGGTTT-3'	genomic					
gSQS-r2	5'-TTGTAACGGTTGGCAGAGAG-3'	sequence of					
5′ -R1	5'-GCTGCTGAATAACAAGACCGA-3'	MsSQS					
5 -K2							
g-degenerate	5'-NTCGA(G/C)T(A/T)T(G/C)G(A/T)GAA-3'						
3'-t1	5'-GCITAICICICIGCCAACCGT-3'						

Table S2. Sequence of primers used in this study.

Note: restriction site of Xho I, Sal I, Xba I and Bam H I was underlined.

Species	gene ID	cDNA (bp)	a.a	kDa	pI
M. Sativa	MsSQS	1439	413	47.25	7.53
M. truncatula	Mt4g071520	2316	413	47.08	7.71
A. thaliana	At4g34640	1902	410	47.14	6.59
	At3g34650	1656	413	47.18	8.01
G. max	Gm12g038200	1851	413	47.11	6.57
	Gm11g112000	1898	413	47.01	6.58
N. tabacum	A4A49_02417	1995	411	46.98	7.86
	A4A49_25438	1353	411	47.06	8.40
	A4A49_10777	1281	403	46.04	7.25
	A4A49_12750	1285	405	47.34	7.25
P. trichocarpa	Pt009g123100v3	2309	413	47.31	7.29
	Pt004g161200v3	1793	476	54.69	8.88
O. sativa	Os03g0805100	1310	403	46.10	7.86
	Os07g0200700	1533	410	46.78	6.97
Z. Mays	Zm00001d013048	1398	401	46.04	6.77
	Zm00001d034516	1417	403	46.18	7.06
T. aestivum	Ta5A02g454500	1706	404	46.35	7.04
	Ta5B02g464600	2123	404	46.49	7.04
	Ta5D02g465000	2327	404	46.38	6.76
C. reinhardt	Cr03g175250v5	2445	461	52.04	6.77
H. sapiens	AAP36671.1	2467	417	48.10	6.52
S. Cerevisiae	ACD03847.1	1350	444	51.73	5.74
Average		1774	416	47.68	7.20

Table S3. Protein property of SQS enzymes in the 12 indicated species.

Note: information on gene accession number is listed in the legend of Figure 1b.

Gene ID	alpha helix	random coil	beta turn	extended strand
MsSQS	69.25%	22.52%	4.12%	4.12%
Mt4g071520	66.34%	22.52%	4.36%	6.78%
At4g34640	70.70%	18.03%	4.23%	7.04%
At3g34650	68.97%	20.00%	4.48%	6.55%
Gm12g038200	67.31%	24.46%	3.15%	5.08%
Gm11g112000	69.49%	22.28%	3.87%	4.36%
A4A49_02417	69.10%	20.68%	3.65%	6.57%
A4A49_25438	68.61%	21.65%	3.65%	6.08%
A4A49_10777	69.73%	23.33%	3.47%	3.47%
A4A49_12750	66.17%	21.98%	3.46%	8.40%
Os03g0805100	70.22%	19.11%	5.21%	5.46%
Os07g0200700	70.00%	20.49%	4.39%	5.12%
Zm00001d013048	67.78%	24.92%	2.74%	4.56%
Zm00001d034516	68.73%	23.82%	3.97%	3.47%
Pt009g123100v3	68.52%	22.03%	3.63%	5.81%
Ta5A02g454500	71.04%	20.05%	3.71%	5.20%
Ta5B02g464600	67.82%	21.78%	4.21%	6.19%
Ta5D02g465000	67.82%	22.03%	4.46%	5.69%
AAP36671.1	67.87%	24.22%	3.12%	4.80%
ACD03847.1	67.79%	24.10%	2.70%	5.41%
Average	68.66%	22.00%	3.83%	5.51%

Table S4. Prediction of the secondary structure of SQS in the indicated species.

information on gene accession number is listed in the legend of Figure 1b.

	GCTTATTCGTAGAAACAAAAG												AAG													
1	ATG	GGA	AGT	ATA	AAA	GCG	ATT	TTG	AAG	AAT	CCA	GAT	GAT	TTT	TTT	CCA	TTA	CTT	AAG	CTG	AAA	ATC	GCG	GCG	AGA	AAC
1	м	G	S	I	к	A	I	L	ĸ	N	P	D	D	F	F	P	L	L	ĸ	L	к	I	A	A	R	N
79	GCCGAGAAGCAGATCCCACCGGAGCCGCATTGGGGATTCTGTTACTCTATGCTTCATAAGGTTTCTAGAAGCTTCGGT																									
27	A	Е	ĸ	Q	I	P	P	Е	P	н	W	G	F	С	Y	s	м	L	н	ĸ	v	s	R	s	F	G
157	CTT	GTT	ATT	CAG	CAG	СТТ	GGT	ccc	GAG	CTT	CGT	GAT	GCT	GTT	TGC	АТА	TTC	TAT	TTG	GTT	СТТ	CGT	GCT	CTT	GAC	ACC
53	L	v	I	Q	Q	L	G	P	Е	L	R	D	A	v	С	I	F	Y	L	v	L	R	A	L	D	Т
235	GTT	GAG	GAT	GAT	ACA	AGC	АТА	GAA	ACA	GAT	GTC	AAG	GTT	ccc	АТА	CTA	ATG	GAT	ттт	CAT	CGT	CAC	ATC	TAT	GAT	ААТ
79	v	Е	D	D	т	S	I	Е	т	D	v	ĸ	v	P	I	L	М	D	F	н	R	H	I	Y	D	N
313	GAT	TGG	CAC	ттт	GGG	TGT	GGC	ACG	ААА	GAG	TAC	AAA	GTT	ста	ATG	GAC	CAG	TTC	САТ	САТ	GTT	TCA	AAG	GCT	ттт	CTG
105	D	W	H	F	G	С	G	т	ĸ	Е	Y	ĸ	v	L	М	D	Q	F	н	н	v	S	ĸ	A	F	L
391	GAA	СТТ	GGA	AAG	AAC	ТАТ	CAG	GAT	GCA	ATC	GAG	GAC	ATT	ACG	ААА	AGA	ATG	GGT	GCT	GGA	ATG	GCG		гтс	АТТ	TGC
131	Е	L	G	ĸ	N	Y	Q	D	A	I	Е	D	I	Т	ĸ	R	м	G	A	G	М	A	ĸ	F	I	С
469	469 ΑΔGGAGGTAGAAACAATTGATGACTACGATGAATATTGTCACTATGTGGCTGGACTTGTTGGGCTGGGCTGGGCTTGATGAAG																									
157	K	Е	v	Е	т	I	D	D	Y	D	Е	Y	С	H	Y	v	A	G	L	v	G	L	G	L	S	ĸ
547	CTT	ттс	TAC	GCA	тст	GGT	ААА	GAA	GAT	CTG	GCT	ACA	GAC	ААА	СТТ	TCA	AAC	TCA	ATG	GGT	TTG	TTT	СТТ	CAG	AAA	ACC
183	L	F	Y	A	S	G	ĸ	Е	D	L	A	т	D	ĸ	L	S	N	S	М	G	L	F	L	Q	ĸ	Т
625	AAC	АТТ	АТТ	CGA	GAT	ТАТ	стс	GAA	GAC	ATC	ААТ	GAG	АТА	CCA	AAG	тса	CGC	ATG	ттт	TGG	CCA	CGG	CAG	ATC	TGG	AGT
209	N	I	I	R	D	Y	L	E	D	I	N	E	I	P	ĸ	S	R	м	F	W	P	R	Q	I	W	S
703	AAA	TAT	GTT	ATC	AAA	CTT	GAG	GAC	TTG	AAA	TAT	GAG	GAA	AAC	TCC	GTT.	AAG	GCT	GTG	CAA	TGC	TTA	AAT	GAC	ATG	ATC
235	ĸ	Y	v	I	ĸ	L	Е	D	L	ĸ	Y	Е	Е	N	S	v	ĸ	A	v	Q	С	L	N	D	м	I
781	ACT	ААТ	GCT	TTG	CTG	CAT	GCT	GAA	GAT	TGC	TTA	CAA	TAC	ATG	TCT	GCA	TTA	CGA	GAC	ccc	TCT	AAT	TTT	CGC	TTT	TGT
261	т	N	A	L	L	н	A	Е	D	С	L	Q	Y	М	S	A	L	R	D	P	S	N	F	R	F	С
859	GCT	ATT	CCT	CAG	GTA	ATG	GCA	ATT	GGA	ACA	CTT	GCA	ATG	TGC	TAT	AAC	AAC	ATT	GGT	GTT	TTC	AGA	GGA	GTA	GTT.	AAA
287	A	I	P	Q	v	м	A	I	G	т	L	Α	м	с	Y	N	N	I	G	v	F	R	G	v	v	ĸ
937	ATG	AGG	CGA	GGT	СТА	ACT	GCC	AAA	GTG	ATT	GAC	CGA	ACA	AAG	ACT	ATG	GCT	GAT	GTC	TAT	GGT	GCT	TTC	TTT(GAT	TTT
313	м	R	R	G	L	т	A	ĸ	v	I	D	R	т	ĸ	т	м	Α	D	v	Y	G	A	F	F	D	F
1015	GCT	TCC	ATG	TTG	GAG	TCC	AAG	GTT	GAC	AAA	AAT	GAT	CCA	AAT	GCA	ACA	AAA	ACA	TCG	AGC	AGG	CTG	GAA	GCT	ATA	CAG
339	A	S	м	L	Е	S	ĸ	v	D	ĸ	N	D	P	N	A	т	ĸ	т	S	S	R	L	Е	A	I	Q
1093	AAA	ACT	TGC	AGA	GAA	TCT	GGT	CTC	CTA	ACC	AAA	AGG.	AAA	TCT	TAC	GTT	TTG	AGG	AAT	GAG	AGC	GCA	TAT	GGC	TCT.	ACC
365	ĸ	т	С	R	Е	S	G	L	L	т	ĸ	R	ĸ	s	Y	v	L	R	N	Е	S	A	Y	G	S	Т
1171	ATG	ATT	CTC	TTA	CTG	GTC.	ATC	TTG	TTG	TCC	ATC	TTT	TTT	GCT	TAT	CTC	TCT	GCC.	AAC	CGT	TAC	AAT	AAC	TAA		
391	м	I	Г	Г	Г	v	I	Г	Г	s	I	F	F	Α	Y	Г	S	Α	N	R	Y	N	N	*		
	TGT	AG	TCT	TTA	TAP	TTT	TGT	TTT	TGG	TAA	ACA	GTG:	TTT1	GA	ATG	CATO	CTA	GAA	TGT	GTG	AGA	AAT	TAA	CAA	AAT	ACT
	AAG' CAGI	TTA!	ICCI AGTO	GT	CTGF AGCF	ATGA AT	LAAI	AGT	TCA	ATT	CTT	TTT	rgt <i>i</i>	AGC	AAC	GGG!	[AT]	TAT	GC	CTTO	CAC	AAA	CATO	GA	'AG(CAA

Figure S1. cDNA sequence of *SQS* cloned from alfalfa and the deduced protein sequence. The ORF was numbered and * represents the stop code (TAA).

GT CRAFT IT GET ET I GGCAGCCGGET A I GET ET GLAGAGAGGACCCI GCAGCAGGGAGGGCE ET I T I CT I CT I GET CG T GAAGGGAGGAGGGAGGCAGGAGGAGGAGGAGGAGGAGGAG	180 360 540
TET ACTCIATEGETICA FARGETICE FARMAGETICEETETTATICAGGAGETIGE CCCCCAGE TIGETGATEGETETTATICATETTICATECETATATICTATITETTITATECTTITETTITE	720
BETCITESTERICITEMANCESTE BETCITESTERICITEMANCESTE BETCITESTERICITEMANCESTE	900
ΤΓΟΤΙΑΑΤΙCΑΑΤΙΤΑΛΑΛΕΛΘΙΤΙΘΑΤΙΤΙΑΤΘΙΘΑΘΕΙΤΙΑΕΙΘΑΘΕΙΤΙΑΕΙΘΑCABATIGIACAAABAAATGATITIGATATIAABAAATTAABAATTAABAATTATTAABAAATCITITITAAAAAACABAABTIGITITGIEITTETTATGGAAATGAAAATGAAATGAAAT	1080
	1260
GGAAAATTTTGGCTTTGAAATAGTGTGATTGATGTAACTCAGACCACTTGTTAGAAACTATAGCCAATTGCAGGCAG	1440
CCATTCTTCAAATTGAGAGGATCTAATGTTTTGTAACTCTTCTTGTTTTGGCAGAGGATGATACAAGATGTTGCATAGATGTCAAGATGTCAAGATTTTCATGTCGACAACTATGATAGATGATGGCATTGGCAGTTTGGCACATCTATGGTAGGATGATAGATGGCAGTTTGGCAGTTTGGCACATCATGGCAGTTGGCACATCATGGCAGTTGGCACATCATGGCAGTTGGCAGTTGGCAGTTGGCAGTTGGCAGTTGGCAGTTGGCAGTGATGATGGCAGTTGGCAGTTGGCAGTTGGCAGTTGGCAGTGATGGCAGTGAGGGAGG	1620
	1800
TACACATECCTCAAACTTTACTEATECTEATECTEATECTATCTTTTTATETAACTACGTEEGEAGEAAAAGTACAAAGTTCTATCGEACAACTTCCTTTACCTTACC	1980
ATTCCGTGATACATGTGGTTTATGACTGCTGTTTATTCCAAAAATCTACCCATTATTGTTTAGGGGAGTGGGTGATGCTAGGGTGGTAATGCAAAATTTGGATATTGGATATTGGATATTGGATATGGATGGTGG	2160
TGATTATTGACTACAGAT TGATGGATCACGATGGGGGCTT TGCATCATGATTGTTTATAATATTGGTTTCTCTATTATATTTTTTCATCTGATGCCATGGACTGCGAATGCCTAGTTAAATCCTTGGTAGGATTTAGGTAAAAAAAA	2340
TIAICIAAIGITICI686161TIAIGITGAAAITAAA661ATTAACAACTAAIG16661CITIG16A1616CIA161T6ACTAIA6GITTACCCCCTITAG1A6CTITICAIG6GIGIAIGTAGATTAGACTAIGACTGIGCACTCIAIGAAAAAATTAAAIGCIG6CCAAICA	2520
TCTTTGCAGGTATCARGEATGTAGGAGATTAGGAATGAGTGCTGGTAATGGGTGGTAGTTGAGGGGAGTGGTAAGTTGTTGGGTAGGATGGTGG	2700
GITTETTATTCTTTTGATECTETEECTTTCTAGTAGTTTGGATTTATGATTTAGTGGBAGGGCAATATAATCAAAAGTCGTGAGGACAAACAGTTATGTTGTGCTACTGAAGTGCAACATTTTGATACTATACTACTATCAATGCGCTCTATTCTAATTC	2880
CABABATCTATCCTTCACAB66ATTICT6CCAT6TTTTEGAATTAB6AA6ATCATCTEGATTTATGCCAA6AATTTTATCTAATTT6CCA6 TA6AAACAGTT6ATCACAAT6ATACAATAGTAGCCT6GCT6GACTT6TG66CT6GACTT6TG66CT6GGCT6GG	3060
TGG YAAGAAGA IC IGGC YAAGAAACT IT CAAAT TCAA TGGA TI IG IT IC IT IC IT CAG TI GG YAAGAAGA IC IGGC YAAGAAACT IT CAAAGAAT TGA TGGA GAAGAAT I GA TGGA GAAGAAT TG TGGG TGG	3240
GIOANTEGET TETT OF TOAGETA TOATEA TETA ATA ATA ATA ATA ATA ATA ATA AGOAAAABAA TA TECTOAGAATA TT TACT TAGETCOAGITA ATT TEGACATAAAAGOAACATT AT TGAGATTA AT TGAGAATTA AT TGAGAATTA AT TGAGATTA AT TGAGAATTA AT TGAGAATTA AT TGAGATTA AT TGAGAATTA AT TGAGATTA AT TGAGATTA AT TGAGATTA AT TGAGATTA AT TGAGATTA AT TGAGATTA AT TGAGAATTA AT TGAGATTA AT TGAGAATTA AT	3420
BOARAICIGEARIANATATEITATCANACITEREEITIGECICTATAAGAATTICTACTIATICCAATCIGAATCACITITICICCCCCATTIGATGATGITAGATAATTIGTAAAAATTGABGATTIGATGGTGAAACAGCITICITIGCGTACIGTTATGITATGATGATGITAGATGATGATAGATTGAAGGATTIGATGGTGAAACAGCITICITIGCGTACIGTTATGITATGATCACCACGAG	3600
TREACT IT I GALLANTER CALLANTER	3780
TAGATEICIGOATTAGEAGACOCCICIAATTICEGUITTEIGUITTEIGUITTEIGUITTEIGUITTEIGUITTEIGUITTEAUTTAATTACTAACTEICAIUITAACTEICAIUITAACTEICAIUITAAATUGUAUGUITTEIGU	3960
TGCCTAEATTTATAAGTGCTCAATCAACAGCGGTTTCCAATTCAAGTTCAAATATATGAAACAACATTATATTATTATCCGTTCTTTAAGTTCAATGCGCTAAAAAATGTGGGTAGTAACAGTGTCGATATACAAATCTTGGGTAGCGCAANTGTTTAACAAAATGTACAGAT	4140
GNACATTAAATAAAANIACITGGTTTTAATTTTCATATTTTAATGTATGTGAATATGAGATAGAT	4320
TTAAACAACAAAATATTTCATGCTTAGAAGTACTAACATTTGGCCAATTATCATGGAGTGGGAATATAAAAATCATGTGATTCCATTTTTTTGGCTTGATAAAAATAAAATCAACACCAACGAAGGTTTGGATCTAGGGGAAGGGGCTAGACCCCAAAGTGGGCGAACCAAAGT	4500
TIGACTCCTARCTGEBAAGGTTACCCACATTTAGTECTCEGECATECCTCAAAAAGGATTACCTCCAGTTGAGGBAACGTATEGBAAACCAAANAATAAATAAATAAATTAAATCGCCCTATGAAAGCAAGCAA	4680
TATCCAACTAATTTTGTGGATCTTATTTCCTTAATACATTTAGACAGTTAATTTTTTGGTTAGTTTTTTCTTTTCTTTC	4860
	5040
AAGGAATGTGAGTATGAATAGTGAATTACTGGAATTTTCTATGTTACTTTATGCTAAATCGATGTTCTTAAAACTAGCATCGTGGGACCCCCTTCGTTGCACTTTTGTACAGTGGTCCTGCCCAATGTCATTGAACTATTTTGTTGAGTTCTCTAATGGATGTCTAGAACTAGCATGTCAAT	5220
ATATTGAAAGCTAAATAGTGGACATTACTAGTTTTGGGACCTACTAATAATACTCGATCTAAATTCAATAGTTTAGGCATGTATATAGTTTCCTCTCATTTGAAAATATATGGTTTTATCGGGGATTCCTAATGGACTAGCTGGTTGCTGTTCTTGCTCATTGTTACG	5400
	5580
AAACAAABTATGATTAGATTTGTAAAAAGAATGTGGATGCTACTCGTGTTTTTACACCTGATGATGCTCCTATTTTATATTCTATAGTCAAAGCAAACACATTAATTGTTAGTGGBGTGAAGAAAAAAGTTGATGCATAGACTCCCTTGCATATGAATTTTCATGTATTTATAGGTGTTGTGTA	5760
TABGCATTITICITBAAGCACTGIAGCAGCAATACTGCAATGATACCEGETCACCGGCCTTGACTAATTAAGCCAGCIACAGCCITGEGETTIEGGAATTCITGTTGTTGTTGTTGTTGTTGTTGAATGCTAGGTATTTGCAAGCATGGTTACCEGGTATTCGTGTTGAAGAATCATA	5940
BCTITITAABBCICTBIBATTABITABBAAAACAACATCITABICABICTCTEBTTITTBCTCATCAATBACTIBBCTTACACAABIBCACABAAAAATTTCCTBBCTBATGEGATACCBATTBTTATTTTCCCAACABAACATTTAATAACTCTTAATTBTCACTABICACCACC	6120
CITICATICCETACCICCATAATTIATAAAASCIGECITITICCIACIAAAASEATICATCATITICCACIETAAEGAAAAAACATEGAACAAAAAACATEGAECABECTEGAABETATACABAAAAACITEGABAAAAATICIGETCICCIAACGAAAAACATEGAACAABEATATACABEAAAAACITEGABAAAAATICIGETCICCIAACGAAAAAACATEGAACAABECTAACABEATATACABAAAAACITEGABAAAATICIGETCICCIAACGAAAAAACATEGABCABECTAACABEATATACABAAAAACITEGABCAABAATICIGETCICCIAACGAAAAAACATEGABCAAAAAACATEGABCABBCTEGAABETATACABAAAAACITEGABCAABAATICIGETCICCIAACGAAAAAACATEGABCAAAAAACATEGABCABBCTEGAABETATACABBAAAACITEGABCAABAAACATEGABCABBCTEGAABETATACABBAAAACITEGABCAABAAAATEGAACAAAAAACATEGABCAABAATEGAACAABAAACATEGABCABBCTEGAABETATACABBAAAACITEGABCAABAAACITEGABCAABAAACATEGABCABBCTEGAABETATACABBAAAACITEGABCAABAAACITEGABCAABAAAATEGABCAAAAAACATEGABCAABAAACATEGABCABBCTEGAABATICATEGABCAABAAAATEGABCAAAAAACATEGABCAAAAAACATEGABCABBCTBAABAAAABTEABAACATEGABCAAAAAAAAAAATEGABCAAAAAACATEGABCAAAAAACATEGABCABAAAACATEGABCAABAAACATEGABCABAAAAATEGABCAAAAAACATEGABCAAAAAACATEGABCAAAAAACATEGABCAAAAAAAATEGA	6300
TOCRANTACTTIAAAAABTATCTTITTACCATTOACABTCTAACAATTTTTTATTGATTGAAGCAGGAAATGTTACGTTTGAAGAATGAGCGCATATGGCTCTACCATTGTTACCATTGTTCTCACTAGTCTTCAAAAATATAAAACT	6480
GATTIAAACTATGCTGCAGATGTGTGTGTGGTGATGTGTGTGCGATGTTTTTGGTTATGCTATGTGTGTG	6660
TO TEAT GAMATAGIT CANTECTIFTITIG TABECARGOOGTATTAT GOCCTEGACAAGAN CATGOALAGAAGANCAGTOG TAGECATGOCCE ACTEGACATGOCCE ACTEGAATTIGCATGCATGOCAGGAGTGATATTGATCATTTGATGCATTGTATTCATTGATGTATTCATTGATGTATTCATTGATGTATTCATTGATGTATTCATTGATGAGTAGGTAG	6840
ATABITICE TABITICE TABITIGEATIBAACITTACCIGTACGITTACCIGTACCCTAMABITATGATIBITATGCABITATITAMA TACACABATCACBITIGAATACBABIGCIACGBABATCAAAACIGCCIGCCICCCCCICCCCCITCTGIGTAACCITGBGITTIATGCCATA ATAITITACTGITGCATIGTATIGATETATTAGITAGITAGATAGITAATAATCAAACICCAAAACCAAACITAATATATATATA	7020 7200 7380

Figure S2. Squence alignment of *MsSQS* showing exon-intron composition.



Figure S3. Image of 3-month-old control and the three transgenic alfalfa lines overexpressing *MsSQS*.