

Supplemental table S2: Expression profiles of selected plant and *S. meliloti* genes in MtSucS1-reduced lines in comparison to control lines.

cluster	DFCI MtGI 8	short annotation	as12 vs. c	as19 vs. c	
I	TC100410	SucS1	-7,85 ^b	-3,04 ^b	
	TC99016	SucS5	-2,97 ^b	-1,16	
	TC99699	Monosaccharide transporter	-7,90 ^b	-2,34 ^a	
	TC107108	Cell wall Inv	-2,52	-1,27	
	NF062D01	Vacuolar acid Inv Psl-1	-3,27 ^b	-1,54	
	TC94273	β -amylase	-1,94	-1,19	
	TC95820	SucS2	-1,60 ^a	-1,91 ^b	
	TC94447	SucS3	-3,14 ^b	-3,77 ^b	
	TC101691	Monosaccharide transporter	-1,29	-1,55	
	TC103015	Tuber-specific & SURE binding factor	-1,82 ^a	-2,36 ^a	
	TC98648	SucS4	-1,98 ^a	-1,90 ^b	
	TC107440	H ⁺ /Monosaccharide cotransporter	-2,05 ^a	-2,20 ^a	
	TC106499	Neutral Inv	-1,96 ^a	-2,03 ^a	
	TC99506	Acid Inv	-3,58 ^b	-2,55 ^a	
	TC107845	Suc transporter 4	-2,23	-1,61	
	EST332714	Suc transporter SUT4	-1,49	-1,14	
	TC101015	Phosphoenolpyruvate carboxylase	-1,91 ^b	-1,57 ^a	
	II	TC96236	Acid beta-fructofuranosidase prec.	-1,04	1,47
		TC110297	α -amylase	-1,24	1,77 ^a
TC103706		Cell wall Inv 2	-1,12	1,71	
TC107513		Suc-P synthase	-1,15	1,81 ^b	
TC100309		Enolase	-1,15	2,10 ^a	
TC100586		Leghemoglobin 29	-1,16	2,03 ^b	
TC94515		Enod40	-1,49	1,61 ^a	
TC106591		Leghemoglobin	-1,01	3,46 ^b	
TC106696		Nodulin 25	-1,07	2,72 ^a	
TC94692		Trehalose 6-P phosphatase	-5,23 ^a	1,47	
TC95549		H ⁺ /hexose cotransporter	-5,01 ^b	1,35	
TC100484		UDP-Glc 6-dehydrogenase	-7,19 ^a	1,24	
TC100391		Asn synthetase 1	-1,56	1,12	
TC101462		Cellulose synthase	-1,84 ^a	1,33	
TC94709		UDP-sugar pyrophosphorylase	-1,91	1,06	
TC107339		Enod18	-1,79	1,12	
III		TC107189	Malate dehydrogenase	1,64 ^a	1,66
		TC107357	Nitrate reductase	3,59 ^a	3,19 ^b
		TC106918	Asp aminotransferase	2,17 ^a	1,89 ^a
	TC106886	Alkaline/neutral Inv	2,60 ^b	1,57	
	TC100558	Pyruvate kinase	1,07	1,58 ^a	
	TC100150	Carbonic anhydrase	1,71 ^a	2,60 ^b	
	TC106913	Gln synthetase	1,31	1,79 ^b	
	TC103232	Suc-P synthase	1,17	1,50 ^a	
	TC100561	Pyruvate decarboxylase 1	1,63	2,16 ^b	
	TC106651	α -1,4-glucan-protein synthase	1,14	1,52 ^b	
	TC94328	UDP-Glc pyrophosphorylase	1,32	2,25 ^b	
	TC94194	Granule-bound glycogen (starch) synthase	1,55	2,49 ^b	
	TC107257	Calmodulin-like protein 1	1,28	2,29 ^b	
	TC96622	Gln synthetase 1	1,49	3,73	
	IV	SMb20611	DctA, C ₄ -dicarboylate transport protein	-1,70	-1,01
		SMa0819	FixB, electron transfer flavoprotein	-1,51	-1,48
		SMc00169	DME, NAD-malic enzyme oxidoreductase	-3,25	-4,76 ^a
		SMb20020	Pyruvate dehydrogenase	-2,03	-3,83 ^b
		SMa0677	put. Glu/Asp transport protein	-1,52	-3,34 ^b
SMb20263		put. ABC transporter periplasm. AA-binding prot.	-1,80	-3,86 ^a	
SMa0831		NifX, N fixation protein	1,03	1,58 ^a	
SMa0817		FixC, oxidoreductase protein	1,08	1,48	

Data represent ratios from mean nodule expression data derived from at least three biological replicates per *MtSucS1*-antisense line and 6 per controls. Each biological replicate was based on nodule pools derived from three individual plants. Significant differences are indicated by ^a and ^b ($p < 0,05$ and $< 0,01$, respectively).