

Supplemental table S1: Primer sequences used for real-time RT-PCR.

<i>MtGl 8</i> ¹⁾	short annotation	forward primer	reverse primer	T _m [°C]	T _m [°C]	amplicon [bp]
EST332714	Suc transporter SUT4	ttgcaactctctcttaaca	cattattagcaacatccaaaa	53.0	53.2	339
NF062D01	Vacuolar acid Inv Psl-1	gattttatccatgaagaac	gacgtacgttgaatctgtaa	53.0	53.0	312
NF112E11	Alkaline/neutral Inv	tggatttttactacgagca	taatagaatgagagagcga	52.9	52.9	339
TC94194	Granule-bound glycogen synthase	gctcttcaactacctgat	gagctcttcaacagagatt	52.9	53.0	351
TC94273	Beta-amylase	taaccaaatcatalgtaatgc	tgctcattaagaacatcaac	52.9	53.1	276
TC94328	UDP-Glc pyrophosphorylase	ctgggagctatagtgactt	gctgaagaacttttactccat	53.1	53.0	346
TC94405	Hexokinase	tctttcatcattgactcag	tcaacatctgagcactctc	53.0	53.0	284
TC94438	Suc transporter	cggtgttctcttactat	agccaatttagtaacaaaac	53.0	53.0	283
TC94447	MtSucS3	atatgagcatctactcccat	tctaagctttggattcctc	53.0	52.9	297
TC94515	Enod40	atatacaaaaggattatgct	aatttcaaaaggaagacaac	53.0	52.8	320
TC94631	Asp aminotransferase 2	tcatactaaagcagataggca	tgcaatcactatgatttgg	53.0	52.9	278
TC94692	Trehalose-6-P phosphatase	ggttactctcttggatcc	tttctagggacaaaataacc	53.0	52.9	370
TC94709	UDP-sugar pyrophosphorylase	ctatogaaccaattgactaca	agtactccacacagaaacct	53.0	53.0	350
TC94780	Glutamate synthase	acacacagtgatgacttagga	atctaccctaataccaccaa	53.0	53.0	251
TC95549	H(+)/hexose cotransporter	attcttcttagctgaaac	aataatcccgaatttgaag	53.0	52.9	284
TC95763	Suc-phosphatase	aaacaactgaggaagagaag	aatcaactctcactgtat	53.0	52.9	343
TC95820	MtSucS2	aaacaaggactgattcact	tcaggataacattglaactcg	53.1	53.0	274
TC96236	Acid beta-fructofuranosidase prec.	ttggaagctgataagaaga	aggagtgtactcagaagagc	53.0	52.9	337
TC96622	Gln synthetase 1	atgcatacaagcaactcatal	ttcacatattatacatccgc	53.0	52.9	297
TC97643	Suc transporter 4	tacagctctctcttaacc	atagcaaaaggacgataattc	53.1	53.0	297
TC98648	SucS2 [MtSucS4]	aagatactcttctgctcacc	gttctcttgaagctgagat	52.9	53.0	332
TC99016	SucS [MtSucS5]	gtagtctctggatcaatgta	gaagaatctccaacaattac	52.9	53.0	332
TC99238	Alkaline/neutral Inv	tctagtctggtagcaatgtg	agatggaataaaatcacgaat	53.2	53.0	313
TC99506	Acid Inv	gtgtaaaggctagttggat	gcaaatagttccagtctct	52.9	53.0	321
TC99699	Monosaccharide transporter	tcaacttctcatagctcaa	tcaatcatgacactaaatgc	53.0	53.7	327
TC100150	Carbonic anhydrase	tctcccaagttatggattt	ggaagataaaccaatttcac	53.1	53.1	326
TC100309	Enolase	ataaccaaccttagttgagc	caccaacaaaaatcgttacta	52.9	53.1	267
TC100391	Asn synthetase	ctagtctctgctgctgaa	gaatccattctcaattctc	53.0	53.0	338
TC100393	Asn synthetase 1	attgtgagtattgacact	tgctagagtacaaatgaccag	53.1	53.2	275
TC100410	MtSucS1	ctttggaattctcagactt	gacatcatctgagcaaaagta	53.0	53.0	368
TC100484	UDP-glucose 6-dehydrogenase	ftcaagacactgattaccag	taaaacataaaagctccaaca	52.9	53.0	365
TC100558	Pyruvate kinase	cagaggcttgatctatatt	gtggacaacacaaaagtta	52.9	52.9	302
TC100561	Pyruvate decarboxylase 1	ggcccattttaagactac	caattttgacagttaacca	52.9	53.1	365
TC100586	Leghemoglobin 29	acaagaggcttggtagtag	caactcttgattgtttga	53.1	53.2	361
TC100851	Multifunctional aquaporin	atcatgtatgcagagatcaa	tctctgcacattaaagaaa	53.2	53.0	337
TC101462	Cellulose synthase	cttgagaggttgcttatact	gtctactcctgcaagaactt	53.1	53.0	332
TC101691	Monosaccharide transporter	tctctatgagcacaattcac	gtcatacaagtgctgagaaa	53.0	53.1	272
TC103015	Tuber-spec. & SURE binding fact.	taataacgctatgattgaa	gattgttcatctctgtga	52.9	52.8	330
TC103232	Suc-P synthase	agagaggaacactagattgga	ccgtgaactactatgagaaca	53.1	53.0	341
TC103335	Hexose transporter HT2	gcttattccaagtgagattt	cctctgtccttaacatacc	53.0	53.1	301
TC103706	Cell wall Inv 2	accattgagtacaaggact	taatccattcccttagaaaag	53.0	53.0	322
TC104674	Impaired Suc ind. 1-like protein	acaaagggatatctggaagt	acatcctccaaaactctaag	53.0	52.8	366
TC106485	Translation elongation factor EF-1 α	ccagtttattttccagttt	caatcaaggacaaatttaca	53.0	53.0	278
TC106499	Neutral Inv	attgacatgttctctct	actgttgacagcatcagtag	53.0	53.0	313
TC106591	Leghemoglobin	attgcaaatcaaatagcaaa	catctcccaataactctctc	53.0	53.0	326
TC106592	Leghemoglobin 1	agaatcaaaagaacctctgt	tgaattgaccataacaacatt	53.0	53.0	279

TC106651	Alpha-1,4-glucan-prot. synthase	ctattggacgttacgatgata	ggatcaatagtccaagtttc	53.0	53.0	297
TC106696	Nodulin 25	cataactgatgaggaactaga	gggataaaaattccttttga	53.1	52.9	293
TC106729	Gln synthetase	gtgttcttcttctcttcac	gggtgaaacatcacaaatcac	53.2	52.9	340
TC106808	Gln synthetase	ctgcctcatttctctctat	gtaactggtcctgtagagtc	53.0	52.9	282
TC106886	Alkaline/neutral Inv	cagatgaaaccagtgattaa	acatgcaattaatgaaacaag	52.9	53.0	294
TC106913	Gln synthetase	cctatatctcaagcaatttt	ccttgaatgagcatcagata	53.0	53.0	340
TC106918	Asp aminotransferase 1	caatcacacaaggttttcaa	cactgcaaaagaaagtaaca	53.0	53.0	265
TC107075	Phosphoenolpyruvate carboxylase	atggagatggttagatgaac	acagatccttgaaactagga	53.1	53.2	336
TC107108	Cell wall Inv	aaatctacgtatgaaccaggt	cacatgagaaccaaatctta	53.0	52.9	329
TC107108	Cell wall Inv	tgttgagatgattatggga	actgggttcatacgtagatt	53.0	53.0	252
TC107189	Malate dehydrogenase	aaattctaaacagaaggggtg	catttgatcctgacagtta	52.9	52.9	260
TC107257	Calmodulin-like protein 1	gataaagcgtatttcagact	ccgtgattgtcaagtaataa	53.0	53.0	281
TC107357	Nitrate reductase	taaacaagatctctcagca	ggttttaactaaaccggata	53.0	53.0	350
TC107440	H(+)/monosacch. cotransporter	gatgtgatgctgattttaga	gacaaatcaacattgaacac	53.0	53.0	357
TC107513	Suc-P synthase	tatgatggtttgatccagta	gatgttcttctaggatctgg	53.1	53.1	305
TC107845	Suc transporter 4	ctggctctattagctattcc	caacactcaaaaataaggtca	52.9	53.0	307
TC109967	Hexokinase 3	aacltctgtattactgctgtg	atcaagacctgtctctcaat	53.0	52.9	365
TC110297	Alpha-amylase	cgtgctgtaacatctact	tcgtgtctatggttatcttg	53.0	53.0	326
Gene ID²⁾						
SMa0677	put. Glu/Asp transport protein	gattccctgatcatagtctc	agaggttctgtctcgatag	52.8	53.8	287
SMa0815	NifA, transcriptional activator	aaagtgtactcctctcctata	aggagagacaagataacagc	53.1	52.9	303
SMa0816	FixX, ferredoxin-like protein	atccgaactgaagagga	gaagacaagcttaccagaac	52.9	53.4	288
SMa0817	FixC, oxidoreductase protein	tagcatcgttttagagaga	agaccatggagagaccttac	53.0	53.1	336
SMa0819	FixB, electron transfer flavoprotein	cttcaagagctgaaggttct	cactgagctaaatgttgattc	53.9	52.6	348
SMa0825	NifH, nitrogenase iron protein	gatgtcgattacgtctcatac	gatcactgtcatcttctgag	52.2	52.2	353
SMa0827	NifD, nitrogenase Fe-Mo	gcaaagctaaatctatccac	aggtcctcataggcagtaata	53.6	53.2	328
SMa0830	NifE, oxidoreductase	caagctttaccactgatgta	aggatattgatgctgtagac	53.2	53.6	351
SMa0831	NifX, N fixation protein	cgattgctactgaagataga	ttgatcggatgaatcttt	53.2	53.0	290
SMb20020	Pyruvate dehydrogenase	tcctttgatattcctttt	aagattctctaccagttctcg	52.5	52.9	367
SMb20263	put. ABC transp. periplasm. AA-binding protein	agtcctcgaagacatgaa	gaacaggtgaggtagttgag	53.1	54.0	337
SMb20611	DctA, C ₄ -dicarboxylate transporter	aagggcatgtagatattggt	ctatctgacgtcttctctt	52.7	53.9	276
SMc00169	DME, NAD-malic enzyme oxidored.	cgactatgctgatgattatt	acataggtatcggtgaagaag	52.1	53.5	296

1) DFCI *Medicago truncatula* Gene Index 8; <http://compbio.dfci.harvard.edu/>

2) *Sinorhizobium meliloti* genome database; <http://bioinfo.genopole-toulouse.prd.fr>

Abbreviations: bp, base pairs; Tm, melting temperature for forward and reverse primer, respectively; P, phosphate