Supplemental Table 1. Genes with statistically significant changes in gene expression identified from microarray analyses of Mt*IFS1*-expressing line B20 and vector control line VC11

TIGR Identifier	Number of ESTs[1]	Fold-change (B20/VC11)	p-value	Gene annotation of closest BLAST homolog
TC45135[2]	4	5.35	0.0045	**Isoflavone synthase**
TC45136[2]	36	4.00	0.0000	**Isoflavone synthase**
TC55222	4	3.47	0.0300	unknown protein (*A. thaliana*)
TC44434	15	2.67	0.0043	DNA-binding protein 3 (*Nicotiana tabacum*)
TC46175[1]	6	2.67	0.0000	3’ UTR of ubiquitin/ribosomal extension protein
TC55546	4	2.49	0.0045	acetoacetyl-CoA thiolase (*A. thaliana*)
TC55319	4	2.13	0.0158	unknown protein (*A. thaliana*)
TC52492	18	2.10	0.0045	GmMYB29A2 gene (*Glycine max*)
TC55406	6	2.07	0.0158	putative ankyrin repeat protein EMB506 Glycine max
TC46537	5	2.02	0.0043	eceriferum3 (CER3) Glycine max
TC45848	11	-2.30	0.0010	hypothetical protein (*Oryza

				sativa)
TC58945	2	-2.30	0.0045	putative glutathione S-transferase T3 (*Lycopersicon esculentum*)
TC49931	2	-2.57	0.0214	transducin family protein / WD-40 repeat family protein (*A. thaliana*)

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[1] Number of ESTs in TIGR *Medicago* Gene Index Release 7.0 (May 2003).

[2] TCs identified as upregulated in both Mt*IFS1*-expressing lines relative to vector control line VC11.