

Supplemental Table 2. Genes with at least a 5-fold reduced RNA level in *tdt-1* mutants

Entries shown in bold were verified by real-time RT-PCR. Relative expression levels determined by this method are shown in parenthesis.

Metabolism, Biosynthesis, Catabolism

Gene name	Fold change	Functional or molecular role
AT4G33790	-9.24	acyl CoA reductase, male sterile 2
AT2G32860	-8.46	glycosyl hydrolase family protein , carbohydrate metabolism
AT3G21560	-5.03	UDP-glucosyltransferase
AT5G14200	-7.81	AtIMD1, 3-isopropylmalate dehydrogenase, leucine biosynthesis
AT5G25980	-5.27	glycosyl hydrolase family 1 protein
AT3G19710	-21.75	BCAT4, branched-chain amino acid aminotransferase
AT3g62040	-6.29	haloacid dehalogenase-like hydrolase family protein
AT5G23020	-17.16	2-isopropylmalate synthase 2 (IMS2) glucosinolate biosynthesis
AT5G23010	-11.18 (-61.3)	2-isopropylmalate synthase 3 (IMS3) glucosinolate biosynthesis
AT3G02020	-10.97	aspartate kinase, aspartate biosynthesis
AT1G06360	-5.79	fatty acid desaturase family protein

Signaling and Responses

AT1G05700	-9.18	leucine-rich repeat protein kinase
AT1G74670	-11.94	gibberellin-responsive protein
AT3G03190	-6.56	AtGSF11, glutathione S-transferase, response to oxidative stress, toxin catabolism
AT5G64110	-5.19	peroxidase, similar to peroxidase ATP3a, response to oxidative stress
AT5G20970	-5.07	heat shock family protein contains similarity to 18.0 kDa class I heat shock protein, response to heat shock
AT5G55250	-7.11	IAMT1, S-adenosyl-L-methionine:carboxyl methyltransferase family protein, converts IAA to its methyl ester, auxin signaling

Transcription

AT1G71692	-5.80	AGL12, MADS-box transcription factor
AT1G68880	-7.31	bZIP transcription factor family protein
AT2G28160	-5.46	FIT1. Transcription factor, regulates Fe uptake in the root

Transport

Gene name	Fold change	Functional or molecular role
AT5G45105	-30.70	similar to putative metal transporter ZIP8, Cation transport
AT1G01580	-28.26 (-81.1)	FRO2, low-iron-inducible ferric chelate reductase responsible for reduction of iron at the root surface for transport
AT1G32450	-5.83	proton-dependent oligopeptide transport (POT) family protein
AT4G19690	-16.08 (-94.7)	IRT1, iron-responsive transporter
AT4G12030	-7.93	bile acid:sodium symporter family protein, Na transport
AT5G23980	-5.54	ferric-chelate reductase (FRO4)
AT3G58810	-6.95	AtMTPA2, zinc transporter
AT5G63850	-7.88	AAP4, amino acid transporter 4, downregulated by dehydration
AT5G09220	-7.73	AAP2, amino acid permease 2

Electron Transport

AT1G06830	-13.17	glutaredoxin family protein
AT1G13710	-8.22	cytochrome P450 family protein, CYP78A5

Other

AT1G70850	-7.73	Bet v I allergen family protein similar to Csf-2 [<i>Cucumis sativus</i>], Pathogenesis-related protein Bet v I family
AT2G40330	-5.74	Bet v I allergen family protein
AT3G54600	-6.60	DJ-1 family protein, similarity to protease I from <i>Pyrococcus furiosus</i>
AT2G32100	-6.60	ovate protein-related contains uncharacterized plant-specific domain TIGR01568
AT2G33790	-5.56	pollen Ole e 1 allergen and extensin family protein
AT3G18200	-5.82	nodulin MtN21 family protein similar to MtN21 involved in root nodule development, <i>Medicago truncatula</i>
AT1G67870	-5.59	glycine-rich protein
AT4G29030	-8.69	glycine-rich protein
AT2G17880	-5.30	DNAJ heat shock protein
AT4G00780	-7.01	meprin and TRAF homology domain and MATH domain-containing protein
AT5G02780	-5.72	In2-1 protein, putative similar to In2-1 [<i>Zea mays</i>]
AT4G12545	-7.96	protease inhibitor/seed storage/lipid transfer protein (LTP) family
AT2G40610	-6.12	ATEXPA8 , expansin 8, cell-wall-loosening
AT4G12550	-5.51	AIR1, auxin induced lipid transfer protein
AT5G45070	-9.49	TIR domain disease resistance protein

Unknown

Gene name	Fold change	Functional or molecular role
AT3G54500	-5.78	expressed protein
AT5G19120	-5.75	expressed protein
AT2G28780	-13.09	expressed protein
AT3G06070	-5.74	expressed protein
AT3G16670	-34.03 (undetectable)	expressed protein
AT2G20670	-5.64	expressed protein
