

Gene	Functional prediction*	Confirmed function <sup>‡</sup>	CACCTG	Up/down <sup>§</sup>	FC
At2g26010	Predicted PR protein	None	Yes	Up	-1.80
At3g31902	Pseudogene, MADS-box protein	None	Yes	Up	-1.58
At2g04395	Telomere maintenance	None	Yes	Up	-1.38
At1g09995	Best <i>Arabidopsis</i> protein match is: helicase related (At1g79890.1)	None		Up	-1.11
At3g23637	Contains DVL domain (DVL21), shoot development	None		Up	-1.22
At2g03445	MIR398A	Targets two Cu/Zn superoxide dismutases (CSD1 and CSD2) (Jagadeeswaran et al., 2009)		Up	-1.27
At1g61224	MIR842A, targets several Jacalin lectin family members	None	Yes	Down	1.58
At4g14811	MIR780A, targets CATION/H+ EXCHANGER 18 (CHX18)	None	Yes	Down	1.25
At4g09775	Best <i>Arabidopsis</i> protein match is: reverse transcriptase-related (At2g02650.1)	None		Down	1.28
At5g02360	Best <i>Arabidopsis</i> protein match is: DC1 domain-containing protein (At1g53340.1)	None		Down	1.29
At2g28755	Best <i>Arabidopsis</i> protein match is: NAD-dependent epimerase/dehydratase family protein (At2g28760.3)	None	Yes	Down	1.50
At5g38378	Encodes a plant thionin family protein	None	Yes	Down	1.26
At3g23680	Best <i>Arabidopsis</i> protein match is: F-box family protein (At3g23685.1)	None		Down	1.12
At5g33210	SHI-RELATED SEQUENCE 8 (SRS8), a member of SHORT INTERNODE (SHI) gene family. <i>Arabidopsis thaliana</i> has ten members that encode proteins with a RING finger-like zinc-finger motif. SRS8 is a putative pseudo-gene (Kuusk et al., 2006)	None		Down	1.30
At4g02950	Best <i>Arabidopsis</i> protein match is: ubiquitin protein (At4g03360.1)	None	Yes	Down	1.35
At3g01345	Contains InterPro domain glycoside hydrolase	None, downregulated in mutants of the SET domain protein SDG4 (Cartagena et al., 2008).		Down	1.26
At5g39290	ARABIDOPSIS THALIANA EXPANSIN A26 (ATEXPA26)	None		Down	1.19
At5g39540	Best <i>Arabidopsis</i> protein match is: anac063 (Arabidopsis NAC (NAM/ATAF1, 2/CUC2) domain 63)	None		Down	1.40

\*Function predicted by sequence similarity.

<sup>‡</sup>Function confirmed by direct assay.

<sup>§</sup>Gene is up- or downregulated in *dpa4*.