

**Supplemental Table 7: Summary of downregulated genes with seed matches to amiRNAs.**

	amiR-lfy-1	amiR-mads-1	amiR-mads-2
Predicted targets, present on array	1	6	18
Predicted targets, present in control	1	4	13
Predicted targets, present in control and downregulated in amiRNA overexpressers	1	1	6
All genes present in control without predicted targets	15367	15364	15355
All genes downregulated without predicted targets	342	141	287
Genes with seed matches, present in control, without predicted targets	1562	2970	2986
Observed downregulated			
Predicted targets	1	1	5
Others	21	27	55
Expected downregulated without predicted targets	34.8	27.3	55.8
$\chi^2$	5.57	0.003	0.62

Downregulated genes among all genes with seed matches to the respective amiRNA. Analysis as in Table 2, using LIMMA and 1% estimated FDR. A  $\chi^2$  test was used to determine statistical significance of the difference between expected and observed downregulated genes among the “non-targets”. A minimal  $\chi^2$  value of 6.63 corresponds to significant differences at  $\alpha = 0.01$ . Use of the logit-T algorithm produced qualitatively similar results (not shown). For amiR-lfy-1, we used the sequence of the 21mer deduced from the mapping of the cleavage product, which was shifted by 2 nucleotides from the intended amiRNA.