Table S6. Gene set enrichment analysis of different gene sets in 35S:*miR396b* in comparison to wild type

Gene set*	Size	NES[†]	Nominal *P*-value	False discovery rate	Significantly different from wild type[‡]
Mitosis-specific genes	79	–5.081	<0.000	<0.000	Yes
Histones	56	–3.922	<0.000	<0.000	Yes
Reference genes	25	0.877	0.597	0.605	No
DEFL	35	1.258	0.218	0.502	No
Photosynthesis	74	1.364	0.136	0.678	No

*Gene set sources. Mitosis-specific genes are from Menges et al. (Menges et al., 2005). *Arabidopsis* histones and histone linker proteins from The Chromatin Database (Gendler et al., 2008). Reference genes are a selection of stably expressed genes (Czechowski et al., 2005) used in this analysis as a negative control. DEFL, defensin-like genes from Silverstein et al. (Silverstein et al., 2005). Photosynthesis, including Calvin cycle and light reactions, extracted from Aracyc (www.arabidopsis.org).

[†] NES, normalized enrichment score. A negative value indicates downregulation in *35S:miR396b* plants.

[‡] A gene set is significantly different in *35S:miR396b* compared to wild type when the nominal *P*-value and false discovery rate are <0.05.

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