

**Table 2.** Delayed exit from the mitotic phase conferred by *CYCD3;1* OE

MIPS ID	Description (2006)	A	B	C	D	Robust change call WT	Robust change call <i>CYCD3</i> OE
At1g44110	Arath;CYCA1;1	1163.85	3043.4	631.45	1350.35	D	
At5g66230	expressed protein	702.95	2146.6	439.65	738.2	D	
At5g55520	similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g26660.1); similar to kinesin heavy chain, putative [Oryza sativa (japonica cultivar-group)] (GB:AAV35794.1)	324.25	758.5	153.85	365	D	
At5g51600	microtubule associated protein (MAP65/ASE1) family protein, low similarity to SP:P50275 Anaphase spindle elongation protein {Saccharomyces cerevisiae}, protein regulating cytokinesis 1 (PRC1) (Homo sapiens) GI:2865521; contains Pfam profile PF03999	507	1077.65	249.1	386.9	D	D
At5g36710	[AT5G36710, expressed protein ];[AT5G36800, expressed protein ]	2311.3	5102.6	1431.45	2353.35	D	
At5g13840	CCS52b	762.45	1985.8	389.1	1206.7	D	NC
At4g33260	[AT4G33270, WD-40 repeat family protein, contains 6 WD-40 repeats (PF00400); WD-repeat protein -Daucus carota,PID:g2253631 ];[AT4G33260, WD-40 repeat family protein, contains 6 WD-40 repeats (PF00400); WD-repeat protein -Daucus carota, PID:g2253631 ]	1394.05	4552.95	718.8	1878.15	D	NC
At4g33400	dem protein-related / defective embryo and meristems protein-related, identical to dem GI:2190419 from (Lycopersicon esculentum)	1170.75	2748.7	678.3	1630.5	D	NC
At4g32830	Aurora-like kinase 2; ALK2	1127	2973.5	680.95	1920.3	D	
At3g25980	mitotic spindle checkpoint protein, putative (MAD2), identical to Swiss-Prot:Q9LU93 mitotic spindle checkpoint protein MAD2 (Arabidopsis thaliana)	883.3	2326.75	486.6	1099.9	D	
At4g05520	calcium-binding EF hand family protein, similar to EH-domain containing protein 1 from {Mus musculus} SP:Q9WVK4, {Homo sapiens} SP:Q9H4M9, receptor-mediated endocytosis 1 from (Caenorhabditis elegans) GI:13487775, GI:13487777, GI:13487779	322.45	701.8	194.65	395.45	D	
At3g14190	expressed protein	1134.1	3263.2	683.9	1552.25	D	NC
At3g12870	expressed protein	1150.85	2679.95	796.75	1203.35	D	NC
At3g02640	expressed protein	2741.7	8121.5	1617.4	3668.85	D	NC
At1g72250	kinesin motor protein-related	310	879.45	169.95	464.4	D	NC
At3g03130	expressed protein; expression supported by MPSS	467.45	684.95	219.8	257.7	D	NC
At1g33940	[AT5G18700, protein kinase-related, contains protein kinase domain, INTERPRO:IPR000719 ];[AT1G33940, expressed protein ]	899.85	1975.2	686.25	1097.35	D	NC
At1g18370	kinesin motor family protein (NACK1), similar to kinesin heavy chain isolog GB:AAB63609 GI:2262101 from (Arabidopsis thaliana)	614.05	1660.3	346.2	792.9	D	NC
At1g02730	cellulose synthase family protein, similar to cellulose synthase catalytic subunit (gi:13925881) from Nicotiana glauca, cellulose synthase-4 (gi:9622880) from Zea mays	3293.35	10152.55	1869.75	4387.45	D	NC
At2g25060	plastocyanin-like domain-containing protein	2876.9	7534	1628.2	3859.5	D	
At1g08560	syntaxin-related protein KNOLLE (KN) / syntaxin 111 (SYP111), identical to SP:Q42374 Syntaxin-related protein KNOLLE (Syntaxin 111) (AtSYP111) {Arabidopsis thaliana}; BAC F22O13 has a deletion of a cytosine at position 7887	2732	8422.9	1572.1	4162.55	D	NC
At2g26760	Arath;CYCB1;4	616.65	1392.05	351.8	418.65	D	NC

Data from the experiment described in SI Table 1 were analyzed by identifying mitotic genes (defined as in legend to SI Table 1) whose signals decrease between 1 week-old and 2 week-old shoots in WT and *CYCD3;1* OE. Twenty-two mitotic genes (1) decrease significantly in older shoots, in contrast to a single gene in older shoots of the *CYCD3;1* OE plants. Columns A-D show the average ATH1 GeneChip signals; A, average signal for 1-week-old WT shoots; B, average signal for 1 week-old *CYCD3;1* OE; C, average signal detected in 2-week-old WT shoots; D, average signal for 2-week-old *CYCD3;1* OE shoots. The robust (defined as in legend to SI Table 1) “difference” calls obtained after pairwise comparisons (2) of values for WT and *CYCD3;1* OE are listed for 1-week-old and 2-week-old shoots in the last columns; “D” indicates a robust “decrease,” and “NC” marks a robust “no change” difference call. Note that only a single mitotic gene is robustly decreased in the sample from *CYCD3;1* OE shoots, compared to the 22 genes identified as robustly decreasing in WT samples.

1. Menges M, de Jager SM, Gruissem W, Murray JA (2005) Plant J 41:546-566.

2. Masubelele NH, Dewitte W, Menges M, Maughan S, Collins C, Huntley R, Nieuwland J, Scofield S, Murray JA (2005) Proc Natl Acad Sci USA 102:15694-15699.