

Table 1. Up-regulation of mitotic genes in shoots conferred by *CYCD3;1* OE

MIPS ID	Description (2006)	A	B	C	D	Robust change call (1 week old shoots)	Robust change call (2 week old shoots)
At2g47500	kinesin motor protein-related	543.9	1090.05	478	465.75	I	
At4g15830	expressed protein	958.8	2551.75	740.8	1203.8	I	
At1g44110	Arath;CYCA1;1	1163.85	3043.4	631.45	1350.35	I	
At5g17160	expressed protein	1348.85	3172.8	870.35	1253.85	NC	
At5g15510	expressed protein	216.05	680.6	163.35	361.7	I	
At5g33300	chromosome-associated kinesin-related, contains weak similarity to chromosome-associated kinesin KIF4A (Chromokinesin) (Swiss-Prot:P33174) (Mus musculus)	354.5	766.95	241.4	672.85	I	
At5g67270	microtubule-associated EB1 family protein, similar to SP:Q9UPY8 Microtubule-associated protein RP/EB family member 3 (Protein EB3) (Homo sapiens); contains Pfam profiles PF00307: Calponin homology (CH) domain, PF03271: EB1 protein	659.5	1747.45	396.25	958.65	I	
At5g66230	expressed protein	702.95	2146.6	439.65	738.2	I	
At5g60930	chromosome-associated kinesin, putative, microtubule-associated motor KIF4, Mus musculus, PIR:A54803	495.9	1417.05	288.6	670.15	I	
At5g48310	expressed protein	442.25	1385.1	232.1	662.35	I	
At5g62550	expressed protein	277.85	900.7	179.9	347.3	I	
At5g55830	lectin protein kinase, putative, similar to receptor lectin kinase 3 (Arabidopsis thaliana) gi:4100060:gb:AAD00733; contains protein kinase domain, Pfam:PF00069; contains legume lectins alpha and beta domains, Pfam:PF00138 and Pfam:PF00139	169.55	597.05	154.45	327.5	I	
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	I	
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	I	
At5g45700	NLI interacting factor (NIF) family protein, contains Pfam profile PF03031: NLI interacting factor [AT5G36710, expressed protein];[AT5G36800, expressed protein]	389.95	812.25	218.3	267.75	I	
At5g36710	similar to kinesin motor protein-related [Arabidopsis thaliana] (TAIR:At5g02370.1); similar to OSJNB0006N15.7 [Oryza sativa (japonica cultivar-group)] (GB:XP_472192.1); contains InterPro domain Kinesin, motor region (InterPro:IPR001752)	2311.3	5102.6	1431.45	2353.35	I	
At5g23910	Kinesin, motor region (InterPro:IPR001752)	200.15	686.15	153.6	371.2	I	
At5g13840	CCS52b	762.45	1985.8	389.1	1206.7	I	
At5g11300	Arath;CYCA2;2	230.2	431.55	241.6	333.2	I	
At5g11510	AtMYB3R4	509.45	1047.25	293.05	446.65	I	
At5g02370	kinesin motor protein-related, kinesin, Xenopus laevis, EMBL:XL249840	355.5	652.05	266.3	343.65	I	
At3g60840	microtubule associated protein (MAP65/ASE1) family protein, low similarity to protein regulating cytokinesis 1 (PRC1) (Homo sapiens) Gi:2865521; contains Pfam profile PF03999: Microtubule associated protein (MAP65/ASE1 family)	468.8	1112.35	386.6	598.05	I	
At3g55660	member of KPP-like gene family, homolog of KPP (kinase partner protein) gene in tomato; expressed protein, contains Pfam profile PF03759: Domain of unknown function (DUF315)	347.4	704.5	160.35	357.5	I	
At3g51280	male sterility MS5, putative, similar to male sterility MS5 (Arabidopsis thaliana) Gi:3859112; contains Pfam profile PF00515 TPR Domain	631.75	1703.5	487.25	682.6	I	
At4g35620	Arath;CYCB2;2	465.2	1147.4	331.65	546.85	I	
At4g33260	WD repeat; CDC20-like	1394.05	4552.95	718.8	1878.15	I	
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	I	
At4g32830	Aurora-like kinase 2; ALK2	1127	2973.5	680.95	1920.3	I	

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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	I	I
At4g28230	[AT4G28230, expressed protein j];[AT4G28220, NADH dehydrogenase-related, similar to 64 kDa mitochondrial NADH dehydrogenase (Neurospora crassa) Gi:4753821, alternative NADH-dehydrogenase (Yarrowia lipolytica) Gi:3718005; contains Pfam profile PF00070: Py expressed protein, weak similarity to phragmoplast-associated kinesin-related protein 1 (Arabidopsis thaliana) Gi:8745333	241.15	771.7	198.05	292.8	I	I
At4g28660	high mobility group (HMG1/2) family protein, similar to HMG2B (Homo sapiens) Gi:32335; contains Pfam profile PF00505: HMG (high mobility group) box	168.95	411.35	104.45	274.1	I	I
At4g23800	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:1348775, Gi:1348777, Gi:1348779	322.45	701.8	194.65	395.45	I	I
At4g05520	kinesin-like protein A, putative, kinesin like protein A, Arabidopsis thaliana, gb:Q07970	486.15	1685.9	266.7	583.05	I	I
At4g02800	expressed protein, similar to A, thaliana hypothetical protein T6B20.12 (1946366)	522.45	756.05	309.9	488.4	I	I
At4g01730	zinc finger (DHC type) family protein, contains Pfam profile PF01529: DHC zinc finger domain spindle checkpoint protein-related, similar to spindle checkpoint protein BubR1 (Gi:22128593) (Xenopus laevis); similar to Mitotic checkpoint serine/threonine-protein kinase BUB1 beta (EC 2.7.1.-) (MAD3/BUB1-related protein kinase)	538.35	1092.05	380.1	660.45	I	I
At2g33560	DNA topoisomerase, ATP-hydrolyzing / DNA topoisomerase II / DNA gyrase (TOP2), identical to SP:P30182 DNA topoisomerase II (EC 5.99.1.3) (Arabidopsis thaliana)	213.1	509.6	149.5	218.35	I	I
At3g23890	expressed protein	608.65	2935.55	416.4	1187.25	I	I
At3g14190	expressed protein	1134.1	3263.2	683.9	1552.25	I	I
At3g19590	WD-40 repeat family protein / mitotic checkpoint protein, putative, contains 5 WD-40 repeats (PF00400) (1 weak); similar to testis mitotic checkpoint protein BUB3 (GB:AAC28439.SP:O43684)(Homo sapiens)	1014	2100.3	715.25	995	I	I
At3g20150	kinesin motor family protein, contains Pfam domain, PF00225: Kinesin motor domain	347.35	1126.95	212	431.6	I	I
At3g12870	expressed protein	1150.85	2679.95	796.75	1203.35	I	I
At3g27330	zinc finger (C3HC4-type RING finger) family protein, contains Pfam profiles: PF00097 zinc finger, C3HC4 type (RING finger), PF01697 Domain of unknown function	233.75	485.6	110.3	184.15	I	I
At3g23670	phragmoplast-associated kinesin-related protein, putative, similar to kinesin like protein GB:CAB10194 from (Arabidopsis thaliana)	210.75	652.15	122.5	304.45	I	I
At3g02640	expressed protein	2741.7	8121.5	1617.4	3668.85	I	I
At1g72250	kinesin motor protein-related	310	879.45	169.95	464.4	I	I
At3g03130	expressed protein; expression supported by MPSS	467.45	684.95	219.8	257.7	I	NC
At3g11520	Arath;CYCB1;3	696.5	1501.65	403	925.75	I	I
At1g20590	Arath;CYCB2;5	455.3	1111.25	330.35	554.6	I	I
At1g34355	forkhead-associated domain-containing protein / FHA domain-containing protein	199.7	631.55	164.65	295.65	I	I
At1g76540	Arath;CDKB2;1	987.2	3669.3	840.65	1706.65	I	I
At1g33940	[AT5G18700, protein kinase-related, contains protein kinase domain, INTERPRO:IPR000719];[AT1G33940, expressed protein]	899.85	1975.2	686.25	1097.35	I	I
At1g69400	transducin family protein / WD-40 repeat family protein, similar to mitotic checkpoint protein (Gi:9294423) (Arabidopsis thaliana); similar to mitotic checkpoint protein (BUB3) (SP:O43684) (Homo sapiens)	173.2	327.8	176.75	337	I	I
At1g34460	Arath;CYCB1;5	302.15	1077.9	286.1	411.35	I	I

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At1g76310	Arath;CYCB2;4	445.8	1250.2	284.65	670.71	I	I
At1g50490	ubiquitin-conjugating enzyme 20 (UBC20), nearly identical to ubiquitin-conjugating enzyme UBC20 (Arabidopsis thaliana) Gi:22530867; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme	1595.6	3312.75	1095.85	1686.71	I	
At1g59540	kinesin motor protein-related, similar to kinesin motor protein (kin2) Gi:2062751 from (Ustilago maydis)	457.2	760.15	189.35	371.351	I	
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	4387.451	I	I
At1g16330	Arath;CYCB3;1	272.9	682.4	206.35	3581	I	
At1g20930	Arath;CDKB2;2	464.6	1326.7	412.95	625.81	I	
At2g17620	Arath;CYCB2;1	234.95	416.25	120.4	255.71	I	NC
At2g28620	kinesin motor protein-related	209.05	538.2	245	256.61	I	
At2g16270	expressed protein, and genefinder; expression supported by MPSS	298.35	753	193.15	220.21	I	
At2g25060	plastocyanin-like domain-containing protein	2876.9	7534	1628.2	3859.51	I	
At1g08560	syntaxin-related protein KNOLLE (KN) / syntaxin 11 (SYP11), identical to SP:Q42374 Syntaxin-related protein KNOLLE (Syntaxin 11) (Arabidopsis thaliana); BAC F22O13 has a deletion of a cytosine at position 7887	2732	8422.9	1572.1	4162.551	I	I
At1g03780	targeting protein-related, similar to microtubule-associated protein / targeting protein for Xklp2 (TPX2) (Gi:8926138) (Homo sapiens); similar to Restricted expression proliferation associated protein 100 (p100) (Differentially expressed in lung cells 2)	398.2	1205.95	245.8	468.251	I	
At1g23790	expressed protein	329.25	912.95	284.45	463.351	I	
At2g22610	kinesin motor protein-related	358.8	703.75	206.8	328.851	I	
At2g25880	Aurora-like kinase 1; ALK1	698	1877.7	393.3	7751	I	
At2g44190	expressed protein, contains Pfam profile: PF04484 family of unknown function (DUF566)	236.7	701.4	213.35	329.151	I	
At2g26760	Arath;CYCB1;4	616.65	1392.05	351.8	418.651	I	
At4g22860	no_match	245.35	493.7	189.75	2181	I	

Eighty-two mitotic genes previously identified as showing tight coexpression with a cohort of mitotic cyclins in suspension-cultured cells using two different synchrony methods (1) were used to assay the extent of mitotic cell cycle activity. Transcript levels for each of the 72 of these mitotic genes were up-regulated in *CYCD3;1* OE plants, and the data for this is shown with MIPS identifiers (MIPS ID) and gene descriptions. Duplicate biological samples for 1-week-old and 2-week-old WT and *CYCD3;1* OE shoots were hybridized to ATH1 Affymetrix GeneChips, and the average signal detected is shown in columns A-D. 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 four times the same) “difference” calls from the four possible individual pair-wise comparisons between the two duplicate samples for each pair of experiments (2) of values between WT and *CYCD3;1* OE are listed for 1-week-old and 2-week-old shoots in the last columns; “I” indicates a robust “increase,” and “NC” marks a robust “no change” difference call. Where no difference call is given the result was defined as not robust, because the same difference call was not generated for all four comparisons using Affymetrix MicroArray Suite 5.0 software. Note the large number of increased (I) calls at both time points.

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.