



## Regulation of Plant Stem Cell Quiescence by a Brassinosteroid Signaling Module

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In the originally published version of this paper, Table S1 was mistakenly reported to have contained primer sequences, microarray data, and quantification of QC division phenotypes. However, Table S1 actually only contained the quantifications of phenotypes, whereas the primer sequences are in the Supplemental Experimental Procedures. In addition, a separate Excel file with microarray data was missing from the paper, and this is now provided as Table S2 and available at GEO with the accession number GSE67144. This error has now been corrected in the online version of the paper. The authors apologize for any confusion this error may have

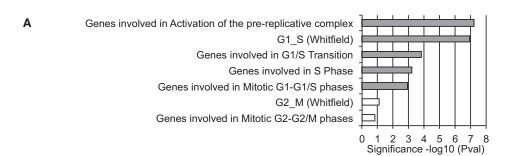
## Weaning Triggers a Maturation Step of Pancreatic β Cells

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In the originally published version of this paper, the order of gene sets in Figure 7A has been flipped, making it incorrectly seem as if mitotic gene sets are induced upon weaning more than G1/S gene sets. The mistake has been corrected online, and the final version of Figure 7 is shown here. The authors apologize for the error and any inconvenience that may have resulted.





В	Gene			
_	Symbol	Description	Fold (wean/suck)	p-value
	Pre-replic	ation complex - reactome		
	Mcm7	minichromosome maintenance deficient 7 (S. cerevisiae)	1.73706	0.013
	Cdk2	cyclin-dependent kinase 2	1.68711	0.007
	Prim1	DNA primase, p49 subunit	1.6583	8E-04
	Mcm3	minichromosome maintenance deficient 3 (S. cerevisiae)	1.55148	0.006
	Mcm4	minichromosome maintenance deficient 4 homolog	1.4731	0.007
	Cdt1	chromatin licensing and DNA replication factor 1	1.43799	0.027
	Mcm6	minichromosome maintenance deficient 6 (MIS5 homolog)	1.3302	0.036
	Mcm10	minichromosome maintenance deficient 10 (S. cerevisiae)	1.30355	0.042
	Orc5	origin recognition complex, subunit 5	1.28069	9E-04
	Orc6	origin recognition complex, subunit 6	1.15932	0.023
	Whitfield_	G1_S		
	Esd	esterase D	1.76822	0.021
	Tipin	timeless interacting protein	1.54832	0.017
	Hells	helicase, lymphoid specific	1.50743	0.01
	Vps72	vacuolar protein sorting 72 (yeast)	1.48138	0.029
	Mcm4	minichromosome maintenance deficient 4 homolog	1.4731	0.007
	Baiap2	brain-specific angiogenesis inhibitor 1-associated protein 2	1.39187	0.046
	Mnx1	motor neuron and pancreas homeobox 1	1.38546	0.009
	Fbxl20	F-box and leucine-rich repeat protein 20	1.3799	0.013
	Pcna	proliferating cell nuclear antigen	1.36892	0.048
	slc25a36	solute carrier family 25, member 36	1.33759	0.028
	Kank2	KN motif and ankyrin repeat domains 2	1.33106	0.002
	Mcm6	minichromosome maintenance deficient 6 (MIS5 homolog)	1.3302	0.036
	Clspn	claspin homolog (Xenopus laevis)	1.30346	0.049
	Bard1	BRCA1 associated RING domain 1	1.26944	0.044
	Nasp	nuclear autoantigenic sperm protein (histone-binding)	1.265	0.02
	Ankrd10	ankyrin repeat domain 10	1.26149	0.049
	Topbp1	topoisomerase (DNA) II binding protein 1	1.22111	0.002
	Arglu1	arginine and glutamate rich 1	1.19051	0.009
	Atad2	ATPase family, AAA domain containing 2	1.15153	0.014

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С	Gene Symbol	I Description		p-value
	Etfa	electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)	1.29462	0.033
	Ndufs6	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)	1.29164	0.007
	Ndufa7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa	1.27237	0.012
	Atp5O	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)	1.24745	0.013
	Ndufa3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa	1.24078	0.044
	Ndufb4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa	1.18531	0.025
	Atp5G2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C2 (subunit 9)	1.18196	0.022
	Ndufb5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa	1.1361	0.029
	Uqcrc2	ubiquinol-cytochrome c reductase core protein II	1.10196	0.037
	Atp5L	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G	1.22204	0.009
	Ndufa4L2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	0.857329	0.008

Figure 7. Transcriptome Changes in  $\beta$  Cells upon Premature Weaning

(A) Cell-cycle-related gene sets that are significantly induced (gray bars) or unchanged (white bars) in β cells of prematurely weaned p25 mice compared with β cells from suckling littermates. Note that gene sets that have changed are preferentially associated with early phases of the cell cycle and not with G2 and mitosis. (B) Cell-cycle-related genes induced in GFP-positive  $\beta$  cells from prematurely weaned mice. Gene sets used were from Reactome pathway analysis and Whitfield et al. (2002).

(C) Oxidative phosphorylation-related genes induced in GFP-positive  $\beta$  cells from prematurely weaned mice. See also Figures S4 and S5 and Table S1.