

**Table S6 Cyclin C-Dependent Genes**

GO-Functional Annotation Clusters for repressed genes in *Ccnc*<sup>-/-</sup> MEFs. The following clusters (1-4) resulting from DAVID-GO Functional Annotation Clustering, represent the genes repressed (2,353 genes).

Cluster	ES <sup>a</sup>	Category <sup>b</sup>	Associated Terms	p-value	Number of Genes Involved
1	19.06	UP KEYWORDS	Mitochondrion	1.52E-26	222
		GOTERM CC DIRECT	Mitochondrion	1.68E-25	327
		UP KEYWORDS	Transit peptide	4.91E-19	121
2	6.78	UP KEYWORDS	Oxidoreductase	8.07E-8	109
		GOTERM BP DIRECT	Oxidation-reduction process	1.91E-7	121
		GOTERM MF DIRECT	Oxidoreductase activity	3.16E-7	110
3	4.49	GOTERM MF DIRECT	Cadherin binding involved in cell-cell adhesion	2.44E-6	59
		GOTERM CC DIRECT	Cell-cell adherens junction	2.67E-5	60
		GOTERM BP DIRECT	Cell-cell adhesion	5.11E-4	38
4	3.23	UP KEYWORDS	Cell cycle	3.32E-7	105
		GOTERM BP DIRECT	Cell cycle	1.76E-5	104
		UP KEYWORDS	Cell division	1.85E-3	57
		GOTERM BP DIRECT	Cell division	1.02E-2	58
		GOTERM BP DIRECT	Mitotic nuclear division	1.73E-2	44
		UP KEYWORDS	Mitosis	2.16E-2	38

<sup>a</sup> ES = Enrichment score produced by Functional Annotation Clustering in DAVID.

<sup>b</sup> Category Terms Defined: UP Keywords = Uniprot Keywords; GOTERM CC DIRECT = GO Term for Direct Localization to Cellular Compartment; GOTERM BP DIRECT = GO Term for Direct Involvement in Biological Process;; GOTERM MF DIRECT = GO Term for Direct Involvement in Molecular Function