

Table S7 Cyclin C-Repressed Genes

GO-Functional Annotation Clusters for induced genes in *Ccnc*^{-/-} MEFs. The following clusters (1-4) resulting from DAVID-GO Functional Annotation Clustering, represent the genes induced (2,482 genes).

Cluster	ES ^a	Category ^b	Associated Terms	p-value	Number of Genes Involved
1	8.39	UP KEYWORDS	Lysosome	3.03E-11	65
		GOTERM CC DIRECT	Lysosomal membrane	1.80E-8	59
		GOTERM CC DIRECT	Lysosome	1.23E-7	73
2	6.68	UP KEYWORDS	Ubl conjugation pathway	3.14E-12	128
		GOTERM MF DIRECT	Ubiquitin-protein transferase activity	2.27E-6	70
		GOTERM BP DIRECT	Protein ubiquitination	3.31E-6	75
		GOTERM MF DIRECT	Ligase activity	8.38E-5	70
3	6.56	UP KEYWORDS	Protein transport	1.35E-10	115
		GOTERM BP DIRECT	Protein transport	5.34E-9	121
		UP KEYWORDS	Transport	9.79E-6	265
		GOTERM BP DIRECT	Transport	8.34E-4	264
4	3.51	KEGG PATHWAY	Melanogenesis	3.80E-6	29
		GOTERM BP DIRECT	Canonical Wnt signaling pathway	2.80E-4	24
		KEGG PATHWAY	Wnt signaling pathway	1.22E-3	30
		KEGG PATHWAY	Basal cell carcinoma	6.99E-3	14

^a ES = Enrichment score produced by Functional Annotation Clustering in DAVID.

^b Category Terms Defined: UP Keywords = Uniprot Keywords; GOTERM CC DIRECT = GO Term for Direct Localization to Cellular Compartment; GOTERM MF DIRECT = GO Term for Direct Involvement in Molecular Function; GOTERM BP DIRECT = GO Term for Direct Involvement in Biological Process; KEGG PATHWAY = KEGG Pathway Association