

Table S3 Oxidative Stress-Repressed Genes in WT MEFs

GO-Functional Annotation Clusters for repressed genes in WT MEFs following oxidative stress. The following clusters (1-4) resulting from DAVID-GO Functional Annotation Clustering, represent the genes repressed (1,966 genes).

Cluster	ES ^a	Category ^b	Associated Terms	p-value	Number of Genes Involved
1	12.41	GOTERM MF DIRECT	Cadherin binding involved in cell-cell adhesion	8.73E-17	76
		GOTERM CC DIRECT	Cell-cell adherens junction	3.83E-15	78
		GOTERM BP DIRECT	Cell-cell adhesion	1.80E-7	43
2	6.88	GOTERM MF DIRECT	Transferase Activity	5.38E-9	210
		GOTERM BP DIRECT	Protein phosphorylation	1.28E-8	99
		GOTERM MF DIRECT	ATP binding	1.42E-8	212
		GOTERM BP DIRECT	Phosphorylation	1.93E-8	103
		GOTERM MF DIRECT	Kinase activity	3.07E-8	111
3	6.84	UP KEYWORDS	Cell cycle	4.25E-10	102
		UP KEYWORDS	Cell division	1.93E-9	69
		GOTERM BP DIRECT	Cell cycle	1.64E-7	100
		GOTERM BP DIRECT	Cell division	1.81E-7	69
		UP KEYWORDS	Mitosis	9.54E-6	45
		GOTERM MF DIRECT	Mitotic nuclear division	4.06E-5	49
4	5.90	UP KEYWORDS	Oxidoreductase	1.69E-7	95
		GOTERM BP DIRECT	Oxidation-reduction process	2.55E-6	100
		GOTERM MF DIRECT	Oxidoreductase activity	4.73E-6	94

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

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