■ **Table S4 Oxidative Stress-Induced Genes in WT MEFs**

GO-Functional Annotation Clusters for induced genes in WT MEFs following oxidative stress. The following clusters (1-4) resulting from DAVID-GO Functional Annotation Clustering, represent the genes induced (1,875 genes).

Cluster	ES[a]	Category[b]	Associated Terms	p-value	Number of Genes Involved
1	**6.38**	GOTERM BP DIRECT	Cellular response to DNA damage stimulus	1.86E-8	72
		UP KEYWORDS	DNA damage	6.44E-8	58
		GOTERM BP DIRECT	DNA repair	1.82E-6	54
		UP KEYWORDS	DNA repair	1.36E-5	45
2	**4.93**	UP KEYWORDS	Ubl conjugation pathway	4.44E-9	95
		GOTERM BP DIRECT	Protein ubiquitination	4.68E-6	58
		GOTERM MF DIRECT	Ubiquitin-protein transferase activity	1.50E-4	49
		GOTERM MF DIRECT	Ubiquitin protein ligase activity	6.26E-3	29
3	**4.15**	GOTERM BP DIRECT	Autophagy	8.16E-6	30
		GOTERM CC DIRECT	Autophagosome	2.05E-4	16
		GOTERM BP DIRECT	Autophagosome assembly	3.38E-3	11
4	**3.46**	UP KEYWORDS	Protein Transport	4.47E-6	79
		GOTERM BP DIRECT	Protein transport	4.43E-5	80
		UP KEYWORDS	Transport	4.55E-3	185
		GOTERM BP DIRECT	Transport	1.55E-2	182

[a] ES = Enrichment score produced by Functional Annotation Clustering in DAVID.
[b] Category Terms Defined: GOTERM BP DIRECT = GO Term for Direct Involvement in Biological Process; UP Keywords = Uniprot Keywords; GOTERM MF DIRECT = GO Term for Direct Involvement in Molecular Function; GOTERM CC DIRECT = GO Term for Direct Localization to Cellular Compartment