

Supplementary table 4: Modulated pathways highlighted by the DAVID functional annotation clustering tool, for cells treated with colloidal silica [10]

<b>Annotation Cluster 1</b> Enrichment Score: 4,18144249257887						
Category	Term	Count	PValue	Genes	Fold Enrichment	FDR
GOTERM_CC_DIRECT	<b>GO:000502~proteasome complex</b>	6	1,09E-05	P97372, Q9CX56, P99026, P46471, Q9R1P1, Q9Z2X2	20,31	0,00044
UP_KEYWORDS	<b>Proteasome</b>	5	6,66E-05	P97372, Q9CX56, P99026, P46471, Q9R1P1	22,75	0,00266
KEGG_PATHWAY	<b>mmu03050:Proteasome</b>	5	3,93E-04	P97372, Q9CX56, P99026, P46471, Q9R1P1	14,01	0,02710
<b>Annotation Cluster 2</b> Enrichment Score: 2,284642433915229						
Category	Term	Count	PValue	Genes	Fold Enrichment	FDR
INTERPRO	<b>IPR002108:Actin-binding, cofilin/tropomyosin type</b>	3	7,77E-04	Q9Z0P5, P18760, Q91YR1	70,21	0,19105
GOTERM_BP_DIRECT	<b>GO:0051016~barbed-end actin filament capping</b>	3	0,00228343	Q9Z0P5, P47754, Q91YR1	41,35	0,96008
UP_KEYWORDS	<b>Actin-binding</b>	4	0,07486874	Q9Z0P5, P47754, P18760, Q91YR1	4,04	0,39930
GOTERM_MF_DIRECT	<b>GO:0003779~actin binding</b>	5	0,074912681	Q9Z0P5, P47754, P18760, Q91YR1, P19973	3,11	0,75848
<b>Annotation Cluster 3</b> Enrichment Score: 2,2736727703379787						
Category	Term	Count	PValue	Genes	Fold Enrichment	FDR
UP_KEYWORDS	NADP	6	6,03E-04	Q923D2, Q9CY64, O88844, Q99LB6, Q8K2T1, Q64105	8,74	0,01609
UP_SEQ_FEATURE	binding site:NADP	3	0,006581131	O88844, Q8K2T1, Q64105	24,29	0,58387
UP_SEQ_FEATURE	nucleotide phosphate-binding region:NADP	3	0,038024095	O88844, Q8K2T1, Q64105	9,64	0,88596
<b>Annotation Cluster 4</b> Enrichment Score: 1,9799880012073776						
Category	Term	Count	PValue	Genes	Fold Enrichment	FDR
UP_KEYWORDS	<b>Tricarboxylic acid cycle</b>	3	0,004213574	O88844, Q9Z2I8, Q8BMF4	30,58	0,05618
KEGG_PATHWAY	<b>mmu01130:Biosynthesis of antibiotics</b>	3	0,004213574	O88844, Q9Z2I8, Q8BMF4	30,58	0,05618

GOTERM_BP_DIRECT	GO:0006099~tricarboxylic acid cycle	7	0,006195389	P12382, Q920E5, O88844, Q9Z0S1, Q9Z2I8, Q8BMF4, Q9D7G0	4,12	0,19892
KEGG_PATHWAY	<b>mmu01200:Carbon metabolism</b>	3	0,007439951	O88844, Q9Z2I8, Q8BMF4	22,81	0,96008
KEGG_PATHWAY	mmu01230:Biosynthesis of amino acids	5	0,012523794	P12382, O88844, Q9Z2I8, Q8BMF4, Q9D7G0	5,43	0,24690
KEGG_PATHWAY	mmu00020:Citrate cycle (TCA cycle)	4	0,021214743	P12382, O88844, Q99LB6, Q9D7G0	6,64	0,34820
		3	0,02555107	O88844, Q9Z2I8, Q8BMF4	11,82	0,35260
<b>Annotation Cluster 5</b>	Enrichment Score: 1,8522219849064838					
Category	Term					
UP_KEYWORDS	NADP	Count	PValue	Genes	Fold Enrichment	FDR
UP_KEYWORDS	<b>Oxidoreductase</b>	6	6,03E-04	Q923D2, Q9CY64, O88844, Q99LB6, Q8K2T1, Q64105 P09528, Q923D2, Q9CY64, O88844, Q9CQU0, P62259, P35700, Q64105	8,74	0,01609
GOTERM_MF_DIRECT	GO:0016491~oxidoreductase activity	8	0,012119744	P09528, Q923D2, Q9CY64, O88844, Q9CQU0, P35700, Q64105	3,19	0,12928
GOTERM_BP_DIRECT	GO:0055114~oxidation-reduction process	7	0,064679029	P09528, Q923D2, Q9CY64, O88844, Q9CQU0, P35700, Q64105	2,44	0,70853
		7	0,082458015	P09528, Q923D2, Q9CY64, O88844, Q9CQU0, P35700, Q64105	2,28	1,00000
<b>Annotation Cluster 6</b>	Enrichment Score: 1,8148662468770735					
Category	Term					
UP_KEYWORDS	<b>Mitochondrion</b>	Count	PValue	Genes	Fold Enrichment	FDR
UP_KEYWORDS	Transit peptide	13	7,77E-04	Q8BFR5, Q60930, P30416, Q9Z2I8, P70444, Q8BMF4, Q99J99, P67778, Q8K1Z0, P38060, O88441, Q9JIY5, Q9QYB1	3,13	0,01777
UP_SEQ_FEATURE	transit peptide:Mitochondrion	6	0,048392576	Q8BFR5, Q8K1Z0, P38060, Q9Z2I8, Q8BMF4, Q9JIY5	3,00	0,33173
		6	0,095493551	Q8BFR5, Q8K1Z0, P38060, Q9Z2I8, Q8BMF4, Q9JIY5	2,45	1,00000
<b>Annotation Cluster 7</b>	Enrichment Score: 1,7170923275646146					

Category	Term					
GOTERM_MF_DIRECT	<b>GO:0098641~cadherin binding involved in cell-cell adhesion</b>	Count	PValue	Genes	Fold Enrichment	FDR
GOTERM_CC_DIRECT	<b>GO:0005913~cell-cell adherens junction</b>	6	0,010125714	P10107, Q9Z0P5, O88844, Q91YR1, P62259, P35700	4,52	0,22185
GOTERM_BP_DIRECT	<b>GO:0098609~cell-cell adhesion</b>	6	0,013145635	P10107, Q9Z0P5, O88844, Q91YR1, P62259, P35700	4,24	0,20527
<b>Annotation Cluster 8</b>	Enrichment Score: 1,691469256512831	4	0,053029287	Q9Z0P5, O88844, Q91YR1, P35700	4,67	1,00000
Category	Term					
UP_KEYWORDS	Magnesium	Count	PValue	Genes	Fold Enrichment	FDR
UP_KEYWORDS	Metal-binding	9	9,45E-04	P12382, Q9QZE7, Q920E5, Q9WUL7, O88844, P55264, Q9Z0S1, Q9D7I5, Q9D7G0	4,40	0,01891
				P09528, Q8BFS6, Q9QZE7, Q920E5, P10107, P55264, Q9CY64, Q99L45, Q9CPU0, P46737, Q8BWU5, P12382, Q9WUL7, O88844, Q9Z0S1, P38060, Q9D7I5, P62137, Q9D7G0, Q3U1C6	1,50	0,35771
GOTERM_MF_DIRECT	GO:0046872~metal ion binding	20	0,060363647	P09528, Q8BFS6, Q9QZE7, Q920E5, P10107, P55264, Q9CY64, Q99L45, Q9Z2I8, Q9CPU0, P46737, Q8BWU5, P12382, Q9WUL7, O88844, Q9Z0S1, P38060, Q9D7I5, P62137, Q9D7G0, Q3U1C6	1,32	0,97571
		21	0,147647788			