

Table S5: Example of annotation clustering from DAVID describing two enriched processes, Glutathione metabolism and transcriptional regulation.					
Category	Term	Count	PValue	List Total	Fold Enrichment
INTERPRO	IPR003081:Glutathione S-transferase, Mu class	4	9.17E-05	275	40.58805195
INTERPRO	IPR004046:Glutathione S-transferase, C-terminal	5	0.001125184	275	10.76198347
INTERPRO	IPR004045:Glutathione S-transferase, N-terminal	5	0.001125184	275	10.76198347
GOTERM_BP_DIRECT	GO:0018916~nitrobenzene metabolic process	3	0.001306243	249	50.02710843
GOTERM_MF_DIRECT	GO:0004364~glutathione transferase activity	5	0.001350374	250	10.20451613
GOTERM_MF_DIRECT	GO:0043295~glutathione binding	4	0.001854759	250	15.817
<b>KEGG_PATHWAY</b>	<b>mmu00480:Glutathione metabolism</b>	<b>6</b>	<b>0.002019562</b>	<b>128</b>	<b>6.569318182</b>
INTERPRO	IPR010987:Glutathione S-transferase, C-terminal-like	5	0.003592444	275	7.892121212
GOTERM_BP_DIRECT	GO:0042178~xenobiotic catabolic process	3	0.004438218	249	28.5869191
GOTERM_BP_DIRECT	GO:0006749~glutathione metabolic process	5	0.004473115	249	7.411423472
KEGG_PATHWAY	mmu00980:Metabolism of xenobiotics by cytochrome P450	5	0.006215115	128	6.690972222
KEGG_PATHWAY	mmu00982:Drug metabolism - cytochrome P450	5	0.007815539	128	6.272786458
UP_SEQ_FEATURE	domain:GST N-terminal	4	0.008489343	255	9.420130719
UP_SEQ_FEATURE	domain:GST C-terminal	4	0.019907987	255	6.892778575
KEGG_PATHWAY	mmu05204:Chemical carcinogenesis	5	0.06493113	128	3.272758152
INTERPRO	IPR012336:Thioredoxin-like fold	5	0.122225117	275	2.630707071
GOTERM_BP_DIRECT	GO:0008152~metabolic process	10	0.291498366	249	1.378157257
Annotation Cluster 2	Enrichment Score: 2.202438644893318				
Category	Term	Count	PValue	List Total	Fold Enrichment
UP_KEYWORDS	Nucleus	86	2.44E-04	281	1.432714499
UP_KEYWORDS	Transcription	42	8.85E-04	281	1.694999913
<b>UP_KEYWORDS</b>	<b>Transcription regulation</b>	<b>39</b>	<b>0.002932861</b>	<b>281</b>	<b>1.626656414</b>
GOTERM_BP_DIRECT	GO:0006351~transcription, DNA-templated	40	0.012933994	249	1.466801787
UP_KEYWORDS	DNA-binding	33	0.014036324	281	1.541673065
GOTERM_MF_DIRECT	GO:0003677~DNA binding	37	0.041367714	250	1.372971261
GOTERM_BP_DIRECT	GO:0006355~regulation of transcription, DNA-templated	39	0.080401663	249	1.285281442