# **Supplementary Material**

Cordeiro et al., Insights on cryoprotectant toxicity from gene expression profiling of endothelial cells exposed to ethylene glycol

SM Table 1 – Three of the Annotation Clusters with the highest enrichment score, for the up-regulated genes at 24h from the comparison Cold/Negative Controls

Up 24h Cold/Negative		
Cluster	Enrichment Score	Number of genes
Response to wounding	8.34	60
Inflammatory response		37
Glycoprotein		258
Disulphide bond	6.49	177
Signal peptide		191
Regulation of cell	6.15	27
migration		

SM Table 2 - Three of the Annotation Clusters with the highest enrichment score, for the down-regulated genes at 24h from the comparison Cold/Negative Controls

Enrichment Score	Number of genes
23.23	103
20.1	75
20.1	29
0.46	104
9.46	
	225

SM Table 3 - Three of the Annotation Clusters with the highest enrichment score, for the up-regulated genes at 72h from the comparison Cold/Negative Controls

Up 72h Cold/Negative		
Cluster	Enrichment Score	Number of genes
Cytokine	10.68	17
Immune response	-	26
Inflammation	3.84	3
Immunosurveillance		5
Cell adhesion	3.38	6
Homeostatic process	-	6

## SM Table 4 - Annotation Cluster with the highest enrichment score, for the down-

regulated genes at 72h from the comparison Cold/Negative Controls

Down 72h Cold/Negative		
Cluster	Enrichment Score	Number of genes
Nucleotide Binding	1.14	3

SM Table 5 - Top 3 annotation clusters with the highest enrichment score of the 24h up-regulated EG vs Normal comparison

Enrichment Score	Number of genes
9.88	28
8.54	63
	34
8.31	242
	9.88 8.54

SM Table 6 - Top annotation clusters with the highest enrichment score of the 24h

down-regulated EG vs Normal comparison

Down 24h EG/Normal		
Cluster	Enrichment Score	Number of genes
Nuclear division	10.37	39
mitosis		39
kinetochore	7.22	15

SM Table 7 - Top annotation clusters with the highest enrichment score of the 72h up-regulated EG vs Normal comparison

Up 72h EG/Normal		
Cluster	Enrichment Score	Number of genes
Inflammatory response	11.14	42
Response to wounding		66
Angiogenesis	9.62	30

SM Table 9 - Top annotation clusters with the highest enrichment score of the 72h

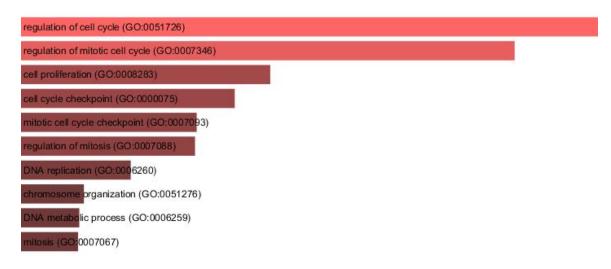
down-regulated EG vs Normal comparison

Down 72h EG/Norma	ıl	
Cluster	Enrichment Score	Number of genes
Mitosis	19.99	61
Kinetochore	15.37	27

cell motion (GO:0006928)	
leukocyte migration (GO:0050900)	
immune system process (GO:0002376)	
signal transduction (GO:0007165)	
cell communication (GO:0007154)	
cell migration (GO:0016477)	
cell motility (GO:0048870)	
locomotory behavior (GO:0007626)	
chemotaxis (GO:0006935)	
regulation of blood pressure (GO:0008217)	

## SM Figure 1 - Gene ontology of the 24h up-regulated Cold/Negative Controls

### comparison



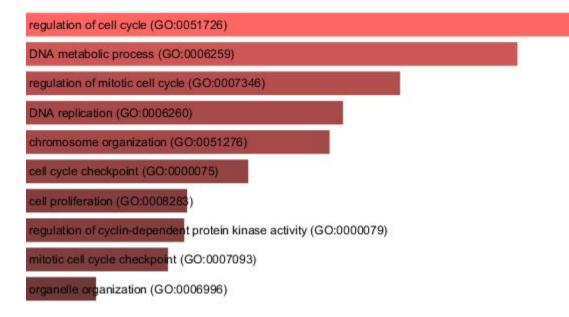
## SM Figure 2 - Gene ontology of the 24h down-regulated Cold/Negative Controls

### comparison

regulation of cell cycle (GO:0051726)
DNA metabolic process (GO:0006259)
regulation of mitotic cell cycle (GO:0007346)
DNA replication (GO:0006260)
chromosome organization (GO:0051276)
cell cycle checkpoint (GO:0000075)
cell proliferation (GO:0008283)
regulation of cyclin-dependent protein kinase activity (GO:0000079)
mitotic cell cycle checkpoint (GO:0007093)
organelle organization (GO:0006996)

### SM Figure 3 – Gene ontology of the 72h down-regulated Cold/Negative Controls

#### comparison



#### SM Figure 4 - Gene ontology of the 72h up-regulated Cold/Negative Controls

#### comparison