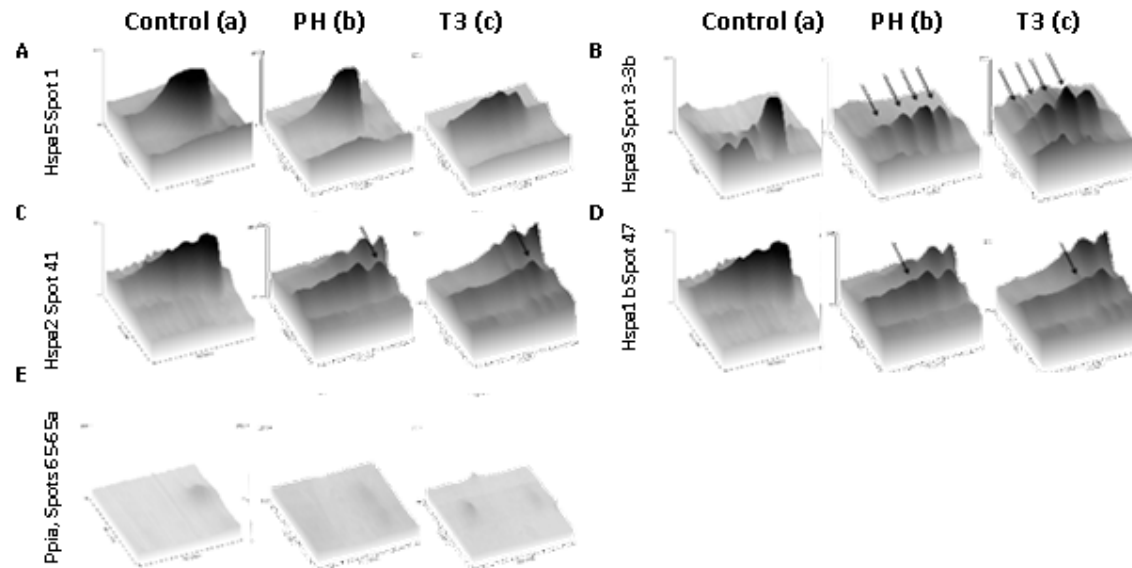
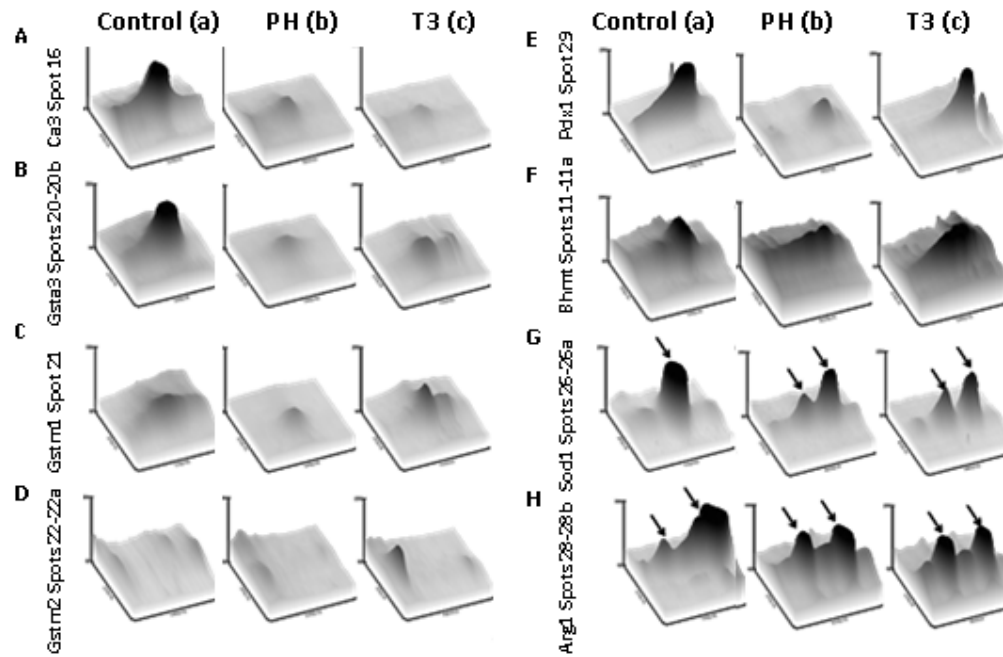


Supporting Information

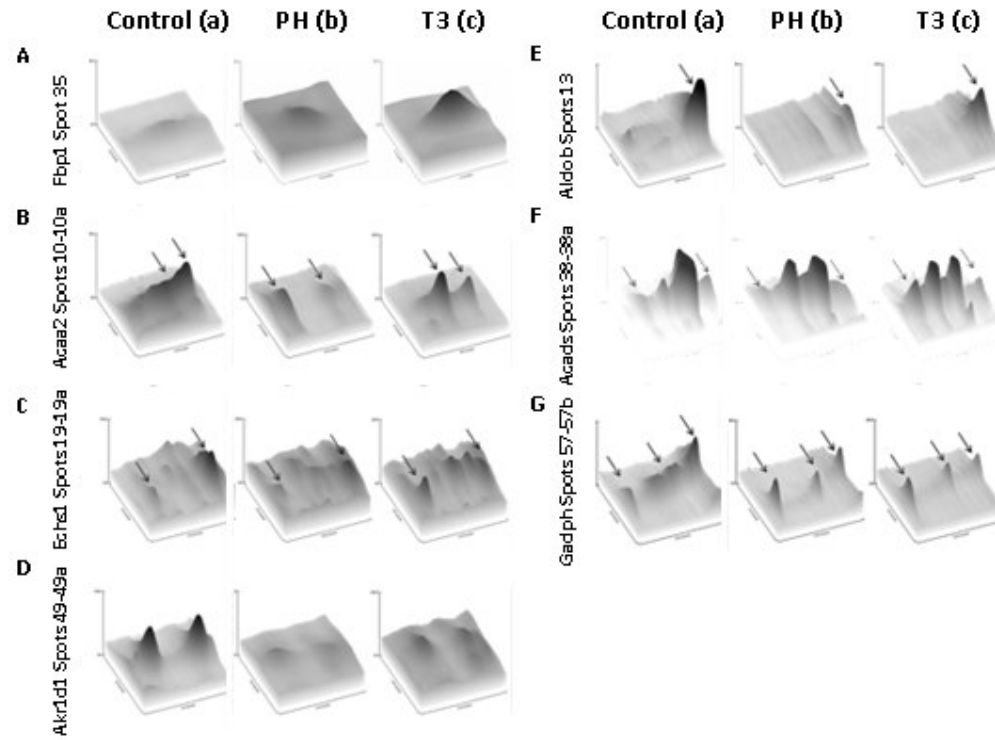
Supplementary Figure 1. Expression profiles of spots corresponding to molecular chaperones, folding catalyst and heat shock proteins. Magnifications related to 78 kDa glucose regulated protein (Hspa5, A), stress 70 protein mitochondrial (Hspa9, B), heat shock related 70 kDa (Hspa2, C), heat shock 70 kDa (Hspa1b, D) and peptidyl-prolyl cis-trans isomerase (Ppia, E) are reported.



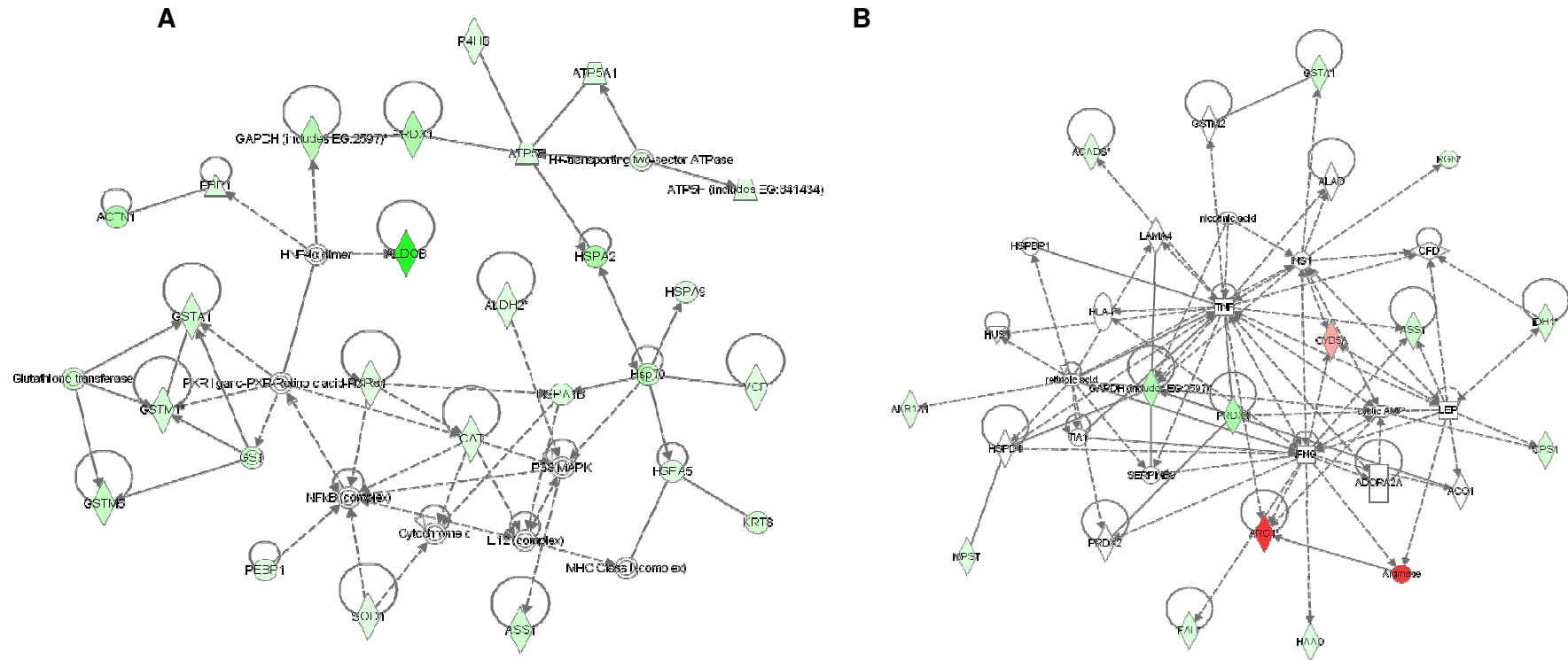
Supplementary Figure 2. Expression profiles of spots corresponding to proteins involved in the oxidative stress response. Magnifications related to carbonic anhydrase III (Ca3, A), glutathione S-transferase Yc 1 (Gsta3, B), Yb1 (Gstm1, C), Yb2 (Gstm2, D), peroxiredoxin 1 (Pdx1, E), betaine homocysteine S-methyltransferase (Bhmt, F), superoxide dismutase (Sod1, G) and liver arginase 1 (Arg1, H) are reported.



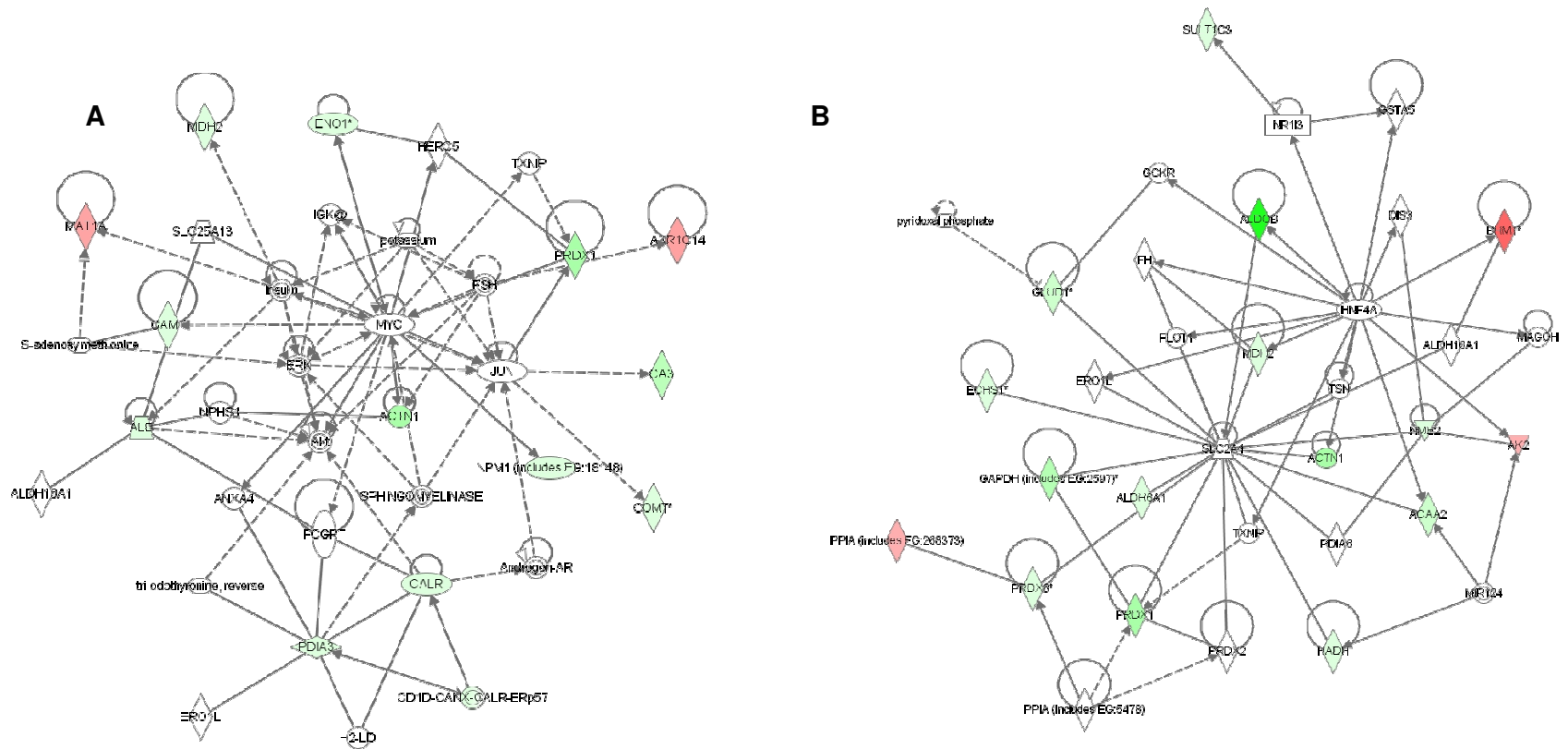
Supplementary Figure 3. Expression profiles of spots involved in metabolic processes. Magnifications related to fructose 1,6 bisphosphatase (Fbp1, A), fructose bisphosphate aldolase B (Aldob, B), 3 ketoacyl CoA thiolase (Acaa2, C), acyl CoA dehydrogenase (Acads, D), enoyl CoA hydratase (Echs1, E), glyceraldehyde 3 phosphate dehydrogenase (Gapdh, F) and 3-oxo-5 beta steroid 4 dehydrogenase (Akr1d1, G) are reported.



Supplementary Figure 4. Protein interaction networks obtained for the differentially expressed proteins identified in PH sample. Gene products are represented as nodes and biological relationships between two nodes as a line. The up- and down-regulated input proteins are coloured in red and green, respectively. The pathway components identified by the algorithm and not detected in the analysis are reported in white. The NFkB-p38MAPK and TNF-INF γ networks are reported in A and B, respectively.



Supplementary Figure 5. The MYC-ERK-AKT and GLUT4 (SLC2A4)-Hepatocyte nuclear factor 4a (HNF4A) networks obtained for the differentially expressed proteins identified in PH sample are reported in A and B, respectively. For network representation details see legend of Supplementary Figure 4.



Supplementary Figure 6. Protein interaction networks obtained for the differentially expressed proteins identified in T3 sample. The NFkB-p38MAPK and GLUT4-Leptin (LEP) networks obtained for the differentially expressed proteins identified in T3 sample are reported in A and B, respectively. For network representation details see legend of Supplementary Figure 4.

