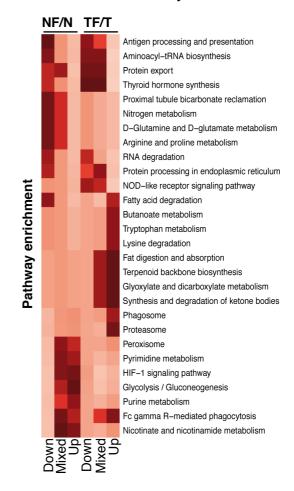
Gene Set Analysis full list

NF/N TF/T Ribosome biogenesis in eukaryotes Aminoacyl-tRNA biosynthesis Protein processing in endoplasmic reticulum Ribosome Pathway ranking 50 Porphyrin and chlorophyll metabolism Glycine, serine and threonine metabolism Protein export 100 RNA transport Valine, leucine and isoleucine biosynthesis 150 Linoleic acid metabolism Retinol metabolism 200 Dorso-ventral axis formation Protein digestion and absorption Basal transcription factors RNA degradation Selenocompound metabolism Tyrosine metabolism Pathway enrichment Vitamin B6 metabolism Drug metabolism - cytochrome P450 Cytokine-cytokine receptor interaction Steroid biosynthesis Fructose and mannose metabolism p53 signaling pathway Nucleotide excision repair Homologous recombination HIF-1 signaling pathway PI3K-Akt signaling pathway **Apoptosis** Terpenoid backbone biosynthesis Biosynthesis of unsaturated fatty acids Synthesis and degradation of ketone bodies Progesterone-mediated oocyte maturation

Ubiquitin mediated proteolysis
Propanoate metabolism
Oocyte meiosis
Fanconi anemia pathway
Mismatch repair
Peroxisome
DNA replication
Lysosome
Cell cycle

Protein Set Analysis full list



S5 Fig. Analysis of transcriptomic and proteomic data using PIANO method. The heatmap shows the result obtained by applying the PIANO tool to gene (A) and protein (B) datasets separately. In particular, the top 10-ranked pathways associated to each comparison, NF/N and TF/T, are shown. The different color of the heatmap represents the rank position of the pathway in the two different comparisons.