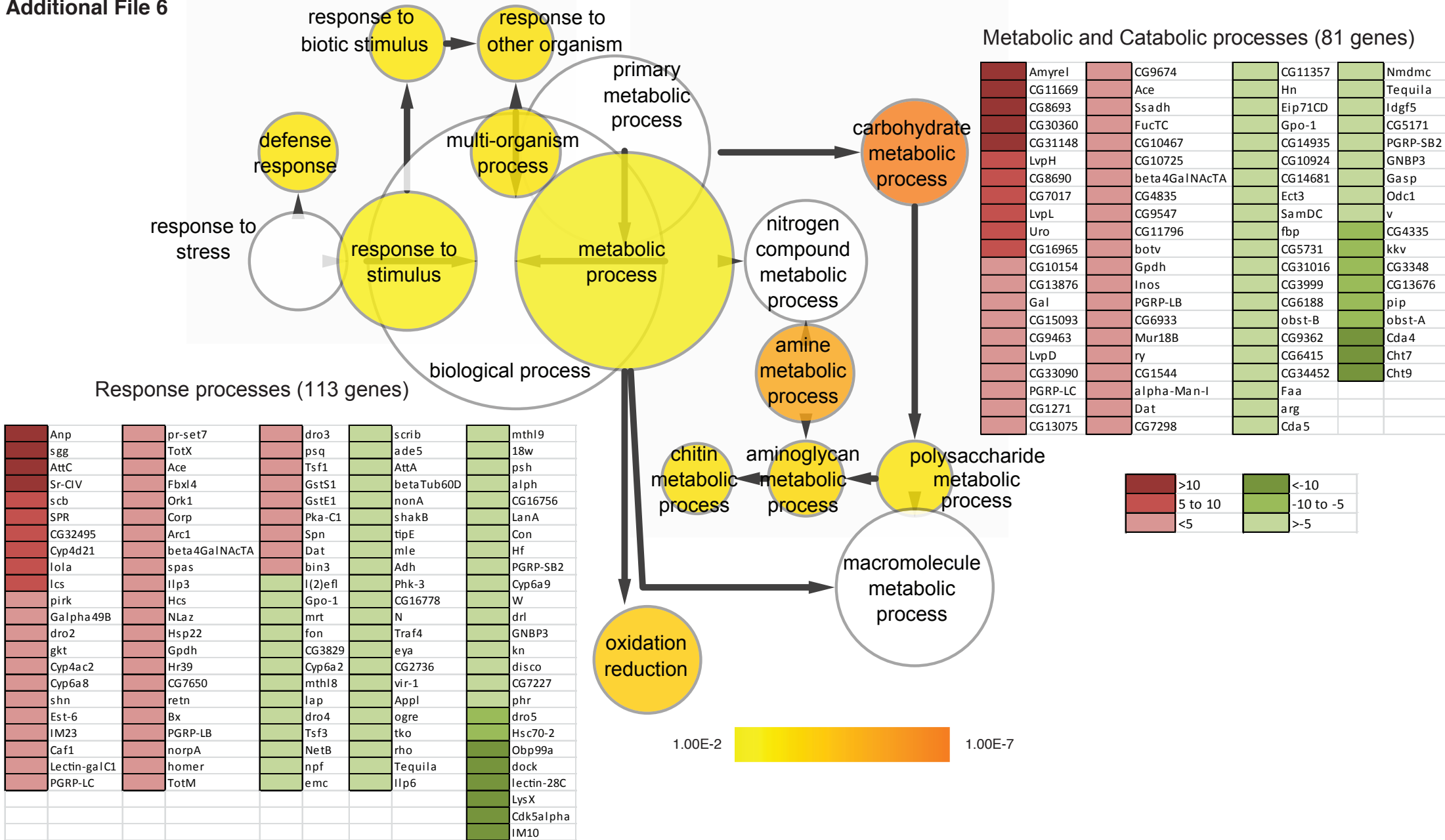


Additional File 6



Additional file 6. GSEA of the 961 differentially expressed transcripts in *nub1* gut. Differentially expressed transcripts (961) were subjected to GSEA and enriched clusters were extracted. This figure should be statistically interpreted as follows: The nodes, corresponding to different Gene Ontology clusters, are either not colored (white) i.e. not found with any statistical power or colored in the scale yellow to orange, where yellow nodes are found with statistical significance after Bonferroni correction $p < 0.01$ and orange colored nodes are found with increasing statistical significance after correction, with a $p < 7 \times 10^{-7}$. The size of the circles reflects the number of genes found in each Biological Process, where a smaller circle contains less genes than a larger. The grey-zoned data highlights statistically enriched clusters of nodes (genes/transcripts), which all are represented under the manually designated heading e.g. 'Response processes' or 'Metabolic and Catabolic processes'. The color-coded table represents the differentially regulated genes found under each grey-zoned heading (different shades of green < -5 fold change, different shades of red > 5 fold change). The three GO processes, including multi-organism process (38 genes), response to biotic stimulus (24 genes) and defense response genes (27 genes) together with additional nodes with similar functions and genes, resulted in a list of 113 unique genes all of which we here call 'Response processes' and this combined cluster is significantly enriched ($p < 0.00001$).