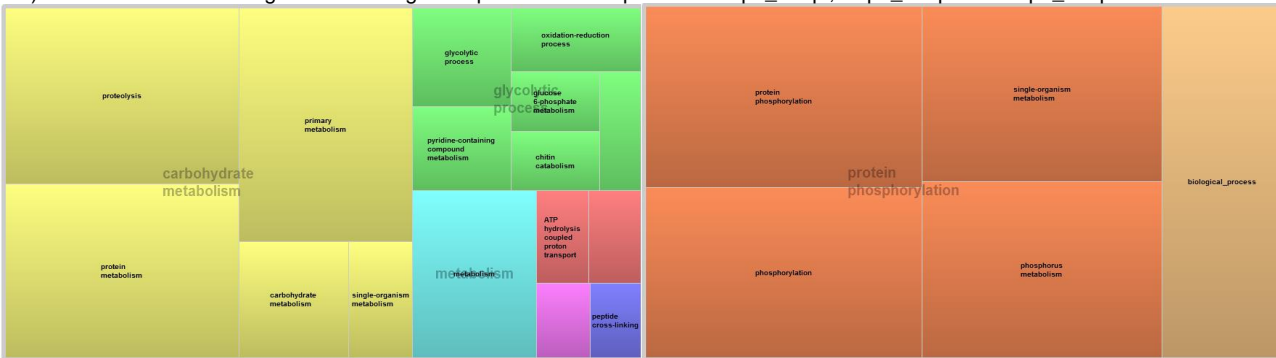


## Higher in lice from gills

## Higher in lice from skin

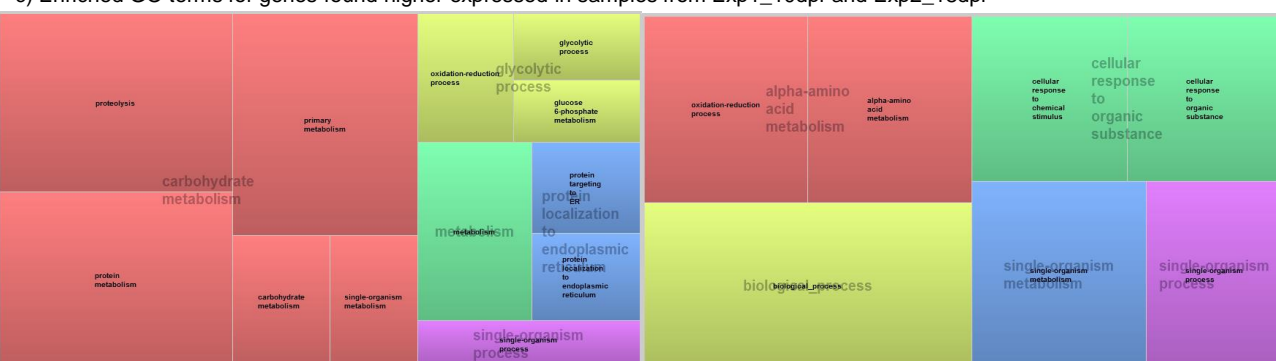
a) Enriched GO terms for genes found higher expressed in samples from Exp1\_10dpi, Exp2\_10dpi and Exp2\_18dpi



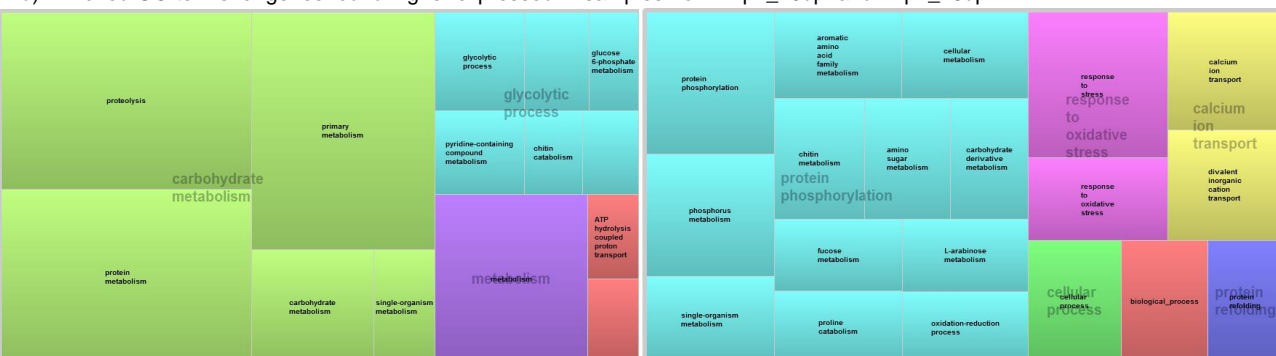
b) Enriched GO terms for genes found higher expressed in samples from Exp1\_10dpi and Exp2\_10dpi



c) Enriched GO terms for genes found higher expressed in samples from Exp1\_10dpi and Exp2\_18dpi



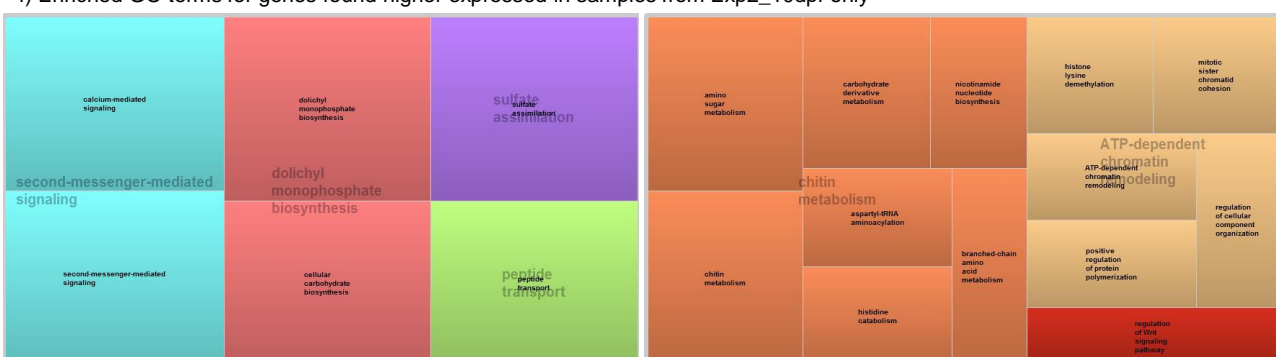
d) Enriched GO terms for genes found higher expressed in samples from Exp2\_10dpi and Exp2\_18dpi



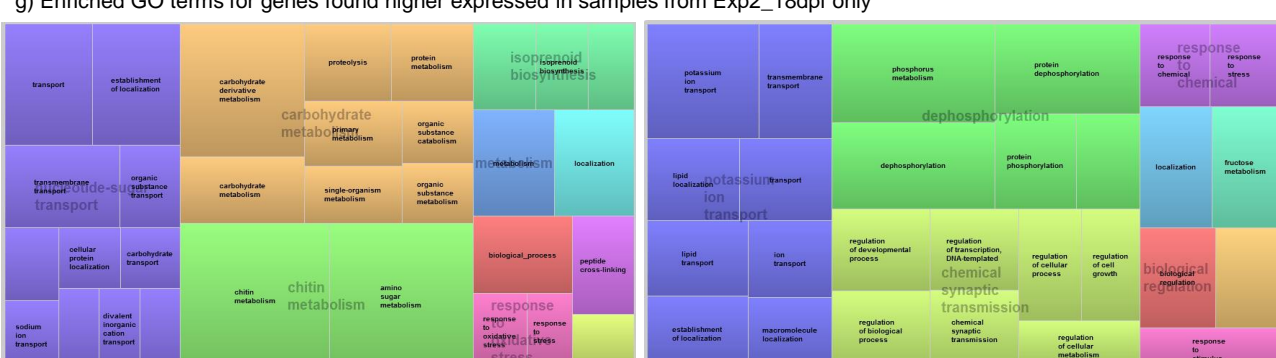
e) Enriched GO terms for genes found higher expressed in samples from Exp1\_10dpi only



f) Enriched GO terms for genes found higher expressed in samples from Exp2\_10dpi only



g) Enriched GO terms for genes found higher expressed in samples from Exp2\_18dpi only



**Figure S1.** Tree maps (Revigo) of enriched GO annotation belonging to biological process. Shown are tree maps for GO annotations enriched in genes found higher expressed in samples from all three samplings (DESeq2; padj < 0.05) (a), of the genes differentially expressed in both samplings at 10 days post-infestation (dpi) (b); and in 2 samplings sampled at different time point (c and d). In e- g are enriched GO annotations shown for genes differentially expressed in one of the three samplings only.