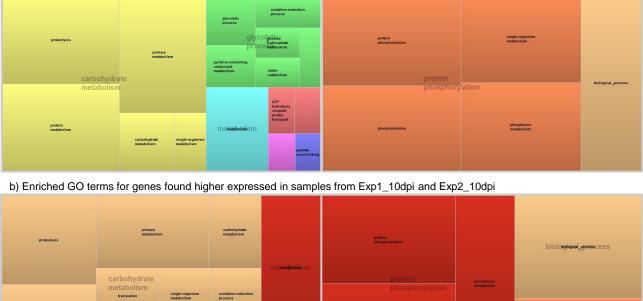
Higher in lice from gills

Higher in lice from skin

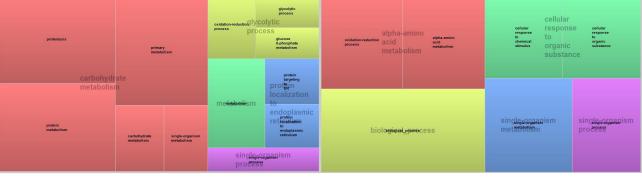
mitachondrial fusitin

a) Enriched GO terms for genes found higher expressed in samples from Exp1_10dpi, Exp2_10dpi and Exp2_18dpi



protein metabolism organic glycolytic organic containing compound metabolism glycolytic metabolism compound metabolism compoun

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

protociyile	primany, metabolism		glycolytic process CIV	colytic	glucose 6-phosphate metabolism	protein phosphorylation	aromatic amino acid family metabolism	;	sellular netabolism	response to FeStress		calcium ion transport	
carbohydrate			process pyridine-containing compound metabolism catabolism				chitin metabolism protein	amino sugar metabolism	carbohydrate dorivative metabolism	to oxidative stress		calcium ion transport divalent inorgania sation	
metabolism					ATP hydrolysis coupled proton transport	phosphorus metabolism	phosphoryla fucose metabolism		arabinose netabolism	to oxidative stress		cation transport	
protein metabolism	carbohydrate single-organism metabolism metabolism	me iadonii sm			single-organism metabolism	proline catabolism	oxidation-reduction process		cellular process	biological_pro	process protein renditing		

e) Enriched GO terms for genes found higher expressed in samples from Exp1_10dpi only

gene expression		organic substance metabolism	DKA conformation change chromosome change organization chromosome organization		transmembrane transport transport		regulation of response to stimulus of intracellular of intracellular			microtubule cytosketen organizatije) croteriorina cytosketeton organization eli						
proteolysis cellular Involved macromolecule translational in metabolism			organelle organization					of small GTPase		termination regulati of G-protein of G-pro coupled coupled receptor recepto signaling protein	on Itein I	division				
protein	cofactor			hydrogen ion transmembrane biological_pro transport		ester			ester@ transport	transduction			biological_proc		loomization	
metabolism metabolism metabolism			protein transport	cellular component organization or biogenesis		phosphotipid amino transport transmem transport			protein phosphorylation protein phos phorylation		phosphorus metabolism					
	mRNA splice											1				
	ellular biosynthesis site selection selection regulation of phosphorus regulation	regulation	me talsoli sm	cellular process	protein folding	vesicle docking involved in executosis	intracellular protein transport	secretion	cellular metabolism	single-organism cellular process	cellular aldehyde metabolism	adfleston	cell adffestion	cellular process		
	involved in etilular protein catabolignen transcription, DNA-templated	probologijste divisionality postanice postanic	protectives in control of the second of the	Protocytical protocytical estimation material materi	Franklikov novovova novovovo novovovo novovovo novovovo novovovo novovo novovo novovo novovo novovovo no novovo no no no no no no no no no	Sector Sector<	Image: state in the state i	Lance Lance State St	Image: Section	$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	$ \begin{tabular}{ c c c c } \hline \begin{tabular}{ c c c c c } \hline \begin{tabular}{ c c c c c c } \hline \begin{tabular}{ c c c c c c c } \hline \begin{tabular}{ c c c c c c c } \hline \begin{tabular}{ c c c c c c c c c c c c c c c c c c c$		$ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \$	$ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \$	$ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \$	

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.