Supplementary figures

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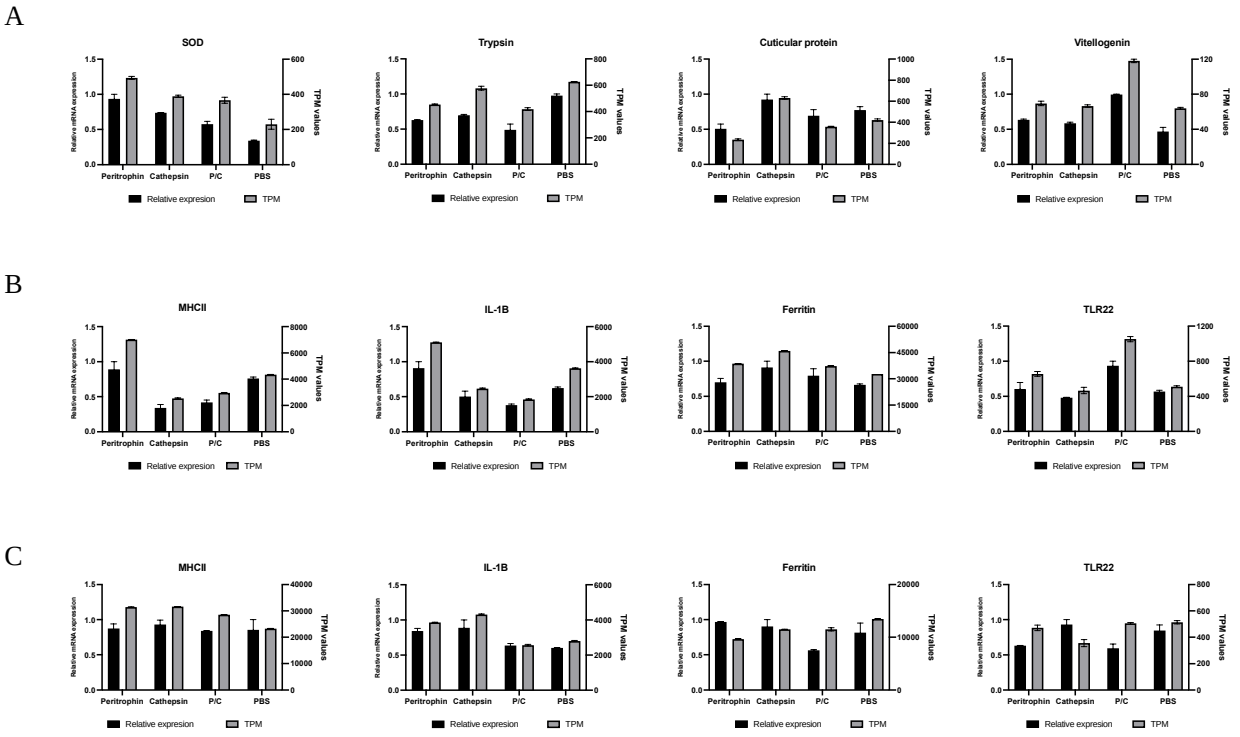

Figure S1. RT-qPCR validation of genes expressed in immunized *Salmo salar* and exposed sea lice. A) RT-qPCR validation of genes expressed in sea lice. B) RT-qPCR validation of genes expressed in *S. salar* skin tissue. C) RT-qPCR validation of genes expressed in *S. salar* head kidney tissue.

Figure S2. GO annotation of Biological Process identifies in genes differentially expressed in vaccinated *S. salar* and *C. rogercresseyi* collected from vaccinated fish. Bars indicate the number of hits for the GO categories.

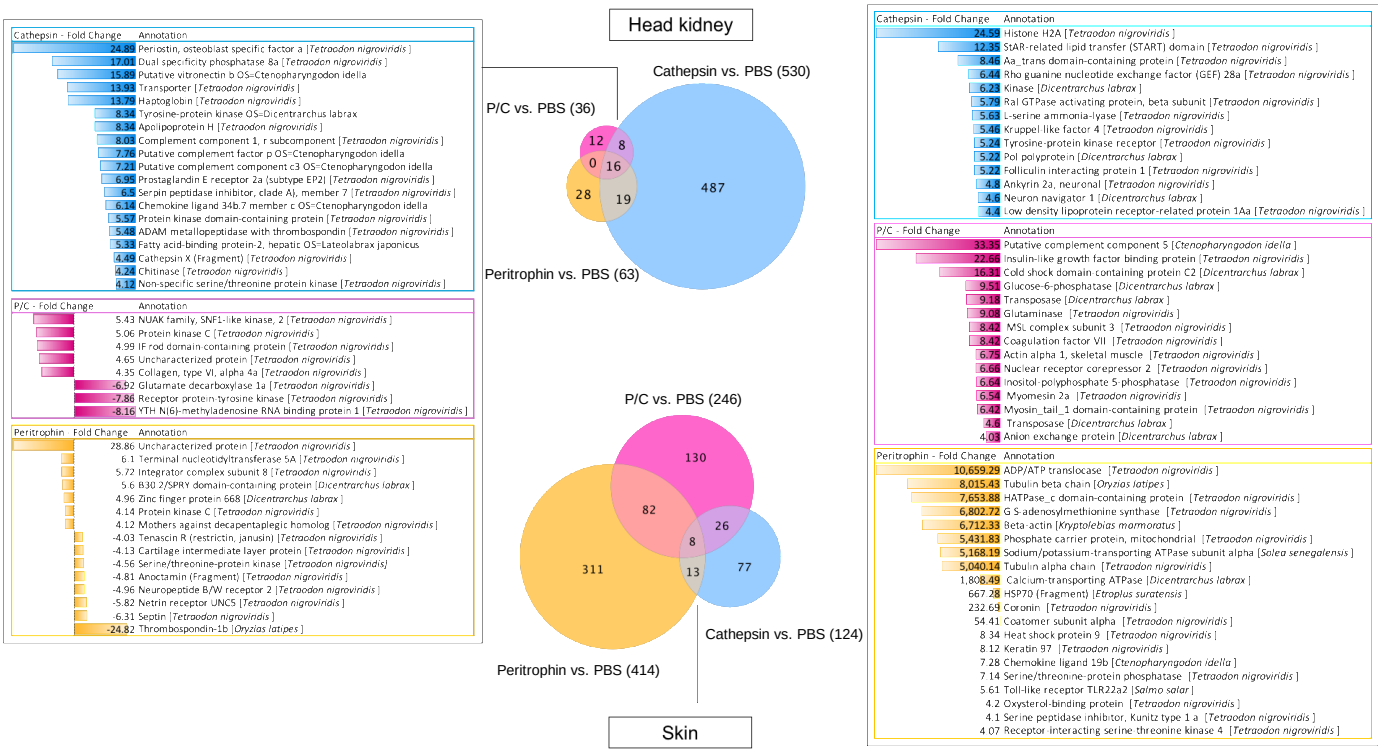

Figure S3. Differential expression analysis of genes associated with chromosomal regions with CGE = 100% in vaccinated Atlantic salmons. Venn diagram showing the distribution of contigs differentially expressed. Colored bars indicate the genes fold change: cathepsin in blue, peritrophin in yellow, and purple for the P/C combination.

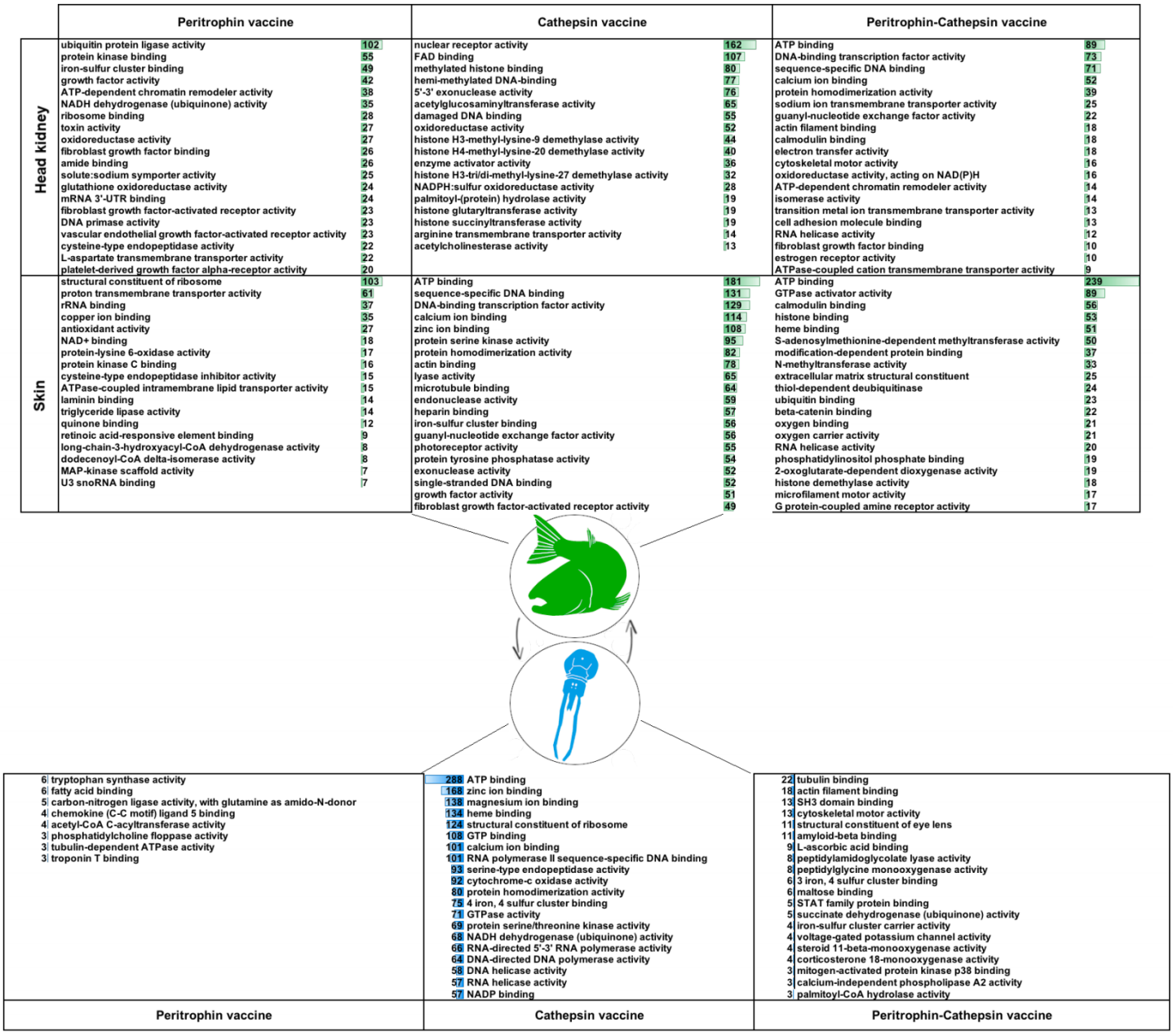

Figure S4. GO annotation of Molecular Function identifies in genes differentially expressed in vaccinated *S. salar* and *C. rogercresseyi* collected from vaccinated fish. Bars indicate the number of hits for the GO categories.

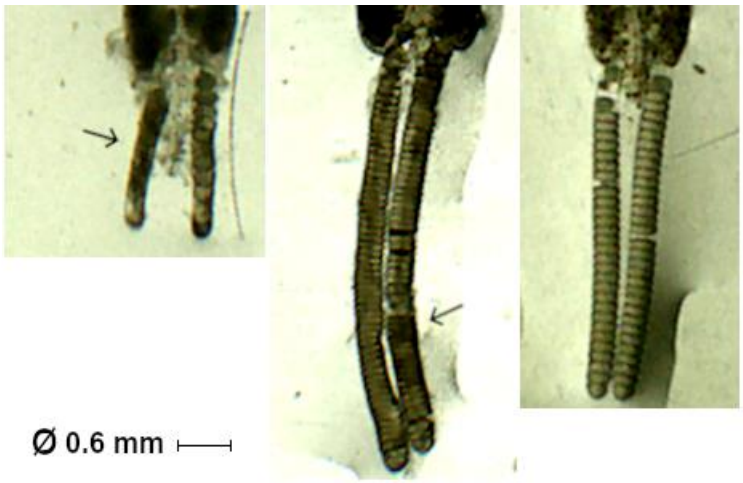

Figure S5. Phenotypic malformations of female *Caligus rogercresseyi* exposed to (A) cathepsin, (B) peritrophin, and (C) PBS-vaccinated fish. Images were taken under the same conditions with a 2X objective lens. The arrows indicate alterations concerning the control groups. The scale of 0.6 mm indicated by the black circle is equivalent in all the images of the figure