

Additional file 2: supplementary Figures

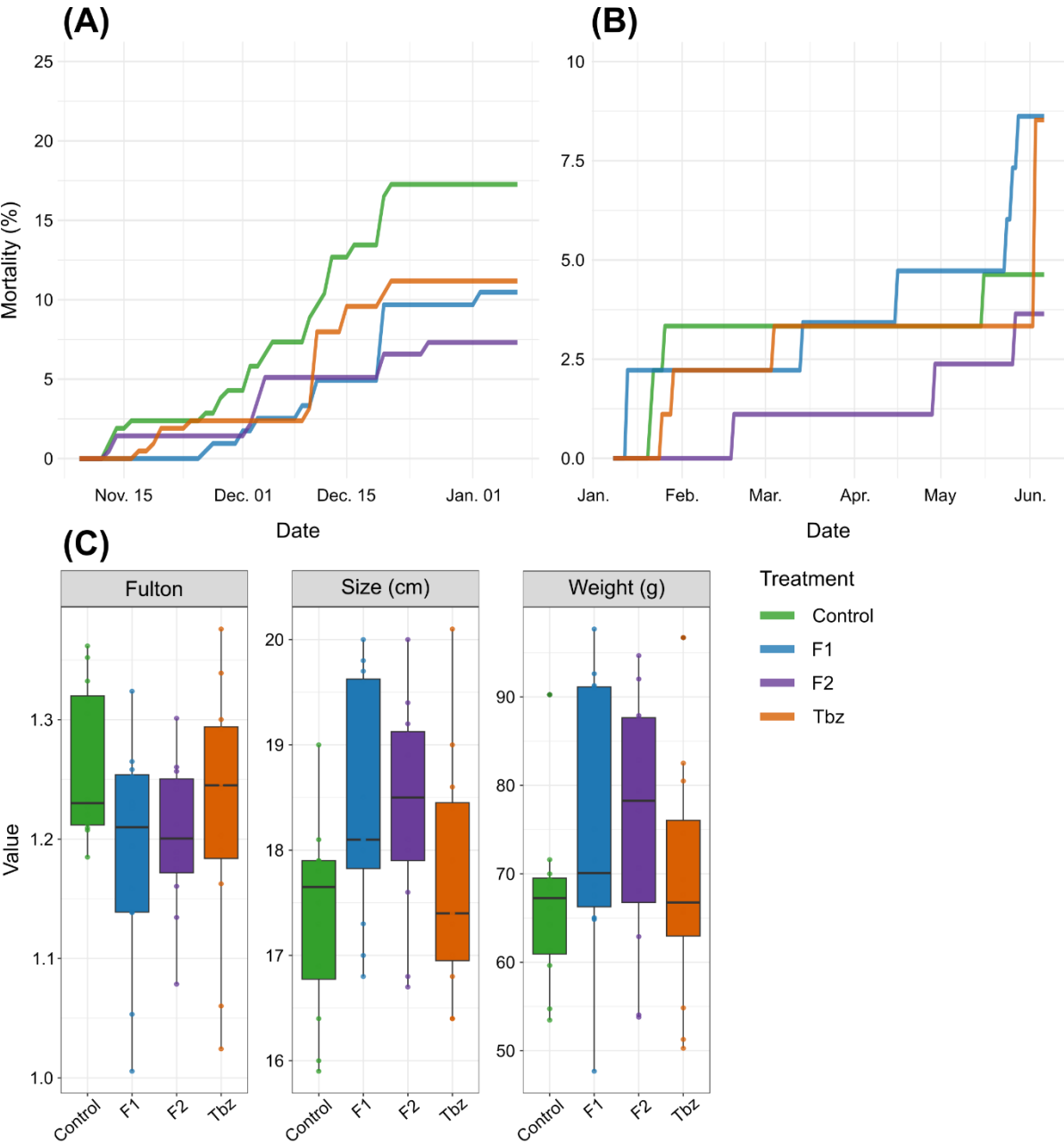


Figure S1. Rainbow trout mortality (A, B) and growth parameter (C). Mortality was recorded daily from November 9, 2023, until June 6, 2024 (sampling day). (A) Mortality until the end of larval stage (maintained in 10 L aquaria). (B) Mortality of juvenile fish (maintained in 50 L aquaria). (C) Fulton index, size (cm) and weight (g) of trout sampled on 06/06/2024. Colours of lines and points indicate the experimental condition.

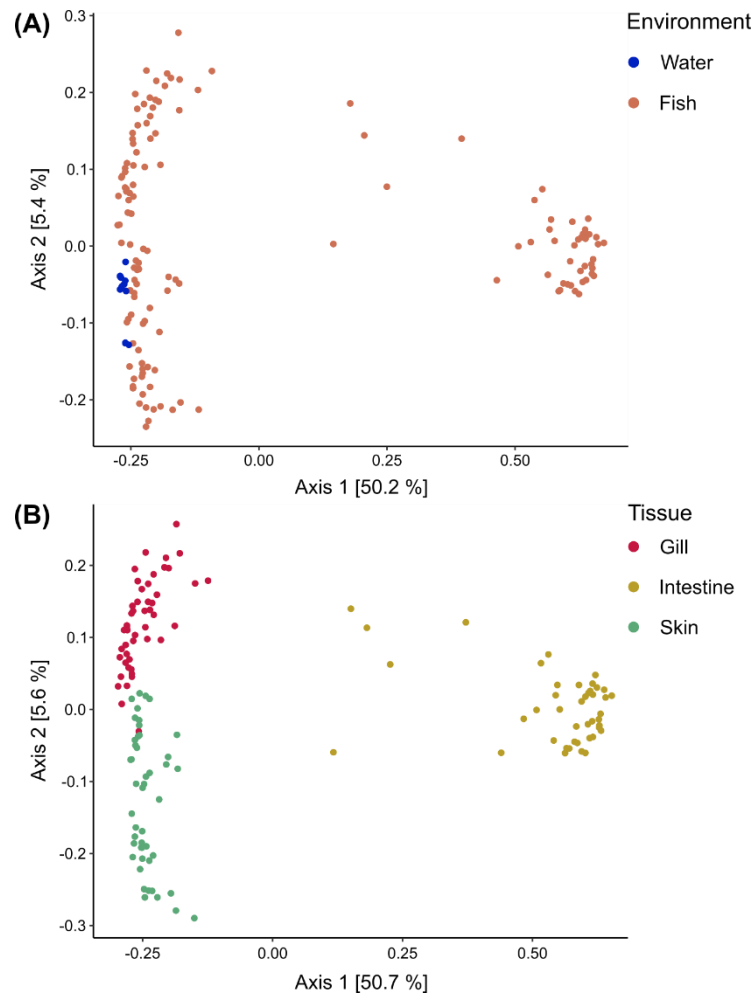


Figure S2. Principal Coordinates Analysis (PCoA) based on Bray-Curtis dissimilarity matrices. Points represent individual samples and are coloured according to (A) environment or (B) tissue. Percentages on the axes indicate the proportion of variance explained by each principal coordinate. Data were normalized using cumulative sum scaling (CSS) prior to ordination.

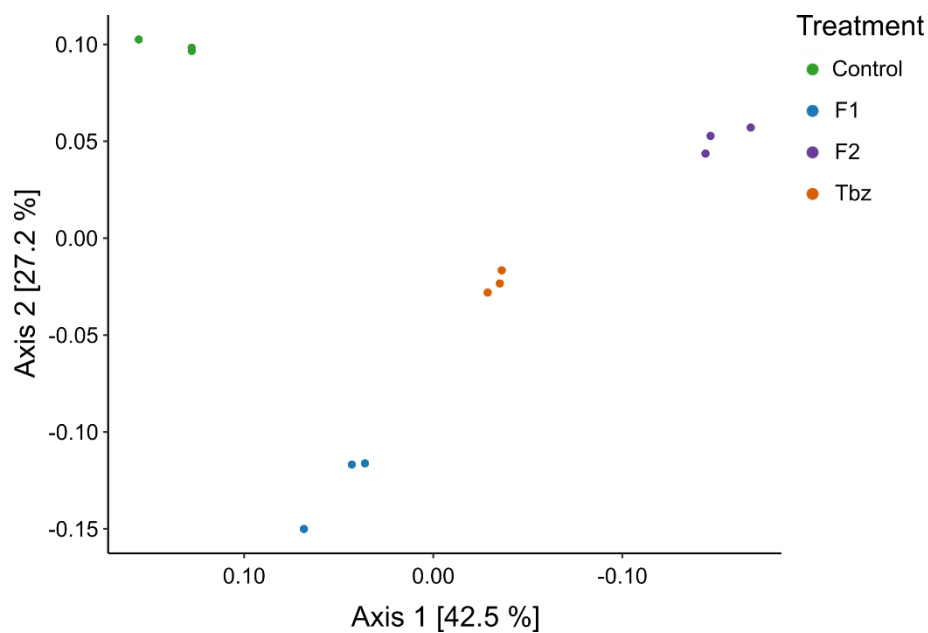
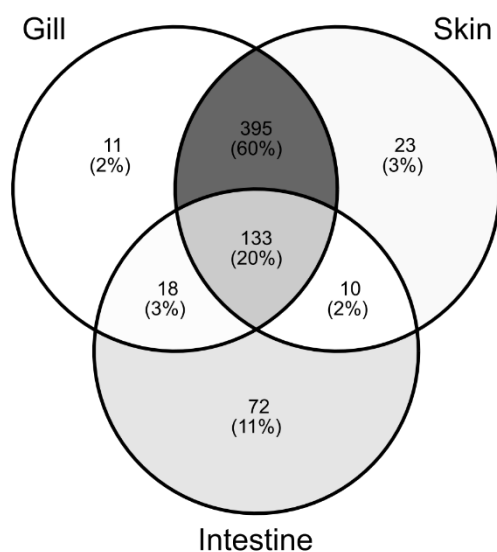
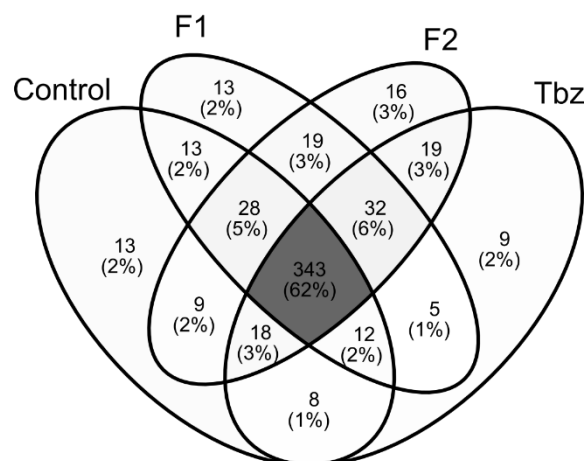


Figure S3. Beta diversity in water samples among treatments (coloured points). Principal Coordinates Analysis (PCoA) based on Bray-Curtis dissimilarity matrices. Percentages on the axes indicate the proportion of variance explained by each principal coordinate. Data were normalized using cumulative sum scaling (CSS) prior to ordination.

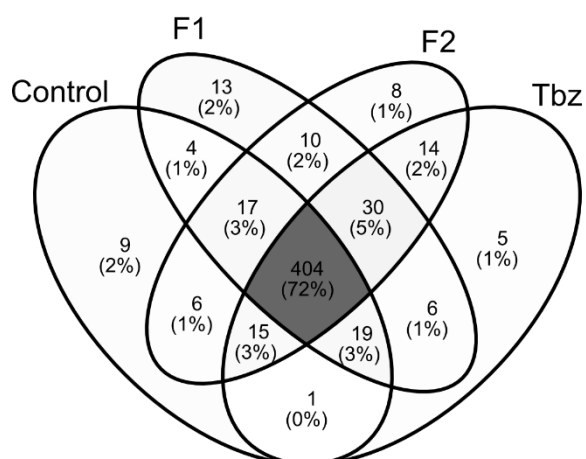
(A) Tissues



(B) Gill



(C) Skin



(D) Intestine

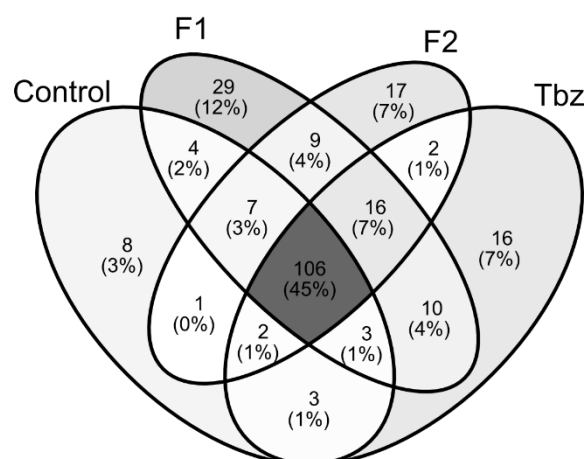


Figure S4. Venn diagrams showing unique and shared ASVs. (A) Shared and unique ASVs among the three tissues (gill, skin, intestine). (B – D) Shared and unique ASVs among the four chemical treatments (Control, F1, F2 and Tbz) in gill (B), skin (C) and intestine (D). Percentages indicated in brackets represent the percentage of ASVs at each intersection relatively to the total number of ASVs considered in the Venn diagram.

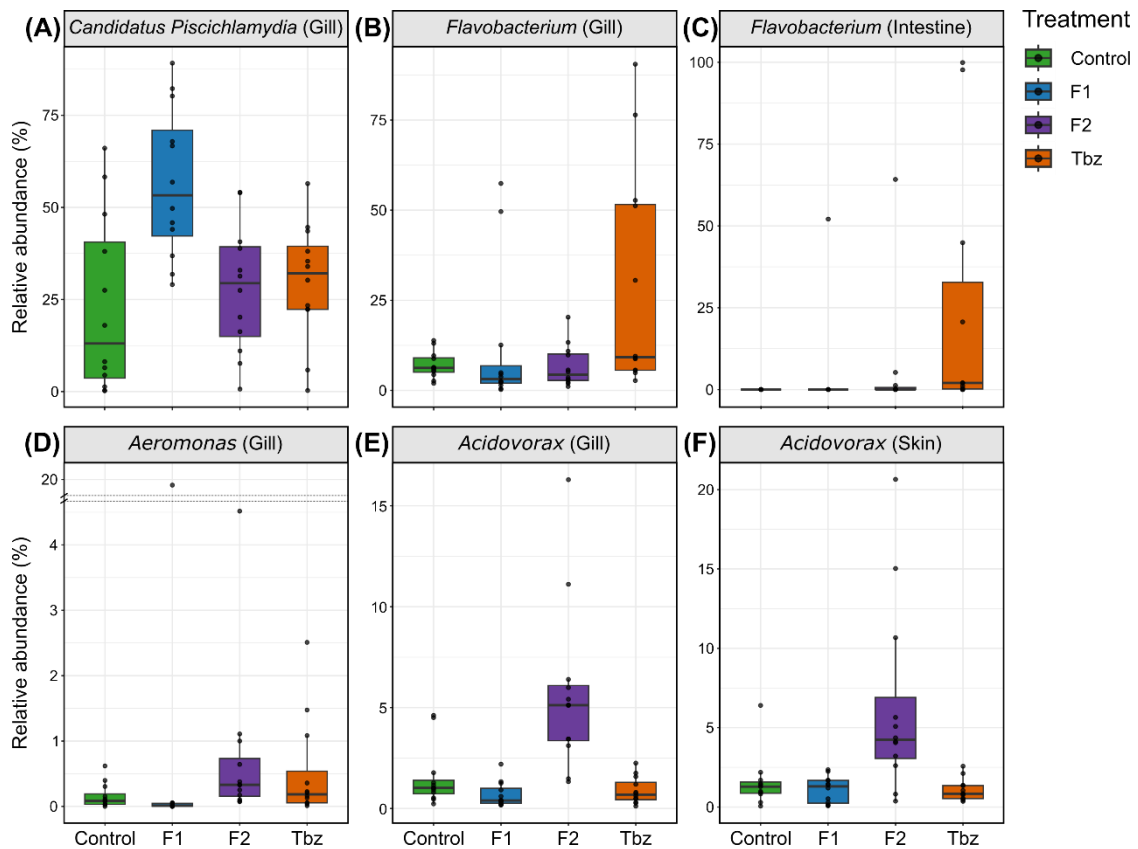


Figure S5. Relative abundance of key genera across tissues and treatments conditions. Relative abundances (%) were calculated at the genus level for *Candidatus Piscichlamydia* in gills (D), *Flavobacterium* in gills (E) and intestine (F), *Aeromonas* in gills (G) and *Acidovorax* in gills (H) and skin (I).

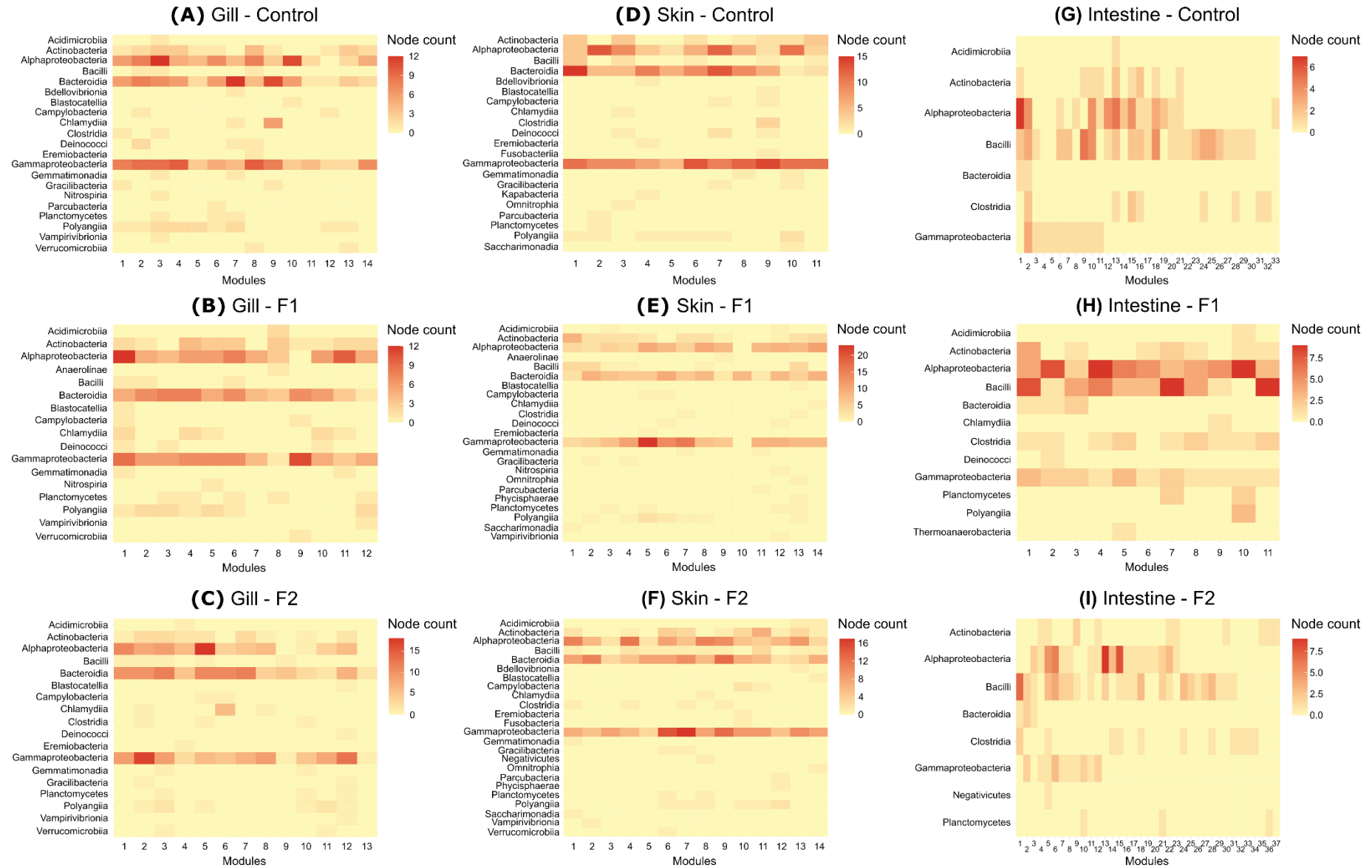


Figure S6. Bacterial classes represented of each module of the cooccurrence networks. Heatmaps in the gill (A – C), skin (D – F) and intestine (G – I) samples are represented under control (A, D, G), F1 (B, E, H) and F2 (C, F, I) treatment conditions.

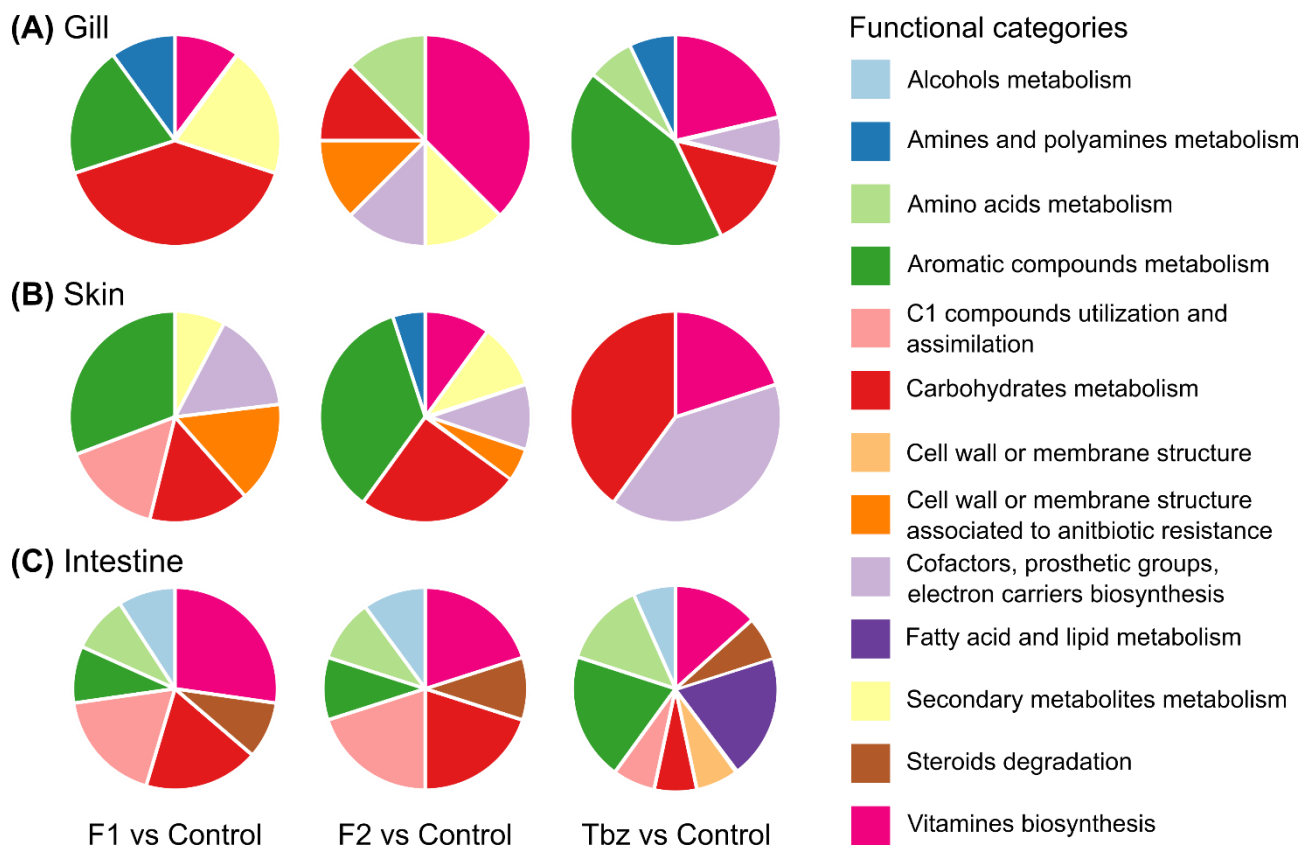


Figure S7. Pie charts representing the number of predicted metabolic pathways differentially expressed between exposed and control treatment conditions in (A) gills, (B) skin and (C) intestine microbiomes. Comparisons (shown below the pie charts) include F1 vs Control, F2 vs Control and Tbz vs Control. Differentially expressed pathways were groups into functional categories, represented by distinct colors.