

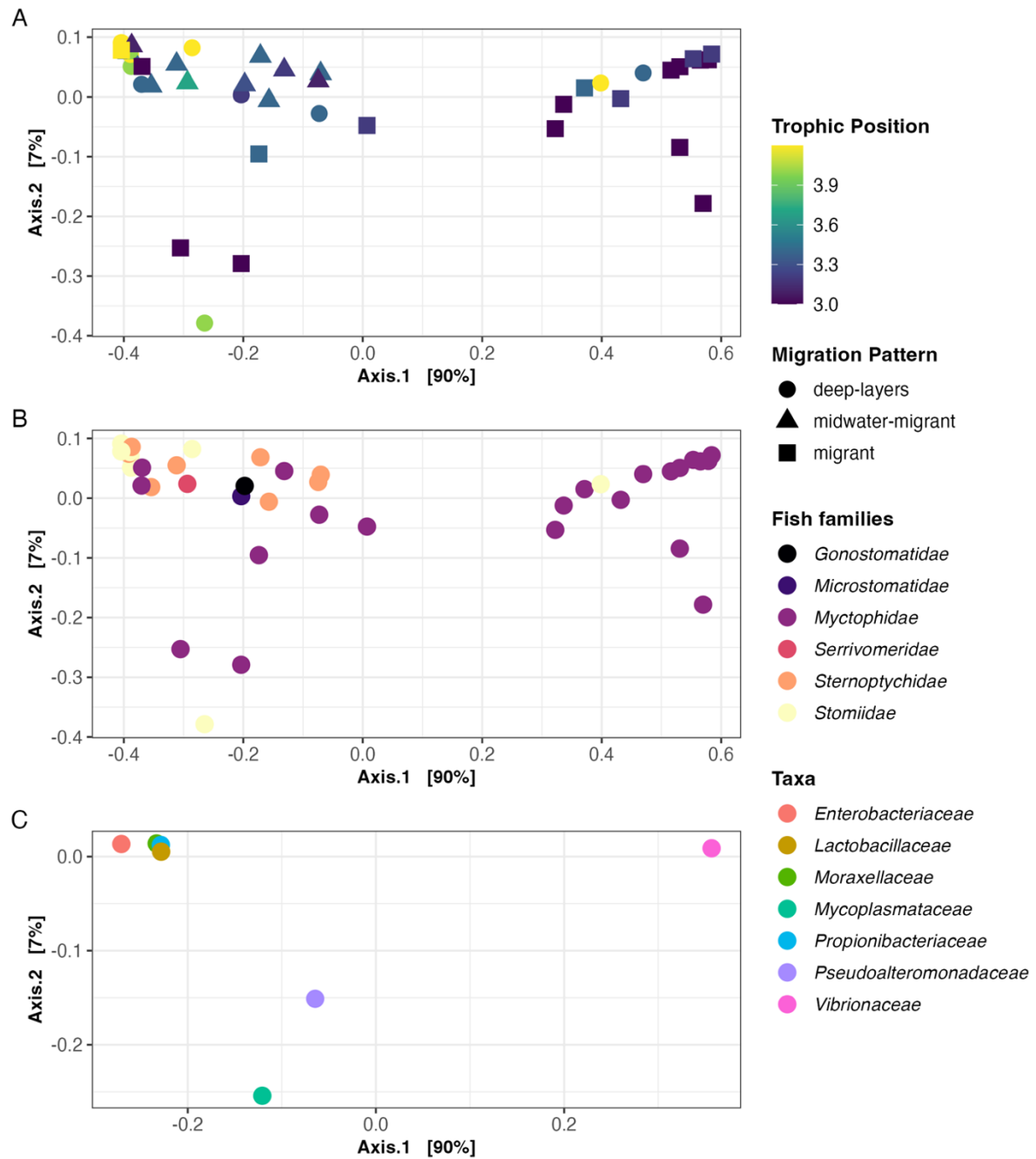


Fig. S1: Principal Coordinates Analysis (PCoA) of liver microbial community composition in mesopelagic fishes, based on Bray-Curtis dissimilarities. Panel A shows samples colored by trophic position and shaped by migratory behavior (circles: deep-layer residents; triangles: midwater migrants; squares: migrants). Panel B displays the same ordination with samples colored by fish family, while Panel C highlights dominant bacterial families (0.5% relative abundance filter applied). The percentages on each axis indicate the variance explained by the corresponding principal coordinate.

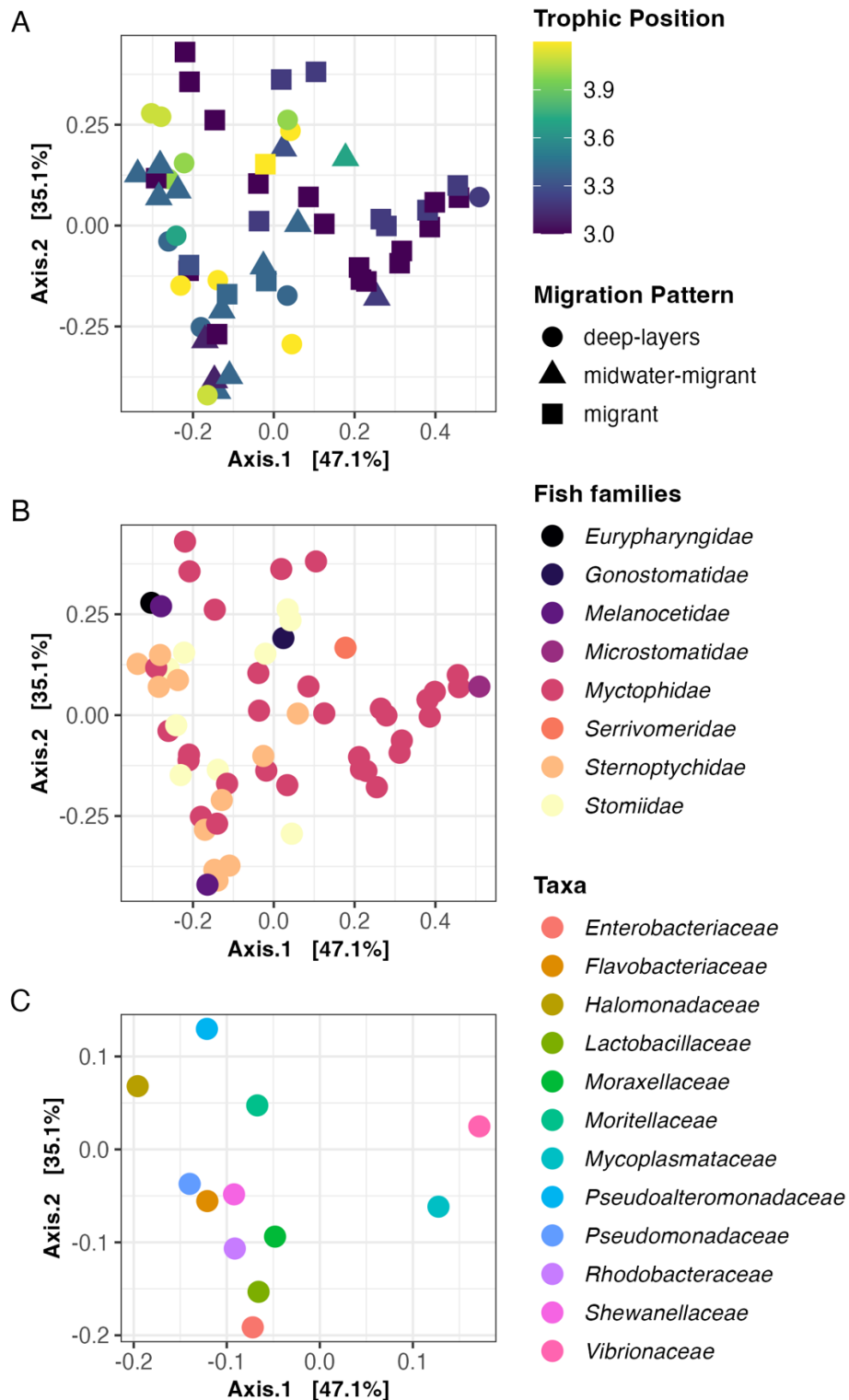


Fig. S2: Principal Coordinates Analysis (PCoA) of skin microbial community composition in mesopelagic fishes, based on Bray-Curtis dissimilarities. Panel A shows samples colored by trophic position and shaped by migratory behavior (circles: deep-layer residents; triangles: midwater migrants; squares: migrants). Panel B displays the same ordination with samples colored by fish family, while Panel C highlights dominant bacterial families (0.5% relative abundance filter applied). The percentages on each axis indicate the variance explained by the corresponding principal coordinate.

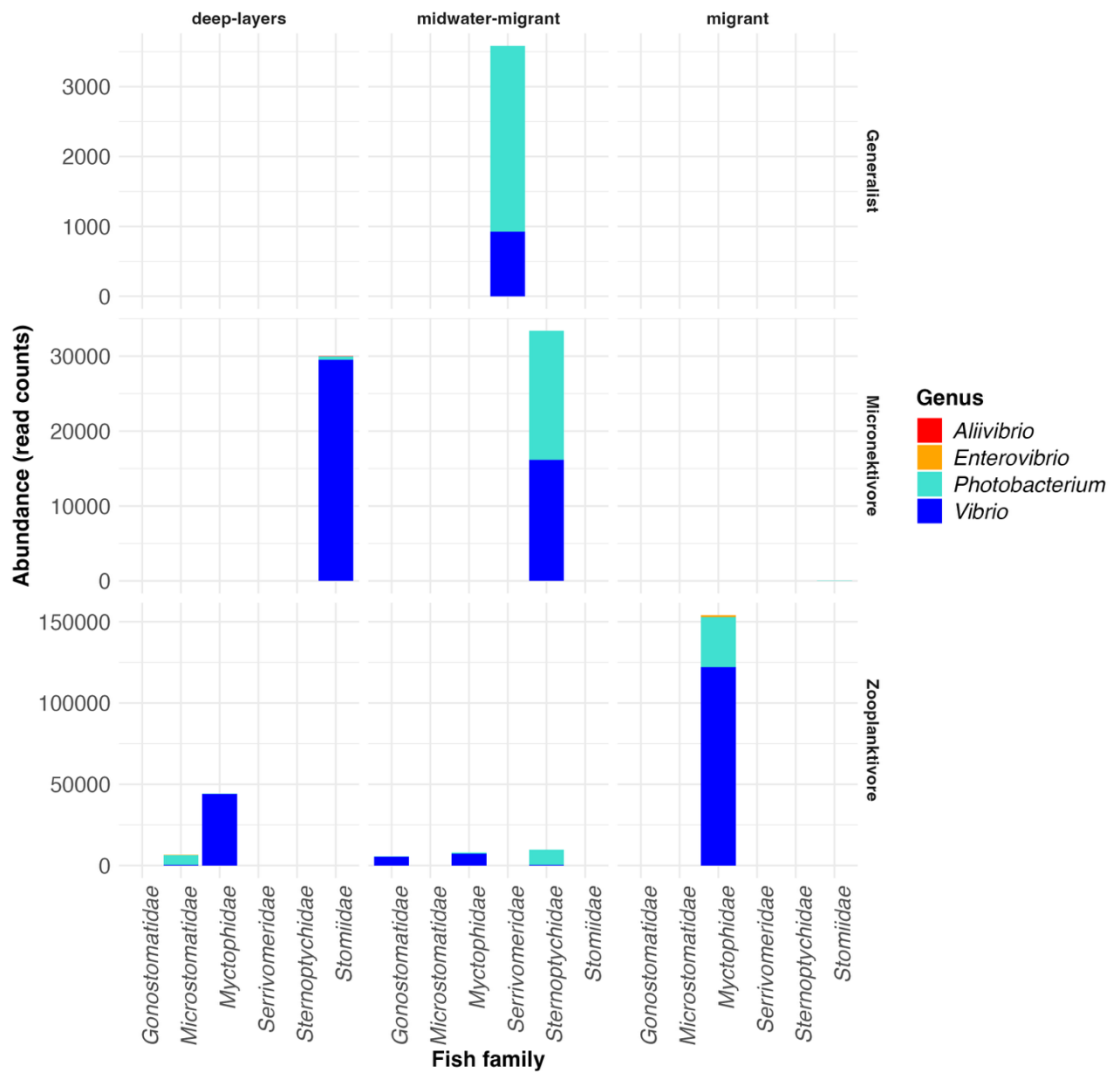


Fig. S3: Abundance of *Aliivibrio*, *Enterovibrio*, *Photobacterium*, and *Vibrio* in the liver microbiomes of mesopelagic fishes, grouped by fish family, vertical distribution (deep-layers, midwater-migrant, migrant). Stacked bar charts show total read counts for each genus across different ecological categories.

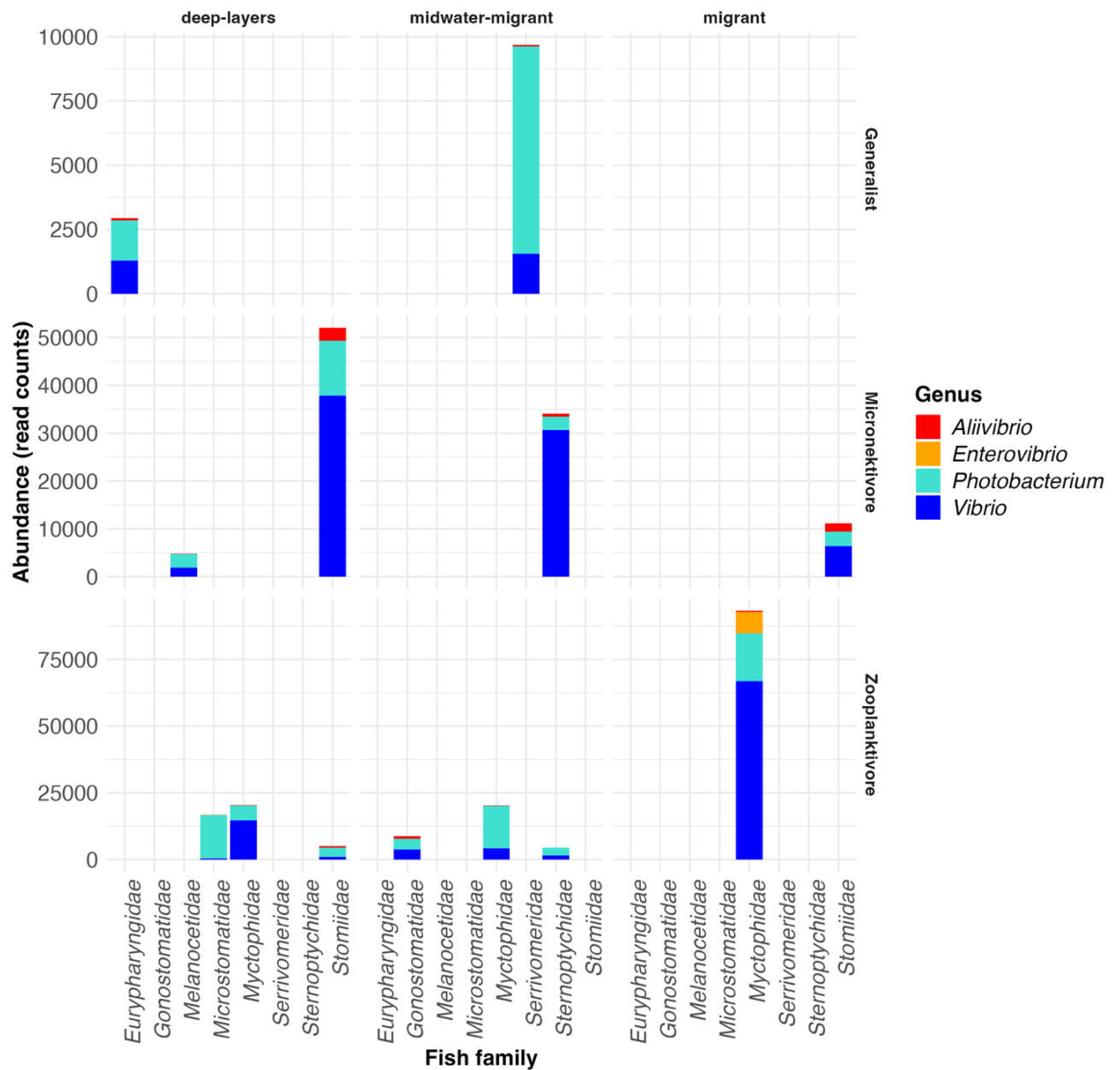


Fig. S4: Abundance of *Aliivibrio*, *Enterovibrio*, *Photobacterium*, and *Vibrio* in the skin microbiomes of mesopelagic fishes, grouped by fish family, vertical distribution (deep-layers, midwater-migrant, migrant). Stacked bar charts show total read counts for each genus across different ecological categories.

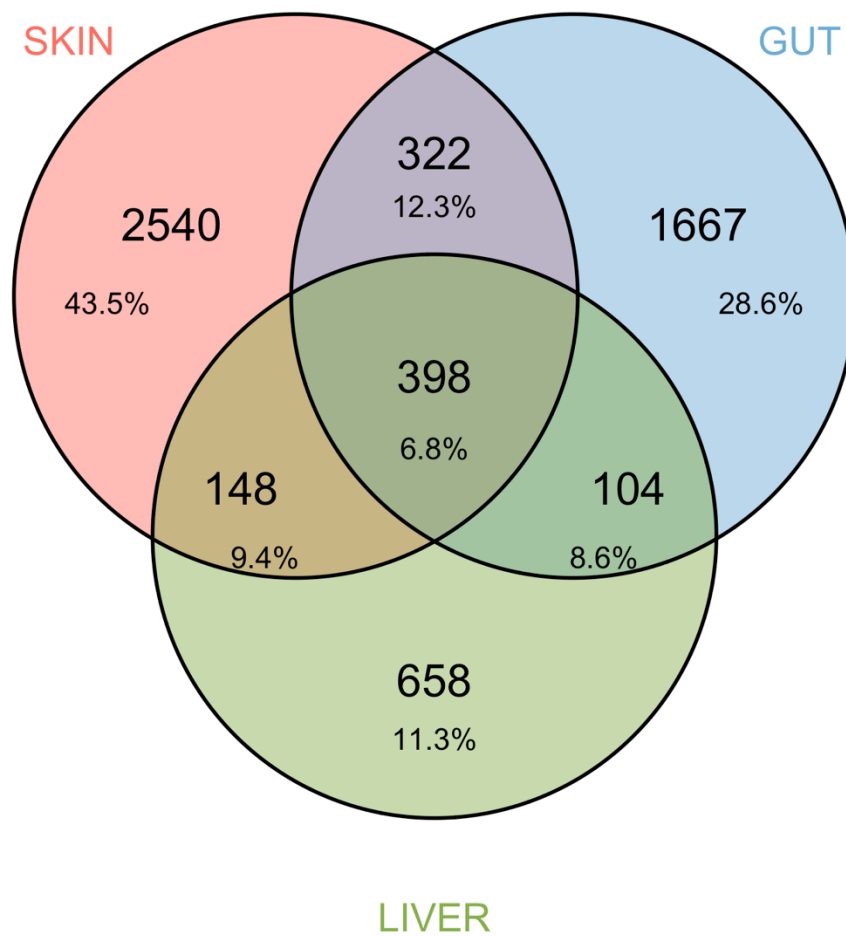


Fig. S5: Venn diagram showing the distribution of microbial taxa (ASVs) across three tissues of mesopelagic fish: gut, skin, and liver. Each circle represents the set of ASVs detected in each tissue, with overlapping areas indicating taxa shared between tissues. Numbers within each section indicate the absolute count of ASVs, along with their relative proportion (%) of the total ASV pool.