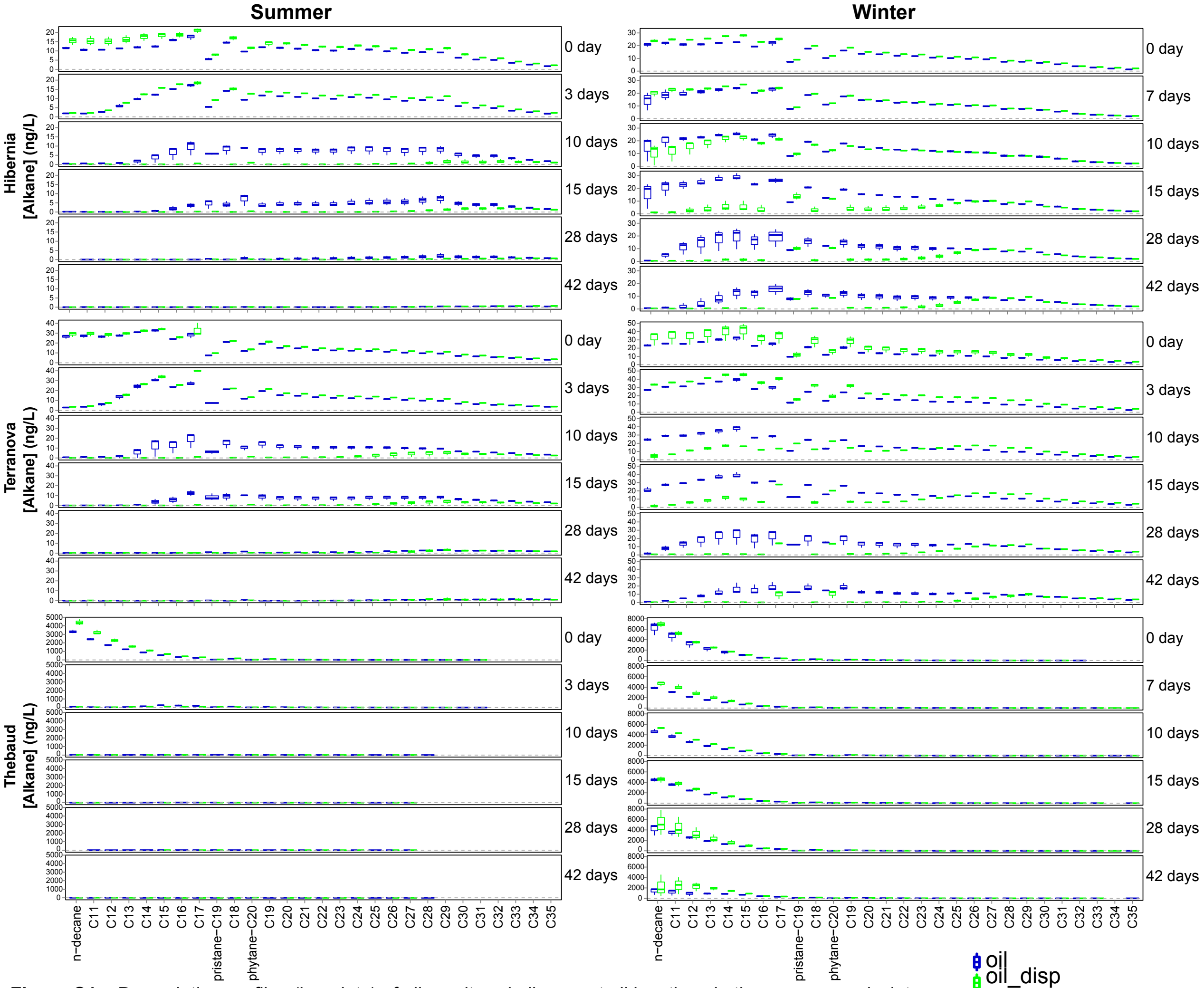


Figure S1a. Degradation profiles (boxplots) of all monitored alkanes at all locations in the summer and winter.

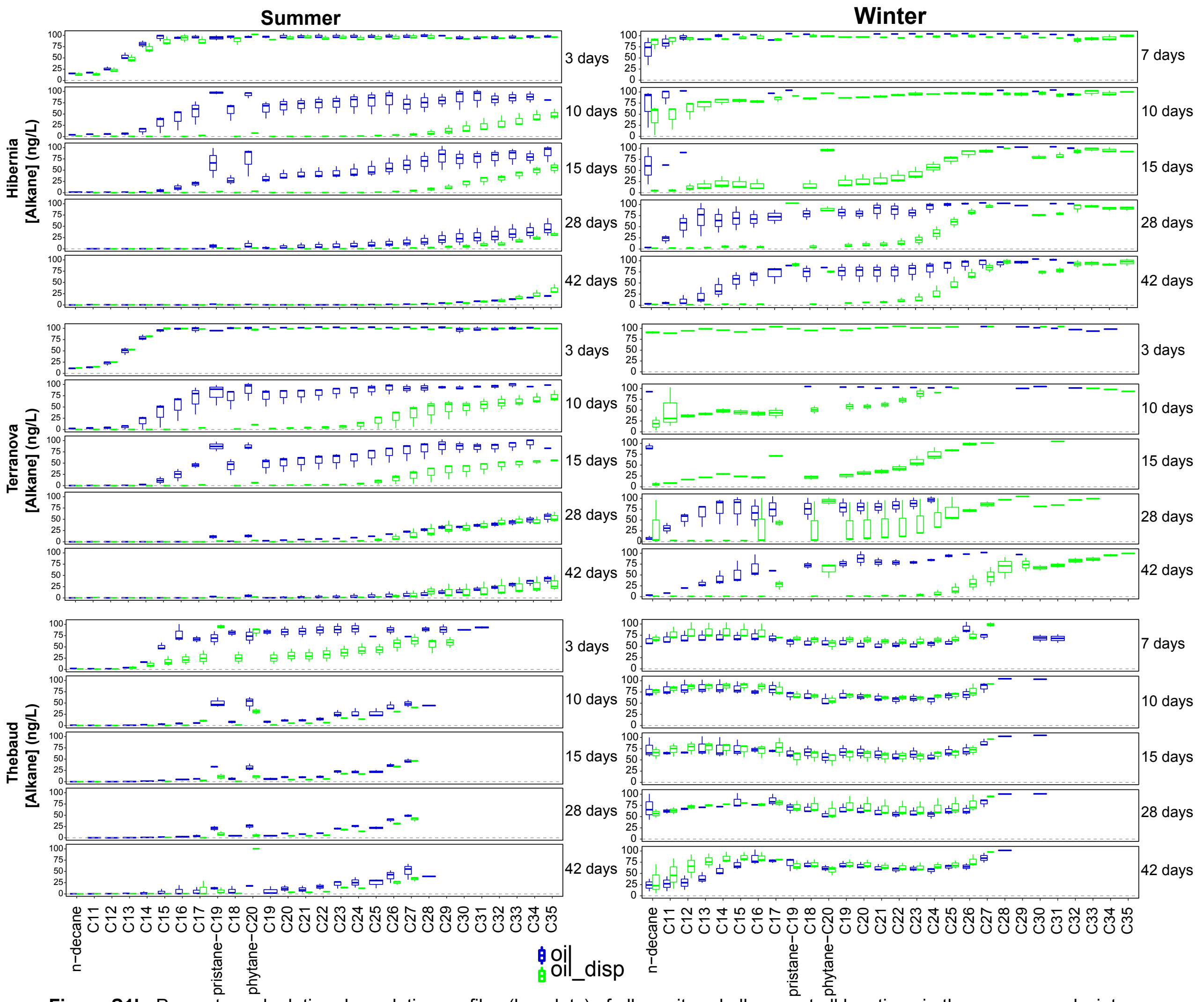


Figure S1b. Percentage depletion degradation profiles (boxplots) of all monitored alkanes at all locations in the summer and winter. Percentage values were obtained by dividing concentration values at 3, 7, 10, 15, 28 or 42 days by concentration values at 0 days.

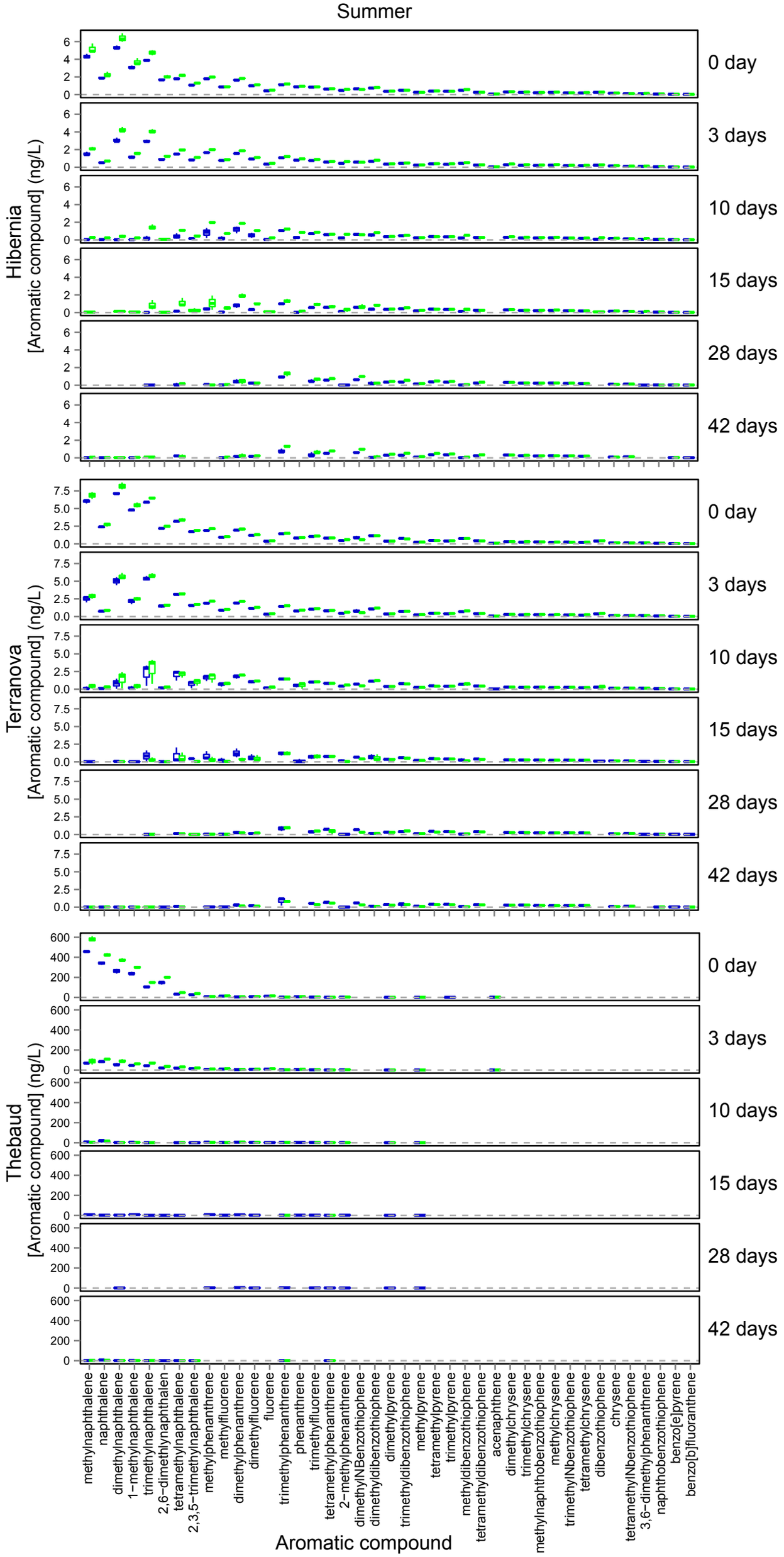


Figure S2a. Degradation profiles (boxplots) of all monitored aromatic compounds at all locations in the summer and winter. *: There was a power failure to the GFI (General Fault Interrupter) plug on the dock that powered the shakers (due to inclement weather so the flasks were not shaking for approximately 72 hours).

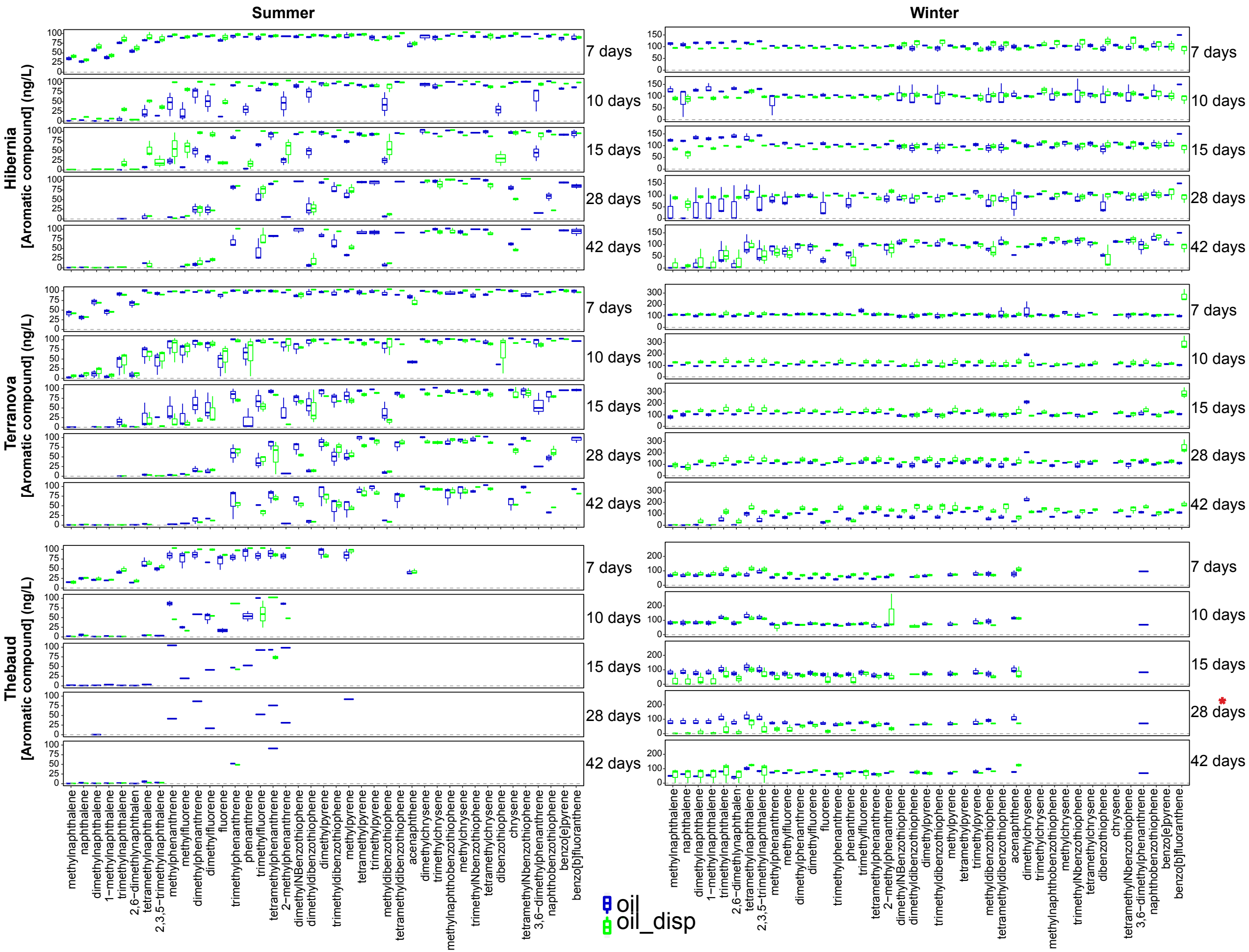


Figure S2b. Percentage depletion degradation profiles (boxplots) of all monitored aromatic compounds at all locations in the summer and winter. *: There was a power failure to the GFI (General Fault Interrupter) plug on the dock that powered the shakers (due to inclement weather so the flasks were not shaking for approximately 72 hours). Percentage values were obtained by dividing concentration values at 3, 7, 10, 15, 28 or 42 days by concentration values at 0 days.

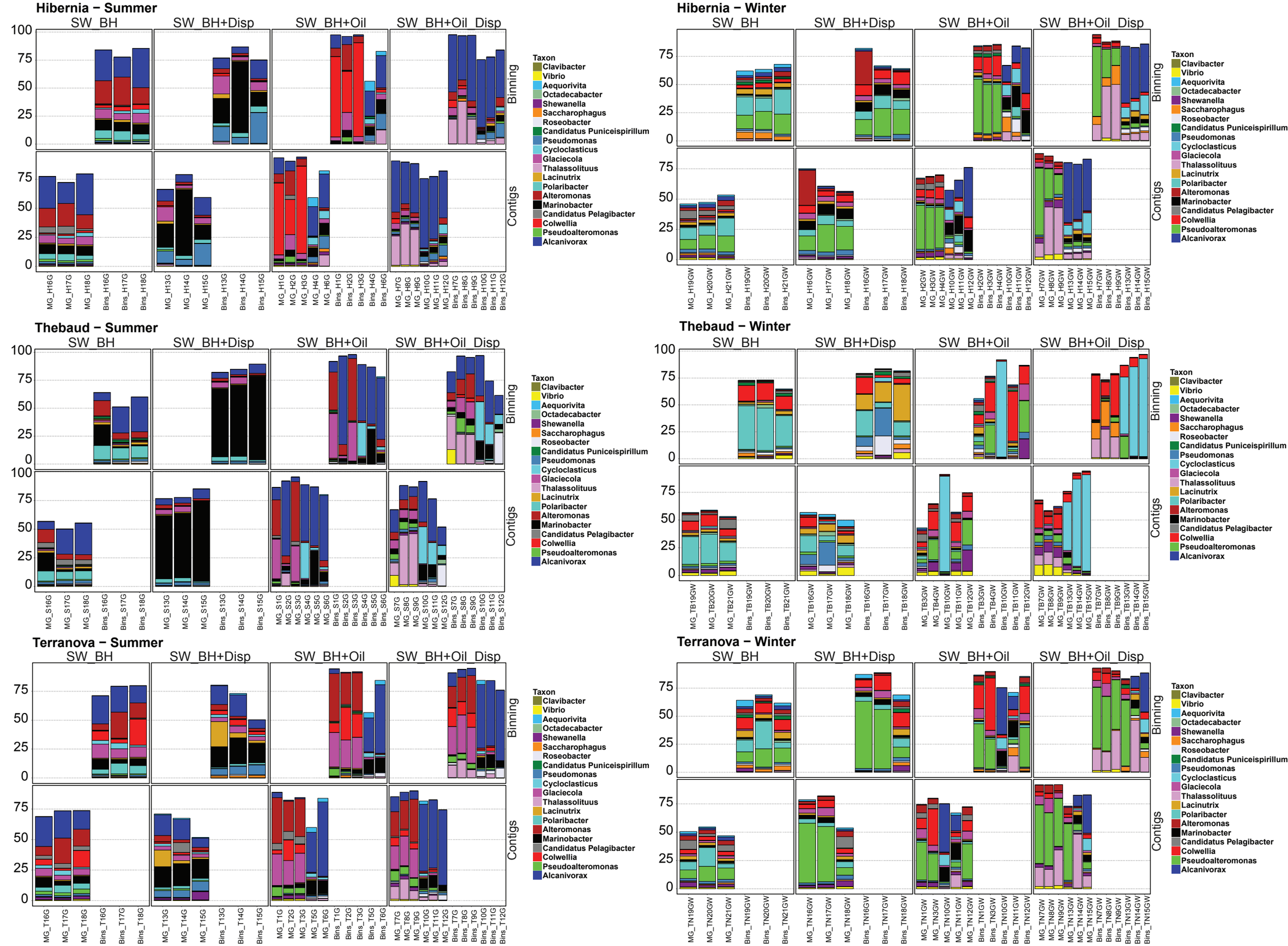


Figure S3. Genus level taxonomy comparison between contigs-centric and bins-based approaches. Contigs-based population profiles were obtained by summarizing taxonomic lineages assigned to each contigs. Metagenome bins population profiles were obtained by summarizing consensus taxonomic lineages as described above (See *Additional file 3 - Metagenome bins validation* for methodology).

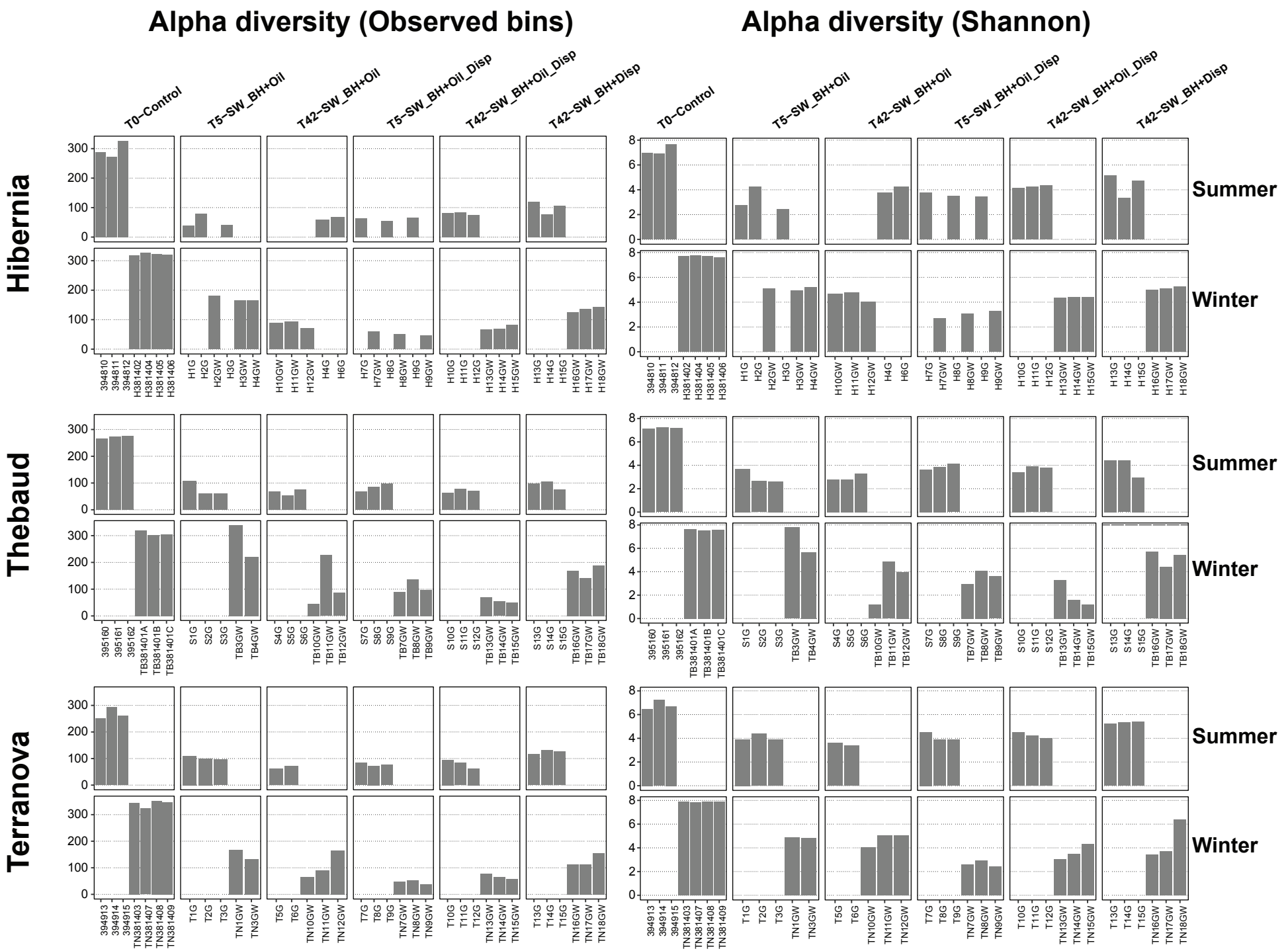


Figure S4. Alpha diversity metrics (Observed species/bins and Shannon indexes) computed from all 601 metagenome bins. Each bar represent a sample. Statistical significance was assessed with an ANOVA followed by a post-hoc Tukey test: For each station and season, all comparisons between T0 and other conditions were significant with an adjusted *p*-value lower than at least 0.05. Y-axis corresponds to sample names. Diversity indices were computed using the bins abundance table (Supplemental Information 2 datasets - Table S3).

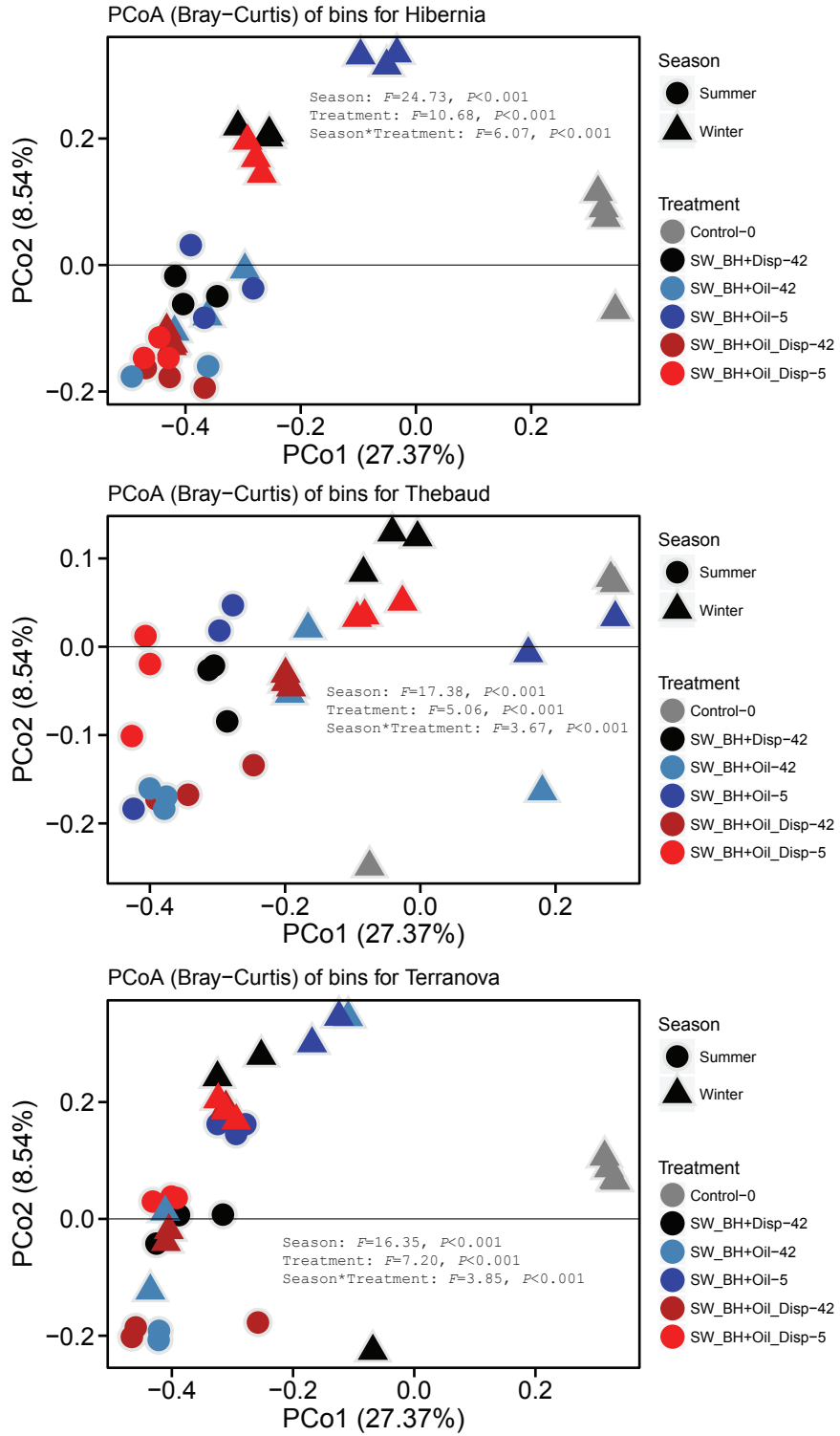
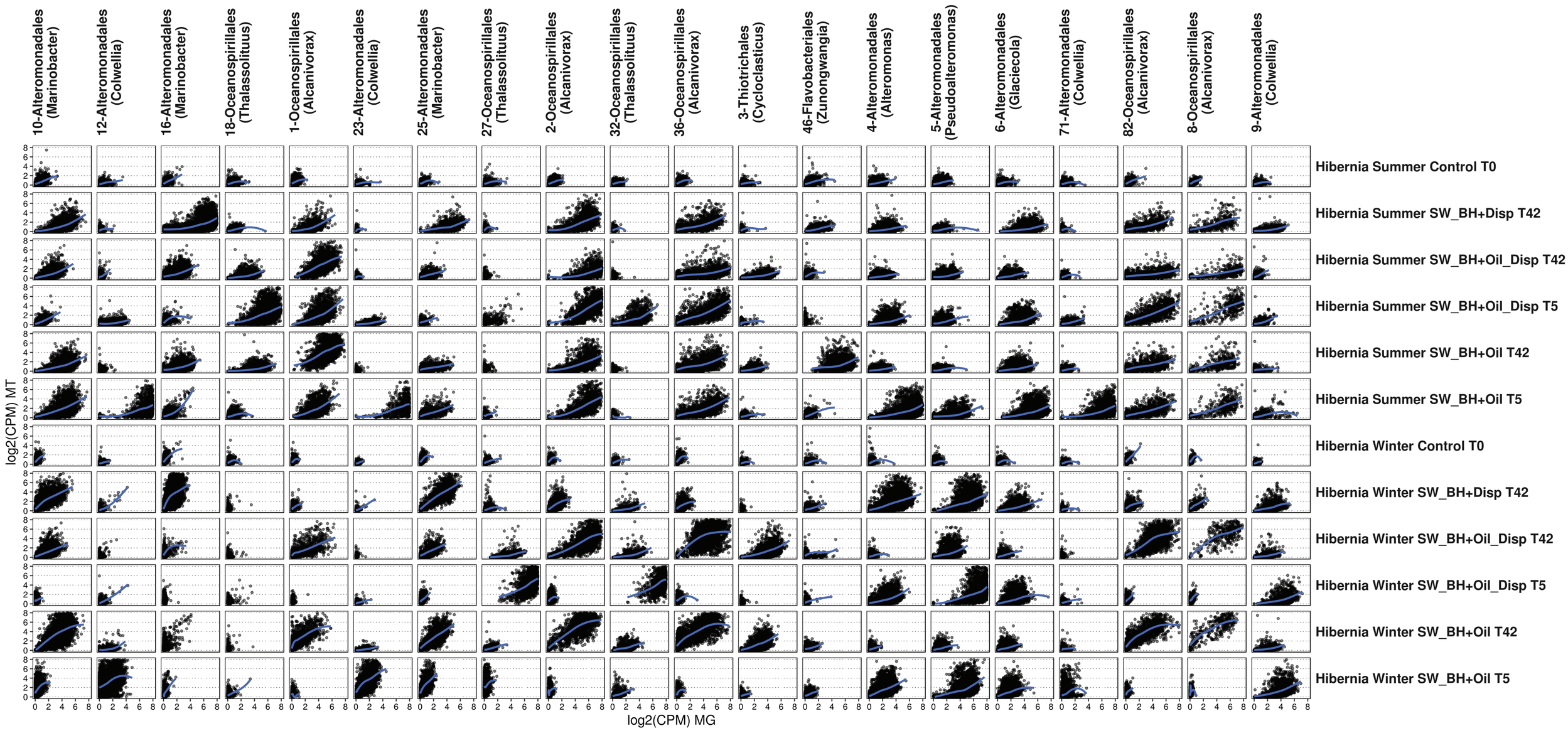


Figure S5. Beta diversity (Bray-Curtis) metrics computed from all 601 metagenome bins (*Supplemental Information 2 datasets - Table S3*). Each point represents a sample. Permanova was performed using the "adonis" function of the vegan library.

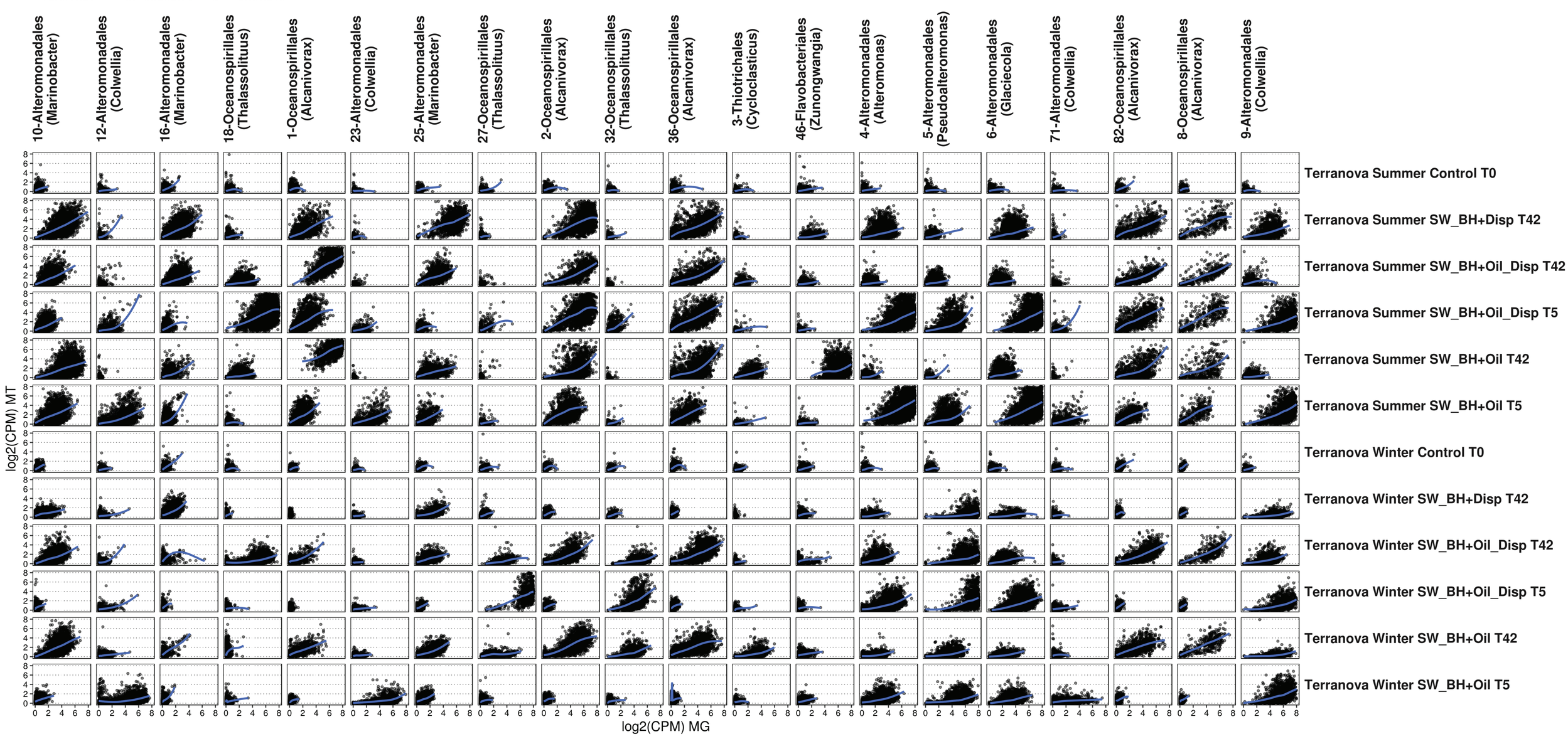
A)

Abundance - MT in function of MG - Hibernia -



Abundance - MT in function of MG - Terranova -

B)



Abundance - MT in function of MG - Thebaud -

C)

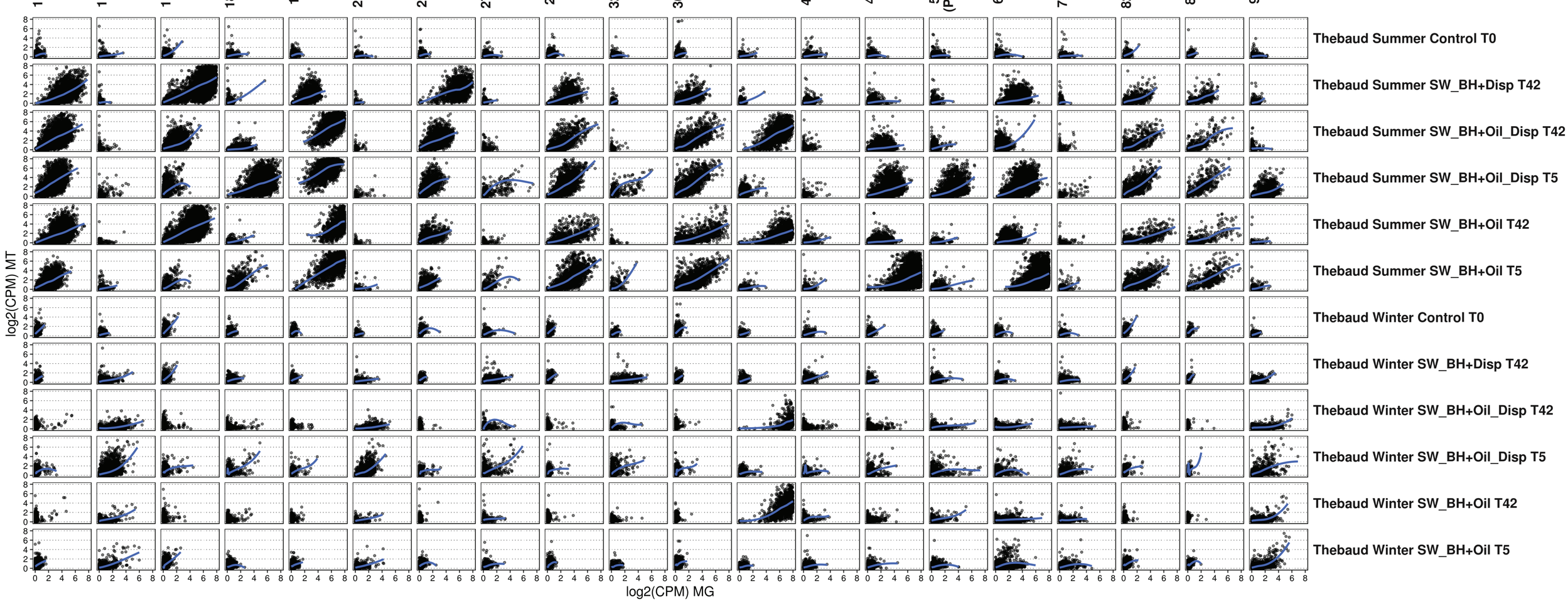


Figure S6. Metatranscriptome gene abundance in function of metagenome gene abundance for each bin at A) Hibernia, B) Terranova and C)Thebaud. Average CPM values of each gene were $\log_2$ transformed for both metatranscriptome and metagenome datasets and ratios of RNA:DNA for each gene of each bin were fitted with a non-parametric smoothing (Loess).