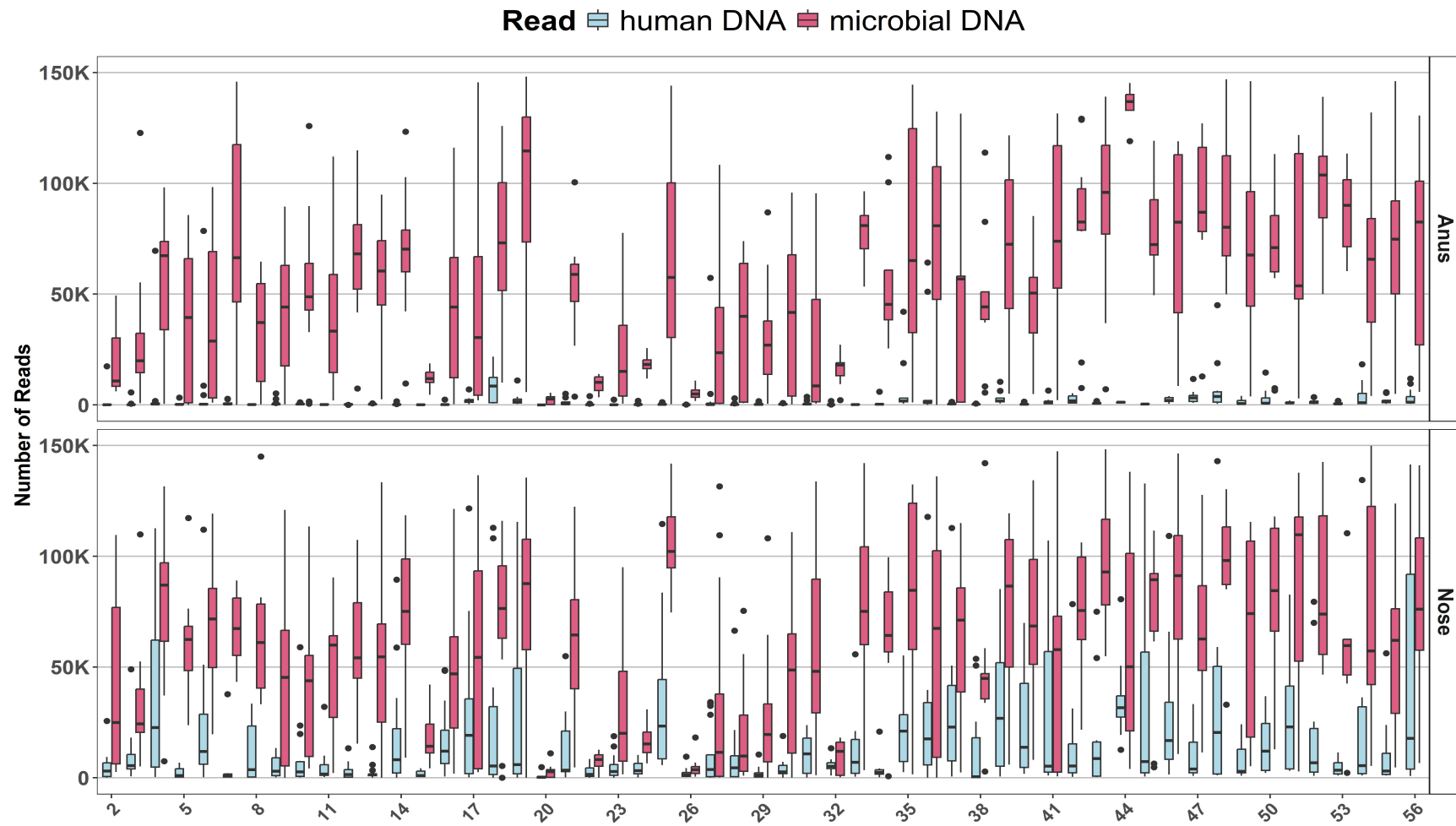
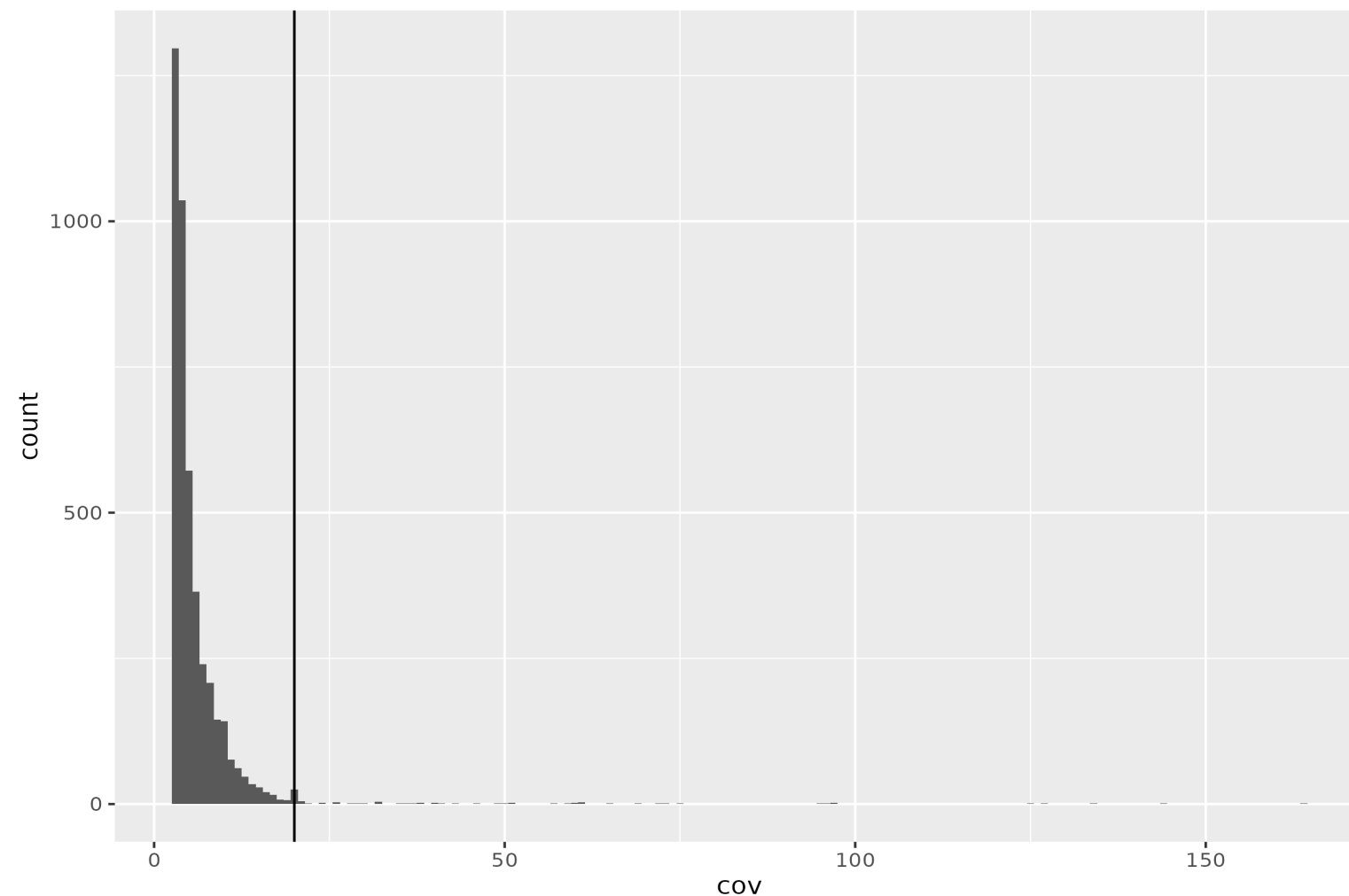


**Supplementary Figure S1. Comparison of adaptive and normal sequencing using Readfish.** A. Number of reads in week 30 at 72 hours of sequencing. B. Proportion of the species classified with Bracken at 72h using normal and adaptive sequencing in the same week (week 30).



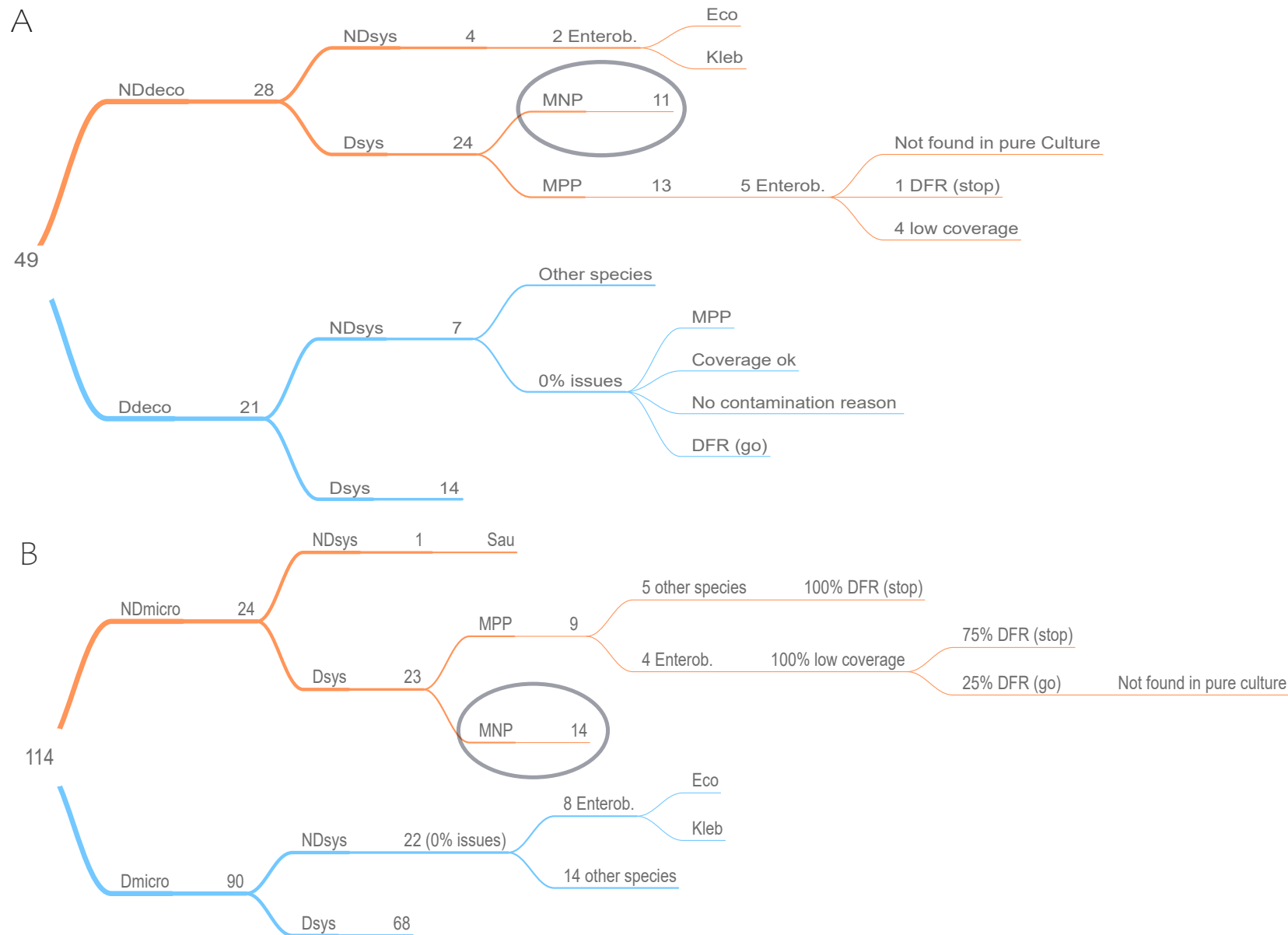
**Supplementary Figure S2. Number of reads in human and microbial DNA.** The reads are chronologically ordered for the sources sampled: anus and nose.



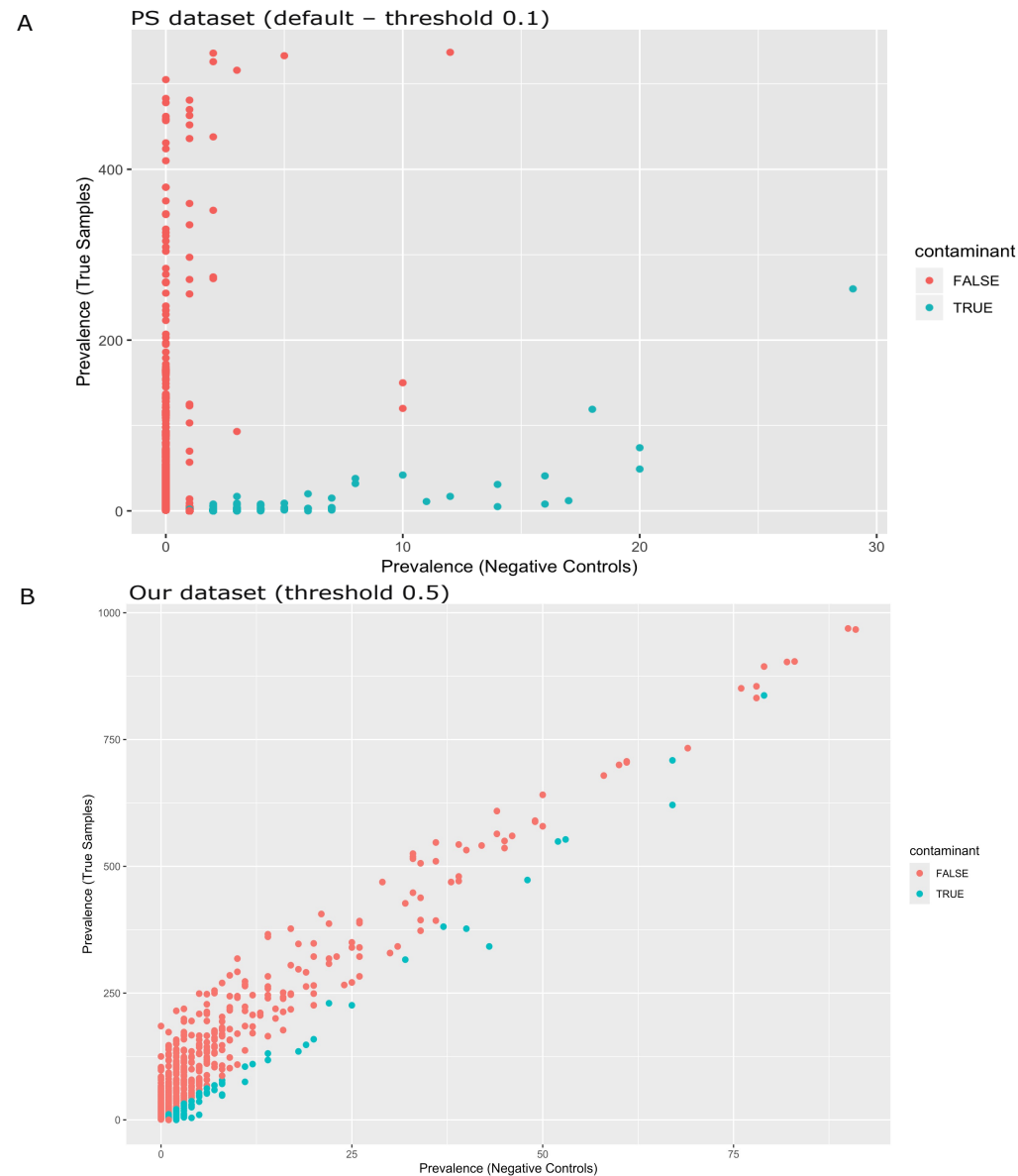
**Supplementary Figure S3. Distribution of the coverage for the negative controls and microbiologically negative samples.** The vertical line refers to the chosen threshold of 20X.





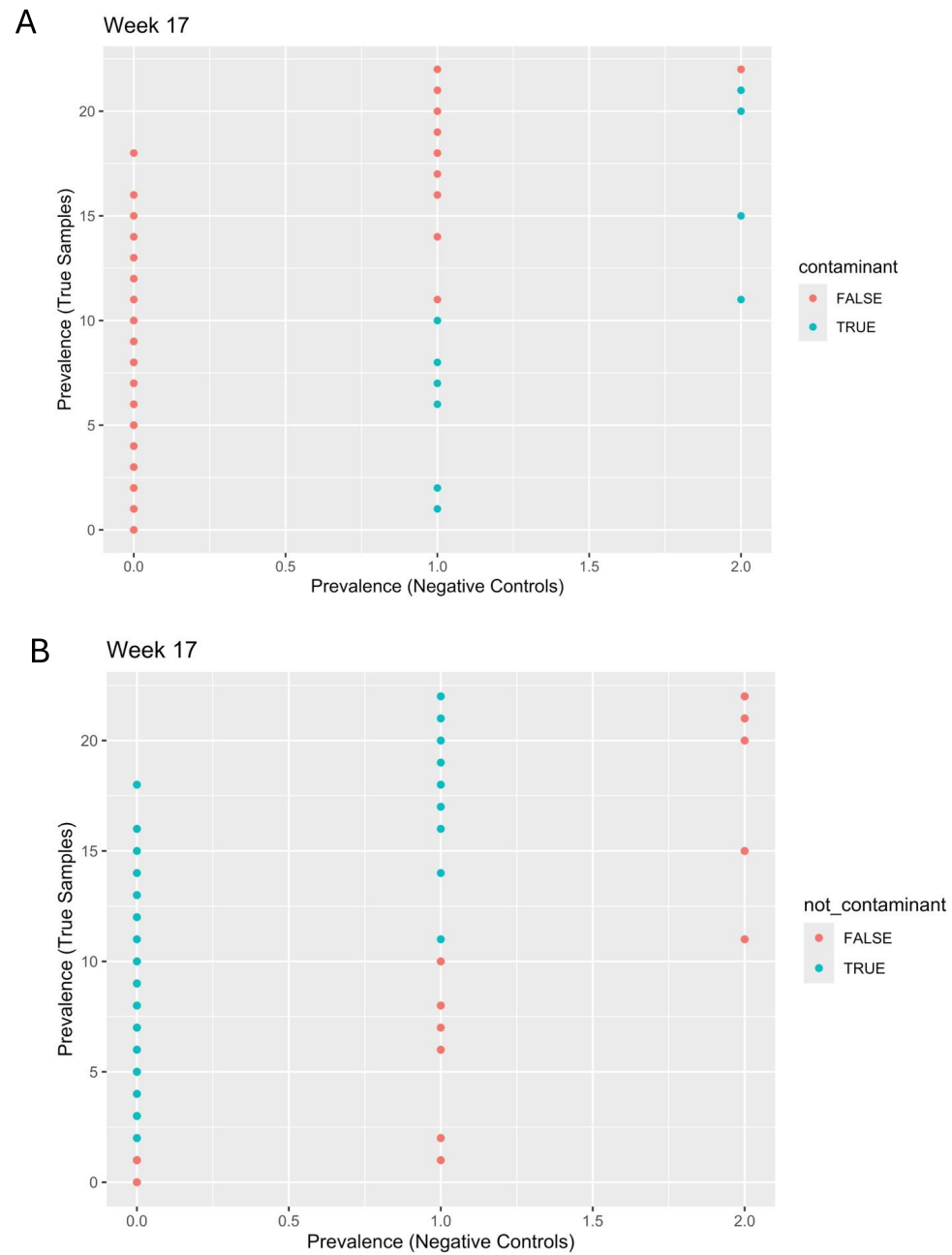


**Supplementary Figure S5. Tree diagram comparing the results for the paired decontamination tools tested.** ND refers to 'not decontaminated', decontaminated (D), A. Decontam (deco), 'Stop-Check-Go' (sys) B. MicroBIEM (micro) 'Stop-Check-Go' (sys).



\*Weeks with suspected cross-contamination were excluded (2, 4, 7, 12, 13, 14, 15, 16, 20, 26, 29, 48)

**Supplementary Figure S6. Result of the prevalence method application (only) from Decontam.** A. PS dataset (published in [https://benjjneb.github.io/decontam/vignettes/decontam\\_intro.html](https://benjjneb.github.io/decontam/vignettes/decontam_intro.html), section 7) with the default threshold (0.1). B. In our dataset, excluding microbiologically negative patients (MNP) and weeks with suspected cross-contamination (with a stricter threshold of 0.5).



**Supplementary Figure S7. Comparison of the prevalence method of Decontam R package on week 17. The functions used are A. *IsContam*, B. *IsNotContam*.**

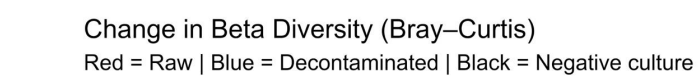
Red = Raw | Blue = Decontaminated | Black = Negative culture



Red = Raw | Blue = Decontaminated | Black = Negative culture



Red = Raw | Blue = Decontaminated | Black = Negative culture

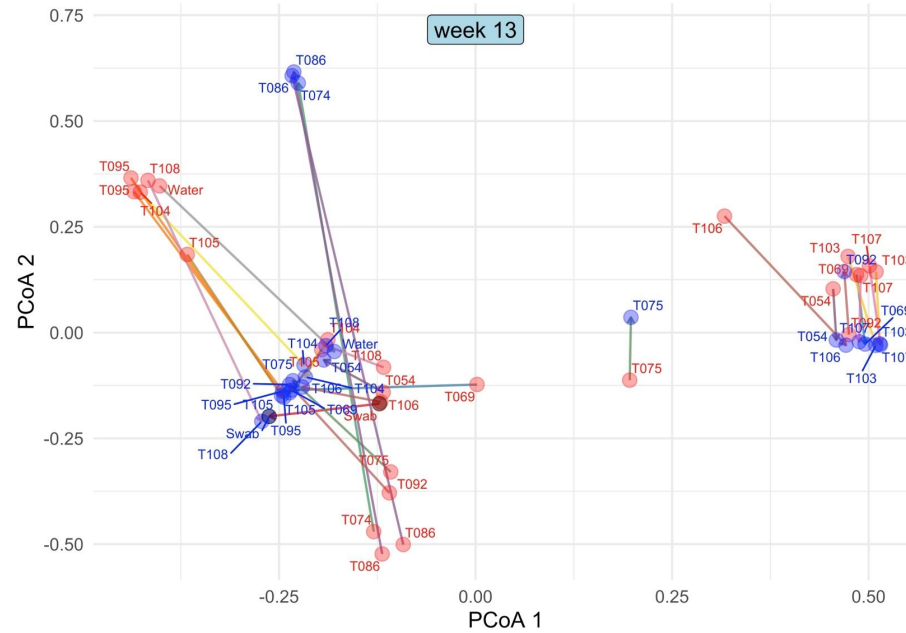


Red = Raw | Blue = Decontaminated | Black = Negative culture



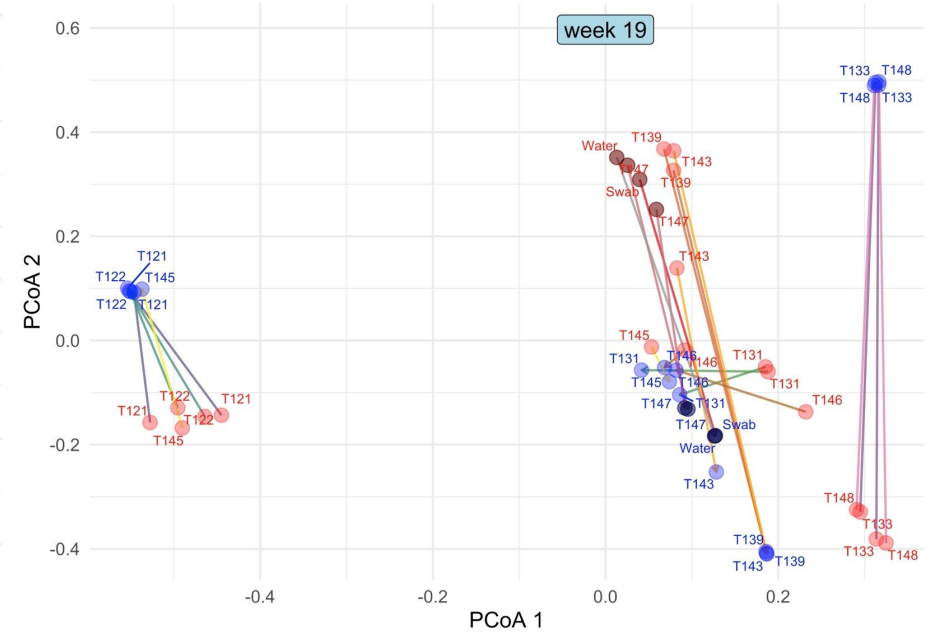
### Change in Beta Diversity (Bray–Curtis)

Red = Raw | Blue = Decontaminated | Black = Negative culture



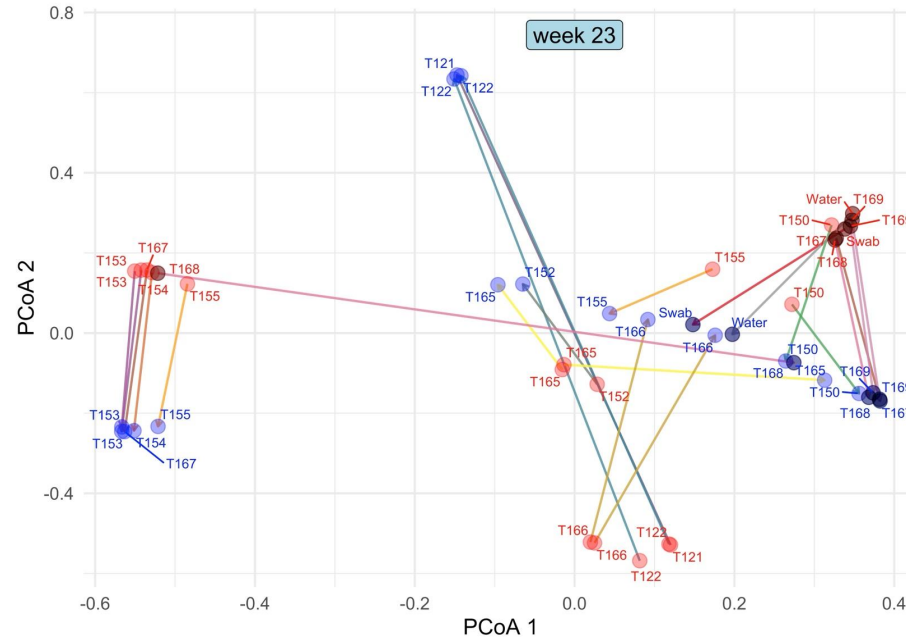
### Change in Beta Diversity (Bray–Curtis)

Red = Raw | Blue = Decontaminated | Black = Negative culture



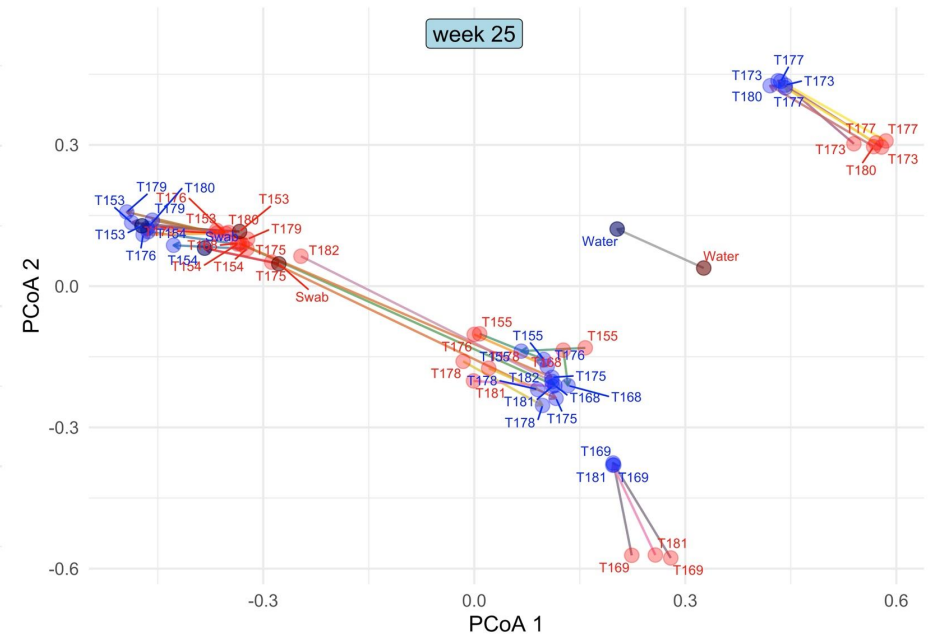
### Change in Beta Diversity (Bray–Curtis)

Red = Raw | Blue = Decontaminated | Black = Negative culture



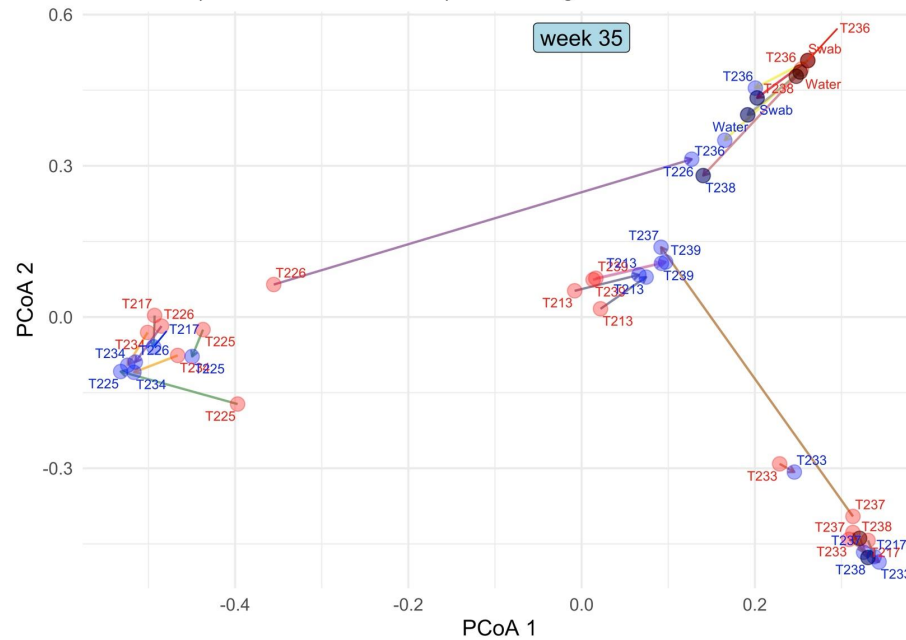
### Change in Beta Diversity (Bray–Curtis)

Red = Raw | Blue = Decontaminated | Black = Negative culture



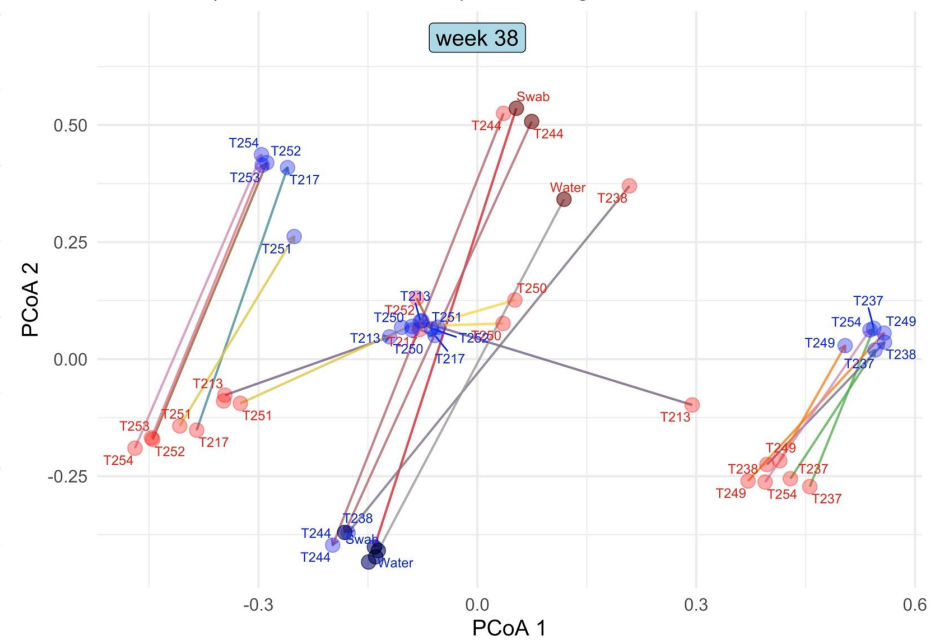
### Change in Beta Diversity (Bray–Curtis)

Red = Raw | Blue = Decontaminated | Black = Negative culture



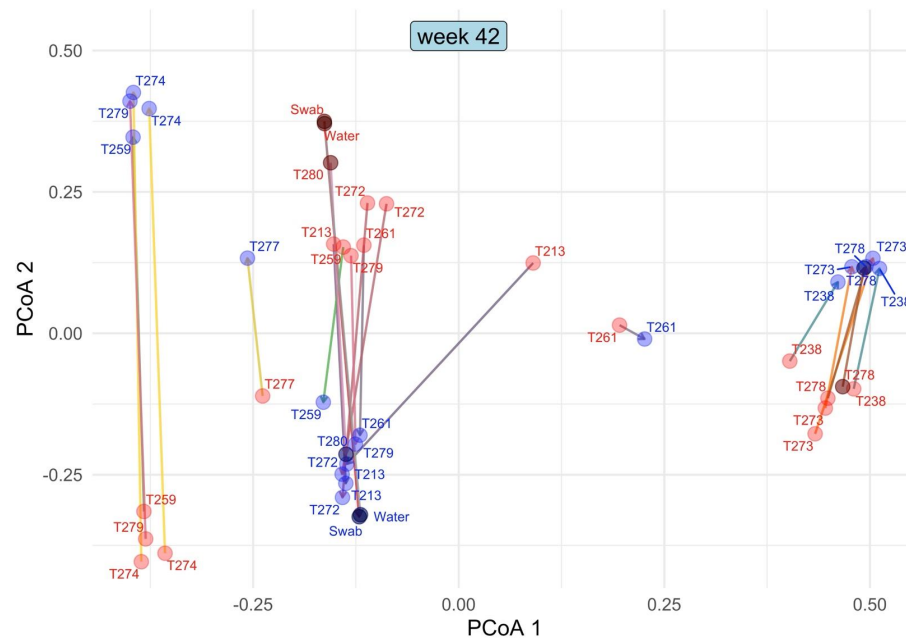
### Change in Beta Diversity (Bray–Curtis)

Red = Raw | Blue = Decontaminated | Black = Negative culture



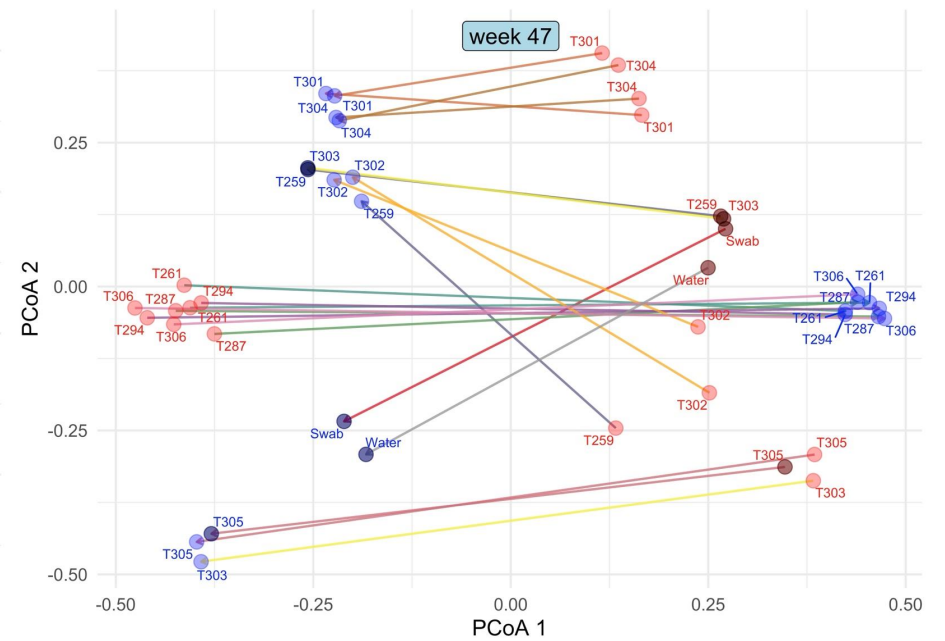
### Change in Beta Diversity (Bray–Curtis)

Red = Raw | Blue = Decontaminated | Black = Negative culture



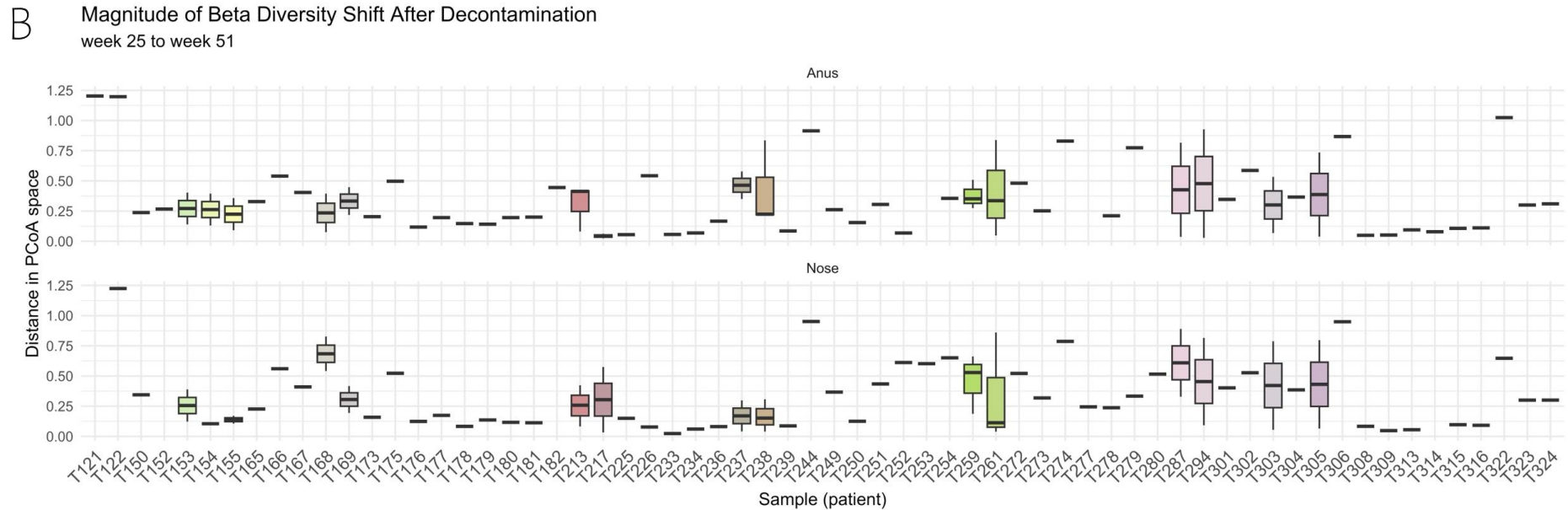
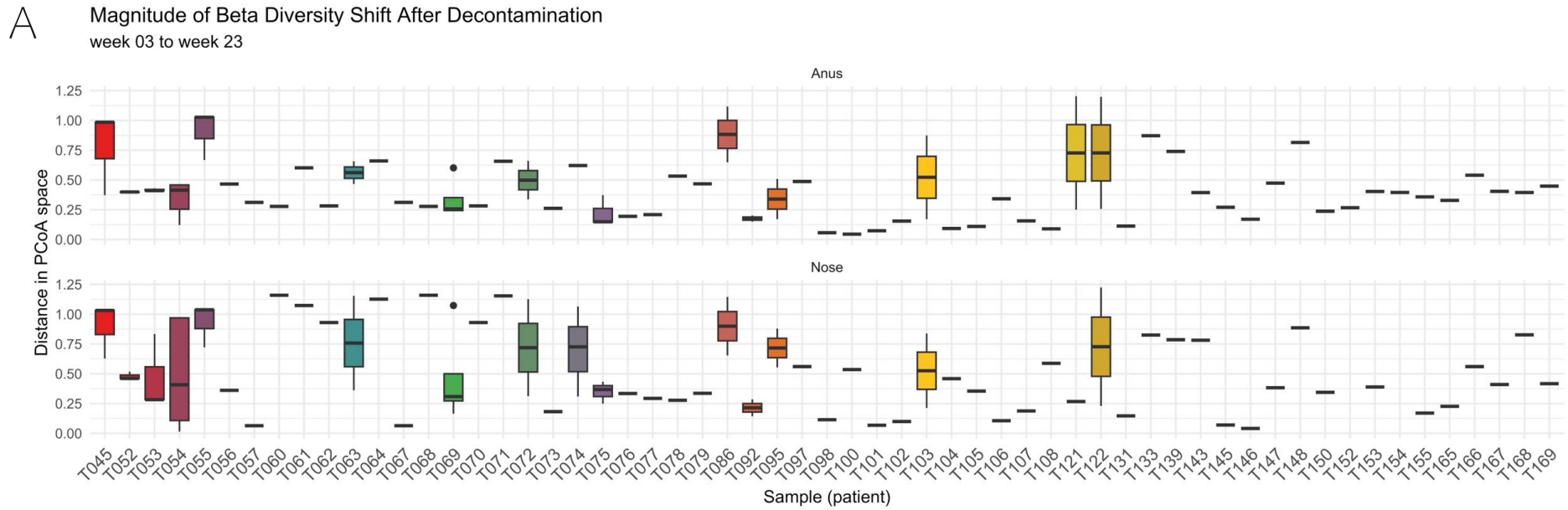
### Change in Beta Diversity (Bray–Curtis)

Red = Raw | Blue = Decontaminated | Black = Negative culture









**Supplementary Figure S9. Magnitude of the shift in the PCoA space for the biom files published in [https://github.com/SAM81221/Stop-Check-Go\\_TAPIR](https://github.com/SAM81221/Stop-Check-Go_TAPIR). Comparison between the raw and the decontaminated samples split by source (anus, nose) from A. Week 03 to week 23, and B. Week 25 to week 51.**