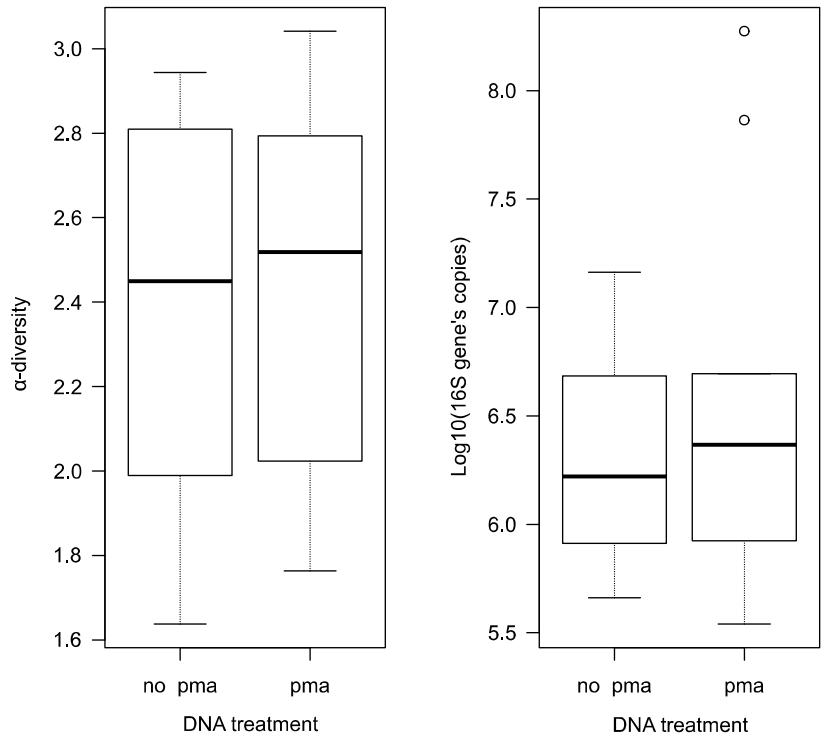


513 **Supplementary Figure 1:** PMA treatment of the DNA did neither influence diversity nor
514 biomass of the CF microbiome in the analyzed cohort.

515 A subset of samples (n=10) from the CF cohort was analyzed for changes in diversity and
516 global biomass with and without PMA treatment. No significant differences were observed.

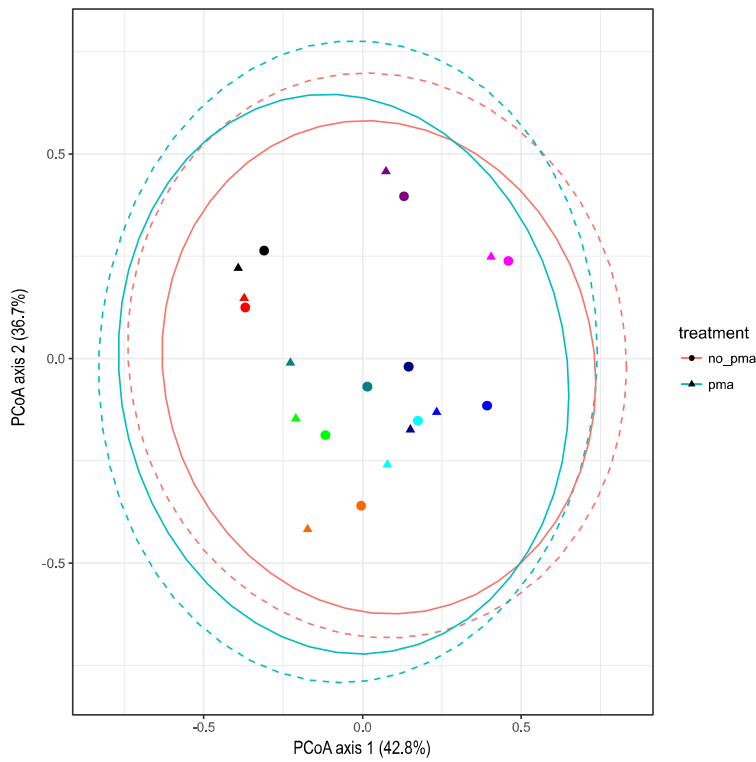


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519 **Supplementary Figure 2:** PMA treatment of the DNA did not influence the structure of the
520 CF microbiome in the analyzed cohort.

521 A subset of samples (n=10) from the CF cohort was analyzed for changes in the microbial
522 structure with and without PMA treatment. No significant differences in the structure of the
523 microbiome were observed. Paired samples are in the same color. The ellipses represent the
524 95% confidence interval assuming assuming a multivariate t-distribution (full lines) or a
525 multivariate normal distribution (dashed lines).



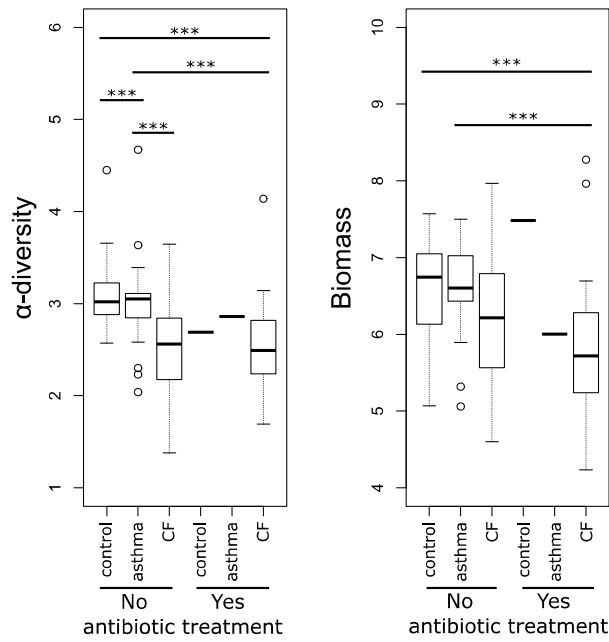
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528 **Supplementary Figure 3:** *Impact of antibiotic therapy prior of sampling on the diversity and*
529 *biomass of the microbiome in the analyzed cohort.*

530 Samples were classified in two groups 'treated' and 'non treated' based on the usage of
531 antibiotic within 4 weeks prior to sampling. Statistical significance was calculated by pairwise
532 Wilcoxon test. P-value code: ***<0.001.

533



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