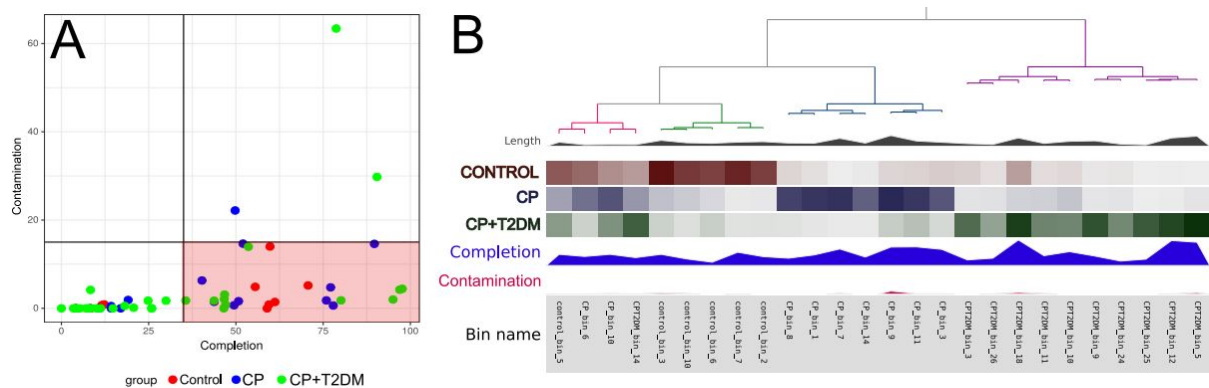


**Fig. S1. Alpha-diversity distribution between study groups. (A) Chao1 index. (B) Shannon index. (C) Simpson index.**



**Fig. S2. MAGs assembly statistics and presence in metagenomic samples. (A) Bins statistic completeness/contamination statistic. The red area indicates MAGs selected for further analysis. (n=26) (B) Anvi'o plot of selected 26 MAGs detection values per group. Proportion of nucleotides in a contig that are covered at least 1x was used as an abundance metric. Hierarchical clustering was performed using the Euclidean distance and ward linkage.**