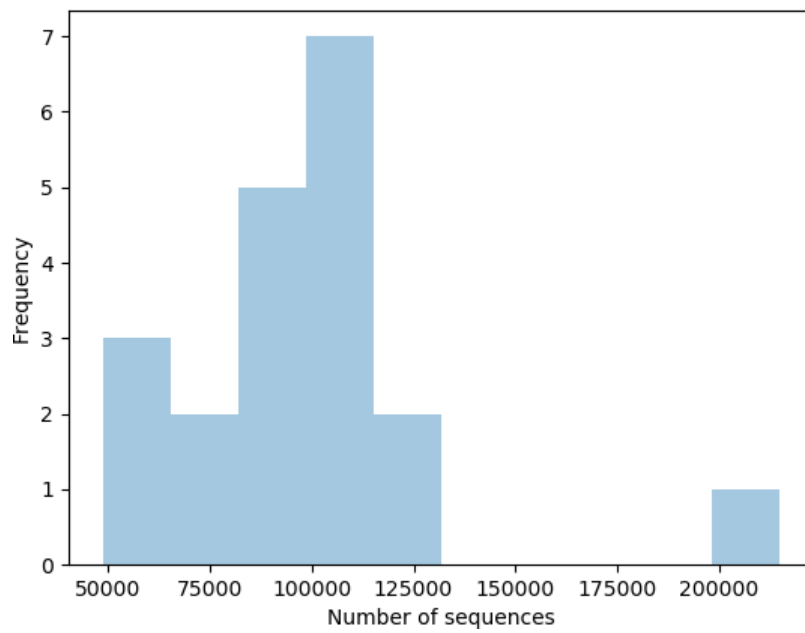
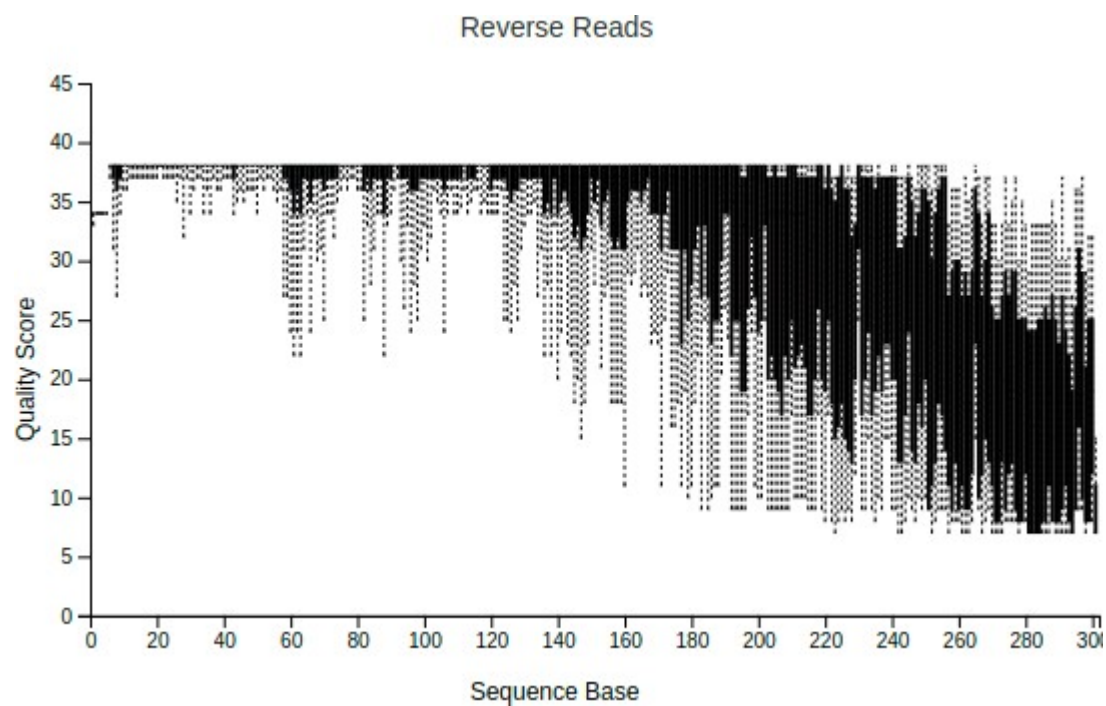
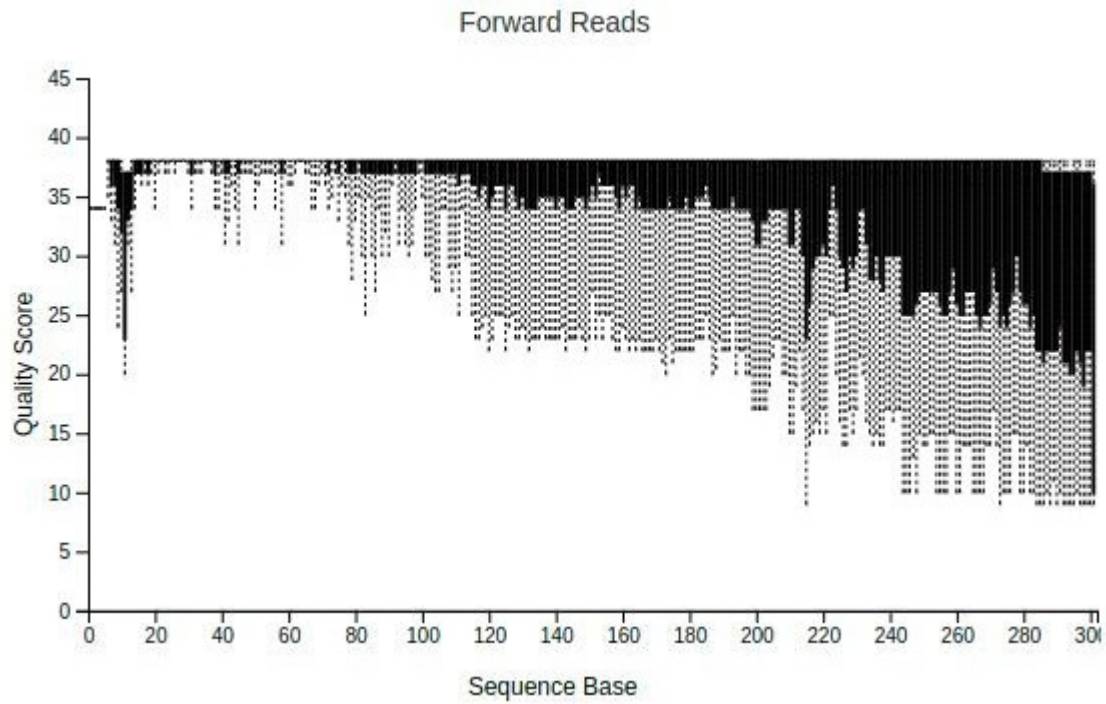


sequence counts summary

| | |
|----------|----------------|
| Minimum: | 48639 |
| Median: | 98827.5 |
| Mean: | 98799.5 |
| Maximum: | 215012 |
| Total: | <u>1975987</u> |



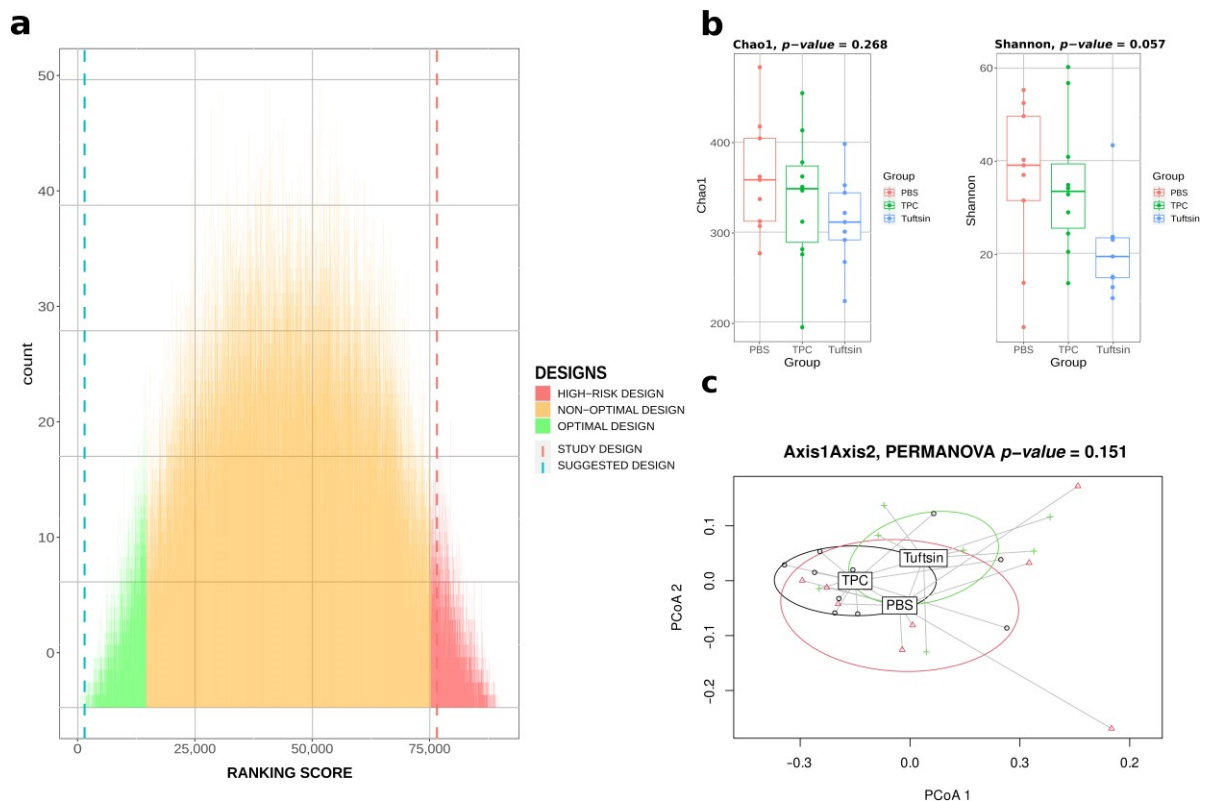
Supplementary Figure S1 | Sequencing data sets generated in this study.



Supplementary Figure S2 | Quality plots for forward and reverse reads.

| SAMPLES NUMBER | NUMBER OF ASVs | MEAN READS BEFORE DADA2 | MEAN READS AFTER DADA2 | FINAL PERCENTAGE OF RETAINED READS |
|----------------|----------------|-------------------------|------------------------|------------------------------------|
| 20 | 947 | 94103.7 | 44753.7 | 47.1 |

Supplementary TableS1 | Summary metrics after DADA2 Denoise and dereplicate paired-end sequences.



Supplementary Figure S3 | Analysis of the mice allocation design selected by the third party study. **a**, Bar chart displaying the ranking score metrics of 90,000 randomly simulated experimental mice allocation designs (integrating the design chosen during the study of Neuman *et al.*) obtained by **Bact-to-Batch** algorithm. The suggested best design of mice allocation in 3 groups proposed by **Bact-to-Batch** is represented by the blue dotted line and the selected design from the Neuman *et al.* study by the red dotted line. **b**, Microbiota α -diversity boxplots (Chao1 and Shannon indices) of the three groups of mice according to the Neuman *et al.* study. **c**, PCoA displaying the microbiota β -diversity of the three groups of mice belonging to the Neuman *et al.* study design.