

### sequence counts summary

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Minimum: 48639

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Median: 98827.5

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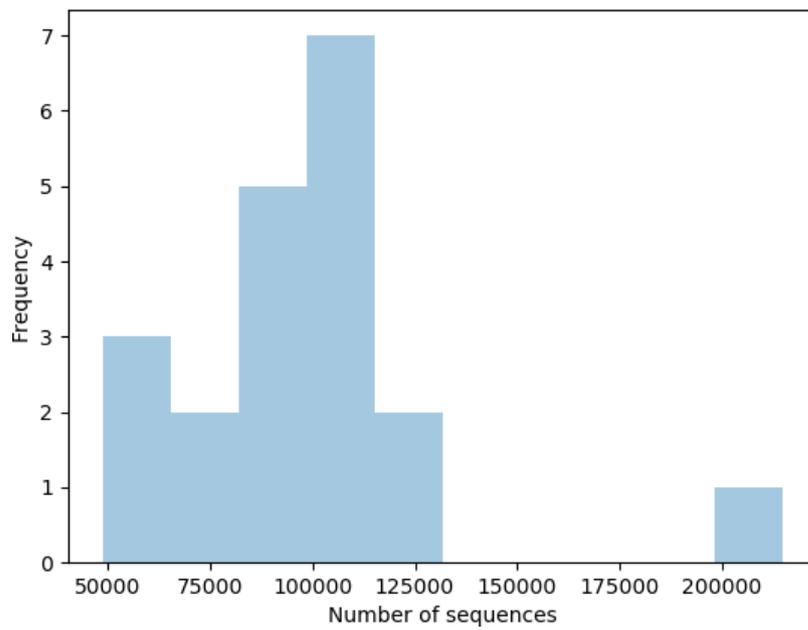
Mean: 98799.5

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Maximum: 215012

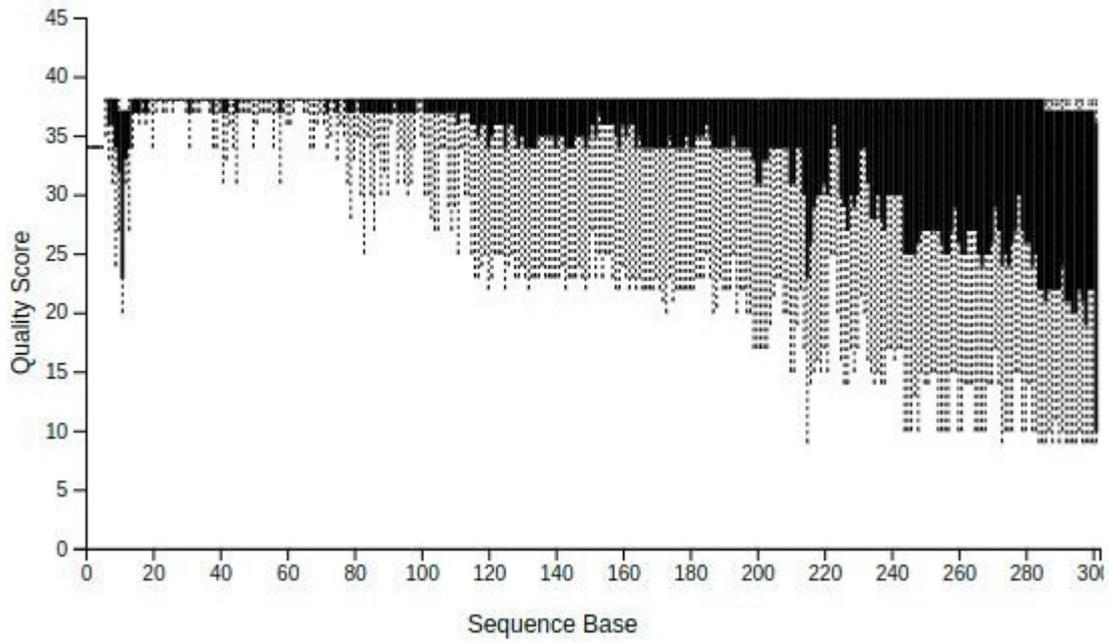
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Total: 1975987

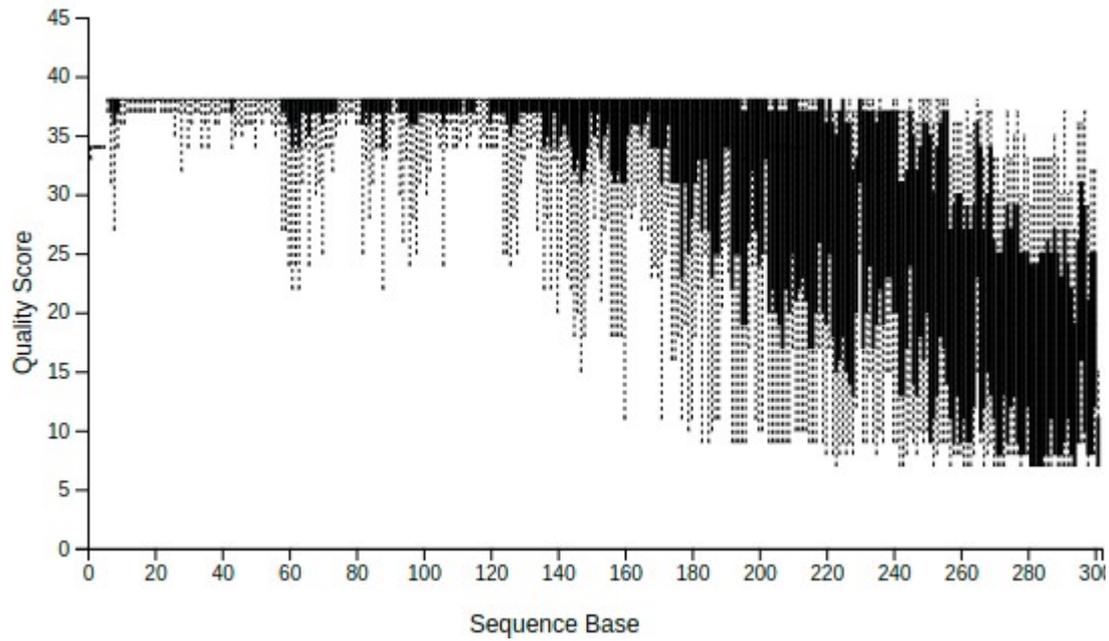


**Supplementary Figure S1 | Sequencing data sets generated in this study.**

### Forward Reads



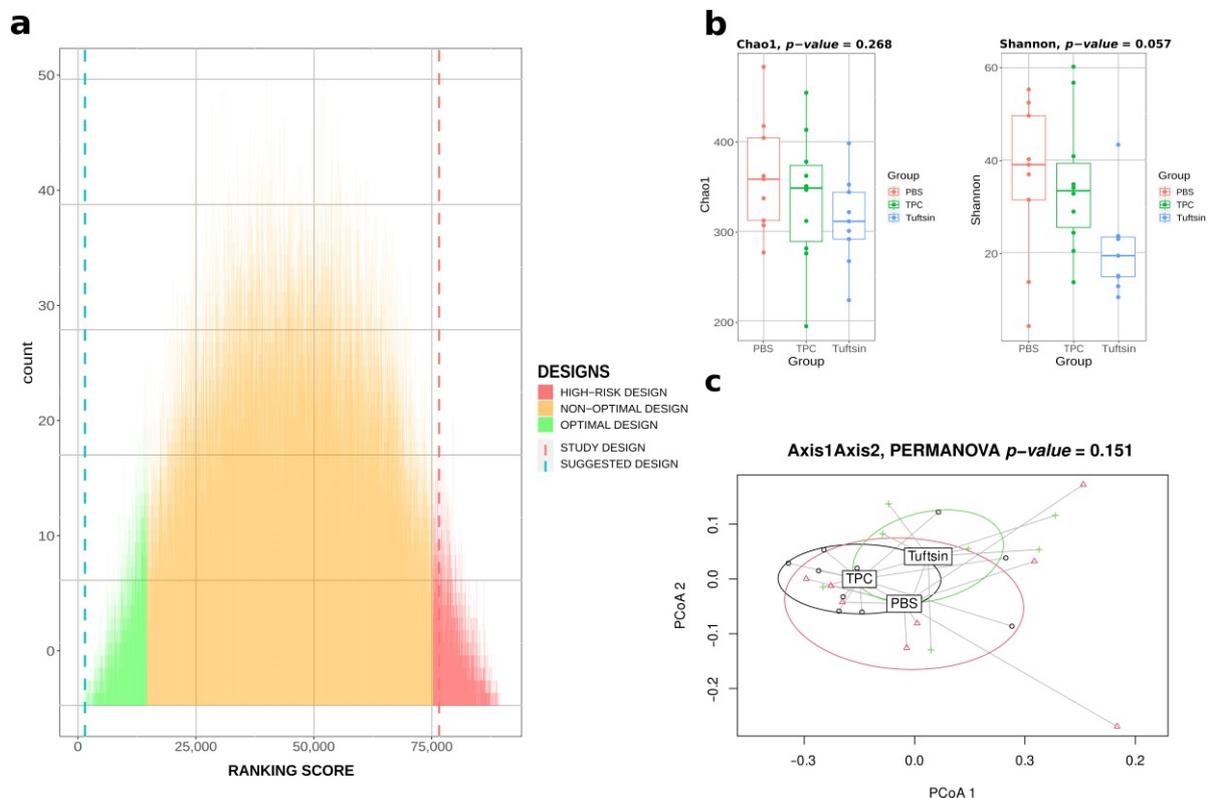
### Reverse Reads



**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  $\alpha$ -diversity boxplots (Chao1 and Shannon indices) of the three groups of mice according to the Neuman *et al.* study. **c**, PCoA displaying the microbiota  $\beta$ -diversity of the three groups of mice belonging to the Neuman *et al.* study design.