

## Supplemental methods

### Assignment of taxonomic annotation and predicted metagenomics

MiSeq FastQ files were created using CASAVA 1.8.2 ([https://support.illumina.com/sequencing/sequencing\\_software/casava](https://support.illumina.com/sequencing/sequencing_software/casava)). The open-source software package DADA2[1] (v.1.10) was used for amplicon-data processing which enables a single-nucleotide resolution of amplicons (amplicon sequence variants, ASVs). Data processing was conducted according to the recommended procedure for large datasets (<https://benjjneb.github.io/dada2/bigdata.html>), adapted to the targeted V1-V2 amplicon. In brief, five bases were truncated from the 5' end of the sequence of both reads. Forward and reverse reads were truncated to a length of 200 and 150 bases, respectively. If the sequence quality dropped below a quality score of five, a shorter resulting read length after truncation was also possible. Exclusion of read-pairs was performed if they contained ambiguous bases, had expected errors higher than two or when originating from PhiX spike-in. To infer error profiles, 1 million reads of the respective sequencing run were used. Subsequently dereplication, error correction and merging of forward and reverse reads was conducted. The `removeBimeraDenovo()` function in consensus mode was used to combine ASV abundance of tables of all samples and to identify and remove chimeric amplicon sequences. For assignment of taxonomic annotation a Bayesian classifier and the Ribosomal Database Project training set (v.16) were used. The functional genomic potential of the faecal microbiota were predicted with PICRUSt2[2] using the standard workflow as described at <https://github.com/picrust/picrust2/wiki/Workflow> and ASVs from the DADA2 pipeline as input. All samples were normalized to 10,000 *16S rRNA*-gene read counts for analysis.

### REFERENCES

- 1 Callahan BJ, McMurdie PJ, Rosen MJ, et al. DADA2: High-resolution sample inference from Illumina amplicon data. *Nat Methods* 2016;13(7):581–83.
- 2 Douglas GM, Maffei VJ, Zaneveld JR, et al. PICRUSt2 for prediction of metagenome functions. *Nat Biotechnol* 2020;38(6):685–88.