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Detailed Author Contribution Statement:

Natalie Jamei Wu-Woods

1. Major contributor to MEM protocol development optimization
2. Performed MEM on all animal and human saliva samples
3. Performed library prep and all bulk and digital quantification experiments
4. Performed 16S rRNA gene and shotgun sequencing analysis
5. Performed all MAG construction
6. Constructed figures 1A-C, 1E-F, 3A, 4, 5, 6. Constructed SI figures 1-5, 7-8, and ED figures 1-5. Constructed tables 1-8.
7. Wrote and edited the manuscript
8. Wrote the supplemental information
9. Co-developed the IRB protocol with JTB to obtain healthy human saliva samples
10. Contributed to obtaining funding

Jacob T. Barlow

1. Designed and validated original MEM protocol
2. Major contributor to MEM protocol development optimization
3. Performed MEM on subset of stool samples and a range of validation samples
4. Designed MEM validation experiments (Fig 1 and 2)
5. Set up clinical sample collaboration with UChicago and Dustin Shaw
6. Designed sampling regime for all clinical samples collected from UChicago in collaboration with DS (Fig 3 and 4)
7. Developed pipeline for raw sequencing analysis of 16S data (Fig 1-4) and shotgun marker gene data (Fig 2,4)
8. Performed analysis for and generated figures 1D-G, 2, 3B-E, and the concept behind 4D
9. Constructed SI figure S6
10. Co-developed the IRB protocol for saliva samples with NW to obtain healthy human saliva samples
11. Wrote initial paper outline (only figures 1-4)
12. Helped edit paper

Florian Trigodet

1. Co-developed analysis plan for figures 5-6 with NW, RFI, and AME
2. Performed SNVs analysis utilized in figure 6
3. Constructed SI figure S9 and table S9-10
4. Co-designed figure 5D and 6A with NW
5. Provided feedback and advice on all shotgun sequencing analysis
6. Wrote and edited the manuscript

Dustin Shaw

1. Performed MEM on human intestinal samples
2. Designed sampling regime for all clinical samples collected from UChicago in collaboration with JTB (Fig 3 and 4)
3. Confirmed feasibility of MEM on samples obtained from the clinic

Anna E. Romano

1. Discussed various techniques for extraction modification of saliva specimens to increase DNA/RNA yield and remove inhibitors.
2. Discussed and researched shotgun sequencing library preparations and sequencing options.
3. Discussed previous research on RNA quality of different mouse SI tissues.
4. Revised methods.
5. Researched the use of MTM prime store as an alternative preservation solution compatible with Qiagen extraction kit.
6. Discussed, troubleshooted, and assisted in shotgun sequencing library prep along side NW. Contributed knowledge about library preparation of low input samples and bubble product formation.

R.F.I. contributed to the design and implementation of the study, to obtaining funding, and to editing the manuscript. A.M.E. oversaw the bioinformatic analysis, contributed to the design and implementation of the study, to obtaining funding, and to editing the manuscript. B.J. supervised the clinical work, contributed to the design and implementation of the study, to obtaining funding, and to editing the manuscript.