

# DPC 2026 - Freiburg

Distangling contaminants from true intratumoural microbial signals in pancreatic ductal adenocarcinoma – A benchmarking approach

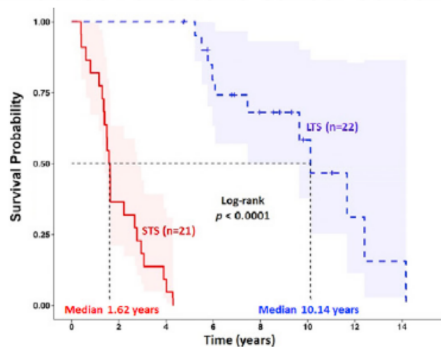
Linh Dang

2026-03-07

# Contamination in Microbiome Study

Cell

## Tumor Microbiome Diversity and Composition Influence Pancreatic Cancer Outcomes



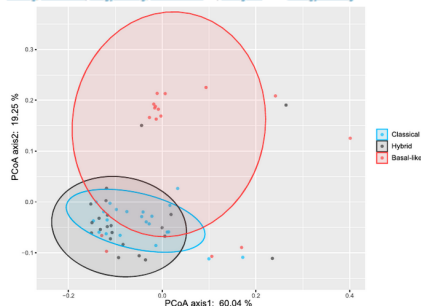
Riquelme et al. Cell 2019

Key taxa: *Streptomyces*, *Pseudoxanthomonas*, *Saccharopolyspora*

Article | [Open access](#) | Published: 31 August 2021

## Tumor microbiome contributes to an aggressive phenotype in the basal-like subtype of pancreatic cancer

[Wei Guo](#), [Yuchao Zhang](#), [Shiwei Guo](#), [Zi Mei](#), [Huiping Liao](#), [Hang Dong](#), [Kai Wu](#), [Haocheng Ye](#), [Yuhang Zhang](#), [Yufei Zhu](#), [Jingyu Lang](#), [Lindian Hu](#) , [Gang Jin](#)  & [Xiangyin Kong](#) 



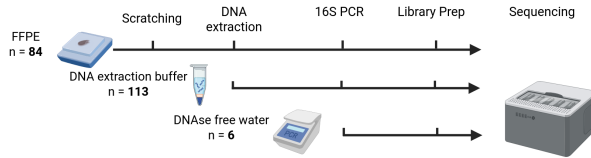
Guo Communication biology 2021

Key taxa: *Acinetobacter*, *Pseudomonas*, *Sphingopyxis*

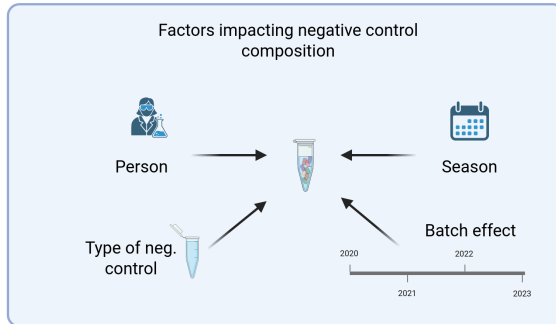
## Section 1

### Negative Control Survey in the Lab

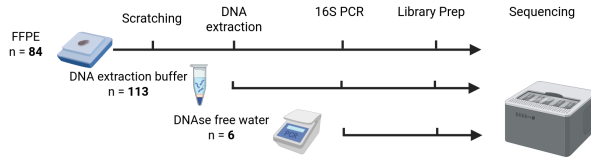
# Negative Sample Collection



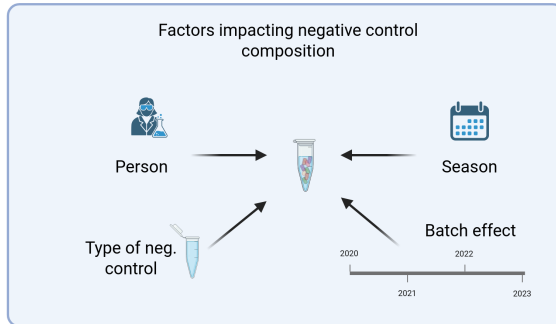
- In total 203 negative control samples over 4 years



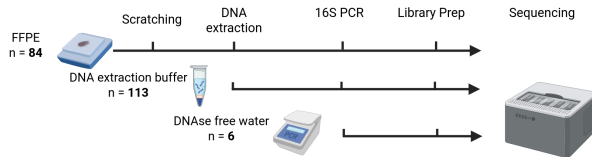
# Negative Sample Collection



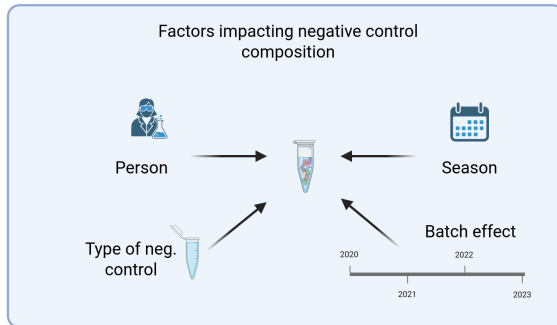
- In total 203 negative control samples over 4 years
  - 113 buffer controls,



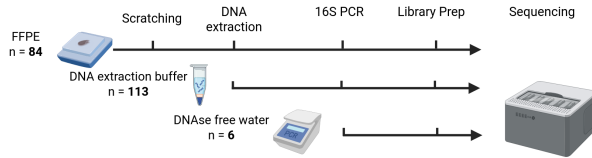
# Negative Sample Collection



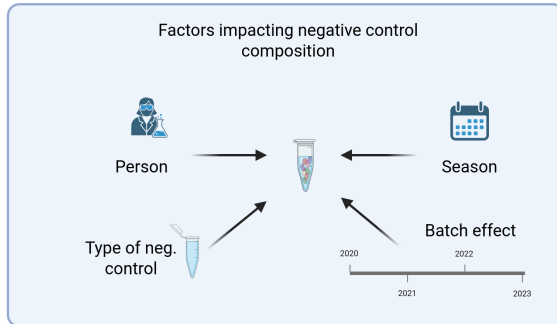
- In total 203 negative control samples over 4 years
  - 113 buffer controls,
  - 84 paraffin controls,



# Negative Sample Collection



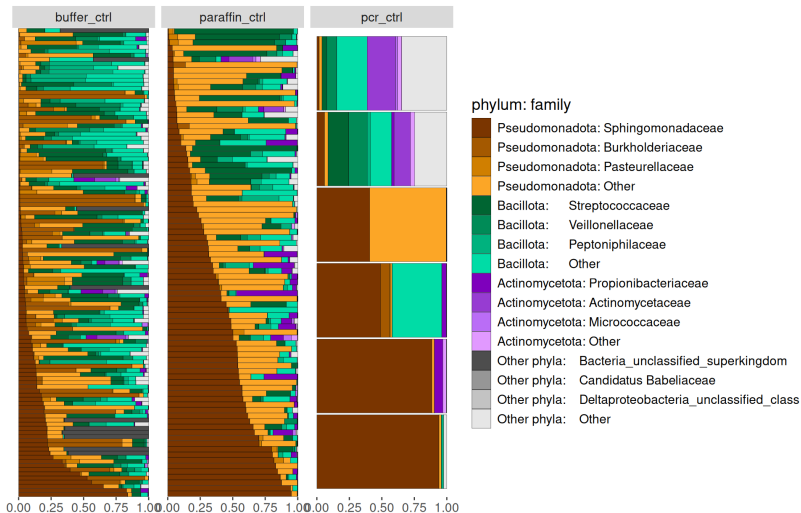
- In total 203 negative control samples over 4 years
  - 113 buffer controls,
  - 84 paraffin controls,
  - 6 PCR control.



# Bacterial Composition

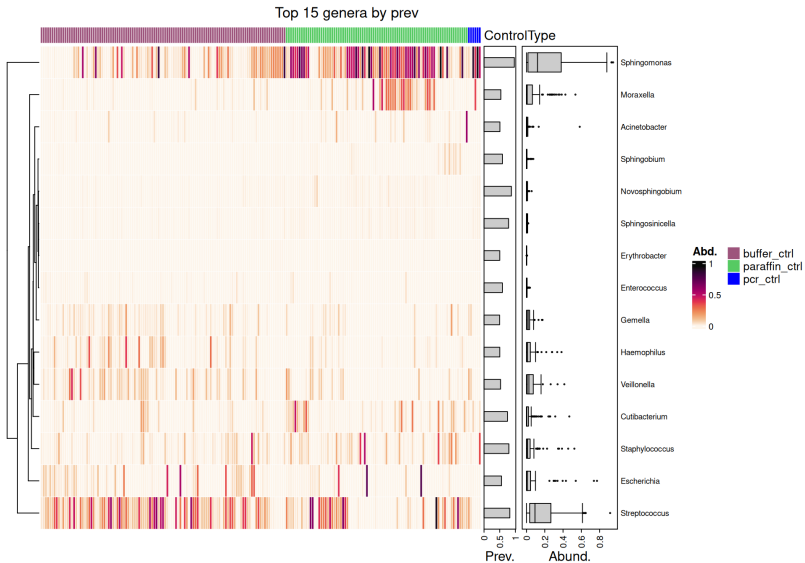
## Composition of NCT Samples

Order by sum





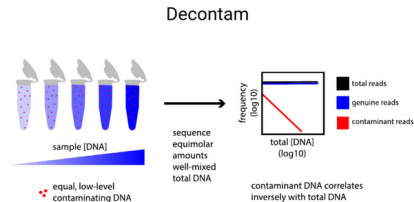
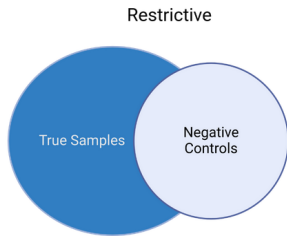
# Heatmap from Negative Controls



## Section 2

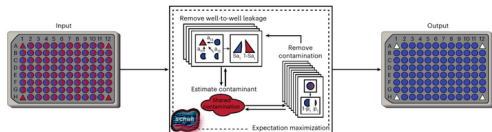
# Intratumor Microbiome in PDAC and Assessment of

# Decontamination Strategies

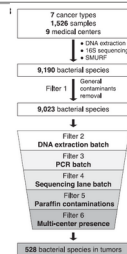


Davis et al. 2018 Microbiome

## SCRuB



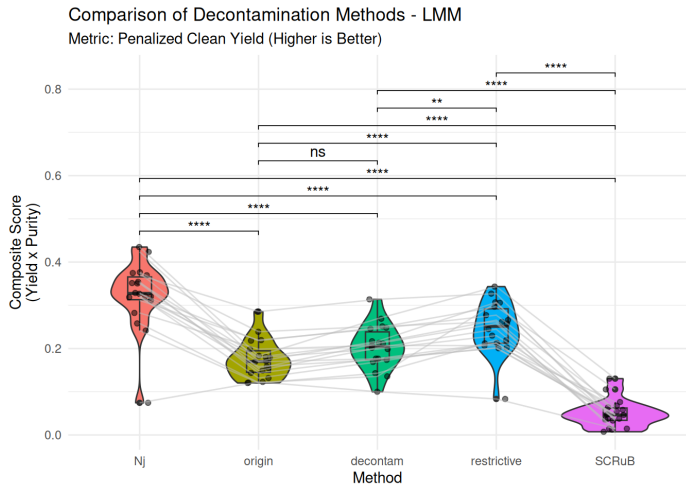
Austin et al. 2023 Nature Biotechnology



Nejman et al. 2020 Science

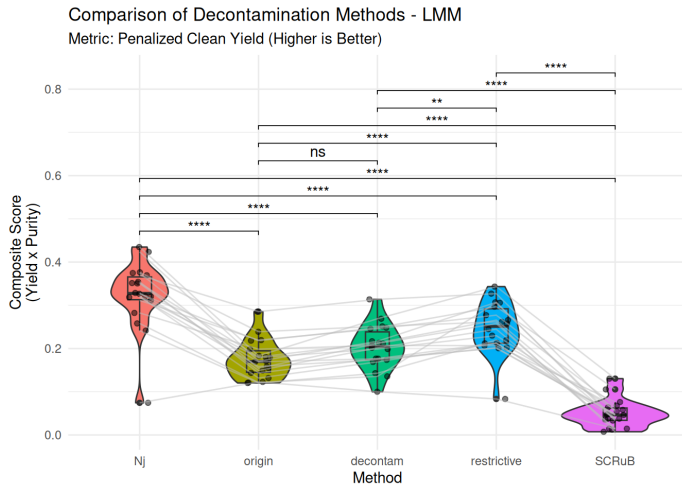
# Assessment of Decontamination Approach

- **Yield:**  
$$\frac{\# \text{ putative true taxa } \notin NCT}{\# \text{ observed species}}$$



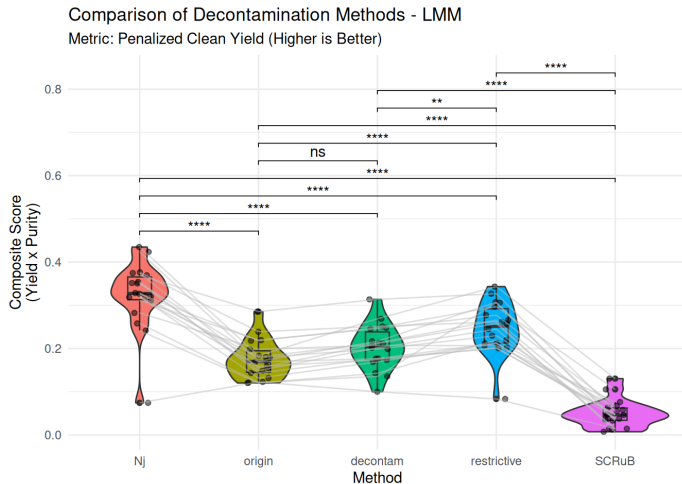
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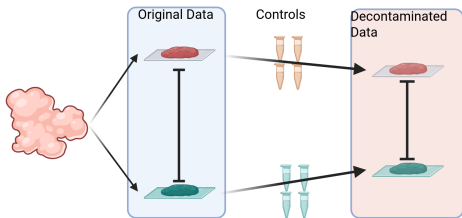
# Assessment of Decontamination Approach

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- **Purity:**  
$$\frac{\# \text{ putative true taxa} \notin NCT}{\# \text{ putative contaminants}}$$
- **Composite Score =**  
$$\text{Yield} \times \text{Purity}$$



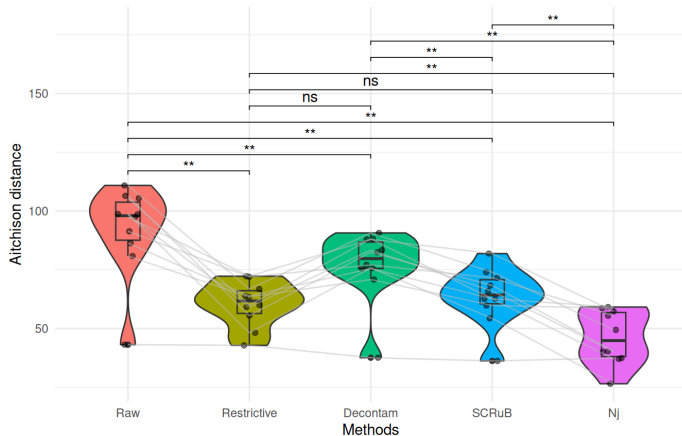
# Integrate Replica

## Utilize Replica for Assessment



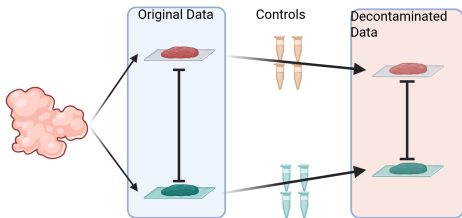
- 10 PDAC sample, each with 2 replica

Paired Wilcoxon test  
The lower the better



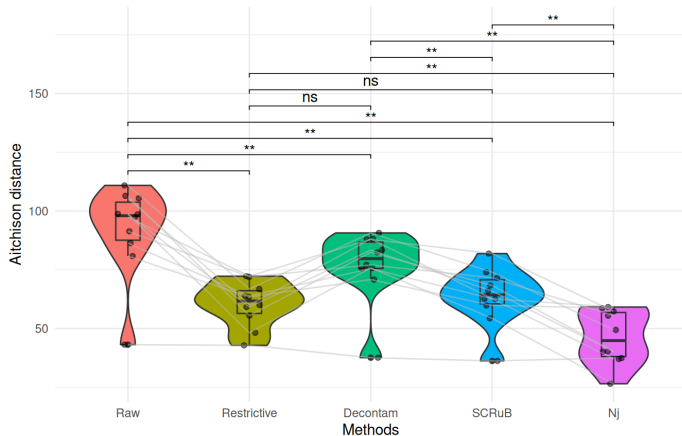
# Integrate Replica

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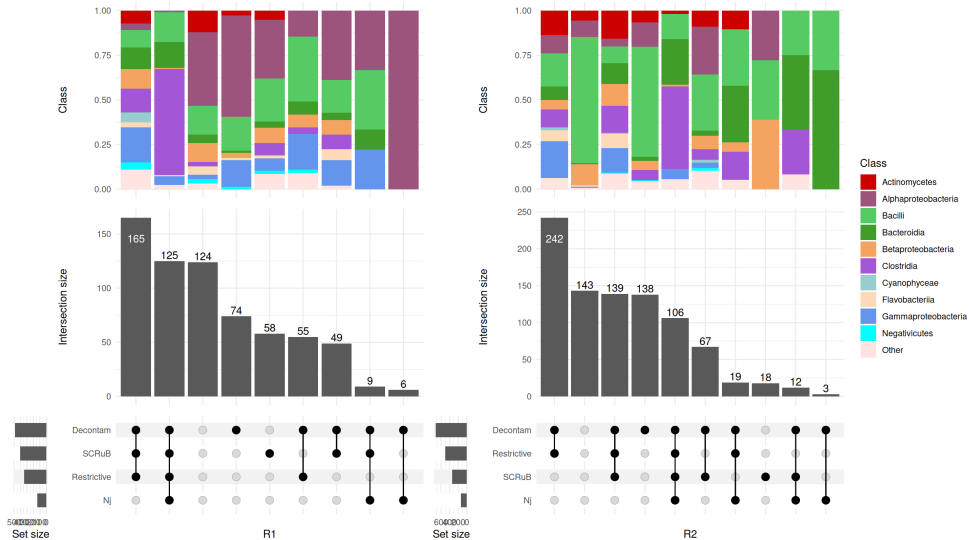
- 10 PDAC sample, each with 2 replica
- Aichison distance with paired Wilcox test.

Paired Wilcox test  
The lower the better

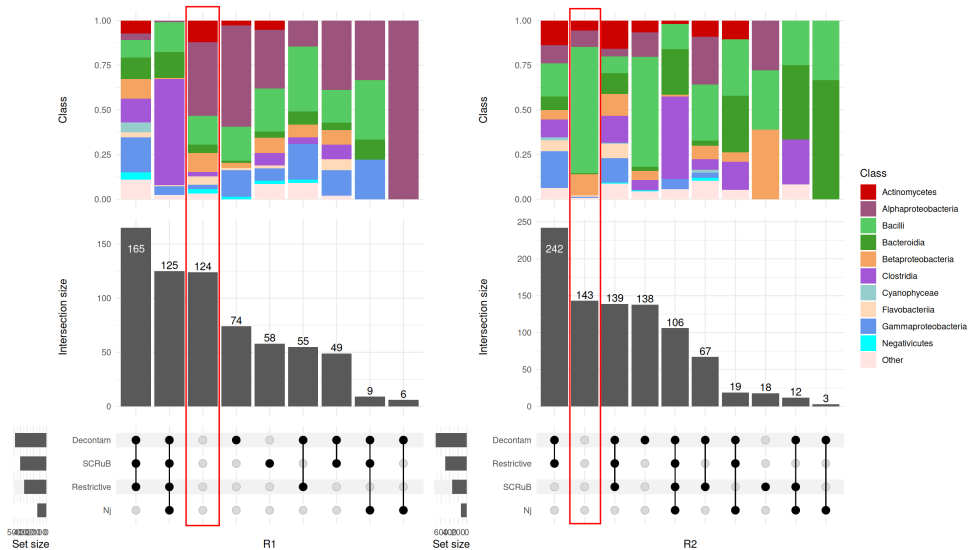




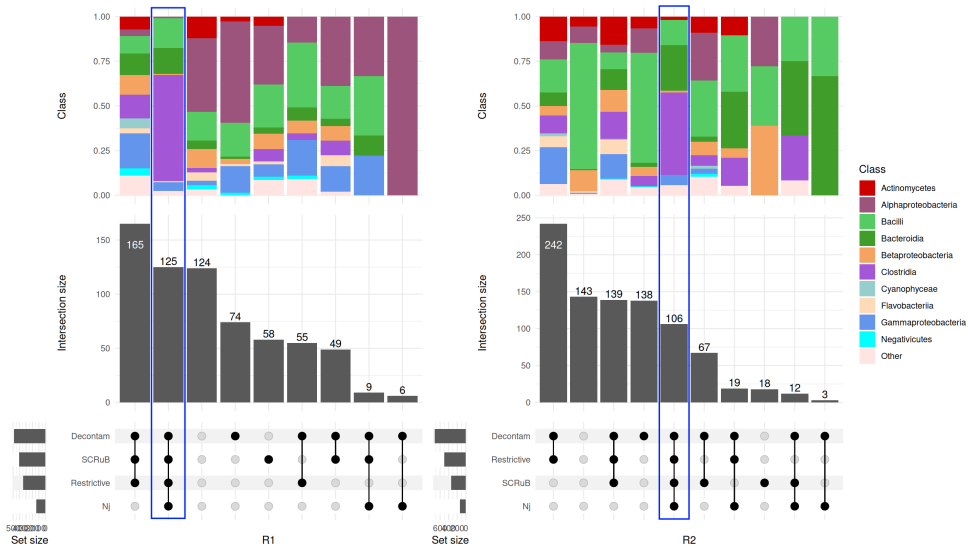
# Overlap - Microbiome profile of PDAC in mice



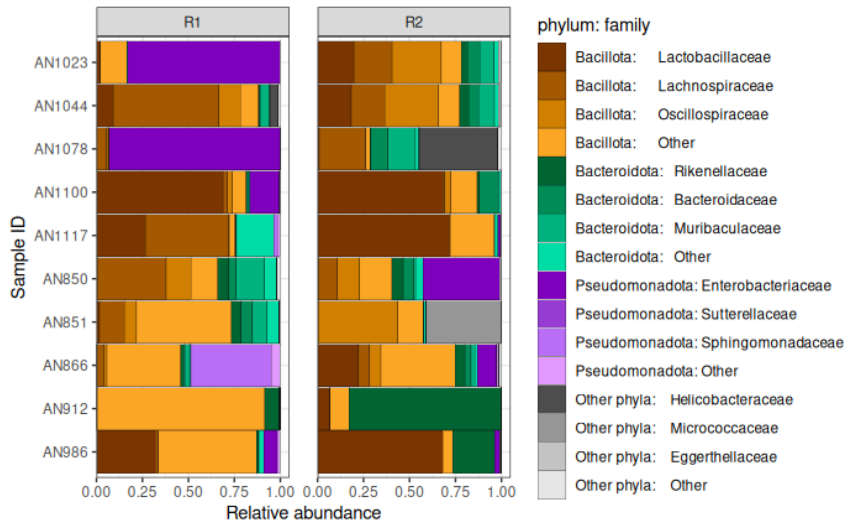
# Overlap - Microbiome profile of PDAC in mice



## Overlap - Microbiome profile of PDAC in mice



# Core microbiome after Nj approach



## Decontamination Methods

- Negative control samples are essential to avoid spurious taxa.

## Intratumor microbiome in PDAC

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## Intratumor microbiome in PDAC

- Re-sequencing and various decontamination methods with proper negative controls could yield a reliable set of intratumor microbiota.



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- Each batch has its own contaminant profile.
- In our study, thoroughly remove contaminant such as Nejman et al. procedure outperforms others.

## Intratumor microbiome in PDAC

- Re-sequencing and various decontamination methods with proper negative controls could yield a reliable set of intratumor microbiota.
- Almost identified taxa are well-known gut microbiota.

# Acknowledgements

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**P-MAPS Consortium**



## Section 3

### Backup Slides

# Core microbiome - All decontamination method - phylum: family

