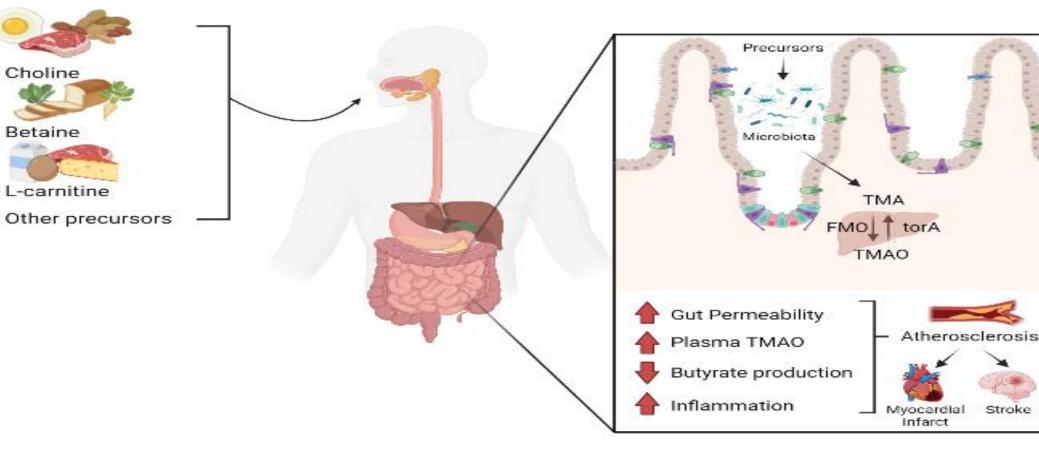


#### Functional Characterization of a High-Throughput in vitro Model to **Predict Faecal Microbiota Transplantation (FMT) Donor Success**

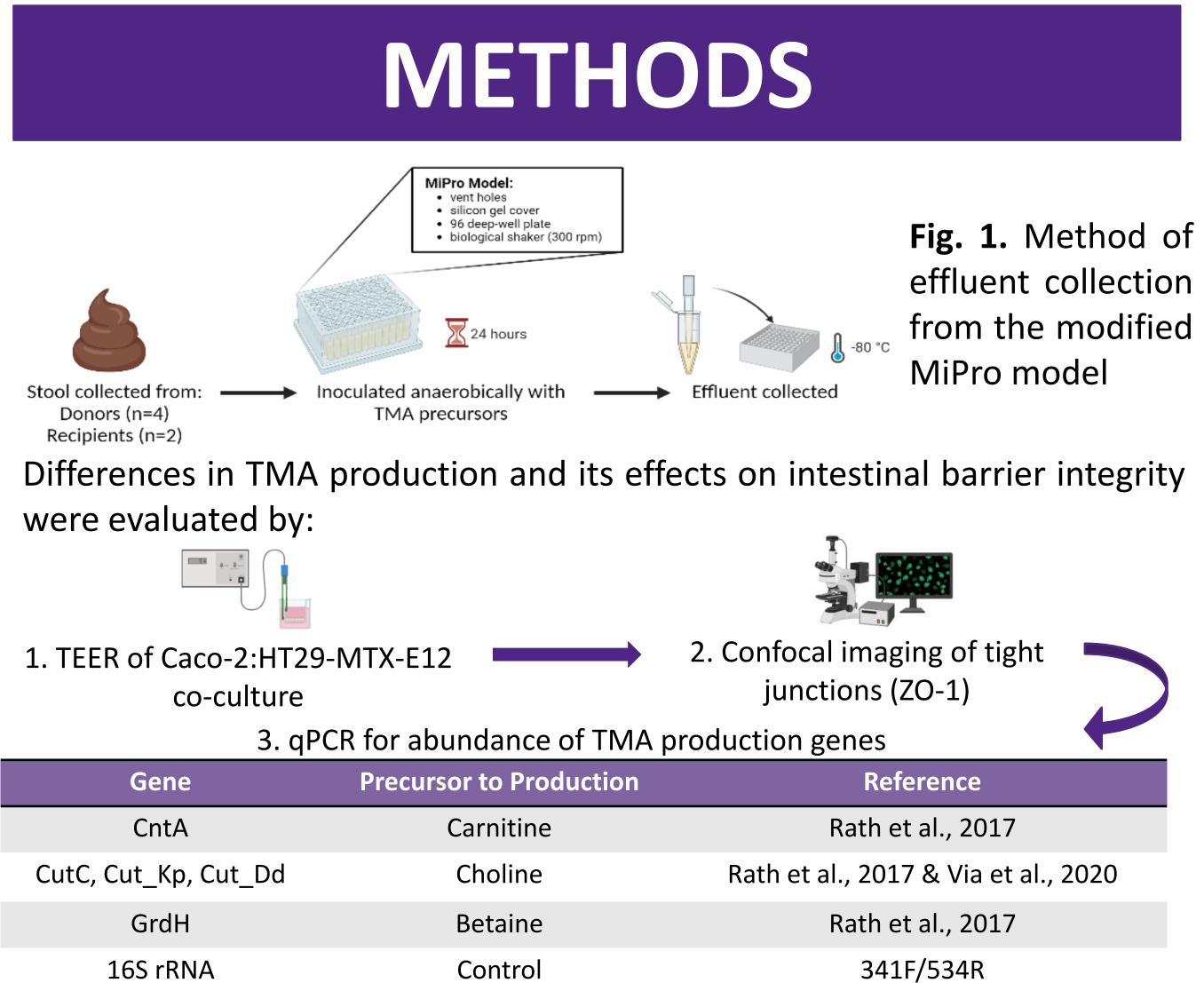
Catherine M. Andary<sup>1</sup>, Shaeley Gibbons<sup>1,4</sup>, Wongsakorn Kiattiburut<sup>1,4</sup>, Kait F. Al<sup>1,4</sup>, Jeremy P. Burton<sup>1,2,4</sup>, and Michael S. Silverman<sup>1,3,4</sup> <sup>1</sup> Department of Microbiology and Immunology, Schulich School of Medicine & Dentistry, Western University, London, ON, Canada <sup>2</sup> Department of Surgery, Schulich School of Medicine & Dentistry, Western University, London, ON, Canada <sup>3</sup> Division of Infectious Disease, St. Joseph's Health Care, London, ON, Canada <sup>4</sup> Lawson Health Research Institute, London, ON, Canada

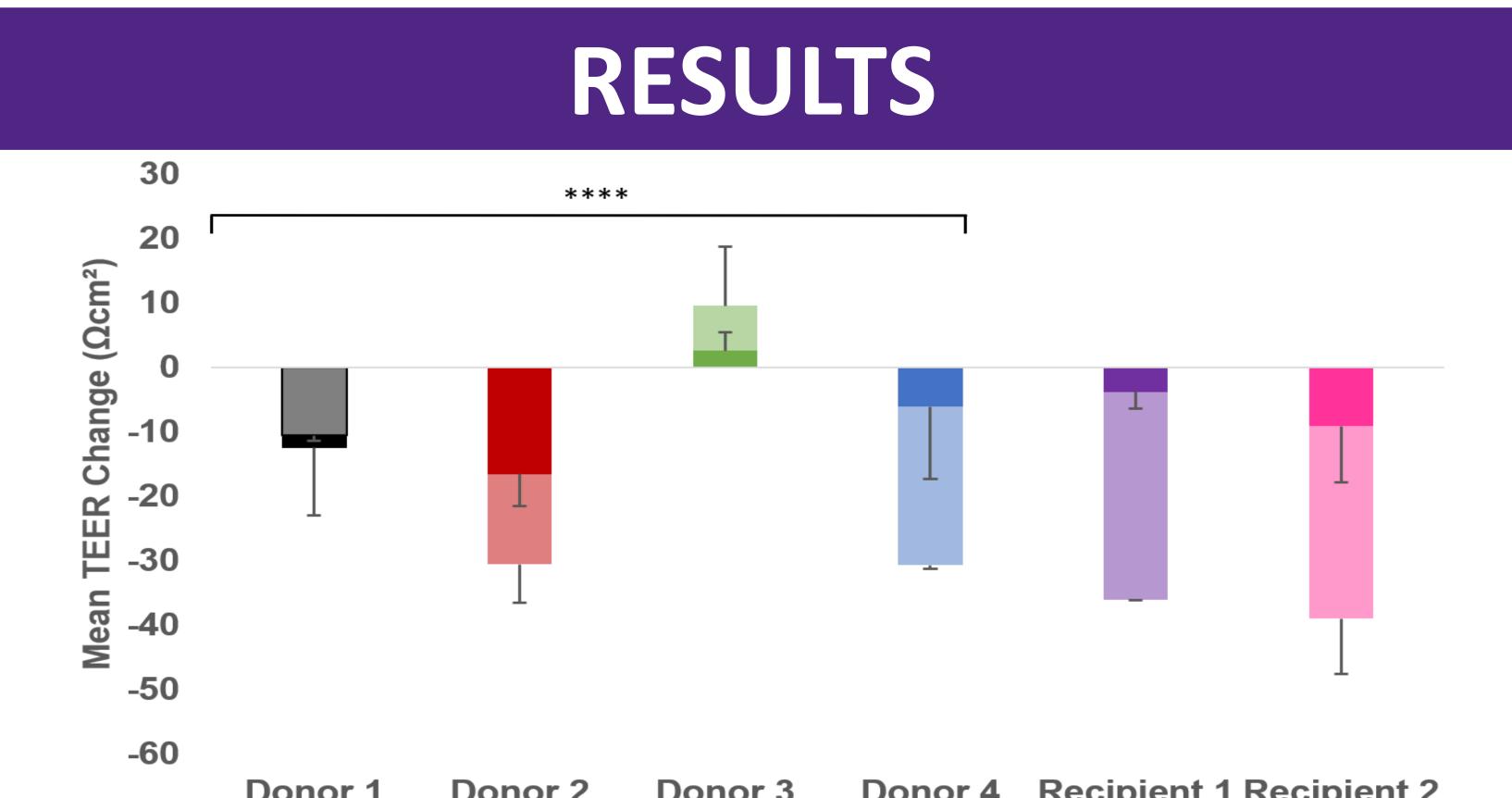
#### INTRODUCTION

- FMT has emerged in recent years as a potential therapy for a variety of microbiome-associated diseases, such as atherosclerosis.
- In vitro models are lacking to study mechanisms of treatment success and donor-recipient compatibility.
- Trimethylamine (TMA) is an atherosclerosis-linked metabolite generated by the gut microbiota from dietary precursors, which is then oxidized to trimethylamine N-oxide (TMAO) by the liver.
- FMT may alter or restore the gut microbiome of recipients to reduce plasma TMAO levels.
- A 96 well plate-based culturing model (MiPro)<sup>1</sup> was adopted and modified to identify the response of FMT donor and atherosclerosis patient microbiomes to TMA metabolites.
- The modified model was used to investigate TMA production and its influence on barrier integrity in a sample population of atherosclerosis patients with high plasma TMAO (n=2) and donors (n=4).

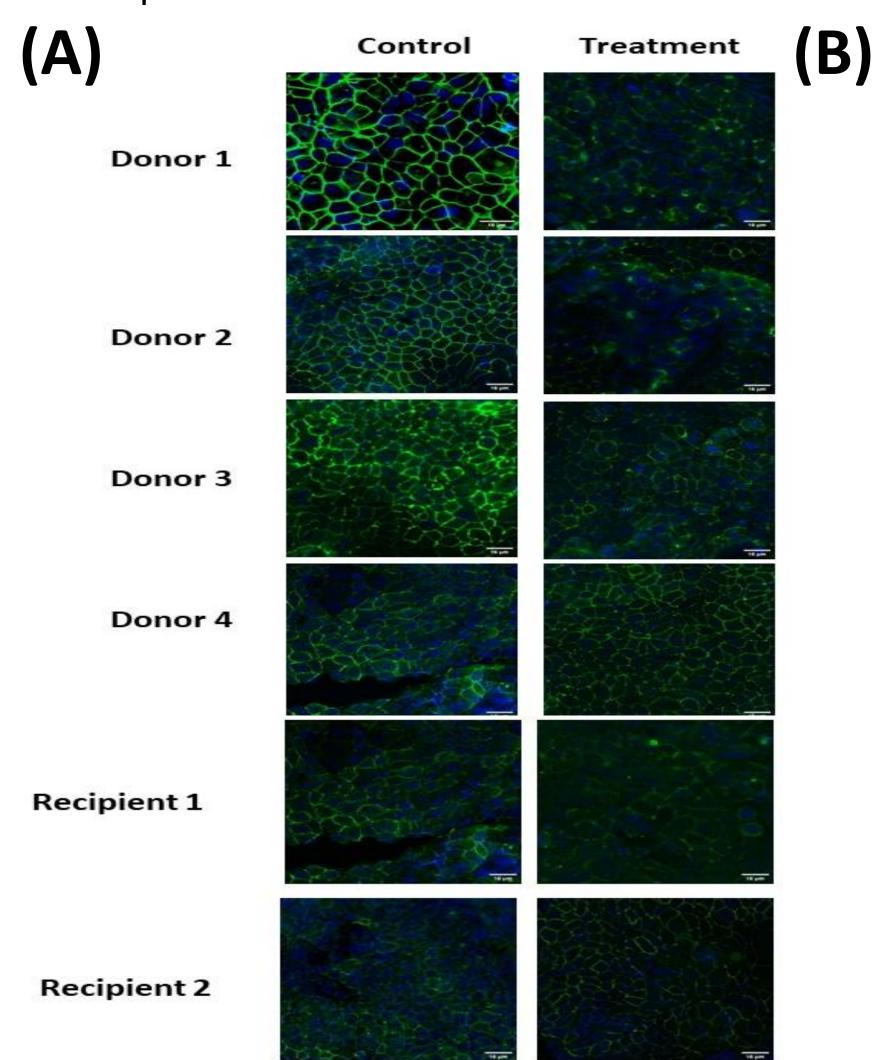


**Objective:** To characterize the effects of microbiome samples from individuals with divergent disease phenotypes on intestinal barrier integrity to identify characteristics implicated in FMT donor success.



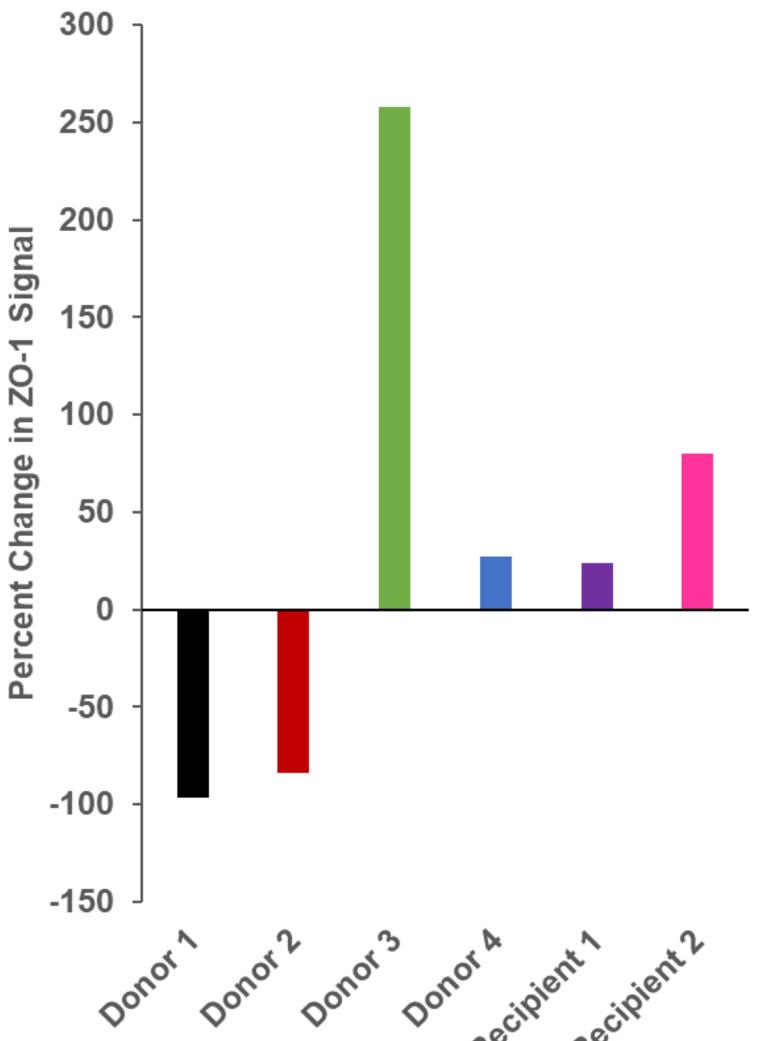


Donor 4 Recipient 1 Recipient 2 Donor 1 Donor 2 Donor 3 Fig. 2. Donors demonstrate significant differences in epithelial barrier permeability following treatment with filtered MiPro effluent. Caco-2:HT29-MTX-E12 cell monolayers were grown to confluency on a nitrocellulose transmembrane over 14 days. The mean change in transepithelial electrical resistance (TEER) ( $\Omega cm^2$ ) was measured using an epithelial volt/ohm meter (EVOM) following 24 hours of filtered effluent treatment. Negative values indicate increased barrier permeability. Significant differences post-treatment (indicated by decreased opacity) were observed between donors (n=4) using a one-way ANOVA at \*\*\*\*p<0.0001. Error bars represent standard errors of the mean.



Ô Chang Pe

Fig. 3. (A) Confocal images and (B) quantified percent change of Zonula occludens-1 (ZO-1) signal are altered following effluent exposure in donors and recipients. Caco-2:HT29-MTX-E12 cell monolayers were grown to confluency on a nitrocellulose transmembrane over 14 days, treated with donor (n=4) or recipient (n=2) filtered effluent for 24 hours, and stained with antibody against ZO-1 before imaging. Expression of ZO-1, a tight junction peripheral membrane protein, is shown in green, while nuclei were stained with DAPI and shown in blue.



# MiPro effluent.

- effluent.
- disrupted

## ACKNOWLEDGEMENTS

This project was supported by the Burton lab, the USRI program, and the Schulich School of Medicine and Dentistry.



## REFERENCES



#### DISCUSSION

• Significant differences in monolayer barrier integrity measured by TEER were observed following treatment with filtered donor

• Donor 3 was especially resilient, with increases in cell barrier integrity observed post-treatment with filtered effluent.

FMT recipients exhibited decreases in monolayer barrier integrity measured by TEER following treatment with filtered

Barrier integrity measured by ZO-1 signal was notably amongst donors and recipients post-effluent treatment, with the largest changes observed in Donor 3.

 This study provides proof of concept of a novel highthroughput *in vitro* model to predict donor microbiota resilience upon exposure to toxic metabolites such as TMA.

Future projects correcting for the small sample size of this study may allow for identification of specific FMT donor microbiota characteristics implicated in therapeutic success.

1. Li, L., Abou-Samra, E., Ning, Z. et al. An in vitro model maintaining taxonspecific functional activities of the gut microbiome. Nat Commun 10, 4146 (2019). https://doi.org/10.1038/s41467-019-12087-8

Rath, S., Heidrich, B., Pieper, D.H. et al. Uncovering the trimethylamineproducing bacteria of the human gut microbiota. Microbiome 5, 54 (2017). https://doi.org/10.1186/s40168-017-0271-9

Dalla Via, A., Gargari, G., Taverniti, V. et al. Urinary TMAO levels are associated with the taxonomic composition of the gut microbiota and with the choline TMA-lyase gene (CUTC) harbored by Enterobacteriaceae. Nutrients, 12, 62 (2019). https://doi.org/10.3390/nu12010062