

1 **Supplementary Figure S 1. Study design. Panel A:** Fifteen subjects with established ESRD  
2 receiving thrice weekly hemodialysis were randomly assigned, in a paired, single-blinded  
3 fashion, to receive either a 250 mg vancomycin or placebo capsule weekly. At 3 months,  
4 the subjects were crossed-over and either received placebo or vancomycin for another 3  
5 months. Pre-dialysis blood samples were collected weekly for one month and then  
6 monthly. Stool samples were collected at baseline and then monthly. **Panel B:** Summary of  
7 subject's samples included in each analysis.

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9 **Supplementary Figure S2. Changes in concentration of solutes from 10 subjects ( 126**  
10 **samples) over the 12-week treatment periods.** Box and whisker plots are shown.

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12 **Supplementary Figure S3. Vancomycin-related changes in relative abundance of**  
13 **genera.** Bar plot of the relative abundance of the top 10 most abundant genera at  
14 baseline and 4 weeks of antibiotics in each subjects. Samples rarefied to 1000.

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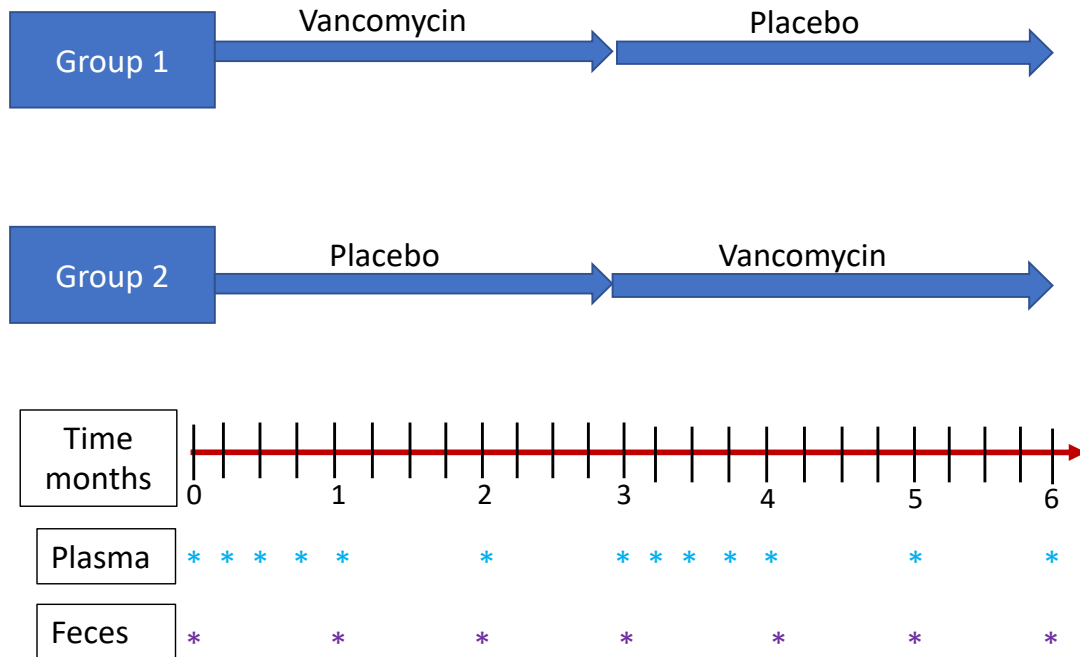
16 **Supplementary Figure S4. IS recovery after 12 weeks vancomycin.** Black line is fitted  
17 mixed model.

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1 **Suppl. Fig. S1**

2 **A**



3 **B**

Baseline
  Receiving Vancomycin
  Receiving Placebo

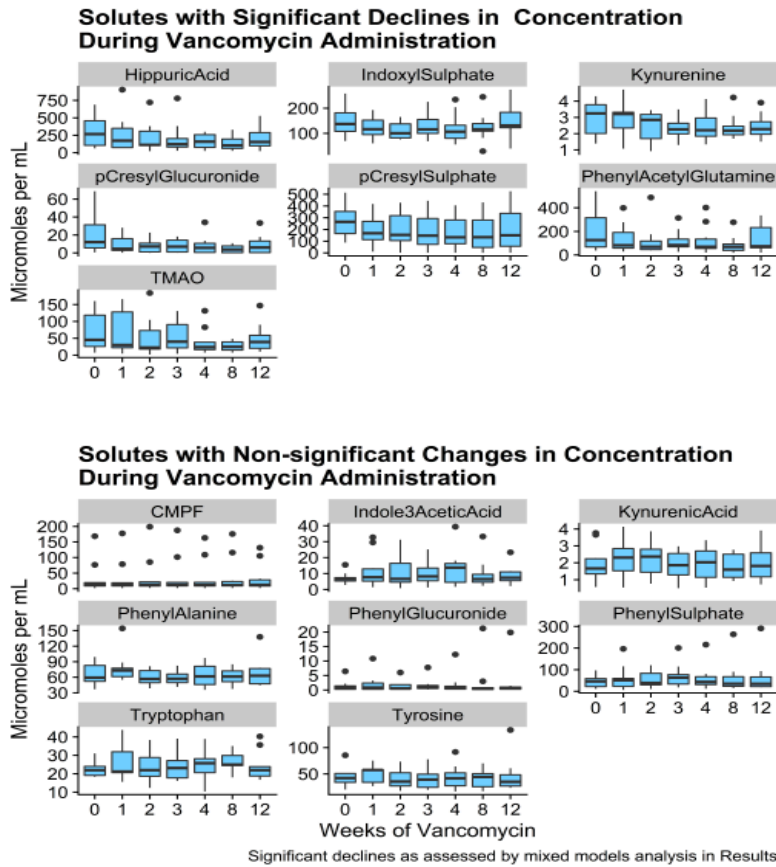
S: Solutes  
 M: Microbiome  
**M: Samples included in DESeq2 analysis**  
 \*: stool samples included in the diversity analysis  
 †: stool samples included in the recovery analysis

Subjects	Weeks 0	1	4	8	12	13	16	20	24
RRA1	SM*	S	S	SM*	SM*	SM*†	S	SM†	SM†
RRA2	SM*	S	S	SM*	SM*	S	S	S	S
RRA4	SM*	S	S	SM*	SM*	SM*†	S	SM†	SM†
RRA5	SM*	S	S	S	SM*	SM*†	S	S	S
RRA8	SM*	S	S	SM*	SM*	SM*†	S	SM†	SM†
RRZ1	SM*	S	S	SM*	SM*	SM*	S	SM*	SM*
RRZ3	SM*	S	S	SM*	SM*	S	S	SM*	SM*
RRZ4	SM*	S	S	SM*	S	S	S	SM*	SM*
RRZ5	SM*	S	S	SM*	SM*	SM*	S	S	SM*
RRZ6	SM*	S	S	SM*	SM*	SM*	S	SM*	SM*

All SM samples were included in the solutes and microbiome correlation analysis

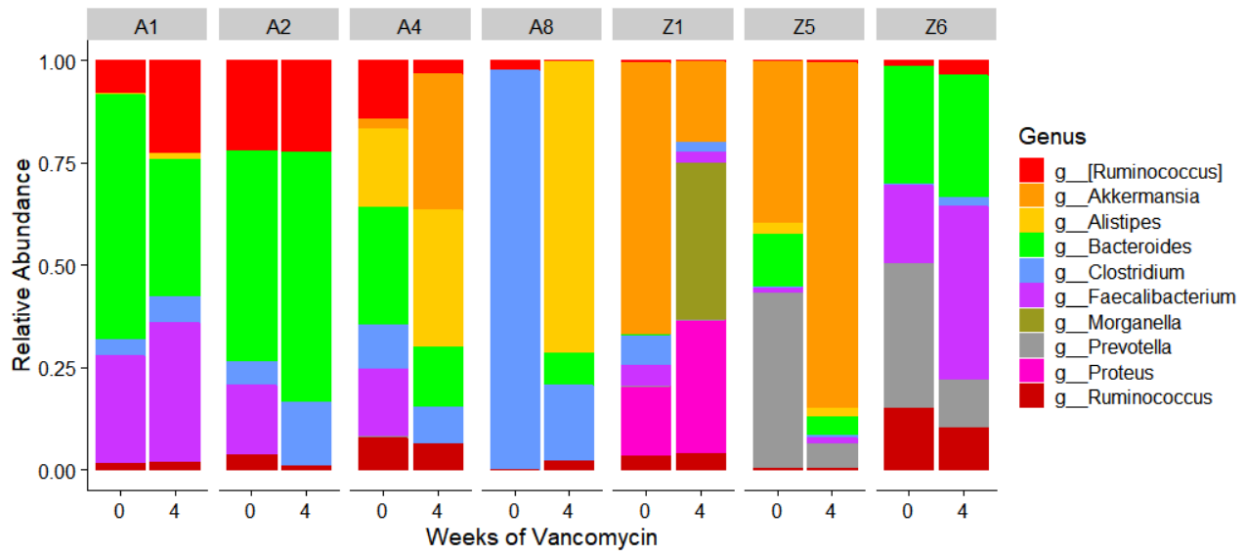
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1 **Suppl. Fig. S2**



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3 **Suppl. Fig. S3**

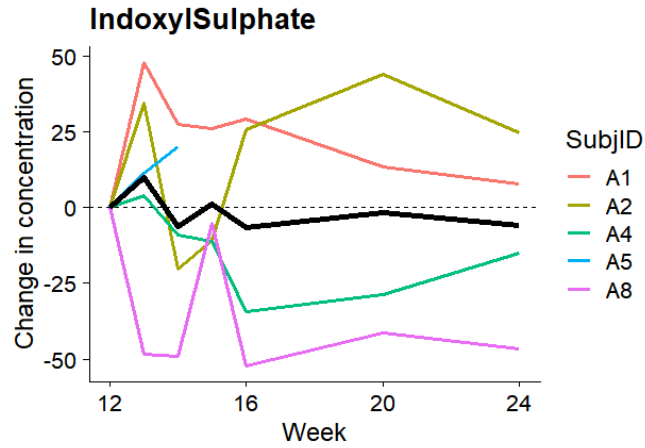


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6 **Suppl. Fig. S4**

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**Table S1: Vancomycin-related changes in relative abundance of genera**

Genus	n	avwk0	avwk4	difference	SE.diff	Paired.t.pval
<b>Prevotella</b>	7	0.067	0.008	-0.058	0.038	0.177
<b>Clostridium</b>	7	0.075	0.033	-0.041	0.05	0.439
<b>Bacteroides</b>	7	0.130	0.094	-0.037	0.021	0.134
<b>Faecalibacterium</b>	7	0.063	0.050	-0.013	0.018	0.506
<b>Ruminococcus</b>	7	0.023	0.019	-0.003	0.009	0.742
<b>Akkermansia</b>	7	0.094	0.095	0.001	0.056	0.985
<b>[Ruminococcus]</b>	7	0.032	0.036	0.005	0.016	0.775
<b>Proteus</b>	7	0.013	0.028	0.015	0.015	0.356
<b>[Eubacterium]</b>	7	0.008	0.042	0.034	0.016	0.078
<b>Alistipes</b>	7	0.013	0.080	0.067	0.049	0.224

4 avwk 0: average relative abundance at week 0  
 5 SE.diff: standard error difference  
 6 Paired.t.pval: p value from paired test comparing 0 and 4 weeks relative abundance.

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