

1 SUPPLEMENTARY INFORMATION

2 **Supplementary Text**

3 **Vancomycin/MoviPrep/SHGM.** Vancomycin targets the majority of colon bacteria. It has
4 previously been shown to be beneficial in treatment of autism; therefore, it is plausible that
5 vancomycin could be targeting some members of the microbiota that drive the symptoms of
6 autism. Vancomycin is also used to treat *C. difficile* infections. Vancomycin is virtually
7 always used before infusion of fecal microbiota in treatment of recurrent *C. difficile*
8 infections by fecal microbiota transplantation. It should be noted that this is the only protocol
9 that is currently clearly associated with substantial engraftment of donor microbiota. From
10 standpoint of microbial ecology, vancomycin treatment is needed to “create space” as a
11 conditioning regimen prior to substantial engraftment of a new microbial community.

12 MoviPrep is a common purgative prior to colonoscopic examinations. The purpose of
13 the bowel lavage here was to ensure clearance of vancomycin from the GI tract, as residual
14 antibiotic could interfere with engraftment of new microbiota. MoviPrep specifically, as
15 opposed to other purgatives, was chosen because of its relatively better tolerability among the
16 general US population undergoing colonoscopic examinations.

17 SHGM is built upon a body of work with patients being treated for recurrent *C.*
18 *difficile* infections. Since the preparation of microbiota is standardized, it is the best we can do
19 at this time to build upon this initial work to enable larger trials and attempts at repeating
20 similar regimens by other groups. Our initial dose was comparable to what is used for FMT
21 treatments, and our maintenance dose is comparable to what Thomas Borody used as a

22 maintenance dose for treating children with ASD (T. Borody, personal communication).
23 Further optimization of dosing is needed in future studies.

24

25 **Safety/Tolerability/Adverse effects.** Children with ASD experienced only temporary adverse
26 effects (primarily mild to moderate hyperactivity and tantrums/aggression) at the beginning of
27 vancomycin treatment, no major changes in blood chemistry or long-term adverse effects
28 were noted. As listed in Additional file 1: Table S3, one participant among the 18 children
29 with ASD (5%) developed an extensive rash, but the rash disappeared when vancomycin was
30 switched from a natural orange flavor to an unflavored form. Within 1-4 days after the start of
31 the vancomycin, 12 children with ASD had a temporary behavioral reaction to the
32 vancomycin either involving hyperactivity (7 out of 12 cases; 39%) or Tantrums/aggression
33 (5 out of 12 cases; 28%). The symptoms lasted 1-3 days in most cases, except for one
34 participant that had symptoms lasting for 3 weeks. After the symptoms disappeared, GI
35 symptoms and behavioral symptoms began improving, which is similar to what Sandler et al.
36 [1] reported in their oral vancomycin therapy for children with autism. Prilosec was generally
37 well-tolerated, but many children had difficulty consuming MoviPrep, due to its taste.
38 Regarding Standardized Human Gut Microbiota (SHGM), rectal administration was
39 remarkably well-tolerated by 6 of 6 recipients. Oral administration of high-dose SHGM was
40 well-tolerated by 12 of 13 recipients, but one participant experienced vomiting and was
41 switched to the rectal route. Oral administration of the low-dose SHGM was well tolerated
42 for 7-8 weeks in all cases.

43 Participants experienced no major changes in Complete Blood Count (CBC) or blood
44 chemistry panel. Minor changes in blood chemistry were observed as follows. There was a

45 5% decrease in average levels of potassium ($p=0.01$) from beginning to end of treatment, but
46 all levels remained in the normal range. After the vancomycin (2nd week of study) there was
47 an 8% increase in platelets ($p=0.03$), but 4 participants had elevated levels at start, and only 2
48 participants had elevated levels after vancomycin. A 26% drop in Blood Urea Nitrogen
49 (BUN) ($p=0.002$) and a 17% increase in Aspartate transaminase (AST) ($p=0.01$) were
50 observed, although all BUN and AST levels remained in normal range. A 6% increase in
51 albumin/globulin (A/G) ratio ($p=0.03$) was observed, with 1 slightly elevated. A 24% increase
52 in alanine transaminase (ALT) ($p=0.003$) was observed, and 1 remained elevated while 2
53 became slightly elevated over time. However, all these results (platelets, BUN, A/G ratio,
54 AST, ALT) returned to similar to baseline at weeks 5 and 10. Slight changes (1-2%) were
55 observed in levels of mean corpuscular volume (MCV), mean corpuscular hemoglobin
56 (MCH), mean corpuscular hemoglobin concentration (MCHC), and red blood cell distribution
57 width (RDW).

58

59 **GI symptoms (GSRS and daily stool records).** A steady and large degree of improvement
60 in most areas of GSRS evaluation was observed, including abdominal pain, indigestion,
61 diarrhea, and constipation (Additional file 3: Figure S1a). There was little change in reflux
62 since no children had significant reflux at the start of the study. Notably, two seemingly
63 opposite GI symptoms- diarrhea and constipation- responded to the FMT treatment
64 effectively.

65 The Daily Stool Record (DSR) was collected and averaged it over two weeks in order
66 to assess changes in stool hardness/softness during the study. Overall, a significant decrease
67 was observed in “% days of abnormal stool” that combines % days of hard, soft/liquid, and no

68 stool, from 62% to 34% ($p=0.001$) during the 10-week FMT treatment (Additional file 1:
69 Table S2 and Additional file 3: Figure S1b). The improvements remained stable for the
70 following 8 weeks during the observation period. In detail, both “% days of hard stools” (type
71 1 or 2) and “% days of soft/liquid stools” (type 6 or 7) significantly decreased during the 10-
72 week FMT treatment, but the decrease in “% days of no stool” was not significant (Additional
73 file 1: Table S2).

74

75 **Autism and Related Symptoms (ABC, VABS-II, and PGI-III).** The Aberrant Behavior
76 Checklist (ABC) was employed to assess treatment effects on aberrant behaviors common in
77 **children with ASD**: irritability, lethargy, stereotypy, hyperactivity, and inappropriate speech.
78 A significant reduction was observed at the end of treatment in all five sub-scales (Additional
79 file 3: Figure S1c).

80 The Vineland Adaptive Behavior Scale II (VABS-II) is a measure of the functioning
81 level in four different domains: Communication, daily living skills, socialization, and motor
82 skills, based on 11 sub-domains. Among 11 subscales, Fine and Gross Motor skills were
83 excluded, since these two subscales for the Vineland are only calculated up to 6.8 years and
84 most **children with ASD** started near or over the limit of the scale. The other 9 subscales and
85 their average were compared between baseline and at the end of the study. The FMT
86 treatment resulted in a significant increase in average developmental age, from 5.4 years at
87 baseline to 6.8 years at the end of the study ($p<0.001$) (Additional file 3: Figure S3). A gain of
88 1.4 years within 18 weeks of the study is a substantial increase, but they still remained below
89 their chronological age of 10.9 years. Significant improvements were also observed in all 9
90 subscale areas with the largest gains in interpersonal skills (2.2 years), personal living skills

91 (1.8 years), and coping skills (1.7 years) (Additional file 3: Figure S3). It is notable that the
92 major impairments in ASD, namely receptive language, expressive language, and
93 interpersonal skills, were among the lowest initial scores, with initial developmental ages of
94 3.1 years, 4.5 years, and 2.9 years, respectively; all three areas had substantial improvements
95 of 1.3, 1.1, and 2.2 years, respectively.

96 By the end of the FMT treatment at week 10, the parents rated the change in their
97 children's autism symptoms using the PGI-III, and the largest improvements were in the GI
98 subscore among 17 subscales and "Overall autism/related symptoms" of the PGI-III
99 (Additional file 3: **Figure S6**). Specifically, the overall scale of PGI-III was rated as Much
100 Better: n= 4 (22%); Better: n= 8 (44%); Slightly Better: n=5 (28%); Little/no change: n=1
101 (6%). The improvement in the other subscales is shown in Additional file 3: **Figure S6**.

102

103 **Stool versus swab microbiome samples.** In addition to stool collection over the 18 week
104 period, fecal swab samples were collected nearly every other week. These samples were
105 obtained by swabbing bottoms or used toilet paper with a sterile swab, and thus are easier to
106 collect than stool samples. The general patterns presented for stool data were present in the
107 swab data, but did not always achieve statistical significance in the tests performed for this
108 study (Additional file 3: **Figure S7**). This may be due to greater variability in the handling of
109 the swab samples, which were shipped to the collection facility at ASU, and thus spent a
110 varied amount of time at ambient temperature, ranging from a few hours to multiple days.

111

112 **Oral versus rectal administration.** No significant difference was observed in efficacy of
113 treatment and changes in gut microbiota after treatment whether FMT was initially

114 administered rectally or orally (Additional file 3: **Figure S8**). However, the sample sizes were
115 too small to identify differences, and a larger trial to evaluate the mode of administration
116 should be performed.

117

118 **Microbiome profiles across even sampling depths and OTU percent identity thresholds.**

119 Recent work [2-4] has highlighted important differences in microbiomes that are apparent
120 only by observing differences in presence, absence, and abundance of closely related taxa
121 that may be grouped into single OTUs at the commonly used 97% similarity threshold. To
122 ensure that this study achieved those maximum OTUs, both 100% and 97% OTUs were
123 defined. Analysis focused on the 100% OTUs, but compared microbiome features to those
124 computed based on 97% OTUs to validate the approach. To validate the method, community
125 richness and composition measures were correlated between the 100% and 97% OTUs, such
126 that if analyses were instead performed on 97% OTUs, the results would be reproducible.
127 Faith PD (Pearson $r=0.97038$, $p<0.001$, $n=569$), unweighted UniFrac (Mantel $r: 0.92999$,
128 $p<0.001$, $n=569$), and weighted UniFrac (Mantel $r: 0.76651$, $p<0.001$, $n=569$) were all highly
129 correlated across the two OTU clustering thresholds, suggesting that the same conclusions
130 would be drawn with either approach. The small differences are expected, as there are many
131 more 100% OTUs than 97% OTUs.

132 Similarly, richness and composition metrics were computed at even sampling
133 (rarefaction) depths of 5,721 and 10,040 on the 100% OTU data. The lower depth allowed us
134 to maximize the number of samples for the analyses, and comparison to the higher depth
135 allows us to confirm that results would be similar if more sequences were retained. Faith PD
136 (Pearson $r=0.99738$, $p<0.001$, $n=548$), unweighted UniFrac (Mantel $r: 0.97296$, $p<0.001$), and

137 weighted UniFrac (Mantel r : 0.99953, $p < 0.001$) were all highly correlated across sampling
138 depths, suggesting that the same conclusions would be drawn based from either sampling
139 depth.

140

141 **Microbiome results across common diversity metrics.** Parallel analyses for multiple
142 diversity metrics were performed to understand the effect of each metric on the findings. With
143 the *Observed OTUs* metric (a count of the number of OTUs observed at least one time in a
144 sample; Additional file 3: Figure S4), the same patterns were observed and presented in Fig.
145 2a (Spearman $\rho = 0.90$, $p < 0.00001$), confirming that both phylogenetic and non-phylogenetic
146 metrics illustrate the same patterns of change in community richness with MTT; i.e., children
147 with ASD initially had lower bacterial richness than controls, but bacterial richness
148 significantly increased after MTT reaching levels closer to those in the neurotypical children.
149 Shannon diversity, a metric which accounts for both the richness and the evenness of samples,
150 also illustrates the same pattern (Spearman ρ to Faith PD: 0.83, $p < 0.00001$; Spearman ρ
151 to Observed OTUs: 0.96, $p < 0.00001$). These increased bacterial richness remained high 8
152 weeks after treatment stopped. Increase in bacterial richness was substantial, from an initial
153 median Faith PD value of 47.2 to a final median value of 57.4, an increase of 22%. Similarly,
154 Observed OTUs increased from 1,296 to 1,475, an increase of 12%, and Shannon diversity
155 increased from 7.2 to 7.9, and increase of 9%.

156 Similarly, pairwise distances were computed between samples using four diversity
157 metrics, a qualitative non-phylogenetic metric (Jaccard distance), and quantitative non-
158 phylogenetic diversity metric (Bray-Curtis distance), a qualitative phylogenetic diversity
159 metric (unweighted UniFrac), and a quantitative phylogenetic diversity metric (weighted

160 UniFrac) (Additional file 3: **Figure S9**). Interestingly, while the pattern was the same between
161 the first three metrics (decrease in distance between recipient and donor), significant
162 engraftment with weighted UniFrac was not observed (though less variation across
163 individuals at weeks 10 and 18 than in earlier time points was observed). Quantitative metrics
164 give more weight to higher abundance OTUs than qualitative metrics. Because differences in
165 composition were observed using a quantitative non-phylogenetic metric (Bray-Curtis) but
166 not observed using a quantitative phylogenetic metric (weighted Unifrac), it suggests that
167 when changes occur in high abundance OTUs, those OTUs are generally closely related (thus
168 the change is down-weighted with a phylogenetic diversity metric relative to a non-
169 phylogenetic diversity metric). Overall, 3 of the 4 metrics demonstrate that engraftment
170 occurred, and remained stable at 8 weeks after treatment stopped.

171

172 **Microbiome results on engraftments using unweighted UniFrac distance.** Similarly to
173 data presented in Fig. 3c, when the unweighted UniFrac distance were compared between the
174 recipient gut and their initial donor sample (instead of their most recent/relevant donor sample
175 as in Fig. 3c), the distance also decreased significantly over time (Additional file 3: **Figure**
176 **S10**; two-tailed Mann-Whitney U-test $p < 0.01$ at three weeks and $p < 0.001$ at 10 and 18 weeks)
177 and remained similar to the donor's bacterial community 8 weeks after treatment stopped. In
178 addition, the distance between the recipient gut bacterial community and the major initial
179 donor's was less than the variation of normal interpersonal bacterial community (showed by
180 comparing the neurotypical children variation) at the end of treatment (week 10) as well as 8
181 weeks after treatment stopped (week 18) (Additional file 3: **Figure S10**).

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184 **References**

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