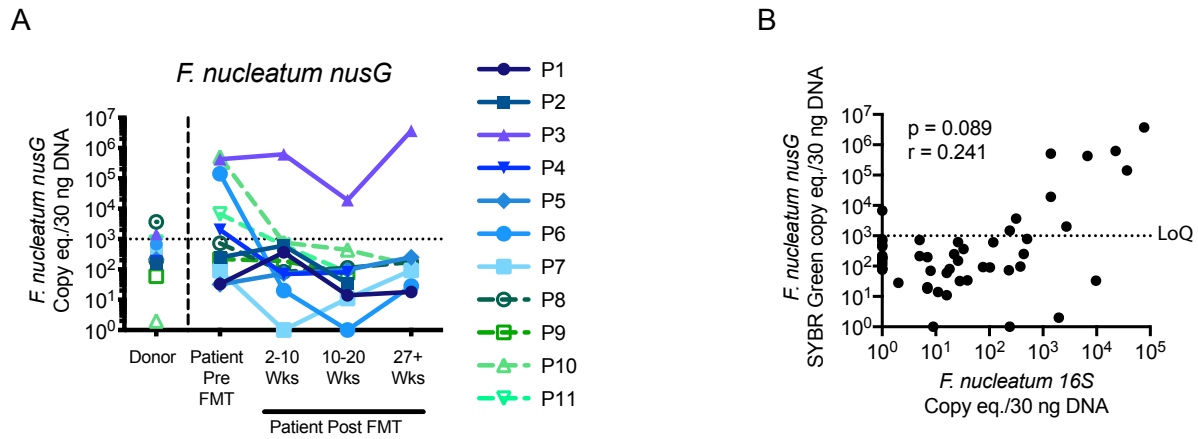


SUPPLEMENTAL MATERIAL

Supplemental Figures & Legends



Supplemental Figure 1. Longitudinal levels of *Fusobacterium nucleatum nusG*. (A) Stool DNA was examined for the presence of the *F. nucleatum*-specific gene *nusG* by SYBR Green qPCR. Data are shown from FMT donors, patients prior to FMT, and patients at various time points post FMT (2-10 weeks, 10-20 weeks, and >27 weeks). Colors denote the source of the FMT donor stool, with familial donors in shades of blue/purple (P1-P7) and commercial stool bank donors shown in shades of green (P8-P11). Undetectable data points were assigned a value of 1 for display purposes on the log₁₀ scale. Due to the use of SYBR green reagents, the background threshold limit (or limit of quantitation, LoQ, dotted line) for *nusG* was 10³ copies per 30 ng DNA, compared to 10⁰ for *F. nucleatum 16S* rDNA and *fadA* genes using Taqman qPCR (see Methods). (B) Spearman's correlation of *nusG* vs. *F. nucleatum 16S* copy numbers in direct stool extracts from the FMT patients and donors.

Supplemental Table 1. qPCR Primers and Probes

Target	Sequence 5' - 3'	Fragment Annealing		Reference
		size (bp)	Temp. (°C)	
<i>E. coli</i> 16S F	CATGCCGCGTGTATGAAGAA	96	60	Arthur <i>et al.</i> , 2012
<i>E. coli</i> 16S R	CGG GTA ACG TCA ATG AGC AAA	96	60	Arthur <i>et al.</i> , 2012
<i>E. coli</i> 16S HEX	HEX - TCGGGTTGTAAAGTACTTTTCAGCGGG - BHQ1		60	This study
<i>clbB</i> (<i>pks</i>) F	GCGCATCCTCAAGAGTAAATA	280	60	Arthur <i>et al.</i> , 2012
<i>clbB</i> (<i>pks</i>) R	GCGCTCTATGCTCATCAACC	280	60	Arthur <i>et al.</i> , 2012
<i>clbB</i> (<i>pks</i>) FAM	FAM - TATTCGACACAGAACAACGCCGGT - BHQ1		60	This study
<i>B. fragilis</i> 16S F	TCRGGAAAGAAAGCTTGCT	163	58	Tong <i>et al.</i> , 2011
<i>B. fragilis</i> 16S R	CATCCTTTACCGGAATCCT	163	58	Tong <i>et al.</i> , 2011
<i>B. fragilis</i> 16S HEX	HEX - AGGGACTGGAAGGCTTTACTGCTTC - BHQ1		58	Tong <i>et al.</i> , 2011
<i>bft</i> F	GCGAACTCGGTTTATGCAGT	281	58	Odamaki <i>et al.</i> , 2012; Boleij <i>et al.</i> , 2015
<i>bft</i> R	GTTGTAGACATCCCACTGGC	281	58	Kato <i>et al.</i> , 2000; Boleij <i>et al.</i> , 2015
<i>bft</i> FAM	FAM - AGCAGAAGGTTATGACGA - NFQ - MGB		58	This study
<i>F. nucleatum</i> 16S F	GGATTTATTGGGCGTAAAGC	162	60	Boutaga <i>et al.</i> , 2005
<i>F. nucleatum</i> 16S R	GGCATTCTACAAATATCTACGAA	162	60	Boutaga <i>et al.</i> , 2005
<i>F. nucleatum</i> 16S HEX	HEX - TGCAGGGCTCAACTCTGTATTGCG - BHQ1		60	This study
<i>fadA</i> F	CAAATCAAGAAGAAGCAAGATTCAAT	121	58	This study
<i>fadA</i> R	GCTTGAAGTCTTTGAGCTCT	121	58	Rubinstein <i>et al.</i> , 2013
<i>fadA</i> FAM	FAM - CGCTGCTAGACAAGCACTAGCACA - BHQ1		58	This study
<i>nusG</i> F	CAACCATTACTTTAACTCTACCATGTTCA	161	60	Castellarin <i>et al.</i> , 2012
<i>nusG</i> R	GTTGACTTTACAGAAGGAGATTATGTA AAAATC	161	60	Castellarin <i>et al.</i> , 2012
<i>nusG</i> probe	N/A - SYBR green used instead		60	N/A

Supplemental Table 2. Percentage of patients positive by direct stool DNA extractions.

Sample	<i>E. coli</i> 16S	<i>pks</i>	<i>B. fragilis</i> 16S	<i>bft</i>	<i>F. nucleatum</i> 16S	<i>fadA</i>
Donors (N=11) ^a	91% (10) ^b	36% (4)	82% (9)	18% (2)	73% (8)	73% (8)
Patients pre-FMT (N=11)	100% (11)	27% (3)	55% (6)	18% (2)	91% (10)	91% (10)
Patients post-FMT (N=11)	100% (11)	36% (4)	82% (9)	27% (3)	64% (7)	64% (7)

^a Total number of donors or patients tested by total stool DNA qPCR

^b Percentage and (number) of donors or patients positive for each respective species-specific *16S* rRNA-encoding gene or virulence factor

Supplemental Table 3. Percentage of patients positive by stool culture.

Sample	<i>E. coli</i> 16S	<i>pks</i>	<i>B. fragilis</i> 16S	<i>bft</i>	<i>F. nucleatum</i> 16S	<i>fadA</i>
Donors (N=11) ^a	91% (10) ^b	64% (7)	100% (11)	73% (8)	91% (10)	82% (9)
Patients pre-FMT (N=11)	100% (11)	45% (5)	55% (6)	18% (2)	73% (8)	91% (10)
Patients post-FMT (N=11)	100% (11)	64% (7)	100% (11)	82% (9)	91% (10)	82% (9)

^a Total number of donors or patients tested by culture

^b Percentage and (number) of donors or patients positive for each respective species-specific *16S* rRNA-encoding gene or virulence factor (at least 1 of 5 colonies were positive if patient was called positive)

Supplemental Table 4. Percentage of all colonies positive by stool culture.

Plate	MacConkey agar		BBE agar		FSA agar	
	<i>E. coli</i> 16S	<i>pks</i>	<i>B. fragilis</i> 16S	<i>bft</i>	<i>F. nucleatum</i> 16S	<i>fadA</i>
Donor colonies (N=50)						
MacConkey, 55 BBE, 51 FSA) ^a	98% (49) ^b	44% (22)	76% (42)	27% (15)	57% (27)	43% (22)
Patient pre-FMT colonies (N=46)						
MacConkey, 45 BBE, 49 FSA)	100% (46)	37% (17)	36% (16)	11% (5)	55% (27)	45% (22)
Patient post-FMT colonies (N=114)						
MacConkey, 140 BBE, 138 FSA)	96% (109)	50% (57)	74% (104)	33% (46)	50% (69)	35% (48)

^a Total number of colonies tested from donors or patients for each respective agar (max of 5 colonies tested per donor/patient per time point, although in some cases fewer than 5 colonies grew; bottom row represents the sum of up to 3 post-FMT time points for the patients)

^b Percentage and (number) of colonies from donors or patients positive for each respective species-specific *16S* rRNA-encoding gene or virulence factor

Supplemental Table 5. Raw culture data from stool samples.

Patient/ Donor Number	Baseline (#positive / #screened)			2-10 wks (#positive / #screened)			10-20 wks (#positive / #screened)			> 6 months (#positive / #screened)		
	<i>Ec16S clbB</i>	<i>Bf16S bft</i>	<i>Fn16S fadA</i>	<i>Ec16S clbB</i>	<i>Bf16S bft</i>	<i>Fn16S fadA</i>	<i>Ec16S clbB</i>	<i>Bf16S bft</i>	<i>Fn16S fadA</i>	<i>Ec16S clbB</i>	<i>Bf16S bft</i>	<i>Fn16S fadA</i>
Donor #1	5/5 5/5	4/5 1/5	5/5 3/5									
Patient #1	5/5 4/5	1/5 0/5	4/5 2/5	5/5 5/5	5/5 3/5	2/5 1/5	1/1 1/1	0/0 0/0	1/5 0/5	5/5 5/5	4/5 3/5	5/5 0/5
Donor #2	5/5 1/5	5/5 2/5	1/1 1/1									
Patient #2	5/5 4/5	0/5 0/5	3/5 3/5	5/5 5/5	3/5 2/5	4/5 3/5	5/5 5/5	1/5 1/5	1/1 1/1			
Donor #3	5/5 0/5	5/5 3/5	4/5 2/5									
Patient #3	5/5 0/5	0/0 0/0	2/2 1/2	3/3 0/3	4/5 0/5	5/5 5/5	1/1 0/1	5/5 2/5	2/2 2/2	5/5 0/5	5/5 3/5	5/5 3/5
Donor #4	0/1 0/1	3/5 2/5	5/5 5/5									
Patient #4	5/5 1/5	0/5 0/5	4/5 1/5	5/5 2/5	5/5 0/5	2/5 2/5	5/5 0/5	5/5 0/5	3/5 3/5			
Donor #5	5/5 0/5	5/5 0/5	1/5 3/5									
Patient #5	1/1 0/1	0/0 0/0	1/5 1/1	0/0 0/0	5/5 0/5	1/5 1/5	6/6 3/6	5/5 0/5	0/5 1/5	2/2 1/2	5/5 0/5	1/5 1/5
Donor #6	5/5 0/5	3/5 2/5	0/5 1/5									
Patient #6	5/5 3/5	0/5 0/5	1/2 1/2	5/5 0/5	5/5 5/5	1/5 1/5	5/5 0/5	2/5 0/5	2/5 1/5	5/5 0/5	0/5 1/5	0/5 1/5
Donor #7	5/5 1/5	2/5 2/5	2/5 1/5									
Patient #7	3/3 0/3	0/5 0/5	4/5 3/5	0/0 0/0	2/5 1/5	3/5 2/5	4/4 0/4	1/5 1/5	3/5 3/5	4/4 0/4	2/5 2/5	2/5 2/5
Donor #8	5/5 5/5	3/5 0/5	2/5 0/5									
Patient #8	5/5 5/5	5/5 2/5	0/5 2/5	5/5 5/5	5/5 0/5	0/5 0/5	5/5 5/5	4/5 2/5	0/5 0/5	5/5 5/5	2/5 1/5	0/5 0/5
Donor #9	5/5 5/5	5/5 0/5	1/5 0/5									
Patient #9	3/3 0/3	4/5 0/5	0/5 0/5	4/4 3/4	5/5 4/5	2/5 0/5	5/5 4/5	4/5 1/5	1/5 0/5			
Donor #10	4/4 0/4	5/5 3/5	3/5 1/5									
Patient #10	4/4 0/4	3/5 3/5	3/5 3/5	4/4 0/4	3/5 3/5	4/5 0/5	0/0 0/0	4/5 2/5	5/5 4/5	0/5 0/5	5/5 4/5	5/5 5/5
Donor #11	5/5 5/5	2/5 0/5	5/5 5/5									
Patient #11	5/5 0/5	3/5 0/5	5/5 3/5	5/5 4/5	3/5 0/5	4/5 1/5	5/5 4/5	5/5 5/5	5/5 3/5			