

Table S1. SCI-induced microbiome compositional differences. ASV-level taxonomic changes from stool microbiomes at 2 weeks post-SCI or sham, with 1% FDR

Endpoint			
Sham vs SCI-Vehicle			
ASV	Sham	SCI-Veh	Adjusted <i>p</i> value (1% FDR)
<i>Bacteroides sp12288 (thetaitotaomicron)</i>	0.0448409	0.0186638	6.94559E-07
<i>Bacteroidales sp12656</i>	0.156247	0.0943178	1.16422E-30
<i>Staphylococcus lentus</i>	0.0334159	0.00351487	1.50293E-08
<i>Lactobacillus johnsonii</i>	0.0577711	0.0290364	5.24441E-08
<i>Clostridium celatum</i>	0.0875609	0	0
<i>Lachnospiraceae sp33565</i>	0.00720456	0.0506877	2.82898E-16
<i>Turicibacter sanguinis</i>	0.124592	0.0603193	8.76368E-33
Sham vs SCI-Inulin			
ASV	Sham	SCI-Inulin	Adjusted <i>p</i> value (1% FDR)
<i>Bacteroides sp12288 (thetaitotaomicron)</i>	0.0448409	0.0757577	5.81151E-08
<i>Bacteroidales sp12550</i>	0.138146	0.028615	0
<i>Bacteroidales sp12656</i>	0.156247	0.188446	1.62892E-08
<i>Staphylococcus lentus</i>	0.0334159	0.000353782	6.74178E-09
<i>Clostridium celatum</i>	0.0875609	0	0
<i>Lachnospiraceae sp33565</i>	0.00720456	0.040268	6.73239E-09
<i>Turicibacter sanguinis</i>	0.124592	0	0
SCI-Vehicle vs SCI-Inulin			
ASV	SCI-Veh	SCI-Inulin	Adjusted <i>p</i> value (1% FDR)
<i>Bacteroides sp12288 (thetaitotaomicron)</i>	0.0186638	0.0757577	1.15921E-15
<i>Bacteroidales sp12550</i>	0.135412	0.028615	0
<i>Bacteroidales sp12656</i>	0.0943178	0.188446	2.24226E-38
<i>Lactobacillus johnsonii</i>	0.0290364	0.061178	5.5047E-06
<i>Turicibacter sanguinis</i>	0.0603193	0	2.91586E-17
Pre-SCI vs Post-SCI			
ASV	SCI-Pre	SCI-2wks	Adjusted <i>p</i> value (1% FDR)
<i>Bacteroidales sp12656</i>	0.158599	0.0943178	2.06832E-30
<i>Lactobacillus johnsonii</i>	0.193283	0.0290364	0
<i>Clostridium celatum</i>	0.022866	0	2.92759E-05
<i>Lachnospiraceae sp33565</i>	0.0128364	0.0506877	6.26693E-12
<i>Turicibacter sanguinis</i>	0.00972012	0.0603193	7.71416E-20

Table S2. LEfSE identified taxonomic changes from stool microbiomes at 2 weeks post-SCI or sham

Bacterial taxa	Group	Effect size	p-value
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Lachnospiraceae.g NA.s sp33760	SCI.Inulin	3.28014007	0.030197383
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f NA.g NA.s sp31072	SCI.Inulin	2.98922362	0.048484305
k Bacteria.p Proteobacteria.c Gammaproteobacteria.o Pseudomonadales.f Moraxellaceae.g Acinetobacter.s radiorensis	SCI.Inulin	3.18049855	0.012764197
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Lachnospiraceae.g NA.s sp32706	SCI.Inulin	3.82883697	0.01334429
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Lachnospiraceae.g NA.s sp32638	SCI.Inulin	3.78461598	0.023383895
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Lachnospiraceae.g NA.s sp33456	SCI.Inulin	3.17262743	0.027158625
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Lachnospiraceae.g NA.s sp33694	SCI.Inulin	3.76036576	0.019757099
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Ruminococcaceae.g NA.s sp34867	SCI.Inulin	3.30028204	0.027323722
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Ruminococcaceae.g Anaerotruncus.s sp34475	SCI.Inulin	2.99522399	0.045806314
k Bacteria.p Proteobacteria.c Gammaproteobacteria.o Pseudomonadales	SCI.Inulin	3.25550068	0.016389554
k Bacteria.p Proteobacteria.c Gammaproteobacteria.o Pseudomonadales.f Moraxellaceae.g Acinetobacter	SCI.Inulin	3.22914314	0.016389554
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Lachnospiraceae.g NA.s sp33417	SCI.Inulin	3.75893236	0.011625603
k Bacteria.p Bacteroidetes.c Bacteroidia.o Bacteroidales.f Bacteroidaceae.g Bacteroides.s sp12288_thetaiotaomicron	SCI.Inulin	4.43785167	0.028207093
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Lachnospiraceae.g NA.s sp33525	SCI.Inulin	3.26973262	0.048484305
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Lachnospiraceae.g NA.s sp32701	SCI.Inulin	3.96461728	0.015562692
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Lachnospiraceae.g NA.s sp33616 sp33639	SCI.Inulin	3.42818688	0.029407217
k Bacteria.p Firmicutes.c Bacilli.o Lactobacillales.f Enterococcaceae.g Enterococcus.s faecalis	SCI.Inulin	3.05716304	0.024861262
k Bacteria.p Proteobacteria.c Gammaproteobacteria.o Pseudomonadales.f Moraxellaceae.g Acinetobacter.s calcoceticus radiorensis variabilis	SCI.Inulin	3.20043929	0.041388896
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Ruminococcaceae.g NA.s sp34731	SCI.Inulin	3.43239165	0.027158625
k Bacteria.p Firmicutes.c Bacilli.o Lactobacillales.f Enterococcaceae	SCI.Inulin	3.0725174	0.024861262
k Bacteria.p Bacteroidetes.c Bacteroidia.o Bacteroidales.f Bacteroidaceae	SCI.Inulin	4.41723887	0.028207093
k Bacteria.p Bacteroidetes.c Bacteroidia.o Bacteroidales.f Bacteroidaceae.g Bacteroides	SCI.Inulin	4.45069433	0.028207093
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Lachnospiraceae.g NA.s sp32758	SCI.Inulin	3.97272763	0.009403563
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Lachnospiraceae.g NA.s sp32623	SCI.Inulin	3.56178608	0.041041078
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f NA.g NA.s sp31116	SCI.Inulin	3.05573343	0.04376775
k Bacteria.p Proteobacteria.c Gammaproteobacteria.o Pseudomonadales.f Moraxellaceae	SCI.Inulin	3.23322001	0.016389554
k Bacteria.p Firmicutes.c Bacilli.o Lactobacillales.f Enterococcaceae.g Enterococcus	SCI.Inulin	3.06357795	0.024861262
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Lachnospiraceae.g NA.s sp33721	SCI.Inulin	3.08898072	0.009139753
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Ruminococcaceae.g NA.s sp35841	SCI	3.08050444	0.030197383
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Lachnospiraceae.g NA.s sp33658	SCI	3.42184273	0.023786517
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Lachnospiraceae.g NA.s sp32702	SCI	3.85317688	0.024861262
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Lachnospiraceae.g Lachnoclostridium.s sp32402	SCI	3.69380202	0.034609178
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Lachnospiraceae.g NA.s sp33739	SCI	3.15551336	0.046329809
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Lachnospiraceae	SCI	5.05697495	0.048668305
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Lachnospiraceae.g NA.s sp33565	SCI	4.28952463	0.027158625
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Lachnospiraceae.g NA.s sp32872	SCI	3.09241069	0.028207093
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Ruminococcaceae.g Oscillibacter.s sp34648	SCI	3.04716797	0.028937471
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Lachnospiraceae.g NA.s sp33718	SCI	3.35285573	0.023786517
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Lachnospiraceae.g NA.s sp32146	SCI	3.27855544	0.027158625
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Ruminococcaceae.g NA.s sp35077	Sham	3.08269556	0.027323722
k Bacteria.p Firmicutes.c Bacilli.o Bacillales.f Staphylococcaceae.g Staphylococcus.s lentus	Sham	4.22428258	0.015562692

Table S2 (continued)			
Bacterial taxa	Group	Effect size	p-value
k Bacteria.p Firmicutes.c Erysipelotrichia.o Erysipelotrichales	Sham	4.77308354	0.015562692
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Clostridiaceae	Sham	4.65015938	0.025161049
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Clostridiaceae.g Clostridium.s celatum	Sham	4.6301129	0.009139753
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Ruminococcaceae.g NA.s sp35361	Sham	3.59813998	0.019660049
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Ruminococcaceae.g NA.s sp35360	Sham	3.08921088	0.041041078
k Bacteria.p Proteobacteria.c Betaproteobacteria.o Burkholderiales.f Alcaligenaceae	Sham	3.43800153	0.011391522
k Bacteria.p Firmicutes.c Bacilli.o Bacillales.f Staphylococcaceae.g Staphylococcus	Sham	4.27885163	0.037902914
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Lachnospiraceae.g NA.s sp33419	Sham	3.32307121	0.015562692
k Bacteria.p Bacteroidetes.c Bacteroidia.o Bacteroidales.f NA.g NA.s sp12550	Sham	4.72904022	0.048484305
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Clostridiaceae.g Clostridium	Sham	4.65240631	0.025161049
k Bacteria.p Firmicutes.c Erysipelotrichia.o Erysipelotrichales.f Erysipelotrichaceae.g Turicibacter.s sanguinis	Sham	4.7786212	0.012764197
k Bacteria.p Firmicutes.c Bacilli.o Bacillales.f Staphylococcaceae.g Jeotgalicoccus	Sham	3.42659395	0.013728404
k Bacteria.p Firmicutes.c Bacilli.o Bacillales.f Staphylococcaceae	Sham	4.30010345	0.037902914
k Bacteria.p Firmicutes.c Erysipelotrichia	Sham	4.76829196	0.015562692
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Lachnospiraceae.g NA.s sp33537	Sham	3.08288654	0.041388896
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f NA.g NA.s sp31125	Sham	3.07776853	0.041388896
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f NA.g NA.s sp31122	Sham	3.42566575	0.034411331
k Bacteria.p Firmicutes.c Erysipelotrichia.o Erysipelotrichales.f Erysipelotrichaceae.g Turicibacter	Sham	4.801587	0.012764197
k Bacteria.p Firmicutes.c Erysipelotrichia.o Erysipelotrichales.f Erysipelotrichaceae	Sham	4.77876752	0.015562692
k Bacteria.p Firmicutes.c Clostridia.o Clostridiales.f Ruminococcaceae.g NA.s sp35498	Sham	3.08729405	0.041388896
k Bacteria.p Proteobacteria.c Betaproteobacteria.o Burkholderiales	Sham	3.41658553	0.011391522
k Bacteria.p Proteobacteria.c Betaproteobacteria	Sham	3.40401102	0.011391522
k Bacteria.p Firmicutes.c Bacilli.o Bacillales	Sham	4.30946747	0.037902914
k Bacteria.p Proteobacteria.c Betaproteobacteria.o Burkholderiales.f Alcaligenaceae.g Parasutterella	Sham	3.41352673	0.011391522
k Bacteria.p Firmicutes.c Bacilli.o Bacillales.f Staphylococcaceae.g Jeotgalicoccus.s halophilus_halotolerans_nan haiensis	Sham	3.4063761	0.013728404
k Bacteria.p Proteobacteria.c Betaproteobacteria.o Burkholderiales.f Alcaligenaceae.g Parasutterella.s excremen tihominis	Sham	3.42627509	0.011391522

Table S3. Bacterial taxa significantly different following SCI in an independent cohort. With 1% FDR correction, alterations between Sham and SCI (a), sham and SCI-inulin (b), or SCI and SCI-inulin (c). Grey boxes indicate significant comparisons (1% FDR) between pre and post-SCI groups at 2wks post injury.

ASV	Sham	SCI-Veh	SCI-Inulin	Sig comparisons by 1% FDR	Identified in independent cohort (Fig 2)
<i>Akkermansia muciniphila</i>	0.032851	0.04787	0.016194	c	
<i>Alistipes sp14336</i>	0.029102	0.067027	0.06584	a, b	
<i>Allobaculum sp36555</i>	0.000152	0.021406	0.006325	a	
<i>Bacteroidales sp12473-sp12526-sp12633</i>	0.074217	0.084304	0.042379	b, c	
<i>Bacteroidales sp12610</i>	0	0.030116	0.013937	a	
<i>Bacteroidales sp12645</i>	0	0.019732	0.058406	b, c	
<i>Bacteroidales sp12656</i>	0.105666	0.052678	0.156417	a, b, c	Yes
<i>Bacteroidales sp12768</i>	0.033087	0.05611	0.04598	a	
<i>Bacteroides sp12288 (thetaitaomicron)</i>	0.080995	0.071137	0.050251	b, c	Yes
<i>Bifidobacterium choerinum-pseudolongum</i>	0.049002	0.002335	0.007556	a, b	
<i>Lachnospiraceae sp32402</i>	0.021026	0.040619	0.01123	c	
<i>Lachnospiraceae sp32778</i>	0.009123	0.043795	0.014431	a, c	
<i>Lactobacillus johnsonii</i>	0.237838	0.079619	0.078155	a, b	Yes
<i>Staphylococcus lentus</i>	0.027879	0.005809	0.019373	a	Yes

Table S4. Independent SCI-induced microbiome compositional differences. ASV-level taxonomic changes from stool microbiomes at 2 weeks post-SCI or sham, with 1% FDR, from independent cohort

Endpoint			
Sham vs SCI-Vehicle			
ASV	Sham	SCI-Veh	Adjusted p value (1% FDR)
<i>Bifidobacterium choerinum-pseudolongum</i>	0.0490019	0.00233502	1.38505E-15
<i>Bacteroidales sp12610</i>	0	0.0301156	2.27912E-07
<i>Bacteroidales sp12656</i>	0.105666	0.0526781	1.42237E-19
<i>Bacteroidales sp12768</i>	0.0330871	0.05611	7.46328E-05
<i>Alistipes sp14336</i>	0.0291018	0.0670273	7.71846E-11
<i>Staphylococcus lentus</i>	0.0278791	0.00580894	0.000146098
<i>Lactobacillus johnsonii</i>	0.237838	0.0796191	0
<i>Lachnospiraceae sp32778</i>	0.00912332	0.0437946	2.64513E-09
<i>Allobaculum p36555</i>	0.00015199	0.0214064	0.000254523
Sham vs SCI-Inulin			
ASV	Sham	SCI-Inulin	Adjusted p value (1% FDR)
<i>Bifidobacterium choerinum-pseudolongum</i>	0.0490019	0.00755608	4.74124E-08
<i>Bacteroides sp12288 (thetaitotaomicron)</i>	0.0809949	0.0502512	4.99359E-05
<i>Bacteroidales sp12473-sp12526-sp12633</i>	0.0742173	0.0423789	2.67067E-05
<i>Bacteroidales sp12645</i>	0	0.0584062	1.67097E-14
<i>Bacteroidales sp12656</i>	0.105666	0.156417	2.43458E-11
<i>Alistipes sp14336</i>	0.0291018	0.0658396	1.27625E-06
<i>Lactobacillus johnsonii</i>	0.237838	0.0781547	0
SCI-Vehicle vs SCI-Inulin			
ASV	SCI-Veh	SCI-Inulin	Adjusted p value (1% FDR)
<i>Bacteroides sp12288 (thetaitotaomicron)</i>	0.0711372	0.0502512	0.00013929
<i>Bacteroidales sp12473-sp12526-sp12633</i>	0.0843043	0.0423789	2.45024E-14
<i>Bacteroidales sp12645</i>	0.0197316	0.0584062	1.95902E-12
<i>Bacteroidales sp12656</i>	0.0526781	0.156417	0
<i>Lachnoclostridium sp32402</i>	0.040619	0.0112297	8.5429E-08
<i>Lachnospiraceae sp32778</i>	0.0437946	0.0144314	8.76893E-08
<i>Akkermansia muciniphila</i>	0.0478695	0.0161938	7.92208E-09
Pre SCI vs Post SCI			
ASV	SCI-Pre	SCI-2wks	Adjusted p value (1% FDR)
<i>Other</i>	0.0400304	0.00230997	3.01332E-20
<i>Bifidobacterium choerinum-pseudolongum</i>	0.0387627	0.00233502	5.35722E-19
<i>Bacteroidales sp12473-sp12526-sp12633</i>	0.0566063	0.0843043	1.20298E-11
<i>Bacteroidales sp12768</i>	0.0328508	0.05611	1.223E-08
<i>Enterococcus faecalis</i>	0.00133197	0.0180171	4.33168E-05
<i>Lactobacillus johnsonii</i>	0.130668	0.0796191	1.57727E-35
<i>Lachnoclostridium sp32402</i>	0.00983318	0.040619	4.98182E-14
<i>Lachnospiraceae sp32778</i>	0.00608032	0.0437946	3.05544E-20
<i>Ruminococcaceae sp35297</i>	0.0262177	0.0028927	1.11286E-08
<i>Allobaculum sp36555</i>	0.0653365	0.0214064	7.94526E-27

Table S5. LEfSE identified taxonomic changes from stool microbiomes at 2 weeks post-SCI or sham, from independent cohort

Bacterial taxa	Group	Effect size	p-value
k_Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__NA.s__sp33761	SCI	3.20746086	0.03938728
k_Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Ruminococcaceae.g__Anaerotruncus.s__sp34475	SCI	3.14434302	0.01455464
k_Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__NA.g__NA.s__sp12473_sp12526_sp12633	SCI	4.29010458	0.03319739
k_Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__NA.s__sp32862	SCI	3.49736231	0.03339209
k_Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__NA.s__sp32735	SCI	3.60307215	0.02671248
k_Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__NA.s__sp32721	SCI	3.47470577	0.02675007
k_Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Ruminococcaceae.g__NA.s__sp33140	SCI	2.96559706	0.02508897
k_Bacteria.p__Actinobacteria.c__Actinobacteria.o__Corynebacteriales.f__Corynebacteriaceae	SCI.Inulin	3.5183703	0.01922687
k_Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__NA.s__sp33731	SCI.Inulin	3.21037177	0.01440632
k_Bacteria.p__Actinobacteria.c__Actinobacteria.o__Corynebacteriales.f__Corynebacteriaceae.g__Corynebacterium	SCI.Inulin	3.51837339	0.01922687
k_Bacteria.p__Actinobacteria.c__Actinobacteria.o__Corynebacteriales	SCI.Inulin	3.51837267	0.01922687
k_Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__NA.s__sp32635_sp32668	SCI.Inulin	3.09090389	0.01922687
k_Bacteria.p__Actinobacteria.c__Actinobacteria.o__Corynebacteriales.f__Corynebacteriaceae.g__Corynebacterium.s__amycolatum	SCI.Inulin	3.51837192	0.01922687
k_Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__NA.s__sp33432	SCI.Inulin	3.16044082	0.01835448
k_Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__Acetatifactor	SCI.Inulin	3.0869611	0.0469165
k_Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__NA.s__sp33421_sp33679	SCI.Inulin	3.69414989	0.00122429
k_Bacteria.p__Firmicutes.c__Bacilli.o__Bacillales.f__Planococcaceae.g__Sporosarcina.s__luteola_pasteurii	Sham	3.15351433	0.04203087
k_Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Lactobacillus	Sham	4.94539917	0.04846866
k_Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae	Sham	4.93387968	0.04846866

Table S5 (continued)			
Bacterial taxa	Group	Effect size	p-value
k_Bacteria.p__Firmicutes.c__Bacilli.o__Bacillales.f__Staphylococcaceae.g__Staphylococcus.s__lentus	Sham	4.0524116 4	0.0234515 3
k_Bacteria.p__Firmicutes.c__Bacilli.o__Bacillales.f__Planococcaceae	Sham	3.1353627 7	0.0420308 7
k_Bacteria.p__Firmicutes.c__Erysipelotrichia.o__Erysipelotrichales.f__Erysipelotrichaceae.g__NA	Sham	3.0456857 4	0.0094330 1
k_Bacteria.p__Firmicutes.c__Erysipelotrichia.o__Erysipelotrichales.f__Erysipelotrichaceae.g__NA.s__sp36786	Sham	3.2849544 8	0.0010709 4
k_Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__NA.s__sp33694	Sham	3.5179440 8	0.0196145 7
k_Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__NA.s__sp33673	Sham	3.2005299 1	0.0242550 8
k_Bacteria.p__Firmicutes.c__Bacilli.o__Bacillales.f__Staphylococcaceae.g__Staphylococcus	Sham	4.2321641 6	0.0446212 7
k_Bacteria.p__Actinobacteria	Sham	4.407117	0.0277423 5
k_Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__NA.s__sp33636	Sham	3.4996426 9	0.0083140 5
k_Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__Marvinbryantia.s__sp32979	Sham	3.5174996 7	0.0032249 9
k_Bacteria.p__Firmicutes.c__Bacilli.o__Bacillales.f__Staphylococcaceae	Sham	4.2207112 5	0.0446212 7
k_Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__Blautia.s__sp32038	Sham	3.5580099	0.0259710 1
k_Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__NA.s__sp33374	Sham	3.3533870 6	0.0270878 6
k_Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__NA.g__NA.s__sp31125	Sham	3.0240336	0.0050210 4
k_Bacteria.p__Firmicutes.c__Bacilli.o__Bacillales.f__Planococcaceae.g__Sporosarcina	Sham	3.1429381 3	0.0420308 7
k_Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__NA.s__sp32622	Sham	3.8416875 7	0.0378540 1
k_Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__NA.s__sp32156	Sham	3.1342279 7	0.0394250 4
k_Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Lachnospiraceae.g__Marvinbryantia	Sham	3.6367098 1	0.0093402

Supplemental Data Table 6. Reagents & Resources.

Antibodies used				
Primary antibodies for Western Blot				
Antibody	Concentration	Host	Supplier	Cat Number
Neuronal nitric oxide synthase (nNOS)	1:1000	Rabbit	Cell Signaling	4231S
Choline acetyltransferase (ChAT)	1:1000	Goat	Sigma	AB144P
Protein gene product 9.5 (PGP9.5)	1:1000	Rabbit	Millipore	AB1761-I
Free fatty acid receptor 2 (FFAR2 / GPR43)	1:1000	Rabbit	Thermo	PA5-111780
Glyceraldehyde 3-phosphate dehydrogenase (GAPDH)	1:1000	Rabbit	Cell Signaling	5174S
β-Actin	1:1000	Rabbit	Cell Signaling	8457S
Secondary antibodies for Western Blot				
Antibody	Concentration	Host	Supplier	Cat Number
Anti-rabbit (HRP-linked)	1:1000	Goat	Cell Signaling	7074S
Anti-goat (HRP-linked)	1:1000	Donkey	Thermo	A16005
Primary antibodies for Immunohistochemistry				
Antibody	Concentration	Host	Supplier	Cat Number
Neuronal nitric oxide synthase (nNOS)	1:100	Rabbit	Cell Signaling	4231S
Anti-HuD + HuC antibody	1:500	Rabbit	Abcam	AB184267
Protein gene product 9.5 (PGP9.5)	1:200	Mouse	Abcam	AB72911
Secondary antibodies for Immunohistochemistry				
Antibody	Concentration	Host	Supplier	Cat Number
Anti-mouse (Alexa Fluor™ 594)	1:200	Goat	Thermo	A-11005
Anti-rabbit (Alexa Fluor™ 488)	1:200	Goat	Thermo	A-11008

ATCC Strains and Growth Conditions				
Bacterium	Medium	Environment	CFU per gavage	ATCC Number
<i>Lactobacillus johnsonii</i>	de Man-Rogosa-Sharpe	Aerobic	10 ¹⁶	33200
<i>Bacteroides thetaiotaomicron</i>	Brain-Heart Infusion	Anaerobic	10 ¹⁴	29148
<i>Clostridium celatum</i>	Chopped Meat Carbohydrate	Anaerobic	10 ¹⁰	27791