

<b>Supplemental Digital Content 1.</b> Characteristics and outcomes of included studies sorted by mammal type and publication year.									
Study (first author, publication year)	Control group? (Y/N)	Model: (mammal, age/life stage, health status, sample size)	Primary study aim	Intervention and group design	Dietary controls	Methods	Gut microbiome composition measures	Significant taxonomy findings	Declared Funding Sources §
<b>Murine (Mouse)</b>									
Evans, 2014	Y	Adult male C57BL/6 mice, healthy, n=48	To determine effect of voluntary exercise vs. no access to exercise on the intestinal microbiome.	1. Control + HFD 2. Wheel access (WA) + HFD 3. Control + Low-fat diet (LFD) 4. WA + LFD	Yes, LFD and HFD groups. LFD: 10% fat HFD: 60% fat (62% saturated; 35.9% mono-; 32% poly-unsaturated).	Terminal restriction fragment length polymorphism (TRFLP), 16S rRNA sequencing of fecal contents.	β-diversity, abundance, bacterial family and phyla, bacteroidetes:firmicutes	<b>1. Control + HFD:</b> <u>Bacteroidetes</u> ↓ S24-7 (f) <u>Firmicutes</u> ↑ Clostridiaceae (f) ↑ Lachnospiraceae (f) ↑ Ruminococcaceae (f) ↓ Turicibacteraceae (f) ↓ Erysipelotrichaceae (f) <u>Actinobacteria</u> ↓ Bifidobacteriaceae (f)  <b>2. WA + HFD:</b> <u>Bacteroidetes</u> ↑ S24-7 (f) <u>Firmicutes</u> ↑ Clostridiaceae (f) ↑ Lachnospiraceae (f) ↑ Ruminococcaceae (f) ↑ Lactobacillaceae (f) ↓ Turicibacteraceae (f) ↓ Erysipelotrichaceae (f)  <b>4. WA + LFD:</b> <u>Bacteroidetes</u> ↑ S24-7 (f) <u>Firmicutes</u> ↑ Lactobacillaceae (f) ↑ Lachnospiraceae (f) ↑ Ruminococcaceae (f) ↓ Turicibacteraceae (f)	G,O

								↓ <u>Erysipelotrichaceae</u> (f) <u>Actinobacteria</u> ↓ <u>Bifidobacteriaceae</u> (f)	
Kang, 2014	Y	Adult male C57BL/6 J mice, healthy, n=40	To determine interaction between habitual dietary conditions and exercise level on intestinal microbiome and behavior	1. Control + High-fat diet (HFD) 2. F. Ex + HFD 3. Control + normal diet (ND) 4. Forced exercise (F.Ex.) + ND	Yes, HFD and ND groups. ND: 10% fat HFD: 60% fat	PCR, 16S rRNA sequencing of fecal contents.	Operational taxonomic units (OTUs), relative abundance, bacteroidetes:firmicutes and bacterial phyla, genus, and family	<b>1. Control + HFD:</b> <u>Firmicutes</u> ↑ <u>Streptococcus</u> (g) ↓ <u>Tenericutes</u>  <b>2. F.Ex + HFD:</b> ↓ <u>Bacteroidetes</u> ↑ <u>Firmicutes</u> ↓ <u>Streptococcus</u> (g) ↓ <u>Tenericutes</u>  <b>4. F.Ex + ND:</b> ↓ <u>Bacteroidetes</u> ↑ <u>Firmicutes</u> ↓ <u>Tenericutes</u>	G,O
Allen, 2015†	Y	Adult male C57BL/6J, healthy, n=29	To compare effects of voluntary exercise via wheel access (WA.) vs. F.Ex. on the intestinal microbiome.	1. F.Ex. 2. WA 3. Control	No, all were fed a standard chow diet.	PCR, 16S rRNA gene sequencing of fecal and cecal contents.	OTUs, α-diversity, richness & evenness, relative abundance, bacteroidetes:firmicutes bacterial genera and phyla	<b>1. F.Ex:</b> <u>Firmicutes</u> ↑ <u>Dorea</u> (g) ↑ <u>Coprococcus</u> (g) ↑ <u>Oscillospira</u> (g) ↑ <u>Ruminococcus</u> (g) ↑ <u>Butyrivibrio</u> (g) ↑ <u>Tenericutes</u> <u>Proteobacteria</u> ↑ <u>Nautilia</u> (g)  <b>2. WA</b> <u>Bacteroidetes</u> ↓ <u>Prevotella</u> (g) <u>Firmicutes</u> ↓ <u>Turicibacter</u> (g) ↑ <u>Anaerotruncus</u> (g)	O
Lambert, 2015 ‡	Y	Adult male C57BL mice, healthy (db/+), and Type 2	To compare the effect of F.Ex. on the intestinal	1. Control + <i>Db/db</i>	No, all were fed a standard chow diet.	PCR, 16S rRNA gene sequencing	Total bacteria, bacterial phyla and species, bacteroidetes:firmicutes relative abundance	<b>1. Control + Db/db:</b> <u>Firmicutes</u> ↓ <u>Clostridium</u> cluster I (g) ↑ <u>Clostridium</u> cluster XI (g)	G,O

		Diabetic [T2D ( <i>db/db</i> )], n= ~36	microbiome in T2D mice when compared to their healthy and sedentary counterparts.	2. F.Ex + <i>db/db</i>  3. Control+ <i>db/+</i>  4. F.Ex + <i>db/+</i>		of cecal contents.		<p><b>2. F.Ex + Db/db:</b>  <u>Bacteroidetes</u>  ↓ Bacteroides (g)  ↓ Prevotella (g)  <u>Actinobacteria</u>  ↓ Bifidobacterium (s)  <u>Proteobacteria</u>  ↓ Enterobacteriaceae (f)  <u>Euryarchaeota</u>  ↓ Methanobrevibacter (g)</p> <p><b>4. F.Ex + Db/+:</b>  <u>Bacteroidetes</u>  ↓ Bacteroides (g)  ↓ Prevotella (g)  <u>Firmicutes</u>  ↑ Clostridium cluster I (g)  <u>Actinobacteria</u>  ↑ Bifidobacterium (s)  <u>Euryarchaeota</u>  ↓ Methanobrevibacter (g)</p>	
Campbell, 2016	Y	Adult male C57BL/6NTac, healthy, n=36	To compare the effects of voluntary exercise vs. sedentary time on intestinal integrity and intestinal microbiome in lean and obese mice.	1. Control + HFD-induced obesity  2. WA + HFD-induced obesity  3. Control + lean  4. WA + lean	Yes, HFD: 45% fat, and ND: 10%	Terminal restriction fragment length polymorphism (TRFLP) and pyro-sequencing of 16S rRNA fecal contents.	OTUs, bacterial genus, phyla, family, species	<p><b>1. Control + HFD-induced obesity:</b>  <u>Firmicutes</u>  ↑ Clostridiales (o)</p> <p><b>2. WA + HFD-induced obesity:</b>  <u>Firmicutes</u>  ↑ Clostridiales (o)  ↑ Faecalibacterium prausnitzii (s)  ↑ Peptococcus (s)  ↑ Allobaculum (s)</p> <p><b>4. WA + lean:</b>  ↑ <u>Firmicutes</u>  ↑ Clostridiales (o)  ↑ Faecalibacterium prausnitzii (s)</p>	G

								↑ Lachnospiraceae (f) ↑ Allobaculum (s) ↑ Clostridium (g)	
Denou, 2016	Y	Adult male C57BL/6 mice, healthy, n=32	To determine the effect of high-intensity interval training (HIIT) on the intestinal microbiome after HFD-induced obesity.	1. Control + ND 2. Control + HFD 3. HIIT + HFD-induced obesity 4. Control + HFD-induced obesity	Yes, HFD: 45% fat and standard chow diet.	PCR, 16S rRNA sequencing of fecal contents.	OTUs, α-diversity, bacterial genus, phyla, relative abundance, bacteroidetes:firmicutes	<b>2. Control + HFD:</b> ↓ <u>Bacteroidetes</u> ↑ <u>Firmicutes</u> <b>3. HIIT HFD-induced obesity:</b> ↑ <u>Bacteroidetes</u> ↓ <u>Bacteroidales (o)</u> ↑ <u>Firmicutes</u>	G,O
Houghton, 2017	Y	PolgA <sup>mut/mut</sup> and wild-type PolgA <sup>+/+</sup> , mitochondrial dysfunction, n=19	To determine how changes in mitochondrial function of aging colonic epithelium influences gut microbiome composition, and whether or not exercise can modulate observed changes in composition in an	1. Control 2. Age + F.Ex. 3. Control + age	No, all were fed a standard chow diet.	PCR, 16S rRNA of fecal contents.	OTUs, α-diversity, bacterial genus, relative abundance, bacteroidetes:firmicutes	<b>2. F.Ex + Age:</b> ↑ <u>Bacteroidetes</u> <u>Proteobacteria</u> ↑ <u>Desulfovibrio (g)</u> ↓ <u>Firmicutes</u> <u>Deferribacteraceae</u> ↑ <u>Mucispirillum (g)</u>	G, O

			accelerated aging model.						
Lamoureux, 2017	Y	Adult C57BL/6 mice, healthy, n=42	To measure effect of exercise on intestinal microbiome in voluntary and forced moderate intensity exercise.	1. Control 2. WA 3. F.Ex.	No, all were fed a standard chow diet.	PCR, 16S rRNA sequencing of fecal samples.	OTUs, $\alpha$ -diversity, $\beta$ -diversity, species richness, relative abundance, bacterial phyla.	No significant taxonomy findings between any groups.	G
Liu, 2017	Y	Adult C57BL/6 mice, healthy n=* *Sample size per group not reported.	To investigate effects of exercise on intestinal microbiome after myocardial infarction (MI).	1. Sed. 2. Sed. + Sham surgery (S.sx) 3. Sed. + MI 4. F.Ex, 5. F.Ex + S.sx 6. F.Ex + MI	No, all were fed a standard chow diet.	16S rRNA sequencing of fecal samples.	OTUs, $\alpha$ -diversity, $\beta$ -diversity, bacterial phyla.  <b>4. F.Ex.</b> <u>Bacteroidetes</u> ↑ Butyricimonas (g) ↑ Prevotella (g) <u>Verrucomicrobia</u> ↑ Akkermansia (g)  <b>5. F.Ex + S.Sx</b> <u>Bacteroidetes</u> ↑ Sphingobacteriales (o) <u>Firmicutes</u> ↑ Erysipelotrichaceae (f) <u>Verrucomicrobia</u> ↑ Akkermansia (g)  <b>6. F.Ex + MI</b> <u>Proteobacteria</u> ↑ Phenyllobacterium (g) ↑ Roseateles (g)		O
<b>Murine (Rat)</b>									
Matsumoto, 2008 ‡	Y	Adult male Wistar rats, healthy, n=14	To determine the effect of WA on the intestinal microbiome.	1.Control 2.WA	Yes, all were fed a 25% casein-sucrose diet.	PCR, 16S rRNA sequencing of cecal contents.	Bacterial species, and n-butyrate producing bacteria.	<b>2. WA:</b> <u>Firmicutes</u> ↑ Ruminococcus hydrogenotrophicus (s) ↑ Clostridium (g) ↑ SM7/11 (s) ↑ Lactobacillus gasseri (s) ↑ T2-87 (f)	Not declared

								<u>Proteobacteria</u> ↑ <i>Escherichia coli</i> (s)	
Queipo-Ortuño, 2013	Y	Adult male Dawley rats, healthy, n=40	To determine the effects of physical activity and nutrition status on the intestinal microbiome.	1. Activity-based anorexia (ABA) 2. Control + ABA 3. WA + ad libitum (ad lib) feeding 4. Control + ad lib feeding.	Yes, ABA groups had food access restricted to 1 hour/day.	PCR, 16S sequencing of fecal contents.	Diversity, abundance, phyla and genera-level bacteria, bacteroidetes:firmicutes	<b>1. ABA:</b> ↓ <u>Bacteroidetes</u> ↑ <i>Bacteroides</i> (g) ↑ <i>Prevotella</i> (g) ↓ <u>Firmicutes</u> ↑ <i>Clostridium</i> (g) ↑ <i>Enterococcus</i> (g) ↓ <i>B. Coccoides-E. rectale</i> (s) ↓ <i>Lactobacillus</i> (g) ↓ <u>Actinobacteria</u> ↓ <i>Bifidobacterium</i> (g) ↑ <u>Proteobacteria</u> ↑ <i>Heliobacter</i> (g) <u>Euryarchaeota</u> ↑ <i>M. smithii</i> (s)  <b>2. Control + ABA:</b> <u>Firmicutes</u> ↑ <i>Enterococcus</i> (g) ↓ <i>B. Coccoides-E. rectale</i> (s) ↓ <i>Lactobacillus</i> (g) <u>Actinobacteria</u> ↓ <i>Bifidobacterium</i> (g) <u>Euryarchaeota</u> ↑ <i>M. smithii</i> (s)  <b>3. WA. + ad lib:</b> <u>Bacteroidetes</u> ↑ <i>Bacteroides</i> (g) ↓ <i>Prevotella</i> (g) ↓ <u>Firmicutes</u> ↓ <i>Clostridium</i> (g) ↓ <i>Enterococcus</i> (g) ↑ <i>B. Coccoides-E. rectale</i> (s) ↑ <i>Lactobacillus</i> (g) ↑ <u>Actinobacteria</u> ↑ <i>Bifidobacterium</i> (g)	G,O

									<b>4. Control + ad lib:</b> <u>Bacteroidetes</u> ↑ Bacteroides (g) ↑ Prevotella (g) <u>Firmicutes</u> ↑ Clostridium (g) <u>Actinobacteria</u> ↓ Bifidobacteria (g) <u>Proteobacteria</u> ↑ Heliobacter (g)
Petriz, 2014	Y	Zucker and Wistar Rats, obese, non-obese, or hyper-tensive, n=9, sex not specified.	To determine the effect of F. Ex. on the intestinal microbiome in the presence of known disease genotypes.	1. F.Ex + Non-obese 2. F.Ex + Obese 3. F. Ex + Hyper-tensive	None, and diet composition not reported.	Pyro-sequencing, PCR, 16S rRNA of fecal contents.	OTUs, $\alpha$ -diversity, bacterial species richness, bacterial phyla, relative abundance	<b>1. F.Ex + Non-obese:</b> <u>Firmicutes</u> ↓ Streptococcus (g)  <b>2. F.Ex + Obese:</b> <u>Firmicutes</u> ↑ Streptococcus alactolyticus (s) ↑ Lactobacillus (g) ↑ Ruminococcus gnavus (s) ↓ Ruminococcus flavefaciens (s) <u>Actinobacteria</u> ↑ Bifidobacterium animalis (s) ↑ Bifidobacterium pseudolongum (s) <u>Proteobacteria</u> ↑ Pseudomonas (g) ↑ Aggregatibacter pneumotropica (s)  <b>3. F. Ex + Hypertensive:</b> <u>Firmicutes</u> ↓ Allobaculum (g) <u>Proteobacteria</u> ↓ Aggregatibacter (g) ↓ Sutterella (g)	G,O

Liu, 2015 ‡	Y	Female high cardio-respiratory capacity (HCR) and low cardio-respiratory (LCR) rats, healthy, n=30	To determine how voluntary exercise alters the intestinal microbiome in ovariectomized rats with intrinsically HCR and LCR fed a HFD.	1. + WA LCR 2. Control + LCR 3. WA + HCR 4. Control + HCR	Yes, 45% HFD after OVX.	PCR, 16S rRNA of cecal contents.	OTUs, $\alpha$ -diversity, $\beta$ -diversity, bacterial phyla, species richness, bacteroidetes:firmicutes	<b>1. WA + LCR:</b> ↓ <u>Firmicutes</u> ↓ Ruminococcus (f) ↓ Christensenellaceae (f) ↑ <u>Proteobacteria</u> ↑ Heliobacteraceae (f) ↑ Desulfovibrionaceae (f) ↑ <u>Cyanobacteria</u> <b>3. WA + HCR:</b> ↑ <u>Firmicutes</u> ↑ Ruminococcus (f) ↑ Christensenellaceae (f) ↑ Clostridium (g) ↓ <u>Proteobacteria</u> ↓ Heliobacteraceae (f) ↓ Desulfovibrionaceae (f) ↓ <u>Cyanobacteria</u>  <b>HCR Control Vs LCR Control:</b>  <u>Bacteroidetes</u> ↑ Porphyromonadaceae (f) <u>Firmicutes</u> ↑ Lachnospiraceae (f) ↑ Peptococcaceae (f) <u>Proteobacteria</u> ↑ Heliobacter (g)	G
Mika, 2015	Y	Male juvenile and adult F344 rats, healthy, n=40	To determine whether juvenile rats would promote a leaner intestinal microbiome phenotype with from 6-weeks of	1. WA + Juvenile 2. Control + Juvenile 3. WA + Adult 4. Control + Adult	No, standard chow diet. Full composition not provided.	PCR, 16S rRNA of fecal samples.	OTUs, $\alpha$ -diversity, $\beta$ -diversity, evenness, richness, relative abundance, bacterial phyla and genus, bacteroidetes:firmicutes	<b>1. WA + Juvenile:</b> ↑ <u>Bacteroidetes</u> ↓ Rikenellaceae g_AF12 (g) ↓ Rikenellaceae g_ (g) ↓ <u>Firmicutes</u> ↑ Blautia (s) ↑ Anaerostipes (s) ↓ <u>Proteobacteria</u> ↑ Desulfovibrio (s)	G



			voluntary wheel running compared to adult counterparts.					↑ <u>Euryarchaeota</u> ↑ <u>Methanosphaera</u> (s)  <b>3. WA + Adult:</b> <u>Bacteroidetes</u> ↑ <u>Rikenellaceae</u> g_AF12 (g) ↑ <u>Rikenellaceae</u> g_ (g)  <u>Firmicutes</u> ↑ <u>Turicibacter</u> (s)	
Welly, 2016 ‡	Y	Juvenile male obesity-prone CD rats (OP-CD), healthy, n=30	To determine how the intestinal microbiome is altered in the presence of energy deficits created from exercise versus diet in an obesity-prone phenotype.	1. WA + HFD  2. Control + HFD  3. Control + HFD weight matched (WM)	Yes, 45% HFD for all groups.	PCR, 16S rRNA of cecal contents	OTUs, bacterial phyla, family, genera, and relative abundance, bacteroidetes:firmicutes .	<b>1. WA + HFD:‡</b> <u>Bacteroidetes</u> ↓ <u>Rikenellaceae</u> (f) ↓ <u>S24-7</u> (f) <u>Firmicutes</u> ↑ <u>Streptoocaceae</u> (f)  <b>3. Control + HFD WM:</b> <u>Firmicutes</u> ↓ <u>Streptococcus</u> (g)	G,O
Batacan, 2017	Y	Adult male Wistar Rats, healthy, n=57	To compare the effects of diet (HFD vs ND) and two exercise intensities on the intestinal microbiome over a 12-week period.	1. Control + ND  2. Control + HFD  3. Control + ND  4. Control + HFD  5. Light-intensity	Yes, ND and 25% HFD were used in all activity groups.	PCR, 16S rRNA of fecal contents	OTUs, $\alpha$ -diversity, $\beta$ -diversity, richness, evenness, bacterial species, family, and class.	<b>5. LIT + ND:</b> <u>Firmicutes</u> ↑ <u>Lactobacillus johnsonii</u> (s) ↑ <u>Clostridium</u> <u>geopufricans</u> (s) ↑ <u>Actinobacteria</u> ↑ <u>Bifidobacteriaceae</u> (f) ↑ <u>Coriobacteriaceae</u> (f) ↑ <u>Proteobacteria</u> ↑ <u>Parasutterella</u> <u>excrementihominis</u> (s) ↑ <u>Tenericutes</u> ↑ <u>Erysipelotrichaceae</u> (f)	O

				training (LIT) + ND				<b>6. LIT + HFD:</b> <u>Firmicutes</u> ↑ Clostridium (c)
				6. LIT + HFD				<b>7. HIIT + ND:</b> <u>Firmicutes</u> ↑ Clostridium saccharolyticum (s)
				7. HIIT + ND				↑ Clostridium geopufricans (s)
				8. HIIT + HFD				<u>Proteobacteria</u> ↑ Parasutterella excrementihominis (s)
								<b>8. HIIT + HFD:</b> <u>Firmicutes</u> ↑ Clostridium (c)
Feng, 2017	Y	Adult male HCR and LCR rats. Exact sample size not specified.	To determine whether exercise can prevent post- operative cognitive decline, neuroinfla- mmation and associated shifts in intestinal microbiome.	1. LCR Control + S.sx  2. HCR Control + S.sx  3. LCR Control + Sx  4. HCR Control + Sx  5. LCR + F.Ex + S.sx  6. HCR + F.Ex + S.sx  7. LCR +	No, standard chow diet. Full compo- sition not provided.	PCR, 16SRNA gene and DNA sequencing of fecal contents.	OTUs, $\alpha$ -diversity, $\beta$ -diversity, bacteroidetes:firmicutes	<b>HCR + Ex:*</b> ↓ <u>Bacteroidetes</u> ↑ <u>Firmicutes</u>  *Surgical condition not specified

F.Ex + Sx									
8. HCR + F.Ex + Sx									
<b>Canine</b>									
Kieler, 2017	N	Adult large- and medium-breed dogs who were sedentary and overweight, healthy, n=18	To determine if exercise influences shifts on intestinal microbiome during weight loss protocol.	1. F.Ex + Diet 2. Control + Diet	Yes, all animals were fed same dry diet food.	PCR, 16S rRNA sequencing of fecal samples.	OTUs, $\alpha$ -diversity, bacterial phyla and genus.	No significant changes to intestinal microbiome as a result of exercise.	O
<b>Equine</b>									
Janabi, 2016	Y	Adult male and female horses (mares and geldings [n=8]), healthy, and older seasonal controls (n=4), healthy	To determine the effects of exercise on the equine intestinal microbiome over 12-weeks.	1. Seasonal control (SC) 2. F.Ex.	No. All animals were fed standard rations of grain and alfalfa, and grass ad-libitum.	PCR, 16S rRNA sequencing of fecal contents.	OTUs, $\alpha$ -diversity, $\beta$ -diversity, relative abundance of bacterial phyla, genera, and species	<b>2. F. Ex. *</b> ↑↓ <u>Bacteroidetes</u> ↑ <u>Dysgonomonas</u> (g) ↑ <u>Firmicutes</u> ↑ <u>Clostridium</u> (g) ↓↓ <u>Proteobacteria</u> ↑↓ <u>Spirochaetes</u> ↑ <u>Treponema</u> (g) * Direction of change varied based on bi-weekly timepoint over 12-week intervention	O
Janabi, 2017	Y	Adult male and female horses (mares and geldings), healthy, n=8.	To determine the acute effect of exercise on	1. SC 1 2. SC 2 3. F. Ex 1	No-all animals were fed standard ration of	PCR, 16S rRNA sequencing of fecal contents.	OTUs, $\alpha$ -diversity, $\beta$ -diversity, relative abundance of bacterial phyla, genera, and species	<b>1. SC 1 *</b> <u>Firmicutes</u> ↓ <u>Clostridium</u> (g) ↓ <u>Fusicatenibacter saccharivorans</u> (s)	O

			the intestinal microbiome before and after a 12-week exercise training protocol.	4. F.Ex 2	grain and alfalfa/ grass hay ad lib.			<u>Spirochaetes</u> ↓ <u>Treponema zioleckii</u> (s) * Direction of change varied based on bi-weekly timepoint over 12-week intervention	
<b>Human</b>									
Clarke, 2014	Y	Adult male rugby players, and weight matched high and low BMI controls, healthy, n=83	To determine the relationship between exercise or sedentary time and the intestinal microbiota.	1. Rugby 2. Low BMI 3. High BMI	No-diets were assessed via food frequency questionnaires (FFQ)	PCR, 16S rRNA sequencing of fecal contents.	OTUs, $\alpha$ -diversity, bacterial phyla, family, and genera.	<b>Rugby vs. High BMI</b> ↓ <u>Bacteroidetes</u> ↑ RC9 gut group (g) ↑ S24-7 (f) ↑ <u>Firmicutes</u> ↑ <u>Succinivibrio</u> (g) ↑ <u>Succinivibrionaceae</u> (f) <u>Verrucomicrobia</u> ↑ <u>Akkermansiaceae</u> (f) ↑ <u>Akkermansia</u> (g)  <b>Rugby vs. Low BMI:</b> ↓ <u>Bacteroidetes</u> ↑ <u>Prevotellaceae</u> (f) ↑ <u>Prevotella</u> (g) ↓ <u>Bacteroides</u> (g) ↑ S24-7 (f) <u>Firmicutes</u> ↓ <u>Lactobacillaceae</u> (f) ↓ <u>Lactobacillus</u> (g) ↑ <u>Erysipelotrichaceae</u> (c) ↑ <u>Succinivibrionaceae</u> (f) ↑ <u>Succinivibrio</u> (g)	G,O
Stewart, 2016	Y	Adults with Type 1 Diabetes (T1D), and Adult non-diabetic controls,	To determine if the intestinal microbiome of physically fit adults with managed	1. T1D 2. Non-T1D	No, diets were assessed with 24-hour dietary recalls.	PCR, 16S rRNA sequencing of fecal samples.	OTUs, $\alpha$ -diversity, abundance, bacterial phyla and species	<b>1. T1D*</b> <u>Firmicutes</u> <u>Lachno-spiraceae</u> (f) <u>Dialister</u> (g) <u>Actinobacteria</u> <u>Actinomyces</u> (g) <u>Collinsella</u> (g)	O

		otherwise healthy, n=20	T1D resembles the intestinal microbiome of physically fit adults without T1D.					<b>2. Non-T1D*</b> <u>Firmicutes</u> Lachno-spiraceae (f) Anoxybacillus (g) Clostridium sensu_stricto (g) Coprococcus (g) <u>Actinobacteria</u> Coriobacteriaceae (f) <u>Proteobacteria</u> Aurantimonas (g) Burkholderales (o) Zoogloea (g) Schlegelella (g) Comamonadaceae (f)  *Direction of results not reported.	
Allen, 2017	Y	Normal weight and obese sedentary (sed.) adults, otherwise healthy, n=32.	To determine influence of longitudinal exercise intervention on the intestinal microbiome where subjects served as their own controls.	1. Sed. + lean 2. Sed. + obese 3. Ex. + lean 4. Ex + obese	Yes, 3-day control diet prior to fecal samples.	PCR, 16S rRNA sequencing	OTUs, $\alpha$ -diversity, $\beta$ -diversity, bacterial genera, species	No significant findings between groups after 6 weeks of exercise or 6 weeks of washout.	O
Bressa, 2017	N	Females, premeno-pausal, healthy, n=40	To observationally compare the intestinal microbiome differences between sedentary	1. Sed 2. Active	No, diets were characterized using FFQs.	PCR, 16S rRNA sequencing	OTUs, $\alpha$ -diversity, $\beta$ -diversity, bacterial phyla, family, genus, and species, bacteroidetes:firmicutes	<b>1. Sed.</b> ↑ <u>Bacteroidetes</u> ↑ <u>Barnesiellaceae</u> (f) ↑ <u>Barnesiellaceae</u> unclassified (g) ↑ <u>Odoribacteraceae</u> (f) ↑ <u>Odoribacter</u> (g) <u>Firmicutes</u>	G, O

			and physically active females.					↑ Turicibacter (g) ↑ Ruminococcaceae unclassified (g) ↑ Ruminococcus (g) <u>Proteobacteria</u> ↑ Desulfovibrionaceae (g)	
								<b>2. Active</b> <u>Bacteroidetes</u> ↑ Paraprevotella (g) <u>Firmicutes</u> ↑ Faecalibacterium prautznii (s) ↑ Roseburia hominis (s) Coprococcus (g) <u>Actinobacteria</u> ↑ Bifidobacterium (g) <u>Proteobacteria</u> ↑ Haemophilus (g) <u>Verrucomicrobia</u> ↑ Akkermansia muciniphila (s)	
Paulsen, 2017	N	Female breast cancer survivors (BCS), otherwise healthy, n=12	To evaluate the influence of CRF and psychosocial factors on the intestinal microbiome in BCS.	1. BCS	No, diets were assessed with 3-day food intake records.	PCR, 16S rRNA sequencing	OTUs, $\alpha$ -diversity, $\beta$ -diversity, bacterial phyla, family, order, and genus	BCS: No quantitatively significant differences.	G, O

Significant results are presented by study within the “Significant bacterial taxonomy findings” column. All significant findings are denoted with an arrow indicating the direction of change, and are categorized within their respective phyla, and further characterized where: (c)=Class; (o)= Order; (f)= Family; (g)=Genus; and (s)=Species. ‡Represents results with cecal contents only. † Represents results with fecal and cecal contents. \*Denotes a study-specific note within the column.