

Table S1. Bodyweight and body condition score measurements in normal and obese cats.

Cat ID	Group	Sex	Female sample collection date	Age at collection	BW at collection (kg)	lean BW (kg)*	% increase in BW	Body Condition Score
D001	obese	male	5/15/2019	6y	7.00	4.08	71.57	9
F001	obese	male	5/15/2019	6y	5.55	3.77	47.21	8
G001	obese	male	5/10/2019	6y	5.35	3.78	41.53	8
H001	obese	male	5/15/2019	6y	6.25	3.20	95.31	9
I001	obese	male	6/28/2019	6y	5.70	4.10	39.02	7
J001	obese	male	5/10/2019	6y	7.00	3.97	76.32	9
K001	obese	male	6/28/2019	6y	6.60	3.70	78.38	9
L001	obese	male	5/10/2019	6y	6.50	3.87	67.96	9
Mean \pm s.d.					6.2 \pm 0.65		64.7 \pm 20.1	
Fc111468	normal	male	8/31/2020	4m	2.20	n/a	n/a	5
Fc111473	normal	male	9/10/2020	4m	2.60	n/a	n/a	5
Fc09Z110	normal	female	8/28/2020	8m	2.41	n/a	n/a	5
Fc09Z113	normal	female	8/28/2020	8m	2.54	n/a	n/a	5
Fc09Z116	normal	male	8/28/2020	8m	3.38	n/a	n/a	5
Fc081392	normal	female	7/12/2018	6y	2.64	n/a	n/a	5
Fc111030	normal	female	10/15/2019	6y	3.26	n/a	n/a	5
Fc111041	normal	male	1/9/2020	6y	4.08	n/a	n/a	5
Mean \pm s.d.					2.9 \pm 0.63		n/a	

* body weight measurement of obese cats when they were lean.

Table S2. Whole genome shotgun metagenomic sequencing yield, control statistics, and mapping rate.

Animal ID	total number of reads	total yield (Gbp)	% adapters & low quality reads	% host sequences	% viral sequences	% read alignment
111468	224,309,608	33.65	1.26%	1.75%	0.06%	96.54%
111473	252,204,562	37.83	0.78%	0.85%	0.05%	97.76%
81392	68,992,950	10.35	1.65%	19.62%	0.04%	78.82%
111030	67,304,938	10.10	1.05%	3.26%	0.05%	95.31%
111041	62,165,458	9.32	1.49%	3.14%	0.05%	95.31%
9Z110	177,167,802	26.58	1.68%	5.54%	0.04%	92.28%
9Z113	187,101,498	28.07	1.23%	3.43%	0.06%	94.74%
9Z116	71,831,380	10.77	1.84%	9.91%	0.05%	88.36%
D001	114,565,502	17.18	2.74%	16.53%	0.03%	81.42%
F001	88,239,704	13.24	3.37%	69.19%	0.01%	27.67%
G001	96,951,866	14.54	3.81%	35.50%	0.02%	61.68%
H001	81,550,038	12.23	2.44%	0.21%	0.04%	98.16%
I001	88,388,090	13.26	2.67%	2.09%	0.03%	95.74%
J001	93,732,658	14.06	3.11%	21.16%	0.02%	76.28%
K001	54,533,852	8.18	2.30%	2.66%	0.03%	95.46%
L001	77,921,032	11.69	3.89%	48.57%	0.02%	48.22%

Table S3. Blood glucose and HOMA-IR measurements in obese cats at the time of fecal sample collection.

Cat ID	Group	Sex	Blood glucose at collection (mg/dL)	Blood glucose reference range	HOMA-IR at collection	HOMA-IR for normal cats
D001	obese	male	127	58~116	2.86	1.3+/-0.9
F001	obese	male	256	58~116	4.60	1.3+/-0.9
G001	obese	male	226	58~116	2.62	1.3+/-0.9
H001	obese	male	203	58~116	3.27	1.3+/-0.9
I001	obese	male	133	58~116	2.14	1.3+/-0.9
J001	obese	male	147	58~116	3.00	1.3+/-0.9
K001	obese	male	285	58~116	3.47	1.3+/-0.9
L001	obese	male	162	58~116	3.37	1.3+/-0.9
Mean \pm s.d.			192.4 \pm 59.3		3.16 \pm 0.72	

Table S4. Top 20 most abundant bacterial genera in the cat rectum microbiota.

Genus name	Phylum	Average relative abundance	STDEV	NCBI taxonomy ID
<i>Prevotella</i>	Bacteroidetes	24.31%	0.177	838
<i>Collinsella</i>	Actinobacteria	12.70%	0.085	102106
<i>Bacteroides</i>	Bacteroidetes	8.17%	0.057	816
<i>Blautia</i>	Firmicutes	4.04%	0.023	572511
<i>Clostridium</i>	Firmicutes	3.24%	0.022	1485
<i>Megasphaera</i>	Firmicutes	2.26%	0.035	906
<i>Sutterella</i>	Proteobacteria	1.76%	0.012	40544
<i>Faecalibacterium</i>	Firmicutes	1.65%	0.02	216851
<i>Megamonas</i>	Firmicutes	1.50%	0.013	158846
<i>Eubacterium</i>	Firmicutes	0.92%	0.01	1730
<i>Roseburia</i>	Firmicutes	0.75%	0.009	841
<i>Flavonifractor</i>	Firmicutes	0.75%	0.007	946234
<i>Ruminococcus</i>	Firmicutes	0.55%	0.004	1263
<i>Lactimicrobium</i>	Firmicutes	0.43%	0.005	2563777
<i>Dorea</i>	Firmicutes	0.42%	0.003	189330
<i>Lachnoclostridium</i>	Firmicutes	0.39%	0.002	1506553
<i>Phascolarctobacterium</i>	Firmicutes	0.38%	0.005	33024
<i>Agathobaculum</i>	Firmicutes	0.37%	0.003	2048137
<i>Parabacteroides</i>	Bacteroidetes	0.27%	0.002	375288
<i>Drancourtella</i>	Firmicutes	0.16%	0.002	1903506

STDEV: standard deviation;

NCBI ID: National Center for Biotechnology Information, taxonomy ID

Table S5. Top 20 most abundant bacterial species in the cat rectum microbiota.

species name	normal average RA	normal STDEV	normal rank	obese average RA	obese STDEV	obese rank	NCBI ID
<i>Prevotella copri</i>	12.863%	0.074	1	19.646%	0.163	1	165179
<i>Erysipelotrichaceae bacterium AU001MAG</i>	3.066%	0.012	2	0.002%	0.000	847	-
<i>Collinsella tanakaei</i>	2.418%	0.016	3	2.399%	0.022	10	626935
<i>Megasphaera elsdenii</i>	1.940%	0.029	4	0.580%	0.007	29	907
<i>Collinsella stercoris</i>	1.833%	0.016	5	4.566%	0.033	2	147206
<i>Clostridium sp. CAG:169</i>	1.700%	0.011	6	0.625%	0.006	28	1262778
<i>Succinatimonas sp. CAG:777</i>	1.568%	0.014	7	0.332%	0.007	46	1262974
<i>Subdoligranulum variabile</i>	1.274%	0.009	8	2.691%	0.023	3	214851
<i>Acidaminococcus sp. CAG:542</i>	1.207%	0.018	9	0.053%	0.000	143	1262687
<i>Blautia sp. CAG:257</i>	1.170%	0.006	10	2.446%	0.019	9	1262756
<i>Prevotella sp. CAG:891</i>	1.157%	0.018	11	2.335%	0.027	11	1262937
<i>Collinsella intestinalis</i>	1.100%	0.015	12	0.677%	0.005	24	147207
<i>Clostridium sp. CAG:299</i>	0.898%	0.006	13	0.429%	0.003	36	1262792
<i>Faecalibacterium prausnitzii</i>	0.851%	0.007	14	0.228%	0.002	57	853
<i>Bacteroides plebeius</i>	0.771%	0.004	15	2.456%	0.021	5	310297
<i>Firmicutes bacterium CAG:424</i>	0.760%	0.004	16	0.379%	0.003	39	1263022
<i>Eubacterium sp. TM06-47</i>	0.683%	0.006	17	0.087%	0.001	111	2292354
<i>Bifidobacterium gallinarum</i>	0.681%	0.013	18	2.503%	0.037	4	78344
<i>Collinsella phocaeensis</i>	0.677%	0.005	19	0.566%	0.004	30	1871016
<i>Bacteroides stercoris</i>	0.633%	0.004	20	2.010%	0.028	289	46506

RA: relative abundance;

NCBI ID: taxonomy ID from National Center for Biotechnology Information.

Table S6. Significantly altered genera in obese cat rectum microbiota compared to normal cat.

Genus name*	obese average RA	normal average RA	adjusted <i>P</i> -value	log ₂ (fold change)	NCBI ID
<i>Anaerolactibacter</i>	0.00%	0.23%	0.006	-11.773	2563783
<i>Solobacterium</i>	0.00%	0.23%	0.006	-11.379	123375
<i>Lactimicrobium</i>	0.00%	0.87%	0.006	-11.125	2563777
<i>Galactobacillus</i>	0.00%	0.18%	0.006	-6.61	2060871
<i>Phascolarctobacterium</i>	0.02%	0.75%	0.006	-5.397	33024
<i>Butyricicoccus</i>	0.07%	0.33%	0.006	-2.188	580596
<i>Holdemanella</i>	0.01%	0.11%	0.008	-3.013	1573535
<i>Butyrivibrio</i>	0.03%	0.13%	0.008	-2.252	830
<i>Fusobacterium</i>	0.00%	0.12%	0.012	-4.743	848
<i>Escherichia</i>	0.01%	0.24%	0.012	-4.157	561
<i>Eubacterium</i>	0.27%	1.57%	0.012	-2.552	1730
<i>Lactobacillus</i>	0.04%	0.48%	0.017	-3.528	1578
<i>Faecalibacterium</i>	0.44%	2.86%	0.017	-2.705	216851
<i>Helicobacter</i>	0.07%	0.70%	0.023	-3.279	209
<i>Succinatimonas</i>	0.37%	1.60%	0.09	-2.099	674963
<i>Bifidobacterium</i>	8.02%	1.61%	0.049	2.32	1678
<i>Dialister</i>	1.94%	0.01%	0.059	7.897	39948

*Genera with an average frequency of at least 0.1% in normal or obese cats and a minimum absolute value of log₂ fold change of 2 were included.

RA: relative abundance; NCBI ID: taxonomy ID from National Center for Biotechnology Information.

Table S7. Significantly decreased species in obese cat rectum microbiota compared to normal cat.

Species name*	obese average RA	normal average RA	adjusted <i>P</i> -value	log ₂ (fold change)	NCBI ID	Phylum
<i>Erysipelotrichaceae bacterium AU001MAG</i>	0.002%	3.066%	0.012	-10.786	-	Firmicutes
<i>Anaerolactibacter massiliensis</i>	0.000%	0.060%	0.012	-9.926	2044573	Firmicutes
<i>Phascolarctobacterium succinatutens</i>	0.002%	0.623%	0.012	-8.572	626940	Firmicutes
<i>Clostridium ventriculi</i>	0.001%	0.176%	0.019	-8.399	1267	Firmicutes
<i>Clostridium colicanis</i>	0.000%	0.050%	0.019	-7.819	179628	Firmicutes
<i>Helicobacter sp. 48519</i>	0.001%	0.149%	0.021	-7.623	2315333	Proteobacteria
<i>Prevotella sp. CAG:755</i>	0.003%	0.069%	0.043	-4.511	1262935	Bacteroidetes
<i>Lactobacillus reuteri</i>	0.007%	0.149%	0.037	-4.413	1598	Firmicutes
<i>Lactobacillus sp.</i>	0.002%	0.051%	0.063	-4.412	1591	Firmicutes
<i>Escherichia coli</i>	0.011%	0.237%	0.016	-4.406	562	Proteobacteria
<i>Faecalibacterium prausnitzii</i>	0.009%	0.129%	0.028	-3.775	718252	Firmicutes
<i>Campylobacter helveticus</i>	0.018%	0.215%	0.026	-3.589	28898	Proteobacteria
<i>Eubacterium sp. AM28-29</i>	0.013%	0.128%	0.026	-3.285	2292349	Firmicutes
<i>Eubacterium sp. TM05-53</i>	0.008%	0.072%	0.021	-3.250	2292353	Firmicutes
<i>Clostridium perfringens</i>	0.023%	0.204%	0.087	-3.138	1502	Firmicutes
<i>Collinsella sp. AM42-18AC</i>	0.006%	0.052%	0.021	-3.058	2292321	Actinobacteria
<i>Allisonella histaminiformans</i>	0.011%	0.088%	0.017	-3.009	209880	Firmicutes
<i>Eubacterium sp. TM06-47</i>	0.087%	0.683%	0.028	-2.966	2292354	Firmicutes
<i>Prevotellamassilia timonensis</i>	0.008%	0.058%	0.028	-2.893	1852370	Bacteroidetes
<i>Helicobacter canis</i>	0.063%	0.453%	0.026	-2.849	29419	Proteobacteria
<i>Blautia wexlerae</i>	0.096%	0.576%	0.028	-2.588	418240	Firmicutes
<i>Collinsella sp. AM18-10</i>	0.018%	0.107%	0.046	-2.565	2292028	Actinobacteria
<i>Roseburia inulinivorans</i>	0.010%	0.054%	0.026	-2.468	360807	Firmicutes
<i>Blautia schinkii</i>	0.046%	0.248%	0.021	-2.419	180164	Firmicutes
<i>Dorea sp. Marseille-P4003</i>	0.024%	0.126%	0.043	-2.404	2040291	Firmicutes
<i>Faecalimonas umbilicata</i>	0.013%	0.068%	0.016	-2.373	1912855	Firmicutes
<i>Succinatimonas sp. CAG:777</i>	0.332%	1.568%	0.043	-2.238	1262974	Proteobacteria
<i>Roseburia hominis</i>	0.092%	0.420%	0.028	-2.188	301301	Firmicutes
<i>Coprococcus sp. AF21-14LB</i>	0.024%	0.108%	0.021	-2.168	2292231	Firmicutes
<i>Lachnospiraceae bacterium</i>	0.013%	0.059%	0.026	-2.164	1898203	Firmicutes
<i>Butyrivibrio pullicaecorum</i>	0.056%	0.250%	0.012	-2.150	501571	Firmicutes
<i>Dorea formicigenerans</i>	0.014%	0.057%	0.046	-2.085	39486	Firmicutes
<i>uncultured Eubacterium sp.</i>	0.019%	0.081%	0.037	-2.084	165185	Firmicutes

*Species with an average frequency of at least 0.05% and a minimum of log₂ fold change of 2 or less were included. RA: relative abundance; NCBI ID: taxonomy ID from National Center for Biotechnology Information.

Table S8. Significantly increased species in obese cat rectum microbiota compared to normal cat.

Species name	obese average RA	normal average RA	adjusted <i>P</i> -value	log ₂ (fold change)	NCBI ID	Phylum
<i>Dialister</i> sp. CAG:486	1.935%	0.001%	0.043	10.598	1262870	Firmicutes
<i>Bifidobacterium adolescentis</i>	2.113%	0.036%	0.017	5.879	1680	Actinobacteria
<i>Megasphaera</i> sp. An286	0.073%	0.002%	0.046	5.261	1965622	Firmicutes
<i>Campylobacter upsaliensis</i>	0.497%	0.020%	0.043	4.640	28080	Proteobacteria
<i>Olsenella provencensis</i>	2.268%	0.115%	0.071	4.300	1852386	Actinobacteria
<i>Bacteroides coprophilus</i> CAG:333	0.099%	0.005%	0.026	4.226	1263041	Bacteroidetes
<i>Bacteroides xylanisolvens</i>	0.122%	0.007%	0.026	4.102	371601	Bacteroidetes
<i>Bifidobacterium longum</i>	0.633%	0.040%	0.019	3.975	216816	Actinobacteria
<i>Phocaeicola coprophilus</i>	0.529%	0.037%	0.037	3.831	387090	Bacteroidetes
<i>Megasphaera stantonii</i>	0.118%	0.011%	0.028	3.456	2144175	Firmicutes
<i>Olsenella</i> sp. An290	0.053%	0.005%	0.037	3.441	1965625	Actinobacteria
<i>Bifidobacterium pseudolongum</i>	0.187%	0.023%	0.071	3.044	1694	Actinobacteria
<i>Bacteroides ovatus</i>	0.101%	0.013%	0.071	2.901	28116	Bacteroidetes
<i>Collinsella</i> sp. An268	0.367%	0.058%	0.028	2.665	1965612	Actinobacteria
<i>Flavonifractor</i> sp. An306	0.119%	0.020%	0.100	2.566	1965629	Firmicutes
<i>Olsenella</i> sp. Marseille-P2300	0.067%	0.016%	0.071	2.083	1805478	Actinobacteria
<i>Olsenella mediterranea</i>	0.071%	0.017%	0.059	2.034	1871031	Actinobacteria
<i>Slackia equolifaciens</i>	0.133%	0.033%	0.028	2.002	498718	Actinobacteria

*Species with an average frequency of at least 0.05% and a minimum of log₂ fold change of 2 or more were included. RA: relative abundance; NCBI ID: taxonomy ID from National Center for Biotechnology Information.

Table S9. Primer sequences for individual bacterial species abundance validation using qPCR.

Target species/strain	Forward Primer	Reverse primer
<i>Bifidobacterium adolescentis</i> strain PRL2019	GCCTCGAAACGCATGTTCC	TTCTTGCCTAATCCCGGAGC
<i>Olsenella provencensis</i>	AGGTTCTTCTCGCCAAGCCGAT	CCCAGCTTGAGCCTGACCTCG
<i>Dialister</i> sp.	GATCCCATTATGCCCCGCCTG	ATATGAACCTTTCCGGCGAAG
<i>Erysipelotrichaceae</i> bacterium AU001MAG	ATGCTGTTGTCTCCTCCGGTA	CGGCAGGATCTAAAAGTCCC
<i>Prevotella copri</i> (primer set 1)	CATAGCCTGTCAATGCGTA	ATTCTATATTCCATTCCGTTGC
<i>Prevotella copri</i> (primer set 2)	ATATTCTGTTCAATTCTCCGTA	GCGATTACCAATTGAGCAAA
<i>Campylobacter upsaliensis</i>	TACTATCGAGGCTTGAGCAT	CGGCAAAATTAGAGCTTCACA
<i>Campylobacter helveticus</i>	CAGCCTTATTATCACTGACA	CGATATGCTCAAGCCTT
<i>Phascolarcobacterium succinatutens</i>	TCGGACCTAAAATGGCCTT	ACCCTCGGAAGTAATGCT