

Figure S1

Library	Organism	Cell Numbers	Library Type	Kit	Kit Version
GBBOG	ZymoBIOMICS™ Microbial Community DNA Standard: D6305	100ng DNA	Shotgun	Kapa Hyper Prep Kit	N/A
CZWOH	ZymoBIOMICS™ Microbial Community Standard cells: D6300	1E8 cells	Hi-C	Phase Genomics	1
CZWON	ZymoBIOMICS™ Microbial Community Standard cells: D6300	2.8E8 cells	Hi-C	Arima/Kapa	1
GPANX	ZymoBIOMICS™ Microbial Community Standard cells: D6300	2.8E8 cells	Hi-C	Arima/Kapa	1
GPANY	ZymoBIOMICS™ Microbial Community Standard cells: D6300	1E8 cells	Hi-C	Phase Genomics	1.5
GPANZ	ZymoBIOMICS™ Microbial Community Standard cells: D6300	1E8 cells	Hi-C	Phase Genomics	1.5
GPAOA	ZymoBIOMICS™ Microbial Community Standard cells: D6300	1E8 cells	Hi-C	Phase Genomics	1.5
GPAOB	ZymoBIOMICS™ Microbial Community Standard cells: D6300	1E8 cells	Hi-C	Phase Genomics	1.5

Figure S2

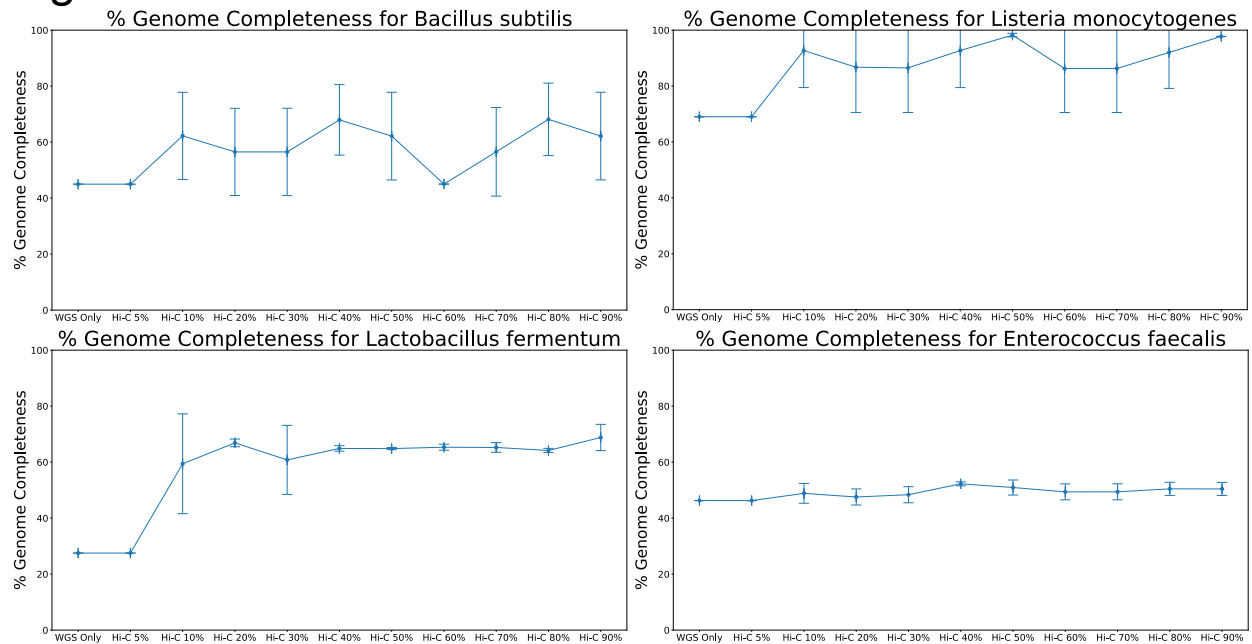


Figure S3

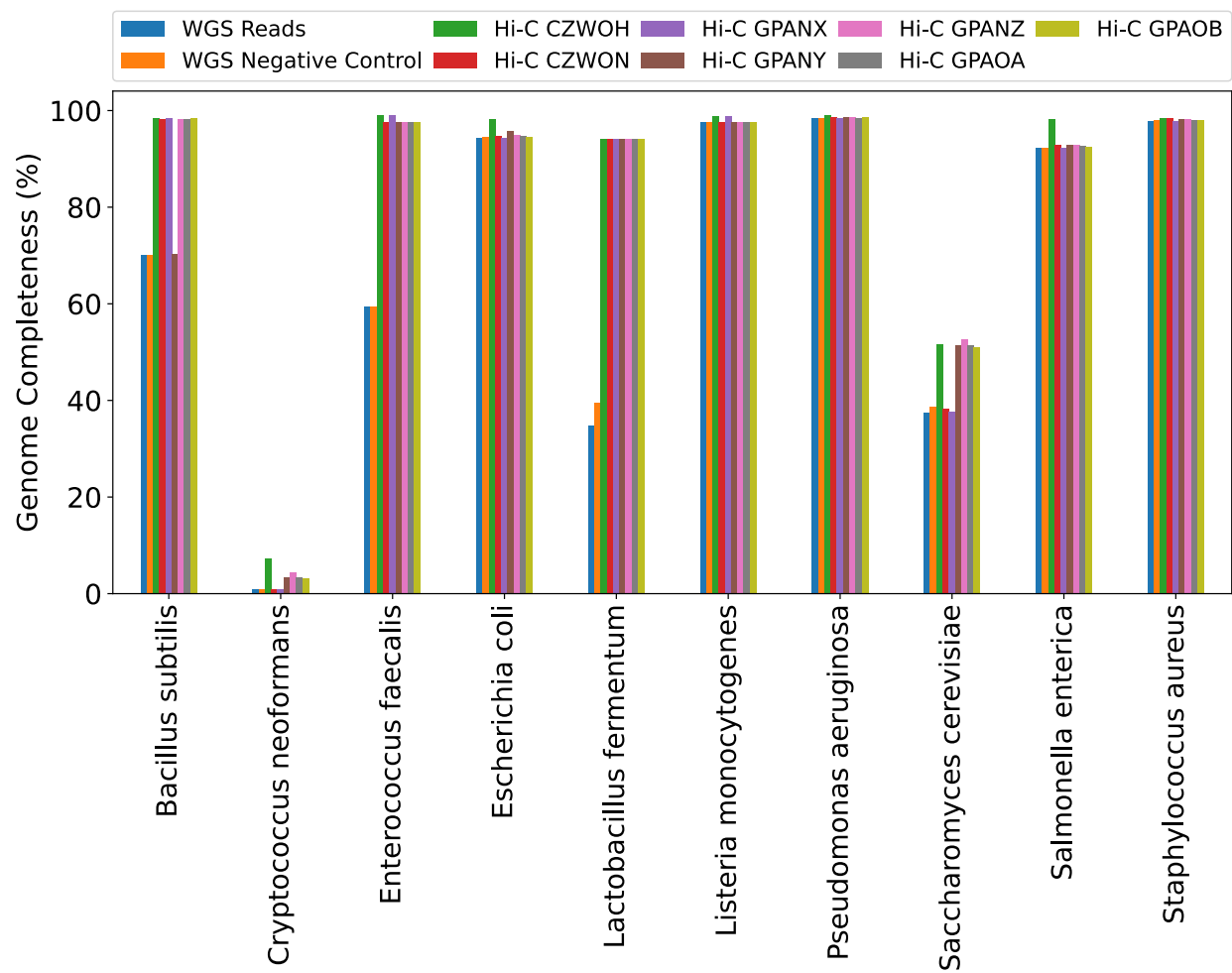


Figure S4

Metabat-LR High Contamination Bins from Cat Fecal Dataset

Completeness	Contamination	Bin Id	Marker lineage
100	57.18	bin.59.fa	k__Bacteria (UID203)
86.41	71.33	bin.14.fa	p__Actinobacteria (UID2112)
70.97	17.1	bin.65.fa	o__Clostridiales (UID1212)
75.65	52.19	bin.62.fa	k__Bacteria (UID203)
62.93	24.92	bin.63.fa	k__Bacteria (UID203)
94.83	11	bin.53.fa	k__Bacteria (UID203)
84.94	12.91	bin.41.fa	o__Clostridiales (UID1226)
96.14	27.59	bin.49.fa	k__Bacteria (UID203)
92.98	11.58	bin.35.fa	o__Clostridiales (UID1226)
65.91	15.38	bin.60.fa	o__Bacteroidales (UID2621)

Metabat_LR High Contamination Bins from Human Fecal Dataset

Completeness	Contamination	Bin Id	Marker lineage
78.62	10.34	bin.95.fa	k__Bacteria (UID203)
94.51	91.69	bin.78.fa	k__Bacteria (UID203)
96.49	18.13	bin.205.fa	k__Bacteria (UID203)
56.14	14.35	bin.202.fa	k__Bacteria (UID203)
88.96	12.96	bin.140.fa	o__Clostridiales (UID1212)
93.67	87.08	bin.123.fa	k__Bacteria (UID203)
92.63	23.15	bin.165.fa	k__Bacteria (UID203)
95.69	34.15	bin.211.fa	k__Bacteria (UID203)
91.07	53.98	bin.221.fa	k__Bacteria (UID203)
97.41	24.44	bin.220.fa	k__Bacteria (UID203)
93.14	20.31	bin.170.fa	o__Clostridiales (UID1212)
63.48	19.3	bin.47.fa	k__Bacteria (UID203)
84.21	17.12	bin.21.fa	k__Bacteria (UID203)
75.76	12.99	bin.130.fa	o__Clostridiales (UID1226)
87	82.7	bin.44.fa	k__Bacteria (UID203)
80.7	12.89	bin.2.fa	o__Clostridiales (UID1226)
72.53	12.97	bin.131.fa	o__Clostridiales (UID1226)
81.34	17.22	bin.137.fa	k__Bacteria (UID203)
99.04	68.5	bin.228.fa	k__Bacteria (UID203)
69.5	14.69	bin.223.fa	o__Bacteroidales (UID2621)
88.97	10.59	bin.66.fa	f__Lachnospiraceae (UID1256)
78.26	38.09	bin.116.fa	o__Clostridiales (UID1226)
94.74	84.56	bin.65.fa	k__Bacteria (UID203)
82.41	16.12	bin.189.fa	o__Clostridiales (UID1212)
60.34	35.06	bin.233.fa	k__Bacteria (UID203)
97.02	16.51	bin.217.fa	k__Bacteria (UID203)
93.42	11.91	bin.126.fa	f__Lachnospiraceae (UID1286)

Figure S5

Metabat-LR Unique Bins from Cat Fecal Dataset

Completeness	Contamination	Bin Id	Marker lineage
100	1.12	bin.57.fa	k__Bacteria (UID2329)
92.36	4.29	bin.55.fa	o__Bacteroidales (UID2657)
86.46	3.15	bin.23.fa	o__Bacteroidales (UID2621)
63.12	3.02	bin.51.fa	f__Lachnospiraceae (UID1256)
62.73	2.98	bin.46.fa	o__Lactobacillales (UID544)
62.37	1.26	bin.42.fa	o__Bacteroidales (UID2654)

Metabat-LR Unique Bins from Human Fecal Dataset

Completeness	Contamination	Bin Id	Marker lineage
99.46	0.54	bin.23.fa	k__Bacteria (UID2569)
94.41	0.89	bin.91.fa	o__Clostridiales (UID1226)
94.19	6.53	bin.210.fa	f__Lachnospiraceae (UID1256)
93.62	1.34	bin.176.fa	o__Clostridiales (UID1212)
93.51	6.02	bin.159.fa	o__Clostridiales (UID1212)
90.66	2.34	bin.109.fa	o__Clostridiales (UID1226)
88.85	0	bin.83.fa	o__Clostridiales (UID1212)
81.7	0	bin.92.fa	o__Bacteroidales (UID2617)
80.31	4.39	bin.184.fa	o__Bacteroidales (UID2657)
78.96	8.97	bin.73.fa	o__Clostridiales (UID1226)
77.71	1.23	bin.144.fa	o__Clostridiales (UID1212)
73.38	4.47	bin.16.fa	o__Clostridiales (UID1212)
73.21	3.51	bin.77.fa	o__Clostridiales (UID1212)
72.58	7.18	bin.145.fa	o__Clostridiales (UID1212)
70.65	2.91	bin.124.fa	o__Clostridiales (UID1212)
69.98	2.13	bin.12.fa	o__Clostridiales (UID1120)
66.4	3.48	bin.155.fa	f__Lachnospiraceae (UID1286)
62.76	7.71	bin.120.fa	o__Clostridiales (UID1212)
59.56	2.92	bin.122.fa	o__Clostridiales (UID1212)
56.32	6.9	bin.125.fa	k__Bacteria (UID203)
54.31	1.72	bin.179.fa	k__Bacteria (UID203)
54.06	0.32	bin.54.fa	o__Clostridiales (UID1226)
51.79	0	bin.134.fa	k__Bacteria (UID203)