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CORRECTION

Correction: Selective colonization ability of human fecal microbes in different mouse gut environments

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Since publication of the original article, the authors realised that Supplementary Tables 2 and 3 were not uploaded with the rest of the supplementary information. These are now uploaded to the HTML version of the article and are produced below.

Supplementary Table 2.

bin ID	Kraken classification (Taxonomic level)	CheckM classification (Taxonomic level)
3	Firmicutes (Phylum)	Lachnospiraceae (Family)
5	Firmicutes (Phylum)	Bacteria (kingdom)
6	- (Root)	Clostridia (Class)
10	Firmicutes (Phylum)	Clostridiales (order)
11	- (Root)	Thermoanaerobacterales (Order)
13	Firmicutes (Phylum)	Clostridiales (order)
14	Firmicutes (Phylum)	Lachnospiraceae (Family)
16	Firmicutes (Phylum)	Bacteria (kingdom)
24	Firmicutes (Phylum)	Lachnospiraceae (Family)
26	Firmicutes (Phylum)	Lachnospiraceae (Family)
28	Firmicutes (Phylum)	Bacteria (kingdom)
29	Firmicutes (Phylum)	Clostridiales (order)
30	Firmicutes (Phylum)	Clostridiales (order)
33	Firmicutes (Phylum)	Clostridiales (order)
36	Firmicutes (Phylum)	Clostridiales (order)
37	Firmicutes (Phylum)	Lachnospiraceae (Family)
39	Firmicutes (Phylum)	Lachnospiraceae (Family)
43	Firmicutes (Phylum)	Clostridiales (order)
47	- (Root)	Lachnospiraceae (Family)
50	Firmicutes (Phylum)	Lachnospiraceae (Family)
51	Firmicutes (Phylum)	Clostridiales (order)
52	Firmicutes (Phylum)	Clostridiales (order)
58	Bacteria (kingdom)	Clostridia (Class)
59	Firmicutes (Phylum)	Clostridiales (order)
65	Firmicutes (Phylum)	Clostridiales (order)
68	Bacteria (kingdom)	Clostridia (Class)
69	Firmicutes (Phylum)	Clostridiales (order)
79	Firmicutes (Phylum)	Clostridiales (order)
80	Firmicutes (Phylum)	Bacteria (kingdom)
82	Firmicutes (Phylum)	Clostridiales (order)
87	Acutalibacter muris (Species)	Clostridiales (order)
88	Firmicutes (Phylum)	Clostridiales (order)
90	Bacteria (kingdom)	Clostridia (Class)
91	- (Root)	Clostridiales (order)
95	Firmicutes (Phylum)	Clostridiales (order)
96	Firmicutes (Phylum)	Lachnospiraceae (Family)
99	Firmicutes (Phylum)	Bacteria (kingdom)
100	Burkholderiales bacterium YL45 (Species)	Proteobacteria (Phylum)
101	Firmicutes (Phylum)	Lachnospiraceae (Family)
104	Firmicutes (Phylum)	Lachnospiraceae (Family)
108	- (Root)	Lachnospiraceae (Family)
116	Firmicutes (Phylum)	Clostridiales (order)
126	Firmicutes (Phylum)	Clostridia (Class)
129	Firmicutes (Phylum)	Lachnospiraceae (Family)
132	Firmicutes (Phylum)	Lachnospiraceae (Family)
133	Firmicutes (Phylum)	Lachnospiraceae (Family)
135	Firmicutes (Phylum)	Lachnospiraceae (Family)
136	- (Root)	Clostridiales (order)
138	Firmicutes (Phylum)	Clostridiales (order)
140	Firmicutes (Phylum)	Clostridiales (order)
146	- (Root)	Clostridiales (order)
148	- (Root)	Lachnospiraceae (Family)
152	Firmicutes (Phylum)	Bacteria (kingdom)
154	Bacteroides thetaiotaomicron (Species)	Bacteroides (Genera)
157	Firmicutes (Phylum)	Bacteria (kingdom)
162	Lactobacillus johnsonii (Species)	Lactobacillus (Genera)
163	Firmicutes (Phylum)	Clostridiales (order)
164	Bacteria (kingdom)	Clostridia (Class)
171	Firmicutes (Phylum)	Clostridiales (order)
174	Akkermansia muciniphila (Species)	Bacteria (kingdom)
181	- (Root)	Bacteria (kingdom)
182	Actinobacteria (Phylum)	Actinobacteria (Phylum)
185	Firmicutes (Phylum)	Clostridiales (order)
187	- (Root)	Clostridiales (order)
192	- (Root)	Clostridiales (order)

Supplementary Table 3.

KO		corrected p value	log2FoldEnriched
NSG vs DONOR			
K13653	AraC family transcriptional regulator	2.33E-220	6.085777164
K03092	RNA polymerase sigma-54 factor	2.67E-205	-7.270532708
K01278	dipeptidyl-peptidase 4	1.78E-198	-12.59251039
K01546	K+-transporting ATPase ATPase A chain	2.10E-193	-9.99100789
K03587	cell division protein FtsI	2.05E-179	-10.2859436
K07037	uncharacterized protein	1.37E-159	-11.05262788
K07263	zinc protease	9.63E-142	-7.352007382
K03332	fructan beta-fructosidase	6.60E-139	-7.187537857
K04518	prephenate dehydratase	6.60E-139	-6.100008843
K00912	tetraacyldisaccharide 4'-kinase	8.98E-135	-10.25290754
C57BL6/J vs DONOR			
K07713	two-component system, NtrC family, response regulator HydG	6.94E-103	-14.05876756
K13653	AraC family transcriptional regulator	7.28E-85	5.687393659
K07043	uncharacterized protein	1.47E-84	-2.799784852
K02121	V/A-type H+/Na+-transporting ATPase subunit E	2.42E-70	-3.153204242
K05516	curved DNA-binding protein	2.42E-70	-6.581666247
K06076	long-chain fatty acid transport protein	6.08E-64	-12.29153314
K03711	Fur family transcriptional regulator, ferric uptake regulator	1.91E-63	-3.626934326
K09790	uncharacterized protein	4.08E-63	-3.264532972
K01235	alpha-glucuronidase	1.70E-60	-3.304631387
K16153	glycogen phosphorylase/synthase	1.76E-60	-9.970604097