

Supplementary Table 4. Recovery of microbial diversity from complex human fecal microbiomes by culturing and mouse colonization. Related to Figures 4 and 7.

(A) Species-level recovery

Human subject	Species detected (whole sample)	% Detected after:		
		Anaerobic Culturing	Aerobic Culturing	Colonized in suckling mice
A	47	40.00%	6%	63%
B	55	29%	2%	55%
C	47	38%	15%	78%
D	39	51%	7%	64%
E	39	46%	7%	74%
F	55	38.00%	14.00%	54%

(B) Genus-level recovery

Human subject	Genera detected (whole sample)	% Detected after:		
		Anaerobic Culturing	Aerobic Culturing	Colonized in suckling mice
A	25	52.00%	12%	92%
B	29	38%	3%	79%
C	28	43%	25%	78%
D	24	58%	13%	75%
E	17	76%	18%	82%
F	31	48.00%	25.00%	65%

(C) Total species-level relative abundance of complete fecal specimen represented by strains recovered after *in vitro* culturing.

Human subject	Total relative abundance (species level) of complex sample recovered	
	Anaerobic Culturing	Aerobic Culturing
A	99%	0%
B	85%	0%
C	91%	1%
D	94%	38%
E	66%	0%
F	88%	97%

(D) Genus-level relative abundance in complex human fecal microbiomes represented by model community members.

Human Subject	% Complex sample genus-level abundance represented by CR model community	% Genus-level abundance of fecal sample colonized in suckling mice represented by CR model community	% Complex sample genus-level abundance represented by DS model community	% Genus-level abundance of fecal sample colonized in suckling mice represented by DS model community
A	62%	47.00%	0.10%	0.30%
B	37.00%	10.00%	0.20%	1.00%
C	55.00%	44.00%	0.30%	1.00%
D	54.00%	30.00%	1.00%	5.00%
E	60.00%	34.00%	0.00%	2.00%
F	73.00%	42.00%	0.05%	0.09%