

Table S2.Most abundant families in the data set, representing 86.9% of all OTUs.

Family	Abundance in all samples (%, mean ; range)	Abundance in mucosal samples (%, mean ; range)	Abundance in stool samples (%, mean ; range)	Abundance in donor Samples (%, mean ; range)
<i>Lactobacillaceae</i>	2.8 (0.0-64.8)	3.0 (0.0-62.3)	2.0 (0.0-64.8)	0.0 (0.0-0.1)
<i>Bacteroidaceae</i>	13.0 (0.0-63.7)	11.8 (0.0-36.2)	14.7 (0.0-62.4)	20.9 (0.0-63.7)
<i>Prevotellaceae</i>	4.2 (0.0-60.6)	4.8 (0.0-60.6)	2.1 (0.0-24.1)	0.2 (0.0-1.3)
<i>Enterococcaceae</i>	3.6 (0.0-39.0)	3.0 (0.0-39.0)	4.3 (0.0-29.6)	0.2 (0.0-0.4)
<i>Clostridiaceae</i>	12.4 (0.0-70.6)	13.1 (0.0-58.5)	14.0 (0.0-70.6)	4.6 (0.0-11.4)
<i>Lachnospiraceae</i>	11.5 (0.0-45.7)	8.6 (0.0-28.7)	9.6 (0.0-38.2)	24.4 (10.7-45.7)
<i>Ruminococcaceae</i>	12.8 (0.0-63.8)	14.1 (0.0-39.0)	11.5 (0.0-63.8)	9.7 (0.0-20.8)
<i>Fusobacteriaceae</i>	4.5 (0.0-66.7)	7.0 (0.0-66.7)	6.3 (0.0-58.9)	1.1 (0.0-3.4)
<i>Alcaligenaceae</i>	3.4 (0.0-33.0)	5.1 (0.0-25.8)	3.0 (0.0-33.0)	0.0 (0.0-0.1)
<i>Enterobacteriaceae</i>	12.5 (0.0-85.6)	10.3 (0.0-80.4)	17.6 (0.0-85.6)	8.6 (0.0-26.1)
<i>Veillonellaceae</i>	3.3 (0.0-35.0)	2.5 (0.0-19.5)	2.6 (0.0-35.0)	3.1 (0.7-7.0)
<i>Erysipelotrichaceae</i>	2.9 (0.0-18.5)	3.0 (0.0-18.5)	2.9 (0.0-16.9)	0.5 (0.3-0.7)