

Supplementary Table 1

Study	Cohort 1: CrohnOmeter	Cohort 2: PREDICT	Cohort 3: MOBIDIC
N	98	284	143
Age, median (years) (Q1; Q3)	30.0 (25.0 ; 41.5)	39.50 (29.00 ; 51.00)	36.0 (28.0 ; 48.0)
Sex (% female)	71.4%	52.8%	55.9%
BMI, median (kg/m ²) (Q1 ; Q3)	21.52 (19.96 ; 24.46)	24.78 (22.09 ; 28.74)	25.11 (21.67 ; 27.14)
Ethnicity	NA	Caucasian – 93% Black – 5.6% Asian – 1.4%	Caucasian – 94.4% Black – 4.9% Asian – 0.7%
Country	EU - 100%	US + Canada – 76.1% EU - 23.9%	US - 25.2% EU - 74.8%
Smoking status	Current smoker – 25.6% No smoker – 74.4%	Current smoker - 17.6% No smoker - 82.4%	Current smoker - 25.2% No smoker - 74.8%
Age at diagnosis (years)	≤16: 12.9% [17- 40]: 83.5% >40: 3.5%	≤16: 19.5% [17- 40]: 62.1% >40: 18.4%	≤16: 17.6% [17- 40]: 65.5% >40: 16.9%
Current localization*	L1 – 38.0% L2 – 5.6% L3 – 56.3% L4 – 7.0%	Ileum – 76.1% Colon – 58.8% Rectum – 14.1% Anal – 9.9%	L1 – 37.3% L3 – 62.7%
Bowel resection (% population)	NA	27.8%	49.7%
CDAI, median (Q1 ; Q3)	NA	130.3 (80.4 ; 195.8)	91.0 (45.4 ; 182.9)
HBI, median (Q1 ; Q3)	2.0 (0.3 ; 4.0)	3.0 (1.0 ; 7.0)	3.0 (1.0 ; 5.3)
Calprotectin**, median (Q1 ; Q3) (mg/kg)	71.9 (50.0 ; 280.9)	205.0 (64.0 ; 786.0)	35.8 (15.6 ; 164.5)

Supplementary Table 2

	Healthy volunteers
N	43
Age, median (years) (Q1 ; Q3)	38 (34.3 ; 43.8)
Sex (% of female)	63%
BMI, median (Q1 ; Q3) (kg/m ²)	22.6 (21.6 ; 24.4)
Country	EU - 100%

Supplementary Table 3

	HV	Cohort 1	Cohort 2
<i>Escherichia coli</i>	1,7E-04	1,2E-03	2,0E-03
<i>Shigella flexneri</i>	7,3E-07	1,3E-05	7,8E-05
<i>Klebsiella pneumoniae</i>	1,4E-06	1,8E-05	4,6E-05
<i>Salmonella enterica</i>	6,5E-07	1,1E-05	1,6E-05
<i>Enterobacter cloacae</i>	1,5E-07	4,4E-06	1,5E-05

	HV	Cohort 1		Cohort 2	
		Quiet	Active	Quiet	Active
<i>Escherichia coli</i>	1,7E-04	1,1E-03	4,0E-03	1,1E-03	6,6E-03
<i>Shigella flexneri</i>	7,3E-07	1,3E-05	3,9E-05	4,3E-05	2,5E-04
<i>Klebsiella pneumoniae</i>	1,4E-06	1,0E-05	6,0E-05	2,9E-05	9,8E-05
<i>Salmonella enterica</i>	6,5E-07	1,0E-05	4,7E-05	1,1E-05	3,6E-05
<i>Enterobacter cloacae</i>	1,5E-07	3,0E-06	8,6E-06	8,2E-06	3,5E-05

Supplementary Table 4

	Information							Mapping against FimH (LF82 as reference)		
Strain ID	Origine	Tissue / Source	Disease	Type of sequencing	Phylogroup quadruplex	Aggregation	%FimS ON	Presence of FimH	% identity LF82	bit score LF82
GI-AIEC02	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	C	Aggregation	25.0	Y	98.004	1567
GI-AIEC04	GIRONA	Intestinal Biopsy	Control	MiSeq 300PE	B2	Aggregation	20.0	Y	99.224	1628
GI-AIEC05	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	B2	Aggregation	0.0	Y	98.004	1567
GI-AIEC06	GIRONA	Intestinal Biopsy	Control	MiSeq 300PE	B2	Aggregation	34.8	Y	99.113	1622
GI-AIEC08	GIRONA	Intestinal Biopsy	Control	MiSeq 300PE	B2	Grey zone	8.0	Y	98.891	1611
GI-AIEC09	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	B2	Aggregation	21.9	Y	99.224	1628
GI-AIEC10	GIRONA	Intestinal Biopsy	Control	MiSeq 300PE	A	Aggregation	18.7	Y	97.783	1555
GI-AIEC11	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	E	Absence of aggregation	0.0	Y	99.667	1650
GI-AIEC12	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	C	Grey zone	0.0	Y	97.672	1550
GI-AIEC14_1	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	B2	Aggregation	26.7	Y	99.113	1622
GI-AIEC15_1	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	B2	Aggregation	51.8	Y	99.113	1622
GI-AIEC16_2	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	B2	Aggregation	9.1	Y	99.113	1622
GI-AIEC19	GIRONA	Intestinal Biopsy	Control	MiSeq 300PE	A	Absence of aggregation	0.0	Y	97.783	1555
GI-AIEC20	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	E	Absence of aggregation	0.0	Y	97.783	1555
GI-AIEC21	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	B2	Aggregation	4.3	Y	99.224	1628
GI-AIEC23	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	A	Aggregation	38.7	Y	97.783	1555
GI-AIEC24	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	C	Absence of aggregation	10.0	Y	98.004	1567
GI-AIEC25	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	B2	Grey zone	0.0	Y	100.000	1666
GI-ECG01	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	B2	Aggregation	13.6	Y	100.000	1666
GI-ECG02	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	B1	Absence of aggregation	0.0	Y	97.672	1550
GI-ECG04	GIRONA	Intestinal Biopsy	Control	MiSeq 300PE	B1	Aggregation	41.0	Y	98.115	1572
GI-ECG05	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	B2	Grey zone	0.0	Y	97.783	1555
GI-ECG09	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	B2	Absence of aggregation	0.0	Y	99.113	1622
GI-ECG15	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	B2	Absence of aggregation	5.4	Y	99.667	1650
GI-ECG16	GIRONA	Intestinal Biopsy	Control	MiSeq 300PE	C	Aggregation	0.0	Y	97.672	1550
GI-ECG17	GIRONA	Intestinal Biopsy	Control	MiSeq 300PE	B2	Aggregation	40.6	Y	100.000	1666
GI-ECG18	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	C	Absence of aggregation	0.0	N	NA	NA
GI-ECG19	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	E	Grey zone	11.8	Y	97.561	1544
GI-ECG21	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	B1	Aggregation	11.1	Y	97.672	1550

Supplementary Table 4

	Information							Mapping against FimH (LF82 as reference)		
Strain ID	Origine	Tissue / Source	Disease	Type of sequencing	Phylogroup quadruplex	Aggregation	%FimS ON	Presence of FimH	% identity LF82	bit score LF82
GI-ECG26	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	B2	Aggregation	11.1	Y	99.335	1633
GI-ECG34	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	E	Aggregation	11.8	Y	97.672	1550
GI-ECG41	GIRONA	Intestinal Biopsy	Control	MiSeq 300PE	B2	Grey zone	0.0	Y	99.224	1628
GI-ECG42	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	E	Aggregation	5.6	Y	97.561	1544
GI-ECG43	GIRONA	Intestinal Biopsy	Control	MiSeq 300PE	B2	Aggregation	22.2	Y	100.000	1666
GI-ECG46	GIRONA	Intestinal Biopsy	Control	MiSeq 300PE	B1	Absence of aggregation	0.0	N	NA	NA
GI-ECG57	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	E	Absence of aggregation	9.1	Y	97.783	1555
GI-ECG63	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	B1	Aggregation	35.7	Y	97.783	1555
GI-ECG64	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	B1	Aggregation	55.0	Y	98.115	1572
GI-ECG65	GIRONA	Intestinal Biopsy	CD	MiSeq 300PE	A	Absence of aggregation	5.6	Y	97.783	1555
CU-08MY_1	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	B2	Aggregation	9.5	Y	100.000	1666
CU-09_396_A	Cornell	Stool	Control	MiSeq 300PE	E	Aggregation	12.5	Y	97.561	1544
CU-09_404_G	Cornell	Stool	Control	MiSeq 300PE	B2	Aggregation	28.8	Y	100.000	1666
CU-09_406_B	Cornell	Stool	Control	MiSeq 300PE	C	Grey zone	0.0	Y	97.783	1555
CU-09_407_A	Cornell	Stool	Control	MiSeq 300PE	E	Absence of aggregation	0.0	Y	97.672	1550
CU-09_410_C	Cornell	Stool	Control	MiSeq 300PE	A	Absence of aggregation	6.9	Y	97.672	1550
CU-09JW_1	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	F	Absence of aggregation	4.8	Y	97.672	1550
CU-09JW_2	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	B1	Aggregation	35.1	Y	98.115	1572
CU-13DK_1	Cornell	Intestinal Biopsy	UC	MiSeq 300PE	B2	Absence of aggregation	0.0	Y	97.894	1561
CU-13DK_9	Cornell	Intestinal Biopsy	UC	MiSeq 300PE	B1	Absence of aggregation	4.3	Y	98.115	1572
CU-14GK_1	Cornell	Intestinal Biopsy	CCD	MiSeq 300PE	B1	Aggregation	0.0	Y	97.783	1555
CU-15MH_1	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	B1	Absence of aggregation	0.0	Y	97.672	1550
CU-17LG_1	Cornell	Intestinal Biopsy	H or non IBD	MiSeq 300PE	C	Absence of aggregation	0.0	Y	97.672	1550
CU-18GB1	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	B1	Absence of aggregation	20.0	Y	98.115	1572
CU-19MD_1	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	B2	Absence of aggregation	0.0	Y	97.894	1561
CU-24LW_1	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	A	Absence of aggregation	0.0	Y	98.004	1567
CU-32SY_1	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	B1	Aggregation	8.1	Y	98.115	1572
CU-355_1	Cornell	Intestinal Biopsy	CCD	MiSeq 300PE	E	Absence of aggregation	0.0	Y	99.667	1650
CU-355_5	Cornell	Intestinal Biopsy	CCD	MiSeq 300PE	B1	Aggregation	21.7	Y	97.783	1555

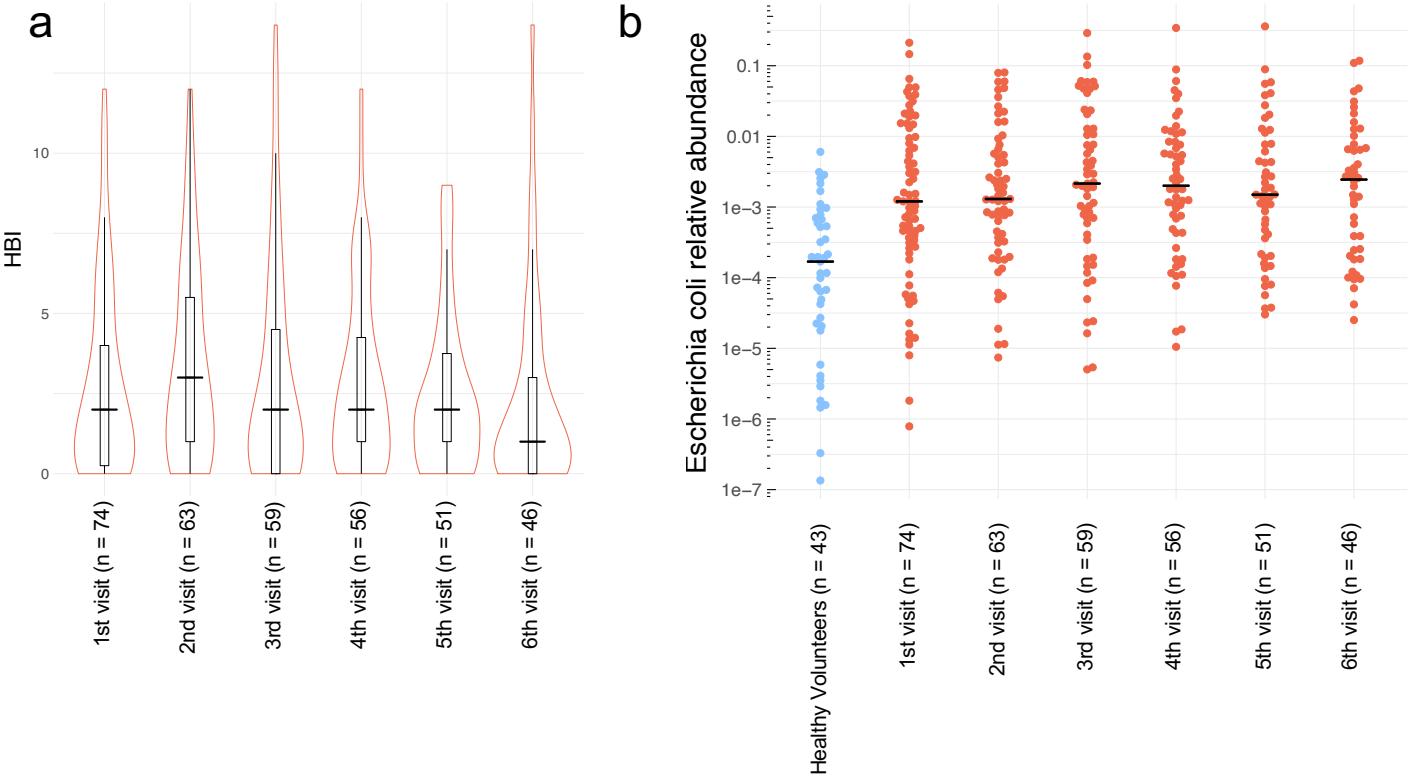
Supplementary Table 4

	Information							Mapping against FimH (LF82 as reference)		
Strain ID	Origine	Tissue / Source	Disease	Type of sequencing	Phylogroup quadruplex	Aggregation	%FimS ON	Presence of FimH	% identity LF82	bit score LF82
CU-35MN_1	Cornell	Intestinal Biopsy	H&non IBD	MiSeq 300PE	B1	Aggregation	33.3	Y	98.004	1567
CU-35MN_4	Cornell	Intestinal Biopsy	H&non IBD	MiSeq 300PE	E	Grey zone	9.4	Y	97.561	1544
CU-37RT_1	Cornell	Intestinal Biopsy	H&non IBD	MiSeq 300PE	C	Absence of aggregation	0.0	Y	97.894	1561
CU-37RT_2	Cornell	Intestinal Biopsy	H&non IBD	MiSeq 300PE	B2	Absence of aggregation	0.0	Y	97.783	1555
CU-38AW_1	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	B1	Aggregation	37.2	Y	98.115	1572
CU-39ES_1	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	B2	Absence of aggregation	0.0	Y	99.224	1628
CU-40EM_1	Cornell	Intestinal Biopsy	UC	MiSeq 300PE	A	Absence of aggregation	0.0	Y	97.672	1550
CU-41CB_1	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	B1	Absence of aggregation	0.0	Y	98.115	1572
CU-41CB_2	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	C	Absence of aggregation	0.0	N	NA	NA
CU-42ET_1	Cornell	Intestinal Biopsy	H&non IBD	MiSeq 300PE	B2	Grey zone	0.0	Y	99.667	1650
CU-43FK_1	Cornell	Intestinal Biopsy	H&non IBD	MiSeq 300PE	B1	Grey zone	3.1	Y	98.004	1567
CU-470_1	Cornell	Intestinal Biopsy	H&non IBD	MiSeq 300PE	F	Aggregation	0.0	Y	97.672	1550
CU-48JD_1	Cornell	Intestinal Biopsy	UC	MiSeq 300PE	B2	Aggregation	7.4	Y	100.000	1666
CU-50PB_1	Cornell	Intestinal Biopsy	H&non IBD	MiSeq 300PE	B2	Aggregation	0.0	Y	97.894	1561
CU-524_2	Cornell	Intestinal Biopsy	CCD	MiSeq 300PE	B1	Aggregation	8.1	Y	97.783	1555
CU-524_6	Cornell	Intestinal Biopsy	CCD	MiSeq 300PE	A	Absence of aggregation	0.0	Y	97.672	1550
CU-52CS_1	Cornell	Intestinal Biopsy	H&non IBD	MiSeq 300PE	C	Absence of aggregation	0	Y	97.894	1561
CU-532_9	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	B2	Aggregation	34.1	Y	99.557	1644
CU-538_10	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	F	Aggregation	7.4	Y	98.448	1589
CU-538_6	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	B1	Absence of aggregation	0.0	Y	98.004	1567
CU-541_1	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	B1	Absence of aggregation	0.0	Y	97.894	1561
CU-541_15	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	A	Absence of aggregation	0.0	Y	97.672	1550
CU-545_4	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	C	Absence of aggregation	0.0	N	NA	NA
CU-546_1	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	B2	Aggregation	18.2	Y	98.448	1589
CU-54AR_1	Cornell	Intestinal Biopsy	H&non IBD	MiSeq 300PE	A	Absence of aggregation	3.8	Y	97.672	1550
CU-552_2	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	B1	Aggregation	0.0	Y	97.783	1555
CU-55AS_1	Cornell	Intestinal Biopsy	H&non IBD	MiSeq 300PE	C	Aggregation	0.0	Y	97.672	1550
CU-568_3	Cornell	Intestinal Biopsy	CCD	MiSeq 300PE	B2	Absence of aggregation	0.0	N	NA	NA

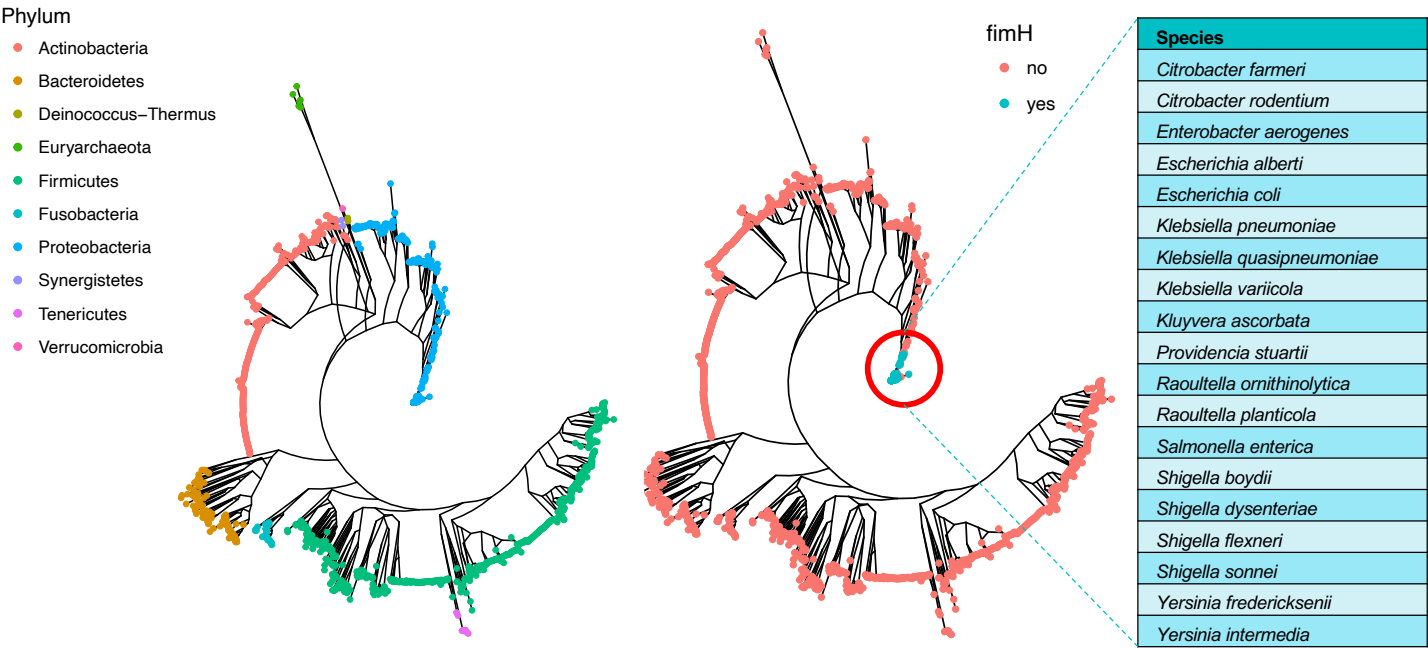
Supplementary Table 4

	Information							Mapping against FimH (LF82 as reference)		
Strain ID	Origine	Tissue / Source	Disease	Type of sequencing	Phylogroup quadruplex	Aggregation	%FimS ON	Presence of FimH	% identity LF82	bit score LF82
CU-576_1	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	E	Grey zone	5.9	Y	97.783	1555
CU-576_10	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	E	Grey zone	3.0	Y	97.783	1555
CU-578_1	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	E	Grey zone	0.0	Y	97.783	1555
CU-584_1	Cornell	Intestinal Biopsy	CCD	MiSeq 300PE	C	Absence of aggregation	0.0	Y	98.004	1567
CU-589_1	Cornell	Intestinal Biopsy	UC	MiSeq 300PE	B2	Absence of aggregation	0.0	Y	97.894	1561
CU-58PP_1	Cornell	Intestinal Biopsy	UC	MiSeq 300PE	B2	Aggregation	2.4	Y	97.894	1561
CU-601_1	Cornell	Intestinal Biopsy	H&non IBD	MiSeq 300PE	B1	Absence of aggregation	0.0	N	NA	NA
CU-602_1	Cornell	Intestinal Biopsy	UC	MiSeq 300PE	B2	Absence of aggregation	0.0	Y	98.004	1567
CU-603_1	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	A	Absence of aggregation	0.0	Y	97.453	1539
CU-60CM_1	Cornell	Intestinal Biopsy	UC	MiSeq 300PE	F	Absence of aggregation	0.0	Y	97.894	1561
CU-73EL_1	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	B1	Aggregation	30.9	Y	97.672	1550
CU-TI_1	Cornell	Intestinal Biopsy	ICD	MiSeq 300PE	C	Absence of aggregation	0.0	Y	97.894	1561

Supplementary Figure 1



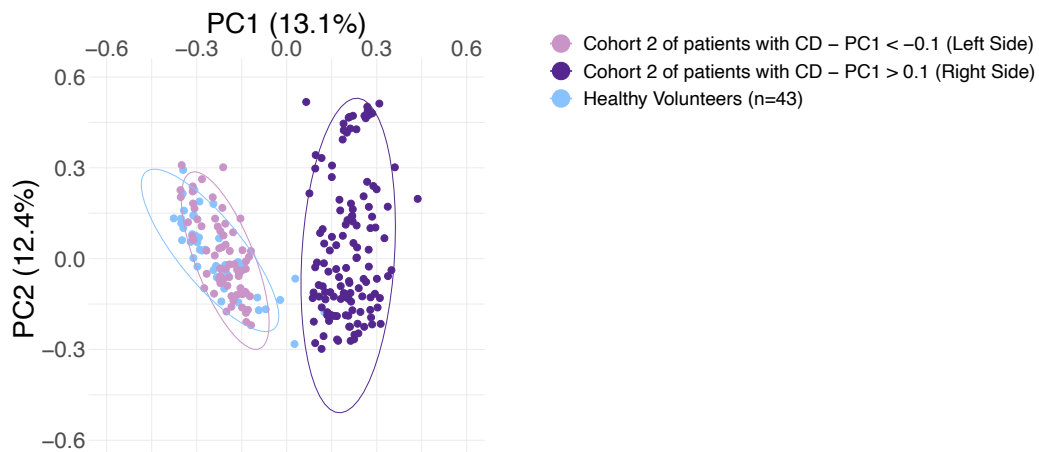
Supplementary Figure 2



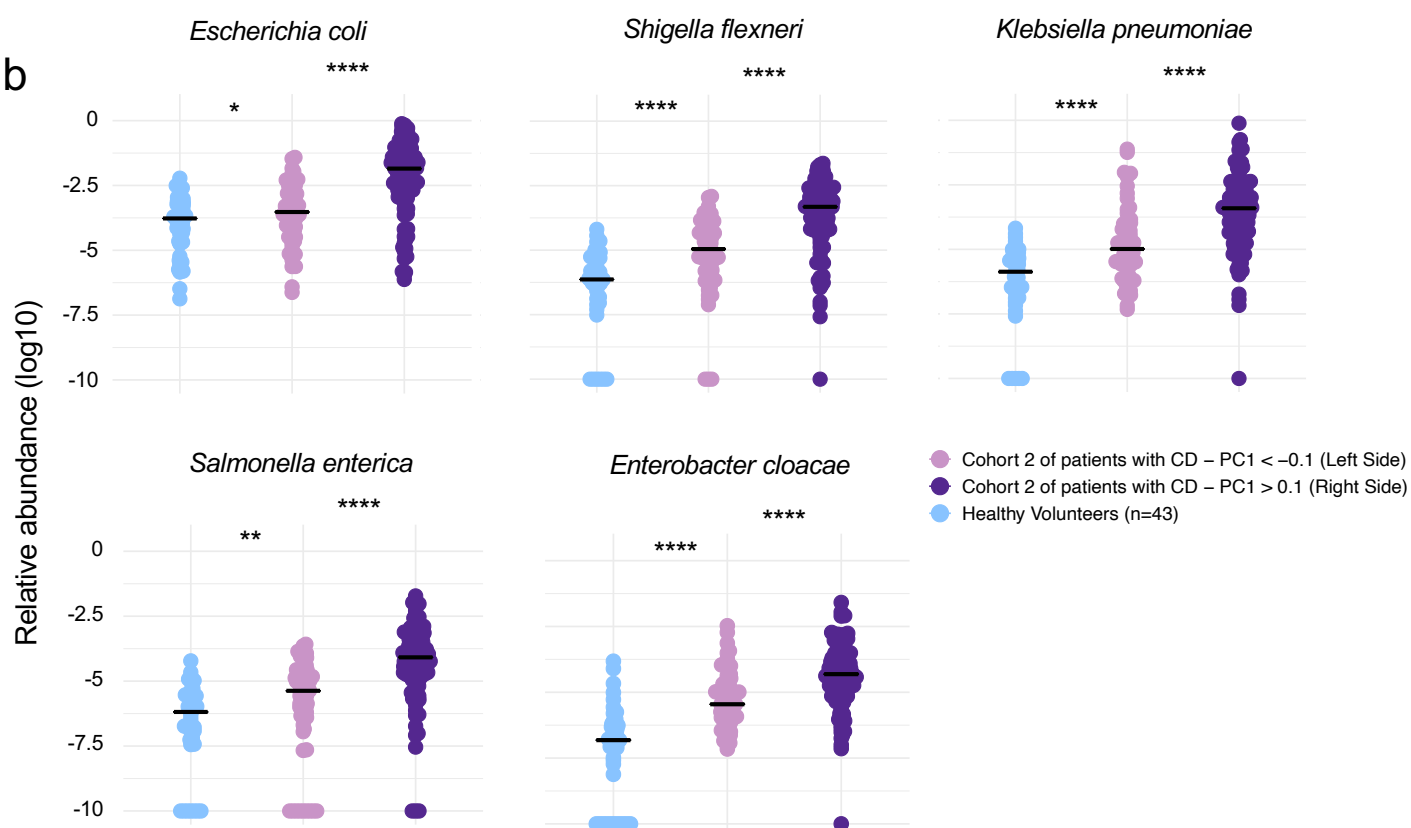
Species
<i>Citrobacter farmeri</i>
<i>Citrobacter rodentium</i>
<i>Enterobacter aerogenes</i>
<i>Escherichia alberti</i>
<i>Escherichia coli</i>
<i>Klebsiella pneumoniae</i>
<i>Klebsiella quasipneumoniae</i>
<i>Klebsiella varicola</i>
<i>Kluyvera ascorbata</i>
<i>Providencia stuartii</i>
<i>Raoultella ornithinolytica</i>
<i>Raoultella planticola</i>
<i>Salmonella enterica</i>
<i>Shigella boydii</i>
<i>Shigella dysenteriae</i>
<i>Shigella flexneri</i>
<i>Shigella sonnei</i>
<i>Yersinia fredericksonii</i>
<i>Yersinia intermedia</i>

Supplementary Figure 3

a

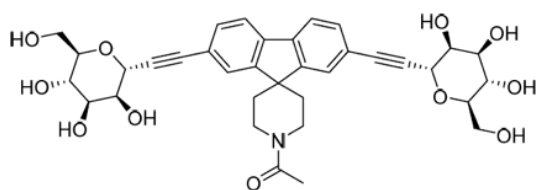


b

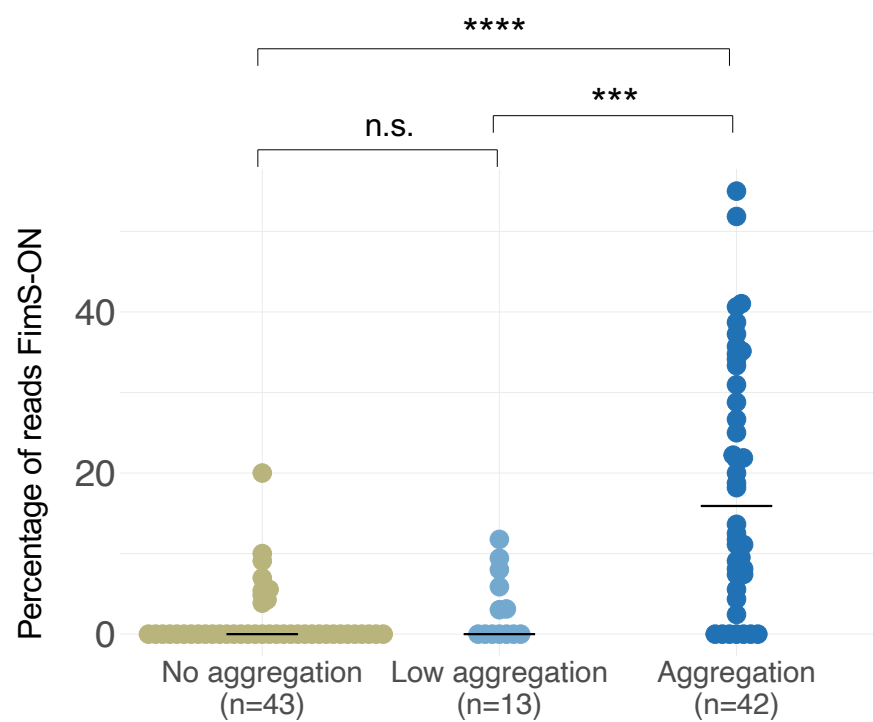


Supplementary Figure 4

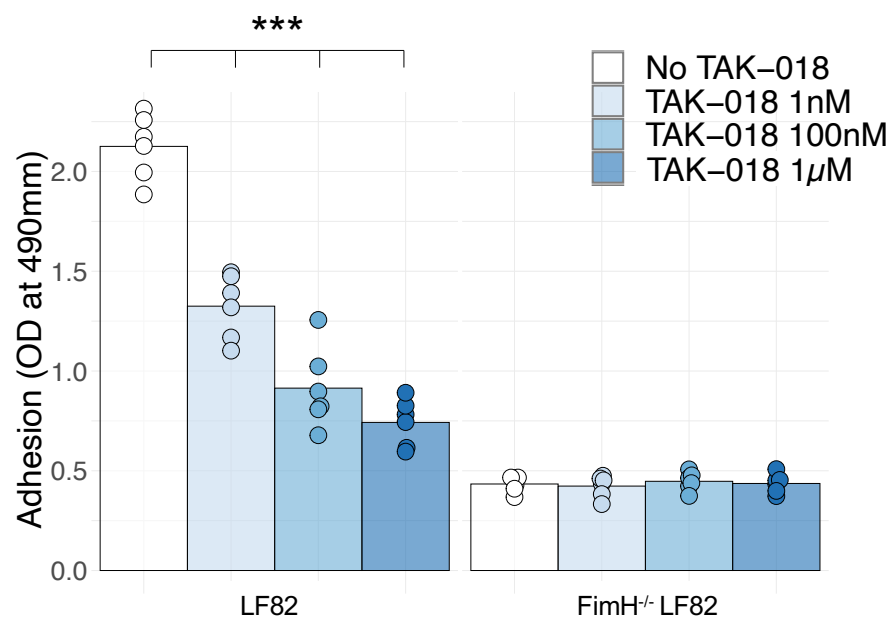
TAK-018



Supplementary Figure 5

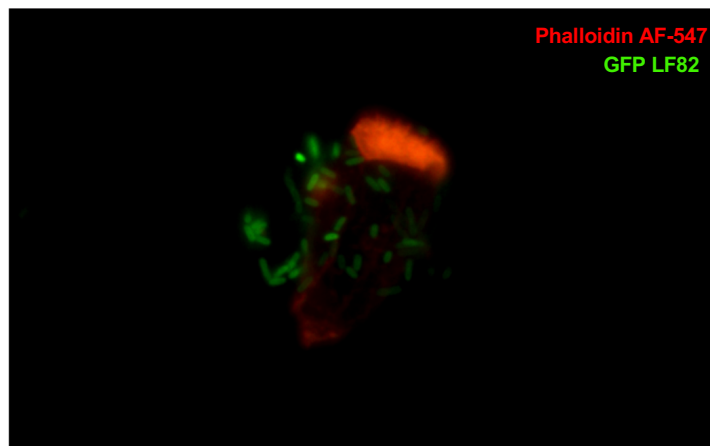
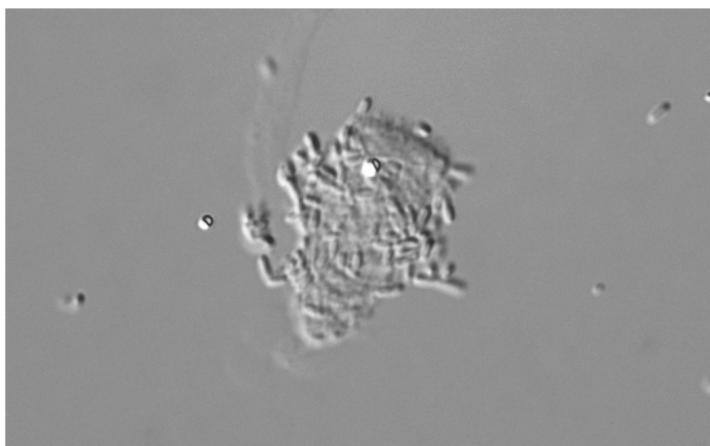


Supplementary Figure 6

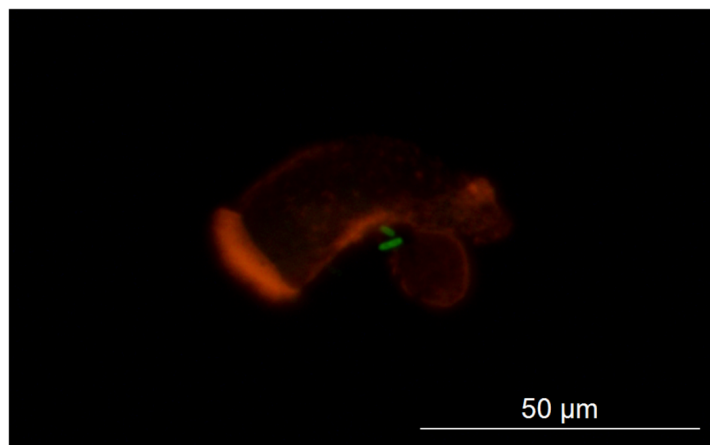


Supplementary Figure 7

GFP LF82



GFP LF82 + TAK-018 3 μ M



Supplementary Figure 8

