

Table S1 Scoring rules for disease activity index and colonic histology score

Rating Scale	Disease Activity Index ¹		
	Weight loss (%) ²	Stool Consistency	Occult Blood or gross bleeding
0	no weight loss	normal	negative
1	1-5	soft	positive within 60–120 s
2	5-10	very soft	positive within 30–60 s
3	10-15	diarrhea	positive within 10–30 s
4	>15	Watery feces	immediate positivity or gross bleeding

¹Disease activity index = combined score of weight loss, stool consistency, and occult blood or gross bleeding.

²Body weight change compared to initial weight.

Table S2 colonic histological score

Rating Scale	Histological Score ¹			
	Epithelium loss (%)	Crypt damage	Depletion of goblet cells	Infiltration of inflammatory cells
0	None	None	None	None
1	0.0-5.0%	0.0-10.0%	Mild	Mild
2	5.0-10.0%	10.0-20.0%	Moderate	Moderate
3	Over 10.0%	Over 20.0%	Severe	Severe

¹Histology score for each mouse was a sum of the score of Epithelium loss,Crypt damage,Depletion of goblet cells,Infiltration of inflammatory cells

Table S3 Colonic immunofluorescence protein expression level

Taxonomy	Average relative abundance (%)											
	NC	DSS	PRE	Probio-M8	PC-01	PM8	SD_NC	SD_DSS	SD_PRE	SD_Probio-M8	SD_PC-01	SD_PM8
ZO-1	61.78	19.02	18.17	45.39	26.1	39.05	10.51	7.84	10.82	14.65	13.99	22.6
MUC2	20.95	4.31	7.01	7.19	15.33	7.8	4.91	3.83	3.53	4.15	2.32	6.53
Occludin	13.52	4.55	10.29	15.04	13.93	15.94	1.19	0.17	1.4	0.81	2.22	5.92

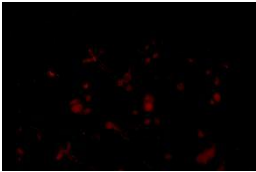
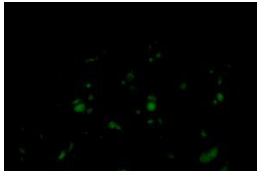
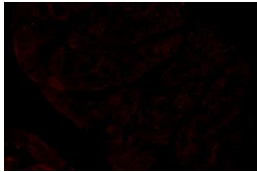
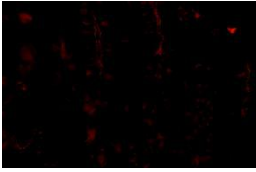
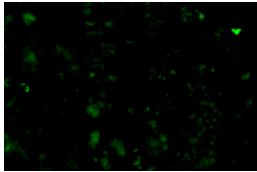
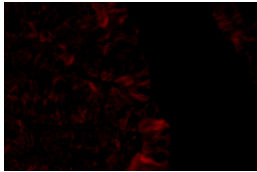
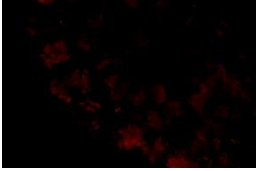
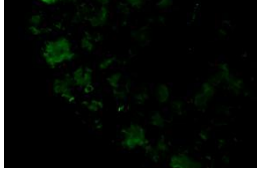
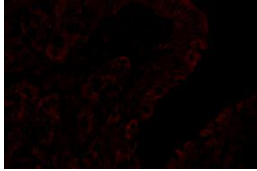
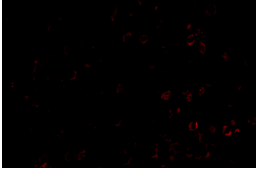
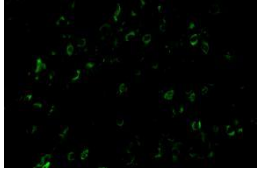
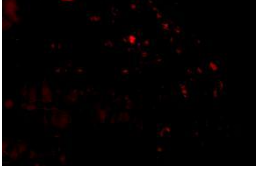
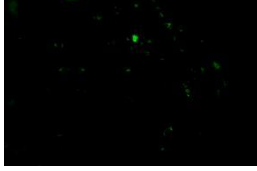
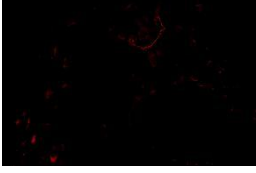
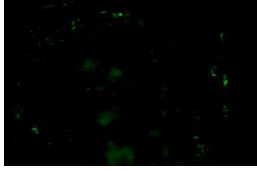
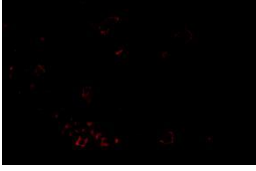
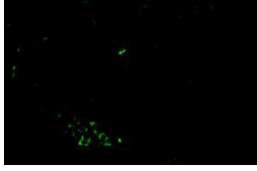
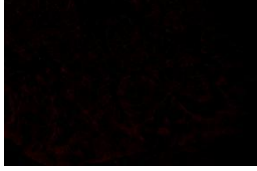
Table S4 Serum biomarker levels

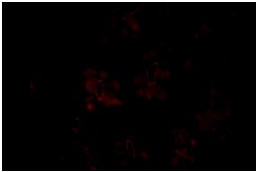
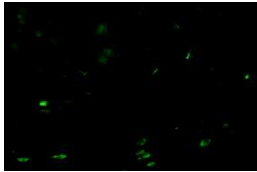
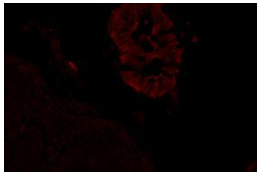
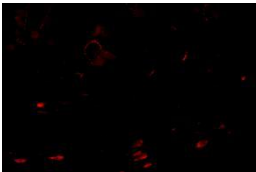
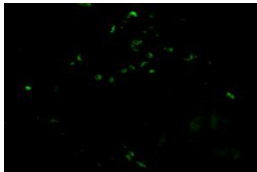
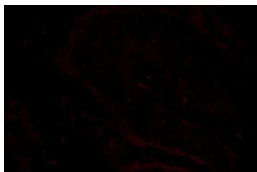
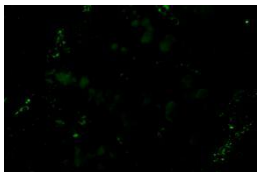
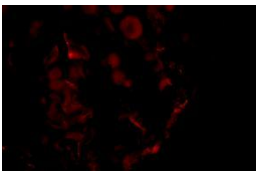
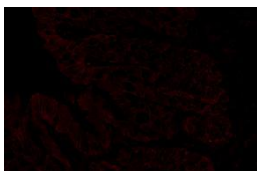
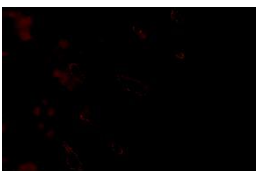
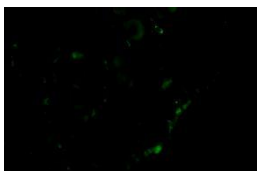
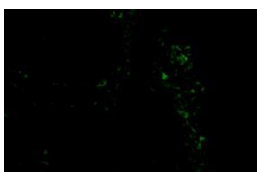
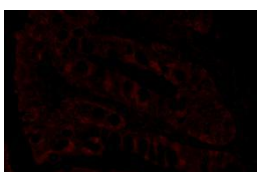
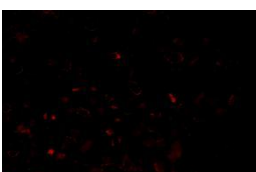
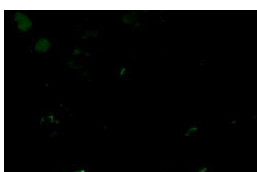
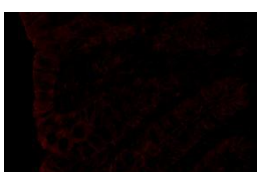
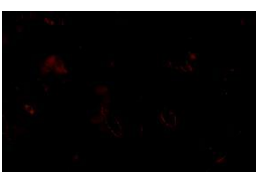
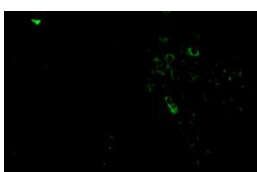
Taxonomy	Average relative abundance (%)											
	NC	DSS	PRE	Probio-M8	PC-01	PM8	SD_NC	SD_DSS	SD_PRE	SD_Probio-M8	SD_PC-01	SD_PM8
LPS	7.5	20.75	16.1	9.7	13.99	13.37	1.14	2.31	2.31	1.4	2.32	2.27
IL-17A	19.24	28.21	20.33	26.67	23.58	23.58	3.12	3.72	3.02	2.9	3.88	3.7
1L-6	50.16	93.52	80.84	76.3	70.16	74.75	10.84	11.71	5.73	8.73	11	8.5
IL-1β	47.98	94.28	75.56	75.01	76.29	69.28	10.66	18.82	8.15	10.3	14.62	13.58
TNF-α	378.69	621.65	556.73	518.89	487.89	389.94	69.12	101.72	80.83	78.33	84.45	67.82
IL-10	47.98	94.28	75.56	75.01	76.29	69.28	10.66	18.82	8.15	10.3	14.62	13.58
SOD	80.93	41.32	42	61.99	53.07	53.33	7.33	9.26	6.99	9.2	8.29	6.68
GSH-PX	148.44	65.23	84.47	126.49	99.69	123.13	21.63	17.07	18.78	20.36	27.38	7.52
MDA	4.23	12.61	11.32	5.21	8.25	8.64	0.93	2.08	1.44	0.78	1.53	1.86

Table S5 Correspondence table of functional pathways annotated to species

cluster	Pathway	Pathway name
1	PWY-6897	thiamine diphosphate salvage II
1	PWY-7357	thiamine phosphate formation from pyrithiamine and oxythiamine (yeast)
1	PWY-7851	coenzyme A biosynthesis II (eukaryotic)
1	PWY-I9	L-cysteine biosynthesis VI (from L-methionine)
1	COA-PWY-1	superpathway of coenzyme A biosynthesis III (mammals)
1	HISTSYN-PWY	L-histidine biosynthesis
2	LIPA-CORESIN-PWY	lipid A-core biosynthesis (E. coli K-12)
2	PWY-6467	Kdo transfer to lipid IVA III (Chlamydia)
2	PWY-6467	Kdo transfer to lipid IVA III (Chlamydia)
2	PWY-7039	phosphatidate metabolism, as a signaling molecule
3	P122-PWY	heterolactic fermentation
4	RHAMCAT-PWY	L-rhamnose degradation I
5	PWY-6151	S-adenosyl-L-methionine salvage I
5	PWY-7851	coenzyme A biosynthesis II (eukaryotic)
5	PWY-5097	L-lysine biosynthesis VI
5	PWY-6143	CMP-pseudamate biosynthesis
5	PWY-6143	CMP-pseudamate biosynthesis
5	PWY-2942	L-lysine biosynthesis III
5	PWY-5686	UMP biosynthesis I
5	PWY-7790	UMP biosynthesis II
5	PWY-7791	UMP biosynthesis III

6	PWY-4041	γ-glutamyl cycle
6	SULFATE-CYS-PWY	superpathway of sulfate assimilation and cysteine biosynthesis
6	PWY0-1261	anhydromuropeptides recycling I
6	PWY-6606	guanosine nucleotides degradation II
6	PWY4FS-7	phosphatidylglycerol biosynthesis I (plastidic)
6	PWY4FS-8	phosphatidylglycerol biosynthesis II (non-plastidic)
6	GLUCOSE1PMETAB-PWY	glucose and glucose-1-phosphate degradation
6	PWY-6284	superpathway of unsaturated fatty acids biosynthesis (E. coli)
6	PWY-5913	partial TCA cycle (obligate autotrophs)
6	SO4ASSIM-PWY	assimilatory sulfate reduction I
7	PWY0-1241	ADP-L-glycero-β-D-manno-heptose biosynthesis
7	PWY-6628	superpathway of L-phenylalanine biosynthesis
7	PWY-7761	NAD salvage pathway II (PNC IV cycle)
7	PWY-5265	peptidoglycan biosynthesis II (staphylococci)
8	PWY66-389	phytol degradation
8	PWY0-1277	3-phenylpropanoate and 3-(3-hydroxyphenyl)propanoate degradation

	ZO-1	MUC2	Occludin
NC			
			
			
DSS			
			
			
PRE			

			
			
Probio-M 8			
			
			
PC-01			
			
			

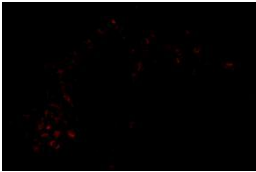
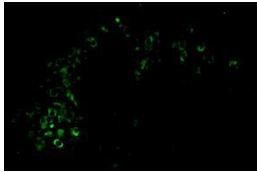
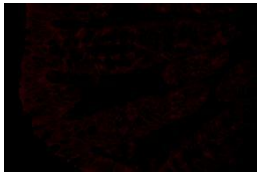
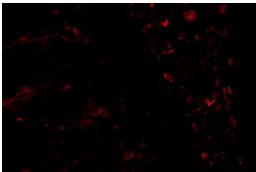
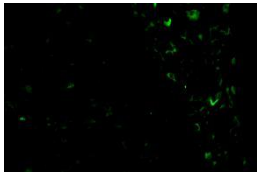
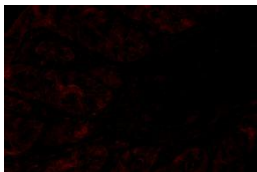
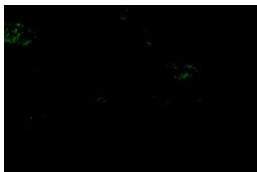
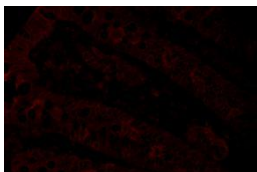
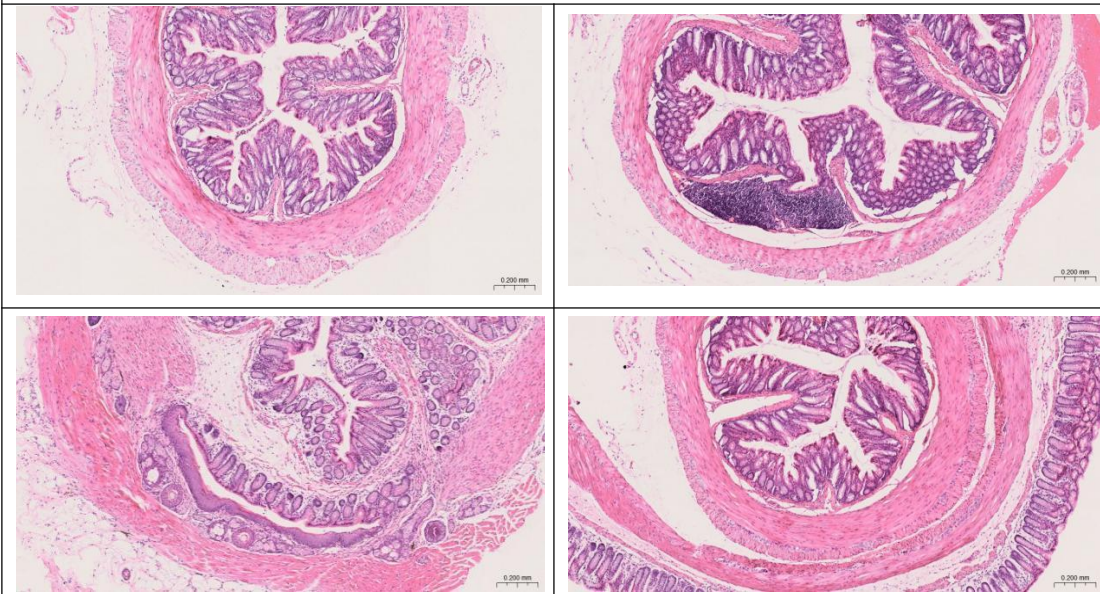
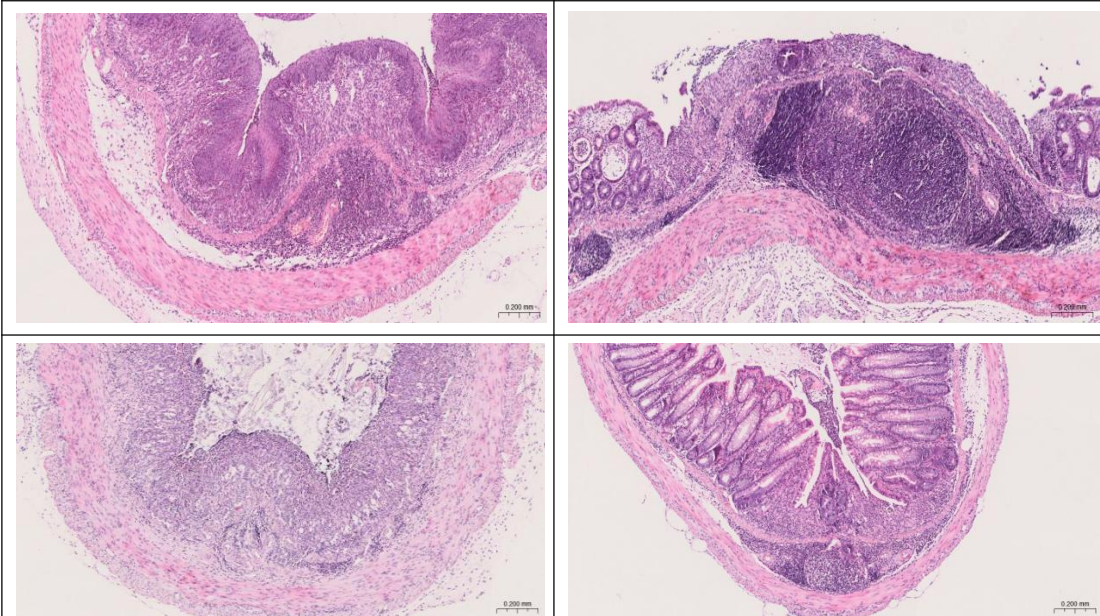
PM8			
			
			

Image of colonic pathological section

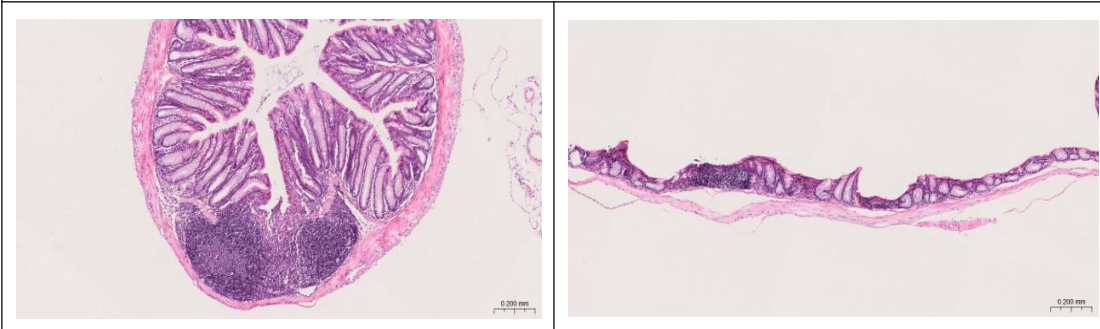
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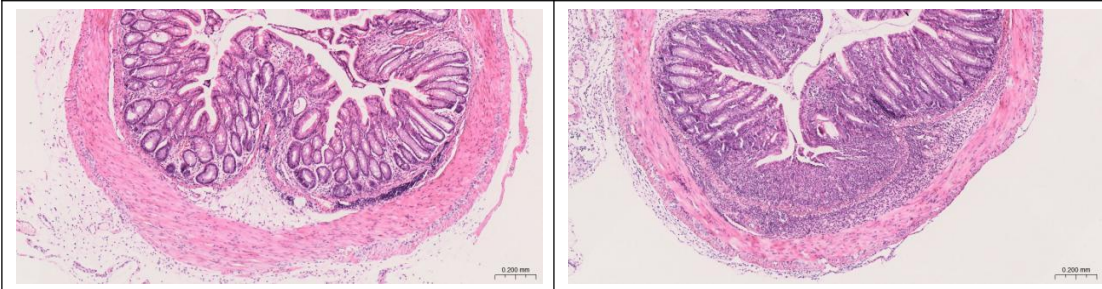


DSS

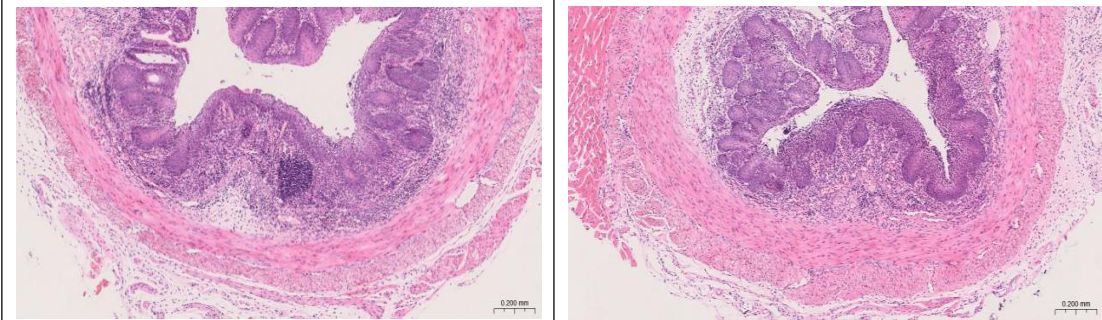
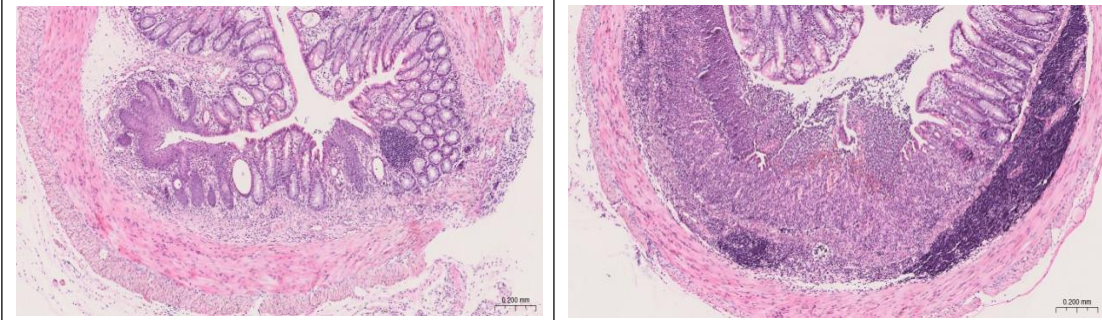


Probio-M8

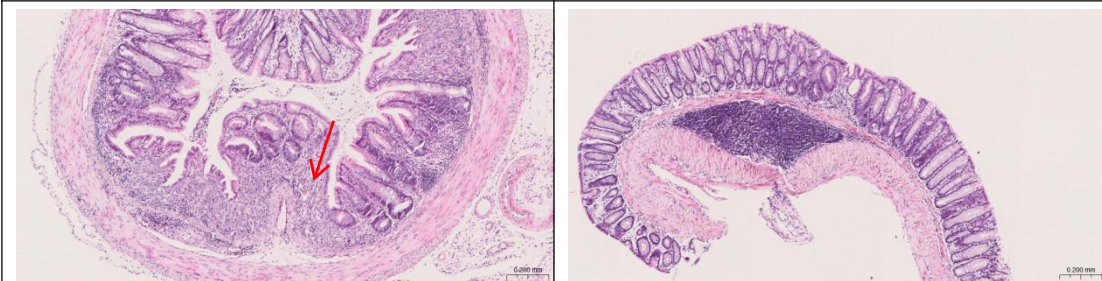
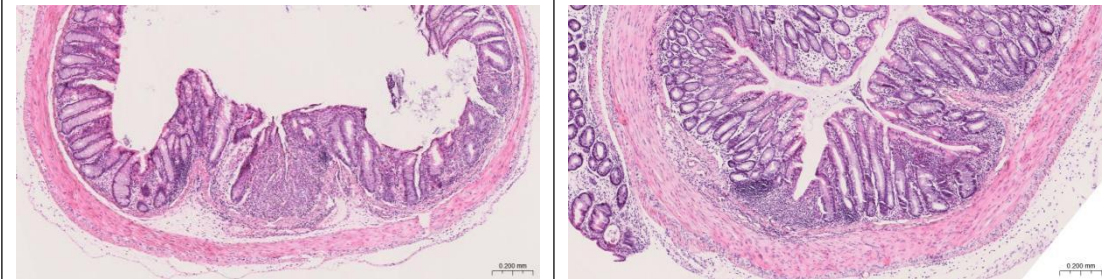




PC-01



PM8



PRE

