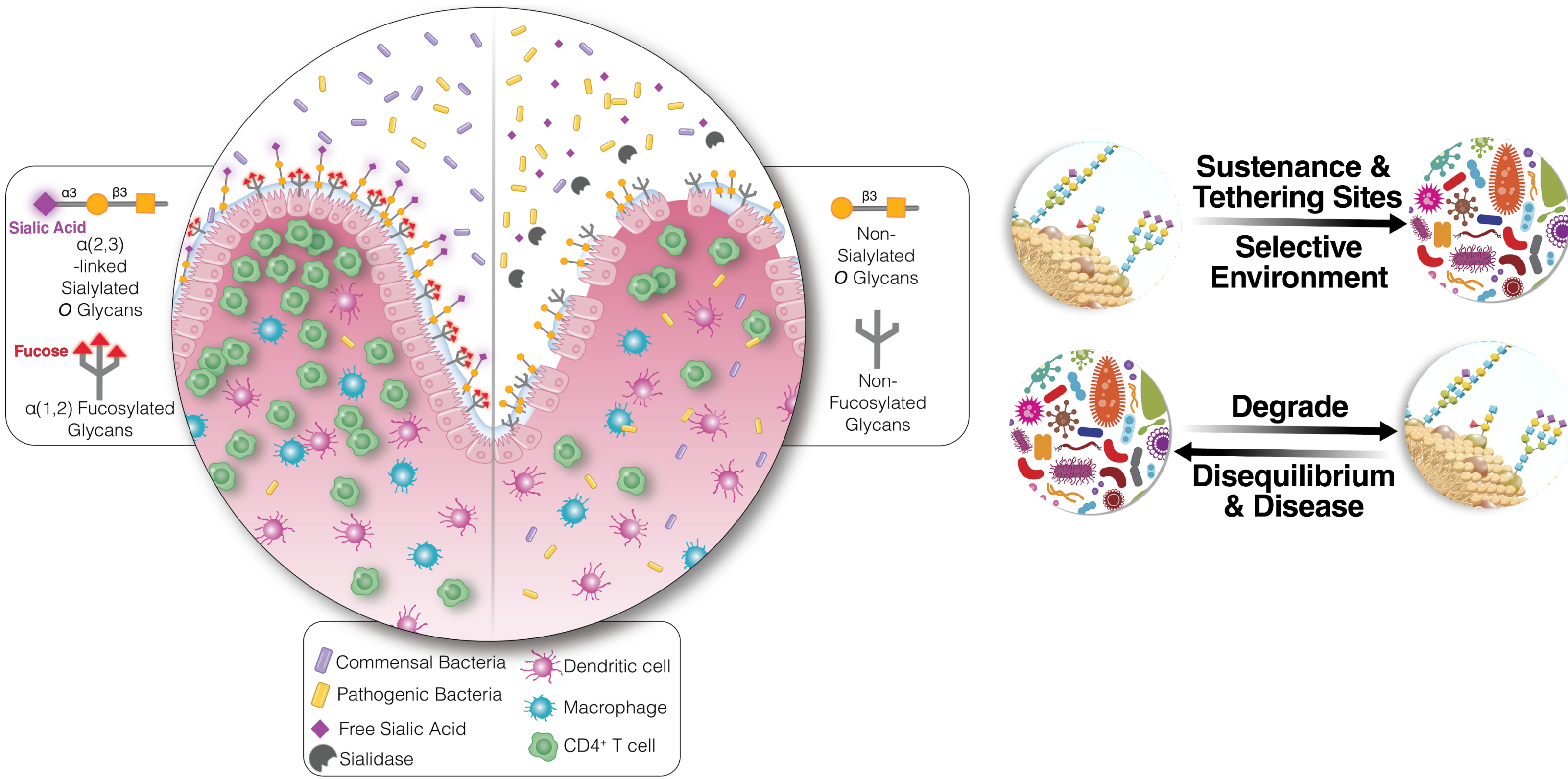


Glycomic Determinants of Gut Microbial Dysbiosis and Translocation During Suppressed HIV Infection

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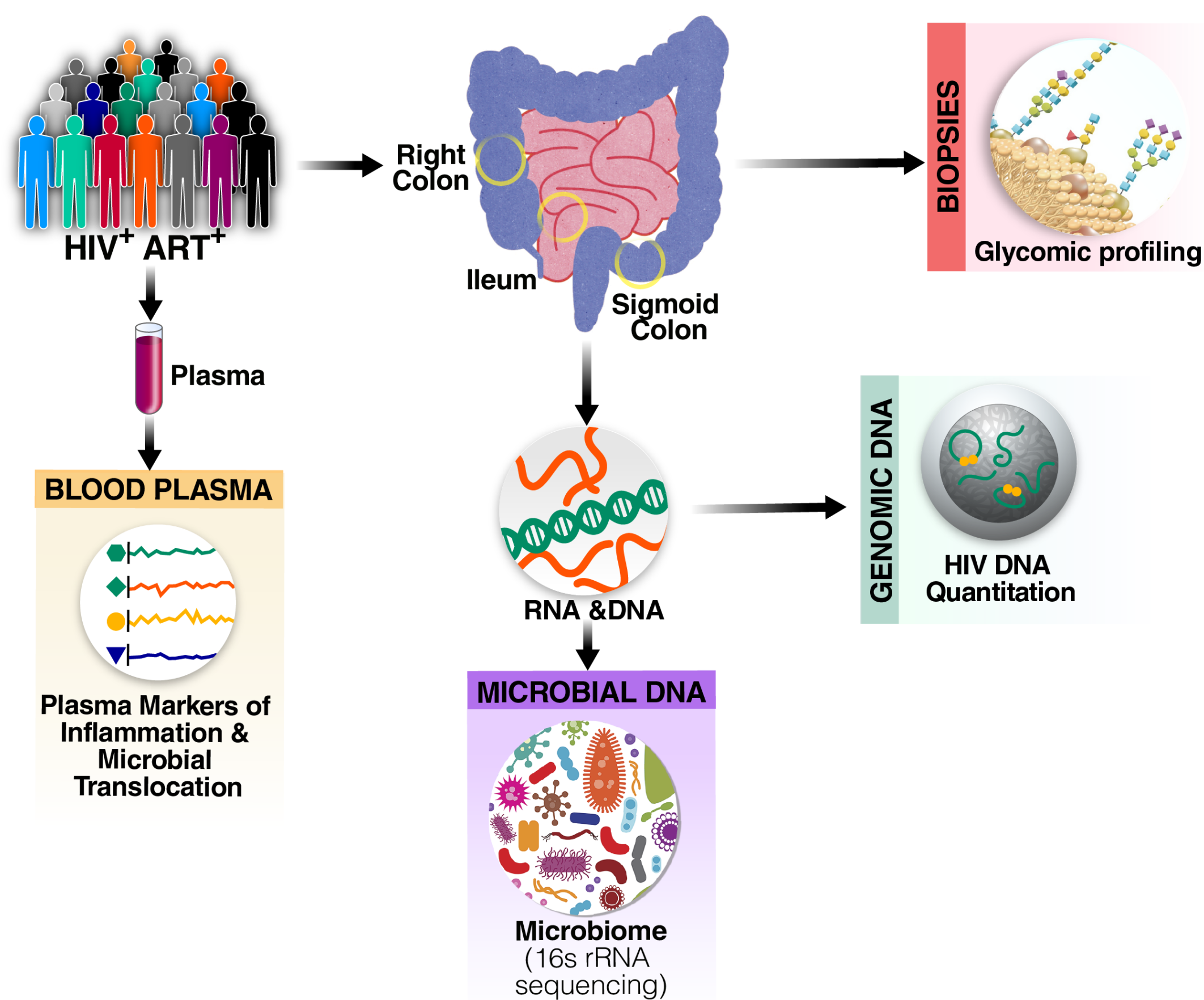
Introduction



- An emerging paradigm suggests that gut glycosylation is a key force in maintaining a homeostatic relationship between the gut and its microbiota. In the general population, changes in the gut glycome can alter the gut microbial composition, leading to microbial dysbiosis and gut inflammation.
- In HIV-infected individuals, microbial dysbiosis and translocation contribute to the vicious cycle between HIV and immune activation/ inflammation. This cycle likely contributes to the development of non-AIDS inflammatory-related illnesses and HIV persistence. However, how gut glycosylation machinery contributes to this cycle is yet to be characterized.
- Here we investigated the role of altered gut glycans in modulating the gut microbiome and mediating HIV-associated gut inflammation.

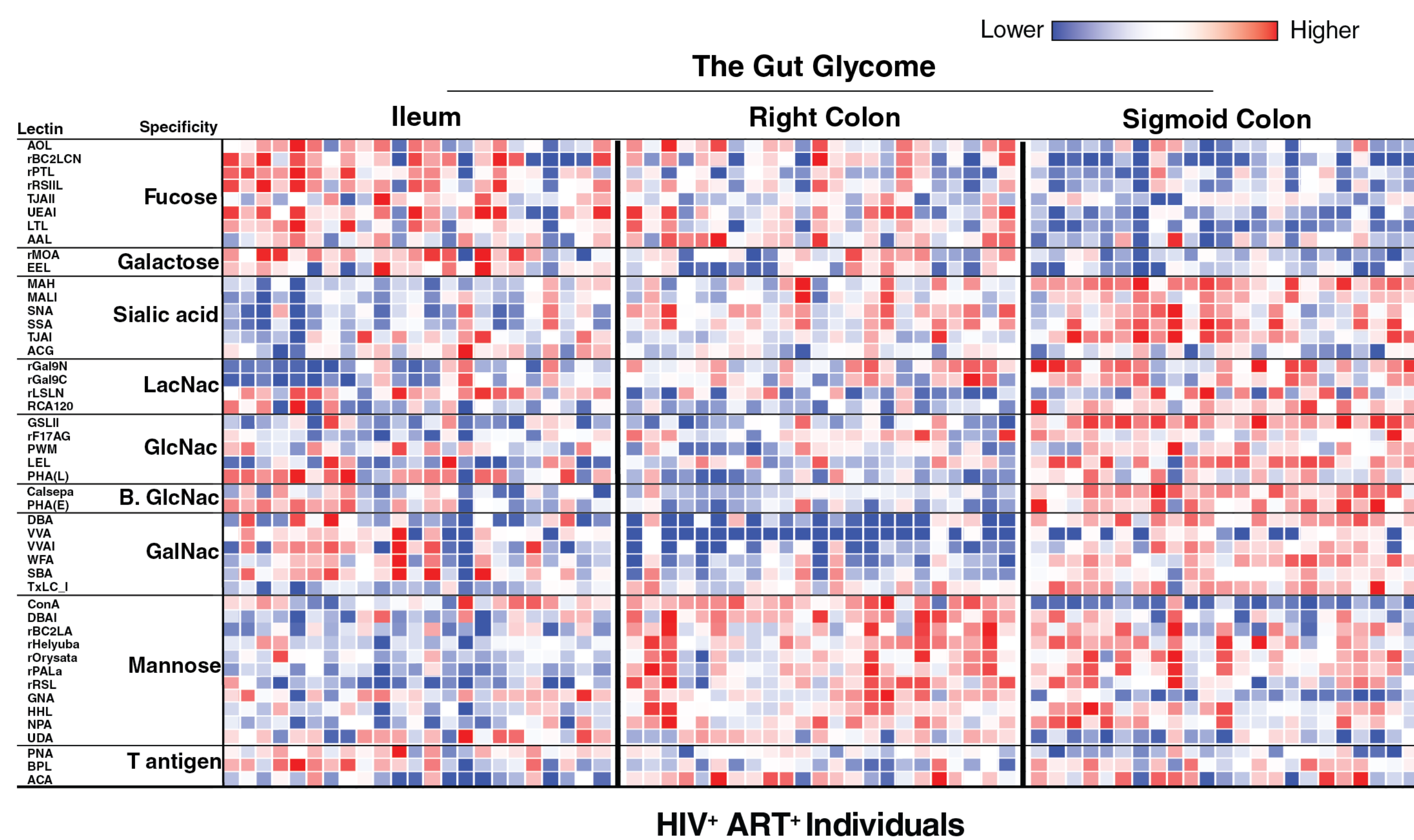
Methods

Characteristic	Value
n	20
Gender (% male)	75
Ethnicity	75% AA, 15% HA, 10% CAU
Age Mean yrs (SD)	51.7 (4.9)
HIV Viral Load (copies/ml)	<40
CD4 Count Mean cells/mm ³ (SD)	500 (261.3)
BMI Mean (SD)	25.7 (3.9)

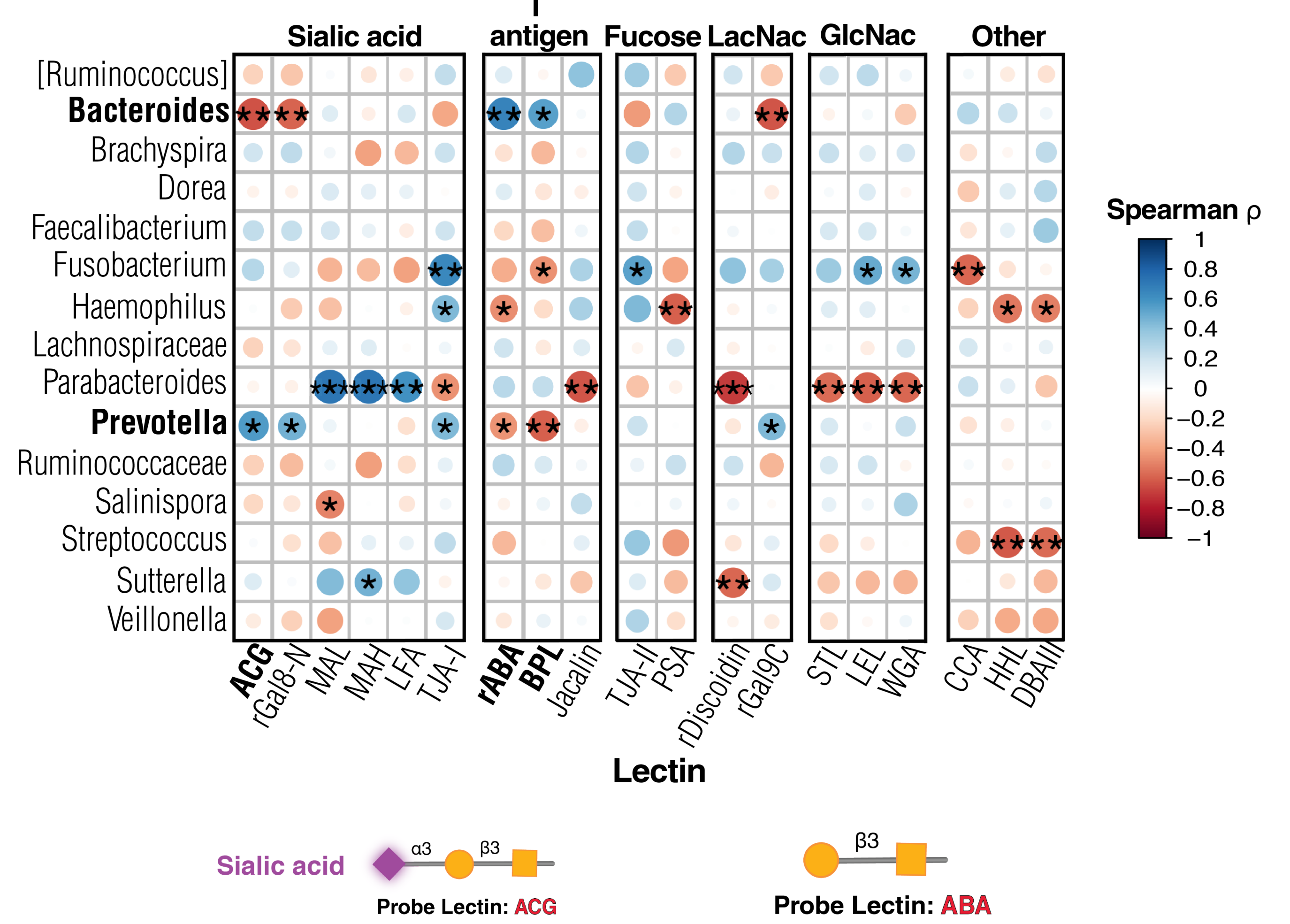


Results

1) The gut glycome is compartmentalized between ileum, right colon, and sigmoid colon. A decrease in fucose, an increase of sialic acid, and an increase of mannose when going from the ileum to the colon. $FDR < 0.05$. Permanova test on euclidean distances < 0.05



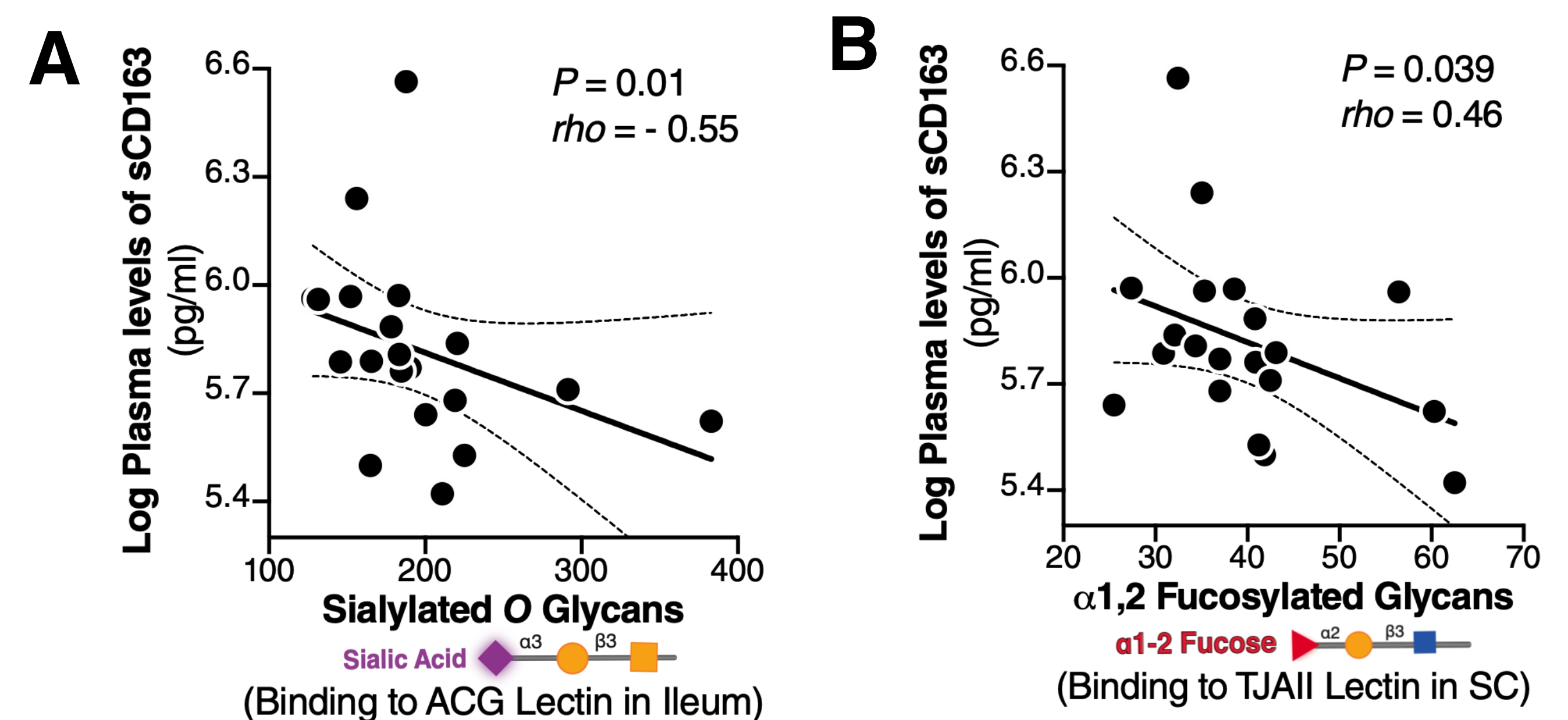
2) Mucosal glycosylation may play a role in microbial composition shift during ART-suppressed HIV infection. Increasing levels of Bacteroides genus correlate with lower sialylated glycans and higher hypo-sialylated glycans (in particular, Gal-GalNAc, also known as T-antigen or TF-antigen). These correlations are compatible with what known that Bacteroides release sialidase.



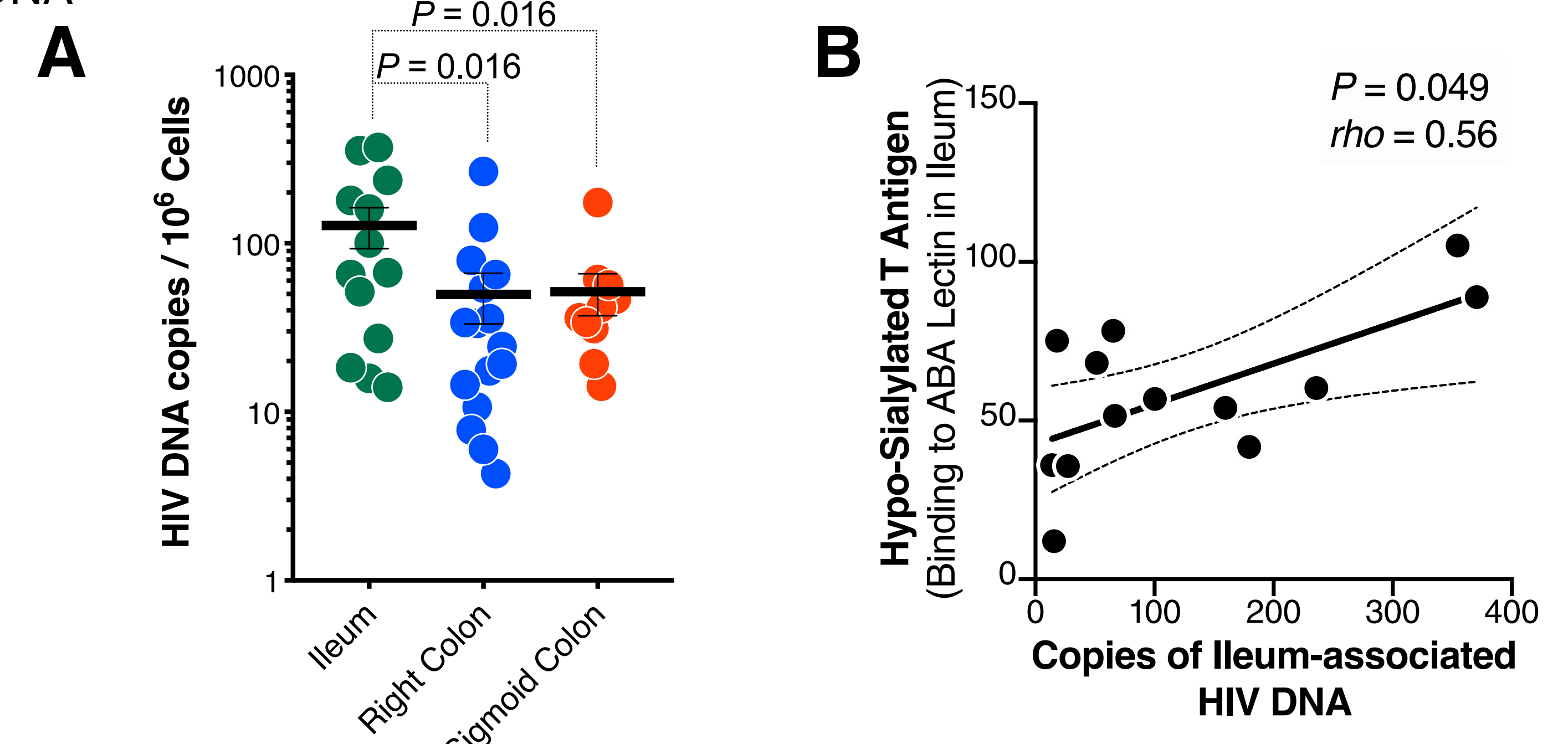
3) Mucosal sialic-acid catabolism and gut fucosylation associate with markers of microbial diversity and dysbiosis during ART-suppressed HIV infection. (A) Correlations with alpha diversity (decreased in HIV infection; the higher the better) and with (B) Bacteroidetes/Firmicutes (increased in HIV infection; the higher the worse)

Panel	P	r	Glycan	Lectin	Metric	Tissue Type
A	0.013	0.55	Sialylated O glycans	ACG	Shannon	Ileum
	0.016	0.53	LacNac, Sialic acid	rGal8N	Shannon	Ileum
	0.001	-0.68	T Antigen, Mostly Hypo-Sialylated	rABA	Shannon	Ileum
	0.005	-0.6	T Antigen, Mostly Hypo-Sialylated	DBA	Shannon	Ileum
	0.032	0.48	α 1,2 Fucose	TJAI	Richness	Ileum
B	0.049	-0.45	Sialylated O glycans	ACG		Ileum
	0.003	0.64	T Antigen, Mostly Hypo-Sialylated	rABA		Ileum
	0.006	0.6	T Antigen, Mostly Hypo-Sialylated	DBA		Ileum
	0.01	0.56	T Antigen, Mostly Hypo-Sialylated	HPA		Ileum
	0.009	-0.57	α 1,2 Fucose	TJAI		Ileum

4) Mucosal sialic-acid catabolism and gut fucosylation associate with markers of inflammation during ART-suppressed HIV infection. (A) Levels of sialylated O-glycans in the ileum correlated with lower levels of sCD163. (B) Mucosal-associated α 1-2 fucose correlated with lower plasma levels of sCD163 in sigmoid colon.



5) Glycomic T antigen correlates with ileum-associated HIV DNA during ART-suppressed HIV infection. (A) Total HIV DNA distribution between tissues. (B) Levels of hypo-sialylated glycans correlated with higher Ileum-associated total HIV DNA



Conclusions

- Our pilot study provides the first proof-of-concept evidence that differential gut glycomic patterns (mainly sialylated and fucosylated glycans) support distinct microbiome compositions that predispose to microbial translocation, inflammation, and HIV persistence.
- Our data are consistent with previous population reports which demonstrated that sialic acid catabolism drives microbial dysbiosis and intestinal inflammation and that gut fucosylation sustains host-commensal symbiosis and prevents gut inflammation.
- Exploiting gut glycosylation machinery may allow the design of strategies to manipulate it to prevent/delay the development of HIV-associated co-morbidities.