

# Silverman - IgA deficiency destabilizes immune homeostasis towards intestinal microbiota and increases the risk of systemic immune dysregulation

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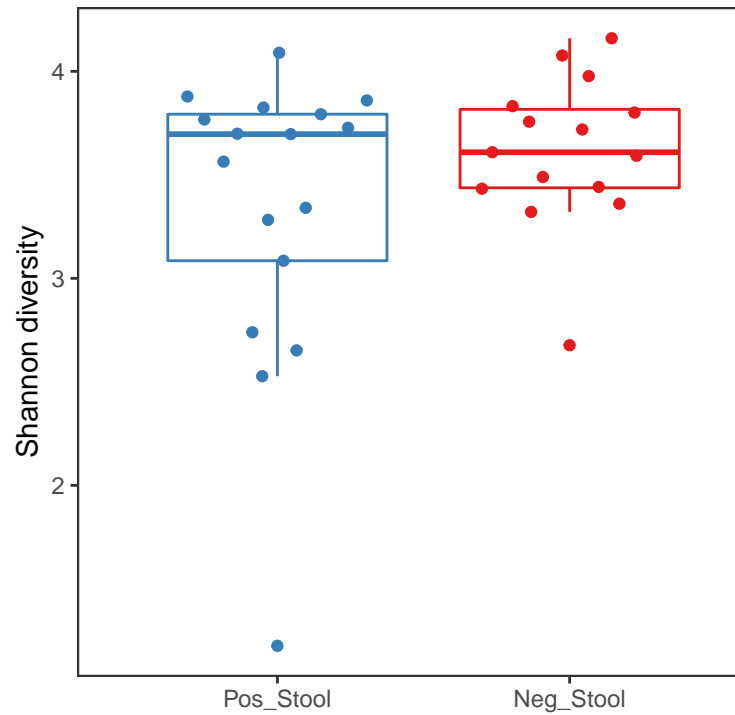
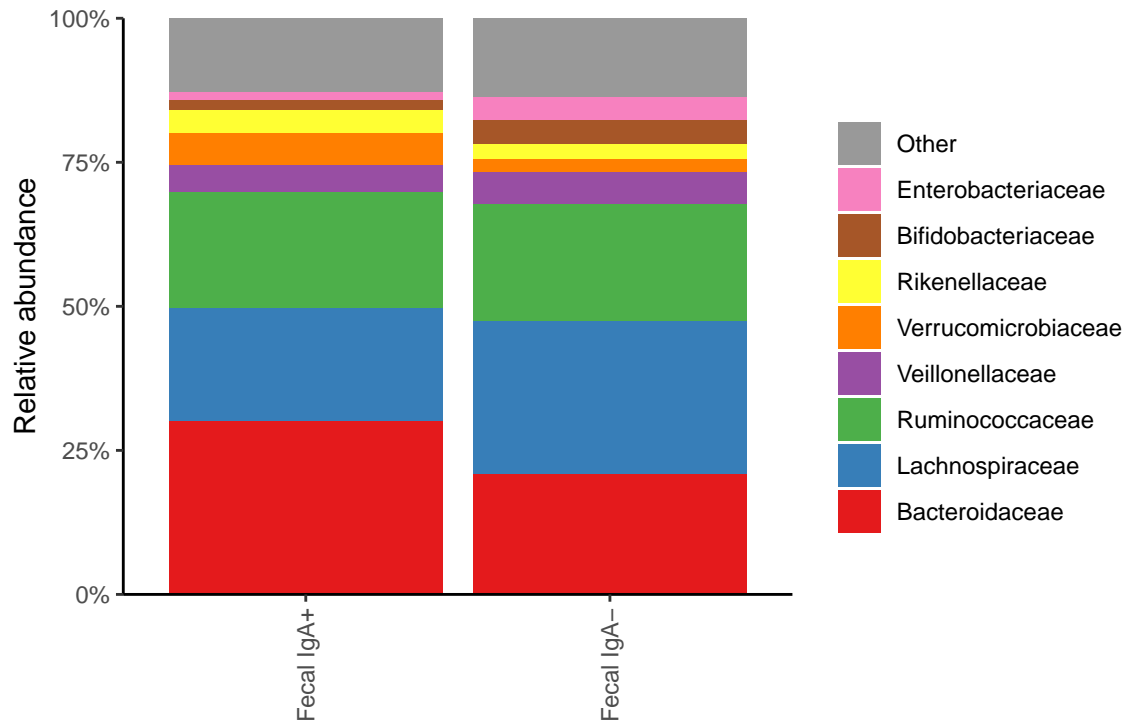
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## Unsorted fecal analysis

Number of samples in each study group and study day.

Table 1: Number of subjects in each household.

F03	F11	F14	F33	F36	F46	F47	F48	F49	F50	F51	F52	F54	F59	F63
2	2	2	2	2	2	2	2	3	2	2	3	2	2	2

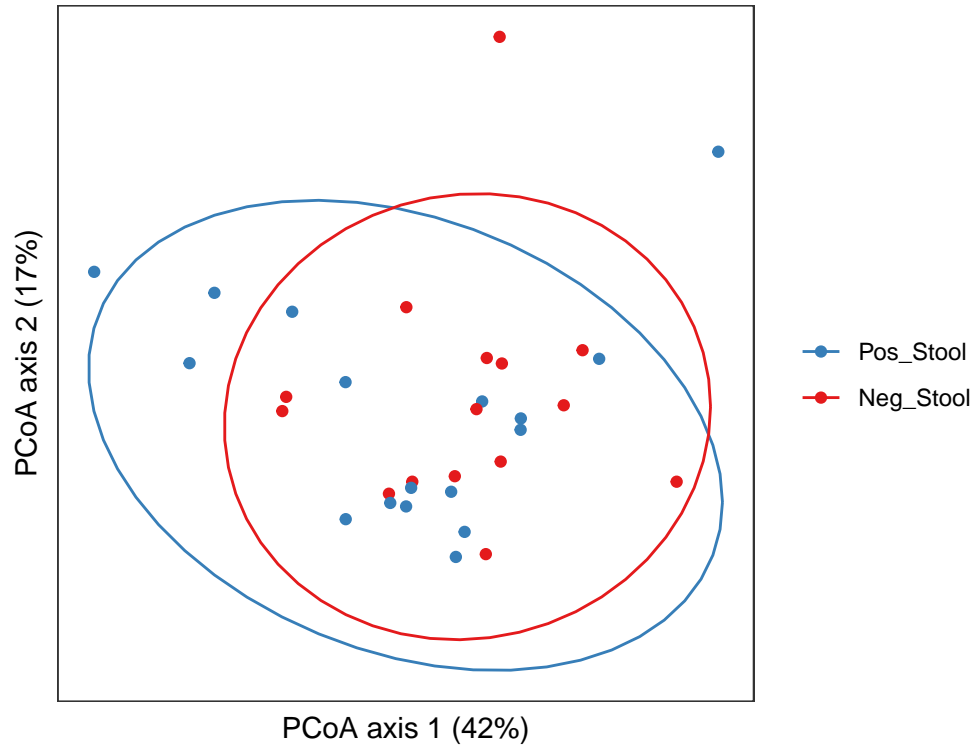


Linear models were used to estimate the difference between cases and controls for each categorization.

term	estimate	std.error	statistic	p.value
Pos - Neg Stool	0.28	0.21	1.4	0.19

Linear mixed effects models were used to estimate the difference between cases and controls for each categorization. Family IDs were used as random effects.

term	Value	Std.Error	DF	t.value	p.value
Pos - Neg Stool	0.25	0.18	16	1.4	0.19



PERMANOVA test on weighted UniFrac distances to test if the centroids of the study groups can be distinguished from each other.

Term	Df	F.Model	R2	p.value
Analysis4	1	1.4	0.044	0.2

## FACS samples - stool only IgA and IgM sorted

Table 5: Sampled populations from each subject.

	IgA-IgM-IgG-	IgA+IgM-	IgM+IgA-	IgM+IgA+
<b>F03.1</b>	1	1	1	1
<b>F03.2</b>	1	0	1	0
<b>F11.1</b>	1	0	1	0
<b>F11.2</b>	1	1	1	1
<b>F33.1</b>	1	0	1	0
<b>F33.2</b>	1	1	1	1
<b>F36.1</b>	1	0	1	0
<b>F36.2</b>	1	1	1	1
<b>F46.1</b>	1	0	1	0
<b>F46.2</b>	1	1	1	1
<b>F47.1</b>	1	0	1	0
<b>F47.2</b>	1	1	1	1

	IgA-IgM-IgG-	IgA+IgM-	IgM+IgA-	IgM+IgA+
<b>F48.1</b>	1	0	1	0
<b>F48.2</b>	1	1	1	1
<b>F49.1</b>	1	0	1	0
<b>F49.2</b>	1	1	1	1
<b>F49.3</b>	1	1	1	1
<b>F50.1</b>	1	1	1	1
<b>F50.2</b>	1	1	1	1
<b>F51.1</b>	1	0	1	0
<b>F51.2</b>	1	1	1	1
<b>F52.1</b>	1	0	1	0
<b>F52.2</b>	1	1	1	1
<b>F52.3</b>	1	1	1	1
<b>F54.1</b>	1	0	1	0
<b>F54.2</b>	1	1	1	1
<b>F59.1</b>	1	0	1	0
<b>F59.2</b>	1	0	1	0
<b>F63.1</b>	1	0	1	0
<b>F63.2</b>	1	1	1	1

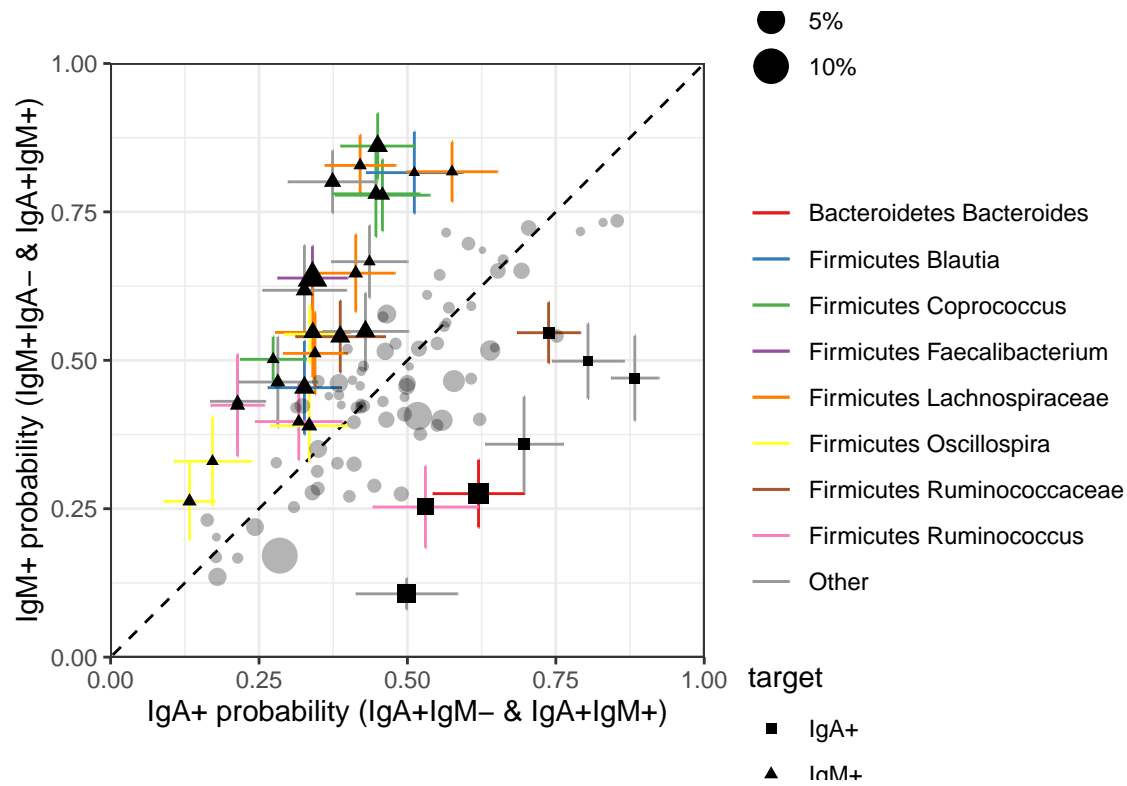
Table 6: Total number of populations sequenced.

IgA-IgM-IgG-	IgA+IgM-	IgM+IgA-	IgM+IgA+
30	16	30	16

### Looking at healthy population only

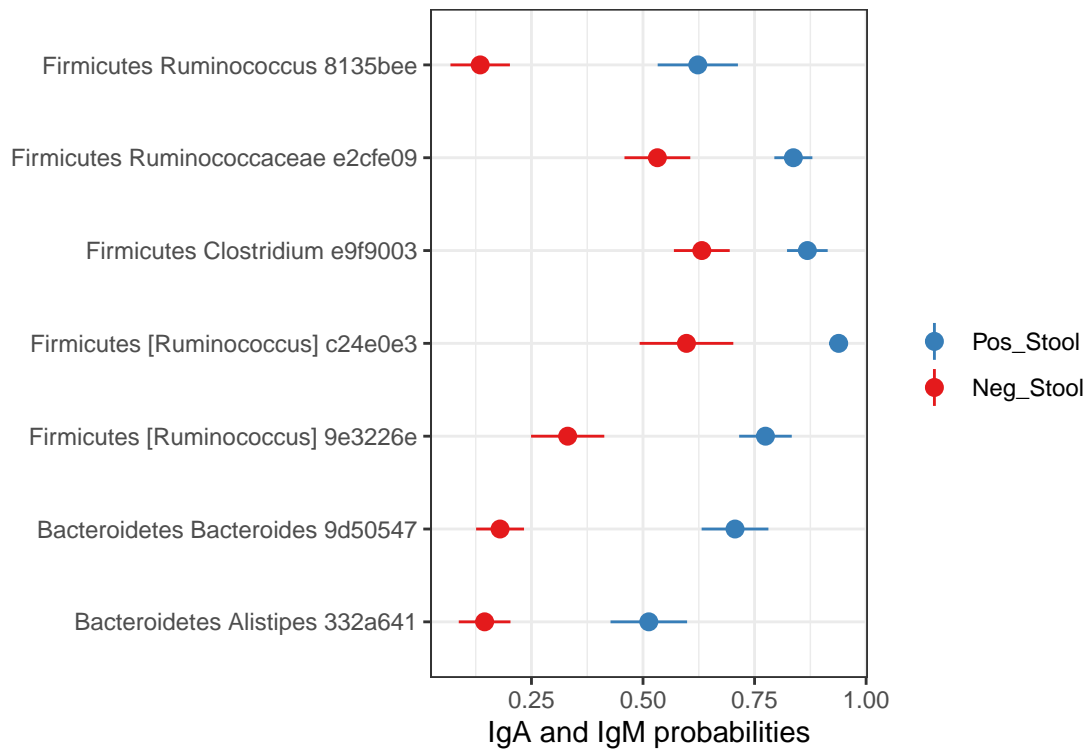
The angle of the vector defining the probability of binding to IgM and probability of binding to IgA are calculated for each subject. M targeted SNVs are defined as having an angle greater than 45 degrees. A targeted SNVs are defined as having an angle less than 45 degrees.

Fig 1C



What are the changes in the SigAD group?

Supp Fig 5D



Result of t test

Taxa	p.value	fdr
Bacteroidetes Alistipes 332a6411ff00b4010ac2397f504c4695	0.0015	0.0027
Bacteroidetes Bacteroides 9d5054752ed33d6a22bd0f96b5618b1c	5.2e-06	3.7e-05
Firmicutes [Ruminococcus] 9e3226efaf559eb14a478f880462cb8a	0.00022	0.00051
Firmicutes [Ruminococcus] c24e0e391aa836b5eae25567c7eb89ee	0.0071	0.0071
Firmicutes Clostridium e9f900358bb9297e10b9fbb1321b1e6e	0.0056	0.0065
Firmicutes Ruminococcaceae e2cfe099d4a73a03ac5f80d4f8369dbc	0.0019	0.0027
Firmicutes Ruminococcus 8135beec331a8d558070c38b580e4b8e	0.00018	0.00051

Results of Wilcoxon rank sum test

Taxa	p.value	fdr
Bacteroidetes Alistipes 332a6411ff00b4010ac2397f504c4695	0.0027	0.0037
Bacteroidetes Bacteroides 9d5054752ed33d6a22bd0f96b5618b1c	0.00014	0.001
Firmicutes [Ruminococcus] 9e3226efaf559eb14a478f880462cb8a	0.0012	0.0029
Firmicutes [Ruminococcus] c24e0e391aa836b5eae25567c7eb89ee	0.008	0.008
Firmicutes Clostridium e9f900358bb9297e10b9fbb1321b1e6e	0.0069	0.008
Firmicutes Ruminococcaceae e2cfe099d4a73a03ac5f80d4f8369dbc	0.002	0.0035
Firmicutes Ruminococcus 8135beec331a8d558070c38b580e4b8e	0.00066	0.0023

## FACS samples - stool only IgG and IgM sorted

Table 9: Sampled populations from each subject.

	IgA-IgM-IgG-	IgG+IgM-	IgG+IgM+	IgM+IgG-
<b>F03.1</b>	1	1	1	1
<b>F03.2</b>	1	1	1	1
<b>F11.1</b>	1	0	1	1
<b>F11.2</b>	1	0	1	1
<b>F33.1</b>	1	1	1	1
<b>F33.2</b>	1	0	1	1
<b>F36.1</b>	1	1	1	1
<b>F36.2</b>	1	0	1	1
<b>F46.1</b>	1	1	1	1

	IgA-IgM-IgG-	IgG+IgM-	IgG+IgM+	IgM+IgG-
<b>F46.2</b>	1	0	1	1
<b>F47.1</b>	1	1	1	1
<b>F47.2</b>	1	1	1	1
<b>F48.1</b>	1	1	1	1
<b>F48.2</b>	1	0	1	1
<b>F49.1</b>	1	1	1	1
<b>F49.2</b>	1	1	1	1
<b>F49.3</b>	1	1	1	1
<b>F50.1</b>	1	0	1	1
<b>F50.2</b>	1	1	1	1
<b>F51.1</b>	1	1	1	1
<b>F51.2</b>	1	0	1	1
<b>F52.1</b>	1	0	1	1
<b>F52.2</b>	1	1	1	1
<b>F52.3</b>	1	1	1	1
<b>F54.1</b>	1	1	1	1
<b>F54.2</b>	1	0	1	1
<b>F59.1</b>	1	0	1	1
<b>F59.2</b>	1	0	1	1
<b>F63.1</b>	1	1	1	1
<b>F63.2</b>	1	0	1	1

Table 10: Total number of populations sequenced.

IgA-IgM-IgG-	IgG+IgM-	IgG+IgM+	IgM+IgG-
30	17	30	30

Analysis4	num_subjects
Pos_Stool	17
Neg_Stool	13

What are the changes in the SigAD group?

Supp Fig 9A

