

## **Effects of a Novel Infant Formula on the Fecal Microbiota in the First Six Months of Life: the INNOVA 2020 study**

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**Supplementary table S1.** Nutritional composition of the standard infant formula (STD) and study formula (INN).

Composition	STD formula			INN formula		
	100 g	100 mL	100 kcal	100 g	100 mL	100 kcal
Energy	514	67		489	67	
Energy	2152	280		2046	279	
Total Fat	27	3.5	5.2	25.6	3.5	5.2
Linoleic acid ( $\omega$ -6)	3.79	493	736	3.147	427	641
$\alpha$ -linolenic acid ( $\omega$ -3)	500	65	97	387	53	79
Araquidonic acid AA ( $\omega$ -6)	53	6.9	10	118	16	24
Docosahexaenoic acid DHA ( $\omega$ -3)	53	6.9	10	118	16	24
Carbohydrates	56.4	7.3	11	54.6	7.4	11.1
Total sugars	56.4	7.3	11	53	7.2	10.8
Lactose	55	7.2	10.7	53	7.2	10.8
Fiber	1.3	0.18	0.22	1.7	0.22	0.33
Proteins	10.6	1.4	2.1	9.4	1.3	1.9
Whey proteins	6.4	0.83	1.2	6.6	0.9	1.3
Caseins	4.2	0.55	0.82	2.8	0.38	0.57
$\alpha$ -casein	20 % of total protein			8% of total protein		
$\beta$ -casein	14 % of total protein			18 % of total protein		

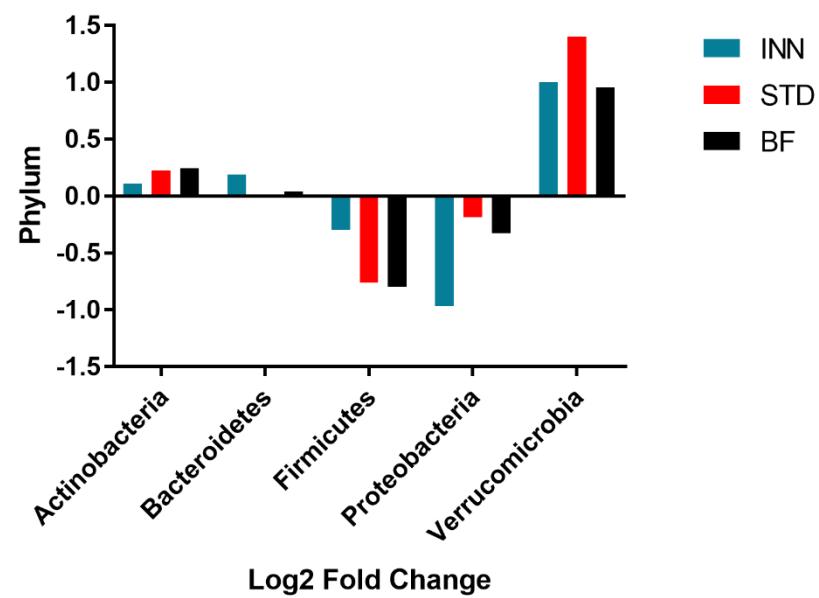
**Supplementary table S2.** Relative abundances at the species levels of fecal bacteria in infants fed the INNOVA (INN) or a standard formula (STD) compared to exclusive breastfed (BF) infants up to 6 months of age

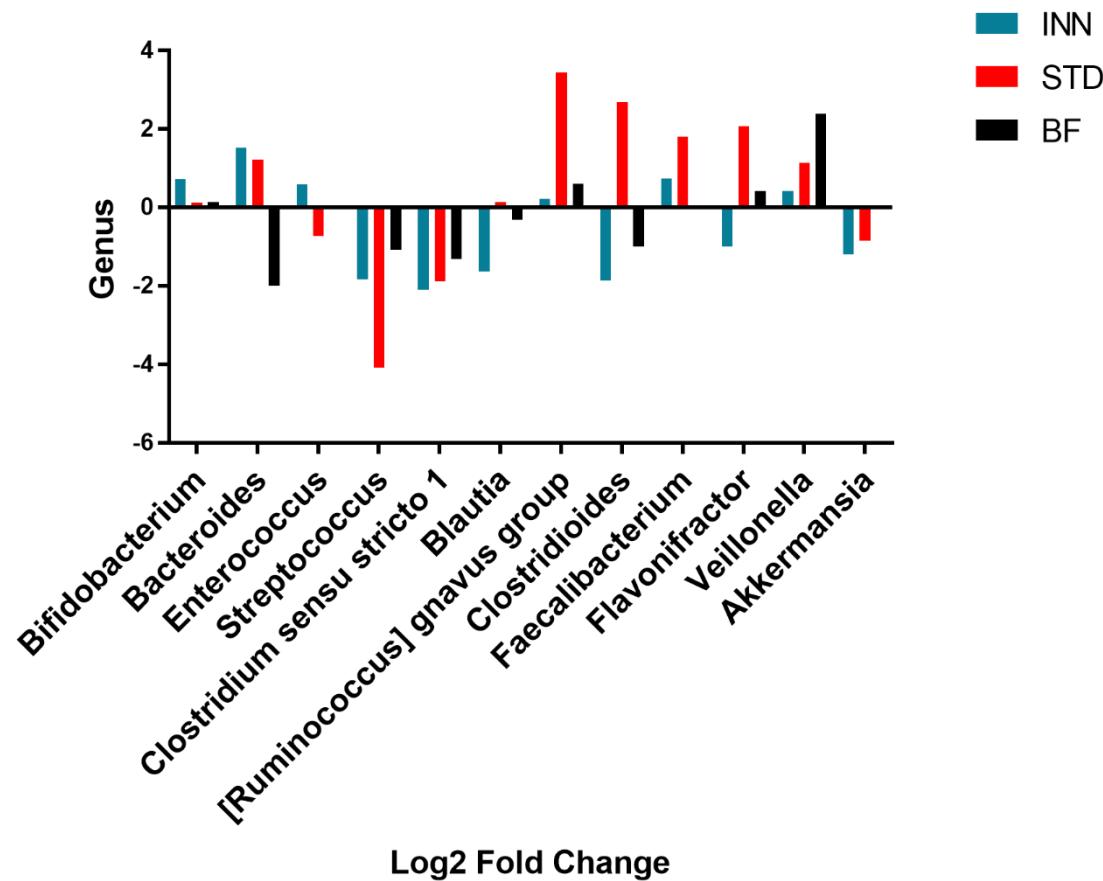
Species	2 months			6 months		
	BF (n=64)	STD (n=64)	INN (n=63)	BF (n=52)	STD (n=55)	INN (n=52)
<i>Bifidobacterium breve</i>	3.2 (0 - 95.2) <sup>a</sup>	0.3 (0 - 7.0) <sup>b</sup>	1.1 (0 - 59.0) <sup>a</sup>	1.8 (0 - 38.3)	0.7 (0 - 20.3)	1.2 (0 - 52.3)
<i>Bifidobacterium longum</i>	47.4 (0.7 - 99.7) <sup>a</sup>	55 (1.4 - 99.3) <sup>b</sup>	79.3 (3.5 - 99.8) <sup>b</sup>	58.2 (2.0 - 99.5)	63.2 (0.4 - 98.1)	77.0 (24.9 - 99.2)
<i>Bifidobacterium bifidum</i>	19.7 (0.04 - 95.7)	7.0 (0.03 - 66.7)	6.9 (0.03 - 95.7)	22.6 (0.05 - 92.1) <sup>a</sup>	8.9 (0.1 - 52.6) <sup>b</sup>	9.4 (0.03 - 47.9) <sup>b</sup>
<i>Akkermansia muciniphila</i>	0.3 (0 - 2.8)	5.1 (0 - 92.1)	1.4 (0 - 74.3)	1.0 (0 - 30.3) <sup>a</sup>	3.0 (0 - 86.5) <sup>b</sup>	1.6 (0 - 36.7) <sup>a</sup>
<i>Ruminococcus gnavus</i>	0.2 (0 - 90.7)	0.2 (0 - 73.8)	0.08 (0 - 10.1)	0.2 (0.01 - 40.9) <sup>a</sup>	1.6 (0 - 46.7) <sup>b</sup>	0.2 (0 - 73.9) <sup>a</sup>
<i>Clostridium difficile</i>	0.04 (0 - 46.7) <sup>a</sup>	0.07 (0 - 24.9) <sup>b</sup>	0.03 (0 - 8.4) <sup>a</sup>	0.04 (0 - 5.7) <sup>a</sup>	0.3 (0 - 24.2) <sup>b</sup>	0.02 (0 - 39.3) <sup>a</sup>
<i>Lactobacillus paracasei</i>	0.02 (0 - 2.5) <sup>a</sup>	0 (0 - 0.2) <sup>b</sup>	0.01 (0 - 0.3) <sup>a</sup>	0 (0 - 0.3)	0 (0 - 0.1)	0 (0 - 0.5)
<i>Staphylococcus aureus</i>	0.01 (0 - 0.4) <sup>a</sup>	0 (0 - 0.1) <sup>b</sup>	0.01 (0 - 0.3) <sup>a</sup>	0 (0 - 0.09)	0 (0 - 0.03)	0 (0 - 0.07)
<i>Streptococcus salivarius</i>	0.1 (0 - 1.4) <sup>a</sup>	0.05 (0 - 0.6) <sup>b</sup>	0.1 (0 - 1.2) <sup>a</sup>	0.09 (0 - 1.4)	0.01 (0 - 0.9)	0.05 (0 - 0.7)

Data are expressed as median and range. Labeled medians with identical letters are not significant. Different letters means significant differences (P < 0.05).

**Supplementary figure S1.** Absolute counts represented by log-fold change between visit 4 (6 months) and visit 1 (21 days). A phylum, B genus by log-fold change are visualized by divergent bar plots.

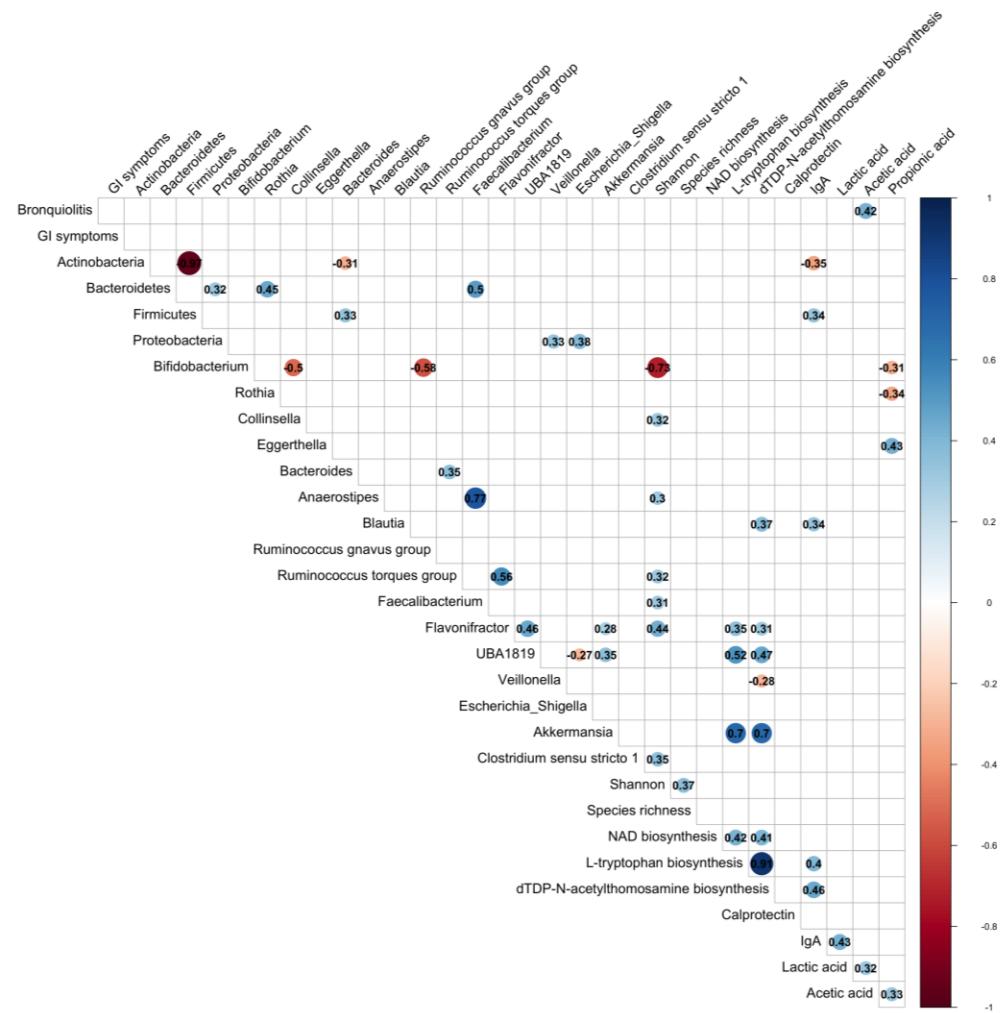
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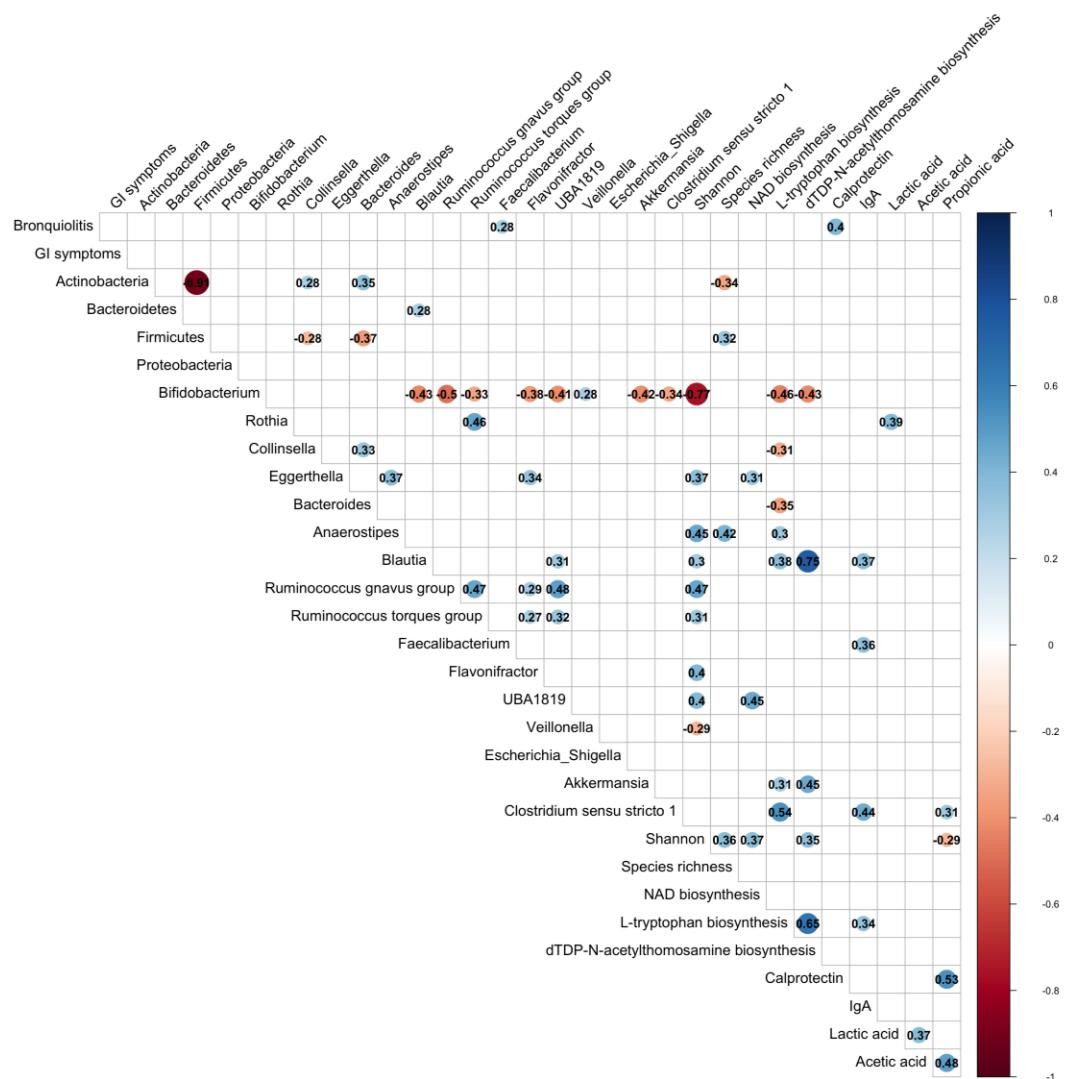


**B**

**Supplementary figure S2.** Correlations between bacterial diversity indices, bacterial variables, SCFAs levels, metabolic traits and clinical outcomes A: Innova formula group; B Standard formula group; C: Breastfed group

A



**B**

C

