

Supplementary Material

Supplementary Table S1. Quantification of flavan-4-ols and anthocyanins in four NILs of corn. C3G: cyanidin-3-glycoside. *Quantification of peak's absorbance at 510 nm, after heating of whole kernel extract. ** Suggested relative abundance of phlobaphenes given that anthocyanins do not shape peaks after heating (see Supplementary Figure 1). np: no peak at 510 nm, no peak displaced after boiling.

NIL of corn	Flavan-4-ol*	Anthocyanins
	Abs/g kernel	mg C3G eq/100g
A	np	-0.7
B	5.03**	0.2
C	np	15.5
D	9.59**	5.3

Supplementary Table S2. Composition of Experimental Diets

Ingredients	Diet P	Diet A	Diet B	Diet C	Diet D
	TD.9718 4	TD.2204 27	TD.2204 28	TD.2204 29	TD.2204 30
	g/kg	g/kg	g/kg	g/kg	g/kg
Casein	200.0	162.5	166.1	162.156	158.582
L-Cystine	3.0	3.0	3.0	3.0	3.0
Corn Starch	392.234	202.0	192.147	189.456	202.679
Maltodextrin	132.0	132.0	132.0	132.0	132.0
Sucrose	100.0	100.0	100.0	100.0	100.0
Soybean Oil	70.0	54.716	58.591	58.604	56.643
Cellulose	50.0	14.0	17.0	23.0	15.0
Mineral Mix, AIN-93G-MX (94046)	35.0	35.0	35.0	35.0	35.0
Vitamin Mix, AIN-93-VX (94047)	15.0	15.0	15.0	15.0	15.0
Choline Bitartrate	2.75	2.75	2.75	2.75	2.75
Vitamin K1, phylloquinone	0.002	0.002	0.002	0.002	0.002
TBHQ, antioxidant	0.014	0.014	0.014	0.014	0.014
Maize NIL A		279.0			
Maize NIL B			278.4		
Maize NIL C				279.0	
Maize NIL D					279.3

Supplementary Table S3. rtPCR primers of colonic inflammatory markers

Gene	Primers
Il1b	Forward: 5'-GCCCATCCTCTGTGACTCAT-3' Reverse: 5'-AGGCCACAGGTATTTTGTCTG-3'
Il6	Forward: 5'-AGTTGCCTTCTTGGGACTGA-3' Reverse: 5'-CAGAATTGCCATTGCACAAC-3'
Tnfa	Forward: 5'-CAAAATTCGAGTGACAAGCCTG-3' Reverse: 5'-GAGATCCATGCCGTTGGC-3'
Nfkb	Forward: 5'-ACCTTTGCTGGAAACACACC-3' Reverse: 5'-ATGGCCTCGGAAGTTTCTTT-3'
Ocl	Forward: 5'-ACGGACCCTGACCACTATGA-3' Reverse: 5'-TCAGCAGCAGCCATGTACTC-3'
Muc2	Forward: 5'-GCTGACGAGTGGTTGGTGAATG-3' Reverse: 5'-GATGAGGTGGCAGACAGGAGAC-3'
Tjp1	Forward: 5'-AGGACACCAAAGCATGTGAG-3' Reverse: 5'-GGCATTCCTGCTGGTTACA-3'
Tlr4	Forward: 5'-AGTGCCCCGCTTTCACCTCT-3' Reverse: 5'-TCCGGCTCTTGTGGAAGCCT-3'
Tlr5	Forward: 5'-GCTTGGAACATATGCCAGACACA-3' Reverse: 5'-AAAGGCTATCCTGCCGTCTGAA-3'
Actb	Forward: 5'-AGCCATGTACGTAGCCATCC-3' Reverse: 5'-CTCTCAGCTGTGGTGGTGAA-3'

Supplementary Table S4. ANCOM-BC analysis for dietary effects on Bacteria Family Relative Abundance. q-values ≤ 0.05 are significant.

Compared with diet P				
Family	dietA	dietB	dietC	dietD
Eggerthellaceae	0.894	0.990	0.908	0.730
Coriobacteriaceae	0.864	0.520	0.839	0.289
Enterobacteriaceae	0.864	0.990	0.908	0.730
o_Enterobacterales	0.894	0.955	0.839	0.515
Sutterellaceae	0.679	0.399	0.877	0.290
Pasteurellaceae	0.634	0.294	0.181	0.186
Erysipelatoclostridiaceae	0.019	0.013	0.908	0.972
Erysipelotrichaceae	0.894	0.257	0.602	0.730
Streptococcaceae	0.207	0.756	0.002	0.622
Enterococcaceae	0.894	0.294	0.602	0.268
Veillonellaceae	0.894	0.296	0.602	0.186
Bacteroidaceae	0.894	0.692	0.702	0.659
Marinifilaceae	0.894	0.990	0.986	0.730
Tannerellaceae	0.894	0.990	0.923	0.730
Rikenellaceae	0.864	0.990	0.908	0.730
f_Anaerovoraceae	0.207	0.990	0.839	0.730
Anaerofustaceae	0.894	0.032	0.908	0.972
Peptostreptococcaceae	0.894	0.990	0.877	0.730
Clostridiaceae	0.894	0.990	0.877	0.542

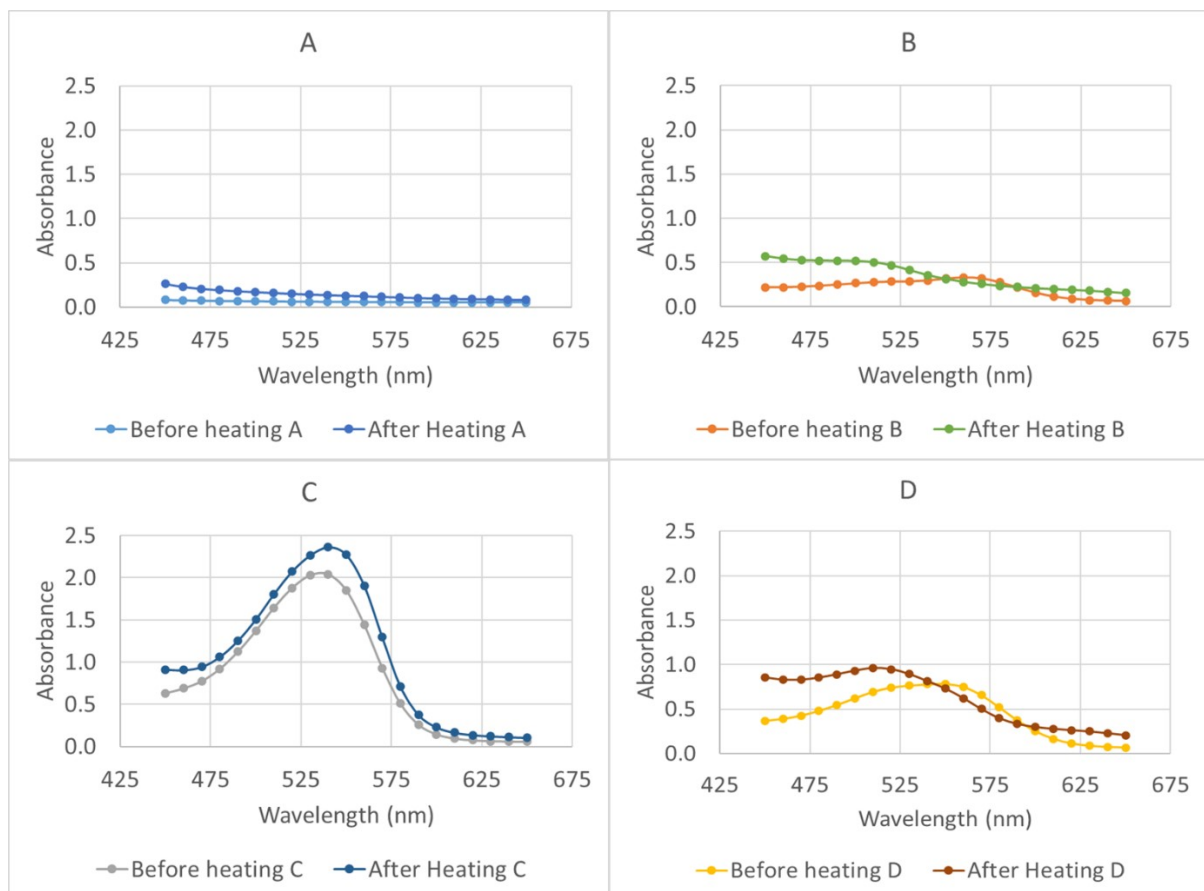
Defluviitaleaceae	0.816	0.990	0.702	0.268
Butyricicoccaceae	0.266	0.520	0.602	0.730
Ethanoligenenaceae	0.864	0.970	0.602	0.824
[Clostridium]_methylpentosum_group	0.019	0.013	0.908	0.988
[Eubacterium]_coprostanoligenes_group	0.894	0.412	0.602	0.186
Oscillospiraceae	0.266	0.016	0.517	0.659
Ruminococcaceae	0.894	0.294	0.877	0.244
Monoglobaceae	0.037	0.089	0.003	0.031
Lachnospiraceae	0.734	0.257	0.839	0.289
Compared to diet A				
Family	dietB	dietC	dietD	dietP
Eggerthellaceae	0.963	0.899	0.960	0.894
Coriobacteriaceae	0.963	0.993	0.687	0.864
Enterobacteriaceae	0.963	0.899	0.960	0.864
o_Enterobacterales	0.963	0.899	0.716	0.894
Sutterellaceae	0.963	0.508	0.870	0.679
Pasteurellaceae	0.963	0.899	0.716	0.634
Erysipelatoclostridiaceae	0.963	0.025	0.074	0.019
Erysipelotrichaceae	0.963	0.899	0.960	0.894
Streptococcaceae	0.963	0.508	0.738	0.207
Enterococcaceae	0.963	0.761	0.377	0.894
Veillonellaceae	0.592	0.575	0.204	0.894
Bacteroidaceae	0.963	0.899	0.716	0.894
Marinifilaceae	0.963	0.899	0.960	0.894
Tannerellaceae	0.963	0.899	0.960	0.894
Rikenellaceae	0.963	0.899	0.936	0.864
f_Anaerovoraceae	0.749	0.618	0.377	0.207
Anaerofustaceae	0.032	0.899	0.960	0.894
Peptostreptococcaceae	0.963	0.899	0.716	0.894
Clostridiaceae	0.963	0.899	0.590	0.894
Defluviitaleaceae	0.963	0.955	0.716	0.816
Butyricicoccaceae	0.963	0.899	0.698	0.266
Ethanoligenenaceae	0.963	0.899	0.960	0.864
[Clostridium]_methylpentosum_group	0.963	0.010	0.022	0.019
[Eubacterium]_coprostanoligenes_group	0.109	0.078	0.014	0.894
Oscillospiraceae	0.963	0.955	0.590	0.266
Ruminococcaceae	0.963	0.993	0.590	0.894
Monoglobaceae	0.971	0.899	0.716	0.037
Lachnospiraceae	0.963	0.899	0.204	0.734
Compared to diet B				
Family	dietC	dietD	dietP	dietA
Eggerthellaceae	0.992	0.931	0.990	0.963
Coriobacteriaceae	0.992	0.799	0.520	0.963

Enterobacteriaceae	0.992	0.881	0.990	0.963
o_Enterobacterales	0.992	0.927	0.955	0.963
Sutterellaceae	0.429	0.899	0.399	0.963
Pasteurellaceae	0.992	0.927	0.294	0.963
Erysipelatoclostridiaceae	0.031	0.093	0.013	0.963
Erysipelotrichaceae	0.992	0.799	0.257	0.963
Streptococcaceae	0.254	0.927	0.756	0.963
Enterococcaceae	0.992	0.927	0.294	0.963
Veillonellaceae	0.992	0.927	0.296	0.592
Bacteroidaceae	0.992	0.927	0.692	0.963
Marinifilaceae	0.992	0.927	0.990	0.963
Tannerellaceae	0.992	0.927	0.990	0.963
Rikenellaceae	0.992	0.927	0.990	0.963
f_Anaerovoraceae	0.992	0.927	0.990	0.749
Anaerofustaceae	0.023	0.000	0.032	0.032
Peptostreptococcaceae	0.992	0.927	0.990	0.963
Clostridiaceae	0.992	0.799	0.990	0.963
Defluviitaleaceae	0.992	0.881	0.990	0.963
Butyricicoccaceae	0.992	0.881	0.520	0.963
Ethanoligenenaceae	0.254	0.799	0.970	0.963
[Clostridium]_methylpentosum_group	0.031	0.093	0.013	0.963
[Eubacterium]_coprostanoligenes_group	0.992	0.881	0.412	0.109
Oscillospiraceae	0.992	0.151	0.016	0.963
Ruminococcaceae	0.992	0.151	0.294	0.963
Monoglobaceae	0.992	0.881	0.089	0.971
Lachnospiraceae	0.992	0.093	0.257	0.963
Compared to diet C				
Family	dietD	dietP	dietA	dietB
Eggerthellaceae	0.930	0.908	0.899	0.992
Coriobacteriaceae	0.930	0.839	0.993	0.992
Enterobacteriaceae	0.930	0.908	0.899	0.992
o_Enterobacterales	0.930	0.839	0.899	0.992
Sutterellaceae	0.661	0.877	0.508	0.429
Pasteurellaceae	0.930	0.181	0.899	0.992
Erysipelatoclostridiaceae	0.953	0.908	0.025	0.031
Erysipelotrichaceae	0.930	0.602	0.899	0.992
Streptococcaceae	0.676	0.002	0.508	0.254
Enterococcaceae	0.930	0.602	0.761	0.992
Veillonellaceae	0.930	0.602	0.575	0.992
Bacteroidaceae	0.930	0.702	0.899	0.992
Marinifilaceae	0.930	0.986	0.899	0.992
Tannerellaceae	0.930	0.923	0.899	0.992
Rikenellaceae	0.930	0.908	0.899	0.992
f_Anaerovoraceae	0.930	0.839	0.618	0.992
Anaerofustaceae	0.930	0.908	0.899	0.023

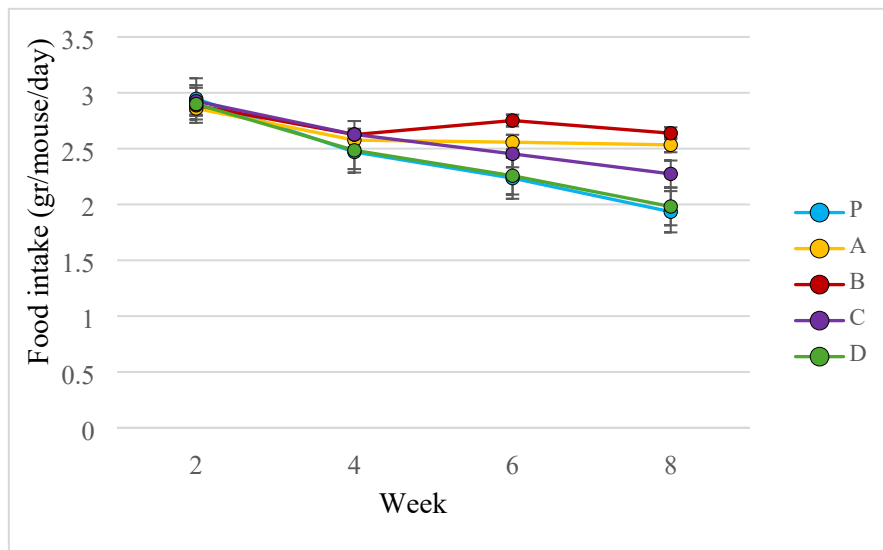
Peptostreptococcaceae	0.930	0.877	0.899	0.992
Clostridiaceae	0.930	0.877	0.899	0.992
Defluviitaleaceae	0.930	0.702	0.955	0.992
Butyricicoccaceae	0.930	0.602	0.899	0.992
Ethanoligenenaceae	0.930	0.602	0.899	0.254
[Clostridium]_methylpentosum_group	0.930	0.908	0.010	0.031
[Eubacterium]_coprostanoligenes_group	0.930	0.602	0.078	0.992
Oscillospiraceae	0.930	0.517	0.955	0.992
Ruminococcaceae	0.930	0.877	0.993	0.992
Monoglobaceae	0.930	0.003	0.899	0.992
Lachnospiraceae	0.930	0.839	0.899	0.992
Compared to diet D				
Family	dietP	dietA	dietB	dietC
Eggerthellaceae	0.730	0.960	0.931	0.930
Coriobacteriaceae	0.289	0.687	0.799	0.930
Enterobacteriaceae	0.730	0.960	0.881	0.930
o_Enterobacterales	0.515	0.716	0.927	0.930
Sutterellaceae	0.290	0.870	0.899	0.661
Pasteurellaceae	0.186	0.716	0.927	0.930
Erysipelatoclostridiaceae	0.972	0.074	0.093	0.953
Erysipelotrichaceae	0.730	0.960	0.799	0.930
Streptococcaceae	0.622	0.738	0.927	0.676
Enterococcaceae	0.268	0.377	0.927	0.930
Veillonellaceae	0.186	0.204	0.927	0.930
Bacteroidaceae	0.659	0.716	0.927	0.930
Marinifilaceae	0.730	0.960	0.927	0.930
Tannerellaceae	0.730	0.960	0.927	0.930
Rikenellaceae	0.730	0.936	0.927	0.930
f_Anaerovoraceae	0.730	0.377	0.927	0.930
Anaerofustaceae	0.972	0.960	0.000	0.930
Peptostreptococcaceae	0.730	0.716	0.927	0.930
Clostridiaceae	0.542	0.590	0.799	0.930
Defluviitaleaceae	0.268	0.716	0.881	0.930
Butyricicoccaceae	0.730	0.698	0.881	0.930
Ethanoligenenaceae	0.824	0.960	0.799	0.930
[Clostridium]_methylpentosum_group	0.988	0.022	0.093	0.930
[Eubacterium]_coprostanoligenes_group	0.186	0.014	0.881	0.930
Oscillospiraceae	0.659	0.590	0.151	0.930
Ruminococcaceae	0.244	0.590	0.151	0.930
Monoglobaceae	0.031	0.716	0.881	0.930
Lachnospiraceae	0.289	0.204	0.093	0.930

Supplementary Table S5. GCA concentration per microbiota donor's recipients. Kruskal-Wallis test was applied to determine significant differences between donors.

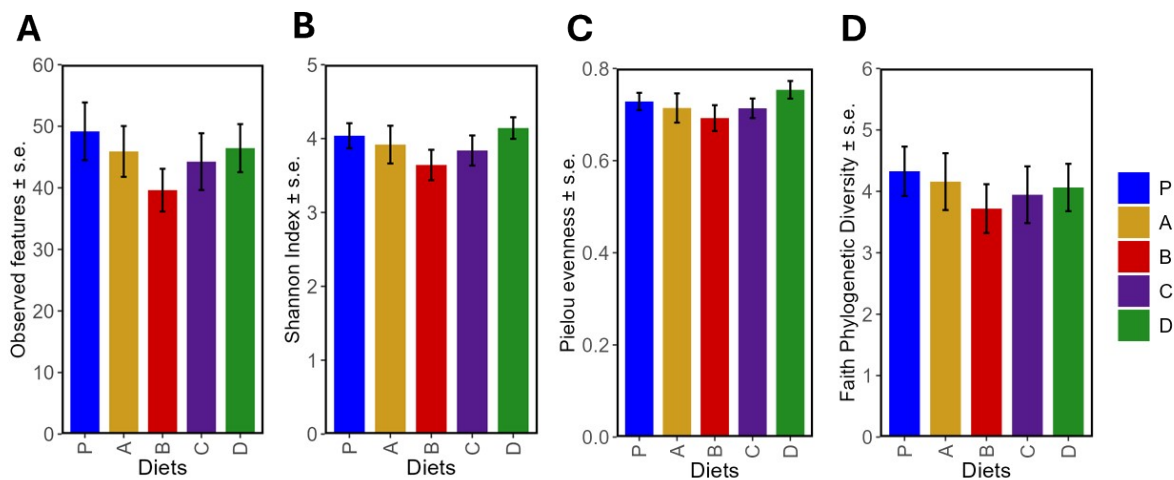
Donor	GCA (ng/ml)		p-value	
	Average	±SD	vs IBD-1	vs IBD-2
IBD-1	19.5163	0.3395	-	0.285
IBD-2	20.3767	0.38101	0.285	-
IBD-3	51.5757	3.6580	<.001	<.001



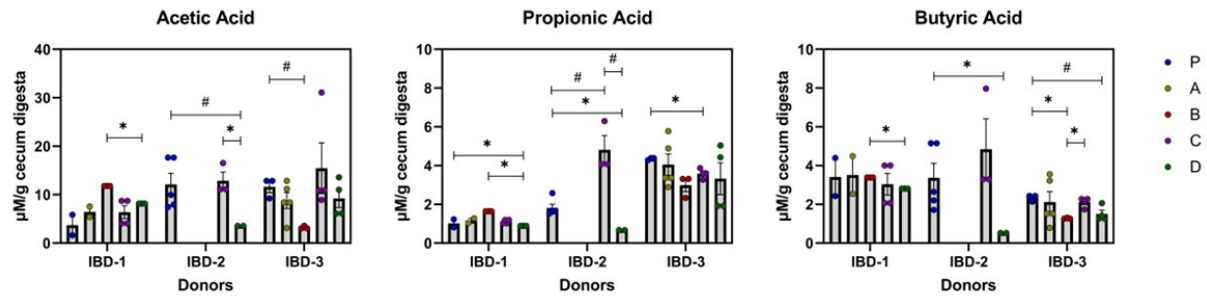
Supplementary Figure S1. Absorption spectra showing earlier accumulation of phlobaphenes (maximum absorbance around 560 nm) and later accumulation of anthocyanins (maximum absorbance around 540 nm) in near-isogenic lines (NILs) of corn B, C and D. A: NIL of corn not expressing 3-deoxyflavonoids (3-DF; phlobaphenes) or 3-hydroxyflavonoids (3-HF; anthocyanins); B: NIL of corn expressing only 3-DF; C: NIL of corn expressing only 3-HF; D: NIL of corn expressing both 3-DF and 3-HF. Only phlobaphenes shift peaks after heating.



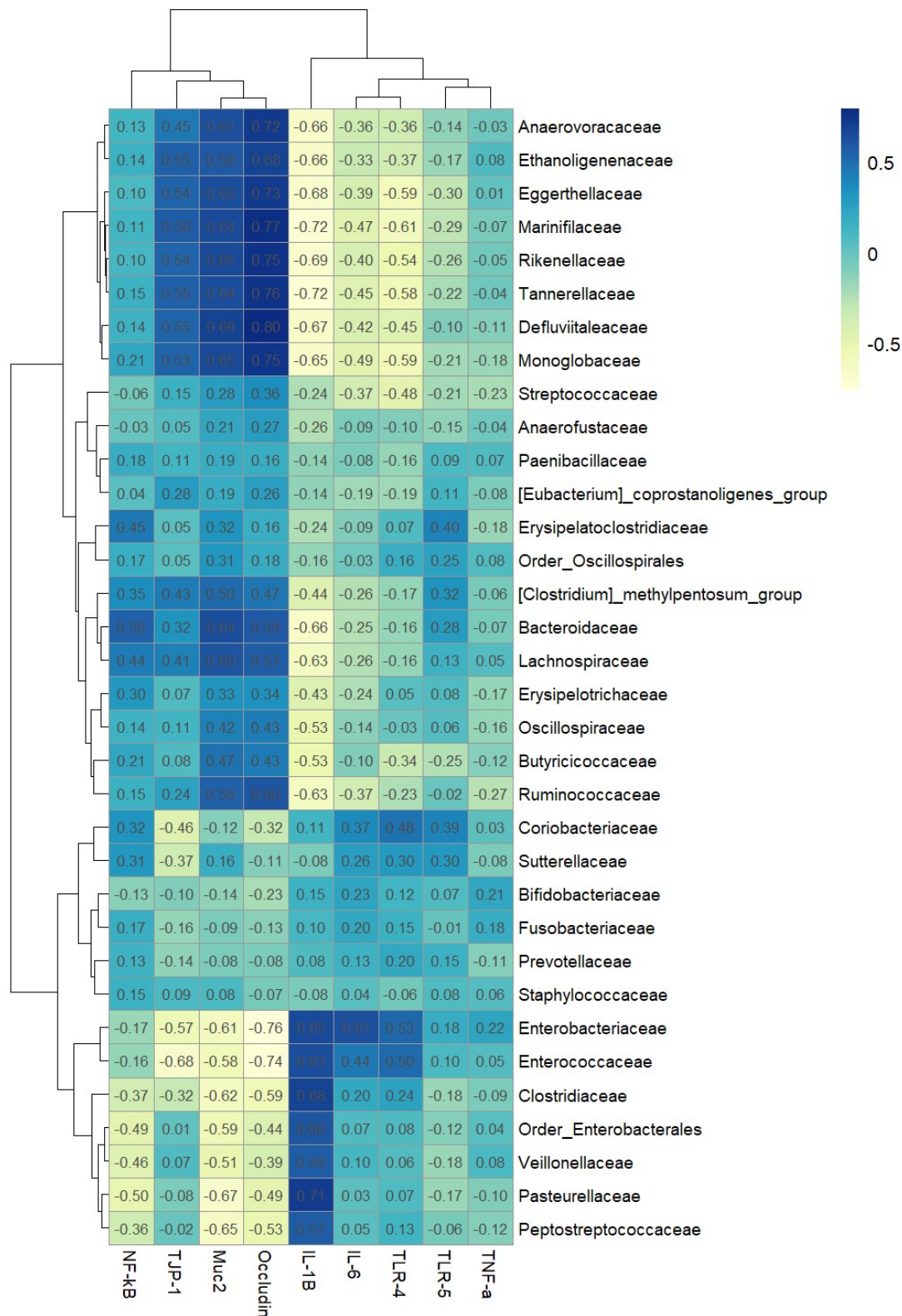
Supplementary Figure S2. Food intake (Average $\pm$ SEM) per treatment (n=9-12) during experimental period. Diets: purified (P), and 25% inclusion of maize NIL with no 3-DF or 3-HF (A) 3-DFs (B), 3-HFs (C) or 3-DF+3-HF (D).



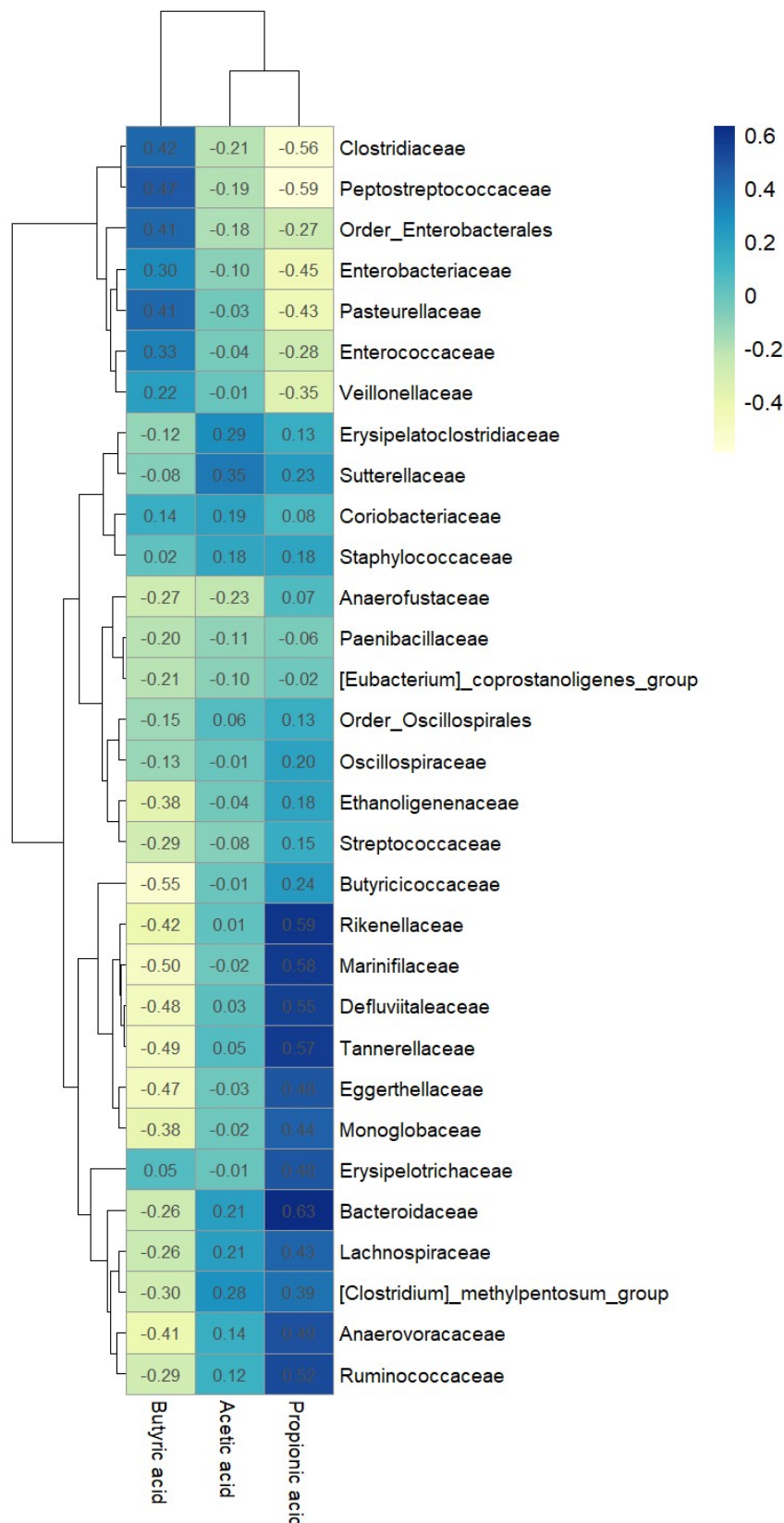
Supplementary Figure S3. Diets do not affect α -diversity indexes. Observed features (A), Shannon Index (B) Pielou evenness (C), and Faith phylogenetic diversity (D). Diets: purified (P), and 25% inclusion of maize NIL with 3-DFs (B), 3-HFs (C), or both 3-DF + 3HF (D). Replicates ($n = 9-12$) are shown for every diet. # $p \leq .10$ and * $p \leq .05$.



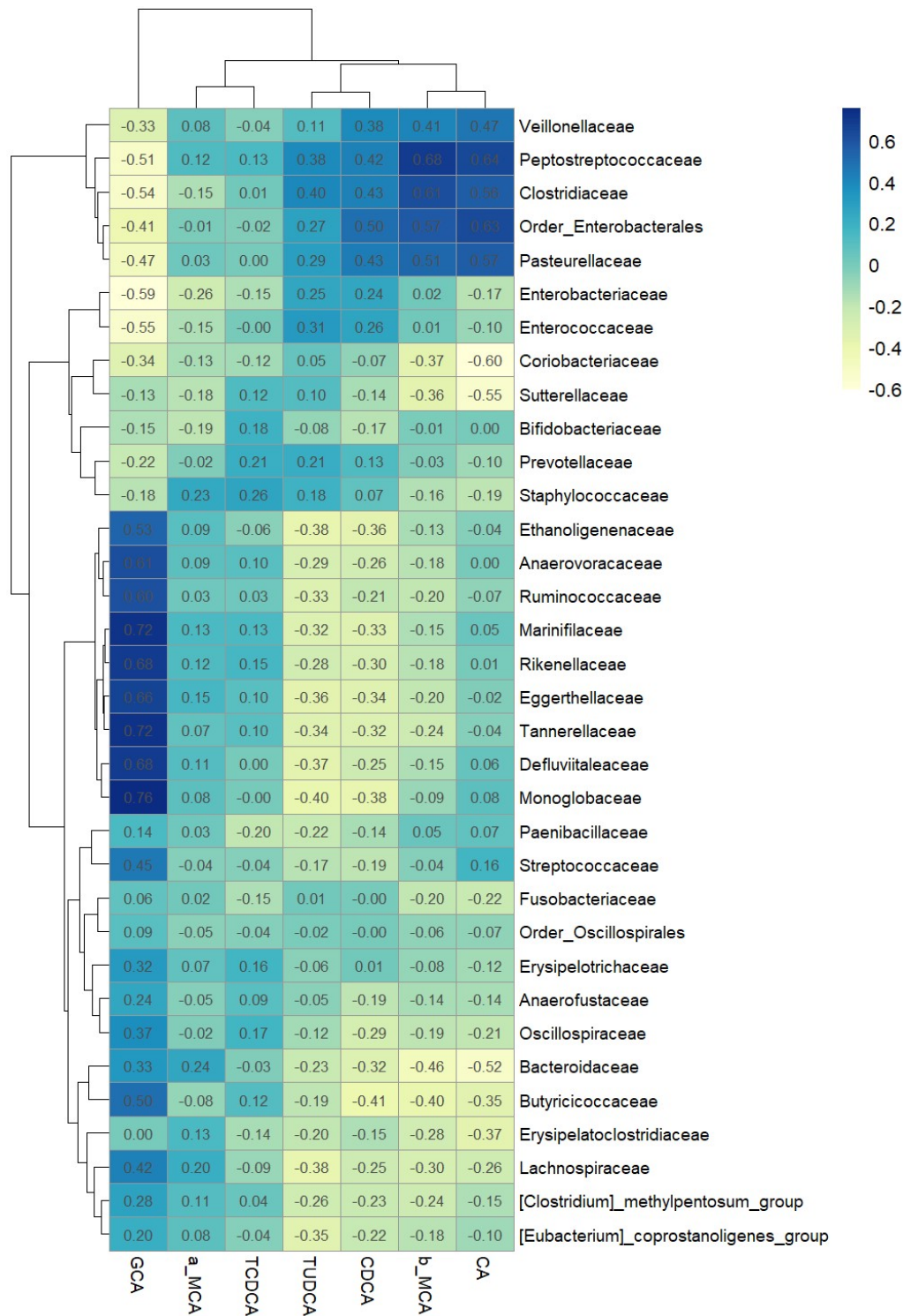
Supplementary Figure S4. Diet treatments affect differently the short-chain fatty acids concentration in cecal content, depending on the donor of the recipient's microbiota. SCFAs: acetate (A), propionate (B), butyrate (C). Dietary treatments: purified (P), and 25% inclusion of maize NILs with no 3-DFs or 3-HFs (Diet A), 3-DFs (Diet B), 3-HFs (Diet C) or both 3-DF+3HF (Diet D). Human donors: IBD-1, IBD-2, IBD-3. Replicates ($n = 3 - 5$) are shown for every diet within each donor's recipient group. # $p \leq .10$ and * $p \leq .05$.



Supplementary Figure S5. Correlation hierarchical heatmap of relative abundance of bacteria families and biomarkers (mRNA expression of pattern recognition receptors, nuclear factor, inflammatory cytokines, tight-junctions and mucus production genes). Darker colors represent higher positive correlations, while lighter represent highly negative correlations. Mild correlations $r < 0.4$, moderate correlations $0.4 < r < 0.6$, strong correlations $r > 0.6$.



Supplementary Figure S6. Correlation hierarchical heatmap of relative abundance of bacteria families and short-chain fatty acids. Darker colors represent higher positive correlations, while lighter represent highly negative correlations. Mild correlations $r < 0.4$, moderate correlations $0.4 < r < 0.6$, strong correlations $r > 0.6$.



Supplementary Figure S7. Correlation hierarchical heatmap of relative abundance of bacteria families and bile acids. Bile acids: glycocholic acid, GCA; taurochenodeoxycholic acid, TCDCA; cholic acid, CA; chenodeoxycholic acid, CDCA; tauroursodeoxycholic, TUDCA; α -murocholic acid, a-MCA; and β -murocholic acid, b-MCA. Darker colors represent higher positive correlations, while lighter represent highly negative correlations. Mild correlations $r < 0.4$, moderate correlations $0.4 < r < 0.6$, strong correlations $r > 0.6$.