Electronic Supplementary Material (ESI) for Food & Function.

Table S1. Total free phenolic content, total flavonoid content, ferric reducing antioxidant power, and DPPH radical scavenging capacity.

		TPC (mg GAE/100mL)	**TFC (mg CAE/100mL)**	**FRAP (mM Fe^{2+} eq./L)**	**DPPH (mg Trolox eq./100 mL)**
Before Digestion					
G	w/o Lc	190.62 ± 10.68^{A}	91.02 ± 2.11^{A}	74.03 ± 4.90^{A}	174.64 ± 3.57^{A}
	Lc	183.46 ± 22.14^{A}	85.33 ± 8.22^{A}	72.20 ± 3.08^{A}	186.55 ± 53.49^{A}
P	w/o Lc	475.89 ± 20.87^{B}	140.4 ± 6.52^{B}	218.69 ± 14.70^{B}	532.48 ± 8.70^{B}
	Lc	473.30 ± 19.37^{B}	147.65 ± 3.22^{B}	195.60± 27.79^{B}	524.95 ± 59.98^{B}
BB	w/o Lc	108.36 ± 2.45^{C}	79.38 ± 2.04^{A}	43.11 ± 2.45^{C}	182.98 ± 17.98^{A}
	Lc	106.20 ± 6.49^{C}	68.30 ± 15.37^{A}	49.78 ± 2.65^{A}	165.12 ± 22.68^{Aa}
BC	w/o Lc	265.72 ± 16.02^{D}	147.65 ± 3.87^{B}	108.14 ±6.45^{D}	218.69 ± 2.06^{C}
	Lc	186.07 ± 18.10^{Da}	133.77 ± 1.08^{Ba}	93.31 ± 14.49^{A}	162.74 ± 6.19^{Aa}
After Small Intestinal Digestion					
G	w/o Lc	52.32 ± 7.49^{A}	21.03 ± 1.30^{A}	30.05 ± 2.59^{A}	56.56 ± 1.81^{A}
	Lc	48.72 ± 19.8^{A}	20.78 ± 1.57^{A}	25.98 ±1.25^{A}	55.51 ± 4.78^{A}
P	w/o Lc	162.72 ± 7.20^{B}	48.31 ± 20.61^{B}	115.86 ± 10.76^{B}	204.73 ± 23.63^{B}
	Lc	167.52 ± 14.55^{B}	44.42 ± 15.58^{AB}	116.96 ± 7.36^{B}	205.77 ± 21.99^{B}
BB	w/o Lc	61.92 ± 9.52^{A}	31.42 ± 2.24^{B}	33.19 ± 8.44^{A}	40.90 ± 14.12^{A}
	Lc	58.32 ± 9.52^{A}	30.12 ± 8.11^{AB}	30.37 ± 2.12^{A}	42.99 ± 12.65^{A}
BC	w/o Lc	79.92 ±7.20^{A}	49.61± 0.05^{B}	38.84 ± 1.78^{A}	70.12 ± 24.45^{A}
	Lc	66.72 ± 8.31^{A}	48.31 ± 0.04^{B}	38.05 ± 2.72^{A}	72.21 ± 23.07^{A}
After Colonic Fermentation					
G	w/o Lc	151.20 ± 36.0^{A}	124.94 ± 5.95^{A}	88.66 ± 8.37^{AB}	162.82 ± 10.17^{A}
	Lc	163.20 ± 55.0^{A}	126.23 ± 3.90^{A}	88.03 ± 10.15^{A}	165.57 ± 14.49^{A}
P	w/o Lc	343.20 ± 54.99^{B}	206.75 ± 23.48^{A}	136.97 ± 34.83^{A}	204.60 ± 0.55^{B}
	Lc	331.20 ± 36.0^{B}	198.96 ± 4.50^{B}	102.78 ± 21.19^{A}	191.13 ± 13.14^{B}
BB	w/o Lc	175.20 ± 41.57^{A}	139.22 ± 11.90^{A}	75.80 ± 13.65^{B}	145.51 ± 44.80^{A}
	Lc	187.20 ± 1.81^{A}	141.82 ± 3.90^{A}	68.58 ± 11.77^{A}	138.73 ± 16.08^{A}
BC	w/o Lc	307.20 ± 41.57^{B}	206.75 ± 59.00^{A}	96.19 ± 8.98^{AB}	165.66 ± 11.36^{A}
	Lc	319.20. ± 20.78^{B}	202.86 ± 22.83^{B}	98.07 ± 9.41^{A}	175.47 ± 10.98^{AB}

Values are expressed as mean ± SD (n=3).

[a] In Lc group significantly differ from the group without Lc for each juice ($p < 0.05$).

[A, B, C, D] Different upper-case letters in the same column indicate significant difference between juice types in the same test ($p < 0.05$).

G: Grape juice; P: Pomegranate juice; BB: Blueberry juice; BC: Black cherry juice. Lc: *L. casei*; w/o Lc: without *L. casei*

Table S2. HPLC-ESI-QTOF-MS/MS identification of phenolic compounds from juice samples before, after gastrointestinal (GI) digestion and colonic fermentation (CF).

Phenolic class	Peak NO	Compound name	Molecular formula	Retention time (min)	Experimental mass	Theoretical mass	Error (ppm)	UV λmax (nm)	Mass fragments	Detected in juice sample											
Positive mode $[M+H]^+$ (m/z)										G			P			BB			BC		
Anthocyanins										Before	After GI	After CF	Before	After GI	After CF	Before	After GI	After CF	Before	After GI	After CF
	1	Delphinidin-3,5-diglc	$C_{27}H_{31}O_{17}$	16.098	627.153	627.1516	2.23	520	303(100)	Y	Y	ND	Y	Y	ND	ND	ND	ND	ND	ND	ND
	2	Cyanidin-3,5-diglc	$C_{27}H_{31}O_{16}$	18.192	611.1632	611.1612	3.27	520	287(100)	Y	Y	ND	Y	Y	ND	ND	ND	ND	ND	ND	ND
	3	Delphinidin-3-glucoside	$C_{21}H_{21}O_{12}$	20.41	465.1031	465.1033	-0.43	520	303(100)	ND	ND	ND	ND	ND	ND	Y	Y	ND	ND	ND	ND
	4	Cyanidin-3-glucoside	$C_{21}H_{21}O_{11}$	21.286	449.108	449.1083	-0.67	520	287(100)	Y	Y	ND	Y	Y	ND	Y	Y	ND	Y	Y	ND
	5	Delphinidin-3-arabinoside	$C_{20}H_{19}O_{11}$	22.717	435.0917	435.0927	-2.30	520	303(100)	ND	ND	ND	ND	ND	ND	Y	Y	ND	ND	ND	ND
	6	Pelargonidin-3-glucoside	$C_{21}H_{21}O_{10}$	23.433	433.1151	433.1134	3.93	520	271(100)	Y	Y	ND	Y	Y	ND	ND	ND	ND	ND	ND	ND
	7	Petunidin-3-glucoside	$C_{22}H_{23}O_{12}$	23.991	479.1185	479.1189	-0.83	520	317(100)	ND	ND	ND	ND	ND	ND	Y	Y	ND	ND	ND	ND
	8	Cyanidin-3-rutinoside	$C_{27}H_{31}O_{15}$	24.407	595.1682	595.1663	3.19	520	593(100) 285(50)	ND	ND	ND	ND	ND	ND	ND	ND	ND	Y	Y	ND
	9	Petunidin-3-arabinoside	$C_{21}H_{21}O_{11}$	28.136	449.1073	449.1083	-2.23	520	317(100)	ND	ND	ND	ND	ND	ND	Y	Y	ND	ND	ND	ND
	10	Malvidin-3-glucoside	$C_{23}H_{25}O_{12}$	29.352	493.1315	493.1346	-6.29	520	331(100)	ND	ND	ND	ND	ND	ND	Y	Y	ND	Y	Y	ND
	11	Malvidin-3-arabinoside	$C_{22}H_{23}O_{11}$	31.758	463.1241	463.124	0.22	520	331(100)	Y	Y	ND	ND	ND	ND	Y	Y	ND	ND	ND	ND
Flavanols																					
	12	Myricetin hexose	$C_{21}H_{20}O_{13}$	39.145	481.0984	480.0904	0.33	365	320(100)	Y	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
	13	Quercetin-3-rutinoside	$C_{27}H_{30}O_{16}$	34.868	611.159	610.1533	-3.51	365	303(100) 165(90)	ND	ND	ND	ND	ND	ND	Y	ND	ND	Y	Y	ND
	14	Quercetin-3-galactoside	$C_{21}H_{20}O_{12}$	35.746	465.1019	464.0954	-2.89	365	301(100)	Y	Y	ND	ND	ND	ND	Y	Y	ND	ND	ND	ND
	15	Quercetin-3-glucoside	$C_{21}H_{20}O_{12}$	36.57	465.1008	464.0954	-5.26	365	303(100)	Y	Y	ND	Y	Y	ND	Y	Y	ND	Y	ND	ND
	16	Quercetin-3-xyloside	$C_{20}H_{18}O_{11}$	40.646	435.0898	434.0849	-6.77	365	303(100)	ND	ND	ND	ND	ND	ND	Y	ND	ND	Y	Y	ND
	17	Kaempferol-3-glucoside	$C_{21}H_{20}O_{11}$	42.46	449.108	448.1006	-0.98	365	287(100) 217(10)	Y	ND	ND	ND	ND	ND	Y	ND	ND	Y	ND	ND
	18	Quercetin-3-rhamnoside	$C_{21}H_{20}O_{11}$	45.785	449.1076	448.1005	-1.65	365	284(100)	ND	ND	ND	ND	ND	ND	Y	ND	ND	ND	ND	ND
	19	Syringetin-3-glucoside	$C_{23}H_{24}O_{13}$	56.106	509.1278	508.1217	-3.42	365	347(100)	ND	ND	ND	ND	ND	ND	Y	ND	ND	ND	ND	ND

Hydroxycinnamic and Hydroxybenzoic Acid Derivatives																				
21	Gallic acid	$C_7H_6O_5$	9.843	171.0285	170.0215	-4.94	280	127(100) 153(70)	Y	Y	Y	Y	Y	Y	ND	ND	Y	ND	ND	Y
22	Protocatechuic acid glucoside	$C_{13}H_{16}O_9$	14.719	317.0854	316.0794	-5.82	280	153(100) 109(10)	Y	Y	ND	ND	ND	ND	ND	ND	ND	Y	ND	ND
23	Chlorogenic acid	$C_{16}H_{18}O_9$	15.000	355.1007	354.0951	-6.33	325	147(100) 163(80)	ND	ND	ND	ND	ND	ND	ND	ND	ND	Y	Y	Y
24	Caffeic acid hexoside	$C_{15}H_{18}O_9$	15.093	343.1013	342.0951	-4.79	325	163(100)	ND	ND	ND	ND	ND	ND	Y	Y	ND	ND	ND	ND
25	Caftaric acid	$C_{13}H_{12}O_9$	16.701	313.0559	312.0481	-0.13	325	179(100) 149(86) 135(81)	Y	Y	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
26	4-Coumaroylquinic acid	$C_{16}H_{18}O_8$	18.849	339.1057	338.1002	-6.92	280 325	148(100)	ND	ND	ND	ND	ND	ND	ND	ND	ND	Y	Y	Y
27	p-Coumaric acid	$C_9H_8O_3$	19.495	165.0543	164.0473	-5.12	280	119(100)	Y	Y	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
28	Coumaric acid	$C_{13}H_{12}O_8$	20.329	297.0597	296.0532	-4.53	280	165(100)	Y	Y	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
29	Chlorogenic acid	$C_{16}H_{18}O_9$	20.46	355.1008	354.0951	-6.04	280 325	163(100)	ND	ND	ND	ND	ND	ND	Y	Y	Y	Y	Y	Y
30	Coumaric glucoside	$C_{15}H_{18}O_8$	26.391	327.1081	326.1002	0.18	280 325	165(100)	Y	Y	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Ellagitannins																				
31	Punicalin	$C_{34}H_{22}O_{22}$	10.053	783.0649	782.0602	-4.02	280,365	289(100) 601(87)	ND	ND	ND	Y	Y	Y	ND	ND	ND	ND	ND	ND
32	Pedunculagin	$C_{34}H_{24}O_{22}$	17.158	785.0788	784.0759	-6.30	280,365	188(100) 427(70) 358(11)	ND	ND	ND	Y	Y	Y	ND	ND	ND	ND	ND	ND
Negative mode [M-H]- (m/z)																				
Flavanols																				
12	Myricetin hexose	$C_{21}H_{20}O_{13}$	39.149	479.0847	480.0904	4.46	365	316(100)	Y	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
13	Quercetin-3-rutinoside	$C_{27}H_{30}O_{16}$	34.887	609.1478	610.1533	3.84	365	301(100) 271(90)	ND	ND	ND	ND	ND	ND	Y	ND	ND	Y	ND	ND
14	Quercetin-3-galactoside	$C_{21}H_{20}O_{12}$	35.776	463.0886	464.0954	2.24	365	301(100)	Y	Y	ND	ND	ND	ND	Y	Y	ND	ND	ND	ND
15	Quercetin-3-glucoside	$C_{21}H_{20}O_{12}$	36.539	463.0882	464.0954	1.38	365	301(100) 271(48)	Y	Y	ND	Y	Y	ND	Y	Y	ND	Y	Y	ND
16	Quercetin-3-xyloside	$C_{20}H_{18}O_{11}$	40.642	433.0808	434.0849	8.62	365	301(100)	ND	ND	ND	ND	ND	ND	Y	ND	ND	Y	ND	ND
17	Kaempferol-3-glucoside	$C_{21}H_{20}O_{11}$	42.501	447.093	448.1006	0.54	365	151(100) 285(25)	Y	ND	ND	ND	ND	ND	Y	ND	ND	Y	ND	ND
18	Quercetin-3-rhamnoside	$C_{21}H_{20}O_{11}$	45.696	447.0941	448.1005	3.21	365	301(100)	ND	ND	ND	ND	ND	ND	Y	ND	ND	ND	ND	ND
19	Syringetin-3-	$C_{23}H_{24}O_{13}$	56.121	507.1164	508.1217	5.00	365	345(100)	ND	ND	ND	ND	ND	ND	Y	ND	ND	ND	ND	ND

	glucoside																			
Hydroxycinnamic and Hydroxybenzoic Acid Derivatives																				
21	Gallic acid	$C_7H_6O_5$	9.831	169.014	170.0215	2.00	280	125(100) 79(12)	Y	Y	Y	Y	Y	Y	ND	ND	ND	ND	ND	ND
22	Protocatechuic glucoside	$C_{13}H_{16}O_9$	14.739	315.0724	316.0794	2.66	280	153(100) 109(10)	Y	Y	ND	ND	ND	ND	ND	ND	ND	Y	ND	ND
23	Chlorogenic acid	$C_{16}H_{18}O_9$	15.005	353.0891	354.0951	5.20	325	191(100) 135(25)	ND	ND	ND	ND	ND	ND	ND	ND	ND	Y	Y	Y
24	Caffeic acid hexoside	$C_{15}H_{18}O_9$	15.095	341.0871	342.0951	-0.47	325	179(100) 234(35)	ND	ND	ND	Y	ND	ND	ND	ND	ND	ND	ND	ND
25	Caftaric acid	$C_{13}H_{12}O_9$	16.693	311.0413	312.0481	3.33	325	179(100) 149(86) 135(81)	Y	Y	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
26	4-Coumaroylquinic acid	$C_{16}H_{18}O_8$	18.851	337.0939	338.1002	4.55	280325	119(100) 163(29)	ND	ND	ND	ND	ND	ND	ND	ND	ND	Y	Y	Y
27	p-Coumaric acid	$C_9H_8O_3$	19.485	163.0395	164.0473	0.24	280	119(100)	Y	Y	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
28	Coutaric acid	$C_{13}H_{12}O_8$	20.359	295.046	296.0532	2.16	280	163(100)	Y	Y	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
29	Chlorogenic acid	$C_{16}H_{18}O_9$	20.463	353.0874	354.0951	0.40	280325	191(100)	ND	ND	ND	ND	ND	ND	Y	Y	Y	Y	Y	Y
30	Coumaric glucoside	$C_{15}H_{18}O_8$	26.395	325.0936	326.1002	3.80	280	163(100) 265(94) 145(74)	Y	Y	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Ellagitannins																				
31	Punicalin	$C_{34}H_{22}O_{22}$	10.103	781.0514	782.0602	-1.23	280,365	289(100) 601(87)	ND	ND	ND	Y	Y	Y	ND	ND	ND	ND	ND	ND
32	Pedunculagin	$C_{34}H_{24}O_{22}$	17.152	783.07	784.0759	2.47	280,365	301(100) 302(87) 167(80)	ND	ND	ND	Y	Y	Y	ND	ND	ND	ND	ND	ND

Abbreviations: Y, detected; ND, not detected; G, grape; P, pomegranate; BB, blueberry; BC, black cherry

Table S3. HPLC-DAD quantification of phenolic compounds from juice samples before, after gastrointestinal (GI) digestion and colonic fermentation (CF). Values are expressed as mg/L ± SD, n=3.

Phenolic class	**Peak NO**	**Compound name**	**Standard used**	**Juice samples**											
				G			**P**			**BB**			**BC**		
				Before	After GI	After CF	Before	After GI	After CF	Before	After GI	After CF	Before	After GI	After CF
Anthocyanins															
	1	Delphinidin-3,5-diglucoside	Delphinidin-3-glucoside	7.70 ± 0.14^{a}	1.28 ± 0.04^{b}	ND	7.23 ± 0.82^{a}	1.33± 0.02^{b}	ND	ND	ND	ND	ND	ND	ND
	2	Cyanidin-3,5-diglucoside	Cyanidin-3-glucoside	11.75 ± 0.78^{a}	5.37 ± 0.14^{b}	ND	32.70± 2.69^{a}	12.05 ± 0.11^{b}	ND	ND	ND	ND	ND	ND	ND
	3	Delphinidin-3-glucoside	Delphinidin-3-glucoside	ND	ND	ND	ND	ND	ND	16.34 ± 1.28^{a}	2.34 ± 0.02^{b}	ND	ND	ND	ND
	4	Cyanidin-3-glucoside	Cyanidin-3-glucoside	23.47 ± 0.42^{a}	10.37 ± 0.82^{b}	ND	12.68 ± 0.78^{a}	6.08 ± 0.78^{b}	ND	7.48 ± 0.97	trace	ND	2.13 ± 0.01	trace	ND
	5	Delphinidin-3-arabinoside	Delphinidin-3-glucoside	ND	ND	ND	ND	ND	ND	10.33 ± 0.27^{a}	1.18 ± 0.13^{b}	ND	ND	ND	ND
	6	Pelargonidin-3-glucoside	Cyanidin-3-glucoside	11.03 ± 0.47^{a}	5.38 ± 0.02^{b}	ND	18.88 ± 0.42^{a}	7.61 ± 0.2^{b}	ND	n.d.	n.d.	ND	ND	ND	ND
	7	Petunidin-3-glucoside	Petunidin-3-glucoside	ND	ND	ND	ND	ND	ND	33.55 ± 1.94^{a}	11.93 ± 1.41^{b}	ND	ND	ND	ND
	8	Cyanidin-3-rutinoside	Cyanidin-3-glucoside	ND	ND	ND	ND	ND	ND	ND	ND	ND	112.78 ± 2.31^{a}	87.15 ± 3.92^{b}	ND
	9	Petunidin-3-arabinoside	Petunidin-3-glucoside	ND	ND	ND	ND	ND	ND	126.23 ± 1.87^{a}	38.66 ± 5.43^{b}	ND	ND	ND	ND
	10	Malvidin-3-glucoside	Malvidin-3-glucoside	ND	ND	ND	ND	ND	ND	11.30 ± 0.92^{a}	8.54 ± 0.13^{b}	ND	7.69 ± 0.40^{a}	6.87 ± 0.15^{b}	ND
	11	Malvidin-3-arabinoside	Malvidin-3-arabinoside	4.55 ± 0.09^{a}	3.48 ± 0.02^{b}	ND	ND	ND	ND	22.72 ± 1.95^{a}	17.50 ± 0.26^{b}	ND	ND	ND	ND
Total Anthocyanins				58.50	25.88		71.49	27.07		227.95	80.15		122.61	94.02	
Loss after GI					55.76%			62.13%			64.84%			23.32%	
Flavonols															
	12	Myricetin hexose	Quercetin-3-galactoside	10.80 ± 1.61	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
	13	Quercetin-3-rutinoside	Quercetin-3-galactoside	ND	ND	ND	ND	ND	ND	3.06 ± 0.10	ND	ND	23.77 ± 0.34^{a}	17.64 ± 1.18^{b}	ND

	14	Quercetin-3-galactoside	Quercetin-3-galactoside	9.70 ± 2.30^{a}	6.54 ± 0.78^{b}	ND	ND	ND	ND	27.83 ± 6.32^{a}	17.19 ± 0.62^{b}	ND	ND	ND	ND
	15	Quercetin-3-glucoside	Quercetin-3-galactoside	7.26 ± 0.08^{a}	5.88 ± 0.20^{b}	ND	46.43 ± 4.20^{a}	17.34 ± 0.03^{b}	ND	8.82 ± 0.08^{a}	6.20 ± 0.31^{b}	ND	2.69 ± 0.30	ND	ND
	16	Quercetin-3-xyloside	Quercetin-3-galactoside	ND	ND	ND	ND	ND	ND	3.93 ± 0.08	ND	ND	3.45 ± 0.19	trace	ND
	17	Kaempferol-3-glucoside	Kaempferol-3-glucoside	1.02 ± 0.04	ND	ND	ND	ND	ND	6.92 ± 0.07	ND	ND	1.82 ± 0.03	ND	ND
	18	Quercetin-3-rhamnoside	Quercetin-3-galactoside	ND	ND	ND	ND	ND	ND	4.66 ± 0.04	ND	ND	ND	ND	ND
	19	Syringetin-3-glucoside	Quercetin-3-galactoside	ND	ND	ND	ND	ND	ND	3.03 ± 0.08	ND	ND	ND	ND	ND
Total flavonols				28.78	12.42		46.43	17.34		58.25	23.39		31.73	17.64	
Loss after GI					56.85%			62.65%			59.85%			44.41%	
Hydroxycinnamic and Hydroxybenzoic Acid Derivatives															
	21	Gallic acid	Gallic acid	17.28 ± 1.61^{a}	12.96 ± 0.02^{b}	1012.94 ± 43.34^{c}	37.61 ± 1.51^{a}	26.44 ± 0.10^{b}	909.30 ± 11.93^{c}	ND	ND	854.55 ± 14.70	ND	ND	1098.25 ± 33.2
	22	Protocatechuic glucoside	Protocatechuic acid	80.46 ± 10.15^{a}	11.40 ± 0.37^{b}	ND	ND	ND	ND	ND	ND	ND	40.43 ±1.89	ND	ND
	23	Chlorogenic acid	Caffeic acid	ND	ND	ND	ND	ND	ND	ND	ND	ND	258.04 ± 6.52^{a}	264.79 ± 0.71^{a}	trace
	24	Caffeic acid hexoside	Caffeic acid	ND	ND	ND	ND	ND	ND	0.45 ± 0.01	trace	ND	ND	ND	ND
	25	Caftaric acid	Caffeic acid	84.48 ± 1.59^{a}	67.32 ± 5.43^{b}	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
	26	4-Coumaroylquinic acid	Caffeic acid	ND	ND	ND	ND	ND	ND	ND	ND	ND	55.16 ± 0.49^{a}	54.58 ± 0.11^{a}	42.47 ± 1.42^{b}
	27	Coumaric acid	*p*-Coumaric acid	5.68 ± 0.16^{a}	4.74 ± 0.06^{b}	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
	28	Coutaric acid	*p*-Coumaric acid	6.07 ± 0.23^{a}	4.84 ± 0.42^{b}	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
	29	Chlorogenic acid	Caffeic acid	ND	ND	ND	ND	ND	ND	232.37 ± 5.21^{a}	194.26 ± 10.51^{b}	9.39 ± 0.79	25.84 ± 0.94^{a}	24.90 ± 0.17^{a}	102.06 ± 1.40^{b}
	30	Coumaric glucoside	*p*-Coumaric acid	7.90 ± 0.12^{a}	3.37 ± 0.26^{b}	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Total hydroxycinnamic and hydroxybenzoic acid derivatives				201.87	104.63	1012.94	37.61	26.44	909.30	232.82	194.26	863.94	379.47	344.27	1242.78

Loss after GI		48.17%		29.70%		16.56%		9.28%
Total phenolics	289.15	142.93	155.53	70.85	519.02	297.80	533.81	455.93
Total loss		50.57%		54.45%		42.62%		14.59%

Different superscripts in the same row indicate significant differences ($P < 0.05$) among the same phenolic concentration at different phase of digestion.

Table S4. HPLC-ESI-QTOF-MS/MS identification and quantification of phenolic metabolites after colonic fermentation.

Phenolic metabolites	Compound name	Molecular formula	Retention time (min)	Experimental mass	Theoretical mass	Error (ppm)	UV λmax (nm)	Mass fragments	Detected in sample after CF			
Negative mode [M-H]- (m/z)												
Peak NO									G	P	BB	BC
M1	Gallic acid	C7H6O5	9.831	169.0137	170.0215	0.24	280	125(100)	Y	Y	Y	Y
M2	Phloroglucinol	C6H6O3	11.599	125.0235	126.0317	-2.86	280	125(100)	ND	Y	ND	Y
M3	Protocatechuic acid	C7H6O4	14.350	153.0189	154.0266	0.91	280	116(100)	Y	Y	Y	Y
M4	Hydroxybenzonic acid	C7H6O3	19.495	137.0241	138.0316	2.46	280	93(100)	ND	Y	ND	Y
M5	Vanillic acid	C8H8O4	22.575	167.0338	168.0423	-3.93	280	108(100)	ND	ND	Y	Y
M6	Syringic acid	C9H10O5	24.182	197.0451	198.052823	0.59	325	153(100)	Y	ND	ND	ND
M7	p-coumaric acid	C9H8O3	29.753	163.0401	164.0473	3.90	325	119(100)	Y	Y	Y	Y
M8	ferulic acid	C10H10O4	33.779	193.0501	194.0579	0.21	325	134(100)	Y	ND	ND	ND
M9	3-(3-hydroxyphenyl)-propanoic acid	C9H10O3	34.067	165.0549	166.0630	-1.57	280	121(100) 119(50)	ND	Y	Y	Y
M10	Benzoic acid	C7H6O2	38.049	121.0285	122.0368	-3.77	280	121(100) 108(10)	ND	Y	Y	Y
Positive mode [M+H]+ (m/z)												
M1	Gallic acid	C7H6O5	9.843	171.0285	170.0215	-4.94	280	127(100) 153(70)	Y	Y	Y	Y
M2	Phloroglucinol	C6H6O3	11.354	127.0391	126.0317	-3.49	280	109(100)	ND	Y	ND	Y
M3	Protocatechuic acid	C7H6O4	ND									
M4	Hydroxybenzoic acid	C7H6O3	19.495	139.0393	138.0316	-1.01	280	77(100)	ND	Y	ND	Y
M5	Vanillic acid	C8H8O4	22.605	169.0501	168.0423	-0.24	280		ND	ND	Y	Y
M6	Syringic acid	C9H10O5	24.098	199.0596	198.052823	-5.37	280	155(100) 140(10)	Y	ND	ND	ND
M7	p-coumaric acid	C9H8O3	29.885	165.0543	164.0473	-5.12	325	119(100)	Y	Y	Y	Y
M8	ferulic acid	C10H10O4	33.739	195.0651	194.0579	-3.30	325	89(100)	Y	ND	ND	ND
M9	3-(3-hydroxyphenyl)-propanoic acid	C9H10O3	ND									

M10	Benzoic acid	C7H6O2	38.047	123.0444	122.0368	-1.97	280	123(100) 95(45)	ND	Y	Y	Y

HPLC-DAD quantification of phenolic metabolites

Peak No	Compound name	Standard used	G	P	BB	BC
M1	Gallic acid	Gallic acid	1012.94 ± 43.34^{a}	909.30 ± 11.93^{b}	854.55 ± 14.70^{c}	1098.25 ± 33.2^{a}
M2	Phloroglucinol	Phloroglucinol	ND	152.19 ± 3.13^{a}	ND	410.24 ±11.08^{b}
M3	Protocatechuic acid	Protocatechuic acid	28.72 ± 4.41^{a}	42.45 ± 3.12^{b}	232.73 ± 17.45^{c}	233.68 ± 7.66^{c}
M4	Hydroxybenzoic acid	Hydroxybenzoic acid	ND	135.99 ± 3.47^{a}	ND	160.48 ± 2.97^{b}
M5	Vanillic acid	Vanillic acid	ND	ND	339.98 ± 11.01^{a}	377.96 ± 20.45^{a}
M6	Syringic acid	Syringic acid	22.49 ± 0.82	ND	ND	ND
M7	*p*-coumaric acid	*p*-coumaric acid	229.13 ± 4.85^{a}	252.84 ± 25.32^{a}	225.50 ± 4.61^{a}	227.65 ± 3.37^{a}
M8	Ferulic acid	Ferulic acid	11.77 ± 0.86	ND	ND	ND
M9	3-(3-hydroxyphenyl)-propanoic acid	Caffeic acid	ND	5.36 ± 0.25^{a}	19.30 ± 0.94^{b}	6.70 ± 1.42^{a}
M10	Benzoic acid	Benzoic acid	ND	158.80 ± 6.24^{a}	152.90 ± 6.48^{ab}	145.31 ± 6.93^{b}
	Total		1305.05	1656.93	1824.96	2660.27

Abbreviations: Y, detected; ND, not detected; G, grape; P, pomegranate; BB, blueberry; BC, black cherry. Different superscripts in the same row indicate significant differences ($P < 0.05$) among the same phenolic concentration in different samples.

Table S5. Composition (%) of bacterial species of different treatment groups

Sample code	k1	k2	k3	BB1	BB2	BB3	BBlc1	BBlc2	BBlc3	BC1	BC2	BC3	BClc1	BClc2	BClc3
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_eggerthii	46.82	46.60	64.98	36.06	34.34	37.33	29.87	42.75	39.87	34.35	34.13	29.57	36.60	47.58	45.20
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_dorei	2.24	2.98	0.57	3.89	4.83	3.44	4.64	6.05	5.09	6.50	4.87	3.50	8.46	8.67	4.45
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_vulgatus	1.24	3.98	0.96	3.79	3.55	2.61	7.69	5.53	5.07	8.29	6.09	2.19	9.99	7.48	6.24
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_massiliensis	0.41	2.85	0.00	9.59	8.67	3.86	23.54	5.24	8.39	11.92	8.31	2.19	9.25	0.92	3.42
d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus_faecalis	6.76	3.13	4.97	3.72	4.64	3.52	2.43	2.21	3.26	8.26	7.98	9.27	0.00	1.50	1.74
d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_thermophilus	4.46	1.69	2.76	2.99	4.09	4.17	1.80	2.14	2.16	2.05	1.65	5.47	0.84	1.34	1.42
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella;__	7.02	2.82	5.89	6.25	4.46	4.05	5.85	4.44	4.01	4.30	5.29	6.81	4.70	5.58	4.51
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_uniformis	4.44	3.26	1.45	2.40	2.09	1.99	2.97	3.91	3.34	2.67	2.49	1.01	4.10	3.45	3.80
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Dorea;__	1.18	2.64	0.00	1.49	1.34	1.66	2.23	2.08	1.73	1.50	2.41	2.41	3.41	0.79	1.34
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae;g__Alistipes;__	1.43	2.56	1.25	1.34	1.57	1.78	0.00	1.55	0.00	1.50	1.45	1.57	1.88	1.58	0.97
d__Bacteria;p__Firmicutes;c__Bacilli;o__Erysipelotrichales;f__Erysipelatoclostridiaceae;g__Erysipelotrichaceae_UCG-003;__	0.72	0.95	1.20	0.75	0.66	0.81	0.22	0.37	0.71	0.44	0.52	0.84	0.00	0.61	0.37
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Blautia;s__human_gut	0.50	0.00	1.13	0.59	1.10	0.53	0.00	0.87	1.24	0.00	0.00	1.03	0.99	0.00	0.69
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Fusicatenibacter;s__uncultured_bacterium	1.45	1.38	1.90	2.33	3.72	4.54	1.67	1.07	3.73	1.50	0.97	4.08	0.00	1.26	1.13
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Hafniaceae;g__Hafnia-Obesumbacterium;s__Hafnia_paralvei	0.00	0.00	0.00	0.62	0.69	1.00	1.13	0.59	1.04	1.92	1.09	2.71	2.62	3.11	2.43
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Dorea;s__uncultured_bacterium	0.60	3.92	0.35	2.74	2.91	2.07	1.24	2.75	1.69	2.07	4.30	6.77	0.00	0.68	1.63
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_stercoris	1.35	0.97	0.27	1.33	1.37	1.18	2.34	3.30	2.04	1.63	1.19	0.82	2.72	3.29	2.89
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;__;__	0.62	0.95	0.85	1.18	1.05	1.63	1.08	0.53	0.35	0.36	2.63	2.29	0.00	0.74	1.03
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Blautia;s__metagenome	1.48	1.95	1.08	2.98	2.91	4.03	0.00	0.53	2.50	1.09	0.46	4.10	0.00	0.00	0.00
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae;g__Alistipes;s__Alistipes_putredinis	0.71	0.00	0.00	0.60	0.83	0.69	0.76	0.00	0.67	0.00	0.00	0.00	0.00	0.00	0.00
d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus_paracasei	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5.34	3.24	4.09
d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus_garvieae	1.64	1.38	0.87	1.59	1.87	2.10	1.32	1.33	2.18	0.93	1.19	1.95	0.00	0.84	0.61
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Anaerostipes;s__metagenome	0.66	0.00	0.82	0.38	0.00	0.91	0.67	0.76	0.71	0.67	1.15	1.03	0.00	0.00	1.21
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_thetaiotaomicron	0.92	2.39	0.87	1.00	1.45	0.99	2.23	2.47	1.28	1.66	2.63	0.94	2.67	1.21	0.95
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__[Ruminococcus]_torques_group;__	0.80	0.82	0.43	0.37	0.71	0.76	0.00	0.85	0.79	0.75	0.54	0.22	0.00	0.66	0.00
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Blautia;__	1.59	5.90	1.60	1.82	2.71	4.00	0.04	1.33	2.67	0.00	0.00	1.51	0.00	0.00	0.61
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_plebeius	0.09	0.00	0.13	0.45	0.51	0.38	0.00	0.68	0.35	0.00	0.34	0.00	0.84	0.47	0.64
d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Strept	0.49	0.00	0.53	0.68	0.69	1.04	0.00	0.00	0.33	0.00	0.00	1.23	0.00	0.00	0.23

ococcus;s__Coregonus_clupeaformis															
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Tannerellaceae;g__Parabacteroides;s__Parabacteroides_distasonis	0.81	1.85	0.60	0.31	0.21	0.00	1.39	1.77	0.16	2.07	2.82	0.48	1.24	1.45	2.31
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Subdoligranulum;__	0.74	0.26	0.28	0.63	0.68	0.88	0.91	0.24	0.67	0.41	0.80	0.62	0.35	0.32	0.15
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Subdoligranulum;s__uncultured_bacterium	0.72	0.74	0.70	1.02	0.62	0.64	0.67	0.35	0.59	0.47	0.32	0.94	0.00	0.53	0.40
d__Bacteria;p__Firmicutes;c__Negativicutes;o__Acidaminococcales;f__Acidaminococcaceae;g__Phascolarctobacterium;s__Phascolarctobacterium_faecium	0.54	0.23	0.00	0.20	0.24	0.30	0.43	0.59	0.00	0.31	0.24	0.50	0.00	0.58	0.26
d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_vestibularis	0.00	0.31	0.00	0.32	0.00	0.51	0.00	0.31	0.00	0.00	0.00	0.00	0.00	0.29	0.21
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__[Eubacterium]_hallii_group;s__unidentified	0.43	0.51	0.30	0.47	0.00	0.00	0.00	0.44	0.39	0.00	0.00	0.52	0.00	0.00	0.15
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Sutterellaceae;g__Parasutterella;s__uncultured_bacterium	0.15	0.18	0.00	0.00	0.00	0.06	0.00	0.83	0.20	0.00	0.52	0.00	0.15	0.87	1.35
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_salyersiae	0.74	0.00	0.17	0.16	0.18	0.14	0.00	0.20	0.20	0.10	0.00	0.00	0.00	0.00	0.23
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__[Eubacterium]_hallii_group;__	0.00	0.00	0.00	0.08	0.86	1.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae;g__Alistipes;s__Alistipes_shahii	0.22	0.23	0.00	0.00	0.00	0.00	0.33	0.26	0.10	0.00	0.26	0.00	0.40	0.00	0.00
d__Bacteria;p__Firmicutes;c__Negativicutes;o__Veillonellales-Selenomonadales;f__Selenomonadaceae;g__Megamonas;s__uncultured_bacterium	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__[Eubacterium]_hallii_group;s__[Eubacterium]_hallii	0.64	0.00	0.60	0.31	0.00	0.00	0.00	0.00	0.45	0.00	0.00	0.46	0.00	0.00	0.29
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__[Ruminococcus]_torques_group;s__uncultured_Firmicutes	0.30	0.33	0.15	0.39	0.44	0.49	0.00	0.18	0.24	0.08	0.00	0.50	0.00	0.00	0.00
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;__	0.33	0.41	0.15	0.17	0.18	0.00	0.54	0.06	0.00	0.83	0.34	0.18	1.24	0.18	0.23
d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus_rhamnosus	0.22	0.00	0.23	0.16	0.14	0.14	0.17	0.00	0.00	0.08	0.32	0.42	0.00	0.00	0.00
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Faecalibacterium;__	0.00	0.00	0.00	0.45	0.29	0.51	0.20	0.37	0.31	0.00	0.00	0.00	0.45	0.00	0.47
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Tannerellaceae;g__Parabacteroides;s__Parabacteroides_merdae	0.22	0.44	0.15	0.24	0.27	0.22	0.15	0.20	0.00	0.18	0.00	0.00	0.49	0.00	0.16
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Dorea;s__Dorea_formicigenerans	0.28	0.00	0.00	0.45	0.56	0.00	0.00	0.00	0.00	0.00	0.54	0.00	0.00	0.00	0.52
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_bacterium	0.56	0.33	0.42	0.28	0.35	0.08	0.00	0.17	0.53	0.13	0.06	0.02	0.49	0.08	0.00
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__[Eubacterium]_hallii_group;s__uncultured_bacterium	0.89	0.00	0.20	0.33	0.00	0.92	0.00	0.00	0.31	0.00	0.00	0.40	0.00	0.00	0.00
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Incertae_Sedis;s__uncultured_bacterium	0.24	0.10	0.25	0.26	0.12	0.13	0.09	0.00	0.16	0.00	0.00	0.00	0.00	0.18	0.13
d__Bacteria;p__Actinobacteriota;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriaceae;g__Collinsella;s__Collinsella_aerofaciens	0.27	0.00	0.18	0.00	0.20	0.19	0.00	0.06	0.00	0.00	0.14	0.22	0.00	0.11	0.11
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Oscillospiraceae;g__uncultured;s__uncultured_rumen	0.26	0.00	0.00	0.25	0.29	0.08	0.00	0.00	0.14	0.00	0.00	0.18	0.00	0.00	0.00
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__human_gut	0.10	0.00	0.00	0.17	0.06	0.00	0.24	0.17	0.00	0.00	0.36	0.00	0.00	0.00	0.00
d__Bacteria;p__Actinobacteriota;c__Coriobacteriia;o__Coriobacteriales;f__Eggerthellaceae;g__Slackia;s__Slackia_sp.	0.29	0.00	0.00	0.00	0.12	0.18	0.00	0.13	0.00	0.00	0.00	0.00	0.00	0.00	0.00
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Hafniaceae;g__Hafnia-Obesumbacterium;__	0.00	0.00	0.00	0.21	0.18	0.00	0.00	0.00	0.00	0.73	0.44	0.00	0.30	0.00	0.69
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_ovatus	0.00	0.00	0.00	0.07	0.00	0.00	0.11	0.00	0.00	0.00	0.28	0.00	0.00	0.16	0.00

d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Lachnoclostridium;s__[Clostridium]_scindens	0.17	0.00	0.00	0.13	0.32	0.27	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Marinifilaceae;g__Odoribacter;s__Odoribacter_splanchnicus	0.19	0.00	0.00	0.00	0.00	0.00	0.22	0.06	0.00	0.00	0.30	0.00	0.00	0.00	0.19
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Anaerostipes;s__Anaerostipes_hadrus	0.35	0.00	0.28	0.26	0.00	0.30	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTHERS	0.73	0.95	0.50	1.74	0.98	1.37	0.85	0.28	0.35	0.23	0.54	1.07	0.49	0.24	0.55

Table S5. Composition (%) of bacterial species of different treatment groups (cont.)

Sample code	G1	G2	G3	Glc1	Glc2	Glc3	P1	P2	P3	Plc1	Plc2	Plc3
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_eggerthii	41.43	33.44	35.60	31.96	45.31	32.72	27.11	39.40	27.71	45.12	44.94	22.00
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_dorei	7.32	6.34	1.20	5.08	6.05	5.75	4.67	6.48	3.81	5.76	5.07	5.23
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_vulgatus	4.60	5.07	3.39	4.71	6.60	11.57	4.05	6.22	4.18	4.78	5.47	12.48
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_massiliensis	1.82	17.02	0.28	13.93	10.07	13.49	11.41	10.35	7.65	3.11	5.56	13.02
d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus_faecalis	3.36	2.52	5.50	3.62	2.52	1.57	8.70	2.61	3.33	2.77	1.60	1.07
d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_thermophilus	4.04	2.35	6.88	3.31	0.95	1.64	2.92	2.83	3.49	2.99	3.47	1.07
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella;__	6.06	2.10	10.22	4.60	6.46	4.61	5.09	4.98	8.21	5.36	5.88	7.47
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_uniformis	2.40	2.51	1.73	2.67	2.52	3.34	1.44	2.08	1.81	2.60	3.26	2.08
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Dorea;__	1.16	2.13	2.50	1.79	6.73	1.12	2.07	2.67	2.57	1.62	1.73	0.00
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae;g__Alistipes;__	0.72	1.00	0.41	0.71	0.00	1.39	1.36	0.00	2.40	1.28	1.58	0.77
d__Bacteria;p__Firmicutes;c__Bacilli;o__Erysipelotrichales;f__Erysipelatoclostridiaceae;g__Erysipelotrichaceae_UCG-003;__	0.90	0.74	1.05	0.40	0.75	0.55	1.00	0.72	0.92	0.82	0.60	0.67
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Blautia;s__human_gut	0.00	0.59	0.81	1.50	0.00	0.40	0.00	0.00	0.85	1.42	0.68	0.97
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Fusicatenibacter;s__uncultured_bacterium	1.35	1.60	3.25	2.21	1.29	0.87	3.86	1.73	2.33	2.33	2.73	2.06
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Hafniaceae;g__Hafnia-Obesumbacterium;s__Hafnia_paralvei	0.85	1.68	0.86	2.21	2.18	1.12	0.00	0.00	0.00	0.00	0.00	0.00
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Dorea;s__uncultured_bacterium	1.72	3.95	5.03	3.62	0.00	2.24	3.88	2.21	3.11	1.97	1.87	0.37
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_stercoris	2.86	1.77	1.48	2.52	2.59	1.84	1.11	2.51	1.41	2.50	1.64	4.17
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;__;__	1.55	1.61	2.39	1.21	0.00	0.82	1.75	0.85	1.76	1.68	0.53	0.00
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Blautia;s__metagenome	0.17	1.40	0.83	2.00	0.00	0.00	3.07	0.00	3.83	1.09	1.66	0.00
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae;g__Alistipes;s__Alistipes_putredinis	0.43	0.00	0.00	0.00	0.75	0.00	0.00	1.20	1.44	0.00	0.00	0.00
d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus_paracasei	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus_garvieae	1.25	0.69	1.02	1.56	0.00	0.82	2.27	1.20	2.18	1.39	1.26	0.57
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Anaerostipes;s__metagenome	0.17	0.62	1.56	0.73	0.00	0.73	0.00	0.91	0.37	1.28	0.00	0.00

d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_thetaiotaomicron	1.66	1.77	0.38	0.79	1.77	2.75	1.94	1.47	2.02	1.57	0.92	1.22
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__[Ruminococcus]_torques_group;__	1.05	0.30	0.64	0.60	0.00	0.12	0.77	0.46	0.50	0.65	0.94	0.00
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Blautia;__	1.26	1.12	0.78	1.64	0.00	0.82	0.65	0.00	2.27	0.35	2.43	0.72
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_plebeius	0.57	0.26	0.30	0.52	0.00	0.48	0.17	0.00	0.85	0.52	0.40	3.82
d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Coregonus_clupeaformis	0.43	0.00	0.00	0.58	0.00	0.00	1.00	0.10	0.94	0.00	0.77	0.00
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Tannerellaceae;g__Parabacteroides;s__Parabacteroides_distasonis	2.58	0.72	2.33	0.77	1.29	2.17	0.48	2.28	0.30	1.03	0.34	2.03
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Subdoligranulum;__	0.33	0.00	0.38	0.58	0.00	0.43	0.94	0.68	0.52	0.59	0.53	0.22
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Subdoligranulum;s__uncultured_bacterium	0.84	1.45	0.52	0.98	1.77	0.65	0.88	0.85	1.98	0.63	0.55	1.41
d__Bacteria;p__Firmicutes;c__Negativicutes;o__Acidaminococcales;f__Acidaminococcaceae;g__Phascolarctobacterium;s__Phascolarctobacterium_faecium	1.04	0.00	2.74	0.42	0.34	0.53	0.27	0.16	0.35	0.66	0.34	2.63
d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__Streptococcus_vestibularis	0.34	0.00	0.25	0.00	0.00	0.00	0.71	0.46	0.00	0.00	0.00	0.00
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__[Eubacterium]_hallii_group;s__unidentified	0.10	0.18	0.34	0.00	0.00	0.00	0.00	0.00	0.63	0.23	0.26	0.00
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Sutterellaceae;g__Parasutterella;s__uncultured_bacterium	0.92	0.17	0.72	0.00	0.00	0.43	0.00	0.72	0.20	0.00	0.17	0.00
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_salyersiae	0.32	0.12	0.19	0.00	0.00	0.22	0.00	0.26	0.22	0.18	0.00	0.00
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__[Eubacterium]_hallii_group;__	0.00	0.24	0.13	0.56	0.00	0.00	1.21	0.00	0.00	0.88	0.26	0.00
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae;g__Alistipes;s__Alistipes_shahii	0.33	0.00	0.00	0.38	0.00	0.42	0.35	0.00	0.33	0.00	0.00	0.00
d__Bacteria;p__Firmicutes;c__Negativicutes;o__Veillonellales-Selenomonadales;f__Selenomonadaceae;g__Megamonas;s__uncultured_bacterium	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	3.67
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__[Eubacterium]_hallii_group;s__[Eubacterium]_hallii	0.42	0.41	0.56	0.00	0.00	0.14	0.00	0.55	0.17	0.00	0.30	0.00
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__[Ruminococcus]_torques_group;s__uncultured_Firmicutes	0.37	0.27	0.63	0.56	0.00	0.07	0.31	0.00	0.50	0.45	0.23	0.00
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;__	0.22	0.56	0.31	0.19	0.00	1.02	0.27	0.00	0.20	0.68	0.09	1.22
d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus_rhamnosus	0.00	0.00	0.33	0.27	0.00	0.17	0.33	0.29	0.22	0.23	0.00	0.72
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Faecalibacterium;__	0.17	0.14	0.00	0.00	0.00	0.17	0.06	0.52	0.67	0.00	0.38	4.29
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Tannerellaceae;g__Parabacteroides;s__Parabacteroides_merdae	0.20	0.24	0.16	0.25	0.00	0.20	0.25	0.23	0.00	0.00	0.00	0.00
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Dorea;s__Dorea_formicigenerans	0.00	0.32	0.72	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__uncultured_bacterium	0.14	0.26	0.00	0.21	0.07	0.32	0.06	0.52	0.18	0.20	0.13	0.00
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__[Eubacterium]_hallii_group;s__uncultured_bacterium	0.00	0.14	0.00	0.00	0.00	0.00	0.44	0.00	0.00	0.00	0.00	0.00
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Incertae_Sedis;s__uncultured_bacterium	0.18	0.08	0.25	0.00	0.00	0.00	0.17	0.20	0.39	0.00	0.30	0.00
d__Bacteria;p__Actinobacteriota;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriaceae;g__Collinsella;s__Collinsella_aerofaciens	0.18	0.00	0.16	0.00	0.00	0.14	0.19	0.23	0.35	0.12	0.23	0.00
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Oscillospiraceae;g__uncultured;s__uncultured_rumen	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.26	0.00	0.00	0.00

d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__human_gut	0.27	0.08	0.00	0.00	0.00	0.34	0.00	0.00	0.06	0.00	0.00	0.62
d__Bacteria;p__Actinobacteriota;c__Coriobacteriia;o__Coriobacteriales;f__Eggerthellaceae;g__Slackia;s__Slackia_sp.	0.13	0.15	0.39	0.00	0.00	0.00	0.00	0.20	0.17	0.14	0.00	0.00
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Hafniaceae;g__Hafnia-Obesumbacterium;__	0.25	0.00	0.00	0.00	0.00	0.17	0.00	0.00	0.00	0.00	0.00	0.00
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Bacteroides_ovatus	0.34	0.30	0.00	0.00	0.00	0.20	0.00	0.00	0.22	0.18	0.00	0.50
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Lachnoclostridium;s__[Clostridium]_scindens	0.14	0.15	0.00	0.00	0.00	0.20	0.25	0.00	0.00	0.00	0.00	0.00
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Marinifilaceae;g__Odoribacter;s__Odoribacter_splanchnicus	0.15	0.27	0.00	0.00	0.00	0.29	0.00	0.29	0.00	0.00	0.00	0.00
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Anaerostipes;s__Anaerostipes_hadrus	0.00	0.15	0.25	0.23	0.00	0.00	0.52	0.00	0.39	0.00	0.00	0.00
OTHERS	0.92	1.04	0.56	0.12	0.00	0.94	2.00	0.59	1.72	0.83	0.92	2.93

Table S6. Significant microbial groups that pass the LDA score (> 2.0) threshold

MICROBIAL GROUP	SCORE	DISTINCTIVE IN
CONTROL (NO JUICE) VS. JUICE		
d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Sutterellaceae.g__Parasutterella.s__uncultured_bacterium	4.20362393	CONTROL
d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae	4.47246924	CONTROL
d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Anaerostipes.s__Lactobacillus_sp_	3.24641694	CONTROL
d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales	4.86497256	JUICE
d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_thetaiotaomicron	4.39991857	CONTROL
d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Anaerostipes.s__Anaerostipes_hadrus	3.54744694	CONTROL
d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_vulgatus	5.26216372	JUICE
d__Bacteria.p__Firmicutes.c__Negativicutes.o__Acidaminococcales.f__Acidaminococcaceae.g__Phascolarctobacterium.s__uncultured_organism	3.24641694	CONTROL
d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Sutterellaceae.g__Parasutterella	4.20362393	CONTROL
GRAPE VS. POMEGRANATE VS. BLACKBERRY VS. BLACK CHERRY		
d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales	4.9400789	POMEGRANATE