

SUPPLEMENTAL FIGURE AND TABLES

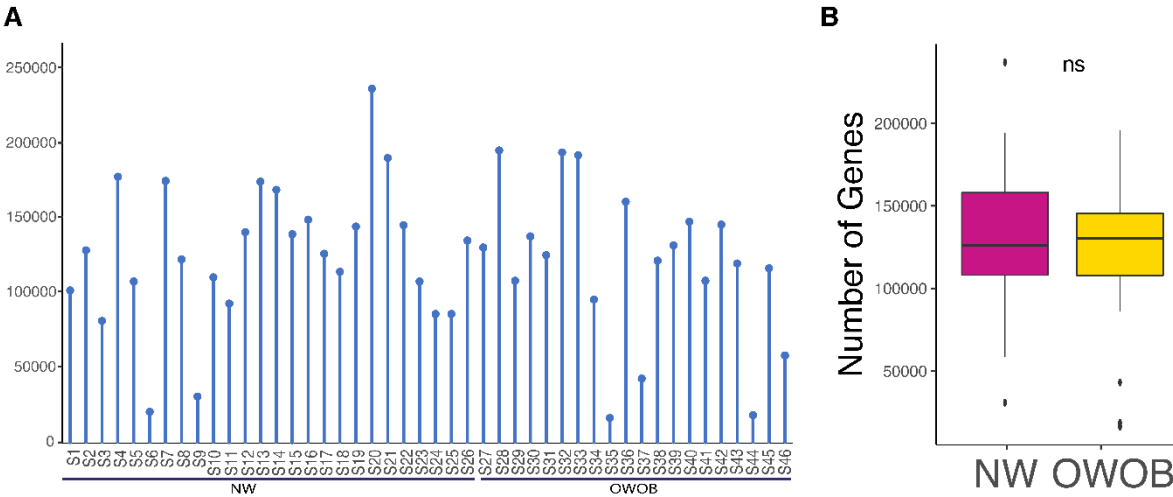


Figure S1: Number of genes predicted for each library **(A)** and pairwise comparison of number of genes predicted in NW vs OWOB **(B)**.

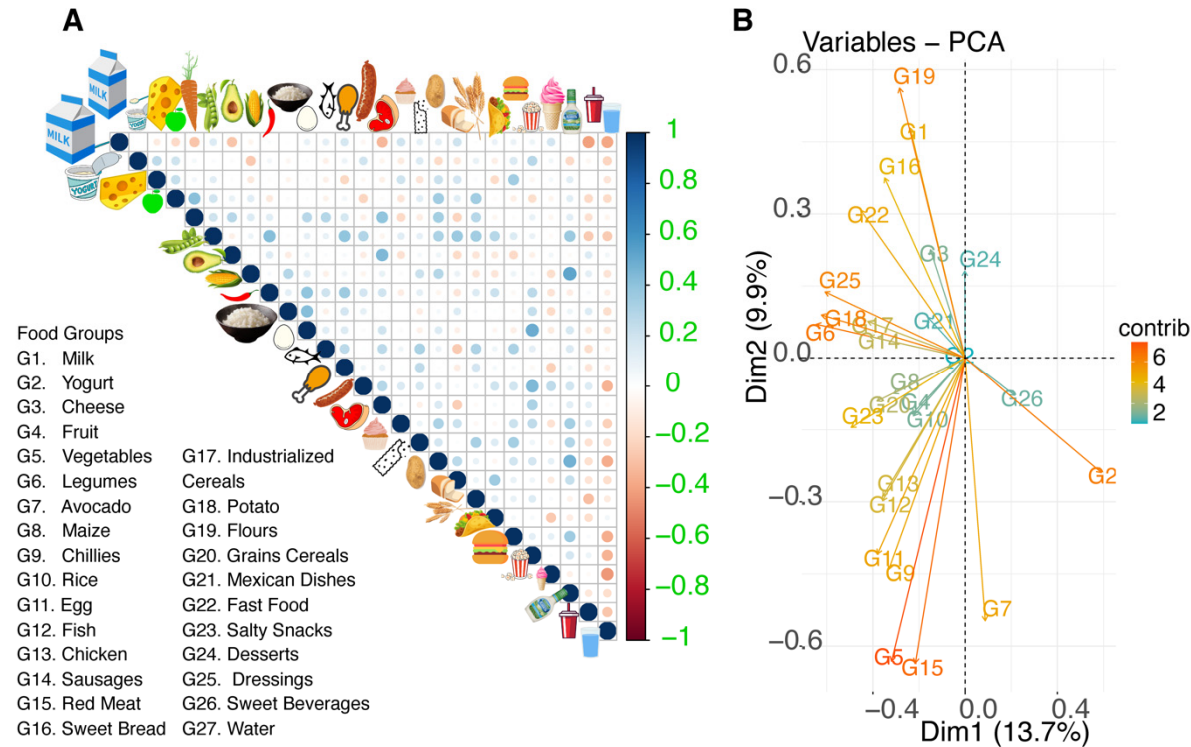


Figure S2: Correlation matrix between food groups that indicates relation between variables (**A**) and Principal Component Analysis (PCA) biplot of the 27 food group vectors where the principal component (PC) 1 explains 13.7% of total variance and PC2 explains 9.9% (**B**).

Table S1: Each of the 107 food items contained in the 11 sections surveyed in the FFQ.

Original FFQ sections		Redefined food groups		Food items
1	Dairy	G1-Milk	1	whole milk (200 ml)
1	Dairy	G1-Milk	2	skim or light milk (200 ml)
1	Dairy	G24-Desserts	3	chocolate milk (200 ml)
1	Dairy	G3-Cheese	4	Oaxaca type cheese (slice)
1	Dairy	G3-Cheese	5	Manchego type cheese (slice)
1	Dairy	G3-Cheese	6	Cream cheese (15 ml)
1	Dairy	G3-Cheese	7	American cheese (slice)
1	Dairy	G2-Yogurt	8	Yogurth (250 ml)
1	Dairy	G24-Desserts	9	Petit Suisse (Danonino or Petizoo, 84 gr)
1	Dairy	G2-Yogurt	10	Yakult, Chamyto or Lalacult (fermented milk, 80 ml)
1	Dairy	G2-Yogurt	11	Activia Flora, Actimel or Svelty Gastro Protect (Probiotic yogurth, 255 ml)
1	Dairy	G24-Desserts	12	Ice cream or sorbet (100 gr)
2	Fruits	G4-Fruit	13	Banana
2	Fruits	G4-Fruit	14	Orange
2	Fruits	G4-Fruit	15	Orange juice (200 ml)
2	Fruits	G4-Fruit	16	Melon (slice)
2	Fruits	G4-Fruit	17	Watermelon (slice)
2	Fruits	G4-Fruit	18	Pineapple (slice)
2	Fruits	G4-Fruit	19	Papaya (slice)
2	Fruits	G4-Fruit	20	Peach
2	Fruits	G4-Fruit	21	Apple
2	Fruits	G4-Fruit	22	Pear
2	Fruits	G4-Fruit	23	Mango
2	Fruits	G4-Fruit	24	Tangerine
2	Fruits	G4-Fruit	25	Strawberries (1/2 cup)

2	Fruits	G4-Fruit	26	Grapes (1/2 cup)
2	Fruits	G4-Fruit	27	Plum (3)
3	Vegetables	G5-Vegetables	28	Tomato
3	Vegetables	G18-Potato	29	Potato
3	Vegetables	G5-Vegetables	30	Jicama
3	Vegetables	G5-Vegetables	31	Cucumber
3	Vegetables	G5-Vegetables	32	Carrot
3	Vegetables	G5-Vegetables	33	Lettuce (a leaf)
3	Vegetables	G5-Vegetables	34	zucchini or squash (1 cup)
3	Vegetables	G5-Vegetables	35	Nopal
3	Vegetables	G7-Avocado	36	Avocado (1/2)
3	Vegetables	G5-Vegetables	37	Broccoli (1 cup)
3	Vegetables	G9-Chillies	38	hot sauce (15 ml) or chlies
3	Vegetables	G9-Chillies	39	Canned chilies
3	Vegetables	G8-Maize	40	Corn
4	Legumes	G6-Legumes	41	Beans (200 gr)
4	Legumes	G6-Legumes	42	Peas (1/2 cup)
4	Legumes	G6-Legumes	43	lentils (200 gr)
5	Eggs, meats, and sausages	G11-Egg	44	Egg
5	Eggs, meats, and sausages	G14-Sausages	45	ham turkey or pork (slice)
5	Eggs, meats, and sausages	G13-Chicken	46	Chicken (1 piece)
5	Eggs, meats, and sausages	G15-RedMeat	47	Beef (125 gr)
5	Eggs, meats, and sausages	G15-RedMeat	48	Pork (125 gr)
5	Eggs, meats, and sausages	G12-Fish	49	Canned tuna (70 gr)
5	Eggs, meats, and sausages	G15-RedMeat	50	Pork rind
5	Eggs, meats, and sausages	G14-Sausages	51	Sausage (turkey or pork)
5	Eggs, meats, and sausages	G15-RedMeat	52	Bacon (slice)

5	Eggs, meats, and sausages	G13-Chicken	53	Liver (1 piece)
5	Eggs, meats, and sausages	G14-Sausages	54	Chorizo (1 piece)
5	Eggs, meats, and sausages	G12-Fish	55	Fish steak
5	Eggs, meats, and sausages	G12-Fish	56	Canned sardines
6	Mexican and typical dises	G21-MexicanDishes	57	Pork taco
6	Mexican and typical dises	G15-RedMeat	58	Barbacoa taco (sheep or lamb)
6	Mexican and typical dises	G21-MexicanDishes	59	Pastor taco (pork)
6	Mexican and typical dises	G21-MexicanDishes	60	Quesadilla, sope or gordita grilled
6	Mexican and typical dises	G21-MexicanDishes	61	Quesadilla, sope or gordita fried
6	Mexican and typical dises	G22-FastFood	62	French fries (1 portion)
6	Mexican and typical dises	G22-FastFood	63	Hamburger
6	Mexican and typical dises	G22-FastFood	64	Hot dog
6	Mexican and typical dises	G22-FastFood	65	Sandwich
6	Mexican and typical dises	G21-MexicanDishes	66	Torta
6	Mexican and typical dises	G22-FastFood	67	Pizza (slice)
6	Mexican and typical dises	G22-FastFood	68	Nuggets (3)
6	Mexican and typical dises	G21-MexicanDishes	69	Tamal
6	Mexican and typical dises	G21-MexicanDishes	70	Pozole (1 portion)
7	Cereals	G8-Maize	71	Maize tortilla
7	Cereals	G19-Flours	72	Flour tortilla (wheat)
7	Cereals	G19-Flours	73	White bread (slice)
7	Cereals	G20-GrainsCereals	74	Wholemeal bread (slice)
7	Cereals	G19-Flours	75	Bolillo or telera
7	Cereals	G16-SweetBread	76	Sweet bread
7	Cereals	G10-Rice	77	Rice (1 portion)
7	Cereals	G19-Flours	78	Soup (1 portion)
7	Cereals	G19-Flours	79	Pasta (1 portion)

7	Cereals	G20-GrainsCereals	80	Oatmeal (1 cup)
7	Cereals	G17-IndCereal	81	Cereal without sugar (1 portion)
7	Cereals	G17-IndCereal	82	Cereal with sugar (1 portion)
7	Cereals	G20-GrainsCereals	83	Cereal with fiber (1 portion)
7	Cereals	G16-SweetBread	84	hot cake (1 piece)
7	Cereals	G23-SaltySnacks	85	Saltines (1 personal package)
8	Beverages	G26-SweetBeverages	86	Cola soda (355 ml)
8	Beverages	G26-SweetBeverages	87	Soda (355 ml)
8	Beverages	G27-Water	88	Natural water (200 ml)
8	Beverages	G26-SweetBeverages	89	Water with natural fruit (200 ml)
8	Beverages	G26-SweetBeverages	90	Water with sweeteners (200 ml)
8	Beverages	G24-Desserts	91	Milkshake (200 ml)
8	Beverages	G26-SweetBeverages	92	Industrialized fruit juice (250 ml)
8	Beverages	G26-SweetBeverages	93	Sports drink (250 ml)
9	Sweets and desserts	G16-SweetBread	94	Cake (slice)
9	Sweets and desserts	G24-Desserts	95	Jam and condensed milk candy (15 ml)
9	Sweets and desserts	G24-Desserts	96	chocolate bar
9	Sweets and desserts	G23-SaltySnacks	97	Peanuts (1 portion)
9	Sweets and desserts	G23-SaltySnacks	98	Fried snacks (1 portion)
9	Sweets and desserts	G16-SweetBread	99	cupcake with creamy filling
9	Sweets and desserts	G16-SweetBread	100	Cookies
9	Sweets and desserts	G23-SaltySnacks	101	Popcorn
9	Sweets and desserts	G24-Desserts	102	Hot tamarind candy
9	Sweets and desserts	G17-IndCereal	103	Cereal bar
10	Fats	G25-Dressings	104	Butter (15 ml)
10	Fats	G25-Dressings	105	Dressing (15 ml)
10	Fats	G25-Dressings	106	Mayonnaise (15 ml)

11	Supplements	NA	107	Vitamins
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Table S2: Z-scores transformed daily intake percentage table for each food group.

SampleID	G1-Milk	G2-Yogurt	G3-Cheese	G4-Fruit	G5-Vegetables	G6-Legumes	G7-Avocado	G8-Maize	G9-Chillies	G10-Rice	G11-Egg	G12-Fish	G13-Chicken	Sausages G14-	RedMeat G15-	SweetBread G16-	Indicereal G17-	G18-Potato	G19-Flours	GrainsCereal G20-	MexicanDish G21-	FastFood G22-	SaltySnacks G23-	G24-Desserts	SweetBecera G25-Dressings	G26-	G27-Water
S117	0.309	0.900	0.193	0.436	0.813	0.549	0.487	1.313	0.940	0.163	0.234	-0.401	-0.067	-0.342	-1.285	-0.175	-0.243	0.501	-0.756	0.134	-0.913	0.679	-0.013	-0.708	0.323	1.130	-1.133
S134	-1.630	-0.882	-0.668	0.444	0.899	-0.126	-0.238	1.151	1.260	0.069	0.137	-0.775	-0.182	-0.667	-0.335	-0.783	-1.037	1.076	1.117	0.840	-0.533	0.578	-0.498	-0.825	-0.030	0.867	0.725
S179	0.272	0.192	0.244	0.428	1.517	0.980	0.712	0.516	0.699	0.075	0.010	1.242	0.356	0.768	0.965	-0.335	0.312	0.334	0.364	0.147	0.710	1.242	0.153	0.332	0.879	0.666	1.199
S201	-1.387	-0.039	0.532	1.315	2.092	0.745	0.178	-0.000	-0.625	-1.308	0.515	0.441	0.910	1.057	-0.707	-0.163	0.540	1.401	0.776	2.039	-0.149	0.575	0.327	0.109	0.589	-0.961	0.526
S329	-0.015	-0.229	0.055	-0.539	-0.979	-0.163	2.723	0.495	0.931	-0.043	-0.853	0.296	0.317	-0.425	-0.700	-0.444	0.388	0.669	0.031	0.634	0.815	0.952	0.338	0.354	0.099	0.720	1.274
S339	0.341	0.474	0.199	-0.501	-1.098	-1.112	3.326	0.647	-0.651	-1.067	-0.782	1.199	-0.060	-0.400	-0.775	-0.753	1.617	-0.609	0.236	-0.731	-0.453	-0.091	0.362	0.544	0.180	-1.166	0.903
S402	0.480	-0.041	1.408	1.790	1.345	1.239	-0.876	0.398	-0.593	2.366	0.346	-0.686	-0.065	-0.529	-0.174	-0.929	-1.277	0.622	2.014	1.473	0.337	-1.212	0.633	0.538	0.095	1.360	-0.158
S573	-0.260	0.561	-0.774	-0.955	-0.301	-0.485	-0.876	-1.037	-0.066	1.464	-0.812	0.831	-0.758	1.516	-0.277	-0.214	1.254	-0.642	1.245	1.096	2.155	2.735	-0.109	-0.538	-0.879	0.802	-0.621
S578	0.342	-0.503	-0.761	-0.193	1.241	3.539	0.852	0.264	4.358	-0.701	-0.029	1.735	2.677	1.416	1.491	-0.271	1.447	-0.467	-0.843	2.050	2.425	-0.583	-0.354	0.446	0.130	0.365	0.553
S847	0.241	0.818	-0.632	0.224	-0.631	1.424	0.769	0.596	0.547	1.954	0.546	0.253	3.162	-0.484	-1.471	-0.203	1.423	0.842	0.367	0.230	0.248	0.146	-0.196	-0.506	0.190	0.661	-1.013
S865	0.954	-0.523	-0.664	1.251	-0.777	1.008	0.867	-0.101	-0.699	0.574	0.655	0.165	0.432	-0.817	-0.480	-0.503	-0.846	-0.461	2.331	-0.879	2.402	-0.921	-0.450	-0.789	1.252	-1.329	0.139
S884	0.912	-0.741	-0.875	1.339	0.643	1.151	-0.017	-0.353	-0.487	0.704	0.965	-0.145	-1.120	0.386	-0.013	-0.597	-0.378	2.669	1.717	0.396	1.923	-0.978	0.439	0.139	-0.719	-0.398	-1.135

S15	0.6	-	0.4	-	-	-	-	-	-	-	-	-	-	0.0	-	-	0.4	-	0.0	1.5	-	1.0	0.0	2.9	-	0.5	-
31	36	0.4	65	1.3	1.3	0.6	0.8	1.0	0.6	0.7	0.7	0.2	0.5	01	0.6	0.8	75	0.8	58	26	0.6	11	74	23	0.8	85	1.0
		97		18	32	25	76	48	99	61	14	82	26		84	37		41		99					79		51
S17	2.6	-	-	-	-	0.5	-	-	-	-	-	-	0.4	-	-	-	0.1	-	0.7	-	-	-	0.6	-	-	-	-
08	04	0.6	0.3	0.4	0.2	90	0.8	0.4	0.0	0.3	0.2	0.7	65	0.5	1.3	0.7	45	0.0	24	0.8	0.1	0.4	0.3	15	0.7	0.0	1.2
		89	67	37	83		76	86	29	53	96	63		75	08	05		78		79	13	77	08		95	94	16
S19	-	-	-	0.0	-	0.0	-	-	-	0.1	-	-	0.1	-	0.7	-	0.5	-	1.2	-	0.9	0.2	-	-	0.8	-	1.6
14	1.1	0.1	1.0	42	0.6	07	0.2	0.6	0.4	29	0.7	0.5	75	0.6	25	0.3	78	0.6	37	0.6	90	91	0.1	0.8	92	0.8	79
	00	49	34		89		10	35	38		95	74		36		80		23		01		83	35		34		
S19	-	-	3.3	-	-	2.7	-	0.3	-	-	-	-	-	0.7	-	3.5	-	1.9	2.5	-	-	2.4	0.1	-	3.0	0.4	-
22	0.2	0.5	61	0.3	0.4	57	0.5	32	0.5	1.1	0.3	0.7	0.7	83	0.2	40	0.8	51	07	0.8	1.0	40	09	0.6	86	07	0.6
	64	01		88	08		10		56	79	51	90	60		55		70			79	26			22		24	
S19	-	-	-	1.2	-	-	-	3.7	-	1.5	-	0.2	-	0.6	-	0.4	3.4	2.0	-	-	-	1.3	-	0.3	3.3	1.0	-
69	0.1	1.1	0.3	10	0.6	0.4	0.8	13	0.6	70	0.3	41	0.7	70	0.5	80	29	76	0.1	0.8	0.8	93	0.0	82	29	41	1.7
	94	29	81		08	56	76		99		14		16		84				59	79	32		65			12	
S19	0.1	2.8	-	-	-	0.0	-	-	1.7	2.1	2.2	-	-	3.2	1.5	0.3	-	0.1	-	-	0.0	-	5.6	0.2	-	0.8	-
72	63	83	0.2	0.9	0.2	82	0.8	0.5	84	38	60	0.6	0.4	61	97	26	0.4	09	0.1	0.0	97	0.3	67	35	0.1	16	1.7
			11	80	54		76	53				79	91				88		12	93		70		87		12	
S21	-	-	-	-	-	0.5	1.0	-	1.6	-	0.8	-	-	-	-	-	0.1	-	0.8	0.8	1.0	-	0.3	-	-	-	1.9
46	0.9	1.1	0.4	0.7	0.1	40	50	0.0	17	0.6	58	0.7	1.0	0.8	0.5	0.8	85	0.3	36	37	28	0.7	75	0.5	0.4	0.8	69
	70	91	90	22	66		48		31		31	98	32	50	82	73		89				37		56	02	29	
S21	-	0.3	2.7	2.6	0.0	0.3	-	-	0.5	0.4	0.5	0.1	-	-	-	-	0.3	0.8	0.5	1.8	-	1.1	-	1.2	-	-	-
48	0.8	37	60	51	79	05	0.0	0.0	46	67	46	74	1.1	0.5	0.0	0.7	43	41	01	89	0.7	47	0.0	98	0.2	0.4	1.0
	87						54	58					52	17	45	26				27		14		94	73	14	
S22	1.3	-	-	-	1.9	0.0	0.1	-	-	-	0.9	4.2	0.7	-	1.6	1.8	1.5	1.2	-	2.1	-	2.1	2.0	-	2.2	-	-
13	31	0.3	0.7	0.3	66	79	07	0.0	0.6	0.9	01	91	23	0.6	49	09	33	29	1.2	60	0.4	44	01	0.3	23	1.1	0.8
		79	12	79				25	30	62				27					88		97		43		14	77	
S22	-	-	-	-	1.7	0.5	1.2	1.8	1.0	2.8	4.1	0.8	0.9	0.1	1.6	-	-	-	-	-	-	-	1.4	-	1.4	-	0.5
16	0.5	0.8	0.4	0.7	75	26	35	52	53	79	62	63	15	29	37	0.2	0.5	0.3	0.5	0.0	0.6	0.6	38	0.6	41	0.5	30
	70	10	54	96												48	82	16	16	98	74	19		18		80	
S22	2.2	-	-	-	-	-	1.5	-	1.1	-	1.3	0.3	1.3	-	-	0.1	0.5	-	-	-	-	-	-	-	-	-	0.8
21	47	1.0	0.9	0.8	0.4	0.4	38	0.5	29	0.4	98	79	11	0.6	1.2	10	55	0.1	0.2	0.4	0.7	0.8	0.4	0.7	0.8	1.4	51
		90	97	15	70	30		65		59				06	01			97	23	72	29	34	83	87	79	85	
S22	0.3	0.5	0.2	0.1	1.4	-	0.5	-	-	0.2	0.2	0.7	-	-	0.4	0.2	-	0.5	0.0	-	-	-	-	2.4	-	-	-
69	96	31	41	19	57	0.5	38	0.6	0.6	19	91	72	1.2	0.4	14	15	1.0	62	05	0.2	0.7	0.3	0.6	67	0.6	0.3	1.1
					57		22	49					50	79		11			61	47	12	57		38	41	11	
S22	-	-	1.4	-	-	-	0.1	-	1.1	0.7	1.3	0.8	0.6	-	0.5	1.6	-	1.1	0.1	-	0.2	0.7	0.4	-	-	2.2	-
70	0.2	0.6	94	0.4	0.8	0.4	48	0.9	04	22	61	27	12	0.1	49	27	0.5	27	62	0.8	99	72	81	0.3	0.8	50	1.2
	66	70		09	93	10		29						13			00			48				42	47		77
S22	-	-	-	-	1.7	-	-	1.8	-	1.1	-	-	1.1	-	2.7	-	-	1.5	-	-	-	0.8	-	-	-	-	0.6
89	0.4	0.8	0.0	0.4	86	0.8	0.5	57	0.6	38	0.4	0.2	18	0.6	37	1.0	1.1	92	0.4	0.7	0.0	73	0.3	0.6	0.6	0.4	94
	65	85	01	95		91	52		99		58	74		79		42	31		55	41	44		78	62	33	50	
S23	0.9	0.5	-	-	-	1.6	-	-	-	-	-	-	0.3	2.2	0.3	-	-	-	-	-	-	1.3	-	3.3	0.2	-	-
45	02	60	1.0	1.1	0.6	87	0.8	0.5	0.6	1.0	0.6	0.5	92	79	86	0.3	1.2	0.4	0.2	0.8	0.3	02	0.1	70	61	0.4	1.3
			21	73	75		76	00	39	07	58	10				09	17	73	64	79	56		46		35	99	

S24	0.5	-	-	0.7	-	0.0	-	0.3	-	-	0.9	-	-	1.1	1.2	-	0.6	1.8	0.0	0.3	0.1	-	-	0.2	1.5	-	0.3
29	68	1.0	0.9	63	0.0	64	0.8	61	0.6	0.1	21	0.9	0.4	78	50	1.0	28	88	38	93	02	0.5	0.3	88	10	1.4	51
		78	51		08		76		99	42		05	38			04						59	81			22	
S24	-	-	-	-	-	-	-	-	-	-	0.0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1.9	1.3
52	1.1	0.9	0.8	1.2	0.9	0.3	0.2	0.4	0.6	0.0	47	0.6	0.2	0.5	1.0	0.4	0.9	0.9	0.7	0.7	1.0	1.0	0.7	0.7	0.7	36	31
	92	88	36	86	06	24	79	85	32	19		43	88	50	69	87	82	12	62	54	70	62	20	22	13		
S24	0.6	-	-	-	0.1	-	-	-	-	0.3	-	-	0.1	-	-	1.1	-	-	-	-	-	-	-	-	0.2	0.9	-
68	42	0.5	0.3	0.4	23	0.8	0.6	0.2	0.6	75	0.9	0.2	90	0.6	0.6	50	1.0	0.8	0.3	0.7	0.9	0.9	0.5	0.6	07	88	0.0
		98	38	06		85	53	67	99		94	80		53	47		30	40	79	10	95	85	04	49			57
S25	-	1.3	-	0.9	-	0.6	-	-	-	-	-	0.0	-	-	-	0.5	1.3	-	-	2.3	0.1	-	-	-	-	-	0.9
27	0.2	26	0.2	63	0.4	92	0.8	0.4	0.5	0.2	0.9	24	0.5	0.2	0.3	92	12	1.0	0.3	49	35	0.3	0.2	0.7	0.8	1.1	02
	63		60		01		76	87	73	01	05		09	57	64				90	45		23	86	71	79	73	
S25	-	-	-	0.2	-	-	2.1	1.6	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.0	-	0.6	0.1
93	0.3	0.1	0.1	75	0.0	0.4	58	11	0.6	0.2	0.9	0.6	0.5	0.6	0.0	0.4	1.1	0.7	1.3	0.6	0.9	0.5	0.5	79	0.0	37	76
	27	58	83		27	23			99	42	19	32	59	25	92	88	78	58	52	73	33	93	39		08		
S26	-	2.4	-	1.6	1.1	0.1	-	-	-	-	-	-	2.1	-	-	-	1.2	-	-	0.6	-	0.6	-	-	-	-	0.0
00	0.7	24	0.8	39	07	30	0.8	0.3	0.6	0.7	0.6	0.1	03	0.5	0.6	0.8	64	0.5	0.3	10	1.0	08	0.2	0.5	0.6	0.3	32
	31		02				76	90	07	30	83	39		17	89	75			01	65		32		62	23	50	89
S26	-	-	-	-	-	-	-	2.2	-	-	-	-	-	-	0.6	0.5	-	-	2.4	-	0.3	-	0.8	-	-	2.1	-
01	0.1	1.0	0.9	1.2	0.9	1.0	0.4	92	0.3	0.8	0.7	1.0	1.2	0.5	24	71	0.0	0.9	07	0.7	85	0.6	12	0.4	0.1	58	0.5
	52	72	86	83	72	92	86		06	28	84	94	72	07			42	94		04		47		32	19		54
S26	0.8	1.8	1.7	-	-	-	-	-	0.6	0.5	-	-	0.3	1.0	-	-	0.3	-	0.1	-	-	0.7	-	-	0.2	0.0	0.0
08	45	52	15	1.4	1.2	0.0	0.0	0.7	94	04	0.9	0.2	47	85	0.6	0.6	43	1.0	19	0.6	0.6	11	0.4	0.1	90	23	70
				96	51	73	36	90				73	06			71	56			53	47	76		72	06		
S26	-	-	-	-	-	-	-	-	-	0.4	-	0.1	0.3	3.1	1.2	1.3	0.3	-	-	-	0.7	-	-	0.5	-	1.3	0.0
27	1.1	1.0	0.7	0.8	0.9	0.9	0.6	0.2	0.4	90	0.6	02	30	06	12	09	98	0.8	0.8	0.8	62	0.6	0.3	12	0.2	38	56
	10	50	68	49	86	32	38	04	94		75						19	36	27			68	41		86		
S26	-	0.2	1.4	-	0.0	-	0.5	-	-	-	-	0.4	-	-	-	-	-	-	-	-	1.7	0.8	-	-	-	-	1.9
32	1.0	85	83	1.1	17	0.7	74	1.1	0.6	0.7	0.7	49	1.2	0.1	0.6	1.0	0.1	1.0	1.0	0.7	84	43	0.5	0.7	0.7	0.5	82
	19			80	77		43	69	98	52		35	34	79	61	26	66	79	91			21	18	22	07		
S26	-	0.8	0.6	1.7	0.7	-	-	-	-	-	-	-	0.3	0.1	1.3	0.1	-	-	-	0.8	-	-	-	-	-	1.3	0.0
63	1.9	44	73	99	72	0.4	0.0	0.6	0.6	0.7	0.9	0.2	28	96	87	64	0.4	0.8	0.4	33	0.1	0.7	0.3	0.7	0.4	08	54
	80					05	44	80	99	23	75	15					06	20	12		27	31	38	56	67		
S26	0.2	0.0	0.1	0.3	1.3	-	0.4	-	0.2	-	0.1	-	-	-	-	-	-	0.4	-	-	-	-	-	2.2	-	-	-
80	00	08	34	05	04	0.6	23	0.6	84	0.8	63	0.1	1.2	0.7	0.6	0.6	0.7	23	1.0	0.5	0.8	0.7	0.2	77	0.4	0.5	0.3
					14		69		51		23	99	32	86	00	77			74	88	21	42	61		57	77	33
S27	-	-	-	-	0.0	-	0.4	-	0.5	-	-	2.8	-	-	1.0	-	-	-	-	-	-	-	-	-	-	0.1	1.7
26	1.0	1.2	0.5	0.6	84	0.5	87	1.0	30	0.8	0.7	52	0.0	0.4	85	1.0	0.9	0.6	1.1	0.2	0.9	0.2	0.5	0.2	0.5	16	60
	78	02	94	51		82		67		29	84		67	95		16	41	11	42	79	21	50	40	75	84		
S28	-	0.6	0.9	1.0	0.8	-	-	-	0.4	-	0.3	-	0.0	-	1.0	-	-	0.6	-	-	-	0.1	0.0	0.4	0.4	0.2	-
17	1.0	67	23	84	18	0.1	0.1	0.7	34	0.7	37	0.3	55	0.2	15	0.2	0.0	13	0.5	0.8	0.6	37	43	30	05	61	0.1
	15				37	48	44		96		43		02			69	22		09	34	51					66	
S28	2.1	1.7	0.9	0.8	-	-	-	-	0.5	-	0.6	-	0.5	-	-	0.3	0.5	-	-	-	0.7	1.2	-	-	-	-	-
46	95	31	87	44	0.8	0.5	0.6	0.1	21	0.6	77	0.0	65	0.8	0.3	24	48	0.8	0.0	0.3	99	83	0.3	0.4	0.8	1.0	1.1
					17	41	24	45		88		58		57	02				00	35	00		15	57	79	41	20

S28	-	1.3	0.7	0.7	0.7	-	-	-	-	-	1.1	-	-	-	0.2	-	-	-	-	-	-	-	-	-	0.4	0.6	
83	0.8	03	82	14	65	1.2	0.8	0.3	0.6	0.5	51	0.1	0.9	0.5	63	0.6	0.9	1.1	1.1	0.8	0.7	0.7	0.4	0.6	0.8	24	14
	28					56	76	05	99	38		42	19	92		87	42	47	12	11	41	32	57	39	11		
S29	-	0.6	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.4	-	-	-	-	-	1.4	0.4
27	0.5	41	0.8	0.4	0.7	0.9	0.8	0.6	0.6	1.0	0.3	0.7	1.4	0.5	1.2	1.1	0.4	0.8	0.9	0.7	50	1.0	0.5	0.0	0.7	93	55
	60		56	79	89	00	76	90	99	09	33	17	91	52	36	20	21	12	76	01		19	68	48	87		
S29	0.7	-	0.0	-	-	-	-	-	-	-	0.0	-	-	-	0.2	1.7	-	0.2	-	-	1.6	-	0.2	-	0.1	-	0.5
67	91	0.7	85	0.8	0.2	0.8	0.8	0.4	0.6	0.0	24	0.8	0.3	0.2	53	41	0.2	71	0.1	0.5	21	0.1	40	0.4	56	0.6	30
		22		97	87	55	76	97	99	41		76	15	40			66		72	90		50		96		98	
S29	0.8	-	-	-	-	-	-	-	-	0.4	-	-	0.3	-	-	-	-	-	-	1.0	-	-	-	0.7	-	0.1	0.0
71	90	0.9	0.6	0.1	1.5	1.0	0.8	0.6	0.6	66	0.6	0.4	01	0.6	0.0	0.1	1.2	0.8	0.6	56	1.0	0.7	0.2	27	0.7	66	33
		80	32	55	59	83	76	86	99		83	17		38	90	64	29	24	00		22	56	04		77		

Table S3: Dietary patterns obtained through PCA factorial analysis and orthogonal rotation.

Food Groups	Foods Included	Pattern 2: Saturated Fat and Simple Carbohydrates	Pattern 1: Proteins and Complex Carbohydrates
1. Milk	Skim and Whole Milk		
2. Yogurt	Yogurt Flavoured, Yakult, Yogurt Actiregularis®, Yogurt Natural		
3. Cheese	Oaxaca, Manchego, American, and Cream Cheese		
4. Fruit	Strawberry, Tangerine, Orange, Banana, Peach, Apple, Pear, Grapes, Mango, Plums, Pineapple, Papaya, Melon, Watermelon, Orange Juice		
5. Vegetables	Tomato, Carrot, Cucumber, Jicama, Lettuce, Zucchini, Nopal, Broccoli		0.5806
6. Legumes	Beans, Peas, Lentils		0.527
7. Avocado	Avocado	-0.41	
8. Maize	Corn Tortilla, Corn		
9. Chillies	Canned Chillies, Hot Sauce		0.5908
10. Rice	Rice		
11. Egg	Eggs		0.5042
12. Fish	Fish, Sardines, Tuna		0.5541
13. Chicken	Chicken and Liver Chicken		0.5857
14. Sausages	Turkey Sausage, Turkey Ham, Pork Sausage, Pork Ham, Chorizo	0.4851	
15. Red Meat	Barbacoa, Beef, Pork, Chicharron, Bacon		0.3861
16. Sweet Bread	Cake, Sweet Cookies and Bread, Filled Cupcakes, Hot Cake	0.5294	

17. Industrialized Cereals	Sweet Cereal, Cereal Bars, Sugar Free Cereal		
18. Potato	Potato	0.5973	
19. Flours	Bolillo, White bread, Pasta	0.424	
20. Grains Cereals	Whole Wheat Bread, Fiber Cereal, Oats		0.4515
21. Mexican Dishes	Torta, Tamale, Pozole, Tacos al pastor (Pork), Sopas, Carnitas (Pork)		
22. Fast Food	Burger, Hot dog, Pizza, Chicken Nuggets, Sandwich, French Fries	0.548	
23. Salty Snacks	Peanuts, Snacks, Crisps, Popcorn	0.434	
24. Desserts	Milkshake, Chocolate Milk, Danonino, Ice Cream, Chocolate, jam, Chamoy Candy		
25. Dressings	Dressing, Mayonnaise, Butter	0.5506	
26. Sweet Beverages	Cola Soft Drink, Fruit Soft Drink, Industrialized Juices, Hydrating Drinks, Water with Artificial Flavoring, Fruit Water		-0.4087
27. Water	Water	-0.7793	

Factor loadings or correlation coefficients between the variables (rows: groups of foods) and factors (columns: patterns 1 and 2).

Table S4: Dietary pattern score obtained for each child that participated based on their reported diet.

SampleID	Pattern1	Pattern2
S117	0.3205371	0.5758733
S134	0.1440915	-0.9681191
S179	-1.170841	-0.4113157
S201	0.9401742	0.143073
S329	0.1623228	-1.05331
S339	-0.0579411	-1.044442
S402	0.5130515	0.2638562
S573	-0.3296513	0.7141154
S578	3.497206	-0.5026956
S847	1.25227	0.5405591
S865	0.4539231	-0.2415238
S884	0.1391787	1.057557
S1531	-1.451602	0.5943944
S1708	-0.6210954	0.3915844
S1914	-0.0851043	-0.7586012
S1922	-0.6085021	2.942155
S1969	-0.0886021	2.483942
S1972	0.6682865	1.843158
S2146	0.6341589	-1.465647
S2148	0.2025058	0.9404573
S2213	2.288327	1.132702
S2216	2.511243	-0.397457
S2221	0.8065155	-1.299773
S2269	-0.3801049	0.3659545
S2270	-0.0431866	0.9992714
S2289	0.5796062	-0.3786825

S2345	-0.8007509	1.265548
S2429	0.4174601	0.4636037
S2452	-1.154805	-1.252507
S2468	-0.9809453	-0.2169433
S2527	0.0232354	-0.6029029
S2593	-0.5400318	-0.8162261
S2600	0.4270049	-0.4282541
S2601	-1.4277	0.4417136
S2608	-0.6509099	0.1371638
S2627	-0.75928	0.1697606
S2632	-0.6678567	-1.465489
S2663	-0.2033831	-0.4476009
S2680	-0.4065396	-0.310024
S2726	0.4214248	-1.822996
S2817	0.1120333	0.1744197
S2846	-0.1584052	0.3756168
S2883	-0.6839789	-0.9429005
S2927	-1.56976	-0.8547883
S2967	-0.6185966	0.125412
S2971	-1.05498	-0.4596928

Table S5. Relative abundance (>0.01%) of bacterial genera detected in fecal samples.

See file.

Table S6: Taxa (at genus or specie level) that contribute the most to beta diversity variation between NW and OWOB groups (SIMPER).

Taxa	Cumulative Relative Abundance	Taxa	Cumulative Relative Abundance	Taxa	Cumulative Relative Abundance
<i>Prevotella copri</i>	0.05639512	<i>[Eubacterium] siraeum</i>	0.43754507	<i>Bacteroides</i> sp.	0.59895415
<i>Bacteroides dorei/vulgatus</i>	0.09469867	<i>Ruminococcus</i> sp. CAG:177	0.45489865	<i>Clostridium</i> sp. CAG:217	0.61009154
<i>Bacteroides stercoris</i>	0.12424528	<i>Ruminococcus bicirculans</i>	0.46307388	<i>Bacteroides intestinalis</i> **	0.62093356
<i>Bacteroides rodentium/uniformis</i> +	0.15170272	<i>Rikenellaceae</i> sp.	0.47121856	<i>Clostridium</i> sp. CAG:343	0.62623611
<i>Bacteroides cellulosilyticus/fragilis</i>	0.17562738	<i>Faecalibacterium prausnitzii</i>	0.48728578	<i>Faecalibacterium prausnitzii</i>	0.64193336
<i>Eubacterium</i> sp. CAG:202	0.19898182	<i>Barnesiella intestinihominis</i>	0.49515177	<i>Dehalococcoides species incertae sedis</i>	0.63151148
<i>Eubacterium</i> sp. CAG:180*	0.2209676	<i>Faecalibacterium</i> sp.	0.50239242	<i>Clostridium</i> sp. CAG:127	0.6367464
<i>Bacteroides caccae</i>	0.24095906	<i>Bacteroides caecimuris</i>	0.50961052	<i>Ruminococcaceae species incertae sedis</i>	0.64704771
<i>Ruminococcus bromii</i>	0.25849825	<i>Bacteroides plebeius</i>	0.51682632	<i>Roseburia inulinivorans</i>	0.65714674
<i>Prevotella species incertae sedis</i>	0.27540254	<i>Firmicutes</i> sp.	0.52392848	<i>Clostridium</i> sp. CAG:465	0.65211104
<i>Alistipes putredinis</i>	0.29225987	<i>Alistipes shahii</i>	0.5307857	<i>Clostridium</i> sp. CAG:567	0.66716776
<i>Bacteroides</i> sp.	0.30876689	<i>Bacteroides coprocola</i>	0.53762254	<i>Alistipes finegoldii</i>	0.67194751
<i>Dialister invisus</i>	0.32493854	<i>Parabacteroides merdae</i>	0.55100433	<i>Methanobrevibacter smithii</i> *	0.67654813
<i>Akkermansia muciniphila</i>	0.33908238	<i>Bacteroides fragilis</i>	0.55758635	<i>Firmicutes species incertae sedis</i>	0.68109163
<i>Bacteroides massiliensis</i>	0.353011	<i>Faecalibacterium prausnitzii</i>	0.56388264	<i>Anaerotruncus</i> sp. CAG:528	0.68548795
<i>[Eubacterium] rectale</i>	0.36521315	<i>Clostridium</i> sp. CAG:510	0.57597579	<i>Bacteroides eggerthii</i> +	0.68972822
<i>Clostridium</i> sp. CAG:302	0.3768737	<i>Bifidobacterium longum</i>	0.58179301	<i>Roseburia species incertae sedis</i> +	0.69395928
<i>Proteobacteria</i> sp.	0.40918866	<i>Akkermansia species incertae sedis</i>	0.58756496	<i>Clostridiales species incertae sedis</i>	0.70223109

<i>Alistipes</i> <i>finegoldii/onderdonkii</i>	0.41935951	<i>Clostridium</i> sp. CAG:594	0.59331688
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Cumulative contributions of most influential species are shown next to each genus. Pairwise comparisons using Wilcoxon rank sum test adjusted by FDR: +: $0.1 \geq p \geq 0.05$, *: $p \leq 0.05$, **: $p \leq 0.01$

Table S7. KO representation analysis.

KO_entr ntry	Name	Definition	log FC	logC PM	F	PValue	FD R	Differentially represented
K16907	K16907	fluoroquinolone transport system ATP-binding protein [EC:3.6.3.-]	4.40 2	5.316	20.8 45	0.000	0.0 02	UP
K02838	frr, MRRF, RRF	ribosome recycling factor	1.09 4	12.07 8	9.32 0	0.003	0.0 41	UP
K02864	RP-L10, MRPL10, rplJ	large subunit ribosomal protein L10	1.18 6	11.94 4	9.79 2	0.003	0.0 34	UP
K14731	mlhB, chnC	epsilon-lactone hydrolase [EC:3.1.1.83]	1.41 4	9.023	8.65 2	0.005	0.0 51	UP
K00949	thiN, TPK1, THI80	thiamine pyrophosphokinase [EC:2.7.6.2]	1.54 9	11.71 0	11.7 09	0.001	0.0 17	UP
K09775	K09775	uncharacterized protein	1.71 5	10.33 1	10.5 79	0.002	0.0 26	UP
K01841	pepM	phosphoenolpyruvate phosphomutase [EC:5.4.2.9]	1.79 3	8.446	8.91 4	0.004	0.0 45	UP
K03366	butA, budC	meso-butanediol dehydrogenase / (S,S)-butanediol dehydrogenase / diacetyl reductase [EC:1.1.1.- 1.1.1.76 1.1.1.304]	1.97 1	4.421	10.5 54	0.002	0.0 30	UP
K19714	kdnB	3-deoxy-alpha-D-manno-octulosonate 8-oxidase [EC:1.1.3.48]	2.02 2	4.427	10.6 60	0.002	0.0 29	UP
K16872	E2.3.1.207	beta-ketodecanoyl-[acyl-carrier-protein] synthase [EC:2.3.1.207]	2.08 0	4.435	10.7 93	0.002	0.0 28	UP
K21400	ortB	2-amino-4-ketopentanoate thiolase beta subunit [EC:2.3.1.263]	2.22 6	4.531	9.83 1	0.003	0.0 34	UP
K18284	K18284	adenosylhomocysteine/aminodeoxyfualosine nucleosidase [EC:3.2.2.9 3.2.2.30]	2.29 1	4.467	11.9 53	0.001	0.0 18	UP
K03821	phbC, phaC	polyhydroxyalkanoate synthase subunit PhaC [EC:2.3.1.-]	2.30 7	4.468	11.4 98	0.001	0.0 21	UP
K15363	FAN1, MTMR15	fanconi-associated nuclease 1 [EC:3.1.21.- 3.1.4.1]	2.33 0	4.472	11.5 66	0.001	0.0 21	UP
K15216	RRN3, TIFIA	RNA polymerase I-specific transcription initiation factor RRN3	2.40 2	4.484	11.7 78	0.001	0.0 19	UP
K00587	ICMT, STE14	protein-S-isoprenylcysteine O-methyltransferase [EC:2.1.1.100]	2.47 3	4.497	12.9 45	0.001	0.0 14	UP

K00814	GPT, ALT	alanine transaminase [EC:2.6.1.2]	2.48 6	4.498	12.0 18	0.001	0.0 18	UP
K07110	ramB	XRE family transcriptional regulator, fatty acid utilization regulator	2.48 7	4.498	12.0 22	0.001	0.0 18	UP
K23160	wabB, rfbU	GlcNAc transferase	2.66 1	4.777	9.07 3	0.004	0.0 43	UP
K05499	cytR	LacI family transcriptional regulator, repressor for deo operon, udp, cdd, tsx, nupC, and nupG	2.67 6	5.493	8.99 1	0.004	0.0 44	UP
K01228	MOGS	mannosyl-oligosaccharide glucosidase [EC:3.2.1.106]	2.68 4	4.534	12.5 61	0.001	0.0 15	UP
K15311	pksG	polyketide biosynthesis 3-hydroxy-3-methylglutaryl-CoA synthase-like enzyme PksG	2.72 2	4.544	12.7 37	0.001	0.0 15	UP
K03528	zipA	cell division protein ZipA	2.80 3	5.809	9.67 3	0.003	0.0 36	UP
K13670	pimF	putative glycosyltransferase [EC:2.4.-.-]	2.81 2	5.320	9.14 3	0.004	0.0 42	UP
K10917	aphA	PadR family transcriptional regulator, regulatory protein AphA	2.84 4	4.941	9.72 0	0.003	0.0 35	UP
K22255	ATPIF1	ATPase inhibitor, mitochondrial	2.85 7	4.572	13.6 06	0.001	0.0 11	UP
K10795	prdD	D-proline reductase (dithiol)-stabilizing protein PrdD	2.87 7	4.778	11.3 60	0.001	0.0 19	UP
K00682	GGCT	gamma-glutamylcyclotransferase [EC:4.3.2.9]	2.89 7	4.582	14.4 37	0.000	0.0 08	UP
K19713	tsdA	thiosulfate dehydrogenase [EC:1.8.2.2]	2.96 6	4.719	11.8 90	0.001	0.0 16	UP
K21405	acoR	sigma-54 dependent transcriptional regulator, acetoin dehydrogenase operon transcriptional activator AcoR	2.97 2	4.751	12.0 96	0.001	0.0 15	UP
K18652	ntdC	glucose-6-phosphate 3-dehydrogenase [EC:1.1.1.361]	3.03 0	4.864	10.0 77	0.002	0.0 32	UP
K11940	hspQ	heat shock protein HspQ	3.03 3	6.083	8.92 8	0.004	0.0 45	UP
K00143	LYS2	L-2-aminoadipate reductase [EC:1.2.1.95]	3.05 0	4.618	13.5 64	0.001	0.0 11	UP
K14989	salR	two-component system, NarL family, secretion system response regulator SalR	3.12 7	6.817	11.9 71	0.001	0.0 16	UP

K21006	pelA	polysaccharide biosynthesis protein PelA	3.14 6	4.639	14.5 90	0.000	0.0 08	UP
K13498	trpCF	indole-3-glycerol phosphate synthase / phosphoribosylanthranilate isomerase [EC:4.1.1.48 5.3.1.24]	3.18 5	7.696	10.1 79	0.002	0.0 30	UP
K01363	CTSB	cathepsin B [EC:3.4.22.1]	3.18 8	4.647	13.7 94	0.001	0.0 10	UP
K04646	CLTC	clathrin heavy chain	3.23 9	4.660	13.9 08	0.001	0.0 10	UP
K20179	VPS11, PEP5	vacuolar protein sorting-associated protein 11	3.50 8	4.735	14.4 74	0.000	0.0 08	UP
K23661	escl	type III secretion system protein	3.59 9	4.766	15.2 72	0.000	0.0 06	UP
K08568	CTSZ	cathepsin X [EC:3.4.18.1]	4.26 2	5.005	15.8 00	0.000	0.0 05	UP
K02656	pilF	type IV pilus assembly protein PilF	4.83 7	5.269	17.9 25	0.000	0.0 03	UP
K16906	K16906	fluoroquinolone transport system permease protein	5.01 9	6.684	19.7 39	0.000	0.0 02	UP
K15868	baiB	bile acid-coenzyme A ligase [EC:6.2.1.7]	5.08 7	6.446	17.1 50	0.000	0.0 03	UP
K16905	K16905	fluoroquinolone transport system permease protein	5.38 7	6.998	20.5 69	0.000	0.0 02	UP
K19161	yafN	antitoxin YafN	5.83 1	7.197	27.4 12	0.000	0.0 00	UP
K21488	yobK	antitoxin YobK	- 4.43 2	6.307	27.4 26	0.000	0.0 00	DN
K01414	prlC	oligopeptidase A [EC:3.4.24.70]	- 5.39 2	7.108	32.8 22	0.000	0.0 00	DN
K19266	E1.2.1.22	lactaldehyde dehydrogenase [EC:1.2.1.22]	- 4.32 1	4.859	23.5 61	0.000	0.0 02	DN
K07728	K07728	putative transcriptional regulator	- 4.14 8	4.800	22.9 77	0.000	0.0 02	DN

K18967	dge1	diguanylate cyclase [EC:2.7.7.65]	- 4.13 9	4.799	23.9 87	0.000	0.0 02	DN
K13942	hmd	5,10-methenyltetrahydromethanopterin hydrogenase [EC:1.12.98.2]	- 4.12 8	4.793	23.1 74	0.000	0.0 02	DN
K17717	pld	phospholipase D [EC:3.1.4.4]	- 3.98 7	4.753	24.4 40	0.000	0.0 02	DN
K10938	acfC	accessory colonization factor AcfC	- 3.93 3	4.744	21.6 42	0.000	0.0 02	DN
K06961	KRR1	ribosomal RNA assembly protein	- 3.92 3	4.865	25.1 11	0.000	0.0 01	DN
K11176	purO	IMP cyclohydrolase [EC:3.5.4.10]	- 3.86 9	4.715	22.1 34	0.000	0.0 02	DN
K03413	cheY	two-component system, chemotaxis family, chemotaxis protein CheY	- 3.79 4	11.95 9	34.8 39	0.000	0.0 00	DN
K09739	mptD	dihydroneopterin aldolase [EC:4.1.2.25]	- 3.76 8	4.687	21.7 72	0.000	0.0 02	DN
K23264	purS	phosphoribosylformylglycinamide synthase subunit PurS [EC:6.3.5.3]	- 3.76 0	4.685	21.0 06	0.000	0.0 02	DN
K00368	nirK	nitrite reductase (NO-forming) [EC:1.7.2.1]	- 3.74 7	4.687	21.7 12	0.000	0.0 02	DN
K09139	K09139	uncharacterized protein	- 3.74 0	4.680	23.0 04	0.000	0.0 02	DN
K07072	mfnF	(4-(4-[2-(gamma-L-glutamylamino)ethyl]phenoxy)methyl)furan-2-yl)methanamine synthase [EC:2.5.1.131]	- 3.72 9	4.677	21.9 31	0.000	0.0 02	DN

K19175	dptH	DNA phosphorothioation-dependent restriction protein DptH	- 3.71 3	5.080	18.0 77	0.000	0.0 03	DN
K18974	sul1	dihydropteroate synthase type 1 [EC:2.5.1.15]	- 3.67 2	4.666	23.6 85	0.000	0.0 02	DN
K22447	cct, ths	archaeal chaperonin	- 3.64 4	4.655	21.6 79	0.000	0.0 02	DN
K01001	ALG7	UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminephosphotransferase [EC:2.7.8.15]	- 3.63 8	4.653	21.4 18	0.000	0.0 02	DN
K00021	HMGCR	hydroxymethylglutaryl-CoA reductase (NADPH) [EC:1.1.1.34]	- 3.62 1	4.649	21.6 10	0.000	0.0 02	DN
K18975	ebr, qacEdelta1	small multidrug resistance pump	- 3.61 7	4.653	23.1 57	0.000	0.0 02	DN
K16509	spxA	regulatory protein spx	- 3.60 7	5.506	16.3 05	0.000	0.0 03	DN
K22081	mgsA	methylamine---glutamate N-methyltransferase subunit A [EC:2.1.1.21]	- 3.55 7	4.634	21.2 77	0.000	0.0 02	DN
K19824	fprB	rubrerythrin	- 3.51 6	4.624	21.2 41	0.000	0.0 02	DN
K02910	RP-L31e, RPL31	large subunit ribosomal protein L31e	- 3.50 8	4.649	29.4 86	0.000	0.0 00	DN
K02243	comGA	competence protein ComGA	- 3.45 5	4.775	20.2 32	0.000	0.0 02	DN
K07765	MBTPS2	S2P endopeptidase [EC:3.4.24.85]	- 3.45 0	4.608	20.9 54	0.000	0.0 02	DN

K01512	acyP	acylphosphatase [EC:3.6.1.7]	- 3.44 9	10.52 0	27.5 56	0.000	0.0 00	DN
K22223	pgp	phosphoglycolate phosphatase [EC:3.1.3.18]	- 3.42 8	4.885	16.5 93	0.000	0.0 03	DN
K14094	ehaC	energy-converting hydrogenase A subunit C	- 3.41 1	4.600	20.8 60	0.000	0.0 02	DN
K01170	endA	tRNA-intron endonuclease, archaea type [EC:4.6.1.16]	- 3.39 0	4.595	20.7 37	0.000	0.0 02	DN
K06875	PDCD5, TFAR19	programmed cell death protein 5	- 3.34 9	4.586	20.5 67	0.000	0.0 02	DN
K14096	ehaE	energy-converting hydrogenase A subunit E	- 3.31 6	4.579	20.4 89	0.000	0.0 02	DN
K12243	pchR	AraC family transcriptional regulator, transcriptional activator of the genes for pyochelin and ferripyochelin receptors	- 3.28 8	4.577	19.5 35	0.000	0.0 03	DN
K09738	K09738	uncharacterized protein	- 3.28 2	4.571	20.2 96	0.000	0.0 03	DN
K00340	nuoK	NADH-quinone oxidoreductase subunit K [EC:7.1.1.2]	- 3.26 2	11.25 9	40.7 44	0.000	0.0 00	DN
K02709	psbH	photosystem II PsbH protein	- 3.25 4	4.566	19.3 15	0.000	0.0 03	DN
K03167	top6B	DNA topoisomerase VI subunit B [EC:5.6.2.2]	- 3.25 0	4.760	17.1 87	0.000	0.0 03	DN
K22224	acdB	acetate---CoA ligase (ADP-forming) subunit beta [EC:6.2.1.13]	- 3.23 8	4.563	21.6 86	0.000	0.0 02	DN

K02966	RP-S19e, RPS19	small subunit ribosomal protein S19e	- 3.23 5	4.562	20.0 72	0.000	0.0 03	DN
K14168	CTU1, NCS6	cytoplasmic tRNA 2-thiolation protein 1 [EC:2.7.7.-]	- 3.22 8	4.560	20.0 11	0.000	0.0 03	DN
K03166	top6A	DNA topoisomerase VI subunit A [EC:5.6.2.2]	- 3.16 4	4.836	14.3 78	0.000	0.0 07	DN
K00584	mtrH	tetrahydromethanopterin S-methyltransferase subunit H [EC:2.1.1.86]	- 3.15 1	4.918	12.9 27	0.001	0.0 11	DN
K03299	TC.GNTP	gluconate:H ⁺ symporter, GntP family	- 3.14 7	12.01 0	32.2 30	0.000	0.0 00	DN
K00094	E1.1.1.251, gatD	galactitol-1-phosphate 5-dehydrogenase [EC:1.1.1.251]	- 3.14 1	4.795	16.0 76	0.000	0.0 04	DN
K16793	aksE	methanogen homoaconitase small subunit [EC:4.2.1.114]	- 3.13 0	4.542	18.8 55	0.000	0.0 03	DN
K14097	ehaF	energy-converting hydrogenase A subunit F	- 3.12 5	4.541	19.6 34	0.000	0.0 03	DN
K17884	E2.7.8.39	archaetidylinositol phosphate synthase [EC:2.7.8.39]	- 3.12 1	4.539	19.6 07	0.000	0.0 03	DN
K02530	lacR	DeoR family transcriptional regulator, lactose phosphotransferase system repressor	- 3.11 2	5.270	13.2 06	0.001	0.0 10	DN
K06914	mfnD	tyramine---L-glutamate ligase [EC:6.3.4.24]	- 3.10 6	4.537	18.7 64	0.000	0.0 03	DN
K12678	aidA-I, misL	autotransporter family porin	- 3.06 8	6.456	11.5 39	0.001	0.0 18	DN

K14080	mtaA	[methyl-Co(III) methanol-specific corrinoid protein]:coenzyme M methyltransferase [EC:2.1.1.246]	- 3.06 3	4.529	19.3 89	0.000	0.0 03	DN
K21306	aglB	dolichyl-phosphooligosaccharide-protein glycotransferase [EC:2.4.99.21]	- 3.04 8	4.526	18.5 39	0.000	0.0 03	DN
K14095	ehaD	energy-converting hydrogenase A subunit D	- 3.02 9	4.523	19.1 94	0.000	0.0 03	DN
K04480	mtaB	methanol--5-hydroxybenzimidazolylcobamide Co-methyltransferase [EC:2.1.1.90]	- 3.02 4	4.522	19.3 09	0.000	0.0 03	DN
K16792	aksD	methanogen homoaconitase large subunit [EC:4.2.1.114]	- 3.02 1	4.521	19.3 40	0.000	0.0 03	DN
K14109	ehaR	energy-converting hydrogenase A subunit R	- 2.99 3	4.516	19.1 22	0.000	0.0 03	DN
K02929	RP-L44e, RPL44	large subunit ribosomal protein L44e	- 2.92 1	4.504	18.7 76	0.000	0.0 03	DN
K09728	K09728	uncharacterized protein	- 2.92 1	4.504	18.8 57	0.000	0.0 03	DN
K08093	hxlA	3-hexulose-6-phosphate synthase [EC:4.1.2.43]	- 2.91 4	5.319	10.3 51	0.002	0.0 29	DN
K11600	RRP41, EXOSC4, SKI6	exosome complex component RRP41	- 2.89 9	4.500	18.7 24	0.000	0.0 03	DN
K00537	arsC	arsenate reductase (glutaredoxin) [EC:1.20.4.1]	- 2.89 2	11.29 5	31.7 61	0.000	0.0 00	DN
K14587	sgcE	protein sgcE [EC:5.1.3.-]	- 2.85 9	4.496	19.4 56	0.000	0.0 03	DN

K0479 7	pfdA, PFDN5	prefoldin alpha subunit	- 2.83 8	4.490	18.4 53	0.000	0.0 03	DN
K0287 7	RP-L15e, RPL15	large subunit ribosomal protein L15e	- 2.82 6	4.669	14.5 08	0.000	0.0 06	DN
K0480 2	PCNA	proliferating cell nuclear antigen	- 2.82 5	4.488	18.2 25	0.000	0.0 03	DN
K1966 5	pssA	archaetidylserine synthase [EC:2.7.8.38]	- 2.81 0	4.485	18.2 40	0.000	0.0 03	DN
K0005 4	mvaA	hydroxymethylglutaryl-CoA reductase [EC:1.1.1.88]	- 2.79 6	5.064	9.87 9	0.003	0.0 34	DN
K1410 8	ehaQ	energy-converting hydrogenase A subunit Q	- 2.79 5	4.483	18.2 93	0.000	0.0 03	DN
K2257 9	rph	rifampicin phosphotransferase [EC:2.7.9.6]	- 2.78 8	4.718	13.3 48	0.001	0.0 10	DN
K0897 1	K08971	putative membrane protein	- 2.74 3	4.475	17.2 92	0.000	0.0 04	DN
K0105 8	pIdA	phospholipase A1/A2 [EC:3.1.1.32 3.1.1.4]	- 2.74 3	9.597	16.8 17	0.000	0.0 03	DN
K0710 1	K07101	uncharacterized protein	- 2.70 9	5.021	9.83 0	0.003	0.0 34	DN
K1121 2	cofD	LPPG:FO 2-phospho-L-lactate transferase [EC:2.7.8.28]	- 2.70 5	4.681	11.9 86	0.001	0.0 16	DN
K0977 6	K09776	uncharacterized protein	- 2.69 7	4.468	17.0 95	0.000	0.0 04	DN

K00579	mtrC	tetrahydromethanopterin S-methyltransferase subunit C [EC:2.1.1.86]	- 2.69 4	4.595	14.4 87	0.000	0.0 06	DN
K07463	K07463	archaea-specific RecJ-like exonuclease	- 2.67 7	4.539	17.2 36	0.000	0.0 03	DN
K18814	ictB	putative inorganic carbon (hco3(-)) transporter	- 2.67 1	9.120	14.7 14	0.000	0.0 06	DN
K18320	IS15, IS26	transposase, IS6 family	- 2.65 6	6.329	9.09 2	0.004	0.0 43	DN
K07700	dpiB, citA	two-component system, CitB family, cit operon sensor histidine kinase CitA [EC:2.7.13.3]	- 2.64 0	5.191	9.17 4	0.004	0.0 42	DN
K07161	K07161	uncharacterized protein	- 2.63 6	4.707	11.7 50	0.001	0.0 17	DN
K19003	mgdA	1,2-diacylglycerol 3-beta-glucosyltransferase [EC:2.4.1.336]	- 2.62 1	5.599	9.30 5	0.003	0.0 41	DN
K07799	mdtA	membrane fusion protein, multidrug efflux system	- 2.59 3	5.585	8.83 8	0.004	0.0 47	DN
K13275	isp	major intracellular serine protease [EC:3.4.21.-]	- 2.57 3	4.453	17.2 92	0.000	0.0 04	DN
K07739	ELP3, KAT9	elongator complex protein 3 [EC:2.3.1.48]	- 2.54 1	5.801	9.27 8	0.003	0.0 41	DN
K22227	ahbD	AdoMet-dependent heme synthase [EC:1.3.98.6]	- 2.52 5	4.749	9.58 7	0.003	0.0 37	DN
K22397	yjhH, yagE	2-dehydro-3-deoxy-D-pentionate aldolase [EC:4.1.2.28]	- 2.52 4	4.877	9.87 3	0.003	0.0 34	DN

K07467	rstA1	phage replication initiation protein	- 2.48 8	11.14 1	22.9 80	0.000	0.0 02	DN
K00442	frhD	coenzyme F420 hydrogenase subunit delta	- 2.46 8	4.476	18.3 83	0.000	0.0 03	DN
K05937	K05937	uncharacterized protein	- 2.41 8	4.432	16.1 35	0.000	0.0 05	DN
K09698	gltX	nondiscriminating glutamyl-tRNA synthetase [EC:6.1.1.24]	- 2.36 2	5.971	8.42 9	0.005	0.0 56	DN
K03264	EIF6	translation initiation factor 6	- 2.34 8	4.608	9.93 0	0.002	0.0 34	DN
K00320	mer	5,10-methylenetetrahydromethanopterin reductase [EC:1.5.98.2]	- 2.33 6	4.648	9.21 3	0.003	0.0 41	DN
K07115	rlmJ	23S rRNA (adenine2030-N6)-methyltransferase [EC:2.1.1.266]	- 2.23 2	8.588	13.0 91	0.001	0.0 11	DN
K02244	comGB	competence protein ComGB	- 2.16 7	4.578	9.50 5	0.003	0.0 38	DN
K12234	cofE, fbiB	coenzyme F420-0:L-glutamate ligase / coenzyme F420-1:gamma-L-glutamate ligase [EC:6.3.2.31 6.3.2.34]	- 2.12 3	4.534	9.27 0	0.003	0.0 41	DN
K00282	gcvPA	glycine dehydrogenase subunit 1 [EC:1.4.4.2]	- 1.81 7	7.858	8.54 0	0.005	0.0 53	DN
K08591	plsY	acyl phosphate:glycerol-3-phosphate acyltransferase [EC:2.3.1.275]	- 1.58 9	11.84 8	17.7 41	0.000	0.0 03	DN
K02860	rimM	16S rRNA processing protein RimM	- 1.55 4	12.34 4	16.7 52	0.000	0.0 03	DN

K02794	manX	mannose PTS system EIIAB component [EC:2.7.1.191]	- 1.55 1	7.940	10.6 25	0.002	0.0 26	DN
K02227	cbiB, cobD	adenosylcobinamide-phosphate synthase [EC:6.3.1.10]	- 1.54 6	10.82 4	20.1 97	0.000	0.0 02	DN
K03215	rumA	23S rRNA (uracil1939-C5)-methyltransferase [EC:2.1.1.190]	- 1.54 4	12.04 1	16.3 74	0.000	0.0 03	DN
K01704	leuD, IPMI-S	3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit [EC:4.2.1.33 4.2.1.35]	- 1.54 1	11.58 9	16.4 09	0.000	0.0 03	DN
K03402	argR, ahrC	transcriptional regulator of arginine metabolism	- 1.44 1	11.78 1	15.3 13	0.000	0.0 05	DN
K00859	coaE	dephospho-CoA kinase [EC:2.7.1.24]	- 1.26 9	11.50 2	17.0 33	0.000	0.0 03	DN
K07566	tsaC, rimN, SUA5	L-threonylcarbamoyladenylate synthase [EC:2.7.7.87]	- 1.16 5	12.16 1	12.4 85	0.001	0.0 13	DN
K00873	PK, pyk	pyruvate kinase [EC:2.7.1.40]	- 1.11 5	12.46 9	12.0 37	0.001	0.0 16	DN
K03702	uvrB	excinuclease ABC subunit B	- 1.09 8	12.53 0	11.6 22	0.001	0.0 18	DN
K02224	cobB-cbiA	cobyrinic acid a,c-diamide synthase [EC:6.3.5.9 6.3.5.11]	- 1.06 1	10.66 0	9.88 8	0.003	0.0 34	DN
K03615	rnfC	Na ⁺ -translocating ferredoxin:NAD ⁺ oxidoreductase subunit C [EC:7.2.1.2]	- 1.02 0	11.80 0	9.34 5	0.003	0.0 40	DN

List of KOs differentially represented in the gut microbiome from NW vs. OWOB populations. (LogFC >1 and <-1, P and FDR adjusted-P <0.05).

Table S8: Enriched pathways as determined by Fisher's test.

<i>path</i>	<i>allFreq</i>	<i>myFreq</i>	<i>pathInt</i>	<i>pathNoInt</i>	<i>backInt</i>	<i>backNoInt</i>	<i>pval</i>	<i>bonferroni</i>	<i>bh</i>	<i>Representation NW vs OWOB</i>
<i>ABC transporters</i>	83	3	3	80	74	2774	0.37327499	1	0.46964551	over
<i>Apoptosis</i>	3	2	2	1	75	2853	0.00200939	0.0221033	0.00736777	over
<i>Butanoate metabolism</i>	24	2	2	22	75	2832	0.12979932	1	0.27068601	over
<i>Chromosome and associated proteins</i>	26	2	2	24	75	2830	0.14790293	1	0.27068601	over
<i>Enzymes with EC numbers</i>	122	4	4	118	73	2736	0.4000396	1	0.46964551	over
<i>Exosome</i>	24	3	3	21	74	2833	0.0237308	0.26103878	0.06525969	over
<i>Lysosome</i>	9	3	3	6	74	2848	0.00130709	0.01437797	0.00718899	over
<i>Membrane trafficking</i>	8	3	3	5	74	2849	0.00088814	0.00976954	0.00718899	over
<i>Peptidases</i>	55	2	2	53	75	2801	0.42695046	1	0.46964551	over
<i>Transcription factors</i>	83	4	4	79	73	2775	0.17225473	1	0.27068601	over
<i>Transporters</i>	284	3	3	281	74	2573	0.98421195	1	0.98421195	over
<i>Chaperones and folding catalysts</i>	31	3	3	28	166	2734	0.26382009	1	0.42320006	under
<i>DNA repair and recombination proteins</i>	46	2	2	44	167	2718	0.75407444	1	0.86578918	under
<i>DNA replication proteins</i>	15	3	3	12	166	2750	0.05133777	1	0.18308884	under
<i>Energy metabolism</i>	18	7	7	11	162	2751	3.47E-05	0.00107624	0.00053812	under
<i>Enzymes with EC numbers</i>	122	5	5	117	164	2645	0.84382502	1	0.90201985	under
<i>Ether lipid metabolism</i>	4	2	2	2	167	2760	0.01836051	0.56917579	0.11383516	under
<i>Folate biosynthesis</i>	15	2	2	13	167	2749	0.21290617	1	0.41250571	under
<i>Function unknown</i>	98	7	7	91	162	2671	0.33489834	1	0.45138472	under
<i>Glycerolipid metabolism</i>	15	2	2	13	167	2749	0.21290617	1	0.41250571	under
<i>Glycerophospholipid metabolism</i>	15	4	4	11	165	2751	0.0088208	0.27344465	0.07847071	under
<i>Glycolysis / Gluconeogenesis</i>	18	2	2	16	167	2746	0.27846123	1	0.42320006	under

<i>Glycosyltransferases</i>	24	3	3	21	166	2741	0.15738499	1	0.34849533	under
<i>Glyoxylate and dicarboxylate metabolism</i>	19	2	2	17	167	2745	0.30033553	1	0.42320006	under
<i>Lipid biosynthesis proteins</i>	17	2	2	15	167	2747	0.25654577	1	0.42320006	under
<i>Lysine biosynthesis</i>	10	2	2	8	167	2754	0.10969305	1	0.26157573	under
<i>Methane metabolism</i>	37	15	15	22	154	2740	4.33E-10	1.34E-08	1.34E-08	under
<i>Nucleotide excision repair</i>	5	2	2	3	167	2759	0.02944864	0.91290799	0.15215133	under
<i>Peptidases</i>	55	3	3	52	166	2710	0.62370322	1	0.80561666	under
<i>Porphyrin and chlorophyll metabolism</i>	31	3	3	28	166	2734	0.26382009	1	0.42320006	under
<i>Prokaryotic defense system</i>	45	2	2	43	167	2719	0.74305535	1	0.86578918	under
<i>Purine metabolism</i>	33	3	3	30	166	2732	0.29590391	1	0.42320006	under
<i>Pyruvate metabolism</i>	29	4	4	25	165	2737	0.08221778	1	0.21239593	under
<i>Replication and repair</i>	13	3	3	10	166	2752	0.03510594	1	0.15546916	under
<i>Ribosome</i>	26	4	4	22	165	2740	0.05906092	1	0.18308884	under
<i>Ribosome biogenesis</i>	33	6	6	27	163	2735	0.01012525	0.31388286	0.07847071	under
<i>Secretion system</i>	75	3	3	72	166	2690	0.81781991	1	0.90201985	under
<i>Terpenoid backbone biosynthesis</i>	8	2	2	6	167	2756	0.07357207	1	0.20733946	under
<i>Transcription factors</i>	83	4	4	79	165	2683	0.71554804	1	0.86578918	under
<i>Transfer RNA biogenesis</i>	37	5	5	32	164	2730	0.0586114	1	0.18308884	under
<i>Transporters</i>	284	7	7	277	162	2485	0.99825834	1	0.99825834	under
<i>Two-component system</i>	91	3	3	88	166	2674	0.90508105	1	0.93525042	under

Over-represented (over) and sub-represented (sub) KEGG pathways in the NW group compared to OWOB. *P-values* were adjusted by FDR according to Benjamini-Hochberg procedure.