

Summary of WD and FMD diets

Western-type diet (WD)									
	Calories (Kcal)	Total fat (g)	Saturated fat (g)	Carbohydrate (g)	Protein (g)	Fiber (g)	G%	CHO%	P%
Day 1	2380,9	135,7	53,2	156,7	122,9	4,4	51	26	21
Day 2	2368,1	130,1	43,6	155,8	135,7	3,1	49	26	23
Day 3	2373,1	130,1	47,1	168,0	122,5	4,8	49	28	21
Day 4	2366,9	134,5	48,2	162,6	116,5	7,4	51	27	20
Day 5	2319,7	126,9	50,6	168,9	123,2	4,9	49	29	21
Day 6	2250,7	127,7	53,9	160,1	106,6	4,1	51	28	19
Day 7	2387,7	146,9	58,0	138,5	120,3	4,0	55	23	20
Media	2349,6	133,1	50,7	158,7	121,1	4,7	51	27	21

Fibre-enriched Mediterranean diet (FMD)									
	Calories (Kcal)	Total fat (g)	Saturated fat (g)	Carbohydrate (g)	Protein (g)	Fiber (g)	G%	CHO%	P%
Day 1	2339,7	51,6	6,6	364,5	83,3	56,3	20	62	14
Day 2	2319,0	47,9	3,4	359,1	96,7	58,8	19	62	17
Day 3	2336,9	55,5	5,1	329,1	92,5	53,8	21	56	16
Day 4	2357,1	49,6	4,3	366,7	93,7	49,9	19	62	16
Day 5	2325,9	54,6	5,4	363,0	81,8	50,6	21	62	14
Day 6	2306,0	45,2	3,1	366,9	95,4	55,3	18	64	17
Day 7	2382,7	43,2	3,8	391,4	91,3	54,4	16	66	15
Media	2338,2	49,6	4,5	362,9	90,7	54,2	19	62	16

Days 1 and 8 FMD

Day 1	gr	Kcal	Fat	Saturated fat	Carbohydrates	Protein	Fiber
Breakfast							
Low-fat milk	200	92,0	3,2	2,2	9,6	6,2	0,0
Bacon	54	188,5	17,1	6,9	0,5	8,0	0,0
Egg	68	102,0	7,5	0,0	0,3	8,5	0,0
Crackets	30	143,4	5,7	0,6	20,1	2,5	0,5
Sugar	14	56,0	0,0	0,0	14,0	0,0	0,0
Lunch							
Bread	21	56,5	0,8	0,1	10,1	1,9	0,6
Bratwurst Sausage	200	399,4	28,1	11,0	2,4	33,6	0,0
Noodles	40	141,6	0,6	0,1	28,8	4,4	1,6
Butter	12	89,2	9,8	6,7	0,1	0,1	0,0
Choco cookie bar	16	85,3	4,7	2,9	9,7	1,0	0,2
Snack							
Milk bread	40	138,0	2,1	1,3	20,4	3,8	0,9
Ham	31,5	62,7	1,6	0,6	0,2	12,0	0,0
Butter	12	89,2	9,8	6,7	0,1	0,1	0,0
Dinner							
Bread	21	36,3	0,3	0,1	7,5	0,9	0,1
Potato omelette	200	316,0	17,8	2,8	28,0	8,8	2,9
Cheese	18	37,9	2,2	1,4	1,6	2,5	0,4
Pork chop	150	316,5	22,5	8,7	0,0	28,5	0,0
Chocolate	5,5	30,8	1,9	1,1	3,2	0,3	0,0
Total		2381	136	53	157	123	7
Breakfast		582	34	10	45	25	1
Lunch		772	44	21	51	41	2
Snack		290	34	13	58	28	4
Dinner		738	43	13	37	41	3

Days 2 and 9 FMD

Day 2	gr	Kcal	Fat	Saturated fat	Carbohydrates	Protein	Fiber
Breakfast							
Low-fat milk	200	92,0	3,2	2,2	9,6	6,2	0,0
Salami	60	277,2	25,2	7,8	3,06	9,6	0
Egg	68	102,7	7,5	0,0	0,3	8,5	0,0
Crackers	30	143,4	5,7	0,6	20,1	2,5	0,5
Sugar	14	56,0	0,0	0,0	14,0	0,0	0,0
Lunch							
Bread	21	56,5	0,8	0,1	10,1	1,9	0,6
Cannelloni with meat, bechamel and cheese	300	513	30,3	8,7	23,4	36	0,0
Snickers	18	86,6	4,1	1,4	11,0	1,5	0,0
Snack							
Milk bread	40	138,0	2,1	1,3	20,4	3,8	0,9
Iberian chorizo	63	286,2	22,6	9,1	0,6	20,0	0,0
Butter	12	89,2	9,8	6,7	0,1	0,1	0,0
Dinner							
Bread	21	56,5	0,8	0,1	10,1	1,9	0,6
Chicken	140	161,0	1,7	0,6	4,3	32,2	0,0
Cheese	18	37,9	2,2	1,4	1,6	2,5	0,4
Ham croquettes	120	241,2	12,0	2,4	24,0	8,9	0,0
Chocolate	5,5	30,8	1,9	1,1	3,2	0,3	0,0
TOTAL		2368	130	44	156	136	3
Breakfast		671	42	11	47	27	1
Lunch		656	31	9	33	38	1
Snack		513	35	17	21	24	1
Dinner		527	19	6	43	46	1

Days 3 and 10 FMD

Day 3	gr	Kcal	Fat (g)	Saturated fat (g)	Carbohydrates (g)	Protein (g)	Fiber (g)
Breakfast							
Low-fat milk	200	92	3,2	2,2	9,6	6,2	0
Ham	60	61,2	1,9	0,7	4,3	6,8	0,0
Egg	68	102,7	7,5	0,0	0,3	8,5	0,0
Crackers	30	143,4	5,7	0,6	20,1	2,5	0,5
Sugar	14	56	0	0	14	0	0,0
Lunch							
Bread	21	56,5	0,8	0,1	10,1	1,9	0,6
Beef	150	165,0	4,5	0,0	0,0	31,4	0,0
Potato omelette	200	316	17,8	2,8	28	8,8	2,88
Macaroon	20	80,2	2,6	0,56	12	1,9	0,58
Snack							
Milk bread	40	138,0	2,1	1,3	20,4	3,8	0,9
Salami	60	277,2	25,2	7,8	3,1	9,6	0,0
Butter	12	89,2	9,8	6,7	0,1	0,1	0,0
Dinner							
Bread	21	56,5	0,8	0,1	10,1	1,9	0,6
Bratwurst sausage	200	399,4	28,1	11,0	2,4	33,6	0,0
Noodles	40	141,6	0,6	0,1	28,8	4,4	1,6
Butter	12	167,5	17,5	12,0	1,6	1,0	0,0
Chocolate	5,5	30,8	1,9	1,1	3,2	0,3	0,0
Total		2373	130	47	168	122	8
Breakfast		455	18	3	34	24	1
Lunch		618	26	3	50	44	4
Snack		504	37	16	24	13	1
Dinner		796	49	24	46	41	2

Days 4 and 11 FMD

Day 4	gr	Kcal	Fat (g)	Saturated fat (g)	Carbohydrates (g)	Protein (g)	Fiber (g)
Breakfast							
Low-fat milk	200	92,0	3,2	2,2	9,6	6,2	0,0
Bacon	54	188,5	17,1	6,9	0,5	8,0	0,0
Egg	68	102,0	7,5	0,0	0,3	8,5	0,0
Crackers	30	143,4	5,7	0,6	20,1	2,5	0,5
Sugar	14	56	0	0	14	0	0
Lunch							
Bread	21	56,5	0,8	0,1	10,1	1,9	0,6
Pork chop	150	316,5	22,5	8,7	0,0	28,5	0,0
Cheese	18	37,9	2,2	1,4	1,6	2,5	0,4
Russian salad	125	274,0	22,5	3,5	10,0	7,1	2,3
Snicker	18	86,6	4,1	1,4	11,0	1,5	0,2
Snack							
Milk bread	40	138,0	2,1	1,3	20,4	3,8	0,9
Iberian chorizo	63	286,2	22,6	9,1	0,6	20,0	0,0
Butter	12	89,2	9,8	6,7	0,1	0,1	0,0
Dinner							
Bread	21	56,5	0,8	0,1	10,1	1,9	0,6
Bolognese lasagna	300	375	9,3	3,6	49,5	21,3	3,9
Cheese	18	37,9	2,2	1,4	1,6	2,5	0,4
Chocolate	5,5	30,8	1,9	1,1	3,2	0,3	0,0
Total		2367	135	48	163	117	10
Breakfast		582	34	10	45	25	1
Lunch		771	48	14	22	40	3
Snack		513	35	17	21	24	1
Dinner		500	14	6	64	26	5

Days 5 and 12 FMD

Day 5	gr	Kcal	Fat (g)	Saturated fat (g)	Carbohydrates (g)	Protein (g)	Fiber (g)
Breakfast							
Low-fat milk	200	92,0	4,0	2,8	12,0	7,8	0,0
Salami	60	277,2	25,2	7,8	3,1	9,6	0,0
Egg	68	102,7	7,5	0,0	0,3	8,5	0,0
Crackers	30	143,4	5,7	0,6	20,1	2,5	0,5
Sugar	14	56	0	0	14	0	0
Lunch							
Bread	21	56,5	0,8	0,1	10,1	1,9	0,6
Pork Burguer	180	381,6	28,8	10,1	5,4	25,2	0,0
Cheese	18	37,9	2,2	1,4	1,6	2,5	0,4
Ham croquettes	120	241,2	12,0	2,4	24,0	8,9	0,0
Choco cookie bar	16	85,3	4,7	2,9	9,7	1,0	0,2
Snack							
Milk bread	40	138,0	2,1	1,3	20,4	3,8	0,9
Pork ham	31	61,7	1,6	0,6	0,2	11,8	0,0
Butter	12	89,2	9,8	6,7	0,1	0,1	0,0
Dinner							
Bread	21	56,5	0,8	0,1	10,1	1,9	0,6
Chicken	140	161,0	1,7	0,6	4,3	32,2	0,0
Milk cream	50	167,5	17,5	12,0	1,6	1,0	0,0
Noodles	40	141,6	0,6	0,1	28,8	4,4	1,6
Chocolate	5,5	30,8	1,87	1,1	3,19	0,264	0
Total		2320	127	51	169	123	5
Breakfast		671	42	11	50	28	1
Lunch		802	44	14	41	38	1
Snack		289	14	9	21	16	1
Dinner		557	22	14	48	40	2

Days 6 and 13 FMD

Day 6	gr	Kcal	Fat (g)	Saturated fat (g)	Carbohydrates (g)	Protein (g)	Fiber (g)
Breakfast							
Low-fat milk	200	92,0	3,2	2,2	9,6	6,2	0,0
Ham	60	61,2	1,9	0,7	4,3	6,8	0,0
Egg	68	102,7	7,5	0,0	0,3	8,5	0,0
Crackers	30	143,4	5,7	0,6	20,1	2,5	0,5
Sugar	14	56,0	0,0	0,0	14,0	0,0	0,0
Lunch							
Bread	21	56,5	0,8	0,1	10,1	1,9	0,6
3 cheese quiche	175	503,7	38,0	23,4	27,7	12,8	0,9
Bacon	53	188,5	17,1	6,9	0,5	8,0	0,0
Choco cookie bar	16	85,3	4,7	2,9	9,7	1,0	0,2
Snack							
Milk bread	40	138,0	2,1	1,3	20,4	3,8	0,9
Iberian chorizo	60	128,4	9,6	3,7	0,3	10,2	0,0
Butter	12	89,2	9,8	6,7	0,1	0,1	0,0
Dinner							
Bread	21	56,5	0,8	0,1	10,1	1,9	0,6
Beef	150	165,0	4,5	0,0	0,0	31,4	0,0
Potato omelette	200	316,0	17,8	2,8	28,0	8,8	2,9
Cheese	18	37,9	2,2	1,4	1,6	2,5	0,4
Chocolate	5,5	30,8	1,87	1,1	3,19	0,264	0
Total		2251	128	54	160	107	7
Breakfast		455	18	3	48	24	1
Lunch		834	61	33	48	24	2
Snack		356	22	12	21	14	1
Dinner		606	27	5	43	45	4

Days 7 and 14 FMD

Day 7	gr	Kcal	Fat (g)	Saturated fat (g)	Carbohydrates (g)	Protein (g)	Fiber (g)
Breakfast							
Low-fat milk	200	92,0	3,2	2,2	9,6	6,2	0,0
Salami	60	277,2	25,2	7,8	3,1	9,6	0,0
Egg	68	102,0	7,5	0,0	0,3	8,5	0,0
Crackers	30	143,4	5,7	0,6	20,1	2,5	0,5
Sugar	14	56,0	0,0	0,0	14,0	0,0	0,0
Lunch							
Bread	21	56,5	0,8	0,1	10,1	1,9	0,6
Pork chop	150	316,5	22,5	8,7	0,0	28,5	0,0
Russian salad	125	274,0	22,5	3,5	10,0	7,1	2,3
Snicker	18	86,6	4,1	1,4	11,0	1,5	0,0
Cheese	18	37,9	2,2	1,4	1,6	2,5	0,4
Snack							
Milk bread	40	138,0	2,1	1,3	20,4	3,8	0,9
Pork Ham	60	128,4	9,6	3,7	0,3	10,2	0,0
Butter	12	89,2	9,8	6,7	0,1	0,1	0,0
Dinner							
Bread	21	41,9	2,9	1,2	0,3	3,5	0,0
Chicken	140	161,0	1,7	0,6	4,3	32,2	0,0
Noodles	40	141,6	0,6	0,1	28,8	4,4	1,6
Butter	12	89,2	9,8	6,7	0,1	0,1	0,0
Chocolate	5,5	30,8	1,87	1,1	3,19	0,264	0
Milk cream	50	167,5	17,5	12	1,55	1	0
Total		2430	150	59	139	124	6
Breakfast		671	42	11	33	27	1
Lunch		734	50	14	31	39	3
Snack		356	22	12	21	14	1
Dinner		590	31	21	38	38	2

Days 1 and 8 WD

Day 1	gr	Kcal	Fat (g)	Saturated fat (g)	Carbohydrates (g)	Protein (g)	Fiber (g)
Breakfast							
Skim milk	200	80,0	0,6	1,0	10,6	7,8	0,0
Sugar	14	56,0	0,0	0,0	14,0	0,0	0,0
Rye bread	110	231,0	1,7	0,3	42,9	5,5	8,8
Strawberry jam	25	54,0	0,1	0,0	13,3	0,1	0,7
Honey	20	66,4	0,0	0,0	16,5	0,1	0,0
Snack							
Walnuts	30	178,5	19,0	0,0	1,0	4,2	1,6
Dates	40	149,2	0,1	0,0	35,1	0,4	3,2
Lunch							
Bread	35	89,3	0,8	0,2	17,9	3,3	1,4
Stewed beans	430	382,7	9,5	3,0	39,1	22,8	25,8
Mix salad	100	27,0	0,2	0,1	3,6	1,3	1,6
Olive oil	5	45,0	5,0	0,0	0,0	0,0	0,0
Pear	205	118,9	0,2	0,0	28,7	0,6	1,0
Snack							
Chocolate soy drink	200	110,0	3,8	0,8	11,0	7,2	1,8
Cereal	40	149,6	0,3	0,0	32,0	3,7	1,9
Dehydrated apple	40	109,6	0,3	0,1	24,0	1,5	2,5
Dinner							
Bread	35	89,3	0,8	0,2	17,9	3,3	1,4
Brown rice	80	212,5	3,4	0,6	38,8	5,0	3,6
Chicken breast	70	80,5	0,8	0,3	2,2	16,1	0,0
Mix salad	100	27,0	0,2	0,1	3,6	1,3	1,6
Olive oil	5	45,0	5,0	0,0	0,0	0,0	0,0
Pineapple	113	63,3	0,0	0,0	14,7	0,6	1,1
TOTAL		2365	52	7	367	85	58
Breakfast		487	2	1	97	14	9
Snack		328	19	0	36	5	5
Lunch		663	16	3	89	28	30
Snack		369	4	1	67	12	6
Dinner		518	10	1	77	26	8

Days 2 and 9 WD

Day 2	gr	Kcal	Fat (g)	Saturated fat (g)	Carbohydrates (g)	Protein (g)	Fiber (g)
Breakfast							
Skim milk	200	80,0	0,6	1,0	10,6	7,8	0,0
Sugar	14	56,0	0,0	0,0	14,0	0,0	0,0
Rye bread	110	231,0	1,7	0,3	42,9	5,5	8,8
Peach jam	25	54,0	0,1	0,0	13,3	0,1	0,5
Honey	20	66,4	0,0	0,0	16,5	0,1	0,0
Snack							
Walnuts	30	178,5	19,0	0,0	1,0	4,2	1,6
Banana	150	133,5	0,5	0,0	30,0	1,8	5,1
Lunch							
Bread	35	89,3	0,8	0,2	17,9	3,3	1,4
Canned Tuna	60	47,4	0,4	0,1	0,3	10,8	0,0
Peas	140	172,2	1,5	0,1	23,8	10,6	11,2
Assorted vegetables	150	51,0	0,3	0,0	8,9	2,1	2,6
Tomato	150	28,5	0,2	0,0	5,3	1,4	1,7
Olive oil	5	45,0	5,0	0,0	0,0	0,0	0,0
Tangerines	180	72,0	0,0	0,0	16,2	1,4	3,4
Snack							
Vanilla soy drink	200	94,0	3,4	0,6	9,0	6,0	1,2
Cereal	40	152,4	0,6	0,1	31,6	4,8	1,2
Dehydrated mango	60	190,2	0,7	0,2	42,0	1,5	4,9
Dinner							
Bread	35	89,3	0,8	0,2	17,9	3,3	1,4
Beef	100	110,0	3,0	0,0	0,0	20,9	0,0
Quinoa	125	153,8	2,8	0,4	24,5	5,6	5,1
Assorted vegetables	150	51,0	0,3	0,0	8,9	2,1	2,6
Artichoke	60	24,6	0,3	0,0	3,6	1,1	2,4
Olive oil	5	45,0	5,0	0,0	0,0	0,0	0,0
Kiwi	200	104,0	1,0	0,0	21,2	2,2	3,8
TOTAL		2319	48	3	359	97	59
Breakfast		487	2	1	97	14	9
Snack		312	19	0	31	6	7
Lunch		505	8	1	72	30	20
Snack		437	5	1	83	12	7
Dinner		578	13	1	76	35	15

Days 3 and 10 WD

Day 3	gr	Kcal	Fat (g)	Saturated fat (g)	Carbohydrates (g)	Protein (g)	Fiber (g)
Breakfast							
Skim milk	200	80,0	0,6	1,0	10,6	7,8	0,0
Sugar	14	56,0	0,0	0,0	14,0	0,0	0,0
Rye bread	110	231,0	1,7	0,3	42,9	5,5	8,8
Turkey breast	30	23,4	0,2	0,1	0,2	5,3	0,0
Straw berry jam	20	66,4	0,0	0,0	16,5	0,1	0,0
Snack							
Walnuts	30	178,5	19,0	0,0	1,0	4,2	1,6
Dried apricots	40	109,6	0,3	0,1	24,0	1,5	2,5
Lunch							
Bread	35	89,3	0,8	0,2	17,9	3,3	1,4
Chikpeas with spinac	430	374,0	14,5	1,7	40,4	16,2	9,8
Assorted vegetables	150	64,5	0,4	0,1	12,3	1,8	2,6
Mixed salad	50	12,0	0,2	0,0	1,4	0,9	0,7
Olive oil	5	45,0	5,0	0,0	0,0	0,0	0,0
Pineapple	113	63,3	0,0	0,0	14,7	0,6	1,1
Snack							
Chocolate soy drink	200	110,0	3,8	0,8	11,0	7,2	1,8
Cereal	40	149,6	0,3	0,0	32,0	3,7	1,9
Dehydrated apple	20	73,0	0,1	0,0	16,6	0,2	2,4
Dinner							
Bread	35	89,3	0,8	0,2	17,9	3,3	1,4
Breast chicken	70	80,5	0,8	0,3	2,2	16,1	0,0
Corn	140	172,2	1,5	0,1	23,8	10,6	11,2
Assorted vegetables	150	64,5	0,4	0,1	12,3	1,8	2,6
Mixed salad	50	12,0	0,2	0,0	1,4	0,9	0,7
Olive oil	5	45,0	5,0	0,0	0,0	0,0	0,0
Tangerines	180	72,0	0,0	0,0	16,2	1,4	3,4
TOTAL		2261	55	5	329	93	54
Breakfast		457	2	1	84	19	9
Snack		288	19	0	25	6	4
Lunch		648	21	2	87	23	16
Snack		333	4	1	60	11	6
Dinner		535	9	1	74	34	19

Days 4 and 11 WD

Day 4	gr	Kcal	Fat (g)	Saturated fat (g)	Carbohydrates (g)	Protein (g)	Fiber (g)
Breakfast							
Skim milk	200	80,0	0,6	1,0	10,6	7,8	0,0
Sugar	14	56,0	0,0	0,0	14,0	0,0	0,0
Rye bread	110	231,0	1,7	0,3	42,9	5,5	8,8
Quince paste	40	90,0	0,0	0,0	22,3	0,1	0,0
Snack							
Walnuts	30	178,5	19,0	0,0	1,0	4,2	1,6
Dehydrated mango	60	190,2	0,7	0,2	42,0	1,5	4,9
Lunch							
Bread	35	86,1	5,7	0,6	3,7	4,3	1,3
Red lentil noodles	100	334	1,7	0,4	50	26	7,6
Mixed salad	50	15	0	0	3	1	1
Assorted vegetables	150	51,0	0,3	0,0	8,9	2,1	2,6
Artichoke	60	20,5	0,25	0	3	0,9	2
Olive oil	5	45,0	5,0	0,0	0,0	0,0	0,0
Pear	205	118,9	0,2	0,0	28,7	0,6	1,0
Snack							
Vanilla soy drink	200	94,0	3,4	0,6	9,0	6,0	1,2
Cereal	40	152,4	0,6	0,1	31,6	4,8	1,2
Dehydrated apple	20	73,0	0,1	0,0	16,6	0,2	2,4
Dinner							
Bread	35	89,3	0,8	0,2	17,9	3,3	1,4
Breast chicken	70	80,5	0,8	0,3	2,2	16,1	0,0
Quinoa	120	153,8	2,8	0,4	24,5	5,6	5,1
Assorted vegetables	150	51,0	0,3	0,0	8,9	2,1	2,6
Mixed salad	50	14,5	0,1	0,0	2,5	0,5	0,9
Olive oil	5	45,0	5,0	0,0	0,0	0,0	0,0
Plum	200	108,0	0,4	0,0	24,0	1,5	4,6
TOTAL		2357	50	4	367	94	50
Breakfast		457	2	1	90	13	9
Snack		369	20	0	43	6	6
Lunch		670	13	1	97	34	15
Snack		319	4	1	57	11	5
Dinner		542	10	1	80	29	15

Days 5 and 12 WD

Day 5	gr	Kcal	Fat (g)	Saturated fat (g)	Carbohydrates (g)	Protein (g)	Fiber (g)
Breakfast							
Skim milk	200	80,0	0,6	1,0	10,6	7,8	0,0
Sugar	14	56,0	0,0	0,0	14,0	0,0	0,0
Rye bread	110	231,0	1,7	0,3	42,9	5,5	8,8
Strawberry jam	25	54,0	0,1	0,0	13,3	0,1	0,5
Turkey breast	30	23,4	0,2	0,1	0,2	5,3	0,0
Snack							
Walnuts	30	178,5	19,0	0,0	1,0	4,2	1,6
Dates	40	149,2	0,1	0,0	35,1	0,4	3,2
Lunch							
Bread	35	89,3	0,8	0,2	17,9	3,3	1,4
Stewed lentils	420	283,8	11,6	1,7	28,8	12,5	7,3
Mixed salad	50	12,0	0,2	0,0	1,4	0,9	0,7
Cucumbrer	150	18,0	0,2	0,0	3,0	1,1	2,7
Olive oil	5	45,0	5,0	0,0	0,0	0,0	0,0
Banana	150	133,5	0,5	0,0	30,0	1,8	5,1
Snack							
Chocolate soy drink	200	110,0	3,8	0,8	11,0	7,2	1,8
Cereal	40	149,6	0,3	0,0	32,0	3,7	1,9
Dehydrated mango	60	190,2	0,7	0,2	42,0	1,5	4,9
Dinner							
Bread	35	89,3	0,8	0,2	17,9	3,3	1,4
Canned tuna	80	63,2	0,6	0,2	0,4	14,4	0,0
Brown rice	80	212,5	3,4	0,6	38,8	5,0	3,6
Tomato	150	28,5	0,2	0,0	5,3	1,4	1,7
Mixed salad	50	12,0	0,2	0,0	1,4	0,9	0,7
Olive oil	5	45,0	5,0	0,0	0,0	0,0	0,0
Tangerine	180	72,0	0,0	0,0	16,2	1,4	3,4
TOTAL		2326	55	5	363	82	51
Breakfast		444	2	1	81	19	9
Snack		328	19	0	36	5	5
Lunch		582	18	2	81	20	17
Snack		450	5	1	85	12	9
Dinner		522	10	1	80	26	11

Days 6 and 13 WD

Day 6	gr	Kcal	Fat (g)	Saturated fat (g)	Carbohydrates (g)	Protein (g)	Fiber (g)
Breakfast							
Skim milk	200	80,0	0,6	1,0	10,6	7,8	0,0
Sugar	14	56,0	0,0	0,0	14,0	0,0	0,0
Rye bread	110	231,0	1,7	0,3	42,9	5,5	8,8
Quince paste	40	90,0	0,0	0,0	22,3	0,1	0,0
Snack							
Walnuts	30	178,5	19,0	0,0	1,0	4,2	1,6
Dehydrated mango	60	190,2	0,7	0,2	42,0	1,5	4,9
Lunch							
Bread	35	89,25	0,84	0,21	17,85	3,325	1,4
Beef steak	100	110,0	3,0	0,0	0,0	20,9	0,0
Peas	140	172,2	1,5	0,1	23,8	10,6	11,2
Assorted vegetables	150	46,5	0,0	0,1	10,4	1,7	2,4
Mix salad	50	12,0	0,2	0,0	1,4	0,9	0,7
Olive oil	5	45	5	0	0	0	0
Kiwi	200	104,0	1,0	0,0	21,2	2,2	3,8
Snack							
Chocolate soy pudding	200	110	2,1	0,6	18,2	3,5	2,2
Cereal	40	152,4	0,6	0,1	31,6	4,8	1,2
Banana	150	133,5	0,5	0,0	30,0	1,8	5,1
Dinner							
Bread	35	89,25	0,84	0,21	17,85	3,325	1,4
Chicken breast	70	80,5	0,84	0,28	2,17	16,1	0
Corn	140	165,2	1,8	0,0	30,8	4,2	4,6
Assorted vegetables	150	46,5	0,0	0,1	10,4	1,7	2,4
Mixed salad	50	12	0,15	0,015	1,4	0,9	0,7
Olive oil	5	45	5	0	0	0	0
Plum	200	108	0,4	0	24	1,5	4,6
TOTAL		2347	46	3	374	96	57
Breakfast		457	2	1	90	13	9
Snack		369	20	0	43	6	6
Lunch		579	12	0	75	40	20
Snack		396	3	1	80	10	9
Dinner		457	8	0	69	24	12

Days 7 and 14 WD

Day 7	gr	Kcal	Fat (g)	Saturated fat (g)	Carbohydrates (g)	Protein (g)	Fiber (g)
Breakfast							
Skim milk	200	80,0	0,6	1,0	10,6	7,8	0,0
Sugar	14	56,0	0,0	0,0	14,0	0,0	0,0
Rye bread	110	231,0	1,7	0,3	42,9	5,5	8,8
Peach jam	25	54,0	0,1	0,0	13,3	0,1	0,5
Honey	20	66,4	0,0	0,0	16,5	0,1	0,0
Snack							
Walnuts	30	178,5	19,0	0,0	1,0	4,2	1,6
Dried apricots	40	109,6	0,3	0,1	24,0	1,5	2,5
Lunch							
Bread	35	89,3	0,8	0,2	17,9	3,3	1,4
Red lentil noodles	100	334,0	1,7	0,4	50,0	26,0	7,6
Tomato	150	28,5	0,2	0,0	5,3	1,4	1,7
Olive oil	5	45,0	5,0	0,0	0,0	0,0	0,0
Plum	200	108,0	0,4	0,0	24,0	1,5	4,6
Artichokes	60	24,6	0,3	0,0	3,6	1,1	2,4
Mix salad	150	51,0	0,3	0,0	8,9	2,1	2,6
Snack							
Chocolate soy pudding	200	110,0	2,1	0,6	18,2	3,5	2,2
Cereal	40	152,4	0,6	0,1	31,6	4,8	1,2
Dehydrated mango	60	190,2	0,7	0,2	42,0	1,5	4,9
Dinner							
Bread	35	89,3	0,8	0,2	17,9	3,3	1,4
Tuna	80	63,2	0,6	0,2	0,4	14,4	0,0
Quinoa	120	153,8	2,8	0,4	24,5	5,6	5,1
Assorted vegetables	150	51,0	0,3	0,0	8,9	2,1	2,6
Olive oil	5	45,0	5,0	0,0	0,0	0,0	0,0
Tangerines	180	72,0	0,0	0,0	16,2	1,4	3,4
TOTAL		2383	43	4	391	91	54
Breakfast		487	2	1	97	14	9
Snack		288	19	0	25	6	4
Lunch		680	9	1	110	35	20
Snack		453	3	1	92	10	8
Dinner		474	9	1	68	27	12

1. COLONIC CONTENT MEASUREMENT

MR imaging examinations of the colon were performed in the pretreatment and treatment phases (both on the challenge diet) using a 1.5-T MR imaging system (Aera; Siemens Healthcare, Erlangen, Germany) with two six-channel phased-array abdominal coils to cover the whole abdomen. The abdomen was imaged obtaining a T2-weighted HASTE sequence in the coronal plane (1400 ms repetition time, 90 ms echo time, 3.5 mm slice thickness, 180° flip angle, and 256x256 matrix resolution) during two apneas of 20 s each and a T1-weighted VIBE Fat-Sat sequence in the coronal plane (3.71 ms repetition time, 1.66 ms echo time, 1.5 mm slice thickness, 10 flip angle and 320x189 matrix resolution) in one apnea of 12 s. No drugs or contrast were used.

Analysis of the images was made using an original software developed for this purpose¹. The program allows semiautomatic segmentation of the colon on the images using a region-growing-based algorithm. First, an anisotropic contrast enhancement filter is applied to enhance the colon's boundary without loss of inside detail. Then, seed points are placed that expand depending on the gray-level mapping defined by the window-level setting of the images. A toolkit was developed to facilitate colonic segmentation, which permits enlarging or reducing the segmentation obtained by the region-growing algorithm. Colonic segmentation was correlated in T2 and T1 images. Nongaseous colonic content was measured in T1 colonic images, and gaseous colonic content was measured by subtracting T1 from T2 colonic volumes. A three-dimensional reconstruction program with 360° rotation over the three dimensions was used to facilitate the measurement of volumes in selected regions of the colon².

2. UNTARGETED METABOLOMIC ANALYSIS

Enzymatic treatment of urine samples

Urine samples (0.5 mL) were incubated with 25 μ L β -glucuronidase and 3 mg sulfatase for 24 h at 37 °C with gentle agitation. After incubation, samples were extracted twice with 2 mL ethyl acetate and evaporated, further re-dissolved in 2 mL MeOH, and analyzed by UPLC-ESI-QTOF-MS.

UPLC-ESI-QTOF-MS analysis

The analyses were carried out using an Agilent 1290 Infinity series LC system coupled to a 6550 I-Funnel Accurate-Mass QTOF (Agilent Technologies, Waldbronn, Germany) with a dual electrospray ionization interface (ESI-Jet Stream Technology) for simultaneous spraying of a mass reference solution that enabled continuous calibration of detected m/z ratios. Urine samples (with or without enzymatic treatment) were injected into a reverse-phase column, a Poroshell 120 EC column (3 x 100 mm, 2.7 μ m) (Agilent Technologies), operating at 30 °C and a flow rate of 0.5 mL/min. The mobile phases used were acidified water (0.1% formic acid) (Phase A) and acidified ACN (0.1% formic acid) (Phase B). Compounds were separated using the following gradient conditions: 0–3 min, 5–18% phase-B; 3–10 min, 18–50% phase-B; 10–13 min, 50–90% phase-B. Finally, phase B content was returned to the initial conditions (5%) for 1 min, and the column re-equilibrated for two more minutes. Data were acquired using the Mass Hunter Workstation software (version B.08.00, Service Pack 1, Agilent Technologies). The system was operated using both negative and positive ion polarity. Data were acquired in centroid and profile mode, with a data storage threshold of 5000 absorbance for MS and 5000 absorbance for MS/MS. The

operating conditions were as follows: gas temperature of 280 °C, drying nitrogen gas of 9 L/min, nebulizer pressure of 45 psi, sheath gas temperature of 400 °C, sheath gas flow of 12 L/min, a capillary voltage of 3500 V, nozzle voltage of 500 V, fragmentor voltage of 100 V, skimmer of 65 V and octopole radiofrequency voltage of 750 V. TOF spectra acquisition rate/time was 1.5 spectra/s and 666.7 ms/spectrum respectively, and transients/spectrum were 5484. The mass range was between 50 and 1100 m/z . At the beginning of the batch, the instrument was calibrated to assure mass accuracy during the MS analysis using a mixture of reference compounds (Tuning Mix). Continuous internal calibration was performed during analyses using signals m/z 112.9855 and m/z 1033.9881 in negative polarity and m/z 121.0509 and m/z 922.0098 in positive polarity. Auto recalibration reference-mass parameters were a detection window of 100 ppm and a minimum height of 1000 counts. MS/MS conditions were collision energy 20 eV and acquisition time 100 ms/spectrum. Data were processed using the Mass Hunter Qualitative Analysis software (version B.08.00, Service Pack 1, Agilent Technologies).

As there was no specific target analytes (untargeted analysis), generic settings were applied to obtain as many compounds as possible. QTOF-MS offers high selectivity, sensitivity, resolution, and high mass accuracy, providing a powerful tool for complex samples' metabolic profiling. All samples were injected in the same batch, and the order of sample injection was randomized to avoid sample bias. A mixture with one replicate of each samples group was used as 'quality control' (QC) and was injected at the beginning and the end of the batch. Besides, MeOH injections were included every three samples as a blank run to avoid the carry-over effect.

Data pretreatment

Batch Feature Finding: MassHunter Profinder

Feature extraction was carried out on Agilent Profinder B.06.00 (Agilent Technologies, Waldbronn, Germany), a stand-alone feature extraction program for LC/MS-based profiling analyses. Profinder was optimized to extract features from large data sets and provide an intuitive user interface to inspect and review each feature across the files associated with the data set. Extracted ion chromatograms and mass spectral data related to each feature were revised and compared simultaneously, and scored by the software.

Once the data files were selected, the recursive feature extraction workflow algorithm was selected, and then, the method for the feature extraction algorithm was edited and reviewed. To find compounds by Molecular Features (MFs) was carried out using a pre-filter to take peaks with a height greater or equal to 10000 counts, allowing only $-H$ and $+HCOO$ as negative ions species and $+H$ as positive ions, a peak spacing tolerance of $0.0025\ m/z$ plus 7.0 ppm, and charge states limited to a maximum of 2. The file obtained with this pre-processing was created for each sample as a CEF file. The final files were exported into the Mass Profiler Professional (MPP) software package (revision B.14.09.01, Agilent Technologies, Santa Clara, CA, USA) for statistical analysis.

A new experiment typed as unidentified was created in MPP, and significance testing and fold change were done. The data source used for the experiment was MassHunter Qual, and the organism was *Homo Sapiens*. In the second step, data were imported from files. The following steps were sample reordering and experiment grouping. After data were imported, several filtering options were

applied, such as a minimum absolute abundance of 5000 counts, minimum mass filtering of 70 and maximum mass filtering of 1200, numbers of ions required greater or equal to 2, and the option to all charge states forbidden.

Alignment

The next step was the alignment of parameters, where unidentified compounds were aligned across the different samples based on their retention times' tolerance and the mass spectral similarity. Compounds from different samples with the same m/z (mass tolerance window: 5 ppm, 2mDa) and retention time (tolerance window: 0.15 min) were considered the same.

Normalization and Baseline Transformation

Next, the baselining pre-processing options were selected. The goal of normalization is to limit systematic non-biological variation to reveal real biological variation. Normalization steps were performed 'within samples' whereas baselining was 'per entity'. Using baseline transformation improved both visualization of abundance pattern similarities and grouping of masses with similar abundance patterns in clustering analysis. Data were transformed to the log 2 scale and centered to the median across samples set to lower the relatively large differences in the respective MFs abundance. All compounds were treated equally regardless of their abundance.

Quality Control on Samples and Entities

Quality control can be performed at both the sample and mass levels to eliminate low-quality samples and unreliable measurements. Carrying over low-

quality samples and masses could limit statistically significant findings or informative clustering results.

'Filter on frequency, on flags, and by abundance' criteria were applied to reduce the dimensionality of the data and select the most representative compounds, which are rarely detected (therefore not very reliable), and filter out entities with non-reproducible measurements within a condition. Only the MFs present in at least 80% of replicates in at least one condition were considered. This entity filtering allowed creating a higher quality data set so that the following multivariate analysis should be more significant.

Multivariate and statistical analysis in the metabolomic analysis

In a second step, statistical comparisons were performed between the Western-type diet (WD) and the fiber-enriched Mediterranean-type diet (FMD). Student's t-test unpaired analyses were applied with a level of significance of $p < 0.05$ with Bonferonni Holm Family-wise Error Rate (FWER) multiple testing corrections and a fold-change cut-off of 2.0. Student's t-test was mainly focused on searching for the null hypothesis's statistical significance between WD and FMD. A list of compounds that significantly differed between groups was generated. Both supervised methods (PLS-DA), suitable for classification, and unsupervised methods (PCA, Clustering) appropriate for pattern identification, were used to visualize statistical results, using the final list of statistically significant MFs.

Compound identification: Molecular structure correlator

The MassHunter MSC (Molecular Structure Correlator) program was used. This software accurately correlated mass MS/MS fragment ions for a compound of interest with one or more proposed molecular structures. Then, each selected formula was used to retrieve one or multiple possible structures from several on-line database and libraries, including the MassHunter compound database (PCDL), METLIN/ChemSpider/KEGG/Lipid Maps, etc., and scored how well each candidate structure correlated with the MS/MS spectrum.

The validation of tentatively identified compounds by the MassHunter program was carried out (whenever possible) by chromatographic comparison with authentic standards. When authentic standards were not available, indirect validation was tried according to the fragmentation by MS/MS and metabolites' elution order.

References

1. Bendezu RA, Mego M, Monclus E, et al. Colonic content: effect of diet, meals, and defecation. *Neurogastroenterol Motil* 2017;29:e12930.
2. Bendezu RA, Barba E, Burri E, et al. Colonic content in health and its relation to functional gut symptoms. *Neurogastroenterol Motil* 2016;28:849-854.

Table S1. Metabolites significantly different in urine after consumption of FMD and WD.

RT (min)	Ionisation mode	Exact Mass	Probable elemental formula	Initial tentative identification	Score (%)	Availability of standard	Metabolite confirmed	Increase (-fold)
<i>Increased metabolites after FMD</i>								
0.9	+	76.0757	CH ₃ N ₃ O	Trimethylamine <i>N</i> -oxide (TMAO)	100.0	YES	TMAO	1.5
3.3	+	381.0800	C ₁₅ H ₁₈ O ₁₀	3,4-Dihydroxyphenyl propionic acid 3- <i>O</i> -glucuronide	96.9	NO	NC*	2.7
4.2	+	281.1134	C ₁₃ H ₁₆ N ₂ O ₅	L-Aspartyl phenylalanine	100.0	YES	L-aspartyl phenylalanine	2.4
4.8	+	134.0603	C ₈ H ₇ N O	Hydroxyindole derivative	97.6	YES	5-hydroxyindole	2.0
5.4	-	250.0718	C ₁₂ H ₁₃ N O ₅	<i>N</i> -Feruloylglycine	98.1	NO	NC	2.0
10.0	-	567.3167	C ₃₀ H ₄₈ O ₁₀	<ul style="list-style-type: none"> • Deoxycholate 3-glucuronide • Hyodeoxycholate 3-glucuronide • Chenodeoxycholate 3-glucuronide • Ursodeoxycholate 3-glucuronide 	96.5	NO	Deoxycholic acid*	2.1
<i>Increased metabolites after WD</i>								
2.3	+	218.1395	C ₁₀ H ₂₀ N O ₄	Propionyl-L-carnitine	100.0	YES	Propionyl-L-carnitine	2.2
2.3	-	216.0332	C ₈ H ₁₁ N O ₄	<i>p</i> -Tyramine 3- <i>O</i> -sulfate	97.6	NO	<i>p</i> -Tyramine*	2.4
6.8	+	242.2122	C ₁₄ H ₂₇ N O ₂	Sphingosine	95.3	YES	NC	17.5
8.4	-	541.2644	C ₂₇ H ₄₂ O ₁₁	Cortolone 3-glucuronide	96.5	NO	Cortolone*	2.0
9.7	-	467.2641	C ₂₅ H ₄₀ O ₈	<ul style="list-style-type: none"> • 18-acetoxy-PGF2α-11-acetate methyl ester • 3-α-Androstanediol glucuronide 	95.9	NO	PGF2 α *	2.0

*Confirmation (or not) of the unconjugated metabolite (commercially available) after treatment of the urine with glucuronidase/sulfatase; FMD, fibre-enriched Mediterranean-type diet (FMD); RT, retention time; WD, Western-like diet; NC, not confirmed.

Table S2. Characteristic microbial gene families present in individuals showing a robust and non-robust microbiota (see **Figure 2**).

Statistically significant ($p < 0.05$) microbial gene families present in individuals showing a robust and non-robust microbiota 8319 significant gene families associated to specific microbial species	
Robust microbiota: 7628 gene families	Non-robust microbiota: 691 gene families
Most abundant species (number of genes):	Most abundant species (number of genes):
<input type="checkbox"/> <i>Bacteroides uniformis</i> (2347)	<input type="checkbox"/> <i>Bacteroides uniformis</i> CAG 3 (237)
<input type="checkbox"/> <i>Bacteroides uniformis</i> CAG 3 (1712)	<input type="checkbox"/> <i>Bacteroides uniformis</i> (173)
<input type="checkbox"/> <i>Bacteroides vulgatus</i> (1597)	<input type="checkbox"/> <i>Ruminococcus bromii</i> (71)
<input type="checkbox"/> <i>Bacteroides vulgatus</i> CAG 6 (952)	<input type="checkbox"/> <i>Bacteroides vulgatus</i> (58)
<input type="checkbox"/> <i>Parabacteroides distasonis</i> (176)	<input type="checkbox"/> <i>Gemmiger formicilis</i> (36)
<input type="checkbox"/> <i>Bacteroides caccae</i> (147)	<input type="checkbox"/> <i>Bacteroides vulgatus</i> CAG 6 (31)
<input type="checkbox"/> <i>Parabacteroides merdae</i> (119)	<input type="checkbox"/> <i>Bacteroides ovatus</i> (21)
<input type="checkbox"/> <i>Bacteroides ovatus</i> (90)	<input type="checkbox"/> <i>Bacteroides caccae</i> (15)
<input type="checkbox"/> <i>Ruminococcus bromii</i> (73)	<input type="checkbox"/> <i>Bacteroides thetaiotaomicron</i> (13)
<input type="checkbox"/> <i>Bacteroides xylanisolvens</i> (52)	<input type="checkbox"/> <i>Parabacteroides distasonis</i> (13)
Robust microbiota: 1322 genes with known functions associated	Non-robust microbiota: 134 genes with known functions associated
Most represented functions (number of genes):	Most represented functions (number of genes):
<input type="checkbox"/> Conserved domain protein (9)	<input type="checkbox"/> ABC transporter ATP-binding protein (2)
<input type="checkbox"/> Peptidyl-prolyl cis-trans isomerase (8)	<input type="checkbox"/> Beta-lactamase (2)
<input type="checkbox"/> TonB-dependent receptor plug domain protein (8)	<input type="checkbox"/> Kinase PfkB family (2)
<input type="checkbox"/> Two component, sigma54 regulator, Fis family (8)	<input type="checkbox"/> L-aspartate oxidase (2)
<input type="checkbox"/> ABC transporter ATP-binding protein (7)	<input type="checkbox"/> Oligopeptide transporter OPT family (2)
<input type="checkbox"/> Glycoside hydrolase family 43 (7)	<input type="checkbox"/> Protein GrpE (2)
<input type="checkbox"/> Transcriptional regulator AraC family (7)	<input type="checkbox"/> Sodium/alanine symporter (2)
<input type="checkbox"/> Transposase (7)	
<input type="checkbox"/> Tyrosine type site-specific recombinase (7)	
<input type="checkbox"/> ABC-2 type transporter (6)	

Table S3. Distinctive microbial metabolic pathways expressed in individuals showing a robust and non-robust microbiota (see **Figure 2**).

Statistically significant ($p < 0.05$) microbial metabolic pathways expressed in individuals showing a robust and non-robust microbiota	
250 significant gene families associated with specific microbial species	
Robust microbiota: 164 metabolic pathways	Non-robust microbiota: 86 metabolic pathways
Most abundant species (number of pathways):	Most abundant species (number of genes):
<input type="checkbox"/> <i>Bacteroides vulgatus</i> (51) <input type="checkbox"/> <i>Bacteroides vulgatus</i> CAG 6 (39) <input type="checkbox"/> <i>Bacteroides uniformis</i> CAG 3 (34) <input type="checkbox"/> <i>Bacteroides uniformis</i> (30) <input type="checkbox"/> <i>Flavonifractor plautii</i> (2) <input type="checkbox"/> <i>Prevotella copri</i> (2)	<input type="checkbox"/> <i>Bacteroides caccae</i> (36) <input type="checkbox"/> <i>Gemmiger formicilis</i> (15) <input type="checkbox"/> <i>Bacteroides vulgatus</i> CAG 6 (8) <input type="checkbox"/> <i>Parabacteroides distasonis</i> (6) <input type="checkbox"/> <i>Bacteroides thetaiotaomicron</i> (5) <input type="checkbox"/> <i>Bacteroides ovatus</i> (4) <input type="checkbox"/> <i>Bacteroides uniformis</i> (3) <input type="checkbox"/> <i>Bacteroides vulgatus</i> (2) <input type="checkbox"/> <i>Blautia obeum</i> (2) <input type="checkbox"/> <i>Blautia wexlerae</i> (2)
Most represented pathways (number of pathways):	Most represented pathways (number of pathways):
<input type="checkbox"/> Glycolysis IV (6) <input type="checkbox"/> Adenosine ribonucleotides de novo biosynthesis (5) <input type="checkbox"/> Calvin-Benson-Bassham cycle (5) <input type="checkbox"/> Pyruvate fermentation to isobutanol (5) <input type="checkbox"/> 5-aminoimidazole ribonucleotide biosynthesis I (4) <input type="checkbox"/> 5-aminoimidazole ribonucleotide biosynthesis II (4) <input type="checkbox"/> Coenzyme A biosynthesis II (4) <input type="checkbox"/> Folate transformations II (4) <input type="checkbox"/> GDP-mannose biosynthesis (4) <input type="checkbox"/> Glycolysis I (from glucose 6-phosphate) (4)	<input type="checkbox"/> Glycolysis IV (4) <input type="checkbox"/> Guanosine ribonucleotides de novo biosynthesis (4) <input type="checkbox"/> dTDP-L-rhamnose biosynthesis I (3) <input type="checkbox"/> Phosphopantothenate biosynthesis I (3) <input type="checkbox"/> 5-aminoimidazole ribonucleotide biosynthesis II (2) <input type="checkbox"/> Adenine and adenosine salvage III (2) <input type="checkbox"/> Adenosine deoxyribonucleotides de novo biosynthesis II (2) <input type="checkbox"/> Adenosine ribonucleotides de novo biosynthesis (2) <input type="checkbox"/> Coenzyme A biosynthesis II (2) <input type="checkbox"/> Folate transformations II (2)

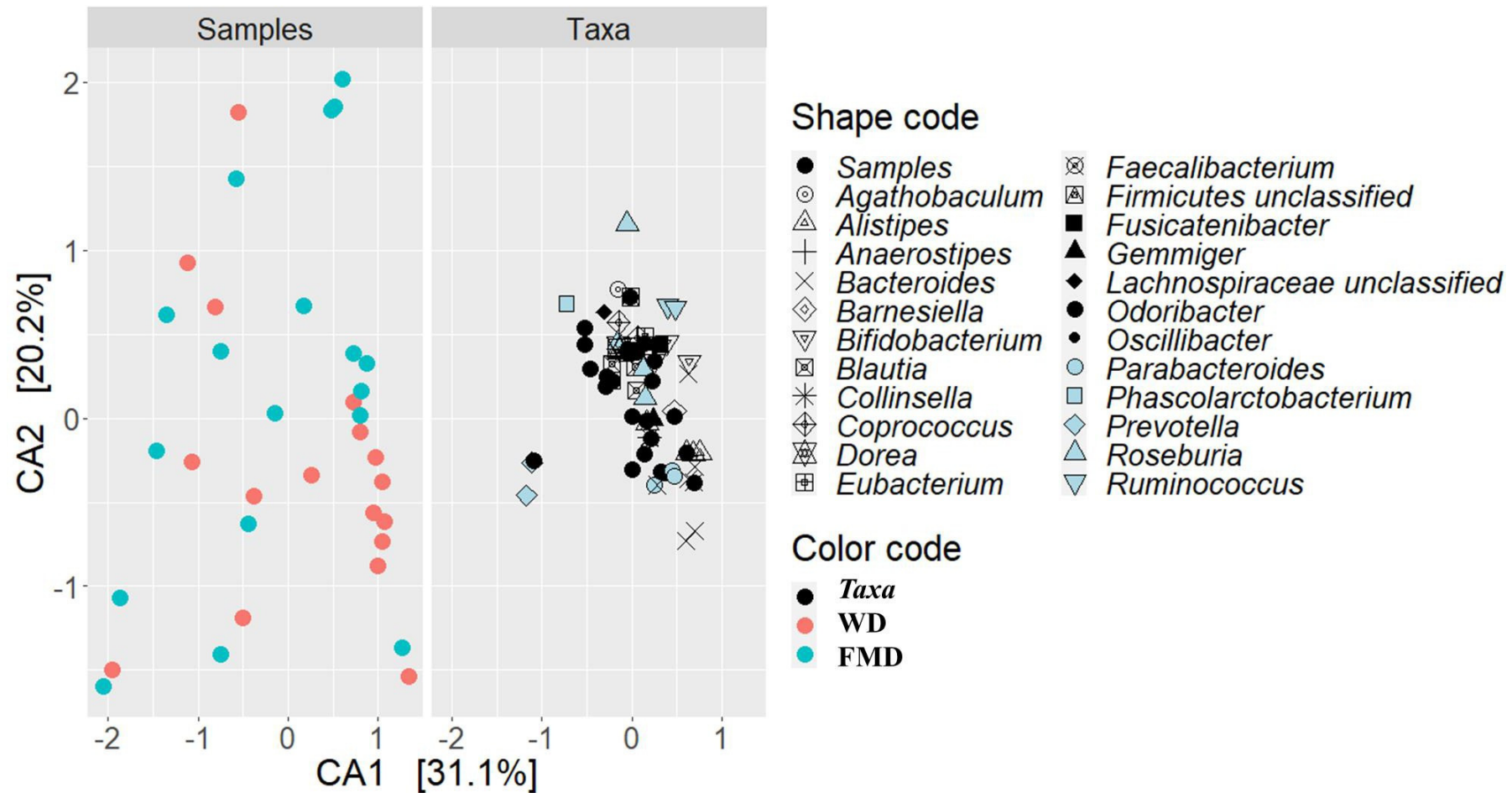


Figure S1. Canonical correspondence analysis (CCA) at genus level of samples obtained after Western-type Diet (WD) or Fiber-enriched Mediterranean-type Diet (FMD) interventions. CA: correspondence analysis. Some samples were grouped similar to principal coordinate analysis (PCoA) (See **Supplementary material Figure S4**). Differences in sample distribution might be due to additional factors other than diet, highlighting the importance of inter-individual variability. The percentage of variance explained by each CA is indicated in the axis.

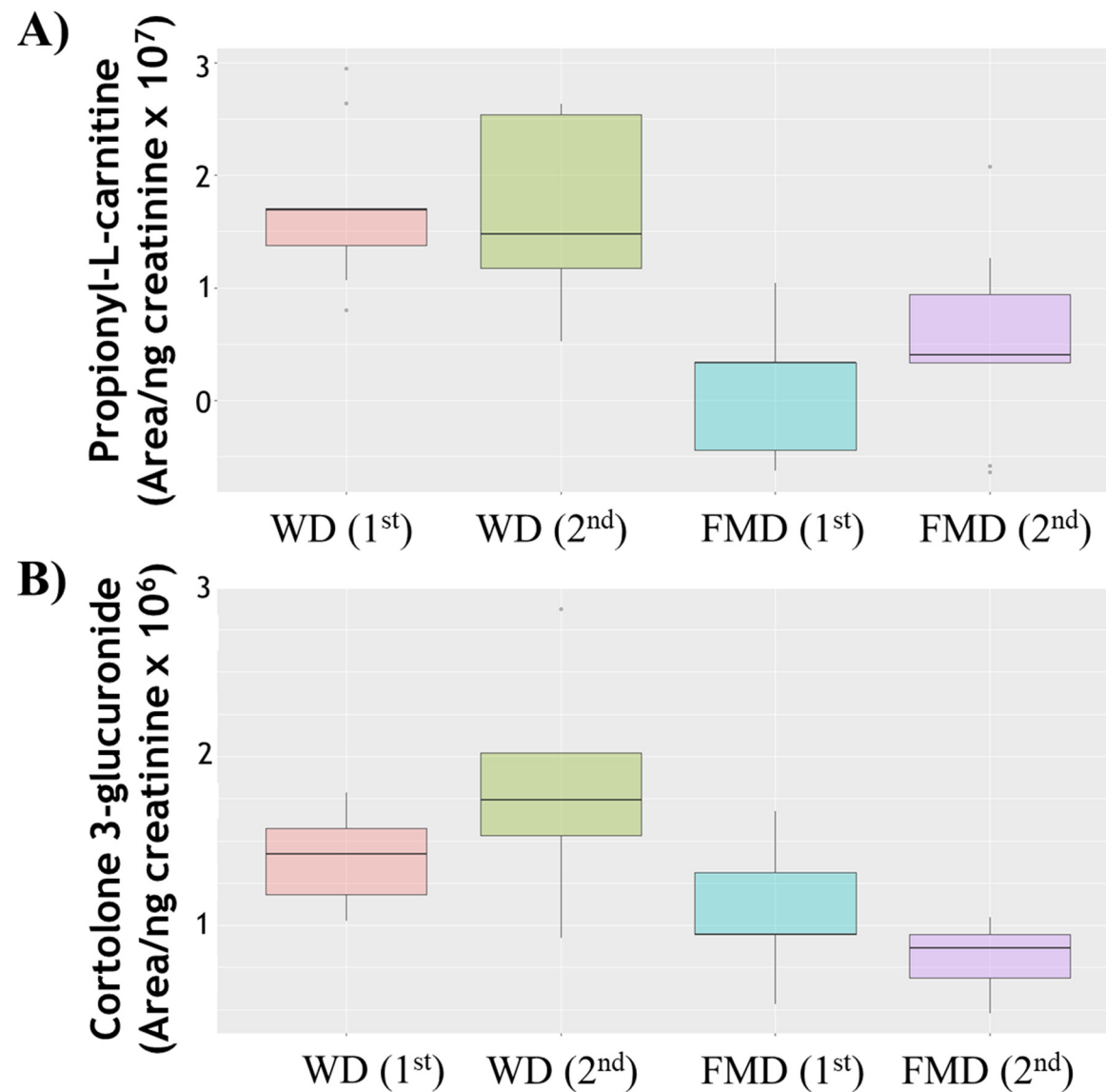


Figure S3. Carry-over effects observed for propionyl-L-carnitine (**A**) and Cortolone 3- glucuronide (**B**) levels in samples obtained after Western-type Diet (**WD**) or Fiber- enriched Mediterranean-type Diet (**FMD**) intervention at 1st or 2nd period.

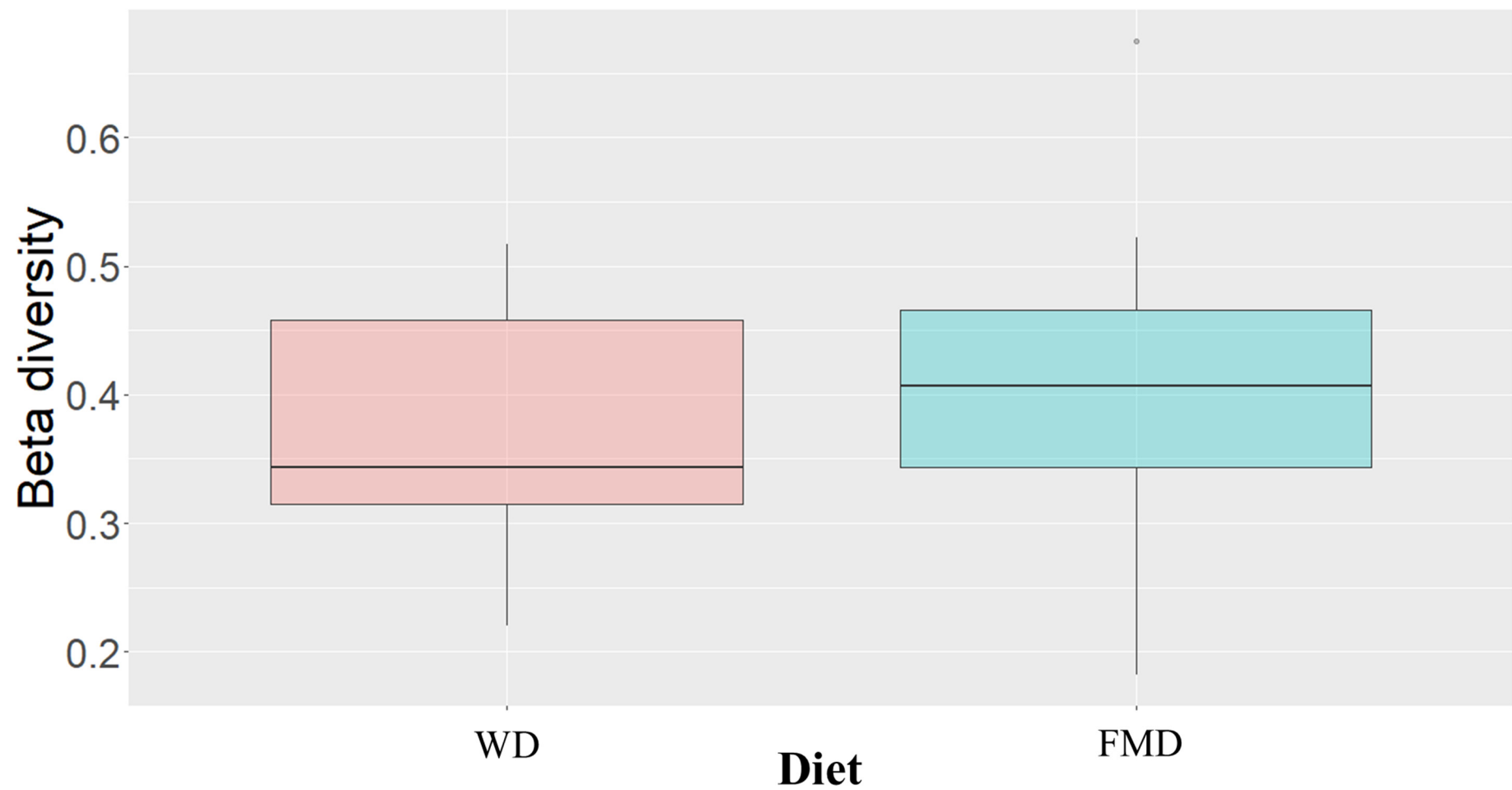


Figure S4. Beta-diversity analysis of metabolic pathways determined in samples obtained after Western-type Diet (**WD**) or Fiber-enriched Mediterranean-type Diet (**FMD**) interventions. The Bray-Curtis method was selected for the calculation. A total of 27 metabolic pathways showed significantly higher expression after FMD intervention.

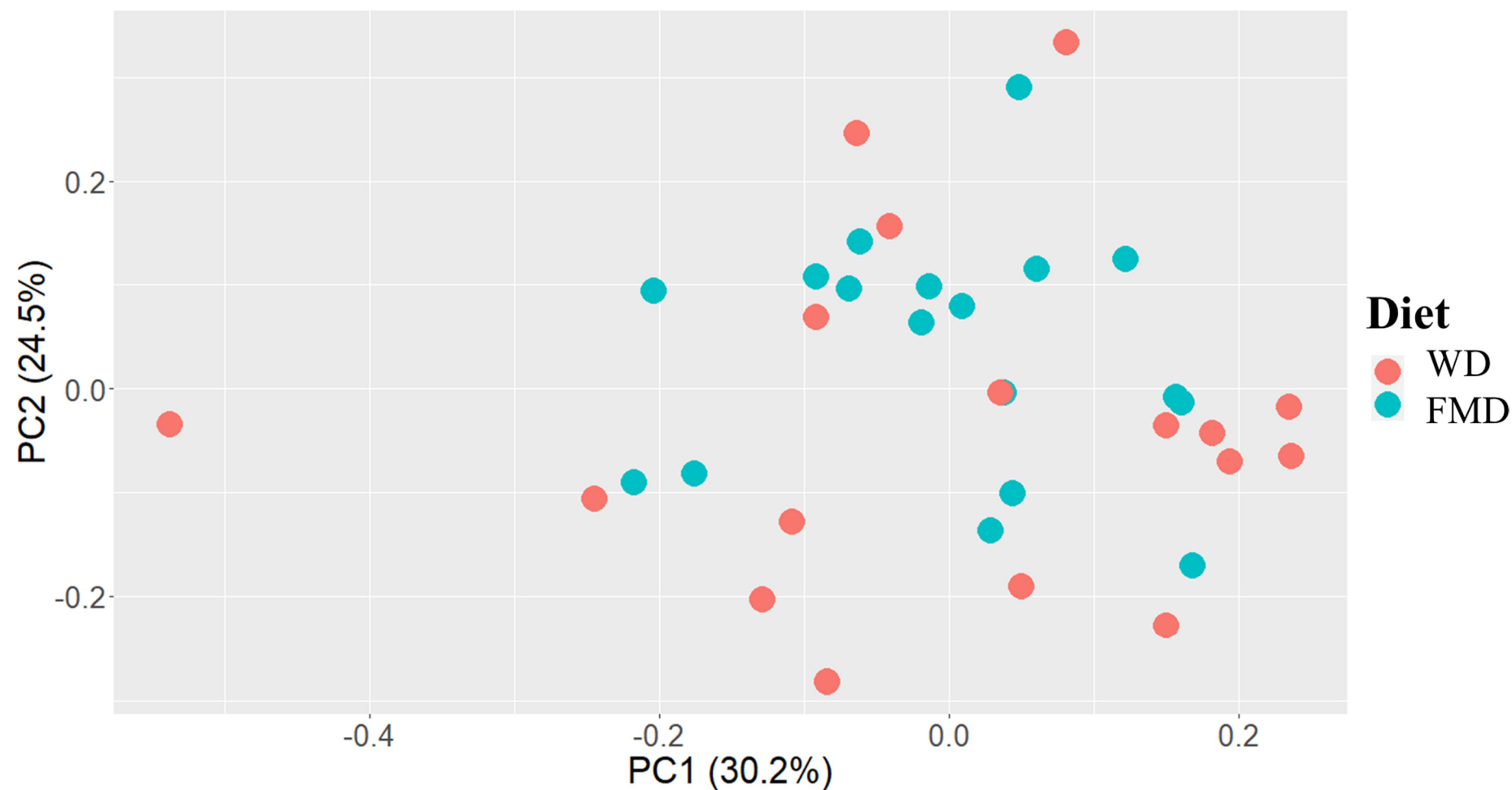


Figure S5. Principal coordinates analysis (PCoA) of taxa present in samples obtained after Western-type Diet (WD) or Fiber-enriched Mediterranean-type Diet (FMD) interventions. No significant differences can be observed in the global taxonomic profiles of participants according to the diet. **PC:** principal coordinate. The percentage of variance explained by each PC is indicated in the axis.

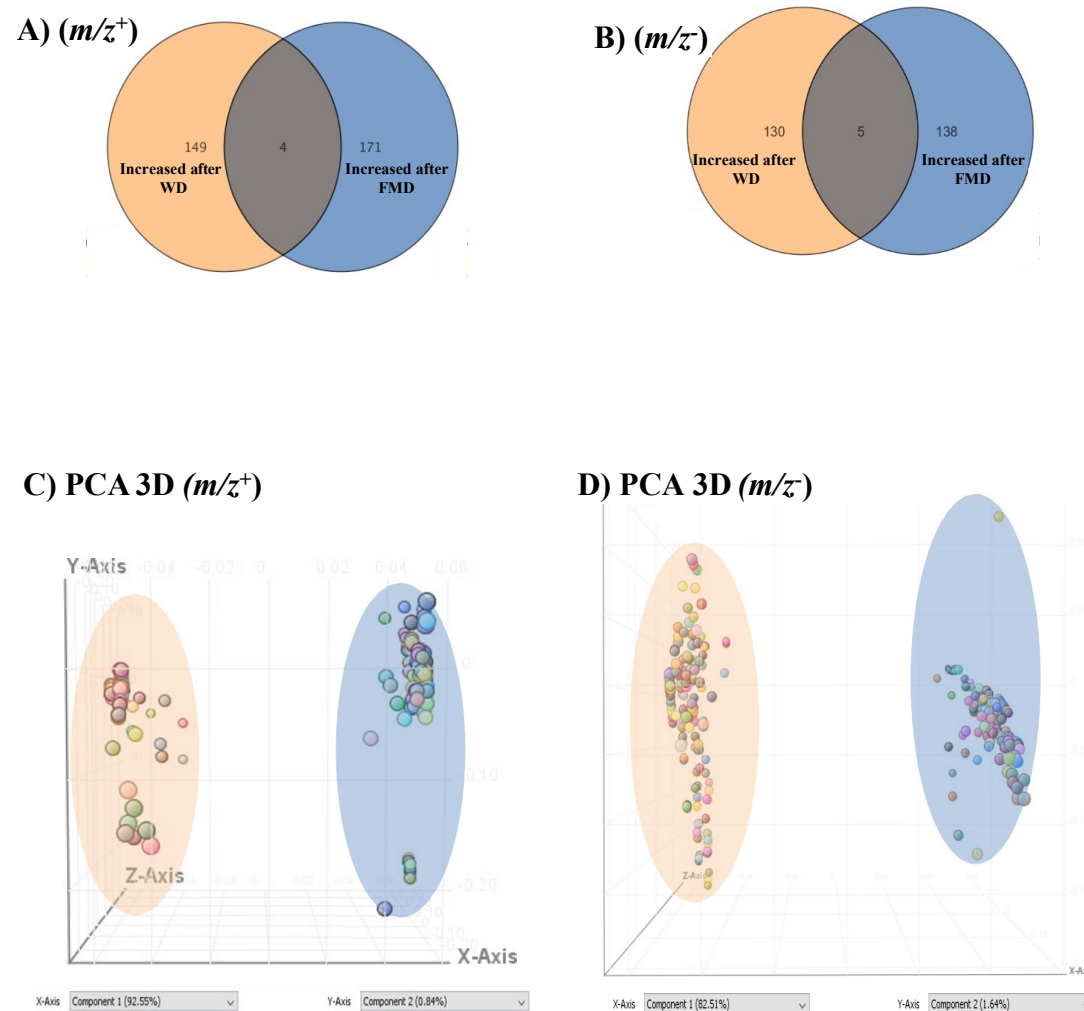


Figure S6. Venn diagrams (**A**, **B**) and three-dimension Principal Component Analyses (PCA) (**C**, **D**) showing those metabolites significantly increased (≥ 2 -fold) after WD (orange colour) and after FMD (blue colour) in UPLC-QTOF-MS positive (**A**, **C**) and negative (**B**, **D**) detection modes.

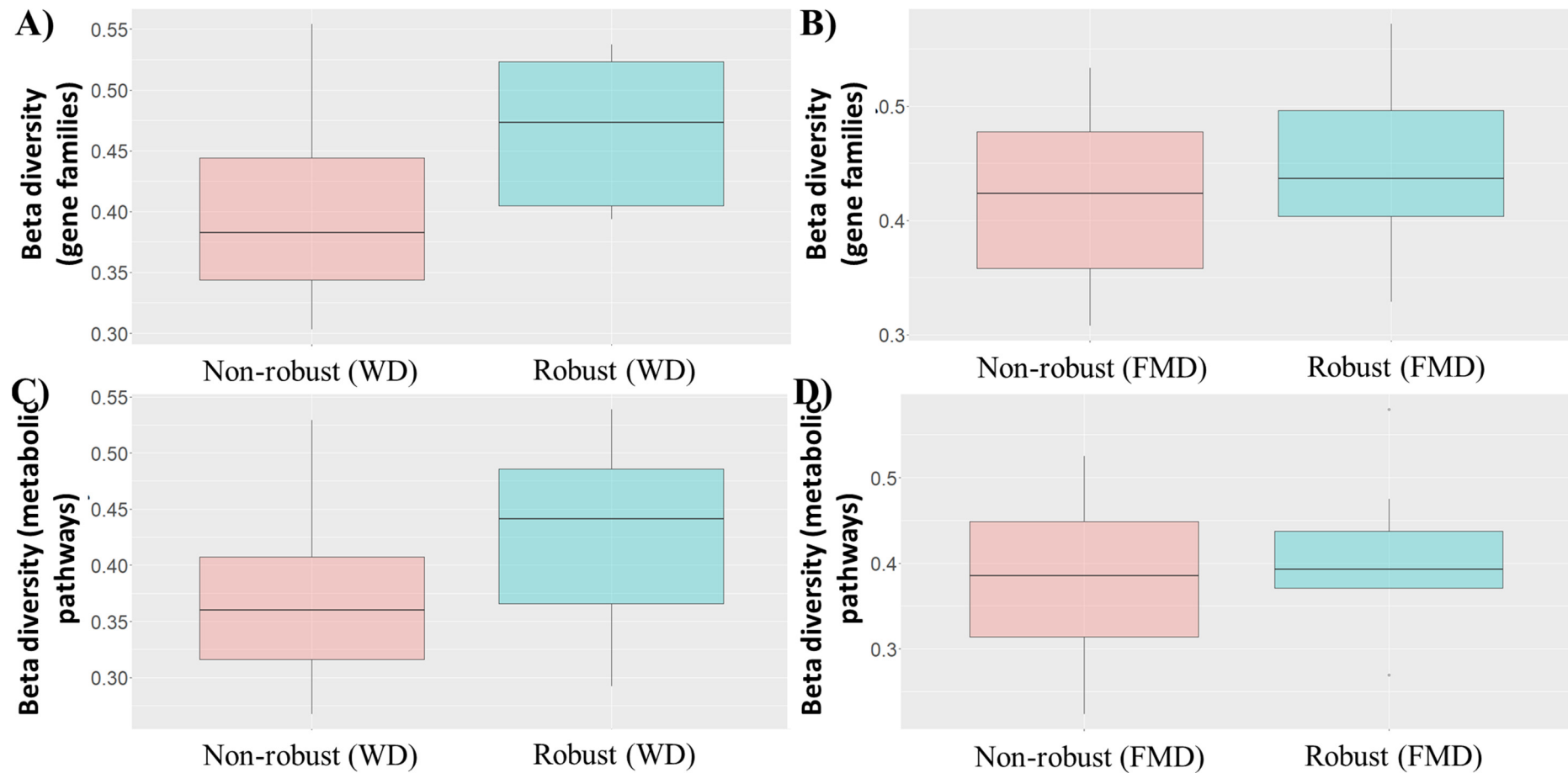


Figure S7. Beta-diversity analysis of gene families (**A, B**) and metabolic pathways (**C, D**) determined in samples from participants showing a robust and non-robust microbiota after Western-type Diet (**WD**) or Fibre-enriched Mediterranean-type Diet (**FMD**) interventions (for further details, see **Figure 2**). The Bray-Curtis method was selected for the calculation. Beta-diversity values were slightly higher in robust microbiotas that did not suffer any relevant change after **WD** (**A, C**).

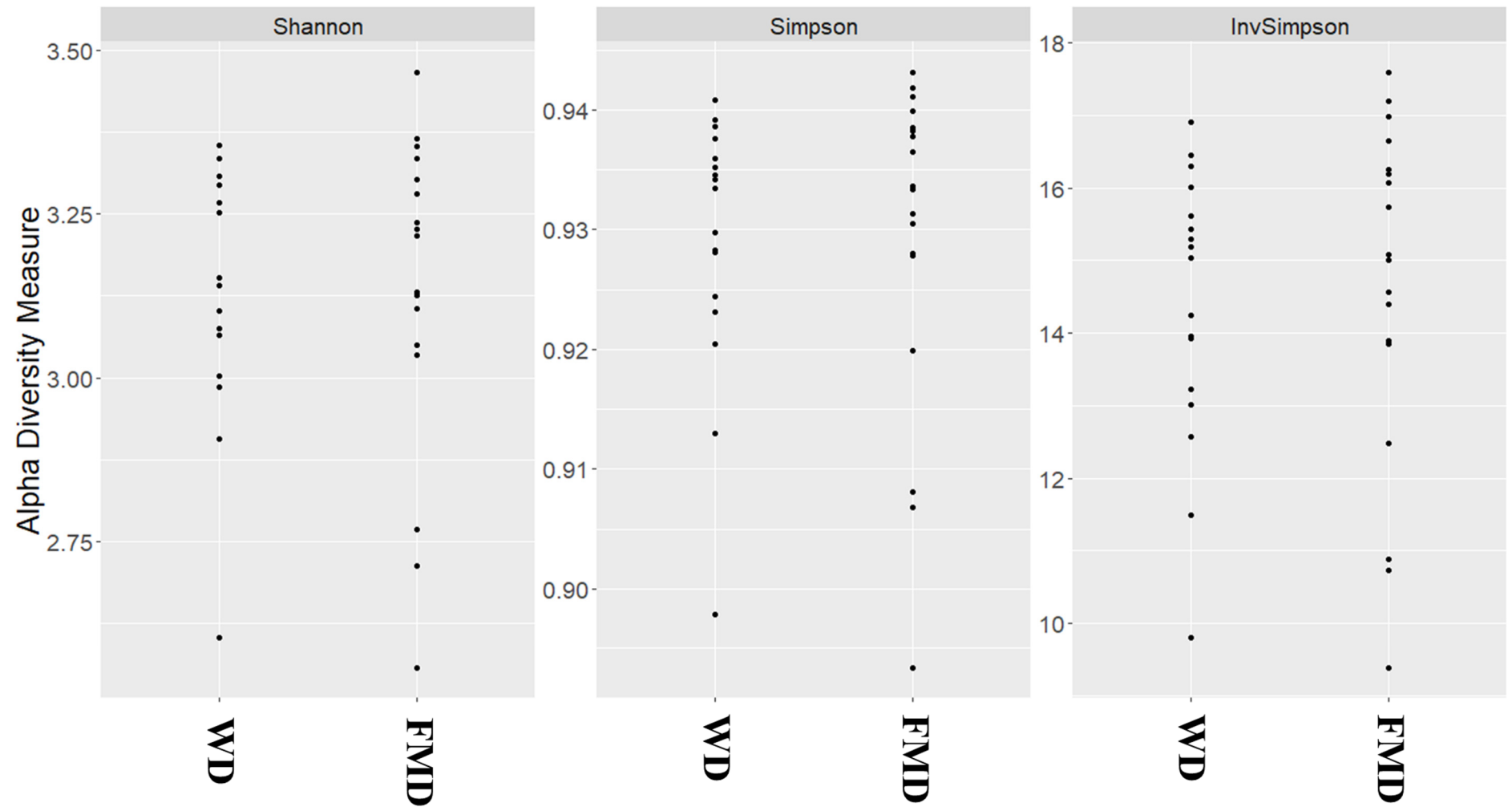


Figure S8. Comparison of different alpha-diversity indicators (Shannon, Simpson and Inverse Simpson) of the relative abundance of taxa determined after Western-type Diet (**WD**) or Fiber-enriched Mediterranean-type Diet (**FMD**) interventions.

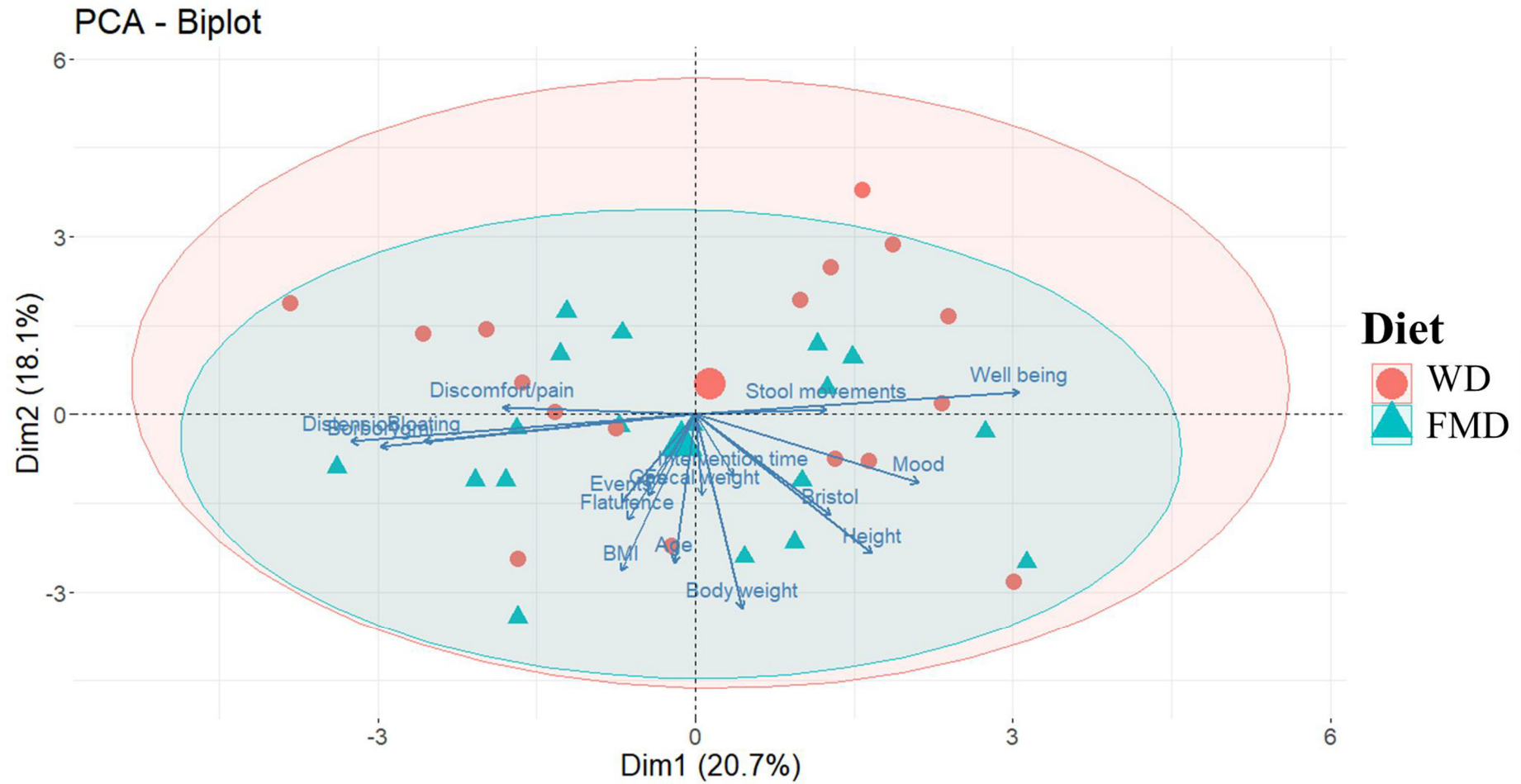


Figure S9. Principal components analysis (PCA) of clinical parameters of participants after Western-type Diet (WD) or Fiber-enriched Mediterranean-type Diet (FMD) interventions. As it can be seen, no relevant differences in clinical symptoms can be observed according to the type of diets administered. **Dim:** dimension (principal component), **BMI:** Body mass index. The percentage of variance explained by each Dim is indicated in the axis.

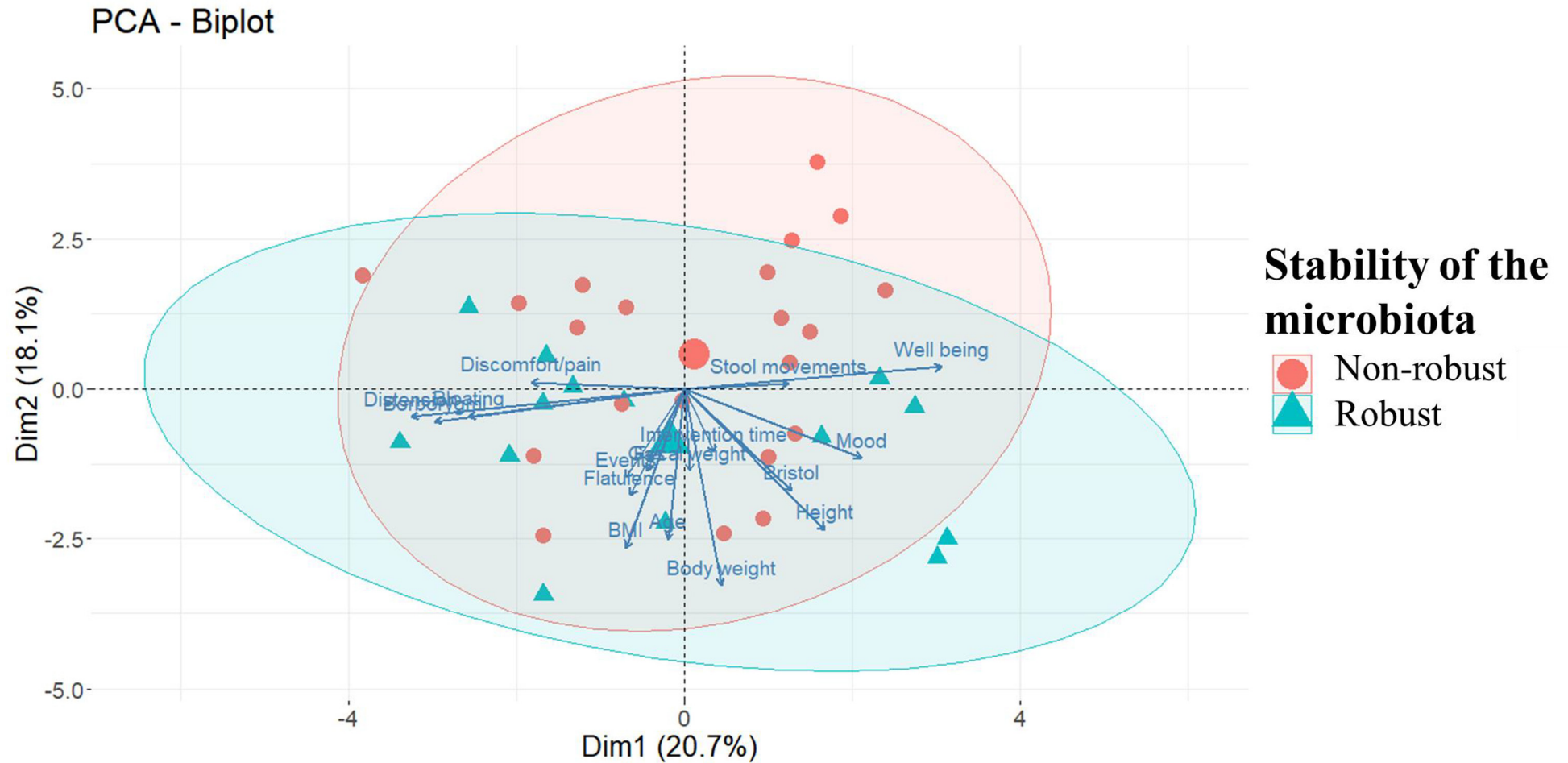


Figure S10. Principal components analysis (PCA) of clinical parameters of participants showing a robust and non-robust microbiota (for further details, see **Figure 2**). No relevant differences in clinical symptoms can be observed according to the stability of the microbiota. **Dim**: dimension (principal component), **BMI**: Body mass index. The percentage of variance explained by each Dim is indicated in the axis.

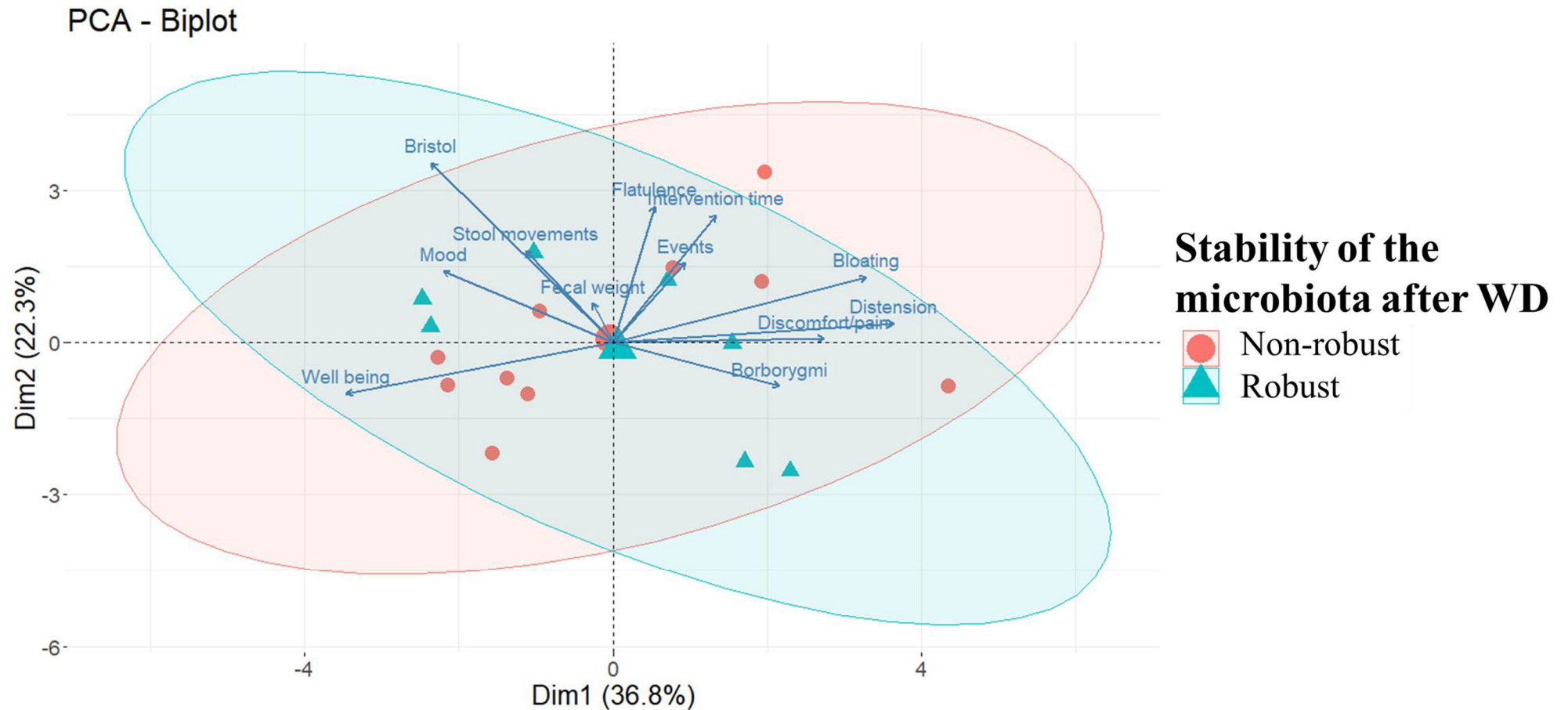


Figure S11. Principal components analysis (PCA) of clinical parameters of participants showing a robust and non-robust microbiota after Western-type Diet (WD) intervention (for further details, see **Figure 2**). No relevant differences in clinical symptoms can be observed according to the stability of the microbiota. **Dim**: dimension (principal component), **BMI**: Body mass index. The percentage of variance explained by each Dim is indicated in the axis.

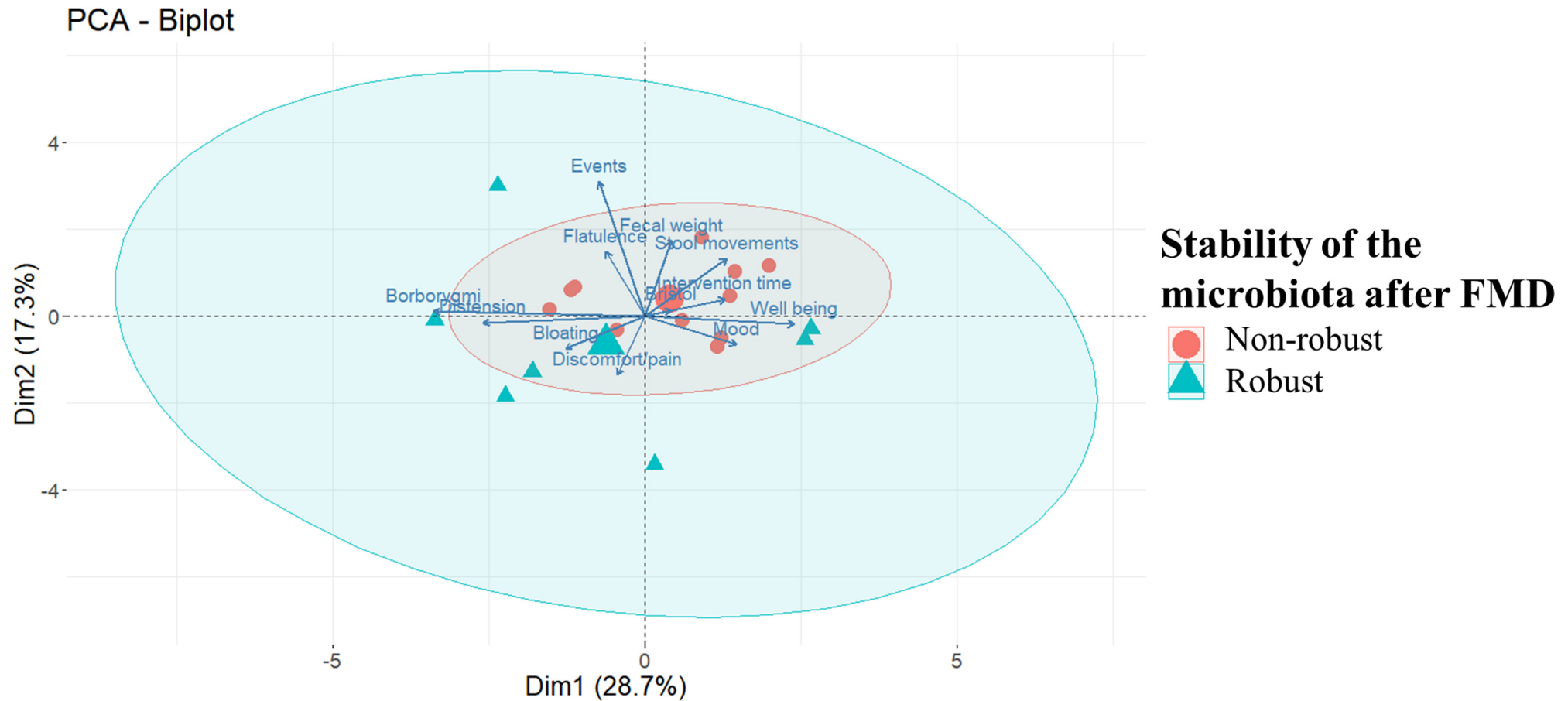


Figure S12. Principal components analysis (PCA) of clinical parameters of participants showing a robust and non-robust microbiota after Mediterranean-type Diet (FMD) intervention (for further details, see **Figure 2**). No relevant differences in clinical symptoms can be observed according to the stability of the microbiota. **Dim**: dimension (principal component), **BMI**: Body mass index. The percentage of variance explained by each Dim is indicated in the axis.

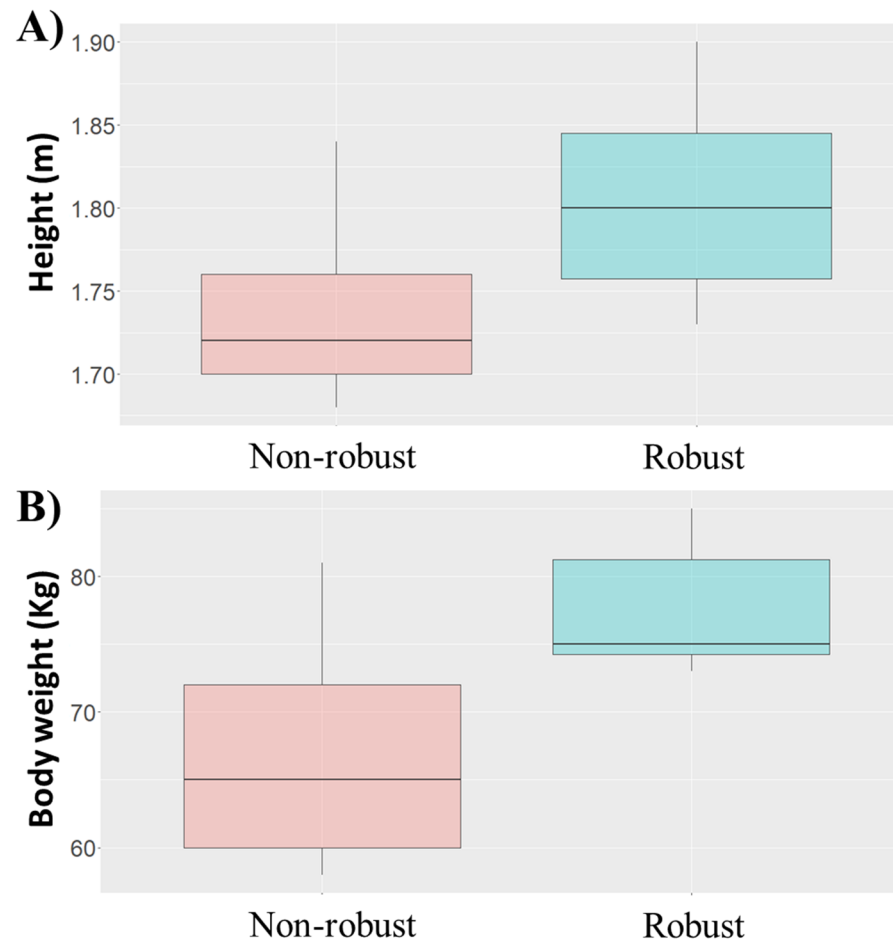


Figure S13. Influence of height and body weight on the stability of the microbiota (for further details, see **Figure 2**). Participants showing higher height and body weight also showed higher microbiota stability after Western-type Diet (**WD**) and Fiber-enriched Mediterranean-type Diet (**FMD**) interventions.

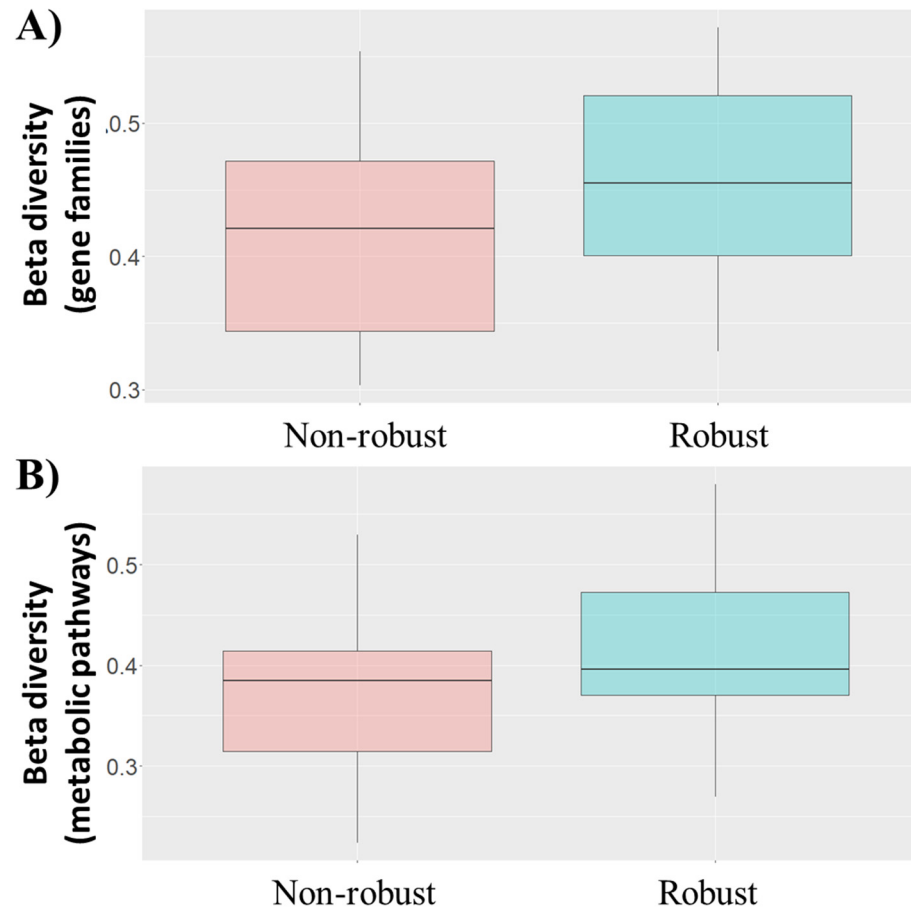


Figure S14. Beta-diversity analysis of gene families (A) metabolic pathways (B) determined in samples from participants showing a robust and non-robust microbiota (for further details, see **Figure 2**). The Bray-Curtis method was selected for the calculation. Beta-diversity values were slightly higher in robust microbiotas that did not suffer any relevant change after Western-type Diet (**WD**) and Fiber-enriched Mediterranean-type Diet (**FMD**) interventions.