

Table S5A. ANCOM analysis of differentially abundant ASVs within segments of treatment and control group.

ASV ID	BLASTn identity	chr	W
Stomach			
ASV-834	Lactococcus taiwanensis strain 0905C15	8.15	435
ASV-654	Clostridium saudeianae strain JCC	7.51	435
ASV-578	Clostridium saudeianae strain JCC	6.51	432
ASV-479	Clostridium saudeianae strain JCC	5.83	427
ASV-756	Clostridium saudeianae strain JCC	5.43	421
ASV-540	Turbidibacter sanguinis strain MCL361	5.37	391
ASV-603	[Clostridium] scindens strain ATCC 35704	5.05	425
ASV-542	[Eubacterium] rectale ATCC 35686	4.94	424
ASV-678	[Clostridium] scindens strain ATCC 35704	4.57	375
ASV-815	[Clostridium] asparagiforme strain N6	4.19	381
ASV-635	Anaerodigium lactifallicum strain G17	3.64	371
ASV-501	[Clostridium] scindens strain ATCC 35704	3.63	381
ASV-654	Kineothrix alysoides strain KNHc209	3.38	380
ASV-862	Acetatifactor muris strain CT-m2	3.45	357
ASV-546	[Clostridium] scindens strain ATCC 35704	3.45	372
ASV-628	Anaerostipes caecae strain L1-62	3.40	366
ASV-791	Neglecta timonensis strain SN17	3.24	368
ASV-651	[Clostridium] scindens strain ATCC 35704	3.01	353
ASV-792	Bacteroides xylophilus strain X5-1	-3.32	353
ASV-895	Eisenbergella tay strain B060562	-3.39	358
ASV-708	Acetatifactor muris strain CT-m2	-3.46	352
ASV-574	Blautia faecicola strain KCMDB1111	-3.75	380
ASV-644	Lachnospirillum pacemense strain Marseille-P3100	-3.92	377
ASV-517	[Clostridium] scindens strain ATCC 35704	-4.38	380
ASV-746	Duncanelia dubosi strain H5	-4.54	397
ASV-733	Kineothrix alysoides strain KNHc209	-4.80	427
ASV-649	[Clostridium] asparagiforme strain N6	-4.95	407
ASV-526	Atlepis onderdonki strain JCM 16771	-5.47	429
Duodenum			
ASV-834	Lactococcus taiwanensis strain 0905C15	7.48	365
ASV-654	Clostridium saudeianae strain JCC	6.58	365
ASV-540	Turbidibacter sanguinis strain MCL361	6.00	349
ASV-733	Kineothrix alysoides strain KNHc209	-4.70	346
ASV-517	[Clostridium] scindens strain ATCC 35704	-4.74	345
ASV-746	Duncanelia dubosi strain H5	-5.48	369
Jejunum			
ASV-834	Lactococcus taiwanensis strain 0905C15	8.84978	328
ASV-654	Clostridium saudeianae strain JCC	6.42407	327
ASV-540	Turbidibacter sanguinis strain MCL361	5.77653	321
ASV-578	Clostridium saudeianae strain JCC	5.19445	327
ASV-479	Clostridium saudeianae strain JCC	3.57336	291
ASV-756	Clostridium saudeianae strain JCC	3.38828	290
ASV-496	Asaccharobacter celatus strain JCM 14811	3.38223	298
ASV-803	[Clostridium] scindens strain ATCC 35704	3.03865	308
ASV-815	[Clostridium] asparagiforme strain N6	2.84024	306
ASV-678	[Clostridium] scindens strain ATCC 35704	2.32251	292
ASV-781	Neglecta timonensis strain SN17	2.01916	280
ASV-651	[Clostridium] scindens strain ATCC 35704	2.01016	271
ASV-554	Blautia faeces strain H05	-2.4873	267
ASV-521	Moryellaformis formicigenus strain L-52	-3.0888	279
ASV-575	Muricoccus intestini strain 2PG-424-CC-1	-3.0857	284
ASV-798	Murimona intestinalis strain SRB-530-5-H	-3.0969	289
ASV-695	Ruminococcus lactus ATCC 29178	-3.2978	288
ASV-588	Paragaeotheria hongkongensis JCM 14552 strain HKU10	-3.5708	301
ASV-733	Kineothrix alysoides strain KNHc209	-3.5758	298
ASV-574	Blautia faecicola strain KCMDB1111	-3.728	301
ASV-877	Murimona intestinalis strain SRB-530-5-H	-3.8224	303
ASV-517	[Clostridium] scindens strain ATCC 35704	-4.9538	317
ASV-746	Duncanelia dubosi strain H5	-5.8099	324
Ileum			
ASV-834	Lactococcus taiwanensis strain 0905C15	8.7069	193
ASV-654	Clostridium saudeianae strain JCC	6.96201	192
ASV-540	Turbidibacter sanguinis strain MCL361	5.81598	189
ASV-526	Clostridium saudeianae strain JCC	4.60098	178
ASV-746	Duncanelia dubosi strain H5	-5.9904	190
Cecum			
ASV-834	Lactococcus taiwanensis strain 0905C15	7.43633	460
ASV-678	[Clostridium] scindens strain ATCC 35704	6.88061	428
ASV-542	[Eubacterium] rectale ATCC 35686	6.38162	440
ASV-815	[Clostridium] asparagiforme strain N6	6.325	418
ASV-603	[Clostridium] rectale ATCC 35704	6.28349	428
ASV-654	Clostridium saudeianae strain JCC	6.12195	436
ASV-564	Kineothrix alysoides strain KNHc209	5.75951	417
ASV-658	[Clostridium] scindens strain ATCC 35704	5.67119	438
ASV-862	Acetatifactor muris strain CT-m2	5.65718	414
ASV-628	Pseudobutyribacterium ruminis strain DSM 9787	5.58964	413
ASV-546	[Clostridium] scindens strain ATCC 35704	5.46603	431
ASV-706	[Clostridium] methylpentosum strain R2	5.35642	416
ASV-653	Faecalimonas unilobata strain EGH7	5.30522	362
ASV-791	Neglecta timonensis strain SN17	5.285	419
ASV-577	[Clostridium] scindens strain ATCC 35704	4.97934	415
ASV-695	[Clostridium] scindens strain ATCC 35704	4.9381	415
ASV-651	[Clostridium] scindens strain ATCC 35704	4.92577	414
ASV-815	[Eubacterium] rectale ATCC 35686	4.89725	415
ASV-540	Turbidibacter sanguinis strain MCL361	4.89784	371
ASV-562	Roseburia intestinalis L1-62	4.88699	367
ASV-518	Procees massiliensis strain Marseille-P2769	4.7916	401
ASV-854	Acetatifactor muris strain CT-m2	4.79106	404
ASV-681	Murimona intestinalis strain SRB-530-5-H	4.78848	411
ASV-526	Clostridium saudeianae strain JCC	4.7888	389
ASV-636	[Clostridium] asparagiforme strain N6	4.72845	391
ASV-774	[Eubacterium] rectale ATCC 35686	4.59478	407
ASV-279	Acetatifactor muris strain CT-m2	4.42648	383
ASV-522	Fusicaeniabacter saccharivorans strain HT03-11	4.36441	370
ASV-612	Fusicaeniabacter saccharivorans strain HT03-11	4.34419	366
ASV-635	Anaerodigium lactifallicum strain G17	4.30498	377
ASV-560	Eubacterium muris strain 420c-B-504-A95	4.28862	368
ASV-841	Anaerotruncus ruberiferus strain MT5	4.23883	403
ASV-722	Procees massiliensis strain Marseille-P2769	4.14799	375
ASV-345	[Clostridium] scindens strain ATCC 35704	4.1288	353
ASV-822	[Clostridium] amygdalium strain BR-10	3.92265	356
ASV-628	Anaerostipes caecae strain L1-62	3.75191	379
ASV-623	[Clostridium] algalivoryticum strain SPL73	3.45523	377
ASV-642	[Clostridium] leptum strain DSM 753	3.33543	364
ASV-654	Anaerotruncus coliformis strain VIAL 14555	2.94023	347
ASV-578	Harellitella acetospora strain V02-281a	2.79771	347
ASV-798	Murimona intestinalis strain SRB-530-5-H	-3.8339	358
ASV-691	Intestinibacter massiliensis strain Marseille-P3216	-3.8547	366
ASV-753	Roseburia hominis A2-183	-3.9795	370
ASV-731	[Clostridium] scindens strain ATCC 35704	-4.0234	361
ASV-344	Anaerodentia torii strain FH02	-4.1257	364
ASV-834	Murimona intestinalis strain 2PG-424-CC-1	-4.2146	391
ASV-792	Bacteroides xylophilus strain X5-1	-4.237	385
ASV-877	Murimona intestinalis strain SRB-530-5-H	-4.2427	387
ASV-809	Anaeroplasmia lactocollum strain JR	-4.253	395
ASV-574	Blautia faecicola strain KCMDB1111	-4.4011	388
ASV-539	[Clostridium] adenense strain RMA 9741	-4.4189	392
ASV-874	Roseburia intestinalis L1-62	-4.4420	397
ASV-895	Eisenbergella tay strain B060562	-5.0762	407
ASV-644	Lachnospirillum pacemense strain Marseille-P3100	-5.2816	434
ASV-575	Atlepis onderdonki strain JCM 16771	-5.8671	455
ASV-733	Kineothrix alysoides strain KNHc209	-6.6002	462
ASV-649	[Clostridium] asparagiforme strain N6	-7.0004	462
Colon			
ASV-834	Lactococcus taiwanensis strain 0905C15	7.8446	463
ASV-678	[Clostridium] scindens strain ATCC 35704	6.71899	448
ASV-654	Clostridium saudeianae strain JCC	6.1597	456
ASV-603	[Clostridium] scindens strain ATCC 35704	6.18609	452
ASV-542	[Eubacterium] rectale ATCC 35686	6.05788	452
ASV-815	[Clostridium] asparagiforme strain N6	6.04324	430
ASV-578	Clostridium saudeianae strain JCC	5.63171	443
ASV-694	Kineothrix alysoides strain KNHc209	5.18454	410
ASV-546	[Clostridium] scindens strain ATCC 35704	4.95055	436
ASV-540	Turbidibacter sanguinis strain MCL361	4.86008	383
ASV-862	Acetatifactor muris strain CT-m2	4.88418	399
ASV-501	[Clostridium] scindens strain ATCC 35704	4.8869	422
ASV-635	Anaerodigium lactifallicum strain G17	4.79195	404
ASV-653	Faecalimonas unilobata strain EGH7	4.73388	362
ASV-626	Pseudobutyribacterium ruminis strain DSM 9787	4.7066	398
ASV-682	Roseburia intestinalis L1-62	4.57395	374
ASV-791	Neglecta timonensis strain SN17	4.4431	407
ASV-706	[Clostridium] methylpentosum strain R2	4.37904	403
ASV-636	[Clostridium] asparagiforme strain N6	4.37358	390
ASV-651	[Clostridium] scindens strain ATCC 35704	4.36887	412
ASV-756	Clostridium saudeianae strain JCC	4.33975	381
ASV-515	[Eubacterium] rectale ATCC 35686	4.32743	407
ASV-479	[Clostridium] scindens strain ATCC 35704	4.28865	408
ASV-595	[Clostridium] scindens strain ATCC 35704	4.17662	369
ASV-518	Procees massiliensis strain Marseille-P2769	4.15084	393
ASV-518	Procees massiliensis strain Marseille-P2769	4.05091	381
ASV-279	Acetatifactor muris strain CT-m2	4.07757	391
ASV-522	Fusicaeniabacter saccharivorans strain HT03-11	4.02569	390
ASV-612	Fusicaeniabacter saccharivorans strain HT03-11	3.91294	386
ASV-681	Murimona intestinalis strain SRB-530-5-H	3.85038	398
ASV-628	Anaerostipes caecae strain L1-62	3.768	381
ASV-654	Acetatifactor muris strain CT-m2	3.65927	371
ASV-722	Procees massiliensis strain Marseille-P2769	3.5043	366
ASV-822	[Clostridium] amygdalium strain BR-10	3.43326	353
ASV-599	Oscillibacter ruminalium GH1	3.06444	358
ASV-830	Faecalimonas unilobata strain EGH7	3.02322	352
ASV-691	Intestinibacter massiliensis strain Marseille-P3216	-3.2442	399
ASV-575	Murimona intestinalis strain 2PG-424-CC-1	-3.6988	371
ASV-539	[Clostridium] adenense strain RMA 9741	-3.7447	369
ASV-798	Murimona intestinalis strain SRB-530-5-H	-3.6241	378
ASV-809	Anaeroplasmia lactocollum strain JR	-3.6345	378
ASV-746	Duncanelia dubosi strain H5	-3.6567	364
ASV-568	Anaerodentia torii strain FH02	-4.1670	401
ASV-895	Eisenbergella tay strain B060562	-4.2435	396
ASV-877	Murimona intestinalis strain SRB-530-5-H	-4.3222	394
ASV-574	Blautia faecicola strain KCMDB1111	-4.604	427
ASV-644	Lachnospirillum pacemense strain Marseille-P3100	-4.9302	431
ASV-733	Kineothrix alysoides strain KNHc209	-6.2221	462
ASV-649	[Clostridium] asparagiforme strain N6	-6.2273	459
ASV-526	Atlepis onderdonki strain JCM 16771	-6.4319	462

*negative CLR indicates differential abundance for control group.

Table S5B. ANCOM analysis of differentially abundant Metacys pathways within segments of treatment and control group.

Metacys ID	Metacys pathway	chr	W
Stomach			
PWY-6876	isopropanol biosynthesis	7.82	285
PWY-4984	urea cycle	7.33	285
PWY-7377	cob(ly)limate a,c-diamide biosynthesis I (early cobalt insertion)	6.95	285
P441-PWY	superpathway of N-acetylneuraminate degradation	-4.40	275
PWY-7371	1,4-dihydroxy-6-naphthoate biosynthesis II	-5.40	284
PWY-6263	superpathway of menaquinol-8 biosynthesis II	-5.90	285
Duodenum			
PWY-4984	urea cycle	6.35	292
PWY-6876	isopropanol biosynthesis	6.82	292
PWY-7377	cob(ly)limate a,c-diamide biosynthesis I (early cobalt insertion)	6.89	292
PWY-6876	isopropanol biosynthesis	6.89	287
PWY-4984	urea cycle	5.81	286
PWY-7377	cob(ly)limate a,c-diamide biosynthesis I (early cobalt insertion)	6.42	286
PWY-6263	superpathway of menaquinol-8 biosynthesis II	-3.07	273
Ileum			
PWY-6478	GDP-D-glycero- α ,D-manno-heptose biosynthesis	4.05	249
PWY-4353	purine nucleotides degradation II (aerobic)	4.45	232
SLA-VQSDHY	adenosine nucleotides degradation I	4.83	252
PWY-6588	pyruvate fermentation to acetone	5.01	251
PWY-4984	urea cycle	5.74	251
PWY-7377	cob(ly)limate a,c-diamide biosynthesis I (early cobalt insertion)	7.14	256
PWY-6876	isopropanol biosynthesis	7.57	256
Cecum			
PWY-5677	succinate fermentation to butyrate	5.09	257
PWY-5022	4-aminobutanoate degradation V	4.85	257
PWY-6363	superpathway of menaquinol-8 biosynthesis II	4.78	249
PWY-7371	1,4-dihydroxy-6-naphthoate biosynthesis II	4.65	249
P441-PWY	superpathway of menaquinol-8 biosynthesis II	4.63	257
PWY-7237	myc, chro- and scillo-inositol degradation	2.42	245
PWY-7377	cob(ly)limate a,c-diamide biosynthesis I (early cobalt insertion)	-4.48	237
PWY-6470	peptidoglycan biosynthesis V (libero-lactam resistance)	3.26	237
PWY-5265	peptidoglycan biosynthesis II (staphylococci)	2.99	236
PWY-6877	myc, chro- and scillo-inositol degradation	2.72	242
PWY-7431	aromatic biogenic amine degradation (bacteria)	-3.18	245
P441-PWY	L-glutamate degradation V (via hydroxylglutamate)	-3.21	242
PWY-6877	succinate fermentation to butyrate	4.54	255
PWY-7371	1,4-dihydroxy-6-naphthoate biosynthesis II	-5.15	253
PWY-6263	superpathway of menaquinol-8 biosynthesis II	-5.39	252

*negative CLR indicates differential abundance for control group.