

**Table S1:** Analyses of Composition of Microbiome (ANCOM) between the four strains of mice i.e. CD1, C57Bl6/J, FVB, NIH-Swiss on normal chow (NC) diet. All the Exact Sequence Variants (ESVs) were identified after applying Benjamini-Hochberg (BH) False Discovery Rate (FDR) correction to P-values (< 0.05).

ESVs	C57BL/6_NC MRF (%)	CD-1_NC MRF (%)	FVB_NC MRF (%)	NIH_NC MRF (%)	p-values (corrected)	Effect size
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__[Odoribacteraceae] ]_g__Odoribacter_s__	0	0.009649078	9.054081445	2.339399793	1.64E-05	0.871099173
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__[Paraprevotellaceae] e]_g__[Prevotella]_s__	0	0	0.995719462	0.002257744	1.32E-05	0.600330676
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__g__s__	0	0.052816007	5.193274372	2.606381017	1.45E-05	0.835264733
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Bacteroidaceae_g__ Bacteroides_s__	2.775805537	11.79927773	2.875019	3.294205303	0.006858033	0.570091943
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Porphyromonadaceae_g__ Parabacteroides_s__distasonis	0.001270245	0	0.005347755	0.045795823	0.001353562	0.618464901
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Rikenellaceae_g__ AF12_s__	0	0.003047077	0.71224852	0.47852924	2.12E-05	0.809342255
p__Firmicutes_c__Bacilli_o__Turicibacterales_f__Turicibacteraceae_g__Tu ricibacter_s__	3.702252816	0.047786737	0.060790304	1.730962078	0.001150899	0.624447502
p__Proteobacteria_c__Betaproteobacteria_o__Burkholderiales_f__Alcaligenaceae_g__ Sutterella_s__	1.224363878	0.07831591	0	0	5.00E-06	0.632381103

\* MRF = mean relative frequency

**Table S2:** Analyses of Composition of Microbiome (ANCOM) between the C57Bl6/J mice on protein deficient (PD) and Normal Chow diet (NC). All the Exact Sequence Variants (ESVs) were identified after applying Benjamini-Hochberg (BH) False Discovery Rate (FDR) correction to P-values (< 0.05).

ESVs	C57BL/6_PD	C57BL/6_NC	p-values	DBM
	MRF (%)	MRF (%)	(corrected)	
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Bacteroidaceae_g__Bacteroides_s__	7.280470717	2.775805537	0.023976024	4.50466518
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__S24-7_g__s__	19.0509963	48.04930871	0.000999001	-28.99831241
p__Deferribacteres_c__Deferribacteres_o__Deferribacterales_f__Deferribacteraceae_g__Mucispirillum_s__schaedleri	1.400407562	0.000648298	0.014985015	1.399759264
p__Firmicutes_c__Bacilli_o__Turicibacterales_f__Turicibacteraceae_g__Turicibacter_s__	1.039937005	3.702252816	0.002997003	-2.66231581
p__Firmicutes_c__Clostridia_o__Clostridiales_f__Lachnospiraceae_g__Coprococcus_s__	1.734292665	0.221109571	0.001998002	1.513183094
p__Firmicutes_c__Clostridia_o__Clostridiales_f__Ruminococcaceae_g__Ruminococcus_s__	0.995763307	2.546279585	0.002997003	-1.550516278
p__Firmicutes_c__Clostridia_o__Clostridiales_NA_NA_NA	1.719289723	0.097669396	0.000999001	1.621620328
p__Firmicutes_c__Erysipelotrichi_o__Erysipelotrichales_f__Erysipelotrichaceae_g__Allobaculum_s__	15.126812	0.103338028	0.002997003	15.02347397
p__Tenericutes_c__Mollicutes_o__RF39_f__g__s__	1.069026606	2.349452393	0.034965035	-1.280425787
p__Verrucomicrobia_c__Verrucomicrobiae_o__Verrucomicrobiales_f__Verrucomicrobiaceae_g__Akkermansia_s__muciniphila	14.16013135	2.809304671	0.035964036	11.35082668

\* MRF = mean relative frequency

\*DBM = Difference between means

**Table S3:** Analyses of Composition of Microbiome (ANCOM) between the CD1 mice on protein deficient (PD) and Normal Chow diet (NC). All the Exact Sequence Variants (ESVs) were identified after applying Benjamini-Hochberg (BH) False Discovery Rate (FDR) correction to P-values (< 0.05).

ESVs	CD-1_PD	CD-1_NC	p-values	p-values	DBM	95.00%	95.00%
	MRF (%)	MRF (%)	(corrected)			lower CI	upper CI
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Bacteroidaceae_g__Bacteroides_s__	5.961170847	11.79927773	0.033966034	0.033966034	-5.838106885	-10.58238902	-1.296465696
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Porphyromonadaceae_g__Parabacteroides_s__	5.218757926	0.680956006	0.000999001	0.000999001	4.537801919	2.395915767	7.03275376
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Rikenellaceae_g__s__	8.609144104	24.77429482	0.000999001	0.000999001	-16.16515072	-21.79474372	-9.936120245
p__Firmicutes_c__Erysipelotrichi_o__Erysipelotrichales_f__Erysipelotrichaceae_g__Allobaculum_s__	12.04060811	0.270857565	0.011988012	0.011988012	11.76975055	3.76720245	20.77508601
p__Tenericutes_c__Mollicutes_o__RF39_f__g__s__	0.550671174	3.106752661	0.001998002	0.001998002	-2.556081487	-4.079267334	-1.336232394
p__Verrucomicrobia_c__Verrucomicrobiae_o__Verrucomicrobiales_f__Verrucomicrobiaceae_g__Akkermansia_s__muciniphila	15.30805802	0.142234966	0.015984016	0.015984016	15.16582305	4.320051176	26.37619697

\* MRF = mean relative frequency

\*DBM = differences between means

**Table S4:** Analyses of Composition of Microbiome (ANCOM) between the FVB mice on protein deficient (PD) and Normal Chow diet (NC). All the Exact Sequence Variants (ESVs) were identified after applying Benjamini-Hochberg (BH) False Discovery Rate (FDR) correction to P-values (< 0.05).

ESVs	FVB_PD	FVB_NC	p-values	DBM	95.00%	95.00%
	MRF (%)	MRF (%)	(corrected)		lower CI	upper CI
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__[Odoribacteraceae]_g__Odoribacter_s__	2.179803547	9.054081445	0.000999001	-6.874277898	-8.829845371	-4.732851243
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__[Paraprevotellaceae]_g__[Prevotella]_s__	3.97616263	0.995719462	0.01998002	2.980443168	1.044897522	4.989784766
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Bacteroidaceae_g__Bacteroides_s__	12.97563937	2.875019	0.003996004	10.10062037	4.935434595	14.98570121
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Porphyromonadaceae_g__Parabacteroides_s__	4.195427289	0.055279888	0.000999001	4.140147401	1.683107711	6.650745806
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Prevotellaceae_g__Prevotella_s__	0.052157205	1.271045616	0.008991009	-1.218888411	-1.826469309	-0.533451963
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Rikenellaceae_g__s__	6.675540043	20.99452387	0.000999001	-14.31898383	-17.51306516	-11.08097071
p__Firmicutes_c__Bacilli_o__Lactobacillales_f__Lactobacillaceae_g__Lactobacillus_s__	0.562483008	7.138844722	0.000999001	-6.576361714	-11.29919933	-2.896728606
p__Firmicutes_c__Bacilli_o__Turicibacterales_f__Turicibacteraceae_g__Turicibacter_s__	2.938128919	0.060790304	0.005994006	2.877338616	0.60765151	5.906260189
p__Firmicutes_c__Clostridia_o__Clostridiales_NA_NA_NA	1.310231443	0.005337011	0.007992008	1.304894432	0.024675569	3.483989987
p__Firmicutes_c__Erysipelotrichi_o__Erysipelotrichales_f__Erysipelotrichaceae_g__Allobaculum_s__	2.628916111	0.012711797	0.036963037	2.616204315	0.042832248	6.370409709

\* MRF = mean relative frequency

\*DBM = differences between means

**Table S5:** Analyses of Composition of Microbiome (ANCOM) between the NIH-Swiss mice on protein deficient (PD) and Normal Chow diet (NC). All the Exact Sequence Variants (ESVs) were identified after applying Benjamini-Hochberg (BH) False Discovery Rate (FDR) correction to P-values (< 0.05).

ESVs	NIH_PD MRF (%)	NIH_NC MRF (%)	p-values (corrected)	DBM	95.00% lower CI	95.00% upper CI
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__g__s__	4.596435755	2.606381017	0.003996004	1.990054738	0.775749617	3.350282479
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Bacteroidaceae_g__Bacteroides_s__	7.870870359	3.294205303	0.006993007	4.576665056	1.831352104	7.339615824
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Porphyromonadaceae_g__Parabacteroides_s__	2.593676576	0.270767954	0.000999001	2.322908622	1.216451802	3.677221329
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Prevotellaceae_g__Prevotella_s__	0.195519067	2.005115036	0.000999001	-1.809595969	-2.591999716	-1.052870551
p__Deferribacteres_c__Deferribacteres_o__Deferribacterales_f__Deferribacteraceae_g__Mucispirillum_s__schaedleri	4.882375652	0.363490914	0.00999001	4.518884738	0.963211265	9.082347456
p__Firmicutes_c__Bacilli_o__Lactobacillales_f__Lactobacillaceae_g__Lactobacillus_s__	4.115939722	9.963881723	0.008991009	-5.847942001	-10.07966238	-1.703718843
p__Firmicutes_c__Bacilli_o__Turicibacterales_f__Turicibacteraceae_g__Turicibacter_s__	0.165375546	1.730962078	0.006993007	-1.565586532	-2.558147174	-0.571966646
p__Firmicutes_c__Erysipelotrichi_o__Erysipelotrichales_f__Erysipelotrichaceae_g__Allobaculum_s__	15.54790187	4.272447977	0.03996004	11.27545389	1.471772376	20.47816567

\* MRF = mean relative frequency

\*DBM = Difference between means

**Table S6:** Analyses of Composition of Microbiome (ANCOM) between the four mice strains i.e. C57Bl6/J, CD1, GVB, NIH-Swiss on protein deficient (PD). All the Exact Sequence Variants (ESVs) were identified after applying Benjamini-Hochberg (BH) False Discovery Rate (FDR) correction to P-values (< 0.05).

ESVs	C57BL/6_PD	CD-1_PD	FVB_PD	NIH_PD	p-values	
	MRF (%)	MRF (%)	MRF (%)	MRF (%)	(corrected)	Effect size
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__[Odoribacteraceae]_g__Butyricimonas_s__	0	0	0	0.598086696	3.94E-05	0.583111289
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__[Paraprevotellaceae]_g__[Prevotella]_s__	0	0.000925412	3.97616263	0	2.79E-05	0.57058755
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Prevotellaceae_g__Prevotella_s__stercorea	0.000993394	0	0.067703184	0	0.000165119	0.4015227
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__VC21_Bac22_g__s__	0	0	0	0.065457026	1.97E-05	0.537290454
p__Cyanobacteria_c__4C0d-2_o__YS2_f__g__s__	0	0	1.204473472	0.008689496	2.06E-05	0.581578549
p__Firmicutes_c__Bacilli_o__Lactobacillales_f__Enterococcaceae_g__Enterococcus_s__	0.000895334	0.032617736	0.624418858	0.172839951	5.52E-05	0.419432724
p__Firmicutes_c__Clostridia_o__Clostridiales_f__Clostridiaceae_g__s__	0.096965297	0.006016408	0.008961138	0.009784228	0.000645956	0.473695009
p__Firmicutes_c__Clostridia_o__Clostridiales_f__Clostridiaceae_g__Clostridium_s__	1.379540459	0	0	0.000822639	2.59E-05	0.495650487
p__Firmicutes_c__Clostridia_o__Clostridiales_f__Lachnospiraceae_g__Coproccoccus_s__	1.734292665	0.147386783	0.583097855	0.611759009	0.001693053	0.49370888
p__Firmicutes_c__Clostridia_o__Clostridiales_f__Peptococcaceae_g__s__	0.011950043	0.007380854	0.117481056	0.053136193	0.000175482	0.510554261
p__Proteobacteria_c__Deltaproteobacteria_o__Desulfovibrionales_f__Desulfovibrionaceae_g__Bilophila_s__	0	0.460395893	0	0	4.67E-05	0.416917741

\* MRF = mean relative frequency

**Table S7:** Analyses of Composition of Microbiome (ANCOM) between the C57Bl6/J and CD1 mice on protein deficient (PD). All the Exact Sequence Variants (ESVs) were identified after applying Benjamini-Hochberg (BH) False Discovery Rate (FDR) correction to P-values (< 0.05).

ESVs	C57BL/6_PD	CD-1_PD	p-values		95.00%	95.00%
	MRF (%)	MRF (%)	(corrected)	DBM	lower CI	upper CI
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Porphyromonadaceae_g__Parabacteroides_s__	0.454178651	5.218757926	0.002997003	-4.764579274	-7.119851549	-2.470188952
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Rikenellaceae_g__s__	5.092540517	8.609144104	0.017982018	-3.516603587	-5.806619098	-0.808456873
p__Firmicutes_c__Clostridia_o__Clostridiales_f__Clostridiaceae_g__Clostridium_s__	1.379540459	0	0.000999001	1.379540459	0.701317811	2.124116226
p__Firmicutes_c__Clostridia_o__Clostridiales_f__Lachnospiraceae_g__Coprococcus_s__	1.734292665	0.147386783	0.000999001	1.586905882	0.960235061	2.273205644
p__Firmicutes_c__Clostridia_o__Clostridiales_f__Ruminococcaceae_g__s__	2.978643617	1.768880004	0.018981019	1.209763613	0.306967833	2.036173214
p__Firmicutes_c__Clostridia_o__Clostridiales_f__Ruminococcaceae_g__Oscillospira_s__	2.103149904	1.006067273	0.002997003	1.097082631	0.496989621	1.710651552

\* MRF = mean relative frequency

\*DBM = Difference between means

**Table S8: Rodent Diet Composition**

	NC	PD
Macronutrients	%	%
Protein	19.1	6.1
Carbohydrate	44.3	75.6
Fiber	4.6	4.6
Fat	5.8	5.5

From Teklad Custom Diet (Envigo):  
Normal Chow (NC): LM-485 (7012)  
Protein deficient diet (PD): TD.90016



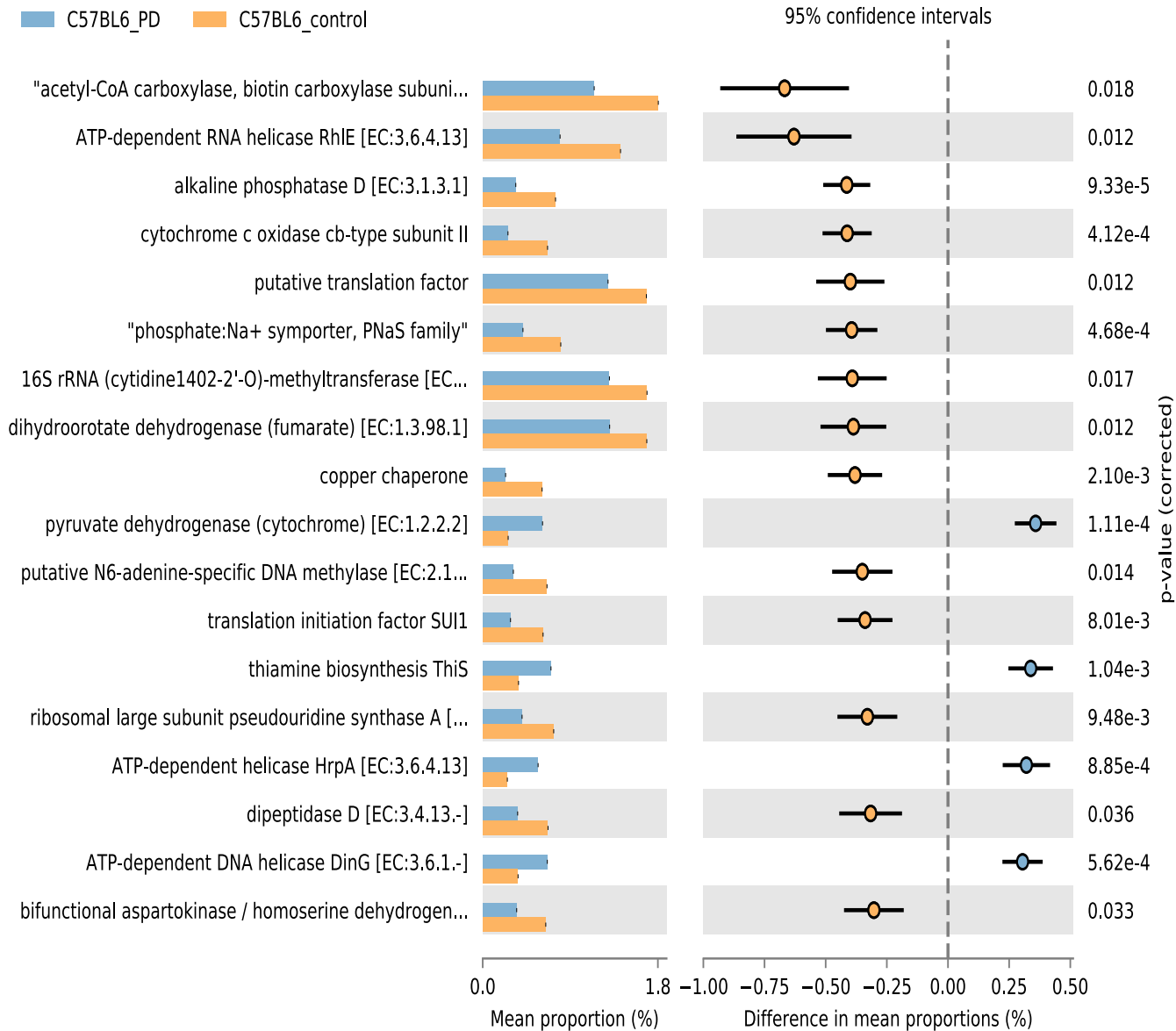
**Table S9:** Overall microbial community profiles in the 4 strain of mice

sOTUs	Mean rel. freq (%)							
	C57BL6PD	C57BL6-NC	CD1-PD	CD1-NC	FVB-PD	FVB-NC	NH-PD	NIH-NC
p_Actinobacteria_c_Actinobacteria_o_Actinomycetales_f_Corynebacteriaceae_g_Corynebacterium_s_	0	0.013777602	0	0.067352988	0.495013613	0.006291682	0.266863701	0.26080287
p_Actinobacteria_c_Actinobacteria_o_Actinomycetales_f_Micrococccaceae_NA_NA	0	0	0.007738032	0.001631348	0	0	0	0
p_Actinobacteria_c_Actinobacteria_o_Bifidobacteriales_f_Bifidobacteriaceae_g_Bifidobacterium_s_pseudolongum	0.921718224	0.505991677	3.367542953	2.081861431	0.042440379	0.030567831	3.272460053	4.396623639
p_Actinobacteria_c_Coriobacteriia_o_Coriobacteriales_f_Coriobacteriaceae_g_s_	0.885752051	0.324172817	0.001028235	0.03866524	0.012243897	0.005966377	0.004153393	0
p_Actinobacteria_c_Coriobacteriia_o_Coriobacteriales_f_Coriobacteriaceae_g_Adlercreutzia_s_	0.027415943	0.045377391	0.165288825	0.124984983	0.06289623	0.03624026	0.051780981	0.066639379
p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_[Odoribacteriaceae]_g_Butyricimonas_s_	0	0	0	0.001251322	0	0	0.614401744	0.053010363
p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_[Odoribacteriaceae]_g_Odoribacter_s_	0.176592919	0	0.001518741	0.010721198	1.567304694	9.187697993	1.671804029	2.369290079
p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_[Paraprevotellaceae]_g_[Prevotella]_s_	0	0	0.001028235	0	3.513471291	1.069619173	0	0.002257744
p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_g_s_	0.826391132	0	1.125643816	0.058684453	3.004722028	5.006375817	4.370949525	2.831867247
p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Bacteroidaceae_g_Bacteroides_s_	6.614145077	2.775805537	6.024272226	11.93812675	14.21901807	2.879747145	7.310922063	3.8541536
p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Bacteroidaceae_g_Bacteroides_s_caccae	0	0	0.306136797	0	0	0	0	0
p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Bacteroidaceae_g_Bacteroides_s_uniformis	0	0	0.472479908	0.273044682	0	0	0.073727503	0
p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Porphyrimonadaceae_g_Parabacteroides_s_	0.504642946	0.000574515	5.278681605	0.667556305	3.380869335	0.060111852	2.777358946	0.087085584
p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Porphyrimonadaceae_g_Parabacteroides_s_distans	0	0.001270245	0	0	0.162631185	0.006016224	0.267023382	0.044475038
p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Prevotellaceae_g_Prevotella_s_	0.008191216	0.320022262	0	0.14607619	0.035627012	1.217967989	0.084091592	2.116542512
p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Prevotellaceae_g_Prevotella_s_stercorea	0.001103771	0	0	0	0.076166082	0.479029917	0	0
p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Rikenellaceae_g_s_	5.418059524	10.21602395	8.682995542	23.78253985	6.86877781	20.45678128	3.771034901	11.58997543
p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Rikenellaceae_g_AF12_s_	0.190156605	0	0	0.003385641	0.450195244	0.716080649	0.489861449	0.502110633
p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_S24-7_g_s_	19.48468664	48.04930871	19.83997043	21.8800574	30.15342456	28.17354865	17.21220596	29.07339548
p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_VC21_Bac22_g_s_	0	0	0	0	0	0	0.063006947	0.023207664
p_Cyanobacteria_c_4C0d-2_o_YS2_f_g_s_	0	0	0	0	1.060972531	0.40959608	0.008689496	0.040046536
p_Cyanobacteria_c_Chloroplast_o_Streptophyta_f_g_s_	0	0	0	0.003568115	0	0.002164127	0	0.002368151
p_Deferribacteres_c_Deferribacteres_o_Deferribacteriales_f_Deferribacteraceae_g_Mucispirillum_s_schaedleri	1.042016887	0.000648298	2.660658547	3.35317471	2.144227305	0.822908683	4.743449026	0.50241754
p_Firmicutes_c_Bacilli_o_Bacillales_f_Staphylococcaceae_g_Jeotgalicoccus_s_	0	0	0	0.003494582	0	0	0.001757901	0.002605015
p_Firmicutes_c_Bacilli_o_Bacillales_f_Staphylococcaceae_g_Staphylococcus_s_	0.00188359	0	0.004207724	0.002574391	0	0.001634094	0.001780444	0
p_Firmicutes_c_Bacilli_o_Bacillales_f_Staphylococcaceae_g_Staphylococcus_s_succinus	0.002918409	0.20887	0.021454738	0.122680582	0.605263907	0.120651376	0.149798758	0.526445946
p_Firmicutes_c_Bacilli_o_Lactobacillales_f_Aerococcaceae_g_Aerococcus_s_	0	0	0.013785498	0.060437359	0.002305989	0.002359381	0.034885619	0.002488813
p_Firmicutes_c_Bacilli_o_Lactobacillales_f_Enterococcaceae_g_Enterococcus_s_	0.000994815	0.000635122	0.036241929	0.001193336	0.610970321	0.07627347	0.175673011	0.045181044
p_Firmicutes_c_Bacilli_o_Lactobacillales_f_Enterococcaceae_g_Vagococcus_s_	0	0	0	0	0.018662108	0	0.00230716	0
p_Firmicutes_c_Bacilli_o_Lactobacillales_f_Lactobacillaceae_g_Lactobacillus_s_	1.32420948	0.739339881	4.162392826	9.309812194	0.486112561	7.823398029	3.466059843	10.6137616
p_Firmicutes_c_Bacilli_o_Lactobacillales_f_Lactobacillaceae_g_Lactobacillus_s_reuteri	0.001638243	0.001391401	0.002110372	0.638675423	0	0.409053955	0	0.472782304
p_Firmicutes_c_Bacilli_o_Lactobacillales_f_Streptococcaceae_g_Lactococcus_s_	0.226716616	0	0.364510489	0.010721198	0.36280839	0.004608012	0.123829436	0.001354646
p_Firmicutes_c_Bacilli_o_Lactobacillales_f_Streptococcaceae_g_Streptococcus_s_	0	0	0.014008422	0.003262696	0.015575843	0	0.001290739	0
p_Firmicutes_c_Bacilli_o_Turicibacteriales_f_Turicibacteraceae_g_Turicibacter_s_	1.150354199	3.702252816	0.66579066	0.053096374	3.2152911	0.068389092	0.134845295	1.761492328
p_Firmicutes_c_Clostridia_o_Clostridiales_f_[Mogibacteriaceae]_g_s_	0.002984446	0.023314102	0.030998266	0.059045969	0.042549026	0.023324496	0.039787298	0.060217639
p_Firmicutes_c_Clostridia_o_Clostridiales_f_g_s_	9.565945255	11.56573548	9.247297507	11.46458303	9.361441787	9.55347265	8.137150681	11.97177046
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Christensenellaceae_g_s_	0.036733726	0.026140508	0.037924475	0.040180377	0.034639709	0.014245897	0.029998001	0.028572587
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Christensenellaceae_g_Christensenella_s_	0	0	0	0	0	0	0	0.010424532
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Clostridiaceae_g_s_	0.100897401	0.038669335	0.006684897	0.024776663	0.01008128	0.010597556	0.007946668	0.014262986
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Clostridiaceae_g_Candidatus_Arthromitus_s_	0	0.016696814	0.013242413	0.879737049	0	0.121021463	0.002258286	0.044908766
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Clostridiaceae_g_Clostridium_s_	1.501179327	0.899128453	0	0.034455739	0	0.005240973	0.000822639	0.416378054
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Dehalobacteriaceae_g_Dehalobacterium_s_	0.063468619	0.103376291	0.105035468	0.08658945	0.094589111	0.053614575	0.089966755	0.101351687
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Eubacteriaceae_g_Anaerofustis_s_	0	0.001270245	0	0.016385788	0	0	0	0.002914968

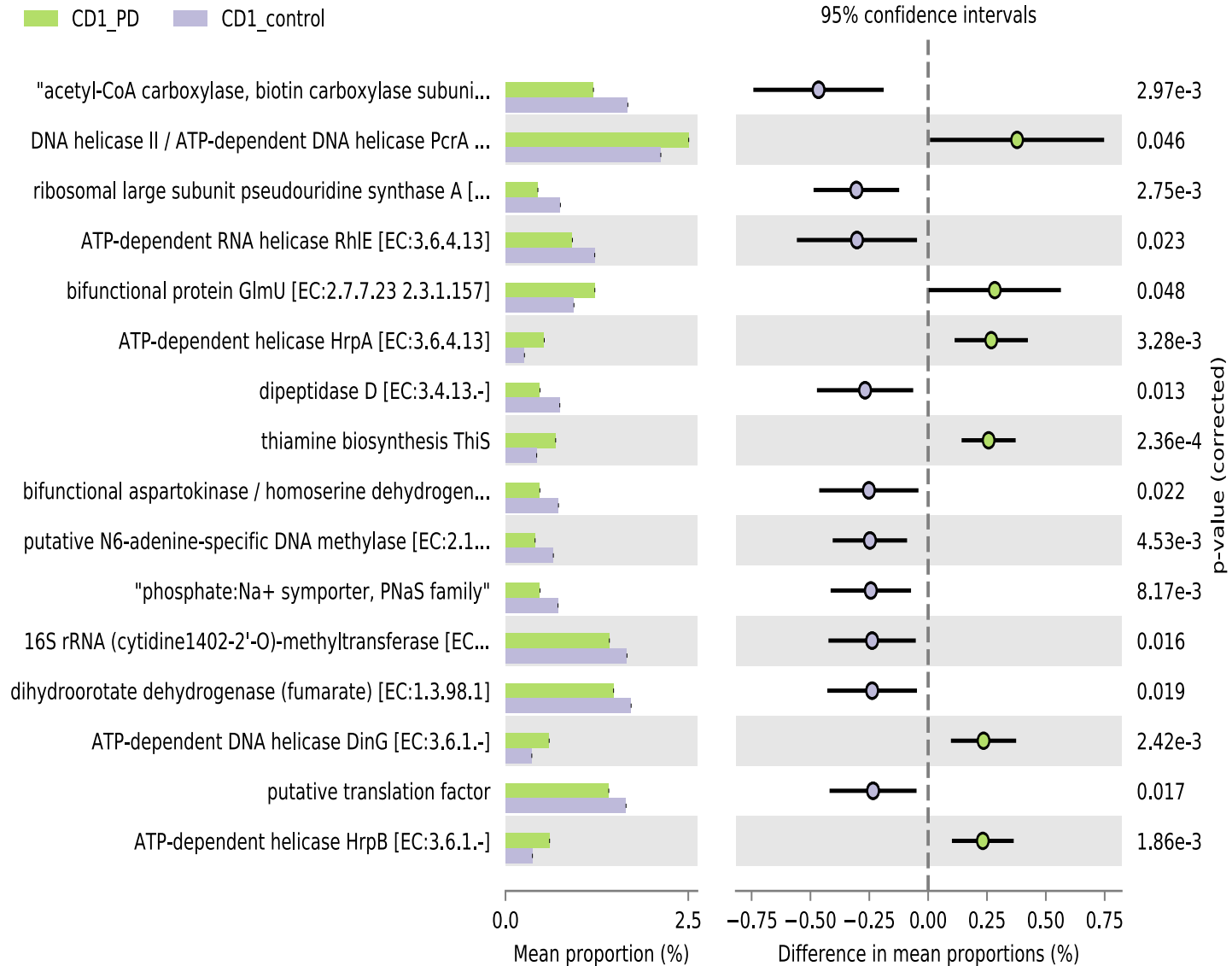
**Table S9 cont**

p_Firmicutes_c_Clostridia_o_Clostridiales_f_Lachnospiraceae_g_[Ruminococcus]_s_gnavus	0.904295862	0.42517821	0.28840447	0.133493162	0.626105427	0.14979878	0.269752834	0.371009317
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Lachnospiraceae_g_s	4.931873455	4.041115447	3.587641521	3.267343769	4.024744667	3.144055626	2.263688731	5.526069613
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Lachnospiraceae_g_Anaerostipes_s	0.028020551	0.489065717	0.003822637	0.034886074	0	0.003358486	0	0.066417607
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Lachnospiraceae_g_Blautia_s	0	0.001574431	0.004657244	0.002447022	0.002620619	0	0	0.001302507
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Lachnospiraceae_g_Coprococcus_s	1.504509639	0.221109571	0.116763018	0.141546679	0.542831309	0.11134934	0.609736508	0.178986905
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Lachnospiraceae_g_Dorea_s	0.009625746	0.017852561	0.04680431	0.025747165	0.059170693	0.015107709	0.007770178	0.019360479
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Lachnospiraceae_g_Epulopiscium_s	0	0	0	0	0.072111135	0.000723045	0.017915463	0
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Lachnospiraceae_g_Roseburia_NA	0	0	0	0	0	0	0.010183299	0
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Lachnospiraceae_g_Roseburia_s	0.001655657	0.024769768	0	0.026735988	0.010832119	0.014342561	0.019966401	0.004481308
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Lachnospiraceae_g_Roseburia_s	0.016325825	0.000618353	0.119256211	0.03850978	0.348080859	0.045232802	0.170454848	0.067241231
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Peptococcaceae_g_s	0.013277826	0.009134025	0.008200949	0.001128547	0.125181387	0.01838288	0.048848553	0.026152058
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Peptococcaceae_g_rc4-4_s	0	0.001471454	0.044922225	0.407664339	0	0	0.00161773	0.001475361
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcaceae_g_s	2.88626658	3.424827019	1.797984465	1.254882728	1.509459999	1.43822216	1.340124081	1.879461335
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcaceae_g_Anaerotruncus_s	0.004227598	0	0.003598824	0	0.008330805	0	0.005632164	0
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcaceae_g_Oscillospira_s	1.98790055	1.209412187	1.048821167	1.27310723	1.276878414	0.749885773	1.166653057	1.623136213
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcaceae_g_Ruminococcus_NA	0	0	0	0	0.025132856	0.664896275	0	0.045760224
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcaceae_g_Ruminococcus_s	0.96358074	2.546279585	0.77133755	1.1026525	0.742637476	0.785880575	0.450691914	0.985185539
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcaceae_g_Ruminococcus_s_flavofaciens	0.002730405	0	0	0.002821368	0	0	0.445415558	0.184081093
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcaceae_g_NA_NA	0.001453193	0	0	0.001631348	0.008105748	0.061938623	0.004448758	0.094681721
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Veillonellaceae_g_Veillonella_s_dispar	0.001103771	0	0.001406915	0.002861349	0	0	0.002397485	0.000903098
p_Firmicutes_c_Clostridia_o_Clostridiales_NA_NA_NA	1.782037843	0.097669396	0.882028945	0.042193383	1.474010373	0.006004137	0.181399202	0.40611353
p_Firmicutes_c_Erysipelotrichi_o_Erysipelotrichales_f_Erysipelotrichaceae_g_s	0.972083581	0.337280746	0.269794993	0.676093083	0.054721426	0.081591172	0.069297669	0.183250213
p_Firmicutes_c_Erysipelotrichi_o_Erysipelotrichales_f_Erysipelotrichaceae_g_Allobaculum_s	15.23138526	0.103338028	12.75570249	0.30095285	2.954736705	0.014300771	18.62396655	1.196383296
p_Firmicutes_c_Erysipelotrichi_o_Erysipelotrichales_f_Erysipelotrichaceae_g_Coprobacillus_s	0.080710933	0.005764974	0	0.007299653	0.000967193	0	0.002075119	0
p_Firmicutes_c_Erysipelotrichi_o_Erysipelotrichales_f_Erysipelotrichaceae_NA_NA	0	0.003400655	0	0.015406603	0.012189176	0.012287071	0.003394433	0.005640226
p_Proteobacteria_c_Alphaproteobacteria_o_f_g_s	0	0	0	0	0.002636436	0.006683894	0	0
p_Proteobacteria_c_Alphaproteobacteria_o_RF32_f_g_s	0.004606312	0.019053668	0.023831064	0.001128547	0.790445153	0.212088548	0.39291771	0.150834603
p_Proteobacteria_c_Alphaproteobacteria_o_Rickettsiales_f_mitochondria_NA_NA	0	0	0	0.001703026	0	0.008226166	0	0.002075119
p_Proteobacteria_c_Betaproteobacteria_o_Burkholderiales_f_Alcaligenaceae_g_Achromobacter_s	0	0	0	0	0.023504101	0.012221464	0	0
p_Proteobacteria_c_Betaproteobacteria_o_Burkholderiales_f_Alcaligenaceae_g_Sutterella_s	1.362927192	1.224363878	0.085997216	0.085358147	0	0	0	0
p_Proteobacteria_c_Betaproteobacteria_o_Burkholderiales_f_Oxalobacteraceae_NA_NA	0	0	0	0.01010026	0	0	0	0
p_Proteobacteria_c_Betaproteobacteria_o_Methylophilales_f_g_s	0.009509681	0	0	0	0.253265044	0.002728776	1.561159882	0.016925208
p_Proteobacteria_c_Betaproteobacteria_o_Rhodocyclales_f_Rhodocyclaceae_g_Dok59_s	0	0	0	0	0.004306333	0.009913493	0.02312655	0.148144712
p_Proteobacteria_c_Deltaproteobacteria_o_Desulfovibrionales_f_Desulfovibrionaceae_g_s	0.304272869	0.349859818	0.059793543	0	0.524147414	0.043222917	0.451466289	0.058980979
p_Proteobacteria_c_Deltaproteobacteria_o_Desulfovibrionales_f_Desulfovibrionaceae_g_Bilophila_s	0	0	0.457207157	0.00998057	0	0	0	0
p_Proteobacteria_c_Deltaproteobacteria_o_Desulfovibrionales_f_Desulfovibrionaceae_g_Desulfovibrio_s	0.406543763	0.129178377	0.369644723	0.087363994	0.486382304	0.239052354	0.566236605	0.463617886
p_Proteobacteria_c_Gammaproteobacteria_o_Enterobacteriales_f_Enterobacteriaceae_g_s	0.016631617	0.011891327	0.573262662	0.079137925	0.302408635	0.198551721	0.403458476	0.102030129
p_Proteobacteria_c_Gammaproteobacteria_o_Enterobacteriales_f_Enterobacteriaceae_g_Proteus_s	0	0	0.01410098	0.002821368	0	0	0	0
p_Proteobacteria_c_Gammaproteobacteria_o_Pasteurellales_f_Pasteurellaceae_g_Haemophilus_s_painfluenzae	0.001103771	0	0	0.001505979	0.001318218	0	0.002035937	0
p_Proteobacteria_c_Gammaproteobacteria_o_Pseudomonadales_f_Moraxellaceae_g_Acinetobacter_s_venetianus	0.001092162	0	0	0	0.017806771	0.001572921	0.020635691	0
p_Tenericutes_c_Mollicutes_o_Anaeroplasmatales_f_Anaeroplasmataceae_g_Anaeroplasma_s	0.356375303	0.55469394	0.053563503	0.001128547	0.393870619	0.420908684	1.018779174	0.138065335
p_Tenericutes_c_Mollicutes_o_RF39_f_g_s	1.174978932	2.349452393	0.5736693	3.117828556	1.11318831	2.511248003	0.449010281	1.888943964
p_TM7_c_TM7-3_o_CW040_f_F16_g_s	0	0.010083915	0.036751632	0.193940334	0.030101949	0.044441779	0.004813242	0.031578478
p_Verrucomicrobia_c_Verrucomicrobiae_o_Verrucomicrobiales_f_Verrucomicrobiaceae_g_Akkermansia_s_muciniphila	14.95522257	2.809304671	13.31063508	0.15471979	0.011773016	0.01950953	9.889472665	0.188600827
	0.002873761	0.002462448	0.029725635	0.179493529	0.055704906	0.097675215	0.04958886	0.047851909

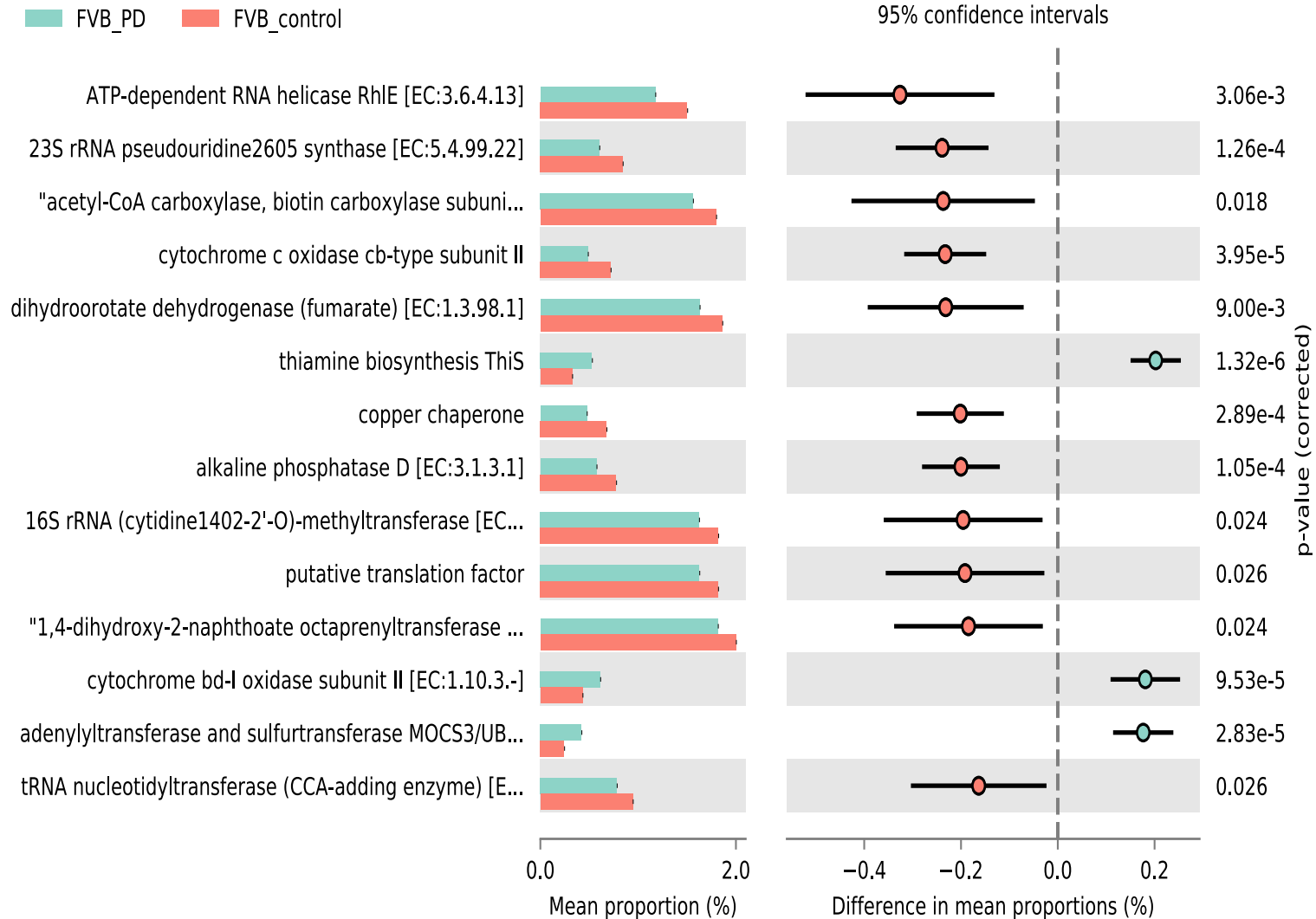
# Fig. S1



# Fig. S2



# Fig. S3



# Fig. S4

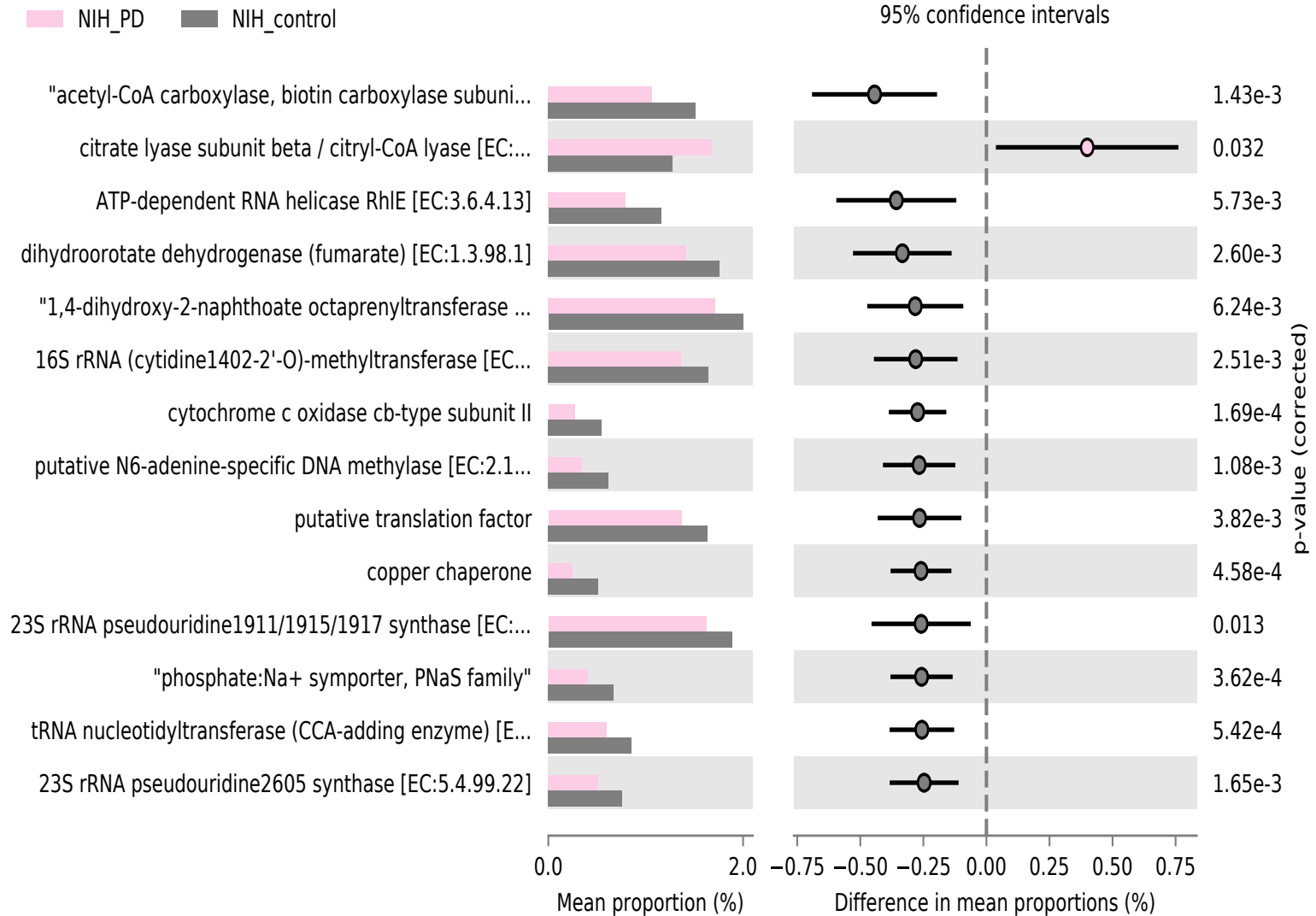


Fig. S5

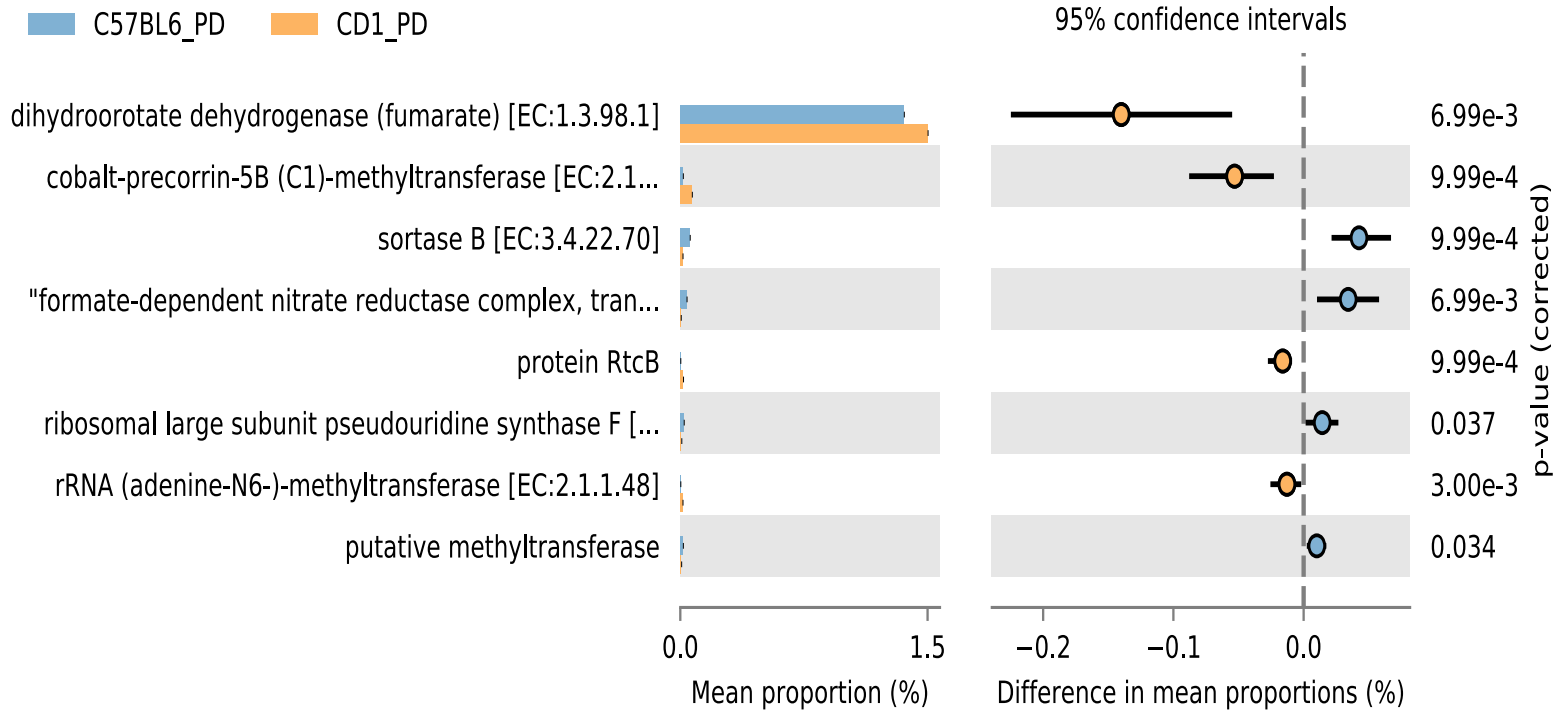


Fig. S6

