Supplementary File 2

Protective Taxa

	MetaCyc pathway types overrepresented by pathways more frequently encoded in the genomes of protective taxa, stratified by outcome?							MetaCyc pathway types overrepresented by pathways less frequently encoded in the genomesof protective taxa, stratified by outcome?					
Outcome	**Pathway Type**	**number of pathways that were significantly MORE prevalent in protective taxa grouped in this MetaCyc Pathway Type / number of pathways that were significantly MORE prevalent in Protective taxa**	**number of pathways that were not differentially prevalent in Protective taxa grouped in this MetaCyc Pathway Type / number of pathways that were not differentially prevalent in Protective taxa**	**Over-representation p-value**	**Adjusted Over-representation p-value**	**Pathways Over-represented within this MetaCyc Pathway Type**	**Protective Taxa Predicted to Carry the Over-represented Pathways**	**number of pathways that were significantly LESS prevalent in protective taxa grouped in this MetaCyc Pathway Type / number of pathways that were significantly LESS prevalent in Protective taxa**	**number of pathways that were not differentially prevalent in Protective taxa grouped in this MetaCyc Pathway Type / number of pathways that were not differentially prevalent in Protective taxa**	**Over-representation p-value**	**Adjusted Over-representation p-value**	**Pathways Over-represented within this MetaCyc Pathway Type**	**Protective Taxa Predicted to Lack the Over-represented Pathways**
Diarrhea	Glycan Pathways	3/11 (27.3%)	7/320 (2.2%)	0.003	0.168	lipid IVA biosynthesis (E. coli) ; Kdo transfer to lipid IVA (four Kdo residues) ; beta-(1,4)-mannan degradation	Bacteroides; Dialister; Veillonella	0/1 (0.0%)	10/330 (3.0%)	1.000	1.000		
Diarrhea	Polymeric Compound Degradation	2/11 (18.2%)	2/320 (0.6%)	0.006	0.169	chondroitin sulfate degradation I (bacterial) ; beta-(1,4)-mannan degradation	Bacteroides	0/1 (0.0%)	4/330 (1.2%)	1.000	1.000		
Serum CFAI IgA V0 to V21	C1 Compound Utilization and Assimilation	0/0 (NaN%)	6/331 (1.8%)	1.000	1.000			1/2 (50.0%)	5/329 (1.5%)	0.036	1.000	Calvin-Benson-Bassham cycle	Akkermansia; Faecalitalea; Merdibacter; Oscillospiraceae_UCG-002
Serum CFAI IgA V0 to V21	Other Biosynthesis	0/0 (NaN%)	6/331 (1.8%)	1.000	1.000			1/2 (50.0%)	5/329 (1.5%)	0.036	1.000	6-hydroxymethyl-dihydropterin diphosphate biosynthesis I	Akkermansia; Faecalitalea; Hungatella; Merdibacter; Oscillospiraceae_UCG-002
Serum CFAI IgA V0 to V31	Amino Acid Biosynthesis;Superpathways	3/4 (75.0%)	13/327 (4.0%)	<0.001	0.021	L-methionine biosynthesis III ; superpathway of L-methionine biosynthesis (by sulfhydrylation) ; superpathway of L-methionine biosynthesis (transsulfuration)	Akkermansia; Catenibacterium; Haemophilus; Hungatella; Lachnospira; Lachnospiraceae__eligens_group	0/2 (0.0%)	16/329 (4.9%)	1.000	1.000		
Serum CFAI IgA V0 to V31	Amino Acid Biosynthesis	3/4 (75.0%)	29/327 (8.9%)	0.003	0.090	L-methionine biosynthesis III ; superpathway of L-methionine biosynthesis (by sulfhydrylation) ; superpathway	Akkermansia; Catenibacterium; Haemophilus; Hungatella; Lachnospira; Lachnospiraceae__eligens_group	0/2 (0.0%)	32/329 (9.7%)	1.000	1.000		

						of L-methionine biosynthesis (transsulfuration)							
Serum CFAI IgA V0 to V31	Carbohydrate Biosynthesis	0/4 (0.0%)	18/327 (5.5%)	1.000	1.000			2/2 (100.0%)	16/329 (4.9%)	0.003	0.162	O-antigen building blocks biosynthesis (E. coli) ; UDP-N-acetyl-D-glucosamine biosynthesis I	Akkermansia; Catenibacterium; Haemophilus; Hungatella; Intestinibacter; Lachnospira; Lachnospiraceae__eligens_group; Prevotella_7; Sellimonas
Serum CFAI IgA V0 to V31	Carbohydrate Biosynthesis;Superpathways	0/4 (0.0%)	5/327 (1.5%)	1.000	1.000			1/2 (50.0%)	4/329 (1.2%)	0.030	0.871	O-antigen building blocks biosynthesis (E. coli)	Akkermansia; Catenibacterium; Haemophilus; Hungatella; Intestinibacter; Lachnospira; Lachnospiraceae__eligens_group; Prevotella_7; Sellimonas

Harmful Taxa

	MetaCyc pathway types overrepresented by pathways more frequently encoded in the genomes of harmful taxa, stratified by outcome?							**MetaCyc pathway types overrepresented by pathways less frequently encoded in the genomesof harmful taxa, stratified by outcome?**					
Outcome	**Pathway Type**	**number of pathways that were significantly MORE prevalent in Harmful taxa grouped in this MetaCyc Pathway Type / number of pathways that were significantly MORE prevalent in Harmful taxa**	**number of pathways that were not differentially prevalent in Harmful taxa grouped in this MetaCyc Pathway Type / number of pathways that were not differentially prevalent in Harmful taxa**	**Over-representation p-value**	**Adjusted Over-representation p-value**	**Pathways Over-represented within this MetaCyc Pathway Type**	**Harmful Taxa Predicted to Carry the Over-represented Pathways**	**number of pathways that were significantly LESS prevalent in Harmful taxa grouped in this MetaCyc Pathway Type / number of pathways that were significantly LESS prevalent in Harmful taxa**	**number of pathways that were not differentially prevalent in Harmful taxa grouped in this MetaCyc Pathway Type / number of pathways that were not differentially prevalent in Harmful taxa**	**Over-representation p-value**	**Adjusted Over-representation p-value**	**Pathways Over-represented within this MetaCyc Pathway Type**	**Harmful Taxa Predicted to Lack the Over-represented Pathways**
ALS LTB IgA V0 to V21	Amino Acid Biosynthesis;Superpathways	1/1 (100.0%)	15/330 (4.5%)	0.048	1.000	superpathway of L-methionine biosynthesis (transsulfuration)	Anaerostipes; Haemophilus; Phascolarctobacterium	0/0 (NaN%)	16/331 (4.8%)	1.000	1.000		
Serum CFAI IgG V0 to V21	Fatty Acid and Lipid Biosynthesis	0/0 (NaN%)	21/331 (6.3%)	1.000	1.000			2/2 (100.0%)	19/329 (5.8%)	0.004	0.223	CDP-diacylglycerol biosynthesis I ; CDP-	Sutterella

												diacylglycerol biosynthesis II	
Serum CFAI IgG V0 to V31	Amino Acid Biosynthesis;Superpathways	1/1 (100.0%)	15/330 (4.5%)	0.048	1.000	superpathway of L-alanine biosynthesis	Raoultibacter; Sutterella	0/2 (0.0%)	16/329 (4.9%)	1.000	1.000		
Serum CFAI IgG V0 to V31	Fatty Acid and Lipid Biosynthesis;Superpathways	0/1 (0.0%)	7/330 (2.1%)	1.000	1.000			1/2 (50.0%)	6/329 (1.8%)	0.042	1.000	superpathway of phospholipid biosynthesis III (E. coli)	Raoultibacter; Sutterella
ALS CFAI IgA V0 to V28	Cell Structure Biosynthesis;Superpathways	1/3 (33.3%)	4/328 (1.2%)	0.045	1.000	peptidoglycan biosynthesis IV (Enterococcus faecium)	Actinomyces; Collinsella; Libanicoccus; Olsenella; Streptococcus	0/0 (NaN%)	5/331 (1.5%)	1.000	1.000		
ALS CFAI IgA V0 to V28	Antibiotic Resistance	1/3 (33.3%)	2/328 (0.6%)	0.027	1.000	peptidoglycan biosynthesis IV (Enterococcus faecium)	Actinomyces; Collinsella; Libanicoccus; Olsenella; Streptococcus	0/0 (NaN%)	3/331 (0.9%)	1.000	1.000		
ALS CFAI IgA V0 to V28	Nucleoside and Nucleotide Biosynthesis	3/8 (37.5%)	27/324 (8.3%)	0.027	1.000	pyrimidine deoxyribonucleotides de novo biosynthesis I ; pyrimidine deoxyribonucleotides de novo biosynthesis II ; superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis (E. coli)	Actinomyces; Anaerovoracaceae__nodatum_group; Bilophila; Lachnospiraceae_ND3007_group; Libanicoccus; Olsenella	0/1 (0.0%)	30/331 (9.1%)	1.000	1.000		
ALS CFAI IgA V0 to V28	Amino Acid Biosynthesis;Superpathways	0/8 (0.0%)	16/324 (4.9%)	1.000	1.000			1/1 (100.0%)	15/331 (4.5%)	0.048	1.000	superpathway of L-aspartate and L-asparagine biosynthesis	Actinomyces; Bilophila; Collinsella; Libanicoccus; Olsenella; Parasutterella; Streptococcus; Sutterella