Table 2, online. Genus-level SS-ANOVA comparisons of control and treatment groups over time

Genus	Interval Start[1]	Interval End[1]	Area[2]	*P* value[3]	Adjusted *P*[4]
Escherichia-Shigella	1	9	-72495.0	<0.0001	<0.0001
Corynebacterium	1	6	1533.9	0.0066	0.0089
Geobacillus	1	9	948.5	<0.0001	<0.0001
Salmonella	1	9	-202.9	<0.0001	<0.0001
Serratia	2	9	-10483.0	<0.0001	<0.0001
Pantoea	2	9	-9964.6	<0.0001	<0.0001
Clostridium	2	9	-3209.4	<0.0001	<0.0001
Tatumella	2	9	-121.6	<0.0001	<0.0001
Streptococcus	3	9	-5586.1	<0.0001	<0.0001
Erwinia	3	7	14.0	0.0435	0.0436
Cedecea	4	9	-100.7	<0.0001	<0.0001
Citrobacter	4	9	-34.2	0.0436	0.0436

Color coding indicates early (green), mid (blue), and late (red) changes.
[1]Start and End indicate the boundaries of the study weeks accounting for differential abundance between groups. Genera are shown with a significant difference between treatment and control groups after Week 0 (following start of treatment) and sustained over at least 4 weeks.
[2]Positive area values indicate the magnitude of greater abundance in Treatment group compared to the Control group. Negative values indicate greater abundance in the Control group compared to the Treatment group.
[3]P values were based on 10,000 scrambled permutations of the groups and SS-ANOVA comparisons to observed data.
[4]P values were adjusted for multiple comparisons using the Benjamini-Hochberg test.

Table 3, online. Imputed KEGG Pathway Abundance Comparisons of Treatment Groups

KEGG2	KEGG3[1]	Interval start[2]	Interval end[2]	Area[3]	*P*	Adjusted *P*[4]
Lipid Metabolism	Fatty acid metabolism	1	6	-20.9	0.0020	0.0053
Metabolism of Terpenoids and Polyketides	Geraniol degradation	1	6	-13.0	0.0031	0.0066
Amino Acid Metabolism	Lysine degradation	1	7	-17.7	0.0004	0.0025
Xenobiotics Biodegradation and Metabolism	Fluorobenzoate degradation	1	8	-4.3	0.0010	0.0040
	Benzoate degradation	1	7	-22.5	<0.0001	<0.0001
	Caprolactam degradation	1	7	-12.0	0.0004	0.0025
Infectious Diseases	Bacterial invasion of epithelial cells	2	9	1.5	<0.0001	<0.0001
	Influenza A	2	7	-0.8	0.0005	0.0029
	Toxoplasmosis	2	7	-0.8	0.0010	0.0040
	Shigellosis	3	9	0.4	<0.0001	<0.0001
Xenobiotics Biodegradation and Metabolism	Metabolism of xenobiotics by cytochrome P450	2	8	-7.3	<0.0001	<0.0001
	Styrene degradation	2	6	-2.5	0.0041	0.0079
	Chlorocyclohexane and chlorobenzene degradation	2	6	-2.4	0.0019	0.0053
	Drug metabolism - cytochrome P450	2	8	-7.7	<0.0001	<0.0001
Lipid Metabolism	Secondary bile acid biosynthesis	2	9	2.2	<0.0001	<0.0001
	Glycerolipid metabolism	3	9	9.2	0.0018	0.0052
Amino Acid Metabolism	Tryptophan metabolism	2	6	-11.8	0.0010	0.0040
	Phenylalanine metabolism	3	7	-7.8	0.0029	0.0065
Metabolism of Other Amino Acids	beta-Alanine metabolism	2	7	-13.2	0.0006	0.0032
Carbohydrate Metabolism	Galactose metabolism	3	9	27.8	<0.0001	<0.0001
Metabolism of Cofactors and Vitamins	Porphyrin and chlorophyll metabolism	3	7	-11.9	0.0023	0.0055
Carbohydrate Metabolism	Amino sugar and nucleotide sugar metabolism	4	9	31.1	0.0026	0.0060
	Fructose and mannose metabolism	4	9	32.5	0.0017	0.0052
Enzyme Families	Cytochrome P450	4	9	-0.04	0.0009	0.0040
Nucleotide Metabolism	Purine metabolism	4	9	37.6	0.0023	0.0055
	Pyrimidine metabolism	5	9	22.0	0.0020	0.0053
Glycan Biosynthesis and Metabolism	Glycosphingolipid biosynthesis - globo series	4	9	2.5	<0.0001	<0.0001
	Glycosphingolipid biosynthesis - ganglio series	5	9	0.7	0.0047	0.0082
	Other glycan degradation	5	9	3.3	0.0001	0.0007
Metabolism of Cofactors and Vitamins	Lipoic acid metabolism	5	9	1.9	0.0046	0.0082

Color coding indicates early (green), mid (blue), and late (red) changes.
[1]KEGG Level 3 categories are shown where the adjusted *P* was ≤0.01 for a time interval of ≥4 weeks duration after initiation of treatment, and the Level 1 category was *Metabolism* or the Level 2 category was *Infectious Diseases*.
[2]Start and End indicate the boundaries of the study weeks with differential abundance between groups.
[3]Positive area values indicate greater abundance in Treatment group compared to the Control group. Negative values indicate greater abundance in the Control group compared to the Treatment group.
[4]*P* values were adjusted for multiple comparisons using the Benjamini-Hochberg test.