



2b. Taxonomic level = Family

Key	
LGG	PLC

	Taxonomy at Baseline (Family level)																LGG	PLC	P				
	Phylum	Class	Order	Family	<i>Bifidobacteriaceae</i>	<i>Coriobacteriaceae</i>	<i>Ruminococcaceae</i>	<i>Veillonellaceae</i>	Undefined Family	<i>Clostridiaceae</i>	undefined	<i>Streptococcaceae</i>	<i>Lactobacillaceae</i>	<i>Bacteroidaceae</i>	<i>Porphyromonadaceae</i>	<i>Prevotallaceae</i>				<i>Enterobacteriaceae</i>			
Taxonomy after 12-months of Treatment	Actinobacteria	Actinobacteria	<i>Bifidobacteriales</i>	<i>Bifidobacteriaceae</i>	S103; S108			S148		S121				S133				4	1	0.11			
			<i>Coriobacteriales</i>	<i>Coriobacteriaceae</i>											S100		S151		1		1		
	Firmicutes	Clostridia	Clostridiales	<i>Ruminococcaceae</i>											S126			S119	2		0		
				<i>Veillonellaceae</i>			S129														1	0	
				<i>Lachnospiraceae</i>				S115													S122	1	1
				<i>Clostridiaceae</i>																		0	0
				Undefined Family								S104										1	0
		Bacilla	Lactobacillales	<i>Streptococcaceae</i>																	S111	0	1
	<i>Lactobacillaceae</i>																				0	0	
	Bacteroidetes	Bacteroidia	Bacteroidales	<i>Bacteroidaceae</i>		S149									S110	S117; S140					0	4	
<i>Prevotallaceae</i>									S134											0	1		
Proteobacteria	Gamma-proteobacteria	Enterobacteriales	<i>Enterobacteriaceae</i>		S112									S156; S154	S152				1	3			
Total number of subjects with longitudinal paired samples																	11	12					

## 2c. Taxonomic level = Order

Key	
LGG	PLC

		Taxonomy at Baseline (Order level)									
Phylum	Class	Order	<i>Bifidobacteriales</i>	<i>Clostridiales</i>	<i>Lactobacillales</i>	<i>Bacteroidales</i>	<i>Enterobacteriales</i>	LGG	PLC	P	
Actinobacteria	Actinobacteria	<i>Bifidobacteriales</i>	S103; S108	S148	S121		S133		4	1	0.02
		<i>Coriobacteriales</i>				S100	S151		1	1	
Firmicutes	<i>Clostridia</i>	<i>Clostridiales</i>	S115	S129; S104		S126	S119; S122	5	1		
	<i>Bacilla</i>	<i>Lactobacillales</i>					S111	0	1		
Bacteroidetes	<i>Bacteroidia</i>	<i>Bacteroidales</i>	S149	S134	S110	S117; S140		0	5		
Proteobacteria	<i>Gamma-proteobacteria</i>	<i>Enterobacteriales</i>	S112			S156; S154	S152	1	3		
Total number of subjects with longitudinal paired samples								11	12		

## 2 d. Taxonomic level = Class

Key	
LGG	PLC

		Taxonomy at Baseline (Class level)								
Phylum	Class	<i>Actinobacteria</i>	<i>Clostridia</i>	<i>Bacilla</i>	<i>Bacteroidia</i>	<i>Gamma-proteobacteria</i>	LGG	PLC	P	
Actinobacteria	<i>Actinobacteria</i>	S103; S108	S148	S121		S133; S100	S151	5	2	0.016
Firmicutes	<i>Clostridia</i>	S115	S129; S104		S126	S119; S122	5	1		
	<i>Bacilla</i>					S111	0	1		
Bacteroidetes	<i>Bacteroidia</i>	S149	S134	S110	S117; S140		0	5		
Proteobacteria	<i>Gamma-proteobacteria</i>	S112			S156; S154	S152	1	3		
Total number of subjects with longitudinal paired samples							11	12		

2e. Taxonomic level = Phylum

Key	
LGG	PLC

		Taxonomy at Baseline (Phylum level)									
		<i>Actinobacteria</i>	<i>Firmicutes</i>		<i>Bacteroidetes</i>		<i>Proteobacteria</i>		LGG	PLC	<i>P</i>
Phylum											
Taxonomy after 12-months of Treatment	<i>Actinobacteria</i>	S103; S108	S148	S121	S133; S100			S151	5	2	0.03
	<i>Firmicutes</i>	S115	S129; S104		S126		S119; S122	S111	5	2	
	<i>Bacteroidetes</i>	S149	S134; S110		S117; S140				0	5	
	<i>Proteobacteria</i>	S112			S156; S154	S152			1	3	
Total number of subjects with longitudinal paired samples									11	12	

**Supplemental Figure 2a-e.** Shift table showing composition of gut microbiota of patients (n=23) having paired samples at baseline (displayed horizontally) and 12-month visit (displayed vertically) are shown at each taxonomic level. Red shading represents patients treated with LGG probiotics (N=11), blue shading represents patient's treated with placebo (N=12). Patients with undefined taxonomy at either visit were excluded from the analysis.

In the 23 patients (that had samples sequenced at baseline and 12-months), there was a statistically significant difference between the distribution of dominant taxa by treatment arms found in the microbiome after 12 months of treatment at the genera ( $P=0.005$ ), order ( $P=0.02$ ), class ( $P=0.016$ ), and phylum ( $P=0.03$ ) levels, but not at the family level ( $P=0.11$ ). All ranks were tested to account for any questions about undefined taxonomic levels within samples. No difference in the distribution of dominant genus was evident at baseline prior to treatment indicating the randomization held for this subset of patients that had fecal samples at 12-months at the genera ( $P=1$ ), family ( $P=1$ ), order ( $P=1$ ), class ( $P=1$ ), and phylum ( $P=0.7$ )