

S3 Table. Summary of generalized linear model (GLM) of bacterial taxa significantly affected by treatment.

Factor	Location	Coeff.	adj-P	Taxon
<i>Metarhizium*</i> <i>Galleria</i>	Root	-10.20	0.03	k_Bacteria; p_Chloroflexi; c_TK10; o_AKYG885; f_Dolo_23
	Soil	-4.15	0.04	k_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Pseudomonadales; f_Moraxellaceae; g_Acinetobacter
		8.78	0.01	k_Bacteria; p_Bacteroidetes; c_Sphingobacteriia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Olivibacter
		10.20	0.01	k_Bacteria; p_Bacteroidetes; c_Sphingobacteriia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Solitalea
		0.80	0.04	k_Bacteria; p_Planctomycetes; c_Planctomycetia; o_Gemmatales; f_Isosphaeraceae
		2.05	0.02	k_Bacteria; p_Chloroflexi; c_Thermomicrobia; o_JG30-KF-CM45; f_un.
		0.90	0.03	k_Bacteria; p_Actinobacteria; c_Thermoleophila; o_Solirubrobacterales; f_un.
<i>Metarhizium</i>	Root	3.75	0.01	k_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Pseudomonadales; f_Moraxellaceae; g_Acinetobacter
		5.35	0.02	k_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Rhizobiaceae; g_un.
		3.89	0.03	k_Bacteria; p_Bacteroidetes; c_Flavobacteriia; o_Flavobacteriales; f_Weeksellaceae; g_Chryseobacterium
		5.02	0.04	k_Bacteria; p_Verrucomicrobia; c_Pedosphaerae; o_Pedosphaerales; f_un.
		2.82	0.04	k_Bacteria; p_Proteobacteria; c_Betaproteobacteria; o_un.
		4.90	0.04	k_Bacteria; p_Actinobacteria; c_Actinobacteria; o_Actinomycetales; f_Microbacteriaceae; g_Microbacterium
		4.70	0.05	k_Bacteria; p_Bacteroidetes; c_Sphingobacteriia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Sphingobacterium
		0.75	0.00	k_Bacteria; p_Verrucomicrobia; c_Spartobacteria; o_Chthoniobacterales; f_Chthoniobacteraceae; g_DA101
	Soil	0.73	0.01	k_Bacteria; p_Nitrospirae; c_Nitrospira; o_Nitrospirales; f_X0319.6A21; g_un.
		0.70	0.02	k_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhodospirillales; f_Rhodospirillaceae; g_un.
		0.67	0.02	k_Bacteria; p_Acidobacteria; c_Chloracidobacteria; o_RB41; f_un.
		0.66	0.02	k_Bacteria; p_Proteobacteria; c_Deltaproteobacteria; o_Syntrophobacterales; f_Syntrophobacteraceae; g_un.
		1.44	0.03	k_Bacteria; p_Nitrospirae; c_Nitrospira; o_Nitrospirales; f_Nitrospiraceae; g_Nitrospira
		0.51	0.03	k_Bacteria; p_Acidobacteria; c_Acidobacteria-6; o_iii1.15; f_un.
		1.00	0.03	k_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Legionellales; f_Coxiellaceae
		<i>Galleria</i>	Root	3.76
5.33	0.02			k_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Rhizobiaceae; g_un.
5.18	0.03			k_Bacteria; p_Verrucomicrobia; c_Pedosphaerae; o_Pedosphaerales; f_un.
2.32	0.04			k_Bacteria; p_Planctomycetes; c_Planctomycetia; o_Planctomycetales; f_Planctomycetaceae; g_Planctomyces
Soil	6.79		0.05	k_Bacteria; p_Acidobacteria; c_Acidobacteria-6; o_iii1-15; f_RB40
	-0.91		0.01	k_Bacteria; p_Actinobacteria; c_Thermoleophila; o_Solirubrobacterales_un.
	-0.76		0.01	k_Bacteria; p_Actinobacteria; c_Thermoleophila; o_Gaiellales; f_Gaiellaceae
	-0.92		0.01	k_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Bradyrhizobiaceae; g_Bradyrhizobium
	-0.82		0.02	k_Bacteria; p_Actinobacteria; c_Thermoleophila; o_Solirubrobacterales; f_Solirubrobacteraceae
	-1.48		0.02	k_Bacteria; p_Chloroflexi; c_Thermomicrobia; o_JG30-KF-CM45; f_un.
	-0.64		0.03	k_Bacteria; p_Planctomycetes; c_Planctomycetia; o_Gemmatales; f_Gemmataceae; g_un.
	-0.68		0.03	k_Bacteria; p_Chloroflexi; c_Ellin6529_un.
	0.49		0.03	k_Bacteria; p_Acidobacteria; c_Chloracidobacteria; o_RB41; f_un.
	-0.69		0.03	k_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Hyphomicrobiaceae; g_Rhodoplanes
	-0.577		0.04	k_Bacteria; p_Bacteroidetes; c_Sphingobacteriia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Solitalea
	-0.45		0.04	k_Bacteria; p_Actinobacteria; c_Acidimicrobia; o_Acidimicrobiales; f_C111; g_un.
	-1.62		0.04	k_Bacteria; p_Actinobacteria; c_Actinobacteria; o_Actinomycetales; f_Frankiaceae; g_un.
1.15	0.05	k_Bacteria; p_Proteobacteria; c_Deltaproteobacteria; o_NB1.j; f_NB1.i		

Coeff. = GLM ($\alpha = 0.05$) coefficient; adj-P = FDR-adjusted P value; un. = unclassified