

S7 Table. Bacterial taxa significantly affected by *Galleria mellonella* treatment determined by Welch's t-test.

Comparison	Location	Effect Size	adj-P	Taxon
I+ M- vs. I- M-	Soil	-2.03	0.03	k_Bacteria; p_Bacteroidetes; c_Sphingobacteriia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Olivibacter
	Root	-4.16	0.01	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Ellin329; f_un.
		2.35	0.02	k_Bacteria;p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_[Weeksellaceae];g_Chryseobacterium
		-2.45	0.02	k_Bacteria;p_Bacteroidetes;c_[Saprospirae];o_[Saprospirales];f_Chitinophagaceae;g_Niastella
		-3.59	0.02	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Shinella
		2.85	0.03	k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_Coxiellaceae;g_Aquicella
		1.93	0.03	k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae;g_Bacillus
		1.88	0.04	k_Bacteria;p_Verrucomicrobia;c_[Spartobacteria];o_[Chthoniobacteriales];f_[Chthoniobacteraceae];g_Chthoniobacter
		2.49	0.04	k_Bacteria;p_Armatimonadetes;c_[Fimbriimonadia];o_[Fimbriimonadales];f_[Fimbriimonadaceae];g_Fimbriimonas
		2.35	0.04	k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Sporichthyaceae
		-2.22	0.05	k_Bacteria;p_Acidobacteria;c_[Chloracidobacteria];o_RB41
		-2.55	0.05	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae
		-2.17	0.05	k_Bacteria;p_Verrucomicrobia;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Verrucomicrobiaceae
		I+ M+ vs. I- M+	Soil	-0.92
3.42	0.01			k_Bacteria; p_Actinobacteria; c_Thermoleophilia; o_Solirubrobacteriales; g_un.
2.69	0.02			k_Bacteria; p_Actinobacteria; c_Thermoleophilia; o_Gaiellales; f_Gaiellaceae; g_un.
2.21	0.04			k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae

Significant taxa determined by pairwise Welch's t-tests with an FDR-adjusted P value adjusted (adj-P; $\alpha = 0.05$)