

**S5 Table. Bacterial taxa significantly affected by *Metarhizium robertsii* amendment determined by Welch's t-test.**

Comparison	Location	Effect Size	adj-P	Taxon
M+ I- vs. M- I-	Soil	-2.98	0.02	k_Bacteria;p_Actinobacteria;c_Acidimicrobiia;o_Acidimicrobiales; f_C111
		-2.10	0.02	k_Bacteria;p_Actinobacteria;c_Thermoleophilia;o_Solirubrobacterales; f_un.
		-2.43	0.03	k_Bacteria;p_Chloroflexi;c_Thermomicrobia;o_JG30-KF-CM45; f_un.
		-2.77	0.03	k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Gemmatales;f_Gemmataceae
		-2.43	0.03	k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Gemmatales;f_Isosphaeraceae
		-2.29	0.03	k_Bacteria;p_Verrucomicrobia;c_Spartobacteria;o_Chthoniobacterales;f_Chthoniobacteraceae;g_DA101
		-2.22	0.04	k_Bacteria;p_Actinobacteria;c_MB-A2-108;o_0319-7L14; f_un.
		-2.10	0.04	k_Bacteria;p_Latescibacteria(WS3);c_PRR-12;o_Sediment-1;f_PRR-10
		-1.99	0.04	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae
		-2.03	0.04	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Kaistobacter
		Root	6.33	0.00
	3.03		0.03	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bradyrhizobiaceae; g_[Bradyrhizobium]
	2.57		0.04	k_Bacteria;p_Chloroflexi; c_Anaerolineae;o_SBR1031;f_A4b
	-4.13		0.01	k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Promicromonosporaceae;g_Promicromonospora
	-2.56		0.03	k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinosynnemataceae
	-1.96		0.04	k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae
	-2.57	0.04	k_Bacteria;p_Firmicutes;	
M+ I+ vs. M- I+	Soil	-2.97	0.01	k_Bacteria;p_Verrucomicrobia; c_Spartobacteria;o_Chthoniobacterales;f_Chthoniobacteraceae;g_DA101
		-3.40	0.01	k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Syntrophobacterales;f_Syntrophobacteraceae
		-2.86	0.02	k_Bacteria;p_Nitrospirae; c_Nitrospira;o_Nitrospirales;f_0319-6A21
		-2.48	0.03	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae; g_un.
		-2.05	0.05	k_Bacteria; p_Acidobacteria; c_Chloracidobacteria; o_RB41; f_un.

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