

**Supplementary Table 2.** Differentially abundant bacterial OTUs in root, stem and leaf compartments of control and infected plants (log2 fold change > 2 and <-2 & FDR<0.01)

OTU	log2FC	FDR	Phylum	Genus	Compartment	Enriched
OTU1580	-2.10679	0.001753	Proteobacteria	<i>g_Methylovirgula</i>	Root	RC
OTU429	5.897181	0.012067	Actinobacteria	<i>g_Mycobacterium</i>	Root	RI
OTU540	3.405582	0.001819	Armatimonadetes	<i>o_Armatimonadales</i>	Root	RI
OTU547	9.590365	1.20E-09	Armatimonadetes	<i>o_Armatimonadales</i>	Root	RI
OTU602	2.159404	0.020353	Planctomycetes	<i>o_Planctomycetales</i>	Root	RI
OTU606	3.087698	0.019017	Planctomycetes	<i>f_Pirellulaceae</i>	Root	RI
OTU693	2.21458	2.63E-06	Bacteroidetes	<i>f_Chitinophagaceae</i>	Root	RI
OTU720	5.194274	0.001286	Bacteroidetes	<i>g_Mucilaginibacter</i>	Root	RI
OTU938	5.225913	0.039073	Patescibacteria	<i>o_Candidatus adlerbacteria</i>	Root	RI
OTU1210	24.78225	2.56E-08	Proteobacteria	<i>f_Enterobacteriaceae</i>	Root	RI
OTU1241	3.105931	0.002449	Proteobacteria	<i>g_Chujaibacter</i>	Root	RI
OTU1247	6.154442	0.001753	Proteobacteria	<i>g_Chujaibacter</i>	Root	RI
OTU1264	3.03073	0.001753	Proteobacteria	<i>f_Rhodanobacteraceae</i>	Root	RI
OTU1530	2.169582	0.019017	Proteobacteria	<i>g_Sphingomonas</i>	Root	RI
OTU1210	127.8042	1.46E-07	Proteobacteria	<i>f_Enterobacteriaceae</i>	Stem	SI
OTU1249	8.62145	6.48E-16	Proteobacteria	<i>g_Stenotrophomonas</i>	Leaf	LI

OTU, operational taxonomic unit; FDR, false discovery rate; FC, fold change; RC, root control (healthy) sample; RI, root infected; SC, stem control; SI, stem infected; LI, leaf infected sample.