

**Table S1.** Primer sets used for qPCR and amplicon metagenomic sequencing used in this study.

Target Gene	Primer Set	Sequence	Reference
<i>qPCR</i>			
16S rRNA gene	338F/534R	5'-CCTACGGGAGGCAGCAG-3' 5'-ATTACCGCGGCTGCTGG-3'	Fierer et al., 2005 [51]
18S rRNA gene	SSU 1536/Fu 1851	5'-ATTGCAATGCMCTATCCCCA-3' 5'-GGAAACTCACCAGGTCCAGA-3'	May et al., 2001 [52]
<i>Amplicon metagenomic sequencing</i>			
16S rRNA gene V3-V4 regions	341F/806R	5'-CCTAYGGRBGCASCAG-3' 5'-GGACTACNNGGTATCTAAT-3'	Youngseob et al., 2005 [50]

**Table S2.** Trimming summary showing the number of initial reads, reads that pass quality control, reads after denoising step, number of sequences after merging them by their 3', and the resulting non-chimeric sequences. B1 = *B. brizantha*/common bean; B2 = *B. brizantha*/*B. brizantha*/common bean; BM = common bean monoculture.

SampleID	Input	Filtered	Denoised	Merged	Non-chimeric
B1R1	165020	147973	139116	92732	76709
B1R2	178822	159876	150726	103001	85990
B1R3	169349	151352	141919	93990	77698
B2R1	152487	136318	127823	85112	70278
B2R2	153882	137960	129386	81468	65603
B2R3	189425	169670	161051	115451	97005
BMR1	175579	157715	148189	97811	79653
BMR2	181736	163465	153122	102363	84574
BMR3	180370	162266	152793	103298	84912

**Table S3.** Mean relative abundance of the 20 most abundant bacterial phyla in the three rhizospheric samples: B1 = *B. brizantha*/common bean; B2 = *B. brizantha*/*B. brizantha*/common bean; BM = common bean monoculture.

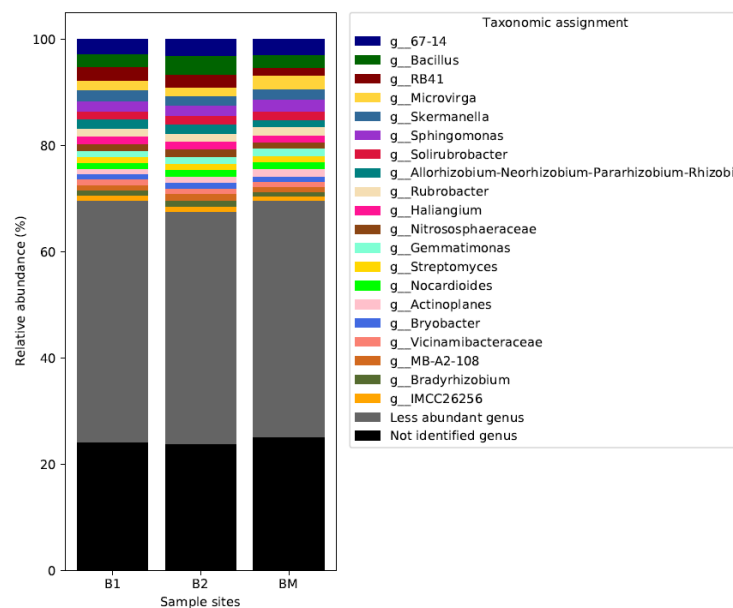
Phylum	B1	B2	BM
Actinobacteriota	30.34 ± 0.51	31.84 ± 1.51	32.36 ± 3.07
Proteobacteria	27.48 ± 2.09	25.60 ± 1.96	26.12 ± 3.64
Acidobacteriota	9.02 ± 0.85	8.45 ± 0.35	7.28 ± 1.04
Chloroflexi	6.12 ± 0.98	7.35 ± 1.3	7.09 ± 0.72
Myxococcota	7.21 ± 0.74	5.89 ± 0.28	7.05 ± 0.18
Gemmatimonadota	5.99 ± 0.30	5.10 ± 0.17	5.64 ± 0.65
Bacteroidota	3.56 ± 0.19	3.37 ± 0.54	3.51 ± 1.29
Firmicutes	2.84 ± 0.29	4.08 ± 0.46	2.99 ± 0.62
Crenarchaeota	2.32 ± 1.48	2.82 ± 0.80	2.79 ± 1.26
Verrucomicrobiota	1.54 ± 0.14	1.97 ± 0.63	1.38 ± 0.34
Entothaeonellaeota	0.63 ± 0.16	0.91 ± 0.06	0.61 ± 0.14
Desulfobacterota	0.68 ± 0.12	0.47 ± 0.19	0.56 ± 0.23
Nitrospirota	0.54 ± 0.14	0.44 ± 0.08	0.41 ± 0.06
Cyanobacteria	0.20 ± 0.10	0.30 ± 0.28	0.57 ± 0.72
Methylomirabilota	0.39 ± 0.05	0.31 ± 0.04	0.24 ± 0.04
Bdellovibrionota	0.24 ± 0.03	0.18 ± 0.04	0.27 ± 0.13
Planctomycetota	0.14 ± 0.05	0.19 ± 0.10	0.25 ± 0.17
Patescibacteria	0.10 ± 0.06	0.16 ± 0.09	0.10 ± 0.04
Armatimonadota	0.11 ± 0.03	0.07 ± 0.03	0.13 ± 0.03
NB1-j	0.13 ± 0.11	0.08 ± 0.02	0.07 ± 0.03

**Table S4.** Mean relative abundance of the 20 most abundant bacterial families in the three rhizospheric samples: B1 = *B. brizantha*/common bean; B2 = *B. brizantha*/*B. brizantha*/common bean; BM = common bean monoculture.

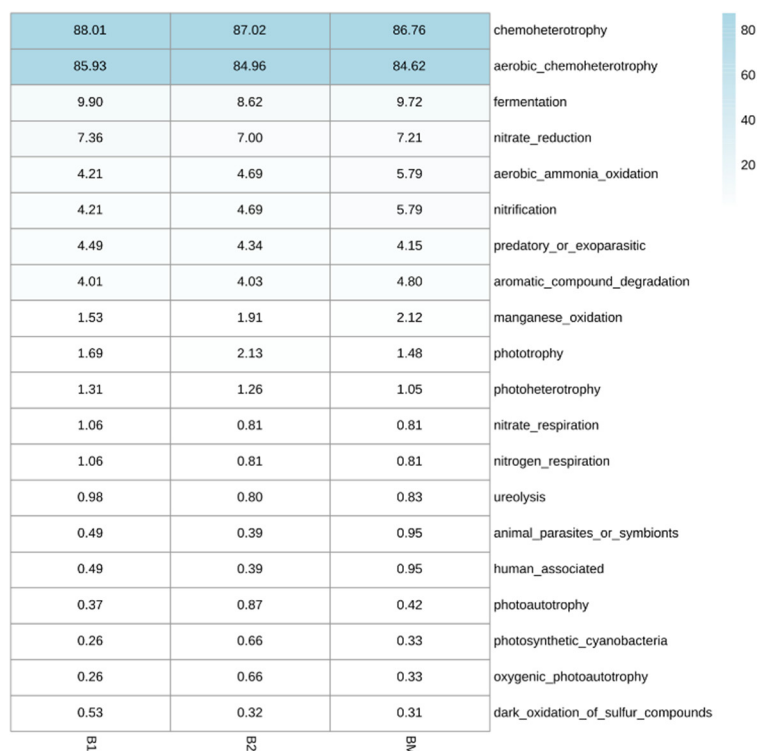
Family	B1	B2	BM
Gemmatimonadaceae	4.89 ± 0.29	4.33 ± 0.13	4.62 ± 0.56
Micromonosporaceae	4.04 ± 0.22	4.53 ± 0.85	4.65 ± 0.58
Roseiflexaceae	2.86 ± 0.64	3.91 ± 1.06	3.07 ± 0.39
67-14	3.00 ± 0.27	3.24 ± 0.17	3.02 ± 0.35
Beijerinckiaceae	2.71 ± 0.32	2.39 ± 0.14	3.90 ± 0.37
Bacillaceae	2.36 ± 0.23	3.58 ± 0.47	2.51 ± 0.55
Sphingomonadaceae	2.85 ± 0.18	2.49 ± 0.17	2.83 ± 0.73
Nitrososphaeraceae	2.32 ± 1.48	2.82 ± 0.80	2.79 ± 1.26
Xanthobacteraceae	2.35 ± 0.03	2.67 ± 0.23	2.00 ± 0.27
Solirubrobacteraceae	2.09 ± 0.08	2.25 ± 0.15	2.60 ± 0.48
Azospirillaceae	2.30 ± 0.25	2.00 ± 0.07	2.22 ± 0.29
Pyrinomonadaceae	2.52 ± 0.29	2.37 ± 0.36	1.42 ± 0.29
Rhizobiaceae	2.28 ± 0.65	2.16 ± 0.91	1.58 ± 0.22
Nocardiodaceae	1.99 ± 0.41	2.00 ± 0.16	2.00 ± 0.65
Pseudonocardiaceae	1.90 ± 0.10	2.20 ± 0.05	1.80 ± 0.25
Comamonadaceae	2.02 ± 0.30	1.69 ± 0.17	1.69 ± 0.24
Myxococcaceae	1.72 ± 0.29	1.31 ± 0.09	1.99 ± 0.47
Chitinophagaceae	1.65 ± 0.03	1.53 ± 0.22	1.55 ± 0.57
Micrococcaceae	1.48 ± 0.14	1.28 ± 0.18	1.90 ± 0.51
Rubrobacteriaceae	1.45 ± 0.15	1.48 ± 0.05	1.56 ± 0.36

**Table S5.** Mean relative abundance of the 20 most abundant bacterial genera in the three rhizospheric samples: B1 = *B. brizantha*/common bean; B2 = *B. brizantha*/*B. brizantha*/common bean; BM = common bean monoculture.

Genus	B1	B2	BM
67-14	3.0 ± 0.27	3.24 ± 0.17	3.02 ± 0.35
Bacillus	2.36 ± 0.23	3.57 ± 0.47	2.51 ± 0.55
RB41	2.52 ± 0.29	2.37 ± 0.36	1.42 ± 0.29
Microvirga	1.83 ± 0.06	1.68 ± 0.16	2.54 ± 0.10
Skermanella	2.07 ± 0.23	1.81 ± 0.06	2.02 ± 0.30
Sphingomonas	1.89 ± 0.15	1.83 ± 0.20	2.15 ± 0.63
Solirubrobacter	1.54 ± 0.12	1.64 ± 0.03	1.77 ± 0.35
Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	1.80 ± 0.58	1.83 ± 0.82	1.24 ± 0.12
Rubrobacter	1.45 ± 0.15	1.48 ± 0.05	1.56 ± 0.36
Haliangium	1.47 ± 0.15	1.34 ± 0.23	1.38 ± 0.27
Unknown Nitrososphaeraceae	1.21 ± 0.86	1.56 ± 0.35	1.13 ± 0.52
Gemmatimonas	1.08 ± 0.13	1.18 ± 0.07	1.38 ± 0.28
Streptomyces	1.26 ± 0.32	1.24 ± 0.21	1.13 ± 0.14
Nocardioides	1.09 ± 0.21	1.15 ± 0.10	1.32 ± 0.40
Actinoplanes	0.88 ± 0.04	1.25 ± 0.27	1.37 ± 0.20
Bryobacter	1.04 ± 0.10	1.03 ± 0.05	1.09 ± 0.06
Unknown Vicinamibacteraceae	1.16 ± 0.19	1.08 ± 0.09	0.89 ± 0.23
MB-A2-108	1.01 ± 0.06	1.17 ± 0.07	0.92 ± 0.03
Bradyrhizobium	0.93 ± 0.08	1.19 ± 0.13	0.81 ± 0.13
IMCC26256	0.91 ± 0.04	1.05 ± 0.11	0.84 ± 0.04



**Figure S1.** Average of relative abundance at genera taxonomic levels in the total bacterial community associated with the common bean rhizosphere under different service crop treatments: B1 = *B. brizantha*/common bean; B2 = *B. brizantha*/*B. brizantha*/common bean; BM = common bean monoculture (control). Relative abundances are based on the proportional frequencies of the ASV that could be classified at the genera levels, and are related to the total ASV identified in the samples.



**Figure S2.** Functional groups of bacteria based on FAPROTAX database. B1 = *B. brizantha*/common bean; B2 = *B. brizantha*/*B. brizantha*/common bean; BM = common bean monoculture.