Supplementary information:

Integrated analysis of root microbiomes of soybean and wheat from agricultural fields

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Supplementary methods:

PGP traits detection

IAA

Isolates were cultured on nutrient agar medium and overlaid with cellulose membrane and incubated for 48h (Bric et al 1991). Salkowski's reagent was added on the cellulose membrane after 48h of incubation. Pink coloration indicated production of IAA (Supplementary Figure S2A).

ACC deaminase

Isolates were screened for their ability to utilize ACC as the sole nitrogen source in DF minimal medium according to the method of Dell'Amico et al. (Dell'Amico et al 2005). Three culture conditions were used: DF minimal medium alone as a negative control; DF minimal medium plus (NH4)2SO4 (2g L−1) as a positive control; and DF minimal medium plus 3 mmol L−1 ACC as the selective medium (Supplementary Figure S2B).

P solubilazation

Phosphorous solubilization was detected using the Pikovskaya's agar medium. In brief, positive strains are capable of producing a halo/clear zone due to the release of organic acids into the surrounding medium (Supplementary Figure S2C) (Katznelson et al 1962).

Nitrogen fixation

Nitrogen fixation was evaluated in 5ml of N-free semisolid medium in 10 ml vials. The inoculation was done into the center of the medium. In general terms, the principle of this semi-solid medium is that it allows for growth of the bacteria under conditions where their nitrogenase requires protection from O2-mediated denaturation (Dalton and Postgate 1968) *i.e.* in early stages of growth when only a small number of cells are starting to multiply and they thus use little oxygen. In later stages, the bacterial cells within the culture medium migrate closer to the surface where there is sufficient oxygen pressure to support aerobic respiration, but not so much that it damages nitrogenase. In this stage a sub-surface growth pellicle is observed. The presence of absence of the pellicle defines the ability to fix nitrogen (i.e. nitrogenase activity, Supplementary Figure S2D) (Baldani et al 2014).

F515-R806 primers bias in rhizospheric soil samples

We observed that 1.5-2.5% reads of the RS fraction were classified as Proteobacteria in rhizospheric soil samples (Supplementary Figure S8). However it has been reported that Proteobacteria usually accounts for over 20% relative abundance in rhizospheric soil communities (Mendes et al 2011, Peiffer et al 2013). Although we have not identified yet the source of this bias, the only methodological difference respect to other published works is the use of a particular TAG sequence (TAG-F 5'-CACGACGTTGTAAAACGAC-3', TAG-R 5'-CAGGAAACAGCTATGACC-3') in the F515- R806 primers (Caporaso et al 2011b). We are aware that this bias was never reported before, but unfortunately, it affected several different pyrosequencing runs, with different sample types (i.e. soil, root tissue, human samples) and only when this combination of primers and TAG was used (data not shown). We hypothesize that this effect was not observed in RA datasets because they are highly dominated by Proteobacteria so even with poor primer hybridization they were successfully amplified. Based on these results, we decided to use RS samples only for diversity analyses, where we considered that the observed richness is equal or most likely lower than it would have been measured with a better Proteobacteria representation.

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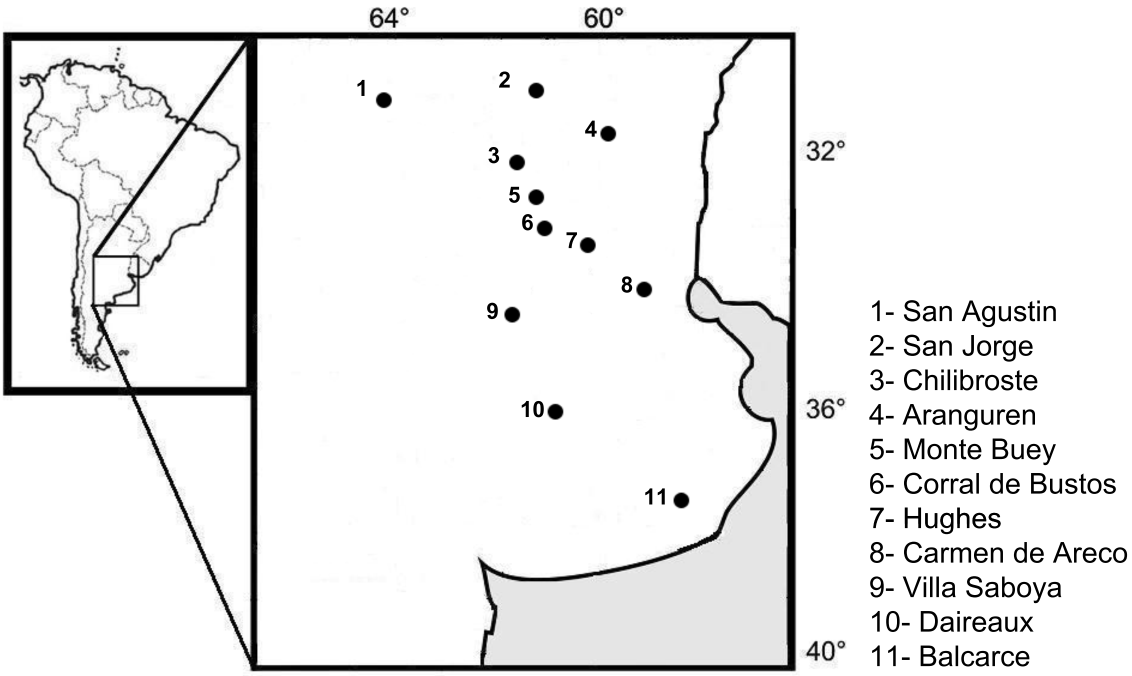
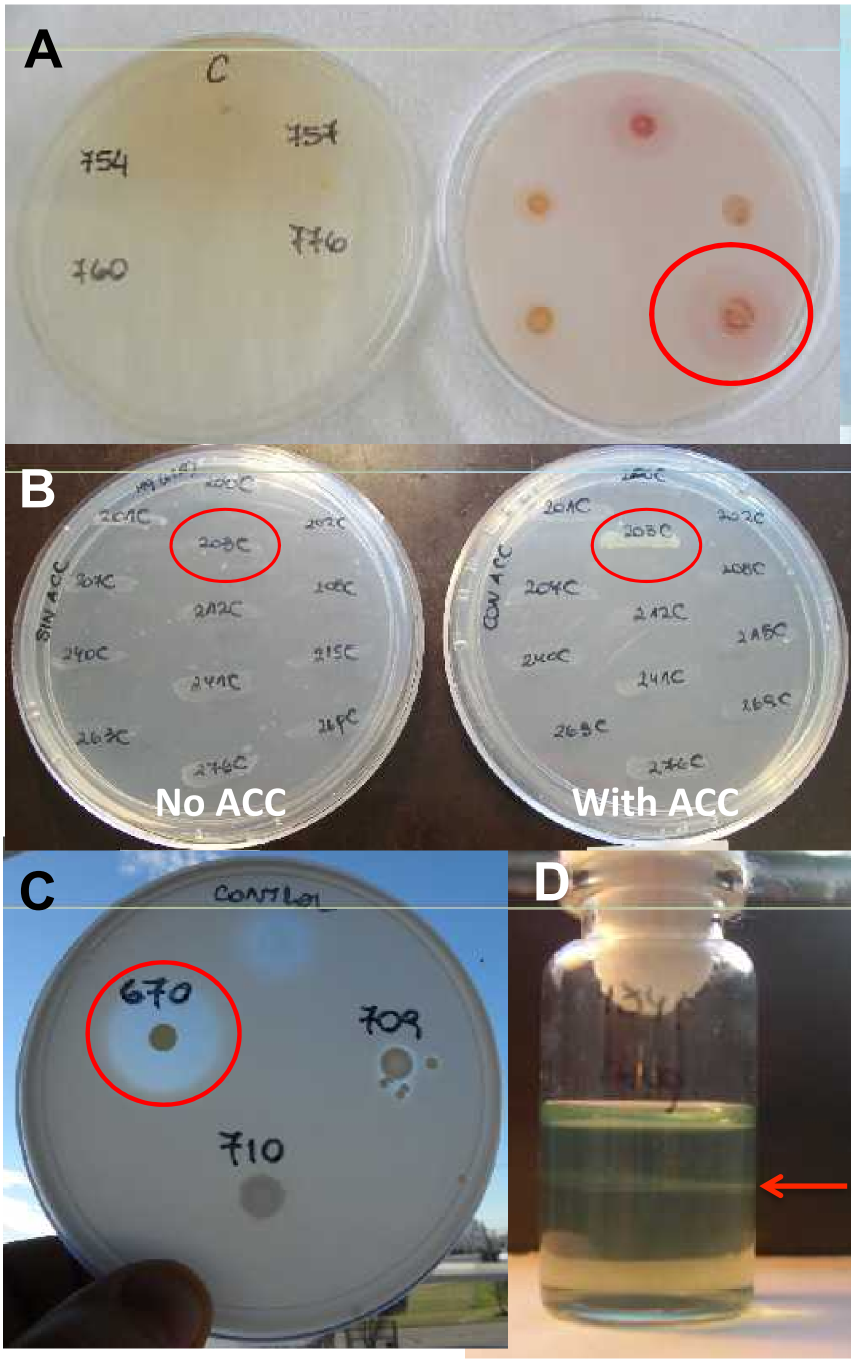
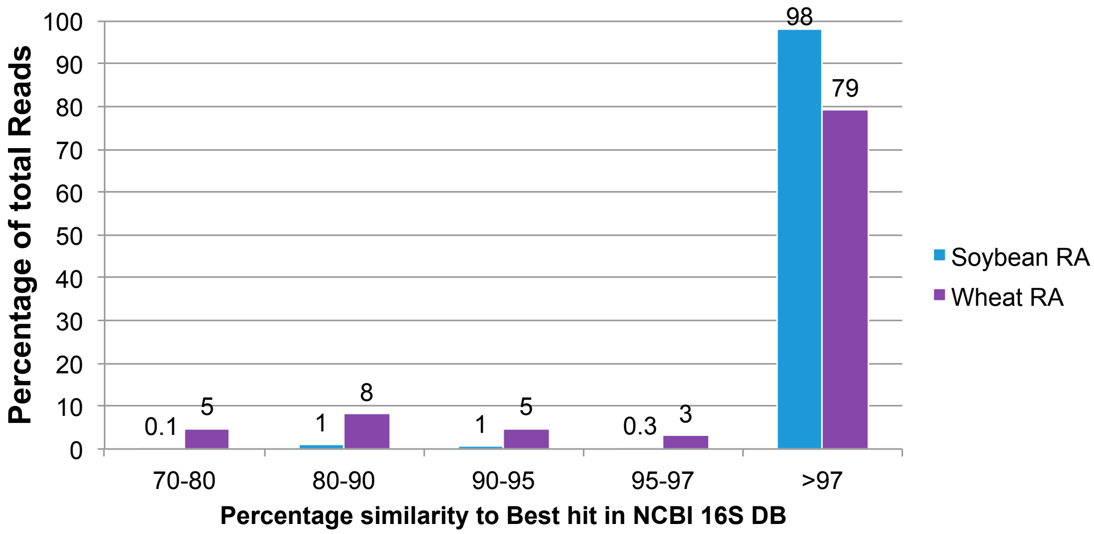
Supplementary figures:



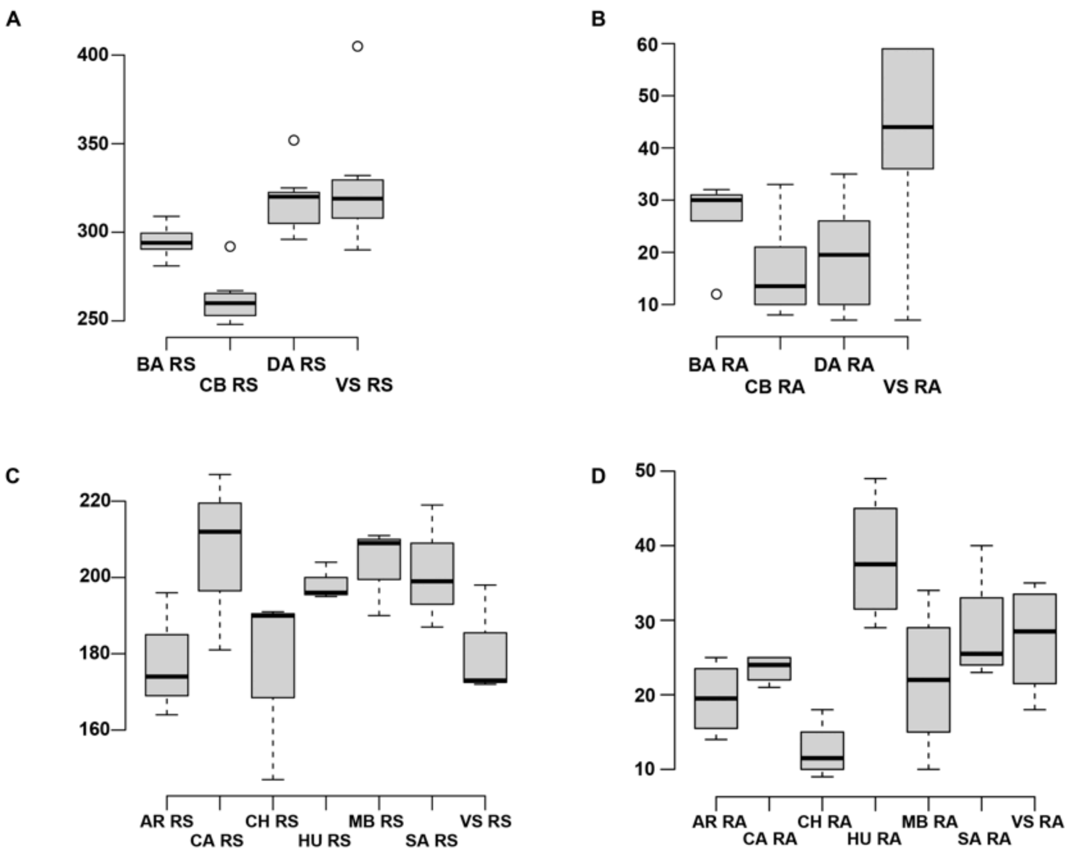
Supplementary Figure S1: Sampling locations. Samples were taken in experimental fields from 11 different locations in Argentine Pampas. The GIS coordinates to build the maps were obtained from DIVA-GIS service (http://www.diva-gis.org/) and imported to gvGIS software (Version: 2.2.0-2313) for visualization (http://www.gvsig.com/). The obtained PDF figures for each map were edited in Adobe Photoshop cs5 (https://www.adobe.com) for final figure formatting.



Supplementary Figure S2: Examples of isolates with positive activities for the four PGP traits. A) Pink coloration indicates production of IAA. B) Growth on ACC selective medium indicates that ACC can be used as a source of nitrogen. C) Strains that are capable of producing a halo/clear zone in the Pikovskaya's agar medium, are able to solubilize P due to the release of organic acids into the surrounding medium D) Since nitrogenase is sensitive to oxygen, the presence of a pellicle at the sub-surface (aerobic region but with lower oxygen pressure) of the N-free semisolid medium indicate the ability to fix nitrogen.

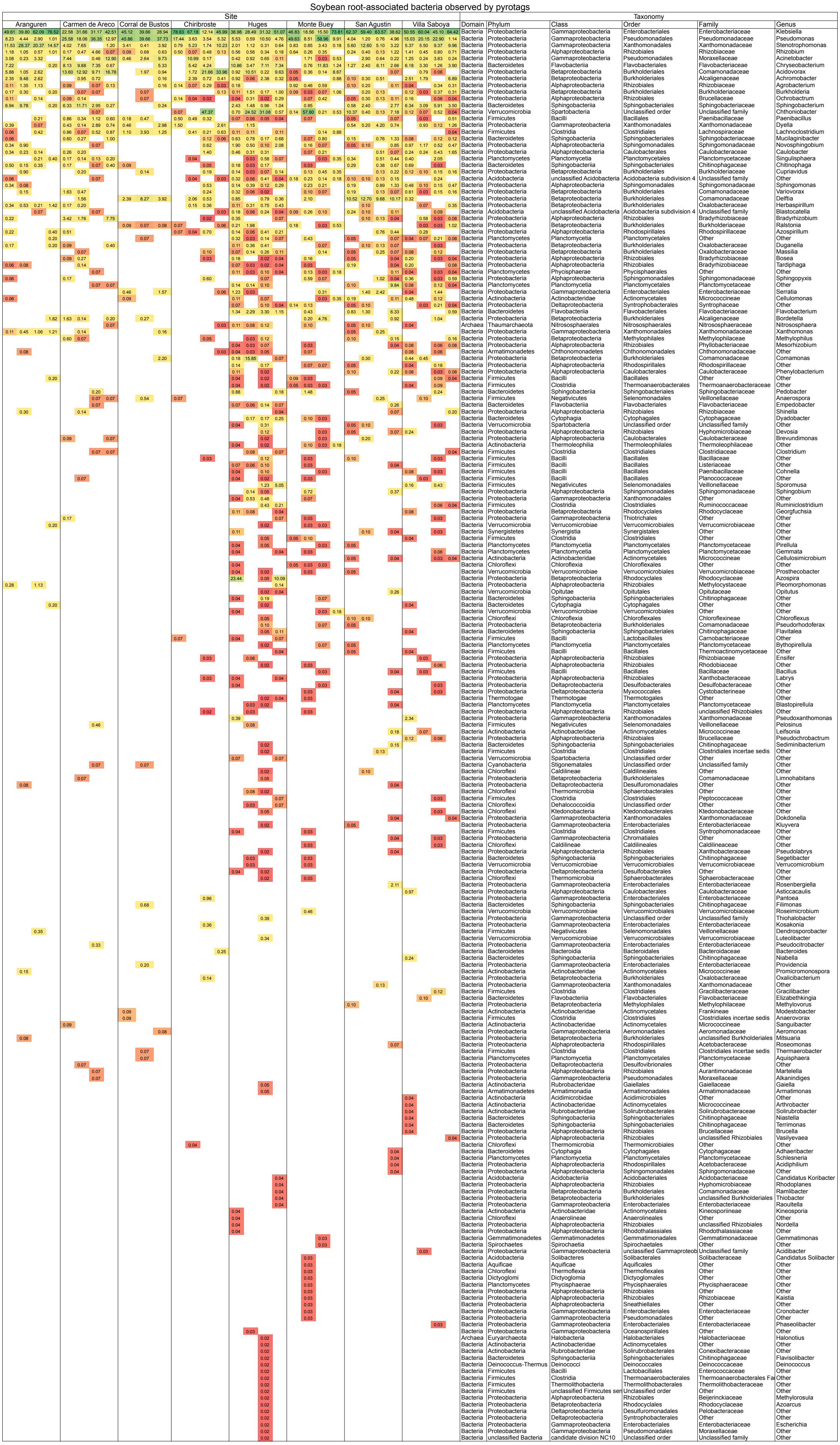


Supplementary Figure S3: Percentage similarity of best blast hits of pyrotag RA data. All root-associated soil pyrotags were blasted against NCBI 16S rRNA database and then grouped according to percentage similarity intervals to best hit.



Supplementary Figure S4: Comparison of alpha diversity between sampling sites. Boxplots represent OTU richness. Kruskal-Wallis Test was used to detect differences in wheat RS mirobiomes (A), wheat RA microbiomes (B), soybean RS mirobiomes (C) and soybean RA microbiomes (D). Sampling sites: AR: Aranguren, CA: Carmen de Areco, CH: Chilibroste, HU: Huges, MB: Monte Buey, SA: San Agustin, VS: Villa Saboya, BA: Balcarce, CB: Corral de Bustos, DA: Daireaux. Significant differences were found for soybean RS and RA microbiomes and for wheat RS microbiomes ($p<0.05$).

Soybean root-associated bacteria observed by pyrotags



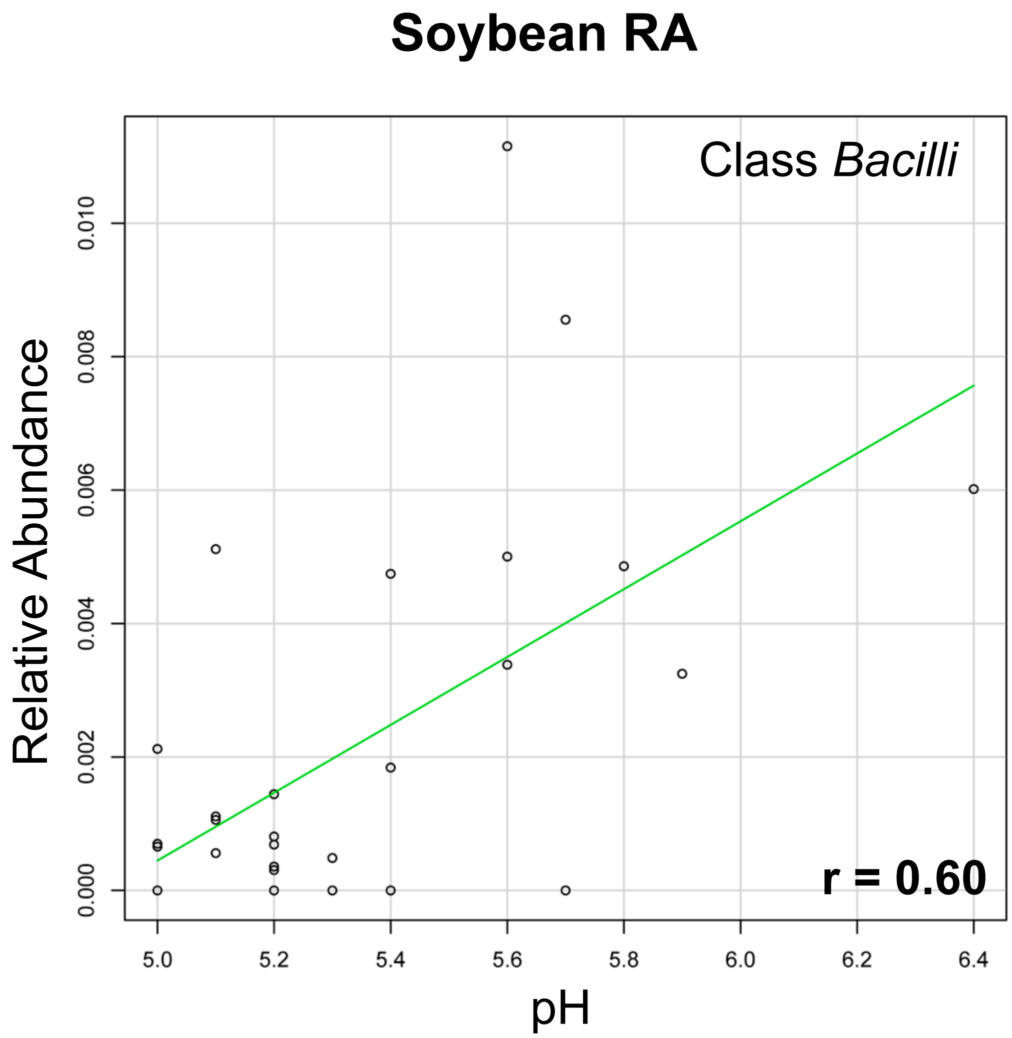
Site																															Taxonomy					
Aranguren				Carmen de Areco				Corral de Bustos			Chiribroste				Huges				Monte Buey				San Agustin				Villa Saboya				Domain	Phylum	Class	Order	Family	Genus
49.61	39.80	62.09	76.52	22.58	31.66	31.17	42.51	45.12	39.66	28.94	78.63	67.18	12.14	45.99	38.98	28.49	31.32	51.07	46.83	18.56	15.50	73.81	62.37	59.40	63.57	38.62	50.55	60.04	45.10	64.42	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella
8.23	4.44	2.90	1.01	25.58	18.06	36.35	12.97	45.86	39.66	37.73	17.44	3.63	3.54	5.32	5.53	0.59	10.50	4.76	49.63	8.51	58.96	9.91	4.04	1.20	0.76	4.96	15.03	20.15	22.90	1.14	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
11.53	28.37	20.37	14.57	4.02	7.65		1.20	3.41	0.41	3.92	0.79	5.23	1.74	10.23	2.01	1.12	0.31	0.64	0.83	0.85	3.43	0.18	5.60	12.60	5.10	3.22	5.37	5.50	9.37	9.96	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomonas
1.18	1.05	0.57	1.01	0.17	0.47	4.66	0.07	0.09	0.68	0.63	0.50	0.07	0.48	0.13	0.56	0.56	0.34	0.18	0.64	0.26	0.35		0.24	0.40	0.13	1.22	1.41	0.45	0.80	0.71	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Rhizobium
3.08	0.23	3.32		7.44		0.46	12.90	0.46	2.64	9.73		10.99	0.17		0.42	0.92	0.65	0.11		1.71	0.03	0.53		2.90	0.64	0.22	1.25	0.24	3.83	0.24	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter
7.22			0.20	8.13	9.88	7.35	0.67			5.33		5.42	4.24		10.86	3.47	7.11	7.34		0.76	11.83	1.24	1.27	2.40	6.11	2.66	6.18	3.30	1.26	3.90	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Chryseobacterium
5.88	1.05	2.62		13.60	12.92	9.71	16.78		1.97	0.94		1.72	21.66	33.96	0.92	10.51	0.22	9.63	0.05	0.36	0.14	8.67				0.07		0.79	0.06		Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Acidovorax
2.35	9.48	2.62			0.95	0.72				0.16		2.39	0.72	0.41	0.92	0.06	2.38	0.32	0.05			0.88	0.10	0.30	0.51		2.51	1.79		6.89	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	Achromobacter
0.11	1.35	1.13		0.09		0.07	0.13			0.16	0.14	0.07	0.29	0.03	0.18				0.92	0.46	0.59		0.10	0.20		0.11	0.04		0.34	0.31	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium
0.17	0.30		0.20		0.07	0.07			0.07					0.13	0.11	1.51	0.17	1.00	0.09	0.03	0.07	1.06		0.20	0.13		0.12	0.03	0.37	0.31	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia
0.11		0.14		0.09	0.14				0.07		0.14	0.04	0.02		0.04	0.31	0.02	0.29		0.07	0.42		0.05	0.30	0.13	0.11	0.16		0.06	0.04	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Brucellaceae	Ochrobactrum
6.94	9.78		0.20	6.33	11.71	2.95	0.27			0.24					2.43	1.48	0.96	1.04		0.85			0.58	2.40		2.77	6.34	3.09	5.91	3.50	Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Sphingobacterium
						0.07					0.07		47.37		0.70	24.52	31.08	0.57	0.14	57.80	0.21	0.53	10.37	0.40	0.13	7.18	0.12	0.07	0.52	0.04	Bacteria	Verrucomicrobia	Spartobacteria	Unclassified order	Unclassified family	Chthoniobacter
		0.21		0.86	0.34	1.12	0.60	0.18	0.47		0.50	0.49	0.32		0.07	0.06	0.05	0.04		0.07			0.05			0.07		0.03		0.51	Bacteria	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Paenibacillus
0.39		0.07		0.43	0.14	2.89	0.74	0.46		2.98	1.50			2.61		1.15							0.54	0.20	4.20	0.74		0.93	0.12	1.26	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Dyella
0.06		0.42		0.86	0.07	0.52	0.87	1.10	3.93	1.25		0.41	0.21	0.63	0.11	0.11		0.11			0.14	0.88								0.04	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnoclostridium
0.06				0.60	0.27		1.00						0.12	0.06	0.63	0.78	0.17	0.68		0.07	0.80		0.15		0.76	1.33	0.08		0.12	0.12	Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Mucilaginibacter
0.34	0.90					0.07							0.62		1.90	0.50	0.10	2.08		0.16	0.07		0.05	0.10		0.85	0.97	1.17	0.52	0.47	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium
0.34	0.23	0.14		0.26	0.20								1.40		0.46	0.31	0.31			0.07	0.21				0.51	0.07	0.24	0.24	0.43	1.65	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Caulobacter
		0.21	0.40	0.17	0.14	0.13	0.20					0.04				0.03	0.58	0.07			0.03	0.35	0.34		0.51	0.44	0.40		2.05		Bacteria	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Singulisphaera
0.50	0.15	0.35		0.17		0.07	0.40	0.09					0.05		0.18	0.03	0.17			0.03			0.29		0.38	0.67	0.69		0.03		Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Chitinophaga
	0.90				0.20				0.14				0.19		0.14	0.03	0.07	0.14		0.13	0.45	0.35			0.13	0.22	0.12	0.10	0.15	0.16	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Cupriavidus
0.06						0.07						0.04		0.03	0.32	0.06	0.41	0.04	0.18	0.23	0.14	0.18	0.10	0.10	0.13	0.15			0.24		Bacteria	Acidobacteria	unclassified Acidobacteria	Acidobacteria subdivision 4	Unclassified family	Other
0.34	0.08												0.53		0.14	0.39	0.12	0.29		0.23	0.21		0.19		0.89	1.33	0.48	0.10	0.15	0.47	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
	0.15			1.63	0.47								0.24		0.32	0.06	0.02			0.10	0.07		0.19		0.13	0.07	0.61	0.03	0.15	0.16	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Variovorax
					1.56			2.39	8.27	3.92		2.06	0.53		0.85		0.79	0.36		2.10			10.52	12.70	9.68	10.17	0.32				Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Delftia
0.34	0.53	0.21	1.42	0.17	0.20							0.15	0.36		0.11	0.31	0.75	0.43						0.10				0.07		0.35	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Herbaspirillum
		0.07				0.07								0.03	0.18	0.06	0.24	0.04	0.09	0.26	0.10		0.24	0.10		0.11			0.09		Bacteria	Acidobacteria	unclassified Acidobacteria	Acidobacteria subdivision 4	Unclassified family	Blastocatella
0.22				3.42	1.76		7.75						0.02		0.35			0.07						0.10	0.13	0.04		0.58	0.03	0.08	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium
								0.09	0.07	0.08	0.07			0.06	0.21	1.98			0.18		0.03	0.53						0.03	0.03	1.02	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Ralstonia
0.22			0.40	0.51							0.07	0.04	0.70		0.14	0.06	0.41	0.21							0.76	0.44		0.28			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Azospirillum
			0.20						0.07						0.32	0.03	0.14	0.07		0.43			0.05			0.07	0.04	0.07	0.21	0.08	Bacteria	Planctomycetes	Planctomycetia	Planctomycetales	Other	Other
0.17			0.20	0.09			0.40								0.11	0.36	0.41				0.07			0.10	0.13	0.07			0.03		Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Duganella
					0.07								0.10		0.07	0.14	0.26	0.11			0.14		0.05		0.25	0.07	0.08		0.12		Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia
				0.09	0.27								0.03		0.18		0.02	0.04		0.16			0.05			0.04	0.20		0.03	0.04	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Bosea
0.06	0.08				0.14										0.07	0.03	0.02	0.04		0.03			0.19			0.04	0.20			0.08	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Tardiphaga
						0.07									0.11	0.03	0.10	0.04		0.13	0.03	0.18				0.11	0.04		0.03	0.04	Bacteria	Planctomycetes	Phycisphaerae	Phycisphaerales	Other	Other
0.06				0.17									0.60				0.07			0.59	0.07				1.02	0.04	0.36		0.03	0.59	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingopyxis
						0.07	0.07								0.14	0.14	0.10						0.10			9.84	0.08		0.12	0.04	Bacteria	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Other
								0.46		1.57				0.06	1.23	0.03					0.31			1.40	2.42		0.04		1.44		Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Serratia
0.06								0.09							0.11		0.07				0.03	0.35	0.19			0.11	0.48		0.12		Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Micrococcineae	Cellulomonas
															0.07		0.10	0.04	0.14	0.13			0.05	0.10				0.03	0.21	0.04	Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	Other
															1.34	2.29	3.30	1.15		0.43			0.83	1.30		6.33				0.59	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
			1.82	1.63	0.14		0.20		0.27											0.20	4.76					0.92			1.04		Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	Bordetella
							0.07							0.03	0.11	0.08	0.12			0.10			0.05	0.10			0.04				Archaea	Thaumarchaeota	Nitrososphaerales	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera
0.11	0.45	1.06	1.21		0.14					0.16													0.05		0.25						Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Xanthomonas
				0.60	0.07								0.05			0.03	0.12						0.10			0.15				0.16	Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	Methylophilus
															0.04	0.03	0.07			0.03						0.04	0.08		0.06	0.08	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	Mesorhizobium
	0.08													0.03	0.04	0.03	0.05			0.07							0.08		0.06		Bacteria	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae	Other
										2.20					0.18	15.85		0.07						0.30			0.44	0.45			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Comamonas
															0.14		0.17			0.07	0.07		0.05				0.04		0.18		Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Other
															0.11		0.02						0.10			0.22	0.08		0.03	0.08	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacterium
			0.20												0.04		0.02		0.09	0.03									0.09	0.04	Bacteria	Firmicutes	Bacilli	Bacillales	Other	Other
															0.04		0.02		0.05	0.03	0.03						0.04		0.09		Bacteria	Firmicutes	Clostridia	Thermoanaerobacterales	Thermoanaerobacteraceae	Other
						0.20									0.88			0.18		1.48			0.05						0.24		Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter
						0.07	0.07		0.54		0.07														0.25			0.10			Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Anaerospora
						0.07									0.07	0.06	0.14	0.07								0.26					Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Empedobacter
	0.30				0.14													0.04								0.07				0.20	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Shinella
																0.17	0.17	0.25		0.10	0.03										Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Dyadobacter
															0.04		0.31						0.05	0.10					0.03		Bacteria	Verrucomicrobia	Spartobacteria	Unclassified order	Unclassified family	Other
																	0.12				0.03		0.05			0.07	0.24				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Devosia
				0.09			0.07										0.02				0.03			0.20							Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas
															0.04		0.02			0.10	0.03	0.18									Bacteria	Actinobacteria	Thermoleophilia	Thermoleophilales	Thermoleophilaceae	Other
						0.07	0.07									0.08		0.07												0.04	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium
													0.03				0.12			0.03			0.10						0.03		Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Other
															0.07	0.06	0.10			0.03						0.04					Bacteria	Firmicutes	Bacilli	Bacillales	Listeriaceae	Other
															0.04		0.10				0.03						0.08		0.03		Bacteria	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Cohnella
					0.07										0.04		0.02			0.03								0.03			Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Other
																	1.23	5.05									0.16		0.43		Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Sporomusa
																0.14	0.05			0.72						0.37					Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingobium
															0.04	0.53	0.48			0.07											Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Other	Other
																	0.43	0.21											0.06	0.04	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminiclostridium
															0.11	0.08		0.04									0.08				Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Georgfuchsia
				0.17														0.07		0.03									0.03		Bacteria	Proteobacteria	Gammaproteobacteria	Thiotrichales	Other	Other
			0.20														0.02			0.03	0.03										Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Other
															0.11									0.10		0.04			0.03		Bacteria	Synergistetes	Synergistia	Synergistales	Other	Other
																	0.05		0.05	0.10							0.04				Bacteria	Firmicutes	Clostridia	Clostridiales	Other	Other
															0.04		0.05				0.03		0.05								Bacteria	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Pirellula
															0.04			0.04		0.03									0.06		Bacteria	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
																							0.05			0.04			0.03	0.04	Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Micrococcineae	Cellulosimicrobium
															0.04				0.05	0.03	0.03										Bacteria	Chloroflexi	Chloroflexia	Chloroflexales	Other	Other
															0.04		0.02			0.03			0.05								Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Prosthecobacter
															23.44		0.05	10.09													Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Azospira
0.28		1.13																0.14													Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Pleomorphomonas
																	0.02	0.04								0.26					Bacteria	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus
															0.04		0.19				0.07										Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Other
			0.20														0.02										0.04				Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Other	Other
															0.04						0.03	0.18									Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Other	Other
																	0.05						0.10	0.10							Bacteria	Chloroflexi	Chloroflexia	Chloroflexales	Chloroflexineae	Chloroflexus
																	0.10				0.07		0.05								Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Pseudorhodoferax
																	0.05	0.11									0.04				Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Flavitalea
											0.07				0.04			0.07													Bacteria	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	Other
																	0.02				0.07		0.05								Bacteria	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Bythopirellula
																		0.04					0.05				0.04				Bacteria	Firmicutes	Bacilli	Bacillales	Thermoactinomycetaceae	Other
													0.03			0.06												0.03			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Ensifer
																	0.02			0.03									0.06		Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhodobiaceae	Other
																					0.03					0.04		0.03			Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus
													0.03		0.04			0.04													Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Labrys
															0.04						0.03								0.03		Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	Other
																				0.03						0.04			0.03		Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Cystobacterineae	Other
																	0.02	0.04		0.03											Bacteria	Thermotogae	Thermotogae	Thermotogales	Other	Other
																0.03	0.02									0.04					Bacteria	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Blastopirellula
													0.02			0.03				0.03											Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	unclassified Rhizobiales	Other
															0.39												2.34				Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Pseudoxanthomonas
						0.46										0.08															Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Pelosinus
																										0.18		0.07			Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Micrococcineae	Leifsonia
																											0.12		0.06		Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Brucellaceae	Pseudochrobactrum
																	0.02									0.15					Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Sediminibacterium
																	0.02								0.13						Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales incertae sedis	Other
															0.07			0.07													Bacteria	Verrucomicrobia	Spartobacteria	Unclassified order	Other	Other
						0.07			0.07																						Bacteria	Cyanobacteria	Stigonematales	Unclassified order	Unclassified family	Other
																	0.02							0.10							Bacteria	Chloroflexi	Caldilineae	Caldilineales	Other	Other
					0.07												0.05														Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Limnohabitans
	0.08																									0.04					Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Other	Other
																0.08	0.02														Bacteria	Chloroflexi	Thermomicrobia	Sphaerobacterales	Other	Other
																		0.07											0.03		Bacteria	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	Other
																0.03		0.07													Bacteria	Chloroflexi	Dehalococcoidia	Unclassified order	Other	Other
																	0.05												0.03		Bacteria	Chloroflexi	Ktedonobacteria	Ktedonobacterales	Ktedonobacteraceae	Other
																										0.04				0.04	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Dokdonella
																	0.02						0.05								Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Kluyvera
															0.04					0.03											Bacteria	Firmicutes	Clostridia	Clostridiales	Syntrophomonadaceae	Other
																										0.04			0.03		Bacteria	Proteobacteria	Gammaproteobacteria	Chromatiales	Other	Other
																				0.03									0.03		Bacteria	Chloroflexi	Caldilineae	Caldilineales	Caldilineaceae	Other
																	0.02									0.04					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Pseudolabrys
																0.03				0.03											Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Segetibacter
																0.03				0.03											Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Verrucomicrobium
															0.04		0.02														Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Other	Other
																	0.02			0.03											Bacteria	Chloroflexi	Thermomicrobia	Sphaerobacterales	Sphaerobacteraceae	Other
																										2.11					Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Rosenbergiella
																											0.97				Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Asticcacaulis
													0.96																		Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Pantoea
									0.68																						Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Filimonas
																				0.46											Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Roseimicrobium
																	0.39														Bacteria	Proteobacteria	Gammaproteobacteria	Unclassified order	Unclassified family	Thiohalobacter
													0.36																		Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Kosakonia
		0.35																													Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Dendrosporobacter
																	0.34														Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Luteolibacter
						0.33																									Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Pseudocitrobacter
														0.25																	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
																											0.24				Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Niabella
									0.20																						Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Providencia
	0.15																														Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Micrococcineae	Promicromonospora
													0.14																		Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Oxalicibacterium
																									0.13						Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Other
																													0.12		Bacteria	Firmicutes	Clostridia	Clostridiales	Gracilibacteraceae	Gracilibacter
																												0.10			Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Elizabethkingia
																							0.10								Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	Methylovorus
								0.09																							Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Frankineae	Modestobacter
								0.09																							Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales incertae sedis	Anaerovorax
				0.09																											Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Micrococcineae	Sanguibacter
										0.08																					Bacteria	Proteobacteria	Gammaproteobacteria	Aeromonadales	Aeromonadaceae	Aeromonas
	0.08																														Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	unclassified Burkholderiales	Mitsuaria
																										0.07					Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas
									0.07																						Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales incertae sedis	Thermaerobacter
									0.07																						Bacteria	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Aquisphaera
					0.07																										Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Other	Other
						0.07																									Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Aurantimonadaceae	Martelella
						0.07																									Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Alkanindiges
																	0.05														Bacteria	Actinobacteria	Rubrobacteridae	Gaiellales	Gaiellaceae	Gaiella
																	0.05														Bacteria	Armatimonadetes	Armatimonadia	Armatimonadales	Armatimonadaceae	Armatimonas
																											0.04				Bacteria	Actinobacteria	Acidimicrobidae	Acidimicrobiales	Other	Other
																											0.04				Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Micrococcineae	Arthrobacter
																											0.04				Bacteria	Actinobacteria	Rubrobacteridae	Solirubrobacterales	Solirubrobacteraceae	Solirubrobacter
																											0.04				Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Niastella
																											0.04				Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Terrimonas
																											0.04				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Brucellaceae	Brucella
																														0.04	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	unclassified Rhizobiales	Vasilyevaea
												0.04																			Bacteria	Chloroflexi	Thermomicrobia	Thermomicrobiales	Other	Other
																										0.04					Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Adhaeribacter
																										0.04					Bacteria	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Schlesneria
																										0.04					Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Acidiphilium
																										0.04					Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Other
																		0.04													Bacteria	Acidobacteria	Acidobacteriia	Acidobacteriales	Acidobacteriaceae	Candidatus Koribacter
																		0.04													Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Rhodoplanes
																		0.04													Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Ramlibacter
																		0.04													Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	unclassified Burkholderiales	Thiobacter
																		0.04													Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Raoultella
															0.04																Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Kineosporiineae	Kineosporia
															0.04																Bacteria	Chloroflexi	Anaerolineae	Anaerolineales	Other	Other
															0.04																Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	unclassified Rhizobiales	Nordella
															0.04																Bacteria	Proteobacteria	Alphaproteobacteria	Rhodothalassiales	Rhodothalassiaceae	Other
																					0.03										Bacteria	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas
																					0.03										Bacteria	Spirochaetes	Spirochaetia	Spirochaetales	Other	Other
																												0.03			Bacteria	Proteobacteria	Gammaproteobacteria	unclassified Gammaproteob	Unclassified family	Acidibacter
																				0.03											Bacteria	Acidobacteria	Solibacteres	Solibacterales	Solibacteraceae	Candidatus Solibacter
																				0.03											Bacteria	Aquificae	Aquificae	Aquificales	Other	Other
																				0.03											Bacteria	Chloroflexi	Thermoflexia	Thermoflexales	Other	Other
																				0.03											Bacteria	Dictyoglomi	Dictyoglomia	Dictyoglomales	Other	Other
																				0.03											Bacteria	Planctomycetes	Phycisphaerae	Phycisphaerales	Phycisphaeraceae	Other
																				0.03											Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Other	Other
																				0.03											Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Kaistia
																				0.03											Bacteria	Proteobacteria	Alphaproteobacteria	Sneathiellales	Other	Other
																				0.03											Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Cronobacter
																				0.03											Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Other	Other
																													0.03		Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Phaseolibacter
																0.03															Bacteria	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Other	Other
																	0.02														Archaea	Euryarchaeota	Halobacteria	Halobacteriales	Halobacteriaceae	Halonotius
																	0.02														Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Other	Other
																	0.02														Bacteria	Actinobacteria	Rubrobacteridae	Solirubrobacterales	Conexibacteraceae	Other
																	0.02														Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Flavisolibacter
																	0.02														Bacteria	Deinococcus-Thermus	Deinococci	Deinococcales	Deinococcaceae	Deinococcus
																	0.02														Bacteria	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Other
																	0.02														Bacteria	Firmicutes	Clostridia	Thermoanaerobacterales	Thermoanaerobacterales Fa	Other
																	0.02														Bacteria	Firmicutes	Thermolithobacteria	Thermolithobacterales	Thermolithobacteraceae	Other
																	0.02														Bacteria	Firmicutes	unclassified Firmicutes sen	Unclassified order	Other	Other
																	0.02														Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylorosula
																	0.02														Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Azoarcus
																	0.02														Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Pelobacteraceae	Other
																	0.02														Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Other	Other
																	0.02														Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Escherichia
																	0.02														Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Other
																	0.02														Bacteria	unclassified Bacteria	candidate division NC10	Unclassified order	Unclassified family	Other

Supplementary Figure S5: Abundance and distribution of all genera found in soybean root-associated samples by pyrotags. All root-associated sequences were taxonomically assigned by BLASTN against NCBI 16S rRNA and were classified to genus (>90% similarity to best-hit), family or order (depending on the case for hits <90% similarity to best-hit). Sequences were grouped by sample, site and classification and relative abundances were calculated according to total number of sequences per sample. Color scales indicate the relative abundances, with a gradual transition between green (high abundant) to red (low abundant).

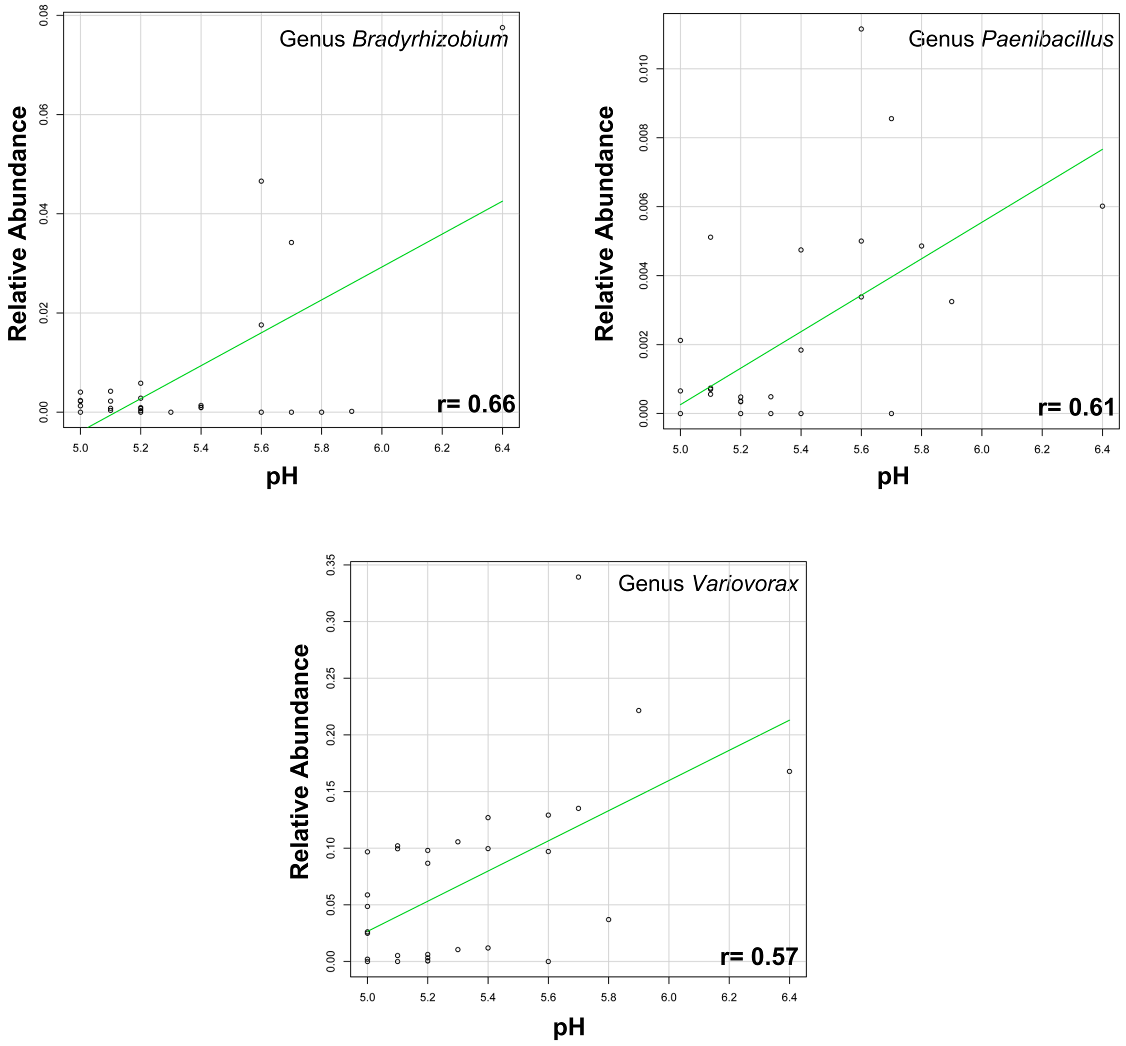
Wheat root-associated bacteria observed by pyrotags

Site																								Taxonomy					
Balcarce						Corral de Bustos						Daireaux						Villa Saboya						Domain	Phylum	Class	Order	Family	Genus
0.33	0.18	0.43	0.36	1.34		0.30	0.20	0.30	1.40	0.72	0.24	18.26	0.66	0.27	0.07	0.36	0.14	10.56	23.30	0.60	13.79	0.22	6.48	Bacteria	Verrucomicrobia	Spartobacteria	Unclassified order	Unclassified family	Chthoniobacter
	0.96	4.07	68.67	0.89	85.41		0.05		6.76	0.36	27.02	21.90	80.73	96.78	86.96	58.20	0.07	10.64	2.06	22.93	1.07	87.55	2.66	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
0.33	0.11	0.43	0.12	0.15	0.16			0.10	1.26	0.24		0.19	0.36	0.18	0.04	0.84	0.43	6.68	7.28	0.45	17.24	0.15	6.03	Bacteria	Planctomycetes	Planctomycetia	Planctomycetales	Other	Other
0.11	0.32			0.97		0.30	0.25	0.45	1.55	0.48	0.24	0.06	0.24				0.22	6.09	5.70		2.79	0.04	6.58	Bacteria	Acidobacteria	unclassified Acidobacteria	Acidobacteria subdivision 4	Unclassified family	Blastocatella
	0.07	0.21		0.15			0.05	0.10	0.81	0.12	0.16			0.59	4.73		0.29	7.19	4.13	62.75	0.90		5.02	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus
52.86	0.02	0.64	2.28		2.46				0.11			0.68	0.30			9.02	74.52	1.83	0.12		0.82	0.04	0.10	Bacteria	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Singulisphaera
0.11	7.37	8.57	0.84		0.66	0.15					0.97	0.43		1.54		1.47		0.29	0.24	0.60	0.08		0.35	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia
1.98	41.11	25.27	1.68		7.70				1.07		6.13	1.11	6.68		0.11	2.27		0.88		0.30			0.05	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Rhizobium
0.22		0.86	0.12	0.22				0.15	0.41		0.16	0.19		0.05					8.74	1.06	8.37		5.27	Bacteria	Acidobacteria	unclassified Acidobacteria	Acidobacteria subdivision 4	Unclassified family	Other
	0.27	0.21	5.40				0.05		1.00			0.49	0.06	0.05		0.04		0.44	3.64		5.50		1.56	Bacteria	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Other
2.31			0.60	1.19					0.04			0.06			0.11		1.79	5.72	0.12	1.36		8.71	4.67	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella
	0.02							0.10	2.18		0.40	0.74	0.30	0.05		0.18		1.61	2.43			0.11	0.15	Bacteria	Planctomycetes	Phycisphaerae	Phycisphaerales	Other	Other
8.68	1.00	9.42			1.48	5.51	0.50				0.08	0.19	7.65			0.44	8.40							Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Streptosporangiaceae	Microbispora
	1.46						41.15				0.56	0.12	1.26	0.41	0.32	0.27	0.07							Bacteria	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Paenibacillus
0.11	0.09	0.21										0.37				0.09		0.07	2.79		1.81		3.77	Bacteria	Firmicutes	Clostridia	Clostridiales	Other	Other
0.11		0.21		0.15		0.15		0.05	0.33							0.09			2.43			0.19		Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Other
0.22			0.36					0.10				0.12							1.70	0.45	4.35		3.87	Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	Other
0.44				0.30					0.07			6.05		0.09				0.22	0.36	0.45				Bacteria	Firmicutes	Bacilli	Bacillales	Other	Other
15.05		38.54	4.56						78.84		14.44							0.44					0.05	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
1.98	24.25		0.84												6.65			0.07		0.15	0.08			Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Caulobacter
	0.07		0.12	0.37														2.64	3.16			0.04	0.15	Bacteria	Chloroflexi	Thermomicrobia	Sphaerobacterales	Other	Other
													0.06				0.22	0.44	1.09		1.15	0.07	3.01	Bacteria	Chloroflexi	Thermomicrobia	Sphaerobacterales	Sphaerobacteraceae	Other
0.77	1.41	2.78	0.36													0.18		0.37			0.16			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium
0.22				0.30							0.24				0.14	0.04				0.15			4.17	Bacteria	Chloroflexi	Caldilineae	Caldilineales	Other	Other
	0.57	0.64											0.24				0.29	0.81		0.45			0.10	Bacteria	Proteobacteria	Gammaproteobacteria	Thiotrichales	Other	Other
	0.16					0.45			0.33			0.12	0.06						0.61	1.36				Archaea	Thaumarchaeota	Nitrososphaerales	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera
	0.16			0.52		6.41	0.81										7.61	0.22						Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Thermomonosporaceae	Actinoallomurus
5.93	2.56		1.44									0.93						0.51	0.12					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	Mesorhizobium
2.42	2.87	0.86	0.12													0.13							0.05	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Dongia
	0.05			0.07								0.19					0.14				3.78		0.10	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Other	Other
	0.02	0.86	0.24		0.49											0.04	0.65							Bacteria	Actinobacteria	Rubrobacteridae	Solirubrobacterales	Solirubrobacteraceae	Solirubrobacter
0.22			0.48		0.82								0.06			0.67							0.05	Bacteria	Actinobacteria	Rubrobacteridae	Solirubrobacterales	Conexibacteraceae	Conexibacter
		0.43		0.15												0.09		0.07				0.11	0.05	Bacteria	Verrucomicrobia	Spartobacteria	Unclassified order	Unclassified family	Other
0.11	0.14	0.21							0.07	0.24	0.08													Bacteria	Chloroflexi	Chloroflexia	Chloroflexales	Other	Other
									0.33	97.35	0.08							0.15			0.08			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Ralstonia
				84.04	0.16													1.61	1.94				2.11	Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Streptomycetaceae	Streptomyces
	0.07			0.07			56.38				7.66					0.04								Bacteria	Firmicutes	Negativicutes	Selenomonadales	Other	Other
				0.22		0.30						25.85				0.04			0.73					Bacteria	Chloroflexi	Ktedonobacteria	Ktedonobacterales	Ktedonobacteraceae	Other
					0.16							14.31						0.37		0.15		0.04		Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Other	Other
	2.65		6.36	0.52								2.71				0.04								Bacteria	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Aquisphaera
											0.65							8.14	0.49	0.90			0.50	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Duganella
									0.55							0.04					8.13	0.04	0.10	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Prosthecobacter
										0.12					0.04			1.39			0.08		4.22	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Variovorax
												0.12	0.06					1.61	1.58				0.55	Bacteria	Cyanobacteria	Oscillatoriophycideae	Oscillatoriales	Unclassified family	Other
0.33	1.71	1.28										0.12				0.13								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Tardiphaga
											0.08					0.04		0.37	0.36				0.45	Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Other	Other
			0.72								30.00	0.25						0.29						Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Dyella
			1.44	0.22														0.07					23.86	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Serratia
		1.93									2.66							1.32				2.30		Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Herbaspirillum
			0.12															4.11	0.24				0.05	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Pantoea
																0.04	0.14		2.31				1.56	Bacteria	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae	Other
												0.06						0.07	1.46				0.10	Bacteria	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Bythopirellula
								0.05							0.07			1.03					0.20	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia
						0.15						0.12						0.95			0.08			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium
			0.96									0.06	0.12			0.04								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Pseudolabrys
	0.05								0.04									0.07		0.60				Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Chryseobacterium
			0.24				0.05													0.15	0.25			Bacteria	Armatimonadetes	Armatimonadia	Armatimonadales	Armatimonadaceae	Armatimonas
	0.05																	0.07		0.30	0.08			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Delftia
	0.05			0.07												0.09	0.22							Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Mycobacteriaceae	Mycobacterium
0.88						84.35					4.27													Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Mucilaginibacter
																		5.72			5.50	0.07		Bacteria	Chloroflexi	Caldilineae	Caldilineales	Caldilineaceae	Other
	7.03											0.68				0.09								Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Micromonosporaceae	Dactylosporangium
		0.21																			3.45		0.05	Bacteria	Chloroflexi	Ktedonobacteria	Ktedonobacterales	Other	Other
	0.02				0.33														2.91					Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Cystobacteraceae	Other
			0.12									0.19				1.95								Bacteria	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Other
													0.18		0.04								1.26	Bacteria	Firmicutes	Bacilli	Bacillales	Listeriaceae	Other
				0.07														0.59					0.65	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Flavobacterium
									0.33										0.85			0.04		Bacteria	Verrucomicrobia	Spartobacteria	Unclassified order	Other	Other
																0.09	0.07	0.88						Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Rickettsiales genera incertae	Other
									0.04			0.74						0.07						Bacteria	Proteobacteria	Gammaproteobacteria	Unclassified order	Unclassified family	Acidibacter
			0.48			0.15						0.19												Bacteria	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas
	0.50											0.12					0.14							Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Micromonosporaceae	Rugosimonospora
						0.30						0.06					0.36							Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Thermomonosporaceae	Actinomadura
															0.04				0.36	0.30				Bacteria	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Blastopirellula
	0.16																	0.15					0.20	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Other	Other
											0.24	0.19					0.07							Bacteria	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Cohnella
				0.07					0.26												0.16			Bacteria	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	Other
							0.05											0.29					0.05	Bacteria	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Other	Other
	0.05					0.15													0.12					Bacteria	Synergistetes	Synergistia	Synergistales	Other	Other
	0.02										0.08												0.20	Bacteria	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bdellovibrionaceae	Other
								0.05	0.15													0.04		Bacteria	Chloroflexi	Chloroflexia	Chloroflexales	Chloroflexaceae	Chloroflexus
									0.04		0.08						0.07							Bacteria	Chloroflexi	Anaerolineae	Anaerolineales	Other	Other
	0.02																		0.12			0.04		Bacteria	Firmicutes	Bacilli	Bacillales	Thermoactinomycetaceae	Other
												0.19				21.01								Bacteria	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Gemmata
				6.26									0.06											Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium
																					4.93		0.05	Bacteria	Acidobacteria	Solibacteres	Solibacterales	Solibacteraceae	Candidatus Solibacter
																					4.19		0.20	Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Other
									0.04														4.07	Bacteria	Firmicutes	Clostridia	Thermoanaerobacterales	Other	Other
																					3.20		0.05	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Other
													0.18						2.79					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhodobiaceae	Other
0.33																	2.58							Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	Legionella
																					2.63		0.25	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Undibacterium
						0.30																	2.01	Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Other	Other
																		1.39	0.73					Archaea	Euryarchaeota	Halobacteria	Halobacteriales	Halobacteriaceae	Halorubrum
												0.68				1.33								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Azospirillum
																		1.47					0.05	Bacteria	Proteobacteria	Gammaproteobacteria	Aeromonadales	Aeromonadaceae	Aeromonas
		1.28	0.12																					Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Inquilinus
																		0.15					1.21	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Cupriavidus
1.21												0.06												Bacteria	Acidobacteria	Acidobacteriia	Acidobacteriales	Acidobacteriaceae	Edaphobacter
												0.06							0.85					Bacteria	Firmicutes	Clostridia	Thermoanaerobacterales	Thermoanaerobacteraceae	Other
																		0.29		0.60				Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomonas
						0.60										0.22								Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Microbacteriaceae	Leifsonia
															0.36					0.45				Archaea	Euryarchaeota	Halobacteria	Halobacteriales	Halobacteriaceae	Halonotius
				0.37						0.36										0.15				Archaea	Euryarchaeota	Halobacteria	Halobacteriales	Halobacteriaceae	Halolamina
0.55																								Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingobium
0.66															0.04									Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	Marinobacterium
																		0.07	0.61					Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	unclassified Burkholderiales	Burkholderiales Genera
			0.48		0.16																			Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Chondromyces
0.55																		0.07						Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium
	0.02								0.59															Bacteria	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Other
							0.20				0.40													Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Streptosporangiaceae	Streptosporangium
				0.45			0.15																	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	Other
																		0.51					0.05	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Curvibacter
			0.12						0.41															Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Geodermatophilaceae	Modestobacter
				0.22																0.30				Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales	Other	Other
												0.06								0.45				Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Other	Other
	0.21								0.30															Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Other	Other
																		0.37					0.05	Bacteria	Cyanobacteria	Oscillatoriophycideae	Oscillatoriales	Other	Other
	0.14	0.21																						Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Brucellaceae	Ochrobactrum
													0.18					0.15						Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	unclassified Burkholderiales	Sphaerotilus
	0.25																	0.07						Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Streptosporangiaceae	Nonomuraea
0.11													0.18											Bacteria	Chloroflexi	Dehalococcoidia	Unclassified order	Other	Other
											0.24											0.04		Bacteria	Chloroflexi	Thermoflexia	Thermoflexales	Other	Other
	0.11								0.15															Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Vulgatibacteraceae	Other
												0.06											0.15	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Bosea
												0.06											0.15	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Other
													0.06							0.15				Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Salmonella
				0.15									0.06											Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Escherichia
																		0.15					0.05	Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Chitinophaga
			0.12						0.07															Bacteria	unclassified Bacteria	Unclassified Class	Unclassified order	Unclassified family	Other
											0.08											0.11		Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Other	Other
							0.10				0.08													Bacteria	Tenericutes	Mollicutes	Acholeplasmatales	Acholeplasmataceae	Other
								0.05				0.12												Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	unclassified Rhizobiales	Other
	0.11																					0.04		Bacteria	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Pirellula
													0.06								0.08			Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Other	Other
	0.02														0.11									Bacteria	Actinobacteria	Rubrobacteridae	Solirubrobacterales	Conexibacteraceae	Other
																		0.07					0.05	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Other
																		0.07					0.05	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Pelomonas
																0.04		0.07						Bacteria	Proteobacteria	Gammaproteobacteria	Thiotrichales	Piscirickettsiaceae	Other
																0.04							0.05	Bacteria	Proteobacteria	Gammaproteobacteria	Chromatiales	Chromatiaceae	Other
															0.04								0.05	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Rugamonas
								98.50																Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Micrococcineae	Curtobacterium
																			4.85					Bacteria	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Zavarzinella
																					4.35			Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	Desulfomonile
																			3.52					Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Microbacteriaceae	Salinibacterium
																		3.45						Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter
																		2.64						Archaea	Thaumarchaeota	Nitrososphaerales	Nitrososphaerales	Nitrososphaeraceae	Other
											2.26													Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Rhodanobacter
																			1.94					Bacteria	Thermotogae	Thermotogae	Thermotogales	Other	Other
																	0.93							Bacteria	Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	Other
	0.75																							Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Streptosporangiaceae	Sphaerisporangium
																		0.73						Bacteria	Proteobacteria	Gammaproteobacteria	Thiotrichales	Piscirickettsiaceae	Thiomicrospira
																				0.60				Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Lysinibacillus
0.55																								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Rhodopila
																			0.49					Bacteria	Chloroflexi	Dehalococcoidia	Unclassified order	Unclassified family	Other
																	0.43							Bacteria	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Other	Other
																					0.41			Archaea	Euryarchaeota	Methanomicrobia	Methanosarcinales	Methanosaetaceae	Methanosaeta
									0.41															Bacteria	Proteobacteria	Epsilonproteobacteria	Nautiliales	Other	Other
												0.37												Bacteria	Proteobacteria	Gammaproteobacteria	Chromatiales	Ectothiorhodospiraceae	Other
																			0.36					Bacteria	Chloroflexi	Caldilineae	Caldilineales	Caldilineaceae	Caldilinea
0.33																								Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter
																					0.33			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Rhodoplanes
											0.32													Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Luteibacter
																				0.30				Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Micrococcaceae	Arthrobacter
																				0.30				Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Xanthomonas
				0.30																				Bacteria	unclassified Bacteria	candidate division NC10	Unclassified order	Unclassified family	Other
						0.30																		Bacteria	Firmicutes	Clostridia	Halanaerobiales	Halobacteroidaceae	Natroniella
																							0.25	Bacteria	Firmicutes	Clostridia	Clostridiales	Symbiobacteriaceae	Other
	0.23																							Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales Family XVII. Inc	Other
	0.23																							Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Labrys
	0.23																							Bacteria	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Pelobacteraceae	Other
																		0.22						Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Pseudoduganella
																		0.22						Bacteria	Proteobacteria	Gammaproteobacteria	Chromatiales	Other	Other
		0.21																						Bacteria	Firmicutes	Clostridia	Clostridiales	Syntrophomonadaceae	Other
												0.19												Bacteria	Chloroflexi	Ktedonobacteria	Ktedonobacterales	Ktedonobacteraceae	Ktedonobacter
																				0.15				Archaea	Euryarchaeota	Halobacteria	Halobacteriales	Halobacteriaceae	Halohasta
																				0.15				Bacteria	Actinobacteria	Thermoleophilia	Thermoleophilales	Thermoleophilaceae	Other
																				0.15				Bacteria	Chloroflexi	Chloroflexia	Chloroflexales	Oscillochloridaceae	Oscillochloris
																				0.15				Bacteria	Firmicutes	Clostridia	Halanaerobiales	Halanaerobiaceae	Halanaerobium
																				0.15				Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Megasphaera
																				0.15				Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Other	Other
																				0.15				Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	Achromobacter
																				0.15				Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Acidovorax
																							0.15	Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Flavisolibacter
																							0.15	Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Niastella
																							0.15	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
				0.15																				Bacteria	unclassified Bacteria	Unclassified Class	Unclassified order	Other	Other
						0.15																		Bacteria	Chloroflexi	Thermomicrobia	Sphaerobacterales	Sphaerobacteraceae	Sphaerobacter
																	0.14							Bacteria	Armatimonadetes	Armatimonadia	Armatimonadales	Armatimonadaceae	Other
																0.13								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Niveispirillum
																			0.12					Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Pseudonocardiaceae	Amycolatopsis
																			0.12					Bacteria	Firmicutes	Clostridia	Halanaerobiales	Other	Other
																			0.12					Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	unclassified Burkholderiales	Aquabacterium
			0.12																					Bacteria	Acidobacteria	Acidobacteriia	Acidobacteriales	Acidobacteriaceae	Other
																							0.10	Bacteria	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Alterococcus
																0.09								Bacteria	Actinobacteria	Rubrobacteridae	Solirubrobacterales	Solirubrobacteraceae	Other
																					0.08			Bacteria	Actinobacteria	Rubrobacteridae	Gaiellales	Gaiellaceae	Gaiella
																					0.08			Bacteria	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	Other
											0.08													Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Pseudonocardiaceae	Pseudonocardia
																		0.07						Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Sphingobacterium
																		0.07						Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium
																		0.07						Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Limnohabitans
																		0.07						Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Polaromonas
																		0.07						Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Collimonas
																		0.07						Bacteria	Proteobacteria	Betaproteobacteria	Neisseriales	Chromobacteriaceae	Paludibacterium
																		0.07						Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Labilitrichaceae	Labilithrix
																		0.07						Bacteria	Proteobacteria	Gammaproteobacteria	Orbales	Orbaceae	Other
																		0.07						Bacteria	Proteobacteria	Gammaproteobacteria	unclassified Gammaproteob	Unclassified family	Other
															0.07									Archaea	Euryarchaeota	Thermoplasmata	Thermoplasmatales	Other	Other
												0.06												Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Micromonosporaceae	Salinispora
												0.06												Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Byssovorax
												0.06												Bacteria	Verrucomicrobia	unclassified Verrucomicrobia	Unclassified order	Other	Other
													0.06											Archaea	Euryarchaeota	Thermoplasmata	Methanomassiliicoccales	Other	Other
													0.06											Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Streptomycetaceae	Streptacidiphilus
													0.06											Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Caenimonas
																							0.05	Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Sporosarcina
																							0.05	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Afipia
																							0.05	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Comamonas
																							0.05	Bacteria	Synergistetes	Synergistia	Synergistales	Synergistaceae	Other
																							0.05	Bacteria	unclassified Bacteria	candidate division SR1	candidate division SR1 bact	Unclassified family	Unclassified genus
																0.04								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Rhizomicrobium
																						0.04		Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Sediminibacterium
									0.04															Bacteria	Acidobacteria	unclassified Acidobacteria	Acidobacteria subdivision 4	Other	Other
									0.04															Bacteria	Actinobacteria	Actinobacteridae	Actinomycetales	Microbacteriaceae	Herbiconiux
															0.04									Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Other
															0.04									Bacteria	Proteobacteria	Gammaproteobacteria	Legionellales	Coxiellaceae	Other
															0.04									Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Other	Other
	0.02																							Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Rufibacter
	0.02																							Bacteria	Firmicutes	unclassified Firmicutes sensu	Unclassified order	Unclassified family	Other
	0.02																							Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Ancylobacter

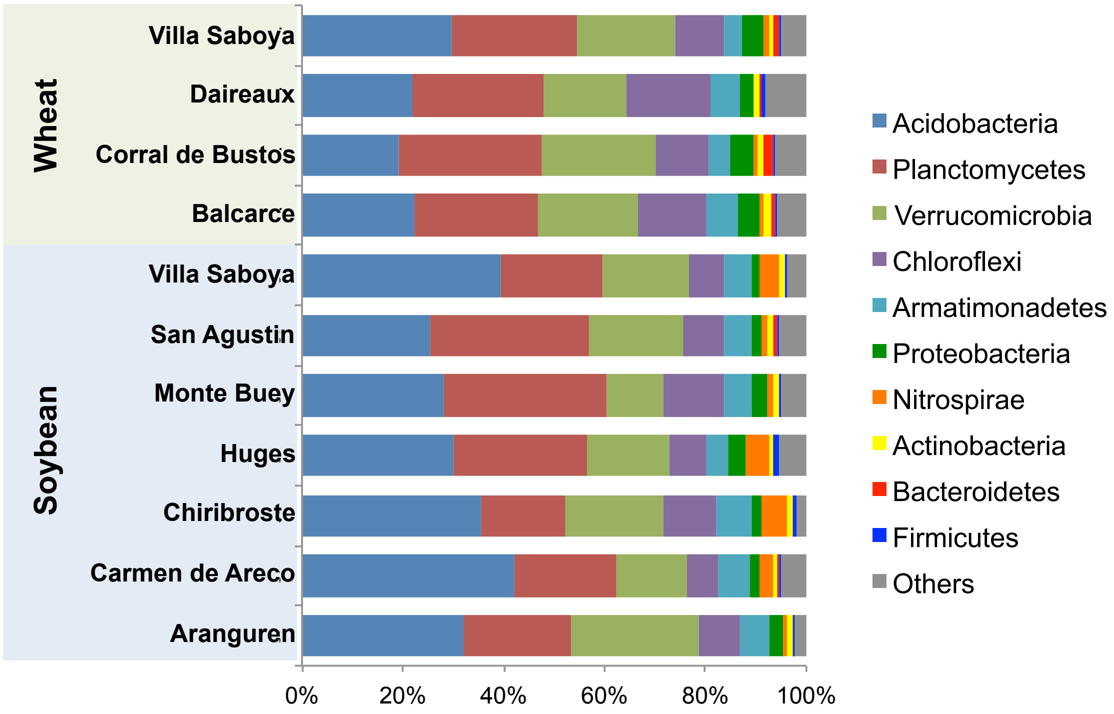
Supplementary Figure S6: Abundance and distribution of all genera found in wheat root-associated samples by pyrotags. All root-associated sequences were taxonomically assigned by BLASTN against NCBI 16S rRNA and were classified to genus (>90% similarity to best-hit), family or order (depending on the case for hits <90% similarity to best-hit). Sequences were grouped by sample, site and classification and relative abundances were calculated according to total number of sequences per sample. Color scales indicate the relative abundances, with a gradual transition between green (high abundant) to red (low abundant).



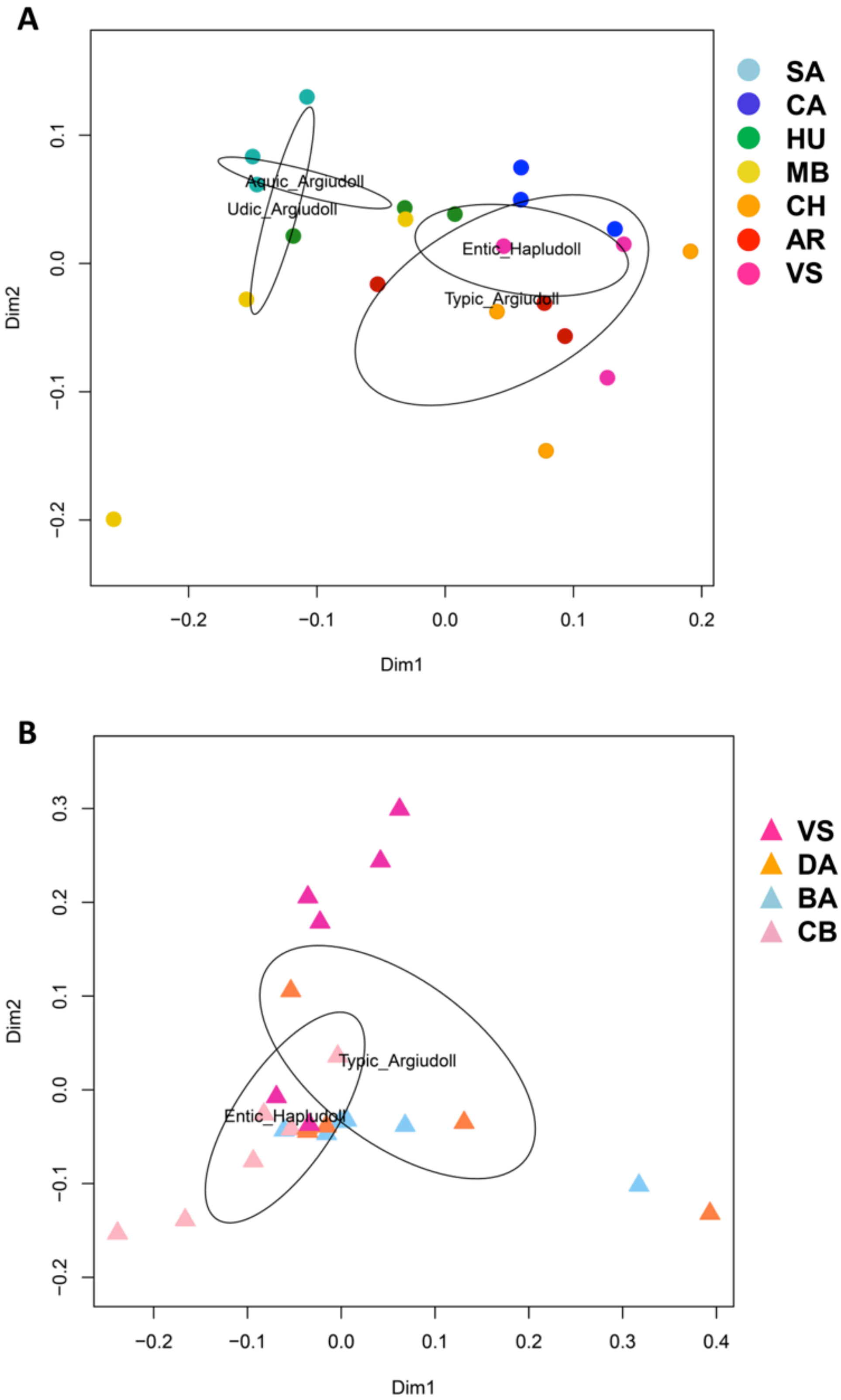
Supplementary Figure S7: Correlation between taxa abundances and soil characteristics. Significant Pearson correlations ($p \leq 0.05$) between relative abundances of Bacilli class and pH in soybean root-associated fraction (RA).



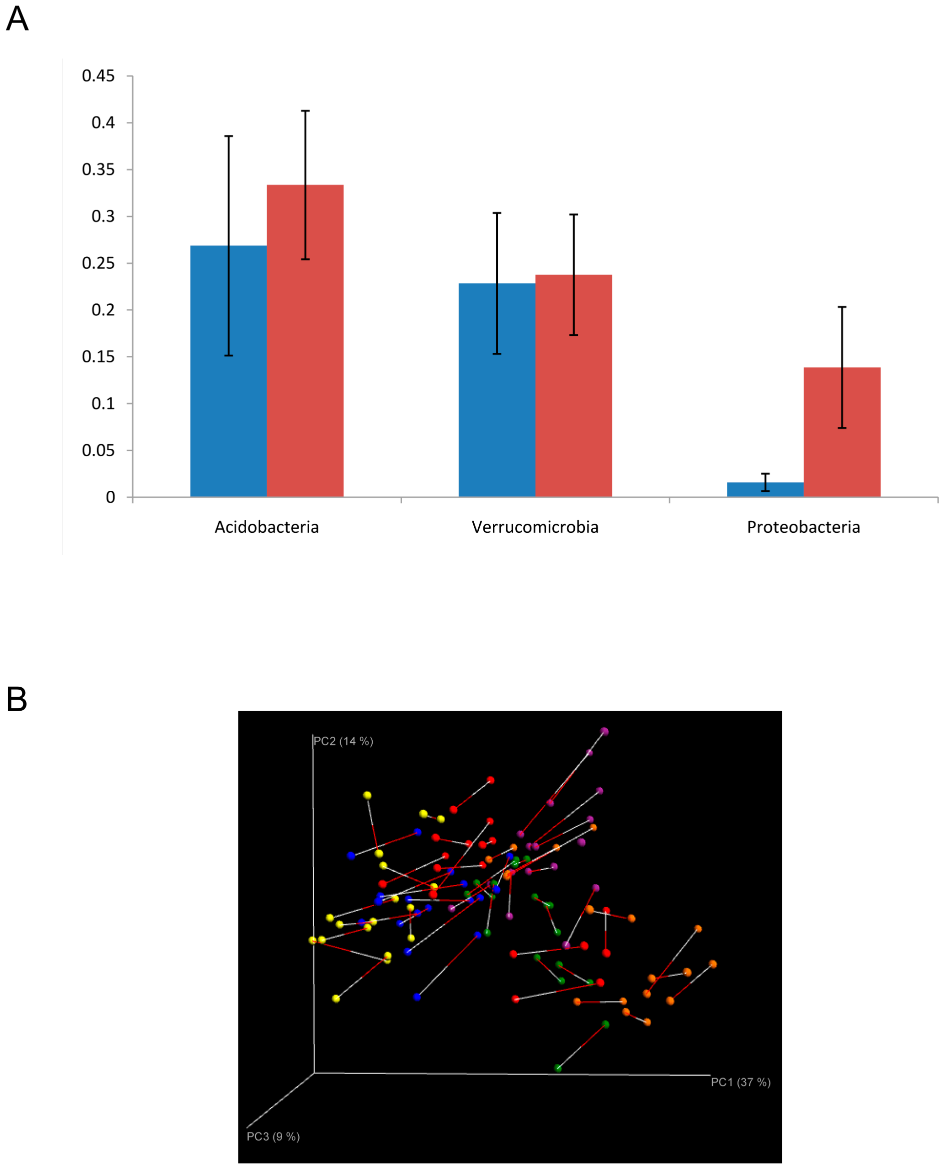
Supplementary Figure S8: Correlation between taxa abundances and soil characteristics. Significant Pearson correlations ($p \leq 0.05$) between relative abundances of taxa (Genus level) in soybean root-associated microbiomes and pH.



Supplementary Figure S9: Taxonomic classification of RS pyrotag datasets. Pyrotag sequences from rhizospheric soil samples were classified at the phylum level. Average values for each site and crop type are shown. An unexpected low abundance of Proteobacteria was observed in all samples and this result is discussed in *supplementary text*.



Supplementary Figure S10: **Principal Coordinate Analysis visualization based on weighted UniFrac distances.** Microbial community assemblies of soybean RS samples (A) and wheat RA samples (B) were significantly structured by soil type. The fitting of factors was done using factorfit() function in “vegan” R package using 100 permutations. Dispersion ellipses represent standard deviation of point scores for each type of soil. AR: Aranguren, CA: Carmen de Areco, CH: Chilibroste, HU: Huges, MB: Monte Buey, SA: San Agustin, VS: Villa Saboya, BA: Balcarce, CB: Corral de Bustos, DA: Daireaux



Supplementary Figure S11: F515-R806 vs. F563-R602 amplification primers. Differences in taxa abundances for external soil microbiome datasets amplified with 515F- 806R (blue bars) and 563F- 802R (red bars) tagged primers (A). External dataset were compared using Procrustes analyses of Principal Coordinate plots based on weighted UniFrac distances (B). Results indicated that beta diversity conclusions were highly reproducible ($p<0.0001$) regardless the primer sets used for amplification. This figure is discussed in *supplementary text*.

Location	Crop	Soil classification	pH	Nitrates (ppm)	Phosphorus (ppm)	Organic Matter (%)	Total Nitrogen (%)	Carbon (%)
Balcarce (BA)	Wheat	Typic Argiudoll	5.097	5.186	23.114	4.026	0.192	2.413
Daireaux (DA)	Wheat	Entic Hapludoll	4.996	5.514	17.300	1.126	0.120	0.650
San Jorge (SJ)	Wheat	Typic Argiudoll	6.143	2.286	33.486	2.520	0.126	1.444
Corral de Bustos (CB)	Wheat	Typic Argiudoll	5.829	5.786	35.429	2.614	0.130	1.506
	Soybean		5.267	3.067	16.300	2.267	0.112	1.307
Villa Saboya (VS)	Wheat	Entic Hapludoll	5.471	2.686	7.771	1.920	0.096	1.100
	Soybean		5.175	18.100	6.475	1.825	0.089	1.035
Monte Buey (MB)	Wheat	Typic Argiudoll	5.929	2.357	75.729	3.229	0.161	1.829
	Soybean		5.067	4.300	171.667	2.533	0.126	1.373
Aranguren (AR)	Soybean	Aquic Argiudoll	5.100	6.867	24.433	4.000	0.200	2.317
Carmen de Areco (CA)	Soybean	Typic Argiudoll	5.900	6.733	32.667	2.867	0.144	1.673
Chilibroste (CH)	Soybean	Udic Argiudoll	5.767	4.267	19.033	2.033	0.102	1.177
Hughes (HU)	Soybean	Typic Argiudoll	5.167	6.633	11.067	3.533	0.177	2.057
San Agustin (SA)	Soybean	Typic Argiudoll	5.167	4.033	25.933	5.117	0.255	3.053

Supplementary Table S1: Soil chemical characteristics from sampled sites. Chemical characteristics (mean) of soils in sampled sites.

(See Supplementary Comma separated file for Supplementary Table S2)

Supplementary Table S2: List of all isolates obtained in this study organized by crop and isolation strategy. The table includes also the assigned taxonomy, the results from PGP studies (when available) and the obtained 16S rRNA sequences.

	Type	Root-Associated bacteria	Rhizospheric soil			
	Growth condition	Nutritive broth	Sporulating	Cetrimide	NFB	Total
Crop	Site					
Wheat	Balcarce	73	82	9	94	258
	Corral de Bustos	77	64	0	42	183
	Daireaux	20	58	0	29	107
	Monte Buey	63	31	0	63	157
	San Jorge	18	5	0	45	68
	Villa Saboya	68	43	63	25	199
	Subtotal	319	283	72	298	972
Soybean	Aranguren	38	38	16	29	121
	Carmen de Areco	38	38	17	37	130
	Chilibroste	30	38	14	30	112
	Corral de Bustos	36	40	11	32	119
	Hughes	41	37	13	26	117
	Monte Buey	35	37	13	38	123
	San Agustin	38	31	13	30	112
	Villa Saboya	39	42	12	32	125
	Subtotal	295	301	109	254	959
	Total	614	584	181	552	1,931

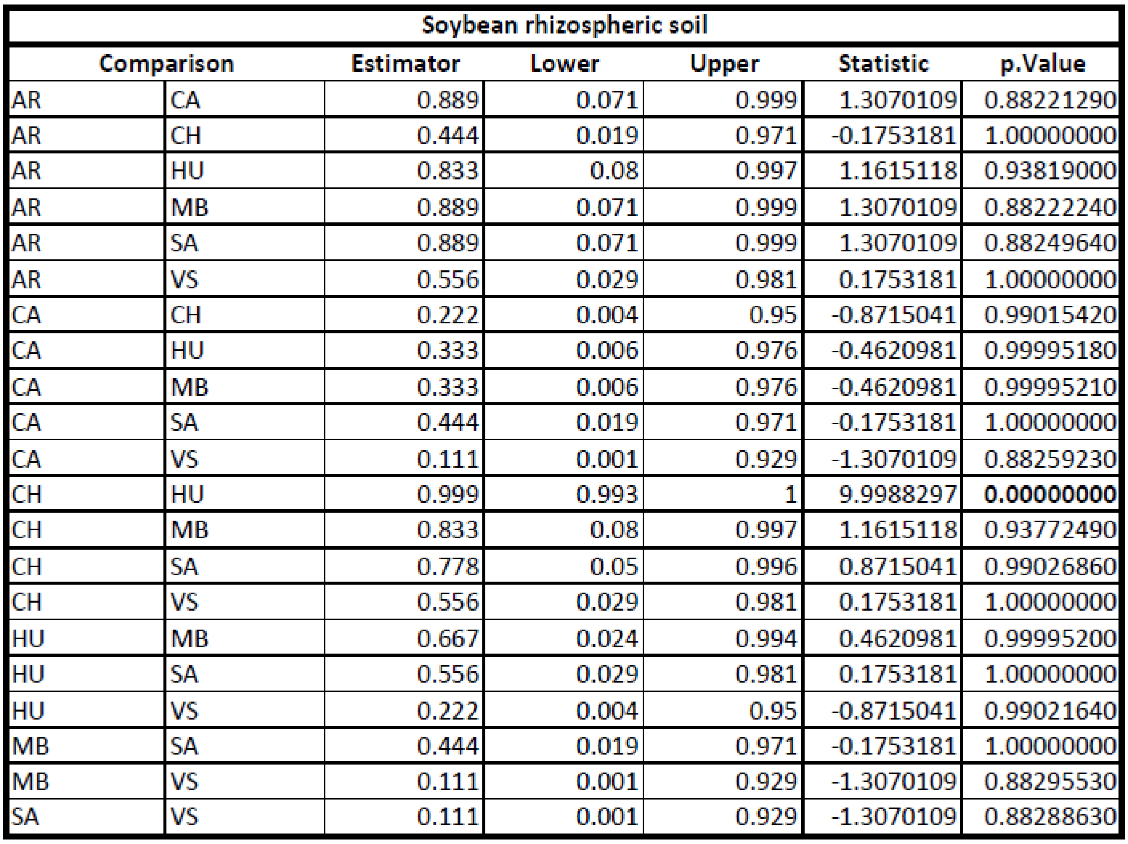
Supplementary Table S3: Number of isolates obtained by isolation strategy and crop.

Soybean Root Asociated

Comparison		Estimator	Lower	Upper	Statistic	p.Value
AR	CA	0.75	0.114	0.986	1.0422351	0.9931536
AR	CH	0.125	0.003	0.88	-1.4745567	0.8899356
AR	HU	0.999	0.994	1	11.5456541	**0.0000000**
AR	MB	0.562	0.062	0.962	0.2527084	1.0000000
AR	SA	0.906	0.163	0.998	1.7330537	0.7292847
AR	VS	0.844	0.151	0.994	1.4728405	0.8908373
CA	CH	0.001	0	0.006	-11.5456541	**0.0000000**
CA	HU	0.999	0.994	1	11.5456541	**0.0000000**
CA	MB	0.375	0.024	0.935	-0.478899	0.9999993
CA	SA	0.781	0.144	0.987	1.2436594	0.9677446
CA	VS	0.688	0.073	0.984	0.7077098	0.9998934
CH	HU	0.999	0.994	1	11.5456541	**0.0000000**
CH	MB	0.812	0.083	0.995	1.1302602	0.9856282
CH	SA	0.999	0.994	1	11.5456541	**0.0000000**
CH	VS	0.969	0.285	1	2.3523145	0.2677536
HU	MB	0.094	0.002	0.837	-1.7330537	0.7293153
HU	SA	0.125	0.003	0.88	-1.4745567	0.8901406
HU	VS	0.188	0.008	0.864	-1.3198596	0.9489530
MB	SA	0.75	0.104	0.987	1.0091398	0.9949752
MB	VS	0.688	0.091	0.98	0.7615348	0.9997497
SA	VS	0.469	0.046	0.942	-0.1280535	1.0000000

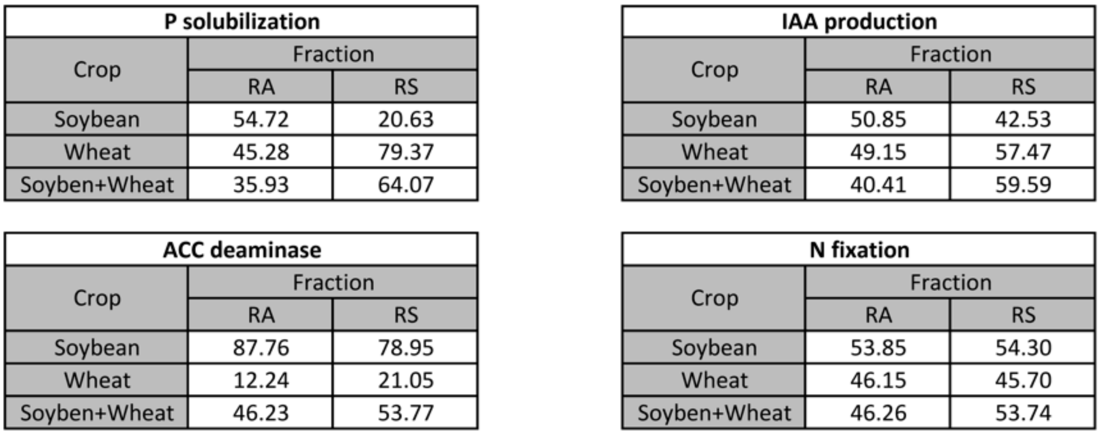
Wheat Root Asociated

Comparison		Estimator	Lower	Upper	Statistic	p.Value
BA	CB	0.236	0.029	0.763	-1.2416262	0.5830740
BA	DA	0.264	0.038	0.766	-1.1502104	0.6469206
BA	VS	0.833	0.203	0.99	1.3411983	0.5137551
CB	DA	0.569	0.167	0.897	0.3682761	0.9904195
CB	VS	0.833	0.203	0.99	1.3411983	0.5141363
DA	VS	0.847	0.227	0.991	1.4453134	0.4440308



Soybean rhizospheric soil						
Comparison		Estimator	Lower	Upper	Statistic	p.Value
AR	CA	0.889	0.071	0.999	1.3070109	0.88221290
AR	CH	0.444	0.019	0.971	-0.1753181	1.00000000
AR	HU	0.833	0.08	0.997	1.1615118	0.93819000
AR	MB	0.889	0.071	0.999	1.3070109	0.88222240
AR	SA	0.889	0.071	0.999	1.3070109	0.88249640
AR	VS	0.556	0.029	0.981	0.1753181	1.00000000
CA	CH	0.222	0.004	0.95	-0.8715041	0.99015420
CA	HU	0.333	0.006	0.976	-0.4620981	0.99995180
CA	MB	0.333	0.006	0.976	-0.4620981	0.99995210
CA	SA	0.444	0.019	0.971	-0.1753181	1.00000000
CA	VS	0.111	0.001	0.929	-1.3070109	0.88259230
CH	HU	0.999	0.993	1	9.9988297	**0.00000000**
CH	MB	0.833	0.08	0.997	1.1615118	0.93772490
CH	SA	0.778	0.05	0.996	0.8715041	0.99026860
CH	VS	0.556	0.029	0.981	0.1753181	1.00000000
HU	MB	0.667	0.024	0.994	0.4620981	0.99995200
HU	SA	0.556	0.029	0.981	0.1753181	1.00000000
HU	VS	0.222	0.004	0.95	-0.8715041	0.99021640
MB	SA	0.444	0.019	0.971	-0.1753181	1.00000000
MB	VS	0.111	0.001	0.929	-1.3070109	0.88295530
SA	VS	0.111	0.001	0.929	-1.3070109	0.88288630

Supplementary Table S4: Tukey non-parametric Test was used to compare OUT richness between pairs of sampled sites: AR: Aranguren, CA: Carmen de Areco, CH: Chilibroste, HU: Huges, MB: Monte Buey, SA: San Agustin, VS: Villa Saboya, BA: Balcarce, CB: Corral de Bustos, DA: Daireaux.



P solubilization		
Crop	Fraction	
	RA	RS
Soybean	54.72	20.63
Wheat	45.28	79.37
Soyben+Wheat	35.93	64.07

IAA production		
Crop	Fraction	
	RA	RS
Soybean	50.85	42.53
Wheat	49.15	57.47
Soyben+Wheat	40.41	59.59

ACC deaminase		
Crop	Fraction	
	RA	RS
Soybean	87.76	78.95
Wheat	12.24	21.05
Soyben+Wheat	46.23	53.77

N fixation		
Crop	Fraction	
	RA	RS
Soybean	53.85	54.30
Wheat	46.15	45.70
Soyben+Wheat	46.26	53.74

Supplementary Table S5: Relative abundance of PGP traits positive isolates by fraction and crop. Results are indicated as percentages (%).

Scripts used:

Here we list the scripts and commands used to analyze DNA sequencing data. The filename used for each script (in bold and underline) is followed by the content of each script. QIIME mapping file is listed at the end of the list.

scripts_and_commands_used.sh

```
#!/bin/bash


# Quality filtering, denoising, chimera checking and sequence split by barcode

ampliconnoise.py -i ../00_Rawdata/H7M6N7102_run73.sff.txt -o run1_amp_noi.fna -m
mapping_run1_pool1.txt --seqnoise_resolution 25.0 -f --platform titanium
ampliconnoise.py -i ../00_Rawdata/IDC449H01_Run79.sff.txt -o run2_pool1_amp_noi.fna -m
mapping_run2_pool1.txt --seqnoise_resolution 25.0 -f --platform titanium
ampliconnoise.py -i ../00_Rawdata/IDC449H02_Run79.sff.txt -o run2_pool2_amp_noi.fna -m
mapping_run2_pool2.txt --seqnoise_resolution 25.0 -f --platform titanium

# Create Directories to compare each group of samples and for each analysis

mkdir 10_soybean_RA_RS
mkdir 11_wheat_RA_RS
mkdir 12_soybean_RA
mkdir 13_soybean_RS
mkdir 14_wheat_RA
mkdir 15_wheat_RS
mkdir 16_wheat_soybean_RA_RS
mkdir 17_wheat_soybean_RA
mkdir 20_RA_pyro_vs_isol


# Create Mapping files for each QIIME analysis

cat mapping_file.txt | awk -F\t '$16 != "Non"' > 10_soybean_RA_RS/mapping_file.txt
cat mapping_file.txt | awk -F\t '$17 != "Non"' > 11_wheat_RA_RS/mapping_file.txt
cat mapping_file.txt | awk -F\t '$18 != "Non"' > 12_soybean_RA/mapping_file.txt
cat mapping_file.txt | awk -F\t '$19 != "Non"' > 13_soybean_RS/mapping_file.txt
cat mapping_file.txt | awk -F\t '$20 != "Non"' > 14_wheat_RA/mapping_file.txt
cat mapping_file.txt | awk -F\t '$21 != "Non"' > 15_wheat_RS/mapping_file.txt
cat mapping_file.txt | awk -F\t '$22 != "Non"' > 16_wheat_soybean_RA_RS/mapping_file.txt
cat mapping_file.txt | awk -F\t '$23 != "Non"' > 17_wheat_soybean_RA/mapping_file.txt

# Filter full fasta file with selected sequences

filter_fasta.py -f all_sequences_qc_filtered.fna --mapping_fp 10_soybean_RA_RS/mapping_file.txt --
valid_states Folder10:10_soybean_RA_RS -o 10_soybean_RA_RS/seqs.fna
filter_fasta.py -f all_sequences_qc_filtered.fna --mapping_fp 11_wheat_RA_RS/mapping_file.txt --
valid_states Folder11:11_wheat_RA_RS -o 11_wheat_RA_RS/seqs.fna
filter_fasta.py -f all_sequences_qc_filtered.fna --mapping_fp 12_soybean_RA/mapping_file.txt --
valid_states Folder12:12_soybean_RA -o 12_soybean_RA/seqs.fna
filter_fasta.py -f all_sequences_qc_filtered.fna --mapping_fp 13_soybean_RS/mapping_file.txt --
valid_states Folder13:13_soybean_RS -o 13_soybean_RS/seqs.fna
```

```
filter_fasta.py -f all_sequences_qc_filtered.fna --mapping_fp 14_wheat_RA/mapping_file.txt --
valid_states Folder14:14_wheat_RA -o 14_wheat_RA/seqs.fna
filter_fasta.py -f all_sequences_qc_filtered.fna --mapping_fp 15_wheat_RS/mapping_file.txt --
valid_states Folder15:15_wheat_RS -o 15_wheat_RS/seqs.fna
filter_fasta.py -f all_sequences_qc_filtered.fna --mapping_fp 16_wheat_soybean_RA_RS/mapping_file.txt
--valid_states Folder16:16_wheat_soybean_RA_RS -o 16_wheat_soybean_RA_RS/seqs.fna
filter_fasta.py -f all_sequences_qc_filtered.fna --mapping_fp 17_wheat_soybean_RA/mapping_file.txt --
valid_states Folder17:17_wheat_soybean_RA -o 17_wheat_soybean_RA/seqs.fna

# Run QIIME analysis for all samples

for i in
{10_soybean_RA_RS,11_wheat_RA_RS,12_soybean_RA,13_soybean_RS,14_wheat_RA,15_wheat_RS,16_wheat_soybean
_RA_RS,17_wheat_soybean_RA}; do cd $i ; cp ../qiime_custom_pipeline.sh . ; cp
../custom_parameters.txt . ; sh qiime_custom_pipeline.sh 2> error.log; cd ..; done

# Trimming isolates Sanger sequences

blastn -task blastn -query all_seqs_raw.fna -db 16SMicrobial -max_target_seqs 1 -outfmt '6 qseqid
qlen length qseq' | tr -d '-' | awk '$3 >= 180' | awk '{print ">"$1" initial_length="$2"
trimmed_length="$3"\t"$4}' | tr '\t' '\n' | fold > all_isolates_seqs_trimmed.fna

# Classify sequences based on BlastN against NCBI
# (All pyrotags sequences and all isolates sequences, without clustering in OTU, were blasted with
this command.
# Classifications of representative sequences were retrieved from these results)

blastn -task blastn -query isolates_or_pyrotag_sequences.fna -db 16SMicrobial -max_target_seqs 1 -
evalue 1E-10 -outfmt '6 qseqid qstart qend qlen sseqid sstart send slen length pident evalue score
staxids stitle' -num_threads 5 -out sequences_vs_NCBI_16S.blastn

# Comparison between pyrotags sequences from Root-Associated samples (soybean 67,373 / wheat 38,870)
vs. all isolates sequences obtained (2007: 960 from soybean, 1047 from wheat).

makeblastdb -in all_isolates_both_crops.fna -dbtype nucl -parse_seqids

blastn -task blastn -query 12_soybean_RA/seqs.fna -db all_isolates_both_crops.fna -max_target_seqs 1
-evalue 1E-10 -outfmt '6 qseqid qstart qend qlen sseqid sstart send slen length pident evalue score'
-max_target_seqs 1 -num_threads 5 -out
20_RA_pyro_vs_isol/soybean_RA_vs_all_isolates_both_crops.blastn
blastn -task blastn -query 14_wheat_RA/seqs.fna -db all_isolates_both_crops.fna -max_target_seqs 1 -
evalue 1E-10 -outfmt '6 qseqid qstart qend qlen sseqid sstart send slen length pident evalue score' -
max_target_seqs 1 -num_threads 5 -out 20_RA_pyro_vs_isol/wheat_RA_vs_all_isolates_both_crops.blastn

OVER97WHEAT=`cat 20_RA_pyro_vs_isol/soybean_RA_vs_all_isolates_both_crops.blastn | awk '$9/$4 >= 0.8
&& $10 >= 97' | wc -l`
COUNTWHEAT=`cut -f 1 20_RA_pyro_vs_isol/soybean_RA_vs_all_isolates_both_crops.blastn | sort -u | wc -
l`
PERCOVER97=$(bc <<<"scale=3;$OVER97WHEAT/$COUNTWHEAT")

echo "Number of Wheat RA pyrotag sequences with over 97% similarity to best hit in isolates:
"$OVER97WHEAT
echo "Total number Wheat RA pyrotag sequences analyzed: "$COUNTWHEAT
echo "Percentage Wheat RA pyrotags with hits over 97% similarity to an isolate= 0"$PERCOVER97

OVER97SOYBEAN=`cat 20_RA_pyro_vs_isol/wheat_RA_vs_all_isolates_both_crops.blastn | awk '$9/$4 >= 0.8
&& $10 >= 97' | wc -l`
COUNTSOYBEAN=`cut -f 1 20_RA_pyro_vs_isol/wheat_RA_vs_all_isolates_both_crops.blastn | sort -u | wc -
l`
```

```
PERCOVER97=$(bc <<<"scale=3;$OVER97SOYBEAN/$COUNTSOYBEAN")

echo "Number of Soybean RA pyrotag sequences with over 97% similarity to best hit in isolates:
"$OVER97SOYBEAN
echo "Total number Soybean RA pyrotag sequences analyzed: "$COUNTSOYBEAN
echo "Percentage Soybean RA pyrotags with hits over 97% similarity to an isolate= 0"$PERCOVER97

# Calculate histograms for the distributions of weigthed Unifrac distances

        # 1) Retrieve the weigthed unifrac distances matrices from each of the 100 repetitions, keep
only the upper triangle (not including zeros at the diagonal) and put all the information in a single
file
for i in {12_soybean_RA,13_soybean_RS,14_wheat_RA,15_wheat_RS}; do for j in {0..99}; do NUMSAMP=`grep
-v '#' ${i}/mapping_*.txt | wc -l`; cat
${i}/97_percent_similarity/60_beta_diversity/weighted_unifrac/rare_dm/weighted_unifrac_rarefaction_40
0_${j}.txt | cut -f 2- | tail -n $NUMSAMP | awk '{for (i=1;i<=NF;i++) printf
"%s%s",(i>NR)?$i:"",FS="\t"; print""}' | tr '\t' '\n' | grep '.' | sort -n >>
${i}/values_WU_distances.txt; done; done
        # 2) Make histograms with values obtained from the 100 repetitions
for i in {12_soybean_RA,13_soybean_RS,14_wheat_RA,15_wheat_RS}; do awk -f histograms.awk 0 1 0.01
${i}/histogram_WU_distances.txt ${i}/values_WU_distances.txt; done
        # 3) Resulting tables are imported to Excel, abundances are transformed into relative values
and plotted
```

qiime_custom_pipeline.sh

```
#!/bin/bash

DIR="$( cd "$( dirname "$0" )" && pwd )"

LEVELS=97        #here other similarity levels may be selected

cd $DIR

echo -e "Step 0 - Determine MIN, MAX and NUM_SAMPLES values"
MIN=`cat seqs.fna | grep '>' | cut -f 1 -d '_' | sort | uniq -c | awk '{print $1}' | sort -n | head -
n 1`
MAX=`cat seqs.fna | grep '>' | cut -f 1 -d '_' | sort | uniq -c | awk '{print $1}' | sort -n | tail -
n 1`
NUM_SAMPLES=`cat seqs.fna | grep '>' | cut -f 1 -d '_' | sort | uniq -c | wc -l`

echo -e "\t\tMIN: $MIN"
echo -e "\t\tMAX: $MAX"
echo -e "\t\tNUM_SAMPLES: $NUM_SAMPLES"

# ### Cluster sequences in OTU and chose the representative sequence
echo -e "Step 1 - Cluster sequences in OTU and chose the representative sequences"
for i in $LEVELS
do
        echo -e "\tSIMILARITY: $i"
        SIM=${i}_percent_similarity
        mkdir -p $SIM/10_pick_otus/
        echo -e "\t\tStep 1.1 - Pick OTUs"
        pick_otus.py -i seqs.fna -s 0.${i} -m uclust -o $SIM/10_pick_otus/ -A
        echo -e "\t\tStep 1.2 - Pick representative set"
        pick_rep_set.py -i $SIM/10_pick_otus/seqs_otus.txt -m most_abundant -f seqs.fna -o
$SIM/10_pick_otus/seqs_rep_set.fasta
done

# ### Align representative sequences and generate phylogenetic analysis
echo -e "Step 2 - Align representative sequences and generate phylogenetic analysis"
for i in $LEVELS
do
        echo -e "\tSIMILARITY: $i"
        SIM=${i}_percent_similarity
        mkdir -p $SIM/20_make_phylogeny/
        echo -e "\t\tStep 2.1 - Align seqs"
        align_seqs.py -i $SIM/10_pick_otus/seqs_rep_set.fasta -p 0.75 -m pynast -a uclust -e 150 -o
$SIM/20_make_phylogeny/pynast_fasttree_method/
        echo -e "\t\tStep 2.2 - Filter alignment"
        filter_alignment.py -i
$SIM/20_make_phylogeny/pynast_fasttree_method/seqs_rep_set_aligned.fasta -o
$SIM/20_make_phylogeny/pynast_fasttree_method/
        echo -e "\t\tStep 2.3 - Make phylogeny"
        make_phylogeny.py -i
$SIM/20_make_phylogeny/pynast_fasttree_method/seqs_rep_set_aligned_pfiltered.fasta -o
$SIM/20_make_phylogeny/pynast_fasttree_method/seqs_rep_set_aligned_pfiltered.tre
done

# ### Assign taxonomy (This is only exploratory and was done to have an initial overview of the
taxonomic distribution)
echo -e "Step 3 - Assign taxonomy"
```

```
for i in $LEVELS
do
        echo -e "\tSIMILARITY: $i"
        SIM=${i}_percent_similarity
        mkdir -p $SIM/30_assign_taxonomy/rdp_method/
        echo -e "\t\tStep 3.1 - Assign taxonomy"
        assign_taxonomy.py -m rdp -c 0.7 --rdp_max_memory=10000 -i
$SIM/10_pick_otus/seqs_rep_set.fasta -o $SIM/30_assign_taxonomy/rdp_method/
done

# ### Create OTU tables
echo -e "Step 4 - Create OTU tables"
STEP=$((($MAX-$MIN)/10))  # Typically this calculation would be used to calculate the step. Here we
used 200 as a fix number
for i in $LEVELS
do
        echo -e "\tSIMILARITY: $i"
        SIM=${i}_percent_similarity
        mkdir -p $SIM/40_otu_tables/rdp_method/
        echo -e "\t\tStep 4.1 - Make OTU table"
        make_otu_table.py -i $SIM/10_pick_otus/seqs_otus.txt -t
$SIM/30_assign_taxonomy/rdp_method/seqs_rep_set_tax_assignments.txt -o
$SIM/40_otu_tables/rdp_method/seqs_otu_table.biom
        echo -e "\t\tStep 4.2 - Convert biom"
        biom convert --table-type "OTU table" --process-obs-metadata "taxonomy" --to-tsv --header-
key "taxonomy" -i $SIM/40_otu_tables/rdp_method/seqs_otu_table.biom -o
$SIM/40_otu_tables/rdp_method/seqs_otu_table.txt
        echo -e "\t\tStep 4.3 - Multiple rarefactions"
#       Normally we would use the following commnand:
#       multiple_rarefactions.py -m $MIN -x $MAX -s $STEP -n 10 -i
$SIM/40_otu_tables/rdp_method/seqs_otu_table.biom -o $SIM/40_otu_tables/rdp_method/rarefied/
#       In this work we used the following:
        multiple_rarefactions.py -m 200 -x 800 -s 200 -n 10 -i
$SIM/40_otu_tables/rdp_method/seqs_otu_table.biom -o $SIM/40_otu_tables/rdp_method/rarefied/
        if [ $i -eq 97 ]
        then
                echo -e "\t\tStep 4.8 - Summarize taxa and make plots"
                for j in {relative,absolute}
                do
                        echo -e "\t\t\t$j"
                        [[ "$j" == "absolute" ]] && IS_ABSOLUTE="-a" || IS_ABSOLUTE=""
                        echo -e "\t\t\t\tIS_ABSOLUTE: ${IS_ABSOLUTE}"
                        echo -e "\t\t\t\tStep 582 - Summarize taxa"
                        summarize_taxa.py -i $SIM/40_otu_tables/rdp_method/seqs_otu_table.biom -o
$SIM/40_otu_tables/rdp_method/summarized_plots_${j}/ $IS_ABSOLUTE
                        echo -e "\t\t\t\tStep 584 - Plot taxa summary"
                        plot_taxa_summary.py -i
$SIM/40_otu_tables/rdp_method/summarized_plots_${j}/seqs_otu_table_L2.txt,$SIM/40_otu_tables/rdp_meth
od/summarized_plots_${j}/seqs_otu_table_L3.txt,$SIM/40_otu_tables/rdp_method/summarized_plots_${j}/se
qs_otu_table_L4.txt,$SIM/40_otu_tables/rdp_method/summarized_plots_${j}/seqs_otu_table_L5.txt,$SIM/40
_otu_tables/rdp_method/summarized_plots_${j}/seqs_otu_table_L6.txt -o
$SIM/40_otu_tables/rdp_method/summarized_plots_${j}/taxa_summary_plots/ $ONE_SAMPLE
                done
        fi
done

# ### Calculate alpha diversity metrics
echo -e "Step 5 - Calculate alpha diversity metrics"
for i in $LEVELS
```

```
do
        echo -e "\tSIMILARITY: $i"
        SIM=${i}_percent_similarity
        echo -e "\t\tStep 5.1 - Alpha diversity on rarefied otu table"
        alpha_diversity.py -t
$SIM/20_make_phylogeny/pynast_fasttree_method/seqs_rep_set_aligned_pfiltered.tre -m
chao1,dominance,equitability,observed_species,shannon,PD_whole_tree -i
$SIM/40_otu_tables/rdp_method/rarefied/ -o $SIM/50_alpha_diversity/10_on_rarefied_otu_table/
        echo -e "\t\tStep 5.2 - Collate data"
        collate_alpha.py -i $SIM/50_alpha_diversity/10_on_rarefied_otu_table/ -o
$SIM/50_alpha_diversity/20_collate_data/
        echo -e "\t\tStep 5.3 - Make rarefaction plots"
        make_rarefaction_plots.py -d 50 -g png -k white -m mapping_file.txt -i
$SIM/50_alpha_diversity/20_collate_data/ -o $SIM/50_alpha_diversity/30_rarefaction_plots/
done

# ### Calculate beta diversity metrics if there are more than 5 samples in the dataset
if [ $NUM_SAMPLES -gt 5 ]
then
        echo -e "Step 6 - Calculate beta diversity metrics"
#       SUBSET=$(($MIN*0.75)) For large and evenly distributed datasets we would use 75% of the
sequences in the smaller sample
#       In this work we used 400:
        SUBSET=400
        echo -e "\tSUBSET: $SUBSET"
        for i in $LEVELS
        do
                echo -e "\tSIMILARITY: $i"
                SIM=${i}_percent_similarity
                mkdir -p $SIM/60_beta_diversity/
                echo -e "\t\tStep 72 - Jackknifed beta diversity"
                jackknifed_beta_diversity.py -e $SUBSET -m mapping_file.txt -f -p
../custom_parameters.txt -t
$SIM/20_make_phylogeny/pynast_fasttree_method/seqs_rep_set_aligned_pfiltered.tre -i
$SIM/40_otu_tables/rdp_method/seqs_otu_table.biom -o $SIM/60_beta_diversity/
        done
fi
```

custom_parameters.txt

```
# qiime_parameters.txt
# WARNING: DO NOT EDIT OR DELETE Qiime/qiime_parameters.txt. Users should copy this file and edit
copies of it.
# split libraries parameters
split_libraries:min-seq-length    180
split_libraries:max-seq-length    400
split_libraries:trim-seq-length
split_libraries:min-qual-score
split_libraries:keep-primer
split_libraries:keep-barcode
split_libraries:max-ambig
split_libraries:max-homopolymer   6
split_libraries:max-primer-mismatch       4
split_libraries:barcode-type      29
split_libraries:max-barcode-errors        3
split_libraries:start-numbering-at
split_libraries:remove_unassigned True
split_libraries:disable_bc_correction
split_libraries:qual_score_window 50
split_libraries:discard_bad_windows
split_libraries:disable_primers
split_libraries:reverse_primers   truncate_only
split_libraries:record_qual_scores

# OTU picker parameters
pick_otus:otu_picking_method      uclust
pick_otus:clustering_algorithm    furthest
pick_otus:max_cdhit_memory        400
pick_otus:refseqs_fp
pick_otus:blast_db
pick_otus:similarity      0.97
pick_otus:max_e_value     1e-10
pick_otus:prefix_prefilter_length
pick_otus:trie_prefilter
pick_otus:prefix_length
pick_otus:suffix_length
pick_otus:optimal_uclust
pick_otus:exact_uclust
pick_otus:user_sort
pick_otus:suppress_presort_by_abundance_uclust
pick_otus:suppress_new_clusters
pick_otus:suppress_uclust_stable_sort
pick_otus:max_accepts
pick_otus:max_rejects
pick_otus:word_length
pick_otus:stepwords
pick_otus:suppress_uclust_prefilter_exact_match

# Parallel options
parallel:jobs_to_start    1
parallel:retain_temp_files        False
parallel:seconds_to_sleep 60

# Representative set picker parameters
pick_rep_set:rep_set_picking_method       first
pick_rep_set:sort_by      otu
```

```
# Multiple sequence alignment parameters
align_seqs:template_fp
align_seqs:alignment_method       pynast
align_seqs:pairwise_alignment_method      uclust
align_seqs:blast_db
align_seqs:min_length    150
align_seqs:min_percent_id 75.0

# Alignment filtering (prior to tree-building) parameters
filter_alignment:lane_mask_fp
filter_alignment:allowed_gap_frac  0.999999
filter_alignment:remove_outliers  False
filter_alignment:threshold        3.0

# Taxonomy assignment parameters
assign_taxonomy:id_to_taxonomy_fp
assign_taxonomy:reference_seqs_fp
assign_taxonomy:assignment_method rdp
assign_taxonomy:blast_db
assign_taxonomy:confidence        0.8
assign_taxonomy:e_value  0.001

# Phylogenetic tree building parameters
make_phylogeny:tree_method        fasttree
make_phylogeny:root_method        tree_method_default

# Beta diversity parameters
beta_diversity:metrics   weighted_unifrac,unweighted_unifrac

# Make 3D plot parameters
make_3d_plots:custom_axes
make_3d_plots:ellipsoid_smoothness   1

# Rarefaction parameters
multiple_rarefactions:num-reps    10
multiple_rarefactions:depth
multiple_rarefactions:lineages_included   False

# Even-depth rarefaction parameters
multiple_rarefactions_even_depth:num_reps 100

# Alpha diversity parameters
alpha_diversity:metrics  PD_whole_tree,chao1,observed_species

# Make rarefaction plots parameters
make_rarefaction_plots:imagetype  png
make_rarefaction_plots:resolution 75
make_rarefaction_plots:background_color   white
make_rarefaction_plots:prefs_path

# Collate alpha
collate_alpha:example_path

# OTU category significance
otu_category_significance:test
otu_category_significance:filter  3
otu_category_significance:threshold
otu_category_significance:otu_include_fp
```

histograms.awk

```
# Bin data for a histogram
# Modifying Tara Murphy's code
# usage: for data values between 0 and 10, with steps of 0.5
# gawk -f histbin.awk 0 10 0.5 data.out data.in

BEGIN {
  m = ARGV[1]      # minimum value of x axis
  ARGV[1] = ""
  M = ARGV[2]      # maximum value of x axis
  ARGV[2] = ""
  w = ARGV[3]      # width of each step
  ARGV[3] = ""
  file = ARGV[4]   # output file for plotting
  ARGV[4] = ""

  b = (M-m)/w      # number of steps

  print "number of steps = "b
  print "width of each step  = "w
  print

  # set up arrays
  for (i = 1 ; i <= b; ++i) {
    n[i] = m+(i*w)        # upper bound of bin
    c[i] = n[i] - (w)   # centre of bin
    f[i] = 0              # frequency count
  }
}

{
  # bins the data
  for (i = 1; i <= b; ++i)
    if ($1 <= n[i]) {
         ++f[i]
         break
    }
}

END {
  # print results to screen
  # and to a file for plotting
  print "bin(centre) = freq"

  for (i = 1; i <= b; ++i) {
    if (f[i] > 0) {
      print "bin("c[i]")", "=", f[i]
      print c[i]"\t"f[i] > file
    }
    else {
      print "bin("c[i]")", "=", 0
      print c[i]"\t"0 > file
    }
  }
}
```

QIIME Mapping File in comma separated values (mapping_file.csv):

(A “>” character was added in between lines to facilitate copy and paste from the online PDF document. In brief: copy and paste the following text in a text editor, eliminate spaces and change of line, convert “>” character into change of line. Optionally, comma can be converted into TAB)

```
#SampleID,BarcodeSequence,LinkerPrimerSequence,ReversePrimer,RunPool,SRAAccession,UsedSamples,Site,Cr
op,PlotID,Stage,Source,454xMIDxID,NumericID,SequencedAfterQC,Folder10,Folder11,Folder12,Folder13,Fold
er14,Folder15,Folder16,Folder17,Description
>
BA2.0.Su.T.31,AGCGTCGTCT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,Balcarce,Wheat,2,Tillering,Rhizospheric_Soil,MID31,31,1326,Non,Non,Non,No
n,Non,15_wheat_RS,Non,Non,BA2.0.Su.T.31
>
BA2.1.Su.T.A.1,ACGAGTGCGT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTA
AT,run1pool1,SRR3330055,NotUsed,Balcarce,Wheat,2,Tillering,Rhizospheric_Soil,MID1,1,953,Non,Non,Non,N
on,Non,Non,Non,Non,BA2.1.Su.T.A.1
>
BA3.0.Su.T.2,ACGCTCGACA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT
,run1pool1,SRR3330055,Used,Balcarce,Wheat,3,Tillering,Rhizospheric_Soil,MID2,2,984,Non,Non,Non,Non,No
n,15_wheat_RS,Non,Non,BA3.0.Su.T.2
>
BA3.1.Su.T.3,AGACGCACTC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT
,run1pool1,SRR3330055,Used,Balcarce,Wheat,3,Tillering,Rhizospheric_Soil,MID3,3,1995,Non,11_wheat_RA_R
S,Non,Non,Non,15_wheat_RS,16_wheat_soybean_RA_RS,Non,BA3.1.Su.T.3
>
BA4.0.Su.T.4,AGCACTGTAG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT
,run1pool1,SRR3330055,Used,Balcarce,Wheat,4,Tillering,Rhizospheric_Soil,MID4,4,1899,Non,11_wheat_RA_R
S,Non,Non,Non,15_wheat_RS,16_wheat_soybean_RA_RS,Non,BA4.0.Su.T.4
>
BA4.1.Su.T.5,ATCAGACACG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT
,run1pool1,SRR3330055,Used,Balcarce,Wheat,4,Tillering,Rhizospheric_Soil,MID5,5,1995,Non,11_wheat_RA_R
S,Non,Non,Non,15_wheat_RS,16_wheat_soybean_RA_RS,Non,BA4.1.Su.T.5
>
BA5.1.0.Su.T.6,ATATCGCGAG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTA
AT,run1pool1,SRR3330055,NotUsed,Balcarce,Wheat,5,Tillering,Rhizospheric_Soil,MID6,6,1813,Non,Non,Non,
Non,Non,Non,Non,Non,BA5.1.0.Su.T.6
>
BA5.1.1.Su.T.7,CGTGTCTCTA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTA
AT,run1pool1,SRR3330055,Used,Balcarce,Wheat,5,Tillering,Rhizospheric_Soil,MID7,7,1733,Non,11_wheat_RA
_RS,Non,Non,Non,15_wheat_RS,16_wheat_soybean_RA_RS,Non,BA5.1.1.Su.T.7
>
BA5.2.1.Su.T.8,CTCGCGTGTC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTA
AT,run1pool1,SRR3330055,NotUsed,Balcarce,Wheat,5,Tillering,Rhizospheric_Soil,MID8,8,1733,Non,Non,Non,
Non,Non,Non,Non,Non,BA5.2.1.Su.T.8
>
BA5.3.0.Su.T.10,TCTCTATGCG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCT
AAT,run1pool1,SRR3330055,NotUsed,Balcarce,Wheat,5,Tillering,Rhizospheric_Soil,MID10,10,1204,Non,Non,N
on,Non,Non,Non,Non,Non,BA5.3.0.Su.T.10
>
BA5.3.1.Su.T.11,TGATACGTCT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCT
AAT,run1pool1,SRR3330055,NotUsed,Balcarce,Wheat,5,Tillering,Rhizospheric_Soil,MID11,11,524,Non,Non,No
n,Non,Non,Non,Non,Non,BA5.3.1.Su.T.11
>
```

```
BA5.2.0.Su.T.33,ATAGAGTACT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run1pool1,SRR3330055,Used,Balcarce,Wheat,5,Tillering,Rhizospheric_Soil,MID33,33,3425,Non,11_wheat_RA_RS,Non,Non,Non,15_wheat_RS,16_wheat_soybean_RA_RS,Non,BA5.2.0.Su.T.33
>
BA2.0.Su.TF.36,CGACGTGACT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run1pool1,SRR3330055,NotUsed,Balcarce,Wheat,2,Flowering,Rhizospheric_Soil,MID36,36,1745,Non,Non,Non,Non,Non,Non,Non,Non,BA2.0.Su.TF.36
>
BA2.1.Su.TF.13,CATAGTAGTG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run1pool1,SRR3330055,NotUsed,Balcarce,Wheat,2,Flowering,Rhizospheric_Soil,MID13,13,811,Non,Non,Non,Non,Non,Non,Non,Non,BA2.1.Su.TF.13
>
BA3.0.Su.TF.14,CGAGAGATAC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run1pool1,SRR3330055,NotUsed,Balcarce,Wheat,3,Flowering,Rhizospheric_Soil,MID14,14,1540,Non,Non,Non,Non,Non,Non,Non,Non,BA3.0.Su.TF.14
>
BA3.1.Su.TF.15,ATACGACGTA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run1pool1,SRR3330055,NotUsed,Balcarce,Wheat,3,Flowering,Rhizospheric_Soil,MID15,15,1586,Non,Non,Non,Non,Non,Non,Non,Non,BA3.1.Su.TF.15
>
BA4.0.Su.TF.16,TCACGTACTA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run1pool1,SRR3330055,NotUsed,Balcarce,Wheat,4,Flowering,Rhizospheric_Soil,MID16,16,1863,Non,Non,Non,Non,Non,Non,Non,Non,BA4.0.Su.TF.16
>
BA4.1.Su.TF.17,CGTCTAGTAC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run1pool1,SRR3330055,NotUsed,Balcarce,Wheat,4,Flowering,Rhizospheric_Soil,MID17,17,1405,Non,Non,Non,Non,Non,Non,Non,Non,BA4.1.Su.TF.17
>
BA5.1.0.Su.TF.18,TCTACGTAGC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run1pool1,SRR3330055,NotUsed,Balcarce,Wheat,5,Flowering,Rhizospheric_Soil,MID18,18,1561,Non,Non,Non,Non,Non,Non,Non,Non,BA5.1.0.Su.TF.18
>
BA5.1.1.Su.TF.19,TGTACTACTC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run1pool1,SRR3330055,NotUsed,Balcarce,Wheat,5,Flowering,Rhizospheric_Soil,MID19,19,879,Non,Non,Non,Non,Non,Non,Non,Non,BA5.1.1.Su.TF.19
>
BA5.2.0.Su.TF.20,ACGACTACAG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run1pool1,SRR3330055,NotUsed,Balcarce,Wheat,5,Flowering,Rhizospheric_Soil,MID20,20,1261,Non,Non,Non,Non,Non,Non,Non,Non,BA5.2.0.Su.TF.20
>
BA5.2.1.Su.TF.21,CGTAGACTAG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run1pool1,SRR3330055,NotUsed,Balcarce,Wheat,5,Flowering,Rhizospheric_Soil,MID21,21,1524,Non,Non,Non,Non,Non,Non,Non,Non,BA5.2.1.Su.TF.21
>
BA5.3.0.Su.TF.22,TACGAGTATG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run1pool1,SRR3330055,NotUsed,Balcarce,Wheat,5,Flowering,Rhizospheric_Soil,MID22,22,1393,Non,Non,Non,Non,Non,Non,Non,Non,BA5.3.0.Su.TF.22
>
BA5.3.1.Su.TF.23,TACTCTCGTG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run1pool1,SRR3330055,NotUsed,Balcarce,Wheat,5,Flowering,Rhizospheric_Soil,MID23,23,1758,Non,Non,Non,Non,Non,Non,Non,Non,BA5.3.1.Su.TF.23
>
MB2.0.Su.T.A.38,TACACGTGAT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run1pool1,SRR3330055,Used,MonteBuey,Wheat,2,Tillering,Rhizospheric_Soil,MID38,38,1586,Non,Non,Non,Non,Non,15_wheat_RS,Non,Non,MB2.0.Su.T.A.38
>
MB2.1.Su.T.24,TAGAGACGAG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run1pool1,SRR3330055,Used,MonteBuey,Wheat,2,Tillering,Rhizospheric_Soil,MID24,24,1415,Non,Non,Non,Non,Non,15_wheat_RS,Non,Non,MB2.1.Su.T.24
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>
MB3.0.Su.T.25,TCGTCGCTCG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,MonteBuey,Wheat,3,Tillering,Rhizospheric_Soil,MID25,25,1447,Non,Non,Non,N
on,Non,15_wheat_RS,Non,Non,MB3.0.Su.T.25
>
MB3.1.Su.T.26,ACATACGCGT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,MonteBuey,Wheat,3,Tillering,Rhizospheric_Soil,MID26,26,1352,Non,Non,Non,N
on,Non,15_wheat_RS,Non,Non,MB3.1.Su.T.26
>
MB4.1.Su.T.28,ACTACTATGT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,MonteBuey,Wheat,4,Tillering,Rhizospheric_Soil,MID28,28,1042,Non,Non,Non,N
on,Non,15_wheat_RS,Non,Non,MB4.1.Su.T.28
>
MB5.0.Su.T.29,ACTGTACAGT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,MonteBuey,Wheat,5,Tillering,Rhizospheric_Soil,MID29,29,722,Non,Non,Non,No
n,Non,15_wheat_RS,Non,Non,MB5.0.Su.T.29
>
MB5.1.Su.T.30,AGACTATACT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,MonteBuey,Wheat,5,Tillering,Rhizospheric_Soil,MID30,30,6311,Non,Non,Non,N
on,Non,15_wheat_RS,Non,Non,MB5.1.Su.T.30
>
VS2.0.Su.T.A.37,TACACACACT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCT
AAT,run1pool1,SRR3330055,Used,VillaSaboya,Wheat,2,Tillering,Rhizospheric_Soil,MID37,37,1415,Non,Non,N
on,Non,Non,15_wheat_RS,Non,Non,VS2.0.Su.T.A.37
>
VS2.1.Su.T.40,TACGCTGTCT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,VillaSaboya,Wheat,2,Tillering,Rhizospheric_Soil,MID40,40,1184,Non,11_whea
t_RA_RS,Non,Non,Non,15_wheat_RS,16_wheat_soybean_RA_RS,Non,VS2.1.Su.T.40
>
VS3.0.Su.T.41,TAGTGTAGAT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,VillaSaboya,Wheat,3,Tillering,Rhizospheric_Soil,MID41,41,1469,Non,11_whea
t_RA_RS,Non,Non,Non,15_wheat_RS,16_wheat_soybean_RA_RS,Non,VS3.0.Su.T.41
>
VS3.1.Su.T.42,TCGATCACGT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,VillaSaboya,Wheat,3,Tillering,Rhizospheric_Soil,MID42,42,1429,Non,11_whea
t_RA_RS,Non,Non,Non,15_wheat_RS,16_wheat_soybean_RA_RS,Non,VS3.1.Su.T.42
>
VS4.1.Su.T.44,TCTAGCGACT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,NotUsed,VillaSaboya,Wheat,4,Tillering,Rhizospheric_Soil,MID44,44,583,Non,Non,N
on,Non,Non,Non,Non,Non,VS4.1.Su.T.44
>
VS5.0.Su.T.45,TCTATACTAT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,VillaSaboya,Wheat,5,Tillering,Rhizospheric_Soil,MID45,45,812,Non,Non,Non,
Non,Non,15_wheat_RS,Non,Non,VS5.0.Su.T.45
>
VS5.1.Su.T.46,TGACGTATGT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,VillaSaboya,Wheat,5,Tillering,Rhizospheric_Soil,MID46,46,1637,Non,11_whea
t_RA_RS,Non,Non,Non,15_wheat_RS,16_wheat_soybean_RA_RS,Non,VS5.1.Su.T.46
>
CB2.0.Su.T.A.32,AGTACGCTAT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCT
AAT,run1pool1,SRR3330055,Used,CorraldeBustos,Wheat,2,Tillering,Rhizospheric_Soil,MID32,32,1563,Non,11
_wheat_RA_RS,Non,Non,Non,15_wheat_RS,16_wheat_soybean_RA_RS,Non,CB2.0.Su.T.A.32
>
CB3.0.Su.T.47,TGTGAGTAGT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,CorraldeBustos,Wheat,3,Tillering,Rhizospheric_Soil,MID47,47,1028,Non,Non,
Non,Non,Non,15_wheat_RS,Non,Non,CB3.0.Su.T.47
>
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CB4.0.Su.T.48,ACAGTATATA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,CorraldeBustos,Wheat,4,Tillering,Rhizospheric_Soil,MID48,48,1314,Non,11_w
heat_RA_RS,Non,Non,Non,15_wheat_RS,16_wheat_soybean_RA_RS,Non,CB4.0.Su.T.48
>
CB5.0.Su.T.49,ACGCGATCGA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,CorraldeBustos,Wheat,5,Tillering,Rhizospheric_Soil,MID49,49,773,Non,11_wh
eat_RA_RS,Non,Non,Non,15_wheat_RS,16_wheat_soybean_RA_RS,Non,CB5.0.Su.T.49
>
CB2.1.Su.T.50,ACTAGCAGTA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,CorraldeBustos,Wheat,2,Tillering,Rhizospheric_Soil,MID50,50,1837,Non,11_w
heat_RA_RS,Non,Non,Non,15_wheat_RS,16_wheat_soybean_RA_RS,Non,CB2.1.Su.T.50
>
CB3.1.Su.T.51,AGCTCACGTA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,CorraldeBustos,Wheat,3,Tillering,Rhizospheric_Soil,MID51,51,1296,Non,11_w
heat_RA_RS,Non,Non,Non,15_wheat_RS,16_wheat_soybean_RA_RS,Non,CB3.1.Su.T.51
>
CB4.1.Su.T.52,AGTATACATA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,CorraldeBustos,Wheat,4,Tillering,Rhizospheric_Soil,MID52,52,1053,Non,11_w
heat_RA_RS,Non,Non,Non,15_wheat_RS,16_wheat_soybean_RA_RS,Non,CB4.1.Su.T.52
>
CB5.1.Su.T.53,AGTCGAGAGA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,NotUsed,CorraldeBustos,Wheat,5,Tillering,Rhizospheric_Soil,MID53,53,666,Non,No
n,Non,Non,Non,Non,Non,Non,CB5.1.Su.T.53
>
SJ5.1.1.Su.T.A.35,CAGTAGACGT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTAT
CTAAT,run1pool1,SRR3330055,NotUsed,SanJorge,Wheat,5,Tillering,Rhizospheric_Soil,MID35,35,1316,Non,Non
,Non,Non,Non,Non,Non,Non,SJ5.1.1.Su.T.A.35
>
SJ2.0.Su.T.A.54,AGTGCTACGA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCT
AAT,run1pool1,SRR3330055,Used,SanJorge,Wheat,2,Tillering,Rhizospheric_Soil,MID54,54,1614,Non,Non,Non,
Non,Non,15_wheat_RS,Non,Non,SJ2.0.Su.T.A.54
>
SJ3.0.Su.T.55,CGATCGTATA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,SanJorge,Wheat,3,Tillering,Rhizospheric_Soil,MID55,55,1277,Non,Non,Non,No
n,Non,15_wheat_RS,Non,Non,SJ3.0.Su.T.55
>
SJ4.0.Su.T.56,CGCAGTACGA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,SanJorge,Wheat,4,Tillering,Rhizospheric_Soil,MID56,56,1044,Non,Non,Non,No
n,Non,15_wheat_RS,Non,Non,SJ4.0.Su.T.56
>
SJ5.2.0.Su.T.A.57,CGCGTATACA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTAT
CTAAT,run1pool1,SRR3330055,NotUsed,SanJorge,Wheat,5,Tillering,Rhizospheric_Soil,MID57,57,935,Non,Non,
Non,Non,Non,Non,Non,Non,SJ5.2.0.Su.T.A.57
>
SJ2.1.Su.T.58,CGTACAGTCA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,SanJorge,Wheat,2,Tillering,Rhizospheric_Soil,MID58,58,1460,Non,Non,Non,No
n,Non,15_wheat_RS,Non,Non,SJ2.1.Su.T.58
>
SJ3.1.Su.T.59,CGTACTCAGA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,SanJorge,Wheat,3,Tillering,Rhizospheric_Soil,MID59,59,1077,Non,Non,Non,No
n,Non,15_wheat_RS,Non,Non,SJ3.1.Su.T.59
>
SJ4.1.Su.T.60,CTACGCTCTA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,SanJorge,Wheat,4,Tillering,Rhizospheric_Soil,MID60,60,876,Non,Non,Non,Non
,Non,15_wheat_RS,Non,Non,SJ4.1.Su.T.60
>
SJ5.1.0.Su.T.61,CTATAGCGTA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCT
AAT,run1pool1,SRR3330055,NotUsed,SanJorge,Wheat,5,Tillering,Rhizospheric_Soil,MID61,61,1034,Non,Non,N
on,Non,Non,Non,Non,Non,SJ5.1.0.Su.T.61
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>
SJ5.2.1.Su.T.62,TACGTCATCA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCT
AAT,run1pool1,SRR3330055,Used,SanJorge,Wheat,5,Tillering,Rhizospheric_Soil,MID62,62,844,Non,Non,Non,N
on,Non,15_wheat_RS,Non,Non,SJ5.2.1.Su.T.62
>
SJ5.3.0.Su.T.63,TAGTCGCATA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCT
AAT,run1pool1,SRR3330055,NotUsed,SanJorge,Wheat,5,Tillering,Rhizospheric_Soil,MID63,63,1147,Non,Non,N
on,Non,Non,Non,Non,Non,SJ5.3.0.Su.T.63
>
SJ5.3.1.Su.T.64,TATATATACA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCT
AAT,run1pool1,SRR3330055,NotUsed,SanJorge,Wheat,5,Tillering,Rhizospheric_Soil,MID64,64,1505,Non,Non,N
on,Non,Non,Non,Non,Non,SJ5.3.1.Su.T.64
>
DA2.0.Su.T.A.34,CACGCTACGT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCT
AAT,run1pool1,SRR3330055,Used,Daireaux,Wheat,2,Tillering,Rhizospheric_Soil,MID34,34,1081,Non,Non,Non,
Non,Non,15_wheat_RS,Non,Non,DA2.0.Su.T.A.34
>
DA2.1.Su.T.65,TATGCTAGTA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,Daireaux,Wheat,2,Tillering,Rhizospheric_Soil,MID65,65,1444,Non,11_wheat_R
A_RS,Non,Non,Non,15_wheat_RS,16_wheat_soybean_RA_RS,Non,DA2.1.Su.T.65
>
DA3.0.Su.T.66,TCACGCGAGA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,Daireaux,Wheat,3,Tillering,Rhizospheric_Soil,MID66,66,918,Non,Non,Non,Non
,Non,15_wheat_RS,Non,Non,DA3.0.Su.T.66
>
DA3.1.Su.T.67,TCGATAGTGA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,Daireaux,Wheat,3,Tillering,Rhizospheric_Soil,MID67,67,1189,Non,11_wheat_R
A_RS,Non,Non,Non,15_wheat_RS,16_wheat_soybean_RA_RS,Non,DA3.1.Su.T.67
>
DA4.0.Su.T.68,TCGCTGCGTA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,Daireaux,Wheat,4,Tillering,Rhizospheric_Soil,MID68,68,1325,Non,11_wheat_R
A_RS,Non,Non,Non,15_wheat_RS,16_wheat_soybean_RA_RS,Non,DA4.0.Su.T.68
>
DA4.1.Su.T.69,TCTGACGTCA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,NotUsed,Daireaux,Wheat,4,Tillering,Rhizospheric_Soil,MID69,69,959,Non,Non,Non,
Non,Non,Non,Non,Non,DA4.1.Su.T.69
>
DA5.0.Su.T.70,TGAGTCAGTA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,Daireaux,Wheat,5,Tillering,Rhizospheric_Soil,MID70,70,1534,Non,11_wheat_R
A_RS,Non,Non,Non,15_wheat_RS,16_wheat_soybean_RA_RS,Non,DA5.0.Su.T.70
>
DA5.1.Su.T.71,TGTAGTGTGA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run1pool1,SRR3330055,Used,Daireaux,Wheat,5,Tillering,Rhizospheric_Soil,MID71,71,1721,Non,11_wheat_R
A_RS,Non,Non,Non,15_wheat_RS,16_wheat_soybean_RA_RS,Non,DA5.1.Su.T.71
>
AR2.0.Su.S.49,ATACGACGTA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,NotUsed,Aranguren,Soybean,2,Vegetative,Rhizospheric_Soil,MID15,49,301,Non,Non,
Non,Non,Non,Non,Non,Non,AR2.0.Su.S.49
>
AR2a11.1.Su.S.50,ACGAGTGCGT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool1,SRR3330056,Used,Aranguren,Soybean,2,Vegetative,Rhizospheric_Soil,MID1,50,742,10_soybea
n_RA_RS,Non,Non,13_soybean_RS,Non,Non,16_wheat_soybean_RA_RS,Non,AR2a11.1.Su.S.50
>
AR3.0.Su.S.51,ACGCTCGACA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,Used,Aranguren,Soybean,3,Vegetative,Rhizospheric_Soil,MID2,51,589,10_soybean_R
A_RS,Non,Non,13_soybean_RS,Non,Non,16_wheat_soybean_RA_RS,Non,AR3.0.Su.S.51
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AR3al1.1.Su.S.52,TACGAGTATG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool1,SRR3330056,Used,Aranguren,Soybean,3,Vegetative,Rhizospheric_Soil,MID22,52,592,10_soybe
an_RA_RS,Non,Non,13_soybean_RS,Non,Non,16_wheat_soybean_RA_RS,Non,AR3al1.1.Su.S.52
>
CA2.0.Su.S.53,AGACGCACTC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,Used,CarmendeAreco,Soybean,2,Vegetative,Rhizospheric_Soil,MID3,53,660,10_soybe
an_RA_RS,Non,Non,13_soybean_RS,Non,Non,16_wheat_soybean_RA_RS,Non,CA2.0.Su.S.53
>
CA2al1.1.Su.S.54,AGCACTGTAG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool1,SRR3330056,Used,CarmendeAreco,Soybean,2,Vegetative,Rhizospheric_Soil,MID4,54,737,10_so
ybean_RA_RS,Non,Non,13_soybean_RS,Non,Non,16_wheat_soybean_RA_RS,Non,CA2al1.1.Su.S.54
>
CA3.0.Su.S.55,TCACGTACTA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,NotUsed,CarmendeAreco,Soybean,3,Vegetative,Rhizospheric_Soil,MID16,55,594,Non,
Non,Non,Non,Non,Non,Non,Non,CA3.0.Su.S.55
>
CA3al1.1.Su.S.56,ATCAGACACG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool1,SRR3330056,Used,CarmendeAreco,Soybean,3,Vegetative,Rhizospheric_Soil,MID5,56,872,10_so
ybean_RA_RS,Non,Non,13_soybean_RS,Non,Non,16_wheat_soybean_RA_RS,Non,CA3al1.1.Su.S.56
>
CB2.0.Su.S.57,ATATCGCGAG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,Used,CorraldeBustos,Soybean,2,Vegetative,Rhizospheric_Soil,MID6,57,379,Non,Non
,Non,Non,Non,Non,Non,Non,CB2.0.Su.S.57
>
CB2a5.1.Su.S.58,CGTGTCTCTA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCT
AAT,run2pool1,SRR3330056,NotUsed,CorraldeBustos,Soybean,2,Vegetative,Rhizospheric_Soil,MID7,58,219,No
n,Non,Non,Non,Non,Non,Non,Non,CB2a5.1.Su.S.58
>
CB3.0.Su.S.59,CTCGCGTGTC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,Used,CorraldeBustos,Soybean,3,Vegetative,Rhizospheric_Soil,MID8,59,255,Non,Non
,Non,Non,Non,Non,Non,Non,CB3.0.Su.S.59
>
CB3al1.1.Su.S.60,CGTCTAGTAC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool1,SRR3330056,Used,CorraldeBustos,Soybean,3,Vegetative,Rhizospheric_Soil,MID17,60,926,Non
,Non,Non,Non,Non,Non,Non,Non,CB3al1.1.Su.S.60
>
CH2.0.Su.S.61,CGACACTATC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,Used,Chilibroste,Soybean,2,Vegetative,Rhizospheric_Soil,MID92,61,933,10_soybea
n_RA_RS,Non,Non,13_soybean_RS,Non,Non,16_wheat_soybean_RA_RS,Non,CH2.0.Su.S.61
>
CH2al1.1.Su.S.62,TACTCTCGTG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool1,SRR3330056,Used,Chilibroste,Soybean,2,Vegetative,Rhizospheric_Soil,MID23,62,624,10_soy
bean_RA_RS,Non,Non,13_soybean_RS,Non,Non,16_wheat_soybean_RA_RS,Non,CH2al1.1.Su.S.62
>
CH3.0.Su.S.63,TCTCTATGCG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,Used,Chilibroste,Soybean,3,Vegetative,Rhizospheric_Soil,MID10,63,860,10_soybea
n_RA_RS,Non,Non,13_soybean_RS,Non,Non,16_wheat_soybean_RA_RS,Non,CH3.0.Su.S.63
>
CH3al1.1.Su.S.64,TAGAGACGAG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool1,SRR3330056,NotUsed,Chilibroste,Soybean,3,Vegetative,Rhizospheric_Soil,MID24,64,570,Non
,Non,Non,Non,Non,Non,Non,Non,CH3al1.1.Su.S.64
>
HU2.0.Su.S.65,TCGTCGCTCG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,NotUsed,Huges,Soybean,2,Vegetative,Rhizospheric_Soil,MID25,65,99,Non,Non,Non,N
on,Non,Non,Non,Non,HU2.0.Su.S.65
>
HU2al1.1.Su.S.66,ACATACGCGT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool1,SRR3330056,Used,Huges,Soybean,2,Vegetative,Rhizospheric_Soil,MID26,66,620,10_soybean_R
A_RS,Non,Non,13_soybean_RS,Non,Non,16_wheat_soybean_RA_RS,Non,HU2al1.1.Su.S.66
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>
HU3.0.Su.S.67,ACGCGAGTAT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,Used,Huges,Soybean,3,Vegetative,Rhizospheric_Soil,MID27,67,547,10_soybean_RA_R
S,Non,Non,13_soybean_RS,Non,Non,16_wheat_soybean_RA_RS,Non,HU3.0.Su.S.67
>
HU3a11.1.Su.S.68,ACTACTATGT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool1,SRR3330056,Used,Huges,Soybean,3,Vegetative,Rhizospheric_Soil,MID28,68,663,10_soybean_R
A_RS,Non,Non,13_soybean_RS,Non,Non,16_wheat_soybean_RA_RS,Non,HU3a11.1.Su.S.68
>
MB2.0.Su.S.69,TCTACGTAGC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,Used,MonteBuey,Soybean,2,Vegetative,Rhizospheric_Soil,MID18,69,1140,10_soybean
_RA_RS,Non,Non,13_soybean_RS,Non,Non,16_wheat_soybean_RA_RS,Non,MB2.0.Su.S.69
>
MB2a11.1.Su.S.70,ACTGTACAGT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool1,SRR3330056,Used,MonteBuey,Soybean,2,Vegetative,Rhizospheric_Soil,MID29,70,652,10_soybe
an_RA_RS,Non,Non,13_soybean_RS,Non,Non,16_wheat_soybean_RA_RS,Non,MB2a11.1.Su.S.70
>
MB3.0.Su.S.71,AGACTATACT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,Used,MonteBuey,Soybean,3,Vegetative,Rhizospheric_Soil,MID30,71,459,10_soybean_
RA_RS,Non,Non,13_soybean_RS,Non,Non,16_wheat_soybean_RA_RS,Non,MB3.0.Su.S.71
>
SA2.0.Su.S.73,AGTACGCTAT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,NotUsed,SanAgustin,Soybean,2,Vegetative,Rhizospheric_Soil,MID32,73,245,Non,Non
,Non,Non,Non,Non,Non,Non,SA2.0.Su.S.73
>
SA2a11.1.Su.S.74,TGTACTACTC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool1,SRR3330056,Used,SanAgustin,Soybean,2,Vegetative,Rhizospheric_Soil,MID19,74,470,10_soyb
ean_RA_RS,Non,Non,13_soybean_RS,Non,Non,16_wheat_soybean_RA_RS,Non,SA2a11.1.Su.S.74
>
SA3.0.Su.S.75,ATAGAGTACT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,Used,SanAgustin,Soybean,3,Vegetative,Rhizospheric_Soil,MID33,75,884,10_soybean
_RA_RS,Non,Non,13_soybean_RS,Non,Non,16_wheat_soybean_RA_RS,Non,SA3.0.Su.S.75
>
SA3a11.1.Su.S.76,CACGCTACGT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool1,SRR3330056,Used,SanAgustin,Soybean,3,Vegetative,Rhizospheric_Soil,MID34,76,501,10_soyb
ean_RA_RS,Non,Non,13_soybean_RS,Non,Non,16_wheat_soybean_RA_RS,Non,SA3a11.1.Su.S.76
>
VS2.0.Su.S.77,ACGACTACAG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,Used,VillaSaboya,Soybean,2,Vegetative,Rhizospheric_Soil,MID20,77,999,10_soybea
n_RA_RS,Non,Non,13_soybean_RS,Non,Non,16_wheat_soybean_RA_RS,Non,VS2.0.Su.S.77
>
VS2a11.1.Su.S.78,CAGTAGACGT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool1,SRR3330056,Used,VillaSaboya,Soybean,2,Vegetative,Rhizospheric_Soil,MID35,78,599,10_soy
bean_RA_RS,Non,Non,13_soybean_RS,Non,Non,16_wheat_soybean_RA_RS,Non,VS2a11.1.Su.S.78
>
VS3.0.Su.S.79,CGTAGACTAG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,NotUsed,VillaSaboya,Soybean,3,Vegetative,Rhizospheric_Soil,MID21,79,370,Non,No
n,Non,Non,Non,Non,Non,Non,VS3.0.Su.S.79
>
VS3a11.1.Su.S.80,CGACGTGACT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool1,SRR3330056,Used,VillaSaboya,Soybean,3,Vegetative,Rhizospheric_Soil,MID36,80,495,10_soy
bean_RA_RS,Non,Non,13_soybean_RS,Non,Non,16_wheat_soybean_RA_RS,Non,VS3a11.1.Su.S.80
>
AR2.0.En.S.49,AGAGCGTCAC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,Used,Aranguren,Soybean,2,Vegetative,Root_Associated,MID81,49,1786,10_soybean_R
A_RS,Non,12_soybean_RA,Non,Non,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,AR2.0.En.S.49
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AR2all.1.En.S.50,AGCGACTAGC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool1,SRR3330056,Used,Aranguren,Soybean,2,Vegetative,Root_Associated,MID82,50,1329,10_soybea
n_RA_RS,Non,12_soybean_RA,Non,Non,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,AR2all.1.En.S.50
>
AR3.0.En.S.51,AGTAGTGATC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,Used,Aranguren,Soybean,3,Vegetative,Root_Associated,MID83,51,1414,10_soybean_R
A_RS,Non,12_soybean_RA,Non,Non,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,AR3.0.En.S.51
>
AR3all.1.En.S.52,CGAGACGCGC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool1,SRR3330056,Used,Aranguren,Soybean,3,Vegetative,Root_Associated,MID93,52,494,Non,Non,12
_soybean_RA,Non,Non,Non,Non,17_wheat_soybean_RA,AR3all.1.En.S.52
>
CA2.0.En.S.53,AGTGACACAC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,Used,CarmendeAreco,Soybean,2,Vegetative,Root_Associated,MID84,53,1169,10_soybe
an_RA_RS,Non,12_soybean_RA,Non,Non,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,CA2.0.En.S.53
>
CA2all.1.En.S.54,AGTGTATGTC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool1,SRR3330056,Used,CarmendeAreco,Soybean,2,Vegetative,Root_Associated,MID85,54,1478,10_so
ybean_RA_RS,Non,12_soybean_RA,Non,Non,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,CA2all.1.En.S.54
>
CA3.0.En.S.55,ATAGATAGAC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,Used,CarmendeAreco,Soybean,3,Vegetative,Root_Associated,MID86,55,1524,10_soybe
an_RA_RS,Non,12_soybean_RA,Non,Non,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,CA3.0.En.S.55
>
CA3all.1.En.S.56,ATATAGTCGC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool1,SRR3330056,Used,CarmendeAreco,Soybean,3,Vegetative,Root_Associated,MID87,56,1496,Non,N
on,12_soybean_RA,Non,Non,Non,Non,17_wheat_soybean_RA,CA3all.1.En.S.56
>
CB2.0.En.S.57,ATCTACTGAC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,Used,CorraldeBustos,Soybean,2,Vegetative,Root_Associated,MID88,57,1086,Non,Non
,12_soybean_RA,Non,Non,Non,Non,17_wheat_soybean_RA,CB2.0.En.S.57
>
CB2a5.1.En.S.58,CACGTAGATC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCT
AAT,run2pool1,SRR3330056,Used,CorraldeBustos,Soybean,2,Vegetative,Root_Associated,MID89,58,1475,Non,N
on,12_soybean_RA,Non,Non,Non,Non,17_wheat_soybean_RA,CB2a5.1.En.S.58
>
CB3.0.En.S.59,CACGTGTCGC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,Used,CorraldeBustos,Soybean,3,Vegetative,Root_Associated,MID90,59,1275,Non,Non
,12_soybean_RA,Non,Non,Non,Non,17_wheat_soybean_RA,CB3.0.En.S.59
>
CB3all.1.En.S.60,CATAGTAGTG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool1,SRR3330056,NotUsed,CorraldeBustos,Soybean,3,Vegetative,Root_Associated,MID13,60,303,No
n,Non,Non,Non,Non,Non,Non,Non,CB3all.1.En.S.60
>
CH2.0.En.S.61,CATACTCTAC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,Used,Chilibroste,Soybean,2,Vegetative,Root_Associated,MID91,61,1399,10_soybean
_RA_RS,Non,12_soybean_RA,Non,Non,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,CH2.0.En.S.61
>
MB3all.1.En.S.72,TGATACGTCT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool1,SRR3330056,Used,MonteBuey,Soybean,3,Vegetative,Root_Associated,MID11,72,565,Non,Non,12
_soybean_RA,Non,Non,Non,Non,17_wheat_soybean_RA,MB3all.1.En.S.72
>
SA3.0.En.S.75,CGAGAGATAC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,Used,SanAgustin,Soybean,3,Vegetative,Root_Associated,MID14,75,785,Non,Non,12_s
oybean_RA,Non,Non,Non,Non,17_wheat_soybean_RA,SA3.0.En.S.75
>
BA3.1.En.TF.8,AGCTCACGTA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,NotUsed,Balcarce,Wheat,3,Flowering,Root_Associated,MID51,8,696,Non,Non,Non,Non
,Non,Non,Non,Non,BA3.1.En.TF.8
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>
BA4.0.En.T.9,AGTATACATA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT
,run2pool1,SRR3330056,NotUsed,Balcarce,Wheat,4,Tillering,Root_Associated,MID52,9,112,Non,Non,Non,Non,
Non,Non,Non,Non,BA4.0.En.T.9
>
BA4.0.En.TF.10,AGTCGAGAGA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTA
AT,run2pool1,SRR3330056,NotUsed,Balcarce,Wheat,4,Flowering,Root_Associated,MID53,10,462,Non,Non,Non,N
on,Non,Non,Non,Non,BA4.0.En.TF.10
>
BA4.1.En.T.11,AGTGCTACGA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,Used,Balcarce,Wheat,4,Tillering,Root_Associated,MID54,11,468,Non,11_wheat_RA_R
S,Non,Non,14_wheat_RA,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,BA4.1.En.T.11
>
BA4.1.En.TF.12,CGATCGTATA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTA
AT,run2pool1,SRR3330056,NotUsed,Balcarce,Wheat,4,Flowering,Root_Associated,MID55,12,182,Non,Non,Non,N
on,Non,Non,Non,Non,BA4.1.En.TF.12
>
BA5.1.0.En.T.13,CGCAGTACGA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCT
AAT,run2pool1,SRR3330056,NotUsed,Balcarce,Wheat,5,Tillering,Root_Associated,MID56,13,95,Non,Non,Non,N
on,Non,Non,Non,Non,BA5.1.0.En.T.13
>
BA5.1.0.En.TF.14,CGCGTATACA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool1,SRR3330056,NotUsed,Balcarce,Wheat,5,Flowering,Root_Associated,MID57,14,269,Non,Non,Non
,Non,Non,Non,Non,Non,BA5.1.0.En.TF.14
>
BA5.1.1.En.T.15,CGTACAGTCA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCT
AAT,run2pool1,SRR3330056,Used,Balcarce,Wheat,5,Tillering,Root_Associated,MID58,15,833,Non,11_wheat_RA
_RS,Non,Non,14_wheat_RA,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,BA5.1.1.En.T.15
>
BA5.1.1.En.TF.16,CGTACTCAGA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool1,SRR3330056,NotUsed,Balcarce,Wheat,5,Flowering,Root_Associated,MID59,16,1412,Non,Non,No
n,Non,Non,Non,Non,Non,BA5.1.1.En.TF.16
>
BA5.2.1.En.T.19,CTACGCTCTA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCT
AAT,run2pool1,SRR3330056,NotUsed,Balcarce,Wheat,5,Tillering,Root_Associated,MID60,19,432,Non,Non,Non,
Non,Non,Non,Non,Non,BA5.2.1.En.T.19
>
BA5.2.1.En.TF.20,CTATAGCGTA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool1,SRR3330056,NotUsed,Balcarce,Wheat,5,Flowering,Root_Associated,MID61,20,984,Non,Non,Non
,Non,Non,Non,Non,Non,BA5.2.1.En.TF.20
>
BA5.3.0.En.T.21,TACGTCATCA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCT
AAT,run2pool1,SRR3330056,Used,Balcarce,Wheat,5,Tillering,Root_Associated,MID62,21,610,Non,11_wheat_RA
_RS,Non,Non,14_wheat_RA,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,BA5.3.0.En.T.21
>
BA5.3.0.En.TF.22,TAGTCGCATA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool1,SRR3330056,NotUsed,Balcarce,Wheat,5,Flowering,Root_Associated,MID63,22,1023,Non,Non,No
n,Non,Non,Non,Non,Non,BA5.3.0.En.TF.22
>
BA5.3.1.En.T.23,TATATATACA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCT
AAT,run2pool1,SRR3330056,NotUsed,Balcarce,Wheat,5,Tillering,Root_Associated,MID64,23,261,Non,Non,Non,
Non,Non,Non,Non,Non,BA5.3.1.En.T.23
>
CB2.0.En.T.25,TATGCTAGTA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,NotUsed,CorraldeBustos,Wheat,2,Tillering,Root_Associated,MID65,25,474,Non,Non,
Non,Non,Non,Non,Non,Non,CB2.0.En.T.25
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CB2.1.En.T.26,TCACGCGAGA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,NotUsed,CorraldeBustos,Wheat,2,Tillering,Root_Associated,MID66,26,430,Non,Non,
Non,Non,Non,Non,Non,Non,CB2.1.En.T.26
>
CB3.0.En.T.27,TCGATAGTGA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool1,SRR3330056,Used,CorraldeBustos,Wheat,3,Tillering,Root_Associated,MID67,27,671,Non,11_whea
t_RA_RS,Non,Non,14_wheat_RA,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,CB3.0.En.T.27
>
BA2.0.En.T.1,TCTATACTAT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT
,run2pool2,SRR3330057,NotUsed,Balcarce,Wheat,2,Tillering,Root_Associated,MID45,1,308,Non,Non,Non,Non,
Non,Non,Non,Non,BA2.0.En.T.1
>
BA2.0.En.TF.2,TGACGTATGT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool2,SRR3330057,NotUsed,Balcarce,Wheat,2,Flowering,Root_Associated,MID46,2,495,Non,Non,Non,Non
,Non,Non,Non,Non,BA2.0.En.TF.2
>
BA2.1.En.T.3,TGTGAGTAGT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT
,run2pool2,SRR3330057,Used,Balcarce,Wheat,2,Tillering,Root_Associated,MID47,3,916,Non,11_wheat_RA_RS,
Non,Non,14_wheat_RA,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,BA2.1.En.T.3
>
BA2.1.En.TF.4,ACAGTATATA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool2,SRR3330057,NotUsed,Balcarce,Wheat,2,Flowering,Root_Associated,MID48,4,1679,Non,Non,Non,No
n,Non,Non,Non,Non,BA2.1.En.TF.4
>
BA3.0.En.T.5,ACGCGATCGA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT
,run2pool2,SRR3330057,NotUsed,Balcarce,Wheat,3,Tillering,Root_Associated,MID49,5,1550,Non,Non,Non,Non
,Non,Non,Non,Non,BA3.0.En.T.5
>
BA3.0.En.TF.6,ACTAGCAGTA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool2,SRR3330057,NotUsed,Balcarce,Wheat,3,Flowering,Root_Associated,MID50,6,1740,Non,Non,Non,No
n,Non,Non,Non,Non,BA3.0.En.TF.6
>
BA3.1.En.T.7,ACGACTACAG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT
,run2pool2,SRR3330057,Used,Balcarce,Wheat,3,Tillering,Root_Associated,MID20,7,4384,Non,11_wheat_RA_RS
,Non,Non,14_wheat_RA,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,BA3.1.En.T.7
>
BA5.2.0.En.T.17,CGTAGACTAG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCT
AAT,run2pool2,SRR3330057,Used,Balcarce,Wheat,5,Tillering,Root_Associated,MID21,17,1343,Non,11_wheat_R
A_RS,Non,Non,14_wheat_RA,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,BA5.2.0.En.T.17
>
BA5.2.0.En.TF.18,AGACTATACT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool2,SRR3330057,NotUsed,Balcarce,Wheat,5,Flowering,Root_Associated,MID30,18,1344,Non,Non,No
n,Non,Non,Non,Non,Non,BA5.2.0.En.TF.18
>
BA5.3.1.En.TF.24,AGCGTCGTCT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool2,SRR3330057,NotUsed,Balcarce,Wheat,5,Flowering,Root_Associated,MID31,24,924,Non,Non,Non
,Non,Non,Non,Non,Non,BA5.3.1.En.TF.24
>
CB3.1.En.T.28,TCGCTGCGTA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool2,SRR3330057,Used,CorraldeBustos,Wheat,3,Tillering,Root_Associated,MID68,28,1987,Non,11_whe
at_RA_RS,Non,Non,14_wheat_RA,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,CB3.1.En.T.28
>
CB4.0.En.T.29,TCTGACGTCA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool2,SRR3330057,Used,CorraldeBustos,Wheat,4,Tillering,Root_Associated,MID69,29,1995,Non,11_whe
at_RA_RS,Non,Non,14_wheat_RA,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,CB4.0.En.T.29
>
CB4.1.En.T.30,TGAGTCAGTA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool2,SRR3330057,Used,CorraldeBustos,Wheat,4,Tillering,Root_Associated,MID70,30,2838,Non,11_whe
at_RA_RS,Non,Non,14_wheat_RA,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,CB4.1.En.T.30
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>
CB5.0.En.T.31,TGTAGTGTGA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,CorraldeBustos,Wheat,5,Tillering,Root_Associated,MID71,31,832,Non,11_wheat_RA_RS,Non,Non,14_wheat_RA,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,CB5.0.En.T.31
>
CB5.1.En.T.32,TGTCACACGA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,CorraldeBustos,Wheat,5,Tillering,Root_Associated,MID72,32,1240,Non,11_wheat_RA_RS,Non,Non,14_wheat_RA,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,CB5.1.En.T.32
>
DA2.0.En.T.33,TGTCGTCGCA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,Daireaux,Wheat,2,Tillering,Root_Associated,MID73,33,1622,Non,11_wheat_RA_RS,Non,Non,14_wheat_RA,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,DA2.0.En.T.33
>
DA2.1.En.T.34,ACACATACGC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,NotUsed,Daireaux,Wheat,2,Tillering,Root_Associated,MID74,34,1639,Non,Non,Non,Non,Non,Non,Non,Non,DA2.1.En.T.34
>
DA3.0.En.T.35,ACAGTCGTGC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,NotUsed,Daireaux,Wheat,3,Tillering,Root_Associated,MID75,35,1810,Non,Non,Non,Non,Non,Non,Non,Non,DA3.0.En.T.35
>
DA3.1.En.T.36,ACATGACGAC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,Daireaux,Wheat,3,Tillering,Root_Associated,MID76,36,1665,Non,11_wheat_RA_RS,Non,Non,14_wheat_RA,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,DA3.1.En.T.36
>
DA4.0.En.T.37,ACGACAGCTC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,Daireaux,Wheat,4,Tillering,Root_Associated,MID77,37,2211,Non,11_wheat_RA_RS,Non,Non,14_wheat_RA,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,DA4.0.En.T.37
>
DA4.1.En.T.38,TACGAGTATG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,Daireaux,Wheat,4,Tillering,Root_Associated,MID22,38,2814,Non,11_wheat_RA_RS,Non,Non,14_wheat_RA,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,DA4.1.En.T.38
>
DA5.0.En.T.39,ACGTCTCATC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,Daireaux,Wheat,5,Tillering,Root_Associated,MID78,39,2252,Non,11_wheat_RA_RS,Non,Non,14_wheat_RA,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,DA5.0.En.T.39
>
DA5.1.En.T.40,ACTCATCTAC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,Daireaux,Wheat,5,Tillering,Root_Associated,MID79,40,1393,Non,11_wheat_RA_RS,Non,Non,14_wheat_RA,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,DA5.1.En.T.40
>
VS2.0.En.T.41,TACTCTCGTG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,VillaSaboya,Wheat,2,Tillering,Root_Associated,MID23,41,1379,Non,11_wheat_RA_RS,Non,Non,14_wheat_RA,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,VS2.0.En.T.41
>
VS2.1.En.T.42,ACGCGAGTAT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,VillaSaboya,Wheat,2,Tillering,Root_Associated,MID27,42,825,Non,11_wheat_RA_RS,Non,Non,14_wheat_RA,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,VS2.1.En.T.42
>
VS3.0.En.T.43,ACTACTATGT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,VillaSaboya,Wheat,3,Tillering,Root_Associated,MID28,43,356,Non,Non,Non,Non,Non,Non,Non,17_wheat_soybean_RA,VS3.0.En.T.43
>
VS3.1.En.T.44,CGAGAGATAC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,VillaSaboya,Wheat,3,Tillering,Root_Associated,MID14,44,663,Non,11_wheat_RA_RS,Non,Non,14_wheat_RA,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,VS3.1.En.T.44
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VS4.0.En.T.45,TCGTCGCTCG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool2,SRR3330057,Used,VillaSaboya,Wheat,4,Tillering,Root_Associated,MID25,45,1219,Non,11_wheat_
RA_RS,Non,Non,14_wheat_RA,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,VS4.0.En.T.45
>
VS4.1.En.T.46,ACTGTACAGT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool2,SRR3330057,NotUsed,VillaSaboya,Wheat,4,Tillering,Root_Associated,MID29,46,485,Non,Non,Non
,Non,Non,Non,Non,Non,VS4.1.En.T.46
>
VS5.0.En.T.47,ACTCGCGCAC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool2,SRR3330057,Used,VillaSaboya,Wheat,5,Tillering,Root_Associated,MID80,47,2699,Non,11_wheat_
RA_RS,Non,Non,14_wheat_RA,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,VS5.0.En.T.47
>
VS5.1.En.T.48,TAGAGACGAG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool2,SRR3330057,Used,VillaSaboya,Wheat,5,Tillering,Root_Associated,MID24,48,2011,Non,11_wheat_
RA_RS,Non,Non,14_wheat_RA,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,VS5.1.En.T.48
>
BA2.1.Su.T.B.1,TACAGATCGT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTA
AT,run2pool2,SRR3330057,Used,Balcarce,Wheat,2,Tillering,Rhizospheric_Soil,MID39,1,1144,Non,11_wheat_R
A_RS,Non,Non,Non,Non,16_wheat_soybean_RA_RS,Non,BA2.1.Su.T.B.1
>
MB4.0.Su.T.B.27,TCGATCACGT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCT
AAT,run2pool2,SRR3330057,Used,MonteBuey,Wheat,4,Tillering,Rhizospheric_Soil,MID42,27,2094,Non,Non,Non
,Non,Non,Non,Non,Non,MB4.0.Su.T.B.27
>
CB2.0.Su.T.B.32,TACGCTGTCT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCT
AAT,run2pool2,SRR3330057,NotUsed,CorraldeBustos,Wheat,2,Tillering,Rhizospheric_Soil,MID40,32,771,Non,
Non,Non,Non,Non,Non,Non,Non,CB2.0.Su.T.B.32
>
DA2.0.Su.T.B.34,ACATACGCGT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCT
AAT,run2pool2,SRR3330057,Used,Daireaux,Wheat,2,Tillering,Rhizospheric_Soil,MID26,34,3574,Non,11_wheat
_RA_RS,Non,Non,Non,Non,16_wheat_soybean_RA_RS,Non,DA2.0.Su.T.B.34
>
VS2.0.Su.T.B.37,TCGCACTAGT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCT
AAT,run2pool2,SRR3330057,Used,VillaSaboya,Wheat,2,Tillering,Rhizospheric_Soil,MID43,37,2263,Non,11_wh
eat_RA_RS,Non,Non,Non,Non,16_wheat_soybean_RA_RS,Non,VS2.0.Su.T.B.37
>
MB2.0.Su.T.B.38,TAGTGTAGAT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCT
AAT,run2pool2,SRR3330057,Used,MonteBuey,Wheat,2,Tillering,Rhizospheric_Soil,MID41,38,2104,Non,Non,Non
,Non,Non,Non,Non,Non,MB2.0.Su.T.B.38
>
VS4.0.Su.T.B.43,TCTAGCGACT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCT
AAT,run2pool2,SRR3330057,Used,VillaSaboya,Wheat,4,Tillering,Rhizospheric_Soil,MID44,43,1774,Non,11_wh
eat_RA_RS,Non,Non,Non,15_wheat_RS,16_wheat_soybean_RA_RS,Non,VS4.0.Su.T.B.43
>
SJ2.0.Su.T.B.54,TACACGTGAT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCT
AAT,run2pool2,SRR3330057,NotUsed,SanJorge,Wheat,2,Tillering,Rhizospheric_Soil,MID38,54,1874,Non,Non,N
on,Non,Non,Non,Non,Non,SJ2.0.Su.T.B.54
>
SJ5.2.0.Su.T.B.81,TACACACACT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTAT
CTAAT,run2pool2,SRR3330057,NotUsed,SanJorge,Wheat,5,Tillering,Rhizospheric_Soil,MID37,81,864,Non,Non,
Non,Non,Non,Non,Non,Non,SJ5.2.0.Su.T.B.81
>
SJ5.1.1.Su.T.B.82,TGATACGTCT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTAT
CTAAT,run2pool2,SRR3330057,NotUsed,SanJorge,Wheat,5,Tillering,Rhizospheric_Soil,MID11,82,435,Non,Non,
Non,Non,Non,Non,Non,Non,SJ5.1.1.Su.T.B.82
>
CH2a11.1.En.S.62,ACGAGTGCGT,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool2,SRR3330057,Used,Chilibroste,Soybean,2,Vegetative,Root_Associated,MID1,62,2675,10_soybe
an_RA_RS,Non,12_soybean_RA,Non,Non,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,CH2a11.1.En.S.62
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>
CH3.0.En.S.63,ACGCTCGACA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,Chilibroste,Soybean,3,Vegetative,Root_Associated,MID2,63,5850,10_soybean_RA_RS,Non,12_soybean_RA,Non,Non,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,CH3.0.En.S.63
>
CH3all.1.En.S.64,AGACGCACTC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,Chilibroste,Soybean,3,Vegetative,Root_Associated,MID3,64,3177,Non,Non,12_soybean_RA,Non,Non,Non,Non,17_wheat_soybean_RA,CH3all.1.En.S.64
>
HU2.0.En.S.65,AGCACTGTAG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,Huges,Soybean,2,Vegetative,Root_Associated,MID4,65,2837,10_soybean_RA_RS,Non,12_soybean_RA,Non,Non,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,HU2.0.En.S.65
>
HU2all.1.En.S.66,ATCAGACACG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,Huges,Soybean,2,Vegetative,Root_Associated,MID5,66,3577,10_soybean_RA_RS,Non,12_soybean_RA,Non,Non,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,HU2all.1.En.S.66
>
HU3.0.En.S.67,ATATCGCGAG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,Huges,Soybean,3,Vegetative,Root_Associated,MID6,67,4159,10_soybean_RA_RS,Non,12_soybean_RA,Non,Non,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,HU3.0.En.S.67
>
HU3all.1.En.S.68,CGTGTCTCTA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,Huges,Soybean,3,Vegetative,Root_Associated,MID7,68,2795,Non,Non,12_soybean_RA,Non,Non,Non,Non,17_wheat_soybean_RA,HU3all.1.En.S.68
>
MB2.0.En.S.69,CTCGCGTGTC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,MonteBuey,Soybean,2,Vegetative,Root_Associated,MID8,69,2174,10_soybean_RA_RS,Non,12_soybean_RA,Non,Non,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,MB2.0.En.S.69
>
MB3.0.En.S.71,TCTCTATGCG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,MonteBuey,Soybean,3,Vegetative,Root_Associated,MID10,71,2858,10_soybean_RA_RS,Non,12_soybean_RA,Non,Non,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,MB3.0.En.S.71
>
SA3all.1.En.S.76,ATACGACGTA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,SanAgustin,Soybean,3,Vegetative,Root_Associated,MID15,76,2703,10_soybean_RA_RS,Non,12_soybean_RA,Non,Non,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,SA3all.1.En.S.76
>
VS2.0.En.S.77,TCACGTACTA,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,VillaSaboya,Soybean,2,Vegetative,Root_Associated,MID16,77,2475,Non,Non,12_soybean_RA,Non,Non,Non,Non,17_wheat_soybean_RA,VS2.0.En.S.77
>
VS2all.1.En.S.78,CGTCTAGTAC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,VillaSaboya,Soybean,2,Vegetative,Root_Associated,MID17,78,2908,10_soybean_RA_RS,Non,12_soybean_RA,Non,Non,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,VS2all.1.En.S.78
>
VS3.0.En.S.79,TCTACGTAGC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,VillaSaboya,Soybean,3,Vegetative,Root_Associated,MID18,79,3269,10_soybean_RA_RS,Non,12_soybean_RA,Non,Non,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,VS3.0.En.S.79
>
VS3all.1.En.S.80,TGTACTACTC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,VillaSaboya,Soybean,3,Vegetative,Root_Associated,MID19,80,2541,10_soybean_RA_RS,Non,12_soybean_RA,Non,Non,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,VS3all.1.En.S.80
>
SA2all.1.En.S.74,CATAGTAGTG,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAAT,run2pool2,SRR3330057,Used,SanAgustin,Soybean,2,Vegetative,Root_Associated,MID13,74,1000,10_soybean_RA_RS,Non,12_soybean_RA,Non,Non,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,SA2all.1.En.S.74
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MB2a11.1.En.S.70,CGACACTATC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATC
TAAT,run2pool2,SRR3330057,Used,MonteBuey,Soybean,2,Vegetative,Root_Associated,MID92,70,3046,10_soybea
n_RA_RS,Non,12_soybean_RA,Non,Non,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,MB2a11.1.En.S.70
>
SA2.0.En.S.73,CGAGACGCGC,CACGACGTTGTAAAACGACGTGCCAGCMGCCGCGGTAA,CAGGAAACAGCTATGACCGGACTACVSGGGTATCTAA
T,run2pool2,SRR3330057,Used,SanAgustin,Soybean,2,Vegetative,Root_Associated,MID93,73,2054,10_soybean_
RA_RS,Non,12_soybean_RA,Non,Non,Non,16_wheat_soybean_RA_RS,17_wheat_soybean_RA,SA2.0.En.S.73
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