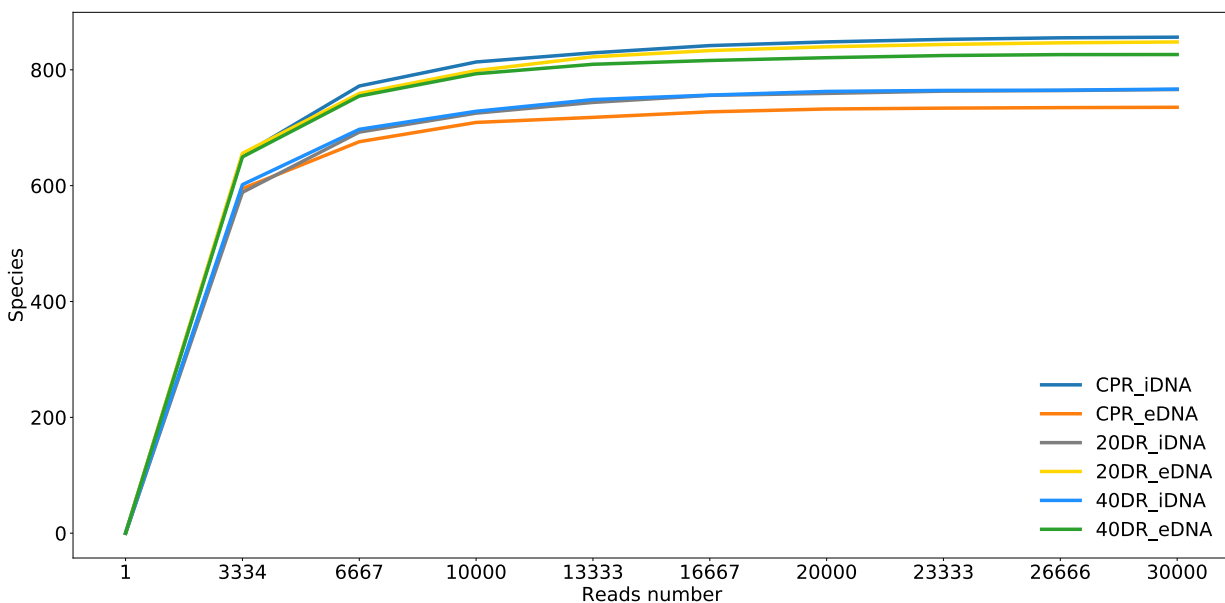


Supplementary Materials: The following supporting information can be downloaded at: www.mdpi.com/xxx/s1,
 Figure S1: title; Table S1: title; Video S1: title.



Supplementary Figure 1: Rarefaction curves.

Supplementary Table 1: Phylum level report of the High-Throughput Sequencing

Taxonomy	CPRi	CPRe	20DRi	20DRe	40DRi	40DRe
<i>Proteobacteria</i>	46.24%	41.83%	51.92%	48.91%	47.60%	46.14%
<i>Gemmatimonadetes</i>	9.87%	10.01%	10.87%	8.26%	11.32%	8.56%
<i>Bacteroidetes</i>	10.27%	10.38%	10.77%	8.31%	9.22%	8.63%
<i>Chloroflexi</i>	5.29%	6.46%	5.84%	9.55%	6.97%	10.88%
<i>Acidobacteria</i>	6.58%	3.70%	8.85%	4.77%	9.40%	5.46%
<i>Actinobacteria</i>	4.02%	4.09%	3.81%	8.68%	4.80%	8.11%
<i>Verrucomicrobia</i>	4.83%	5.82%	2.91%	5.11%	4.99%	6.48%
<i>Firmicutes</i>	7.58%	13.12%	0.52%	0.96%	0.89%	1.24%
<i>Patescibacteria</i>	1.48%	1.43%	0.83%	1.65%	1.04%	1.65%
Taxa below 0.5%	1.15%	0.79%	1.21%	1.14%	1.17%	0.81%
Planctomycetes	1.09%	0.92%	0.29%	1.17%	0.82%	0.81%
Armatimonadetes	0.60%	0.53%	0.77%	0.54%	0.97%	0.57%
Cyanobacteria	0.36%	0.40%	0.20%	0.58%	0.35%	0.42%
uncultured soil bacterium WS2	0.40%	0.10%	1.06%	0.19%	0.41%	0.14%
Spirochaetes	0.23%	0.43%	0.17%	0.18%	0.05%	0.12%

Supplementary Table 2: Genera level report of the High-Throughput Sequencing: OTUs detected in controls and do not in treated samples.

OTUs			CPR_iDNA	CPR_eDNA	20DR_iDNA	20DR_eDNA	40DR_iDNA	40DR_eDNA
<i>Lutispora</i>	AN	Gv	0,77%	1,34%	0,00%	0,00%	0,00%	0,00%
<i>Eisenbergiella</i>	AN	Gv	0,36%	0,73%	0,00%	0,00%	0,00%	0,00%
<i>Desulfotobacterium</i>	sAN	+	0,36%	0,39%	0,00%	0,00%	0,00%	0,00%
<i>Anaerovorax</i>	sAN	Gv	0,31%	0,34%	0,00%	0,00%	0,00%	0,00%
<i>Anaerobacterium</i>	AN	+	0,24%	0,64%	0,00%	0,00%	0,00%	0,00%
<i>Oxalobacter</i>	AN	-	0,23%	0,25%	0,00%	0,00%	0,00%	0,00%
<i>Veillonella</i>	AN	-	0,22%	0,22%	0,00%	0,00%	0,00%	0,00%
<i>Desulfovibrio</i>	AN	-	0,20%	0,17%	0,00%	0,00%	0,00%	0,00%
<i>Clostridium sensu stricto 12</i>	AN	+	0,19%	0,21%	0,00%	0,00%	0,00%	0,00%
<i>Desulfotomaculum</i>	AN	+	0,12%	0,14%	0,00%	0,00%	0,00%	0,00%
<i>Clostridium sensu stricto 3</i>	AN	+	0,12%	0,14%	0,00%	0,00%	0,00%	0,00%
<i>Thermincola</i>	AN	+	0,11%	0,11%	0,00%	0,00%	0,00%	0,00%
<i>Clostridium sensu stricto 16</i>	AN	+	0,09%	0,13%	0,00%	0,00%	0,00%	0,00%
U. m. of Ruminococcaceae family	sAN	+	0,09%	0,17%	0,00%	0,00%	0,00%	0,00%
<i>Kaistia</i>	sAE	-	0,09%	0,17%	0,00%	0,00%	0,00%	0,00%
U. m. of Clostridiales order	AN	+	0,07%	0,10%	0,00%	0,00%	0,00%	0,00%
<i>Oxobacter</i>	AN	+	0,06%	0,04%	0,00%	0,00%	0,00%	0,00%
<i>Propioniceella</i>	fAN	+	0,06%	0,07%	0,00%	0,00%	0,00%	0,00%
<i>Niabella</i>	sAE	-	0,04%	0,06%	0,00%	0,00%	0,00%	0,00%
U. m. of Christensenellaceae family	AN	-	0,04%	0,04%	0,00%	0,00%	0,00%	0,00%
<i>Haliscomenobacter</i>	sAE	-	0,03%	0,04%	0,00%	0,00%	0,00%	0,00%
<i>Niveispirillum</i>	AE	-	0,03%	0,07%	0,00%	0,00%	0,00%	0,00%
<i>Propionivibrio</i>	AN	-	0,03%	0,02%	0,00%	0,00%	0,00%	0,00%
<i>Sedimentibacter</i>	sAN	+/-	0,02%	0,06%	0,00%	0,00%	0,00%	0,00%
<i>Dechloromonas</i>	AN	-	0,01%	0,02%	0,00%	0,00%	0,00%	0,00%

Gv: cells stained Gram-negative, the cell-wall ultrastructure resembles Gram-positive bacteria; +: gram stain positive; -: gram stain negative; +/-: Gram stain positive or negative. AE: aerobic; sAE: strict aerobic; AN: anaerobic; sAN: strict anaerobic; fAN: facultative anaerobic

Supplementary Table 3: Plant Growth Promoting Rhizobacteria (PGPR) microorganisms

	Nitrogen fixation	Phytohormones production	Siderophore production	(ACC) deaminase	Phosphate solubilization	Overcoming environmental stress	
<i>Acetobacter</i>					+		[48, 66]
<i>Advenella</i>		+	+		+		[66]
<i>Allorhizobium</i>	+						[68]
<i>Anabaena</i>	+						[48]
<i>Arthrobacter</i>					+		[66, 68]
<i>Aulosira</i>	+						[48]
<i>Azorhizobium</i>	+						[65, 68]
<i>Azospirillum</i>	+	+	+			+	[69, 48, 65, 66, 68]
<i>Azotobacter</i>	+	+					[48, 65]
<i>Bacillus</i>	+	+		+	+	+	[69, 48, 66]
<i>Bradyrhizobium</i>	+	+					[66]
<i>Burkholderia</i>	+	+	+	+	+		[65, 66]
<i>Cedecea</i>					+		[66]
<i>Cellulosimicrobium</i>		+	+		+		[72]
<i>Chryseobacterium</i>			+		+		[65, 66]
<i>Citrobacter</i>			+				[68]
<i>Cronobacter</i>					+		[66]
<i>Delftia</i>					+		[66]
<i>Enterobacter</i>		+			+		[66]
<i>Escherichia</i>		+					[66]
<i>Flavobacterium</i>					+		[68]
<i>Frankia</i>	+						[66]
<i>Frateuria</i>						+	[69]
<i>Gluconacetobacter</i>	+					+	[48, 66]
<i>Gordonia</i>					+		[66]
<i>Grimontella</i>		+	+				[66]
<i>Herbaspirillum</i>	+		+		+		[66, 66]
<i>Klebsiella</i>		+	+		+		[66]
<i>Mesorhizobium</i>	+						[66, 73]
<i>Methylobacterium</i>	+						[71]
<i>Micrococcus</i>					+		[68]
<i>Mycobacterium</i>						+	[65]
<i>Nostoc</i>	+						[48]
<i>Ochrobactrum</i>				+			[66]
<i>Paenibacillus</i>		+			+		[65, 66]
<i>Pantoea</i>	+	+			+		[66]
<i>Phosphobacter</i>					+	+	[48]
<i>Phyllobacterium</i>			+		+		[65, 66]
<i>Plectonema</i>	+						[48]
<i>Pseudomonas</i>		+	+	+	+	+	[48, 65, 66]
<i>Rahnella</i>		+					[66]
<i>Rhizobium</i>	+	+	+	+	+		[65, 70]
<i>Rhodococcus</i>					+		[66]
<i>Scytonema</i>	+						[48]
<i>Serratia</i>					+		[66]
<i>Sinorhizobium</i>	+					+	[65]
<i>Stenotrophomonas</i>			+			+	[48]
<i>Tetrathibacter</i>					+		[66]
<i>Tolypothrix</i>	+						[48]

Supplementary Table 4: PGPR bacteria distribution detected in iDNA and eDNA. Treated samples OTUs abundance compared to controls. Bold and underlined show OTUs with higher and lower abundance, respectively

	CPR_iDNA	20DR_iDNA	40DR_iDNA	CPR_eDNA	20DR_eDNA	40DR_eDNA
<i>Allorhizobium</i>	0,19%	<u>0,15%</u>	0,19%	0,22%	0,23%	<u>0,20%</u>
<i>Azospirillum</i>	0,13%	<u>0,00%</u>	<u>0,10%</u>	0,29%	<u>0,06%</u>	<u>0,23%</u>
<i>Pseudomonas</i>	0,30%	<u>0,16%</u>	<u>0,08%</u>	0,21%	0,21%	0,22%
<i>Bacillus</i>	1,65%	<u>0,07%</u>	<u>0,50%</u>	4,24%	<u>0,51%</u>	<u>0,73%</u>
<i>Bradyrhizobium</i>	0,00%	0,00%	0,20%	0,00%	0,21%	0,12%
<i>Chryseobacterium</i>	0,00%	0,00%	0,01%	0,00%	0,01%	0,01%
<i>Enterobacter</i>	0,00%	0,00%	0,03%	0,00%	0,00%	0,04%
<i>Mesorhizobium</i>	0,41%	<u>0,37%</u>	<u>0,35%</u>	0,35%	0,51%	<u>0,33%</u>
<i>Paenibacillus</i>	0,00%	0,02%	0,02%	0,00%	0,03%	0,02%
<i>Pantoea</i>	0,00%	0,02%	0,02%	0,00%	0,03%	0,02%
<i>Pseudomonas</i>	0,30%	<u>0,16%</u>	<u>0,08%</u>	0,21%	0,21%	0,22%
<i>Rhizobium</i>	0,19%	<u>0,15%</u>	0,19%	0,22%	0,23%	<u>0,20%</u>
<i>Stenotrophomonas</i>	0,02%	<u>0,00%</u>	<u>0,00%</u>	0,00%	0,00%	0,00%