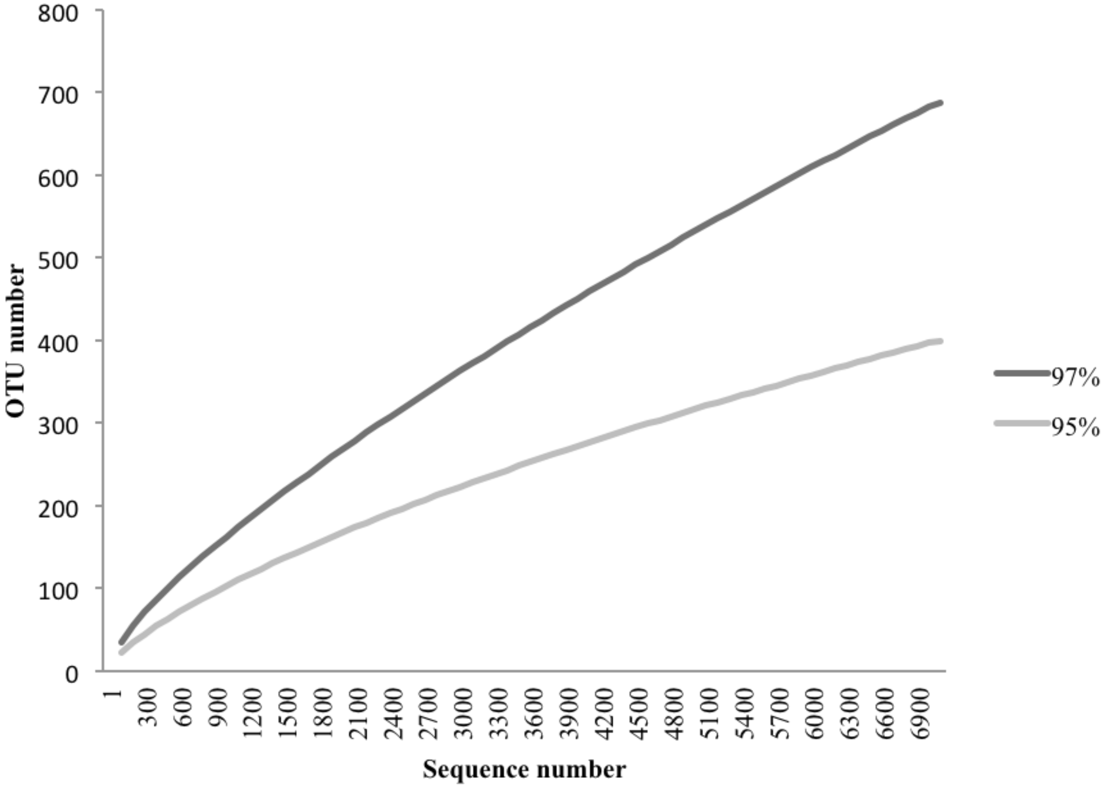

Figure S1. Rarefaction analysis of the 16S rDNA sequences from culturable bacterial isolates from maize rhizospheres. Curves were constructed based on 95 and 97 % sequence identity. Curves did not reach a plateau, indicating that sample saturation was not reached.

Supplementary Table S1. Physicochemical properties of sampled soils.

Site	pH (1:2)	EC	OM (%)	TN (ppm)	P (mg/Kg)	K (Cmol/Kg)	Ca (Meq/100g)	Mg (Cmol/Kg)	Na (Cmol/Kg)	Snd (%)	St (%)	Cy (%)	Texture type	Maize hybrid	Days after sowing
I	6.3^{a}	0.03^{a}	0.35^{a}	47.4^{a}	11.52^{a}	0.98^{a}	8.62^{a}	2.88^{a}	1.35^{a}	57.06	32.70	10.24	Sandy-loam	Pioneer / 30P49	40-45
II	7.6^{b}	0.08^{a}	0.38^{a}	52.6^{a}	18.34^{a}	1.49^{b}	11.23^{a}	3.32^{a}	1.70^{a}	51.6	54.70	14.24	Clay	Dekalb / Dk2020	80-90
III	7.4^{b}	0.10^{a}	0.40^{a}	54.8^{a}	17.89^{a}	1.39^{b}	10.78^{a}	3.84^{a}	1.81^{a}	27.06	56.70	10.24	Clay	Syngenta / Renacer	60-70
IV	7.1^{b}	0.09^{a}	0.50^{a}	54.2^{a}	37.80^{b}	1.60^{b}	16.10^{b}	5.71^{b}	1.48^{a}	8.34	40.70	50.96	Silty clay	Pioneer / 30P49	70-80
V	7.3^{b}	0.09^{a}	0.46^{a}	55.1^{a}	8.66^{a}	1.08^{a}	10.29^{a}	5.42^{b}	1.85^{a}	18.34	28.70	52.96	Clay	Dekalb / Dk2020	120-130

Electric conductivity (EC), organic matter (OM), total nitrogen (TN), bioavailable phosphate (P), potassium (K), calcium (Ca), magnesium (Mg), sodium (Na), sand (Snd), silt (St), clay (Cy). Different lower case letters in the same column indicate differences ($P<0.01$) between sites.

Supplementary Table S2. OTUs and its best match and percentage of identity.

OTU	Best match	% Identity	Accession Number
OTU 1	*Bacillus subtilis* DY7	100.0	EU096316
OTU 2	*Bacillus cereus* SG4	100.0	KX817272
OTU 3	*Bacillus aryabhattai* MML5326	98.2	MF687955
OTU 4	*Bacillus megaterium* UIS0181	99.0	MT178181
OTU 5	*Bacillus* sp. NIASMJP5N	97.7	LC467356
OTU 6	*Bacillus flexus* 4-1	100.0	EU594560
OTU 7	*Bacillus* sp. DU40	97.7	HM567096
OTU 8	*Bacillus subtilis* CLW-BA1-5	98.9	HQ334986
OTU 10	*Staphylococcus saprophyticus* HBUAS51564	100.0	FJ854568
OTU 12	*Bacillus subtilis* R7	98.6	GQ122328
OTU 13	*Bacillus endophyticus* EH6	99.8	GU339236
OTU 15	*Bacillus cereus* V34	93.9	HM439506
OTU 16	*Bacillus subtilis* CCGB:1271	98.4	GQ482980
OTU 17	*Bacillus cereus* SG4	99.5	KX817272
OTU 18	*Bacillus subtilis* GHt1-7	98.1	GU434357
OTU 19	*Bacillus firmus* EK-29	99.5	EU910249
OTU 20	*Bacillus flexus*	98.8	GU395997
OTU 21	*Bacillus megaterium* Y18-04	97.2	GU143908
OTU 22	*Enterobacter* sp.	99.7	FJ976548
OTU 23	*Bacillus flexus* 4-1	96.6	EU594560
OTU 25	*Bacillus* sp. DU32(2010)	98.1	HM567087
OTU 26	*Bacillus* sp. CNE 9	94.6	FR749864
OTU 30	*Terribacillus* sp. J31	100.0	EU435359
OTU 34	*Bacillus* sp. FO-011	98.9	AF234842
OTU 36	*Pseudomonas* sp. Sk0927	99.7	FJ751243
OTU 37	*Pseudomonas* sp. KUS3	91.2	LN794843.1
OTU 39	*Pseudomonas* sp. YT3	86.7	HQ143572
OTU 43	*Bacillus subtilis* B-12	92.0	HQ009797
OTU 46	*Pseudomonas* sp. sk0927	92.9	FJ751243
OTU 50	*Pseudomonas* sp. sk0927	92.9	FJ751243
OTU 51	*Bacillus* sp. EK-25	93.7	EU910245
OTU 52	*Bacillus* sp. SRC_DSF15	94.3	GU797297
OTU 54	*Bacillus subtilis* APBSMLB98	92.3	MG705877.1
OTU 55	*Klebsiella pneumoniae* kpwiq51	98.2	MT102634
OTU 56	*Pseudomonas putida* AQ	91.3	JF751057
OTU 59	*Klebsiella pneumoniae* A17KP0004	98.2	CP052560
OTU 60	*Bacillus* sp. Cafi13c	99.2	AY859753
OTU 75	*Pseudomonas putida* SEM	95.4	FN600412
OTU 79	*Bacillus subtilis* strain RP24	91.0	EF154418
OTU 82	*Pantoea* sp. OSA17	99.8	HM222646
OTU 84	*Bacillus pumilus* L2 ecto 7	96.3	FN555460
OTU 94	*Lysinibacillus fusiformis* MB-13	99.7	HM055955
OTU 95	*Bacillus megaterium* DSM319	98.6	CP001982
OTU 98	*Bacillus subtilis* CLW-BA1-5	98.5	HQ334986
OTU 103	*Paenibacillus polymyxa* BCHMAC42	99.6	GU188910
OTU 104	*Cronobacter sakazakii* fmb03	97.7	JF330129
OTU 112	*Massilia timonae* 205	99.6	EU730926
OTU 113	*Bacillus licheniformis* strain SD2	97.9	HM055611
OTU 114	*Arthrobacter* sp. TXc7-10	99.5	HQ333015
OTU 117	*Bacillus* sp. TSH18	98.8	AB508884
OTU 118	*Bacillus* sp. LX1	95.5	HQ660811

OTU 120	*Acinetobacter* sp. CNE 4	99.2	FR749854
OTU 121	*Bacillus* sp. DU40(2010)	98.5	HM567096
OTU 123	*Bacillus subtilis* DmB4	93.1	HQ111352
OTU 124	*Bacillus flexus* IK-MB14-518F	97.3	FJ906742
OTU 125	*Bacillus subtilis* DmB4	96.1	HQ111352
OTU 126	*Bacillus* sp. ITCr14	99.7	FR823403
OTU 127	*Bacillus subtilis* CLW-BA1-5	97.8	HQ334986
OTU 128	*Bacillus flexus* IK-MB14-518F	97.1	FJ906742
OTU 129	*Bacillus endophyticus* EH6	94.0	GU339236
OTU 130	*Bacillus* sp. MTCC 5513	95.4	HM222944
OTU 131	*Bacillus pumilus* BPRIST037	100.0	JF431426
OTU 134	*Bacillus subtilis* DmB4	98.3	HQ111352
OTU 137	*Bacillus* sp. TXc2-2	96.4	HQ333033
OTU 138	*Bacillus subtilis* CLS-BA8-7	81.8	HQ334981
OTU 141	*Bacillus pumilus* TW3	91.7	GU204972
OTU 151	*Bacillus* sp. DU40(2010)	98.0	HM567096
OTU 156	*Bacillus pumilus*CLW-A5-5	92.6	HQ334983
OTU 157	*Bacillus* sp. R12(2010)	94.9	GU433443
OTU 159	*Bacillus cereus*SV1	96.4	EU327888
OTU 162	*Bacillus* sp. DU40(2010)	94.6	HM567096
OTU 163	*Bacillus* sp. M1(2009)	92.8	GU086455
OTU 164	*Acinetobacter calcoaceticus* GWRVA20	95.7	EU921458
OTU 167	*Acinetobacter calcoaceticus*	90.6	DQ187381
OTU 168	*Pseudomonas plecoglossicida* S4	95.4	DQ095893
OTU 169	*Acinetobacter schindleri* IBP-SL13	94.7	HQ689693
OTU 172	*Bacillus anthracis* F9	85.3	FJ009400
OTU 174	*Sinomonas atrocyanea* DSM 20127	99.6	X80746
OTU 175	*Bacillus cereus* CNE 11	93.3	FR749859
OTU 179	*Bacillus* sp. IMER-B2-29	99.8	FJ715743
OTU 183	*Bacillus cereus* MB-24	95.7	HM055966
OTU 185	*Pseudomonas luteola* Marseille	93.8	AY574976
OTU 190	*Bacillus* sp. OSM29	98.2	HM222647
OTU 195	*Bacillus cereus* SO16	98.2	GQ891107
OTU 196	*Bacillus cereus* CNE 11	93.5	FR749859
OTU 197	*Bacillus* sp. MB-5	100.0	HM055947
OTU 202	*Bacillus* sp. DU27(2010)	90.1	HM567081
OTU 208	*Bacillus licheniformis* XJSL4-3	95.5	GQ903412
OTU 212	*Bacillus cereus* MB-29	96.5	HM055971
OTU 216	*Enterobacter* sp. IPPBC-W27	97.4	HQ840768
OTU 220	*Bacillus* sp. DB23(2010)	96.8	HM566906
OTU 221	N/D		
OTU 224	*Bacillus* sp. DU118(2010)	95.5	HM566998
OTU 228	*Bacillus* sp. ICB415	88.6	HM748070
OTU 231	*Bacillus subtilis* RSNPB23	95.3	HM588163
OTU 239	*Stenotrophomonas maltophilia* MHF ENV 22	99.8	HQ661377
OTU 240	*Stenotrophomonas maltophilia* SH-3 16S	95.2	GQ884174
OTU 243	*Sphingobacterium multivorum* DW-18	99.9	EU240955
OTU 248	*Arthrobacter nitroguajacolicus* Rue61a	99.8	AJ785758
OTU 251	*Bacillus subtilis* CLS-BA8-7	99.1	HQ334981
OTU 252	*Bacillus* sp. M71_S46	96.9	FM992827
OTU 253	*Bacillus* sp. SC131(2010)	96.1	HM566485
OTU 254	*Bacillus* sp. DU40(2010)	99.1	HM567096
OTU 259	*Bacillus subtilis* CLS-BA8-7	97.3	HQ334981
OTU 260	*Bacillus cereus* BAC-B2	92.5	DQ884352

OTU 261	*Bacillus megaterium* 3BS3	96.4	HM161867
OTU 262	*Bacillus* sp. SRC_DSF15	88.2	GU797297
OTU 266	*Bacillus thuringiensis* Y4-36	98.7	GU143905
OTU 267	*Bacillus flexus* IK-MB14-518F	98.2	FJ906742
OTU 268	*Bacillus mojavensis* TKLS-C4-5	96.2	HQ334989
OTU 269	*Bacillus* sp. IBP-SL8	98.5	HQ689689
OTU 270	*Bacillus* sp. IHB B 4014	96.4	HM233989
OTU 272	*Bacillus cereus* MB-29	97.9	HM055971
OTU 273	*Bacillus* sp. SWL-3	99.4	AM689971
OTU 274	*Brevibacillus* sp. GI-9	99.3	FR686596
OTU 275	*Bacillus pumilus* IK-MB13-518F	89.0	FJ906741
OTU 281	*Paenibacillus pabuli*	99.4	AB366401
OTU 282	*Pseudomonas mendocina*	97.6	AF094734
OTU 288	*Bacillus subtilis* CLS-BA8-7	96.5	HQ334981
OTU 289	*Rhizobium* sp. BZ3	100.0	HQ588847
OTU 313	*Klebsiella aerogenes* UIS0178	97.3	MT178070
OTU 314	*Pantoea agglomerans* 4GW7	95.7	GU991862
OTU 321	*Bacillus cereus* BAC-B2	93.0	DQ884352
OTU 324	*Bacillus pumilus* SB 3129	92.7	GU191902
OTU 325	*Bacillus pumilus* RRLJ SMAD	87.5	DQ299945
OTU 331	*Bacillus subtilis* CLS-BA8-7	94.6	HQ334981
OTU 335	*Enterobacter* sp BMC3	84.8	JN053269
OTU 336	*Bacillus* sp. SGE173(2010)	92.3	HM566699
OTU 365	*Bacillus megaterium* Z3-4	93.7	HQ268535
OTU 368	*Enterobacter cloacae* OsEp_A&N_15A7	94.4	JQ830772
OTU 372	*Bacillus* sp. RKZ11261	97.2	EU835568
OTU 375	*Lysinibacillus* sp. 3405BRRJ	89.7	JF309274
OTU 381	*Bacillus cereus* BAC-B2	93.4	DQ884352
OTU 383	*Pseudomonas* sp. Y3-3	98.8	HM057106
OTU 385	*Lysinibacillus fusiformis* DB-1	96.2	GU084135
OTU 387	*Paenibacillus* sp. Dg-904	99.1	EU497636
OTU 388	*Bacillus* sp. DV9-46	100.0	GQ407190
OTU 390	*Bacillus* sp. MTCC 5513	96.6	HM222944
OTU 392	*Lysinibacillus sphaericus*	91.6	FR846534
OTU 393	*Lysinibacillus* sp. TSSAS2-47	89.5	GQ284508
OTU 394	*Paenibacillus lautus* DS19	96.7	EU834247
OTU 398	*Bacillus cereus* PPB11	97.1	HM771666
OTU 401	*Bacillus cereus* SO16	89.3	GQ891107
OTU 409	*Bacillus subtilis* Z3-1	84.3	HQ290082
OTU 411	*Bacillus* sp. OSM29	98.0	HM222647
OTU 412	*Bacillus* sp. NK7	95.2	AY654898
OTU 416	*Bacillus* sp. PN13	97.6	DQ523735
OTU 419	*Pseudomonas* sp. T2P35	89.7	FM212008
OTU 421	*Pseudomonas* sp. J14	99.8	EU099380
OTU 422	*Paenibacillus* sp. SWCH-2	97.9	EU700193
OTU 423	*Bacillus marisflavi*	96.1	AB617551
OTU 433	*Bacillus* sp. IHB B 4014	91.7	HM233989
OTU 441	*Terribacillus* sp. 3404BRRJ	87.2	JF309273
OTU 451	*Bacillus* sp. SRC_DSF10	92.1	GU797292
OTU 453	*Paenibacillus* sp. Y412MC10	91.1	CP001793
OTU 454	*Bacillus pumilus* MW-1	98.3	HM027879
OTU 456	*Bacillus* sp. Can6	94.0	EU831296
OTU 459	*Bacillus* sp. SGE173(2010)	95.4	HM566699
OTU 464	*Bacillus amyloliquefaciens* TA208	93.1	CP002627

OTU 469	*Bacillus* sp. OSM29	97.1	HM222647
OTU 489	*Bacillus* sp. MB104	93.1	AB518947
OTU 490	*Bacillus* subtilis AR-2	91.6	FJ866758
OTU 494	*Bacillus* sp. SRC_DSF8	92.1	GU797290
OTU 495	*Bacillus megaterium*DCU41	94.2	HM594691
OTU 505	*Bacillus* sp. DU87(2010)	95.1	HM567144
OTU 510	*Bacillus* sp. CCBAU 13239	92.8	EF377308
OTU 521	*Bacillus flexus* strain IK-MB14-518F	98.3	FJ906742
OTU 523	*Bacillus flexus* strain IK-MB14-518F	97.1	FJ906742
OTU 541	*Bacillus subtilis* strain TXc1-2	99.0	GU434365
OTU 567	*Bacillus* sp. IHB B 2287	96.6	HM233977
OTU 568	*Bacillus aquimaris* strain 44-B-6A	96.3	EU927415
OTU 575	*Bacillus subtilis* strain GHt1-7	95.1	GU434357
OTU 576	*Bacillus megaterium* strain 3DL144M	92.2	HM163494
OTU 577	*Bacillus* sp. PaH3.30a	96.1	GQ406788
OTU 584	*Bacillus* sp. SRC_DSF24	95.0	GU797306
OTU 592	*Bacillus* sp. J21(2010)	91.8	HM624045
OTU 593	*Bacillus megaterium* strain D4	95.8	FJ755786
OTU 596	*Bacillus megaterium* strain Y18-04	90.3	GU143908.
OTU 600	*Pseudomonas corrugata* isolate PSB35	94.9	HQ242748
OTU 607	*Bacillus cereus* EK-15	89.5	EU910235
OTU 625	*Bacillus* sp. EK-22	85.8	EU910242
OTU 642	*Bacillus* sp. FZ-3	97.6	HM242293
OTU 650	*Aeromonas veronii* B565	99.8	CP002607
OTU 661	*Pseudomonas fluorescens* HN1205	89.2	HQ610446
OTU 662	*Bacillus* sp. EK-22	92.2	EU910242

N/D not defined.