

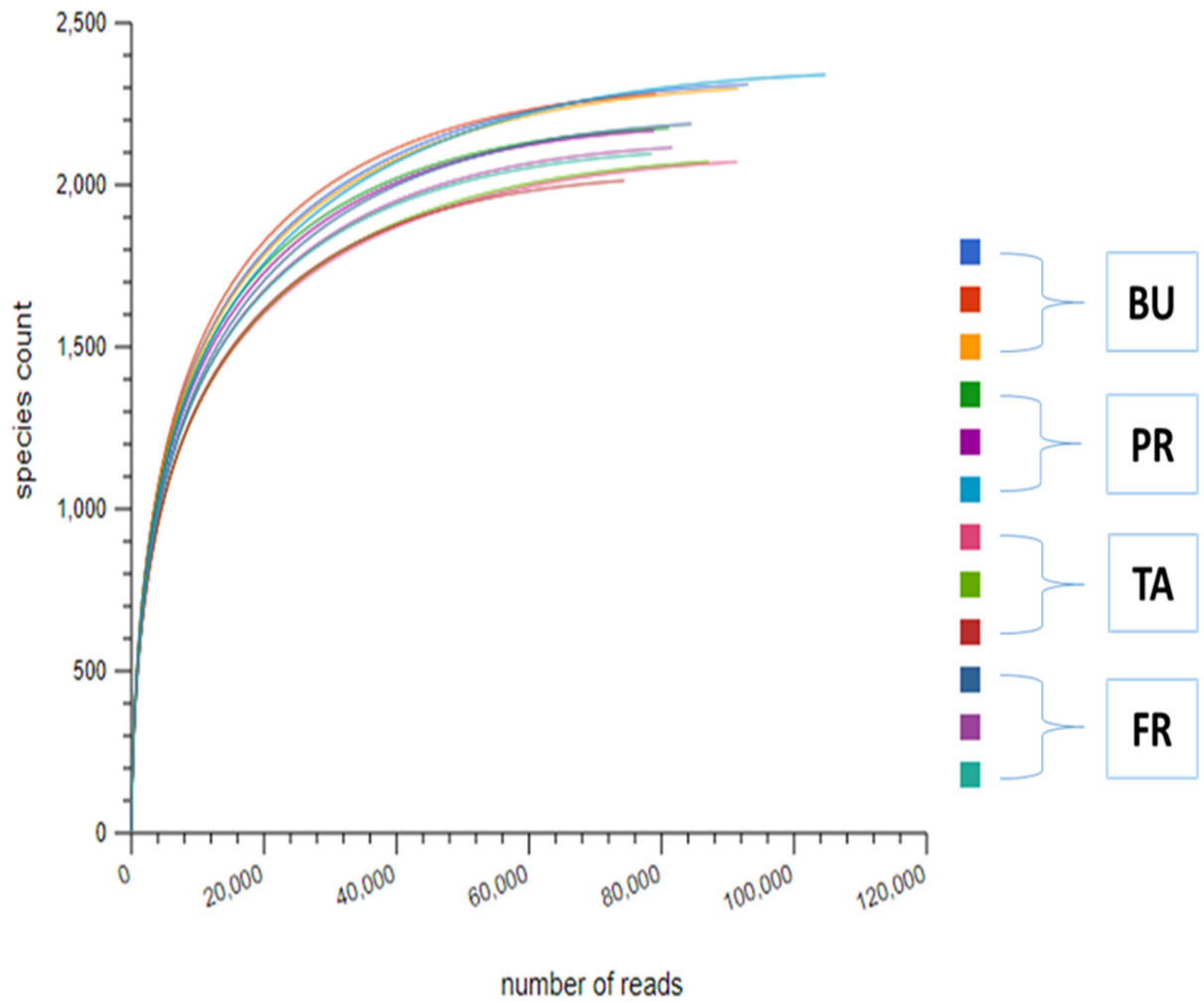
**Table S1.** 16S amplicon sequence information for maize rhizosphere across different growth stages.

SAMPLE	DATA BEFORE QC					DATA AFTER QC			
	Size (bp)	No. of raw sequence reads	Mean sequence length(bp)	Mean GC content(%)	No of artificial duplicate read	Size (bp)	No. of sequence reads	Mean sequence length (bp)	Mean GC content (%)
BU1	399998 74	93132	429 ± 60	59 ± 5	78725	55444 47	13981	397 ± 92	59 ± 4
BU2	339592 50	79190	429 ± 62	58 ± 5	66328	49222 16	12368	398 ± 91	59 ± 4
BU3	394392 63	91569	431 ± 59	58 ± 4	78070	52090 32	13189	395 ± 94	58 ± 4
PR1	347650 82	81200	428 ± 61	59 ± 4	68091	50731 52	12759	398 ± 91	59 ± 4
PR2	338905 51	78866	430 ± 57	59 ± 4	66470	48404 35	12182	397 ± 91	59 ± 4
PR3	450883 95	104815	430 ± 60	58 ± 5	89330	59627 07	14913	400 ± 88	59 ± 4
TA1	390883 84	91384	428 ± 60	58 ± 5	77224	53870 58	13644	395 ± 91	59 ± 4
TA2	370520 55	87143	425 ± 69	58 ± 7	73348	50254 26	12809	392 ± 94	59 ± 4
TA3	314582 63	74393	423 ± 67	58 ± 6	61962	45577 68	11824	385 ± 95	59 ± 4
FR1	357286 55	84510	423 ± 66	58 ± 5	69749	54864 05	14237	385 ± 95	58 ± 4
FR2	344999 59	81697	422 ± 68	58 ± 6	66905	53813 58	14139	381 ± 100	58 ± 5
FR3	333578 78	78587	424 ± 64	58 ± 5	65154	50888 29	13101	388 ± 95	59 ± 4

BU- Bulk soil, PR- Pretasseling stage rhizosphere, TA- Tasseling stage rhizosphere, FR- Fruiting stage rhizosphere.

**Table S2:** Beta diversity evaluation of nitrifying bacteria and archaea

	BU	PR	TA	FR	P-value	R
BU	0.000	0.020	0.020	0.000	0.01	0.58
PR	0.020	0.000	0.000	0.020		
TA	0.020	0.000	0.000	0.020		
FR	0.000	0.020	0.020	0.000		



**Figure S1.** Rarefaction curve showing the richness of species sequences across the different vegetative growth. BU= samples from bulk soil, PR= samples from pretasseling growth stage, TA= samples from tassel growth stage, FR= samples from fruiting growth stage.