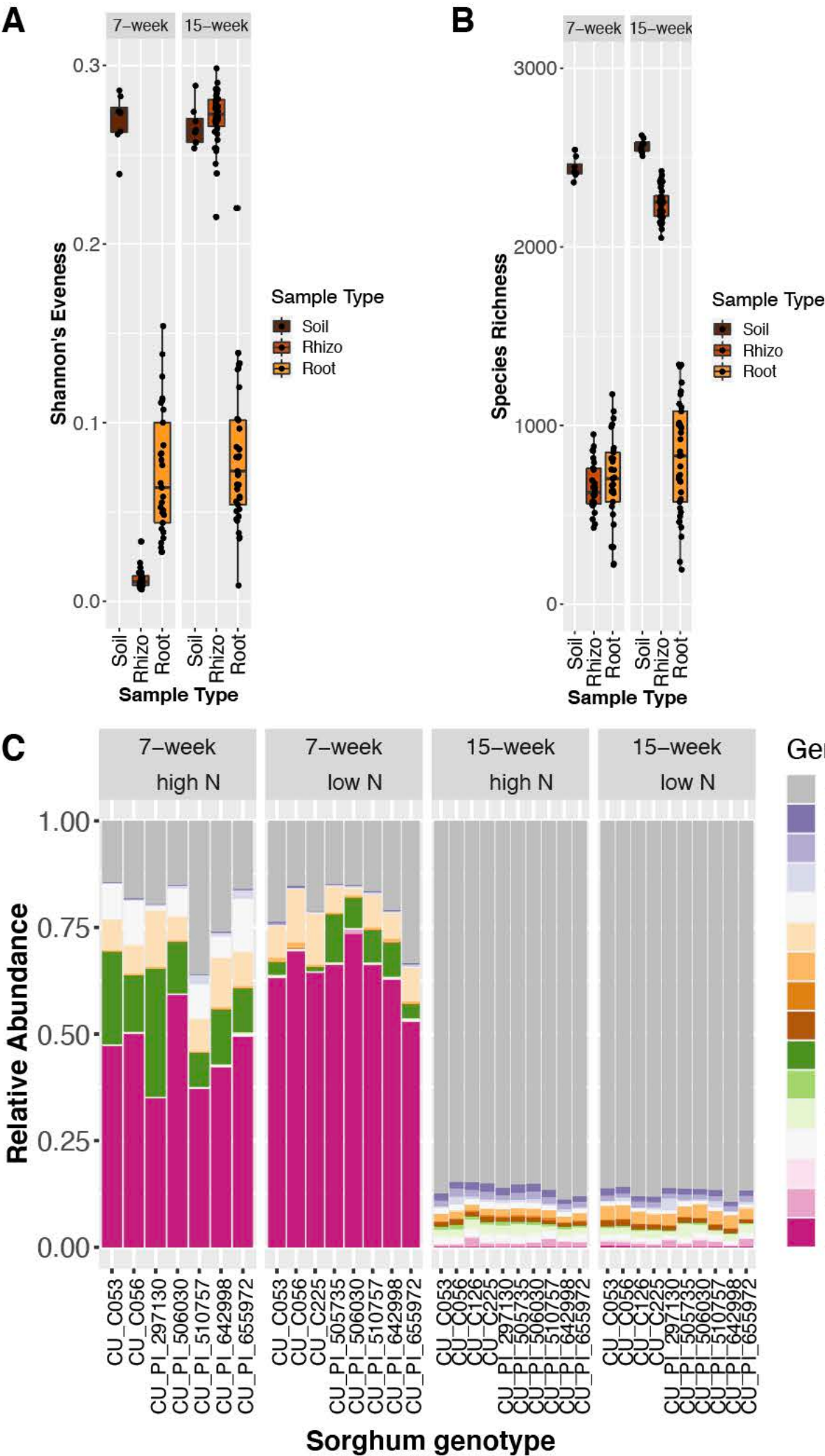
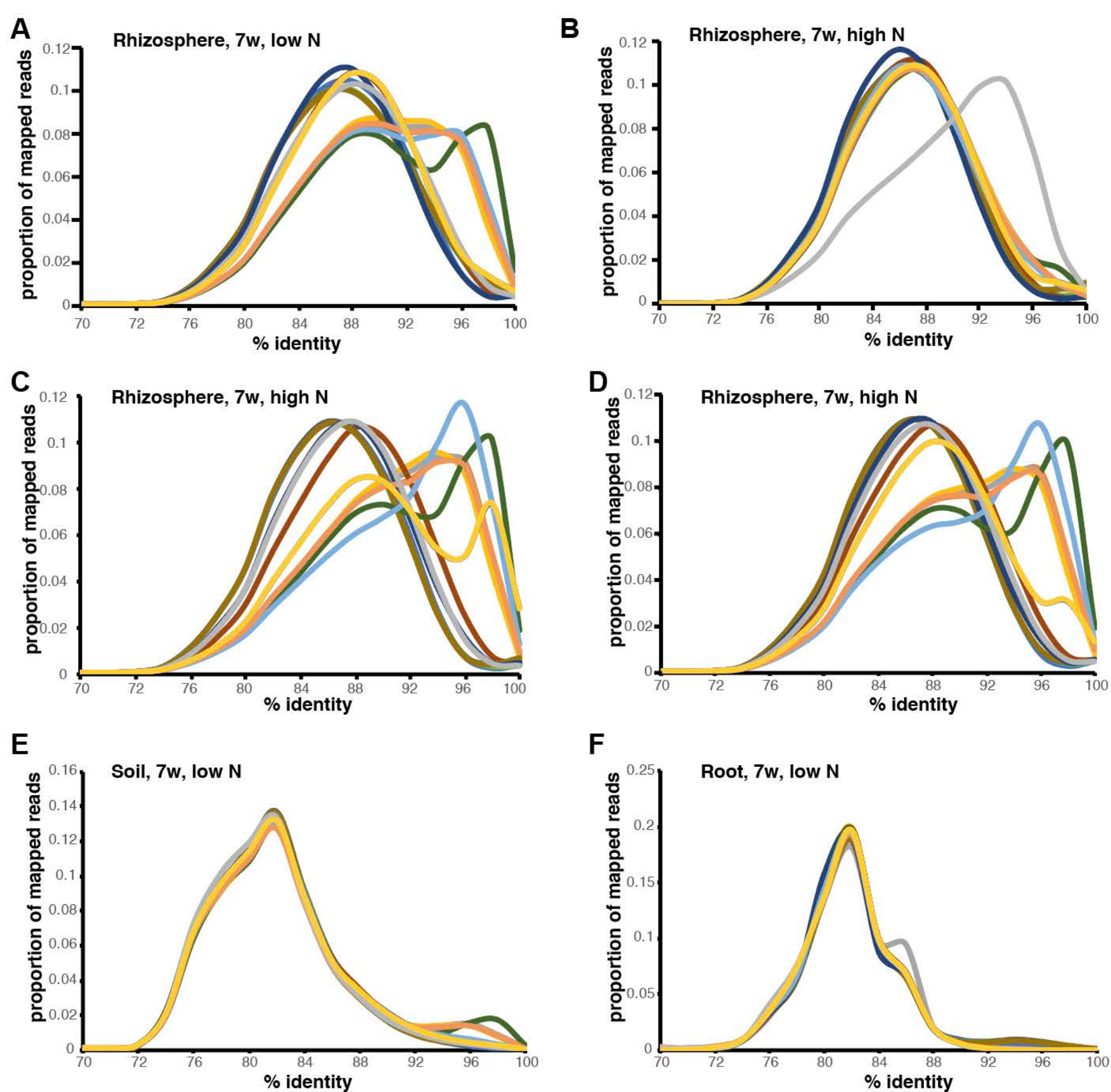


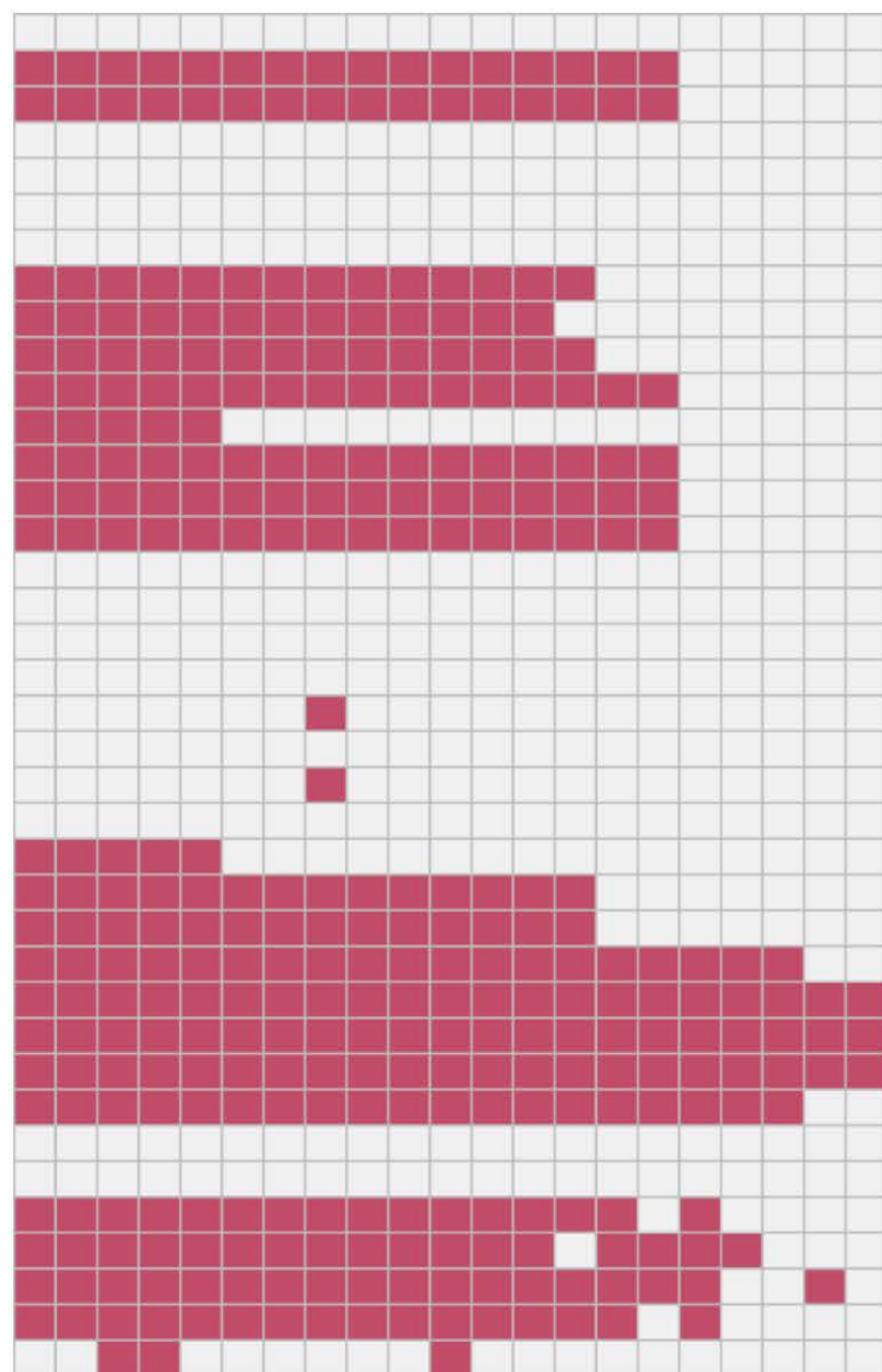


Supplemental Figure S1. Amplicon data reveals components of Shannon's diversity and *Pseudomonas* expansion across nitrogen treatments in the sorghum rhizosphere. **A**, Boxplots of Shannon's evenness for soil, rhizosphere and root samples at the 7-week (left panel) and 15-week (right panel) time points using the 97% clustered OTU dataset. **B**, Boxplots of species richness for soil, rhizosphere and root samples at the 7-week (left panel) and 15-week (right panel) time points using the 97% clustered OTU dataset. **C**, Relative abundance barplots for the top fifteen most abundant genera in the 97% clustered OTU dataset as plotted for individual rhizosphere samples within the 7-week time point (left two panels) and 15-week time point (right two panels) for each of the two nitrogen treatments (individual panels). These data demonstrate a large increase in *Rhodanobacter* in high nitrogen samples that is not seen in the low nitrogen samples (ANOVA, $p < 0.001$, $F = 45.93$). Additionally, these data demonstrate that while *Janthinobacterium* abundance remains relatively equivalent between treatment groups in the rhizosphere 7w time point (ANOVA, $p = 0.62$, $F = 0.26$), the genus *Pedobacter* is higher in the high nitrogen compared to low nitrogen (ANOVA, $p < 0.01$, $F = 10.31$) and the genus *Pseudomonas* is higher in the low nitrogen than high nitrogen (ANOVA, $p < 0.001$, $F = 16.49$).



— *Pseudomonas frederiksbergensis* AS1
 — *Pseudomonas fluorescens* C3
 — *Pseudomonas fluorescens* H24
 — *Pseudomonas koreensis* CRS05-R5
 — *Pseudomonas* sp. RIT288
 — *Pseudomonas frederiksbergensis* KNU-15
 — *Pseudomonas* sp. 655
 — *Pseudomonas* sp. JAI1 15
 — *Pseudomonas* sp. 424
 — *Pseudomonas prosekii* LMG 26867
 — *Pseudomonas* sp. OV341
 — *Pseudomonas arsenicoxydans* CECT 7543
 — *Pseudomonas frederiksbergensis* LMG 19851
 — *Pseudomonas jessenii* LMG 21605
 — *Pseudomonas umsogensis* KD5_MF50

Supplemental Figure S2. Genome wide alignment of assembled shotgun metagenomic reads with 15 closest isolate genomes based on long read 16S data. Plots of metagenome data for individual field samples selected for metagenomic sequencing: **A**, rhizosphere 7-week time point from low N field. **B**, **C**, **D**, three replicates of rhizosphere 7-week time point from high N field. **E**, soil 7-week time point from low N field, **F**, root 7-week time point from low N field. For each panel, 15 fully sequenced *Pseudomonas* isolates were selected from the IMG database based on similarity to the 10 most abundant full-length *Pseudomonas* sequences in our single-molecule data and subsequently we mapped the QC-filtered raw metagenomic reads to these genomes. Plots represent the proportion of mapped reads (y-axis) as a function of mapped percent identity (x-axis) for 15 selected genomes. The majority of rhizosphere samples exhibit high levels of mapping to multiple *Pseudomonas* species, including *P. frederiksbergensis* LMG 19851 (IMG database ID: 2636416079), *P. arsenicoxydans* CECT 7543 (IMG database ID: 2636416065, and a relative of *P. lini*) and *Pseudomonas* sp. OV341 (IMG database ID: 2757320528).



type III effector protein AvrRpm1
 type III effector protein AvrPtoB
 type III secretion system translocator protein
 HrpZ protein
 HrpF protein
 type III effector protein AvrF
 type III secretion apparatus protein HrpB
 putative type III negative regulator of Hrp expression (HrpV)
 HrpD
 type III secretion protein D
 HrpL
 type III secretion protein W
 type III secretion protein Q
 type III secretion protein U
 type III secretion protein C
 Hrps
 type III secretion protein S
 type III secretion protein R
 type III secretion protein J
 type III secretion protein T
 type III secretion protein V

Pseudomonas arsenicoxydans CECT 7543
 Pseudomonas brassicacearum BS3663
 Pseudomonas brassicacearum subsp. brassicacearum NFM421
 Pseudomonas corrugata
 Pseudomonas corrugata BS3649
 Pseudomonas corrugata CFBP5403
 Pseudomonas corrugata TEIC1148
 Pseudomonas extremaustralis DSM 17835
 Pseudomonas extremorientalis BS2774
 Pseudomonas fluorescens ATCC 13525
 Pseudomonas fluorescens F113
 Pseudomonas fluorescens N2C3
 Pseudomonas fluorescens N2E2
 Pseudomonas fluorescens Pf29Arp
 Pseudomonas fluorescens Q8r1-96
 Pseudomonas frederiksbergensis BS3655
 Pseudomonas koreensis BS3658
 Pseudomonas lini BS3782
 Pseudomonas mediterranea CFBP 5447
 Pseudomonas mediterranea CFBP5444
 Pseudomonas mediterranea DSM 16733
 Pseudomonas mediterranea TEIC1105
 Pseudomonas moraviensis BS3668
 Pseudomonas reinekei BS3776
 Pseudomonas simiae DSM 18861
 Pseudomonas synxantha LMG 2190
 Pseudomonas syringae 31R1
 Pseudomonas syringae pv. apii BS0426
 Pseudomonas syringae pv. apii BS2900
 Pseudomonas syringae pv. fabae BS2730
 Pseudomonas syringae pv. lachrymans BS2122
 Pseudomonas vancouverensis BS3656
 Soil metagenome
 Rhizosphere metagenome 1
 Rhizosphere metagenome 2
 Rhizosphere metagenome 3
 Rhizosphere metagenome 4
 Endophyte metagenome

Present
 Absent

Supplemental Figure S3. Presence/absence of Hrp-family T3SS orthologs in Pseudomonas isolate genomes and sorghum metagenomes. Isolates identified in green represent isolates with known commensal relationships with plants whereas isolates in red represent known pathogenic isolates. Proteins associated with each gene in the island are labeled on the bottom of the heatmap.