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A - Papers appearing in refereed journals

Fu, Q., Abadie, M., Blaud, A., Carswell, A. M., Misselbrook, T. H., Clark, I. M. and Hirsch, P. R. 2019. Effects of urease and nitrification inhibitors on soil N, nitrifier abundance and activity in a sandy loam soil . *Biology And Fertility Of Soils.*

The publisher's version can be accessed at:

- https://dx.doi.org/10.1007/s00374-019-01411-5

The output can be accessed at: https://repository.rothamsted.ac.uk/item/96z51/effects-of-urease-and-nitrification-inhibitors-on-soil-n-nitrifier-abundance-and-activity-in-a-sandy-loam-soil.

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Supplementary Fig. 1. Daily measurements at Woburn of soil temperature (10 cm depth) and rainfall after urea application.
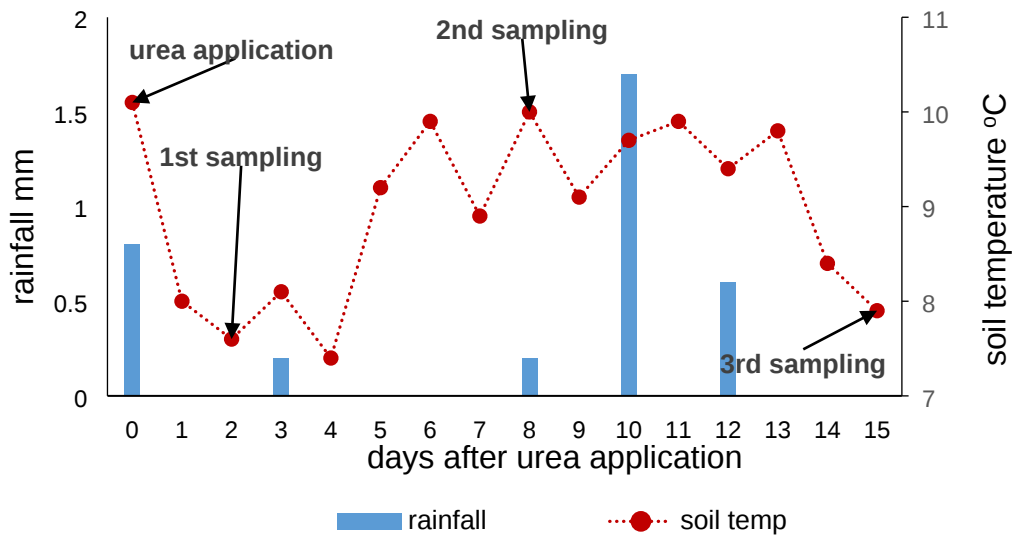

Supplementary Fig. 2. Wheat grain and straw N offtake and net N recovery in all treatment plots (n = 6). Letters above columns denote significantly different means according to Tukey's post-hoc test on ANOVA, α = 0.05. AN – ammonium nitrate fertilizer applied at same N rate as urea.
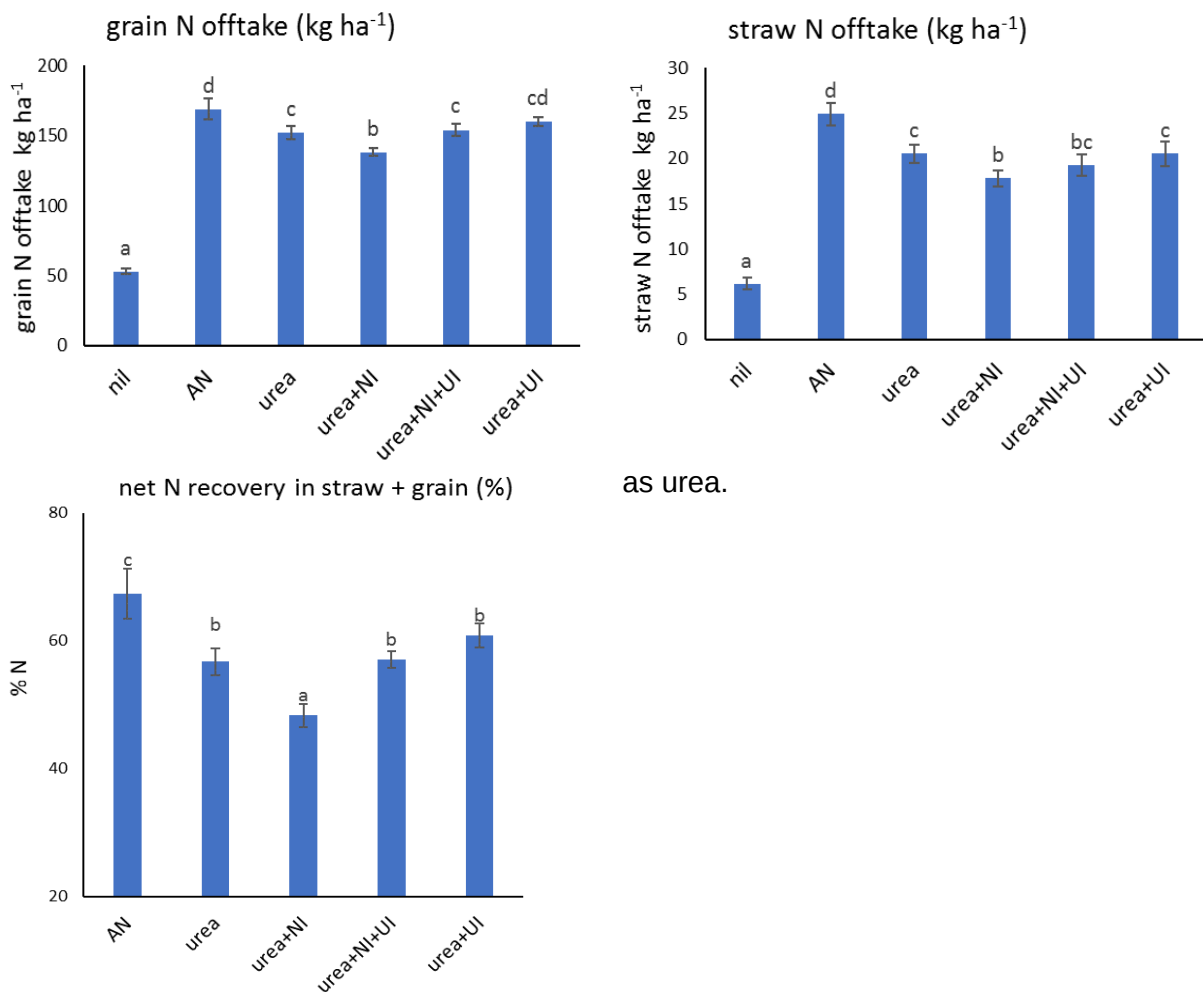
Supplementary Fig. 3. NMDS plot, Bray-Curtis matrix, for 16S rRNA amplicon diversity (2000 most abundant OTU) in all treatments 2 d after urea application.
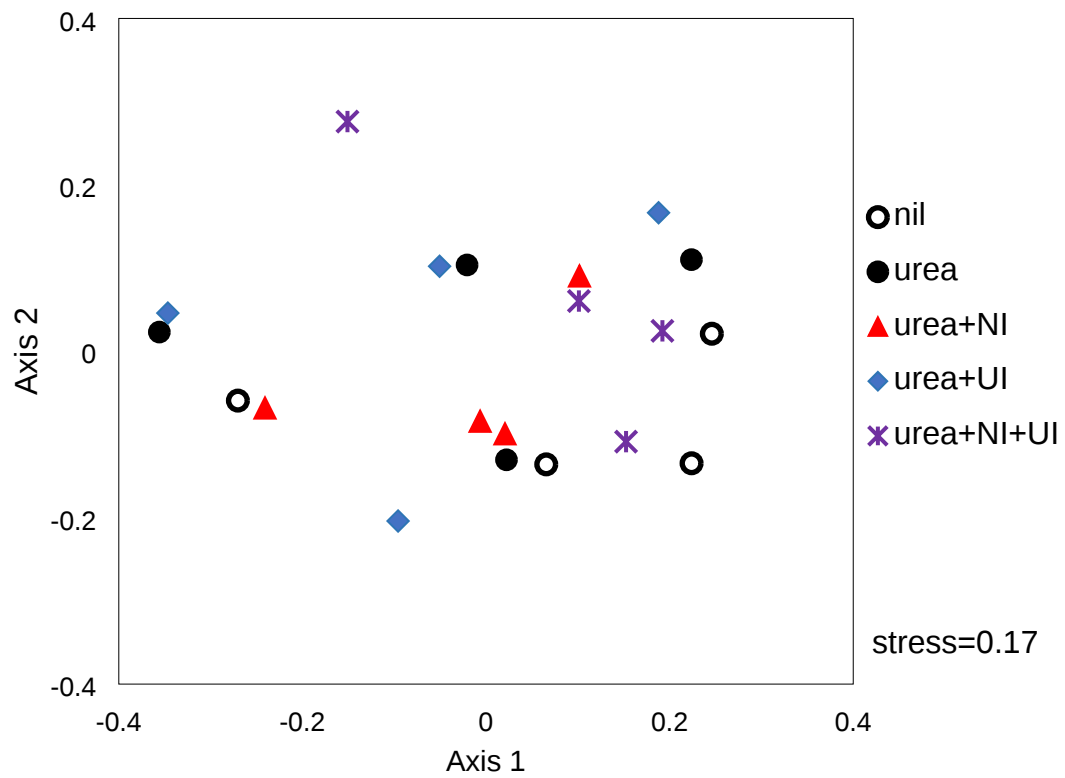
Supplementary Fig. 4. Mean abundance for all treatments of genes at each time point. All genes were significantly less abundant at 15 days compared to two days after urea addition (Tukey's post-hoc *α* = 0.05) except *nxr Nitrospira* and *amoA* Archaea (NSD).
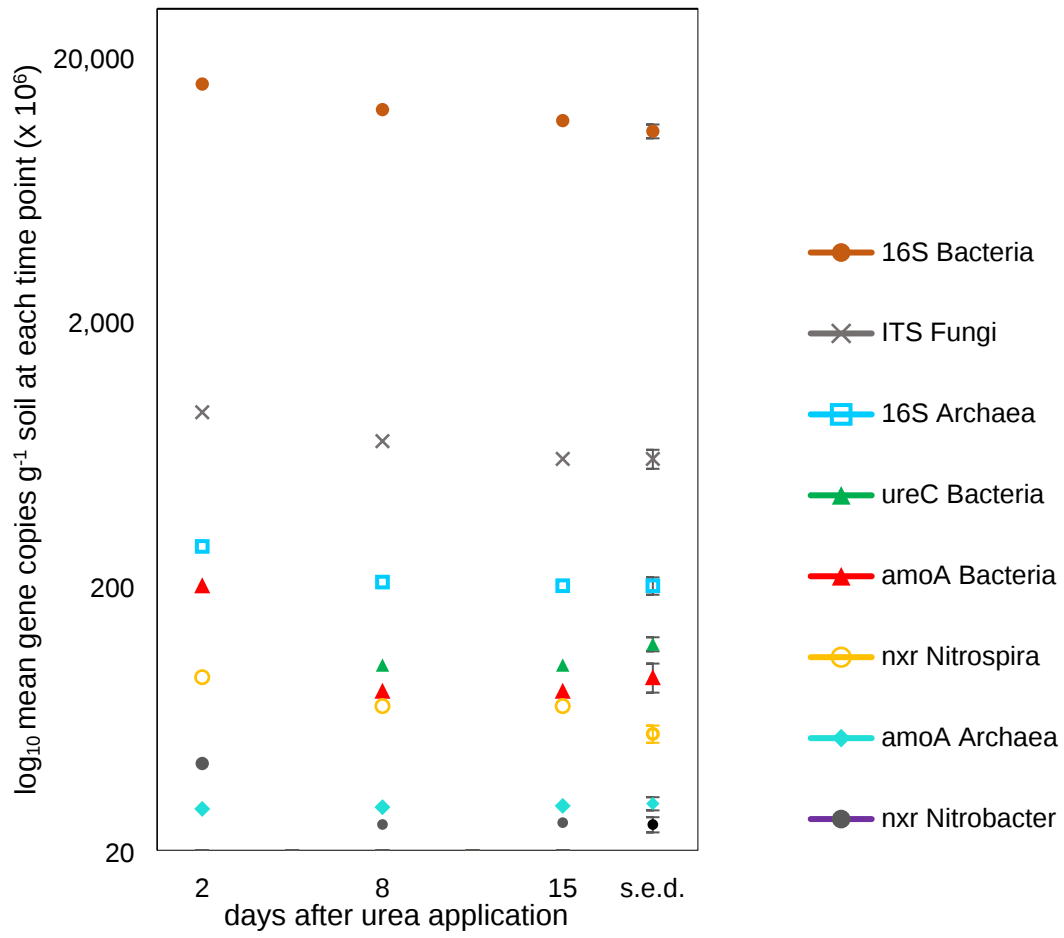
Supplementary Fig. 5. Mean abundance for all treatments of transcripts at each time point. All transcripts were significantly more abundant at 15 days compared to two days after urea addition except *amo* Bacteria which was significantly less abundant (Tukey's post-hoc α = 0.05).
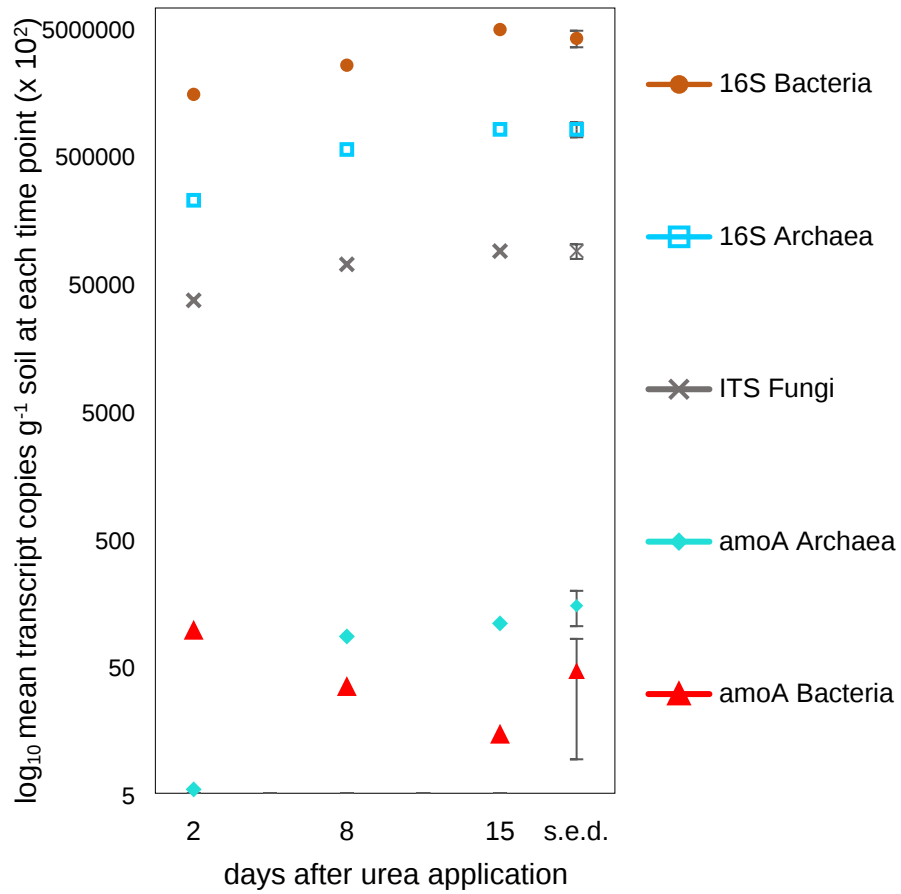
Supplementary Table 1. PCR efficiency of primer sets

	Efficiency	r²	slope	y-int
16S Bacteria	84.8%	0.995	-3.749	36.359
ITS Fungi	87.30%	0.998	-3.669	35.258
16S Archaea	100.10%	0.995	-3.319	33.365
ureC **Bacteria**	95.40%	0.997	-3.437	31.779
amoA **Bacteria**	82.20%	0.997	-3.837	35.908
nxr **Nitrospira**	92.70%	0.999	-3.511	31.665
amoA **Archaea**	86%	0.997	-3.709	33.318
nxr **Nitrobacter**	93.30%	0.999	-3.494	33.457

Supplementary Table 2. PCR efficiency of primer sets in RNA RT-qPCR

	Efficiency	r²	slope	y-int
16S Bacteria	78.8%	0.999	-3.962	36.922
16S Archaea	93.40%	0.995	-3.491	33.852
ITS Fungi	91.90%	0.998	-3.532	34.095
amoA **Archaea**	90%	0.997	-3.601	32.279
amoA **Bacteria**	90.50%	0.999	-3.572	34.172

	pH	NO_3^-	NH_4^+	min N	16S Bact	16S Arch	ITS Fun	ureC Bact	amoA AOB	amoA AOA	nxrA spira	nxrA bacter	16S RNA Bact	16S RNA Arch	ITS RNA Fungi	amoA RNA AOB
NO_3^-	-0.46															
NH_4^+	-0.46	0.55														
mineral N	-0.44	**0.62**	**0.99**													
16S Bacteria	-0.02	0.21	0.18	0.19												
16S Archaea	0.08	0.17	0.12	0.13	**0.76**											
ITS Fungi	-0.25	0.32	0.36	0.36	**0.61**	**0.66**										
ureC **Bacteria**	-0.06	0.18	0.18	0.19	**0.69**	**0.85**	**0.76**									
amoA **Bacteria**	-0.38	**0.64**	0.46	0.51	0.49	0.43	0.62	0.46								
amoA **Archaea**	0.13	-0.02	-0.04	-0.03	0.36	**0.64**	0.27	0.48								
nxrA Nitrospira	-0.06	0.06	0.13	0.13	**0.70**	**0.81**	**0.75**	**0.82**	0.46	0.59						
nxrA Nitrobacter	-0.10	0.21	0.24	0.25	**0.66**	**0.72**	**0.70**	**0.74**	**0.62**	0.34	**0.81**					
16S RNA Bacteria	-0.02	-0.35	-0.14	-0.19	-0.25	-0.24	-0.30	-0.30	-0.36	0.07	-0.24	-0.41				
16S RNA Archaea	-0.11	-0.18	-0.08	-0.11	-0.17	-0.15	-0.23	-0.21	-0.28	0.11	-0.13	-0.30	**0.75**			
ITS RNA Fungi	-0.23	-0.05	0.05	0.03	-0.21	-0.21	-0.14	-0.22	-0.13	-0.01	-0.18	-0.26	**0.65**	**0.87**		
amoA **RNA AOB**	-0.41	0.37	0.25	0.27	0.28	0.25	0.30	0.29	0.39	0.04	0.15	0.33	-0.29	-0.23	-0.15	
amoA **RNA AOA**	-0.19	-0.04	0.00	-0.01	-0.06	-0.06	-0.09	-0.11	-0.22	0.13	-0.08	-0.24	**0.61**	**0.91**	**0.84**	-0.09

Supplementary Table 3. Spearman's rank correlation (r_s) for all samples, plots and times. Statistically significant correlations ($P <0.05$) are highlighted yellow; strong positive or negative correlations ($>.6$) are in **bold.**