

Table S1. Median and interquartile range of the relative abundance of the genera in Nellore steers influenced by the use of post-ruminal urea in relation to conventional urea during the dry season.

Domain	Phylum	Genera	Treatments			P-value
			CONT	PRU	U+PRU	
Bacteria	Actinobacteriota	<i>Actinomycetospora</i>	NI ^b	0.000 ± 0.005 ^{ab}	0.001 ± 0.013 ^a	0.030
		<i>DNF00809</i>	0.065 ± 0.017 ^b	0.089 ± 0.031 ^a	0.068 ± 0.390 ^{ab}	0.051
		<i>Ilumatobacteraceae</i>	0.003 ± 0.012 ^{ab}	0.012 ± 0.030 ^a	NI ^b	0.035
		<i>Jatrophihabitans</i>	NI ^b	0.000 ± 0.013 ^{ab}	0.000 ± 0.015 ^a	0.089
		<i>Kineococcus</i>	NI ^b	NI ^b	0.000 ± 0.001 ^a	0.039
		<i>Kineosporia</i>	NI ^b	0.000 ± 0.044 ^{ab}	0.048 ± 0.058 ^a	0.091
		<i>Kribbella</i>	NI ^b	0.000 ± 0.008 ^a	NI ^{ab}	0.060
		<i>Uncultured</i>	NI ^b	NI ^b	0.008 ± 0.012 ^a	0.003
	Bacteroidota	<i>Uncultured</i>	0.412 ± 0.191 ^a	0.296 ± 0.123 ^b	0.252 ± 0.108 ^b	0.013
		<i>U29.B03</i>	0.075 ± 0.045 ^a	0.033 ± 0.015 ^b	0.034 ± 0.029 ^b	0.014
	Bdellovibrionota	<i>Bdellovibrio</i>	NI ^b	NI ^b	0.000 ± 0.003 ^a	0.037
	Chloroflexi	<i>Gitt.GS.136</i>	NI ^b	0.004 ± 0.014 ^a	NI ^b	0.058
		<i>Uncultured</i>	NI ^b	NI ^b	0.000 ± 0.005 ^a	0.039
	Desulfobacterot	<i>Desulfuromonas</i>	NI ^b	0.000 ± 0.002 ^a	NI ^b	0.039
		<i>Desulfobulbus</i>	NI ^b	0.000 ± 0.006 ^a	NI ^b	0.039
	Elusimicrobiota	<i>Endomicrobium</i>	0.005 ± 0.005 ^a	0.000 ± 0.005 ^b	0.007 ± 0.001 ^{ab}	0.095
	Fibrobacterota	<i>Fibrobacter</i>	0.943 ± 0.262 ^a	0.631 ± 0.172 ^b	0.655 ± 0.201 ^b	0.013
	Firmicutes	<i>Allobaculum</i>	NI ^b	NI ^b	0.013 ± 0.066 ^a	0.040
		<i>Anaerovorax</i>	0.266 ± 0.071 ^b	0.335 ± 0.032 ^a	0.266 ± 0.055 ^b	0.017
		<i>Bacteroides_pectinophilus_group</i>	NI ^b	0.000 ± 0.011 ^{ab}	0.013 ± 0.014 ^a	0.049
		<i>Clostridia_vadinBB60_group</i>	0.007 ± 0.017 ^b	0.027 ± 0.005 ^a	0.021 ± 0.018 ^{ab}	0.054
		<i>Uncultured</i>	0.030 ± 0.012 ^{ab}	0.035 ± 0.011 ^a	0.019 ± 0.007 ^b	0.036
		<i>Eubacterium</i>	NI ^b	0.003 ± 0.005 ^a	NI ^{ab}	0.070
		<i>Flavonifractor</i>	NI ^b	0.000 ± 0.001 ^a	NI ^b	0.076
		<i>Howardella</i>	NI ^b	0.006 ± 0.017 ^a	NI ^{ab}	0.067
		<i>Lachnospiraceae_NK3A20_group</i>	0.921 ± 0.377 ^{ab}	0.834 ± 0.287 ^a	0.611 ± 0.207 ^b	0.078
		<i>Lachnospiraceae_NK4B4_group</i>	0.021 ± 0.009 ^{ab}	0.009 ± 0.012 ^b	0.016 ± 0.008 ^a	0.079
		<i>Lachnospiraceae_XPB1014_group</i>	0.893 ± 0.214 ^{ab}	1.002 ± 0.273 ^a	0.817 ± 0.237 ^b	0.088
		<i>Lysinibacillus</i>	NI ^b	0.013 ± 0.021 ^a	0.012 ± 0.016 ^a	0.030
		<i>Peptoclostridium</i>	NI ^b	0.007 ± 0.603 ^{ab}	0.536 ± 1.006 ^a	0.037

		<i>Peptococcus</i>	NI ^b	NI ^b	0.000 ± 0.015 ^a	0.039
		<i>Staphylococcus</i>	NI ^b	NI ^{ab}	0.004 ± 0.009 ^a	0.021
		<i>Weissella</i>	NI ^b	NI ^b	0.004 ± 0.013 ^a	0.026
	Myxococcota	<i>P3OB.42</i>	0.003 ± 0.003 ^a	NI ^b	0.003 ± 0.003 ^{ab}	0.097
	Planctomycetota	<i>vadinHA49</i>	NI ^{ab}	NI ^b	0.000 ± 0.005 ^a	0.092
	Proteobacteria	<i>Allorhizobium.Neorhizobium.Pararhizobium.Rhizobium</i>	0.012 ± 0.014 ^b	0.048 ± 0.036 ^a	0.091 ± 0.083 ^a	0.001
		<i>1174.901.12</i>	NI ^b	NI ^b	0.000 ± 0.013 ^a	0.011
		<i>Belnapia</i>	NI ^b	NI ^b	0.000 ± 0.001 ^a	0.039
		<i>Caulobacter</i>	NI ^{ab}	0.000 ± 0.005 ^a	NI ^b	0.092
		<i>Comamonas</i>	0.004 ± 0.010 ^b	0.002 ± 0.010 ^b	0.012 ± 0.013 ^a	0.065
		<i>Devosia</i>	0.000 ± 0.002 ^b	0.014 ± 0.043 ^{ab}	0.022 ± 0.035 ^a	0.040
		<i>Hyphomicrobium</i>	NI ^b	0.000 ± 0.006 ^{ab}	0.000 ± 0.009 ^a	0.070
		<i>Massilia</i>	0.007 ± 0.024 ^b	0.010 ± 0.038 ^b	0.047 ± 0.083 ^a	0.019
		<i>Pseudomonas</i>	0.033 ± 0.153 ^b	0.189 ± 0.173 ^{ab}	0.206 ± 0.089 ^a	0.055
		<i>Uncultured</i>	NI ^b	NI ^{ab}	0.000 ± 0.007 ^a	0.088
		<i>Uncultured</i>	0.021 ± 0.019 ^b	0.023 ± 0.005 ^a	0.013 ± 0.014 ^a	0.027
		<i>Rubellimicrobium</i>	NI ^b	NI ^b	0.000 ± 0.062 ^a	0.039
	Spirochaetota	<i>Treponema</i>	1.015 ± 0.285 ^a	0.735 ± 0.431 ^{ab}	0.729 ± 0.317 ^b	0.061
	Verrucomicrobiota	<i>ADurb.Bin063.1</i>	0.000 ± 0.004 ^a	NI ^{ab}	NI ^b	0.091
Archaea	Halobacterota	<i>Methanomicrobium</i>	1.521 ± 1.116 ^b	2.206 ± 0.412 ^{ab}	2.648 ± 0.909 ^a	0.037

NI: not identified. SEM: Standard error means. CONT: conventional urea; PRU: post-ruminal urea; U+PRU: conventional urea+ post-ruminal urea. Values followed by superscript letters indicate statistical differences (P < 0.05) based on Kruskal-Wallis test.