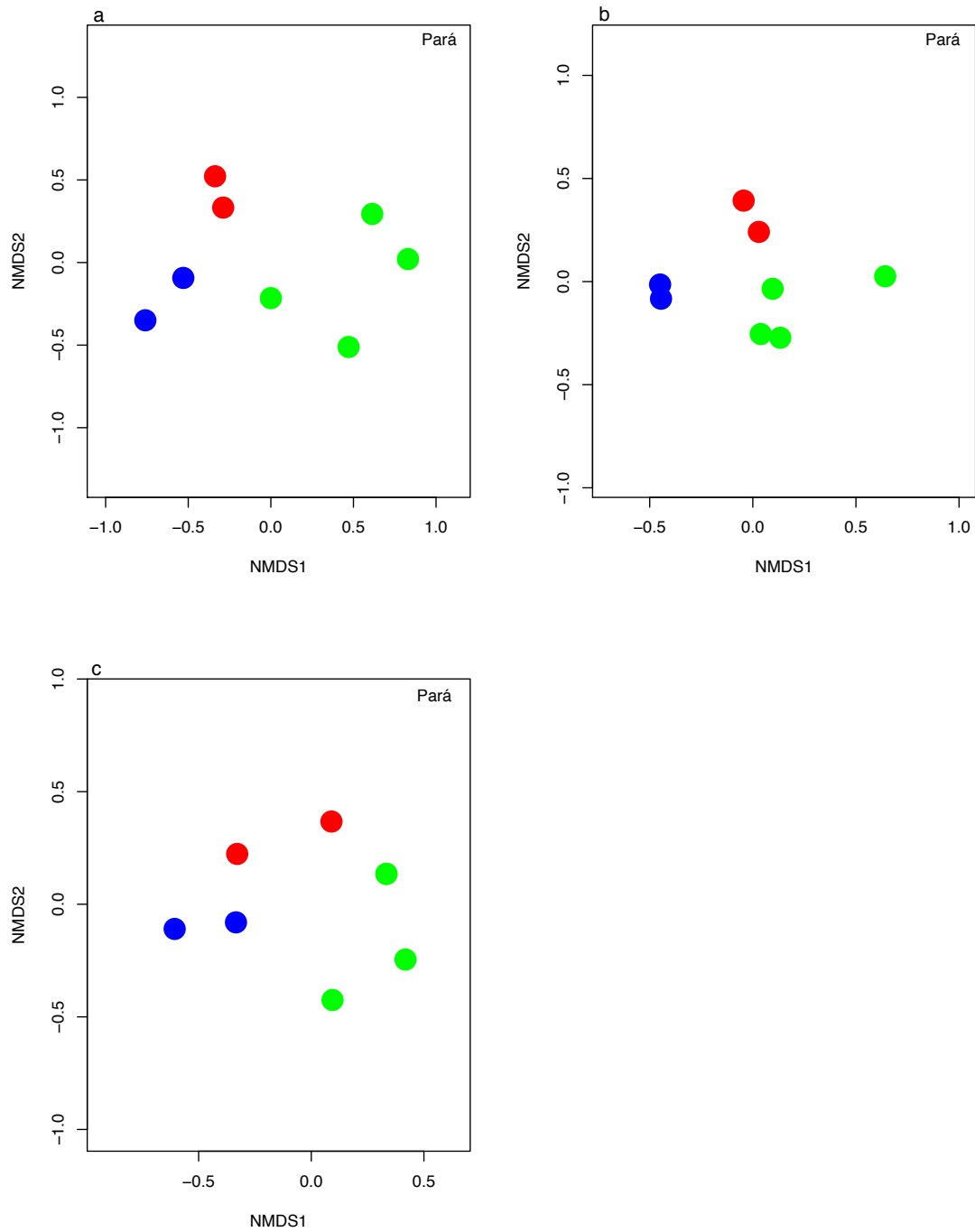


## **SUPPLEMENTAL FIGURES**

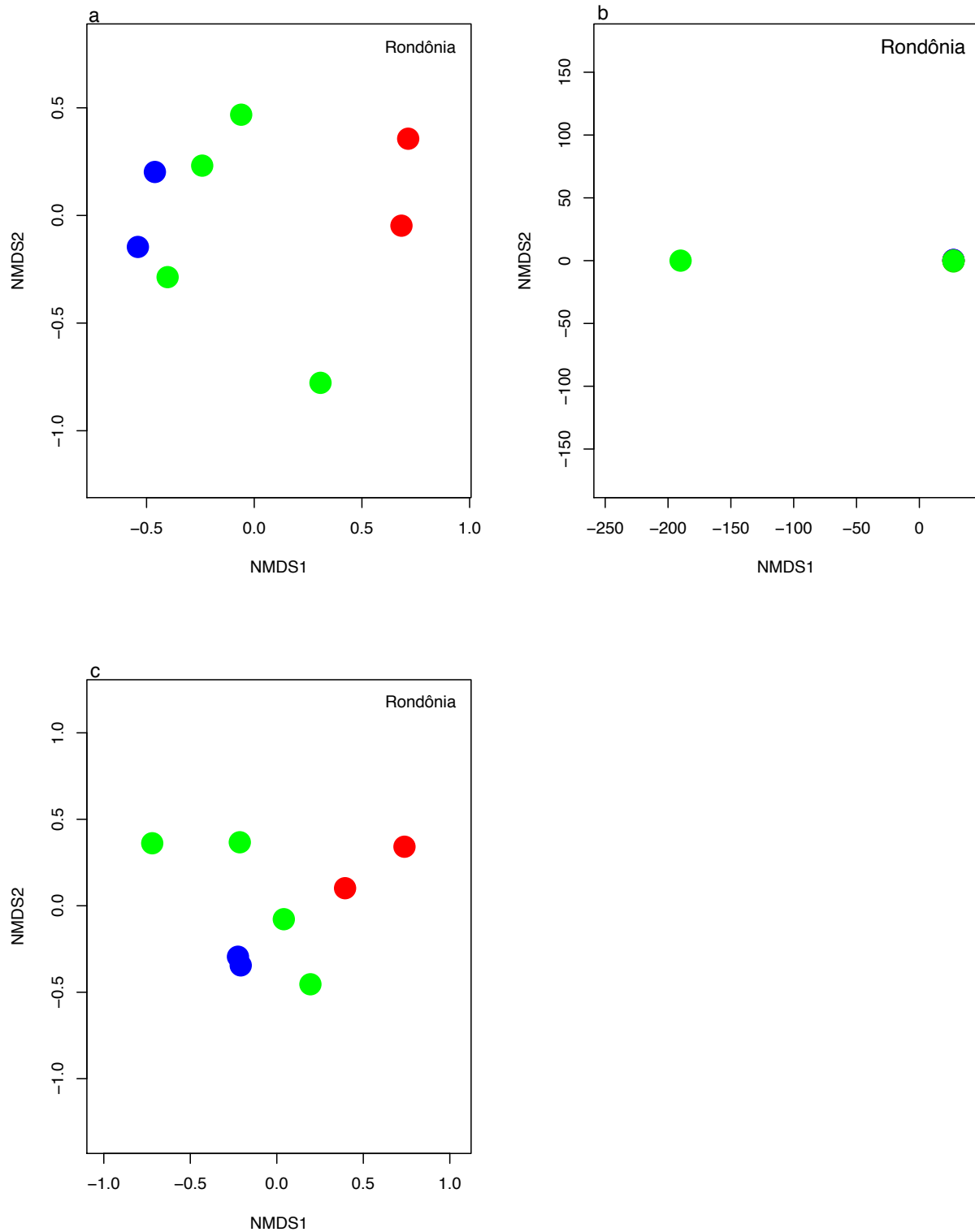
for Kroeger et al. "Rainforest-to-pasture conversion stimulates soil methanogenesis across the Brazilian Amazon"

This file contains Supplemental Figures 1 - 7.

**Suppl. Figure 1.** Non-metric multidimensional scaling indicating how similar the active soil microbial communities are for the substrates (a)  $^{13}\text{CH}_4$ , (b)  $^{13}\text{CO}_2$ , (c)  $^{13}\text{NaAOc}$  from Pará. The plot was created using a Bray–Curtis dissimilarity matrix among all samples. Primary rainforest = green, pasture = red, and secondary rainforest = blue.

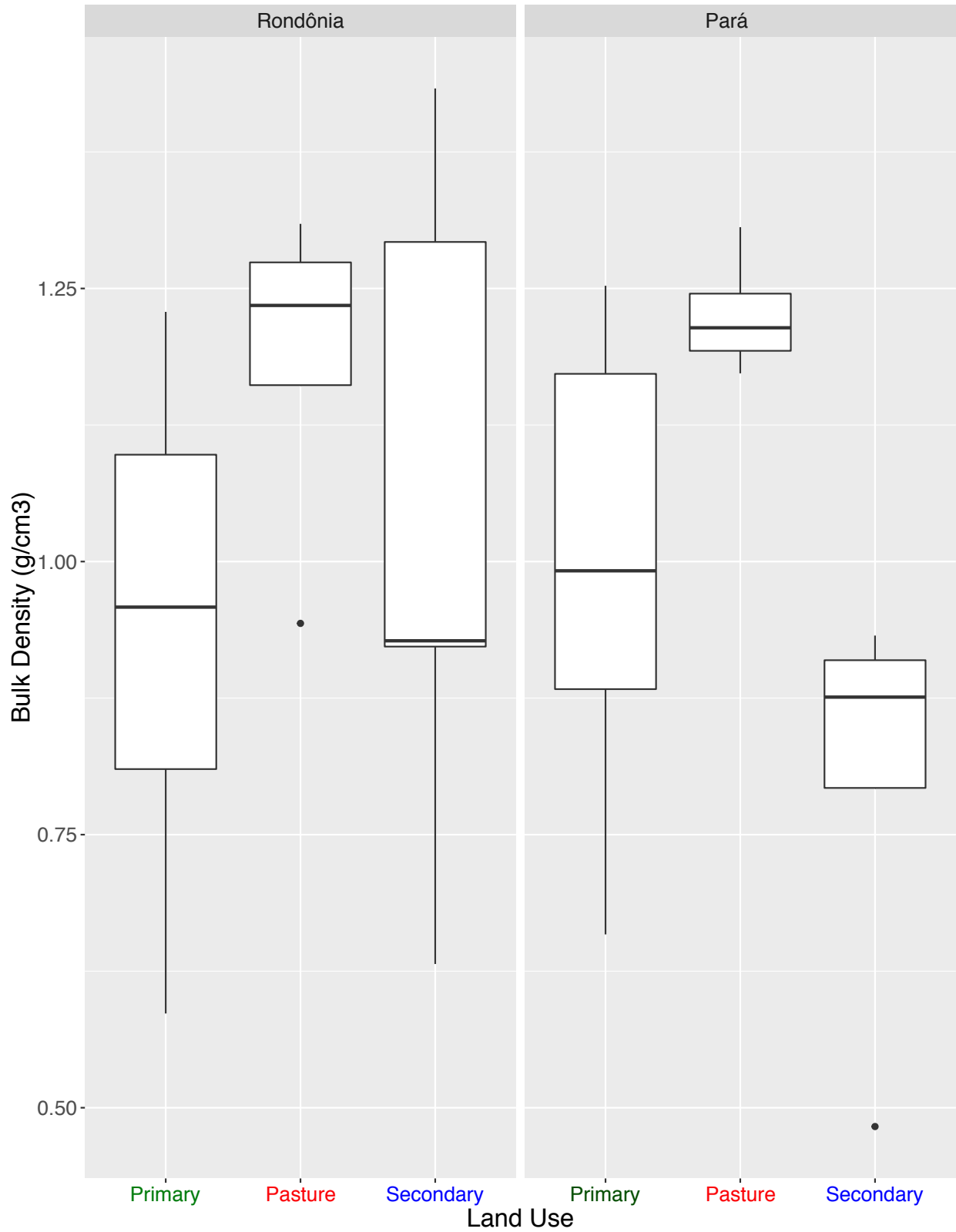


**Suppl. Figure 2.** Non-metric multidimensional scaling indicating how similar the active soil microbial communities are for the substrates (a)  $^{13}\text{CH}_4$ , (b)  $^{13}\text{CO}_2$ , (c)  $^{13}\text{NaAOc}$  from Rondônia. The plot was created using a Bray–Curtis dissimilarity matrix among all samples. Primary rainforest = green, pasture = red, and secondary rainforest = blue.

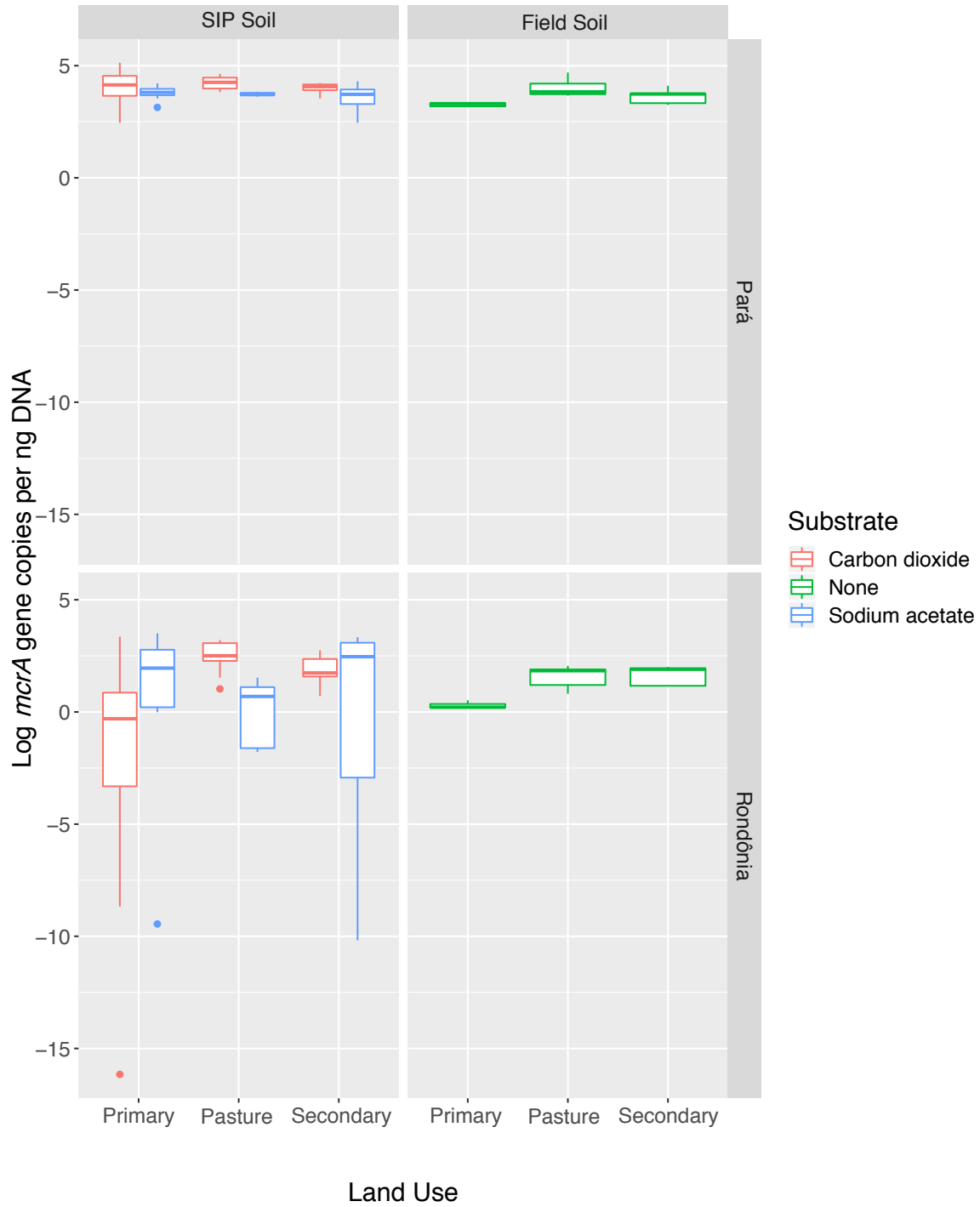




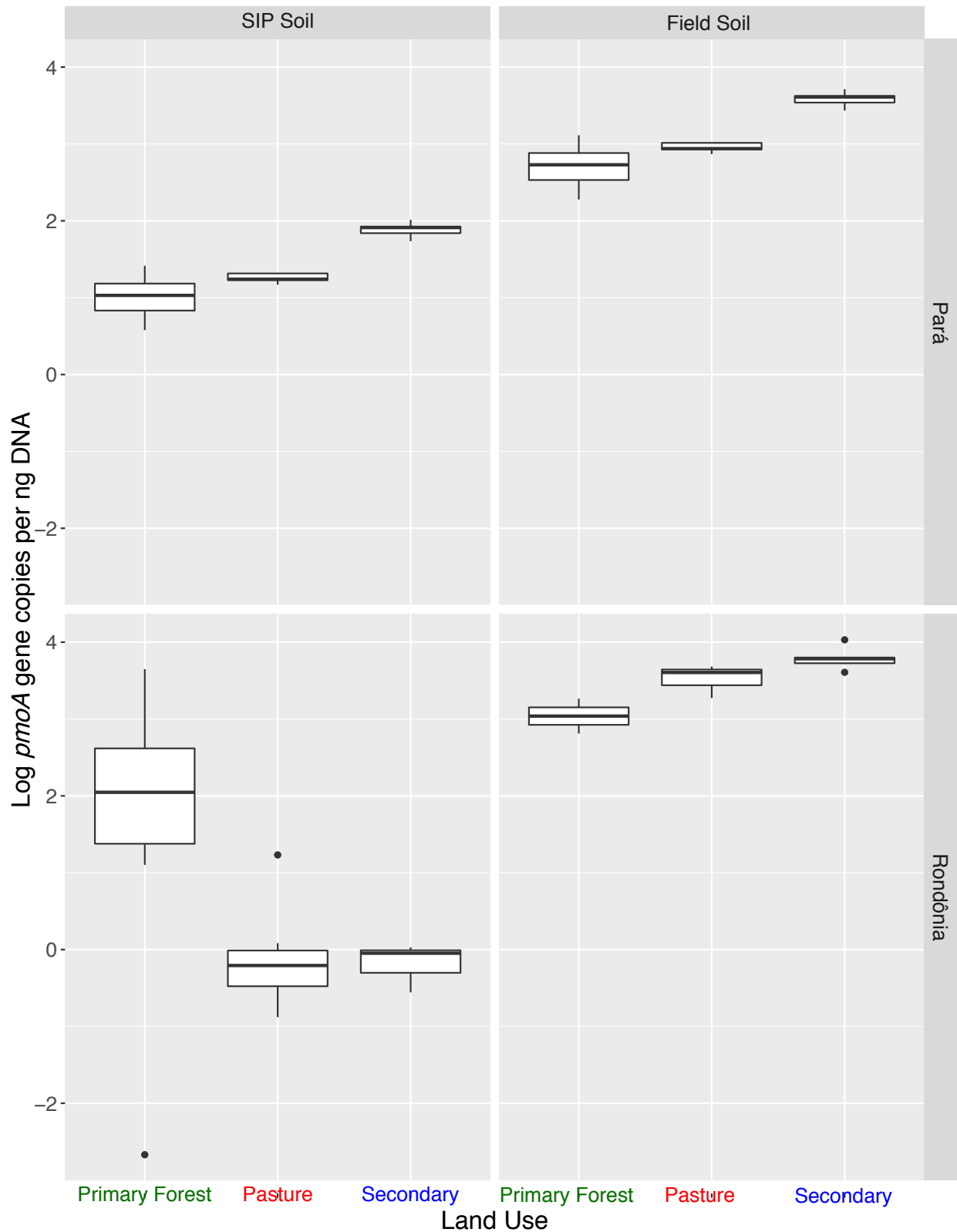
**Suppl. Figure 4.** The soil bulk density ( $\text{g}/\text{cm}^3$ ) for each land use (primary rainforest, pasture, secondary rainforest) and geographic location (Rondônia and Pará).



**Suppl. Figure 5.** The log *mcrA* gene copies per ng of DNA for soils from three land-use types (primary rainforest, pasture, and secondary rainforest) in Rondônia and Pará incubated with  $^{13}\text{CO}_2$ ,  $^{13}\text{NaAOc}$ , or no incubation (field soil).  $^{13}\text{CO}_2$  samples = red,  $^{13}\text{NaAOc}$  samples = blue, unaltered samples = green.



**Suppl. Figure 6.** The log *pmoA* gene copies per ng of DNA for soil from three land-use types (primary rainforest, pasture, and secondary rainforest) in Rondônia and Pará incubated with  $^{13}\text{CH}_4$  or no incubation (field soil).



**Suppl. Figure 7.** Non-metric multidimensional scaling indicating if the original soil and the  $^{12}\text{C}$ -controls (heavy and light fractions combined) are dissimilar from one another based on substrate (square = carbon dioxide, circle=methane, diamond=no substrate (i.e. original soil), triangle=sodium acetate), land-use (primary rainforest = green, pasture = orange, secondary rainforest = blue), and location (light grey = Pará, dark grey = Rondônia). The plot was created using a Bray–Curtis dissimilarity matrix of rarefied 16S rRNA amplicon sequences.

