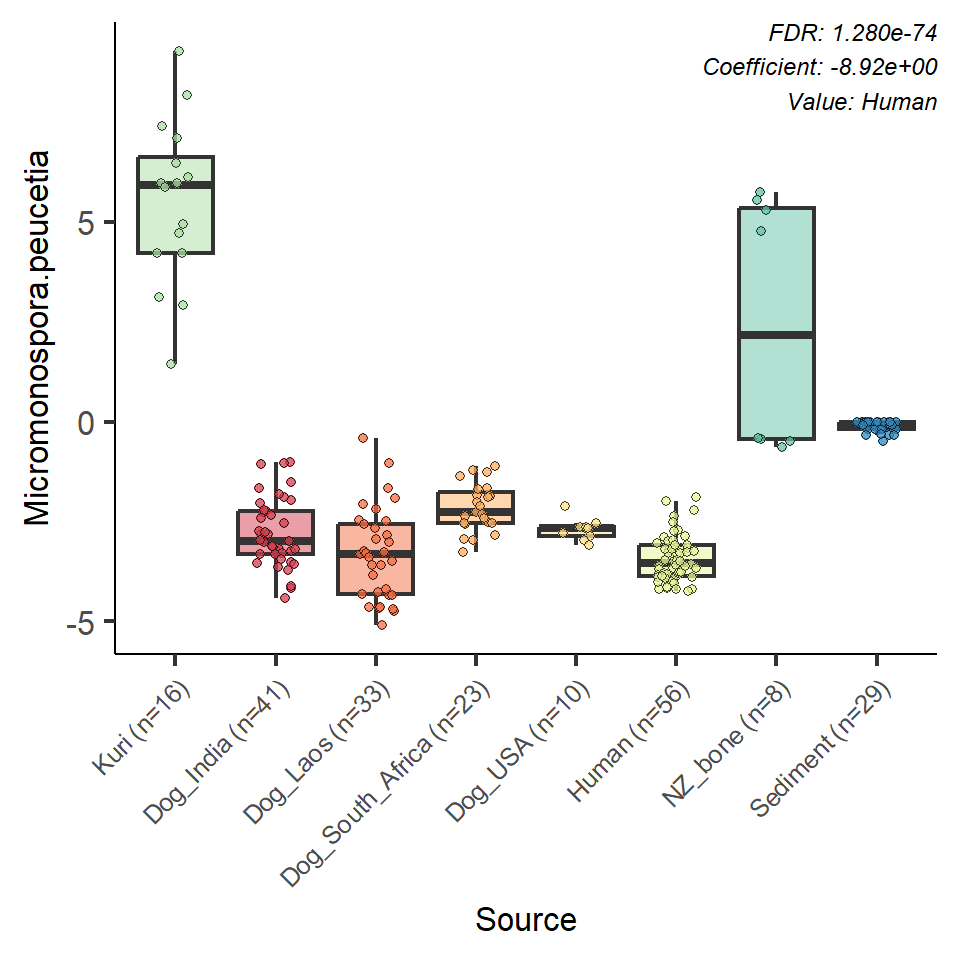
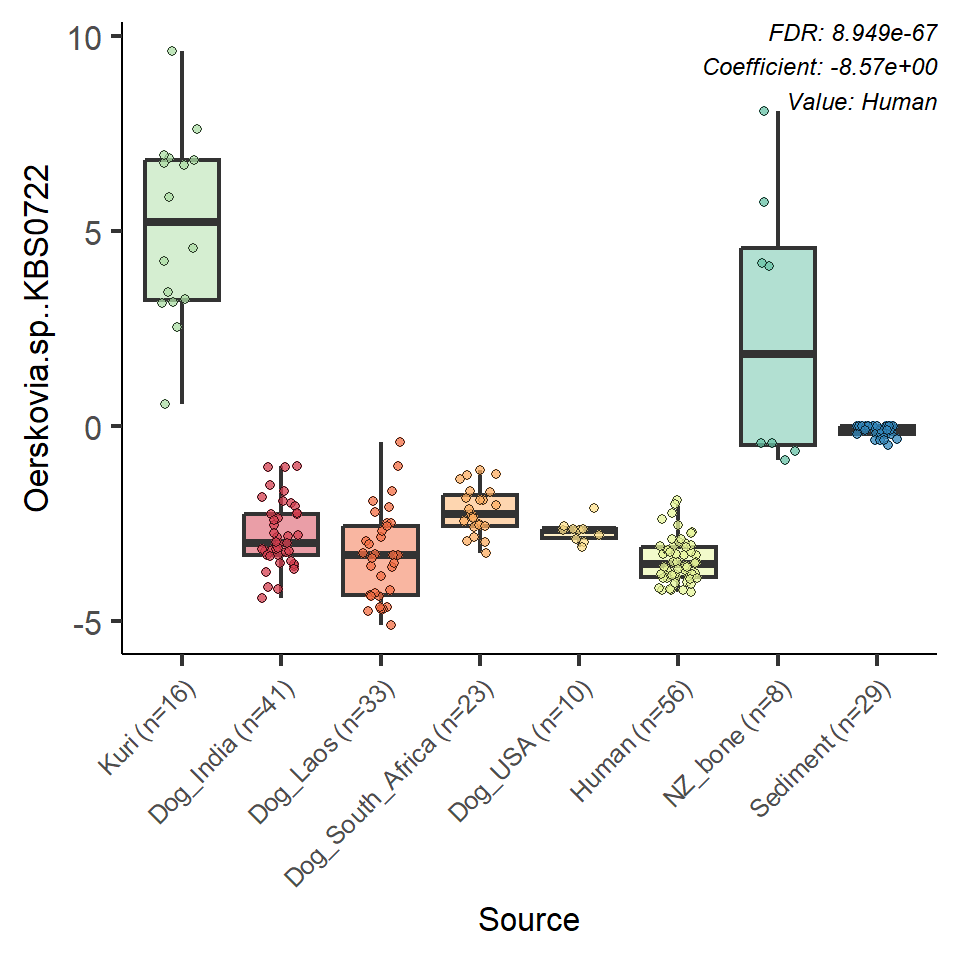
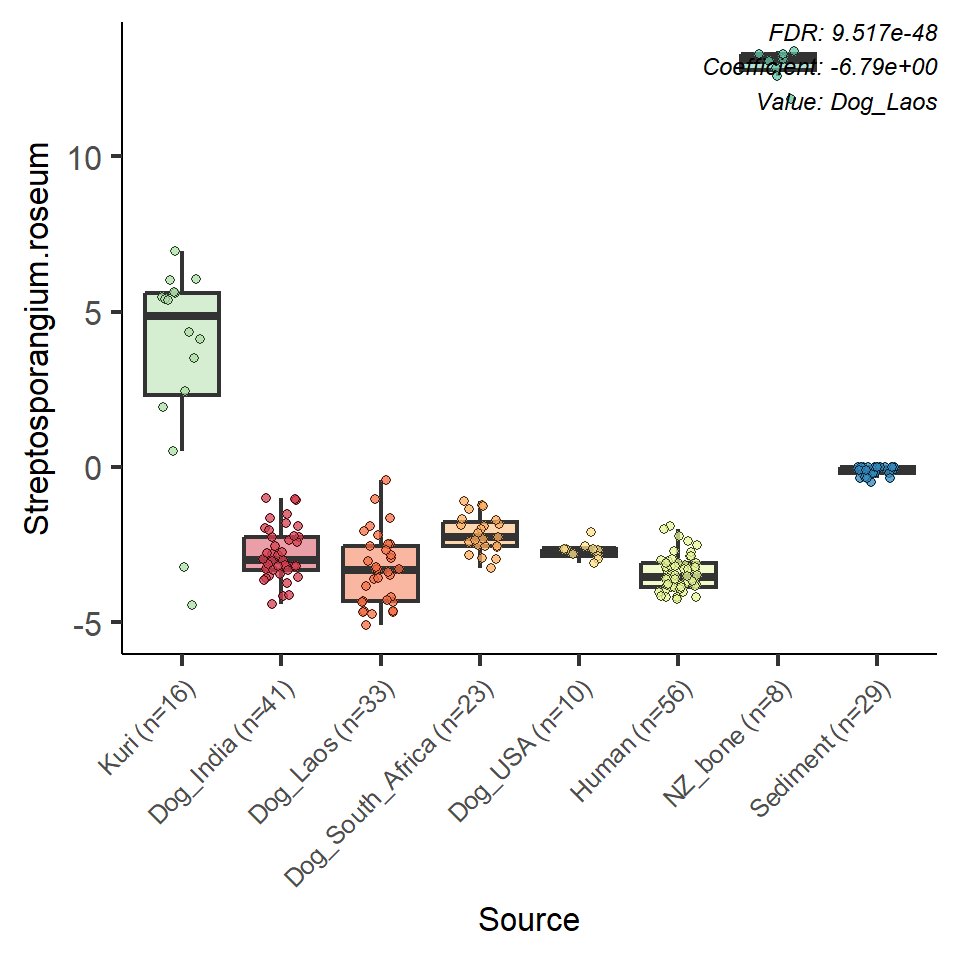
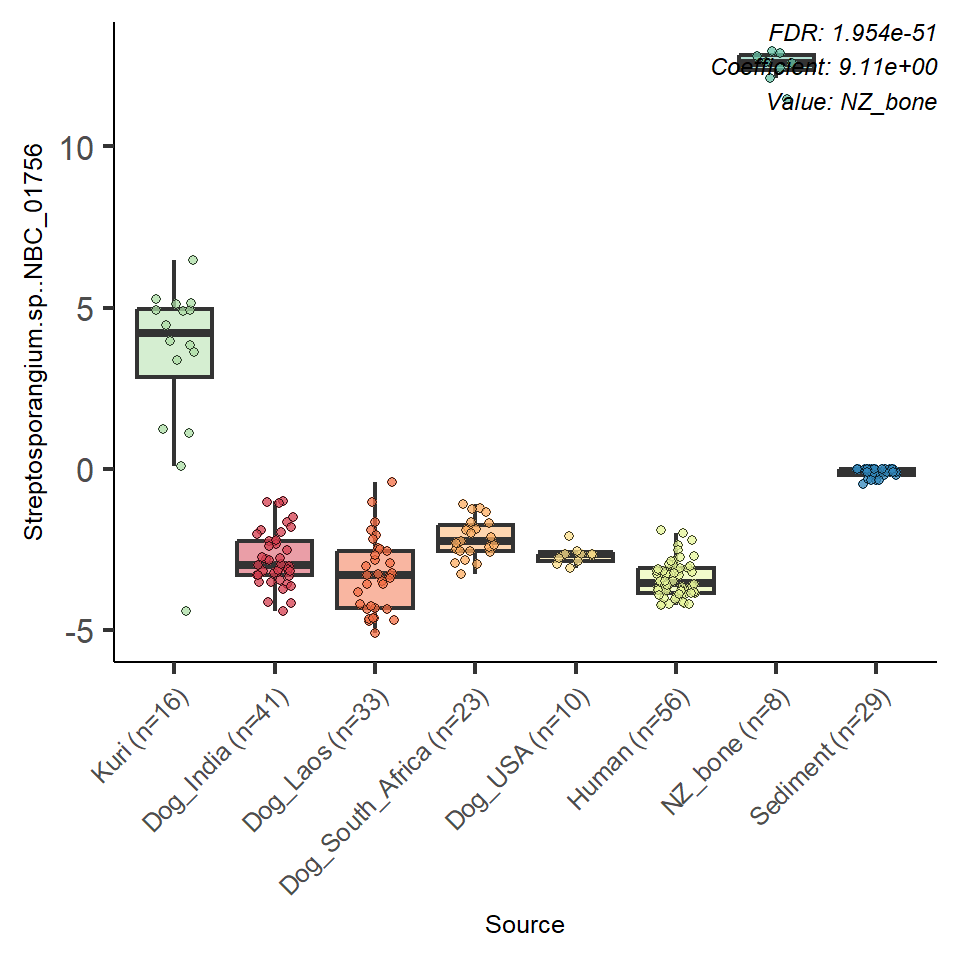
**Figure 1. MaAsLin2 results showing boxplots of shared contaminant species (based on CLR transformed data)**



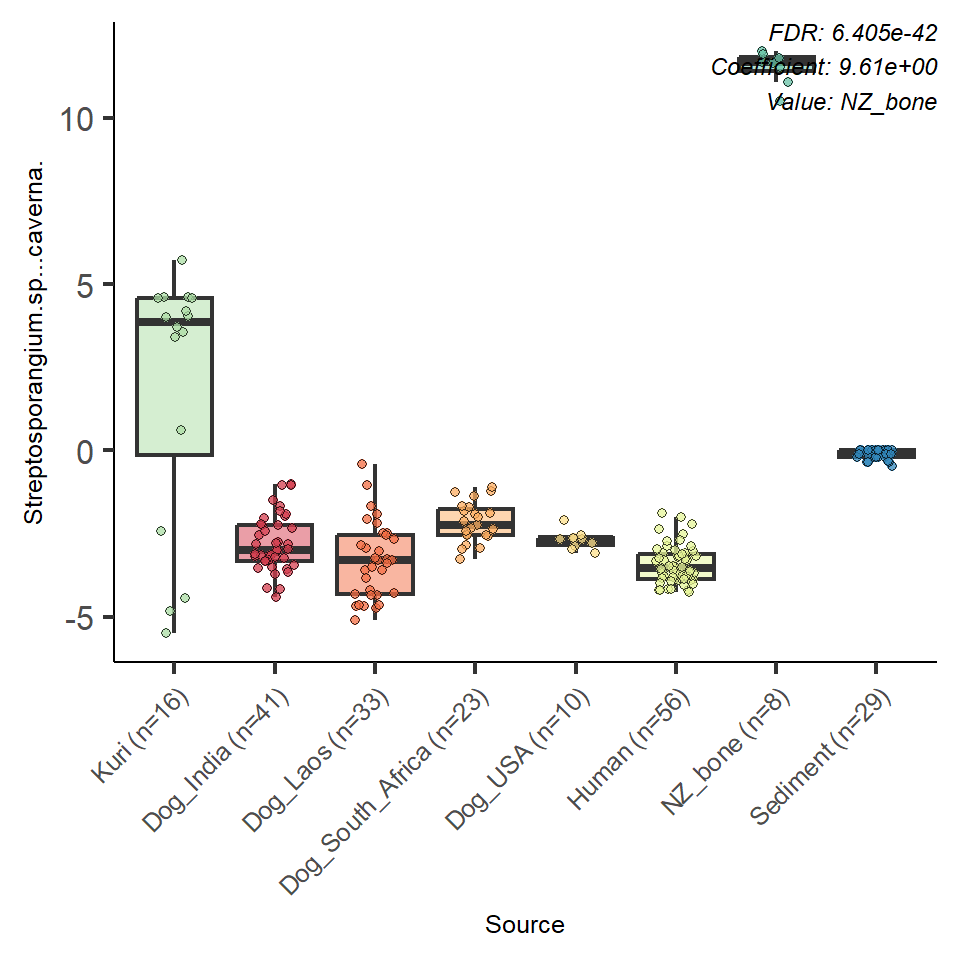


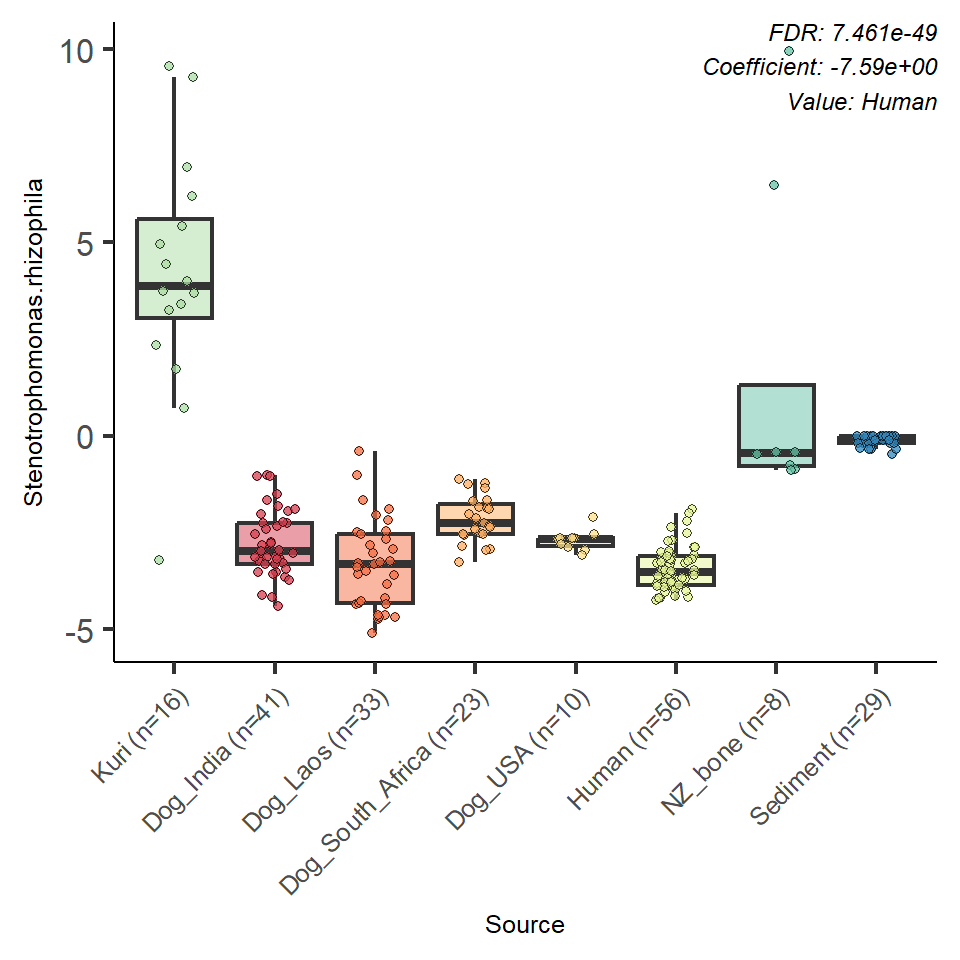
**Figure 1. continued**



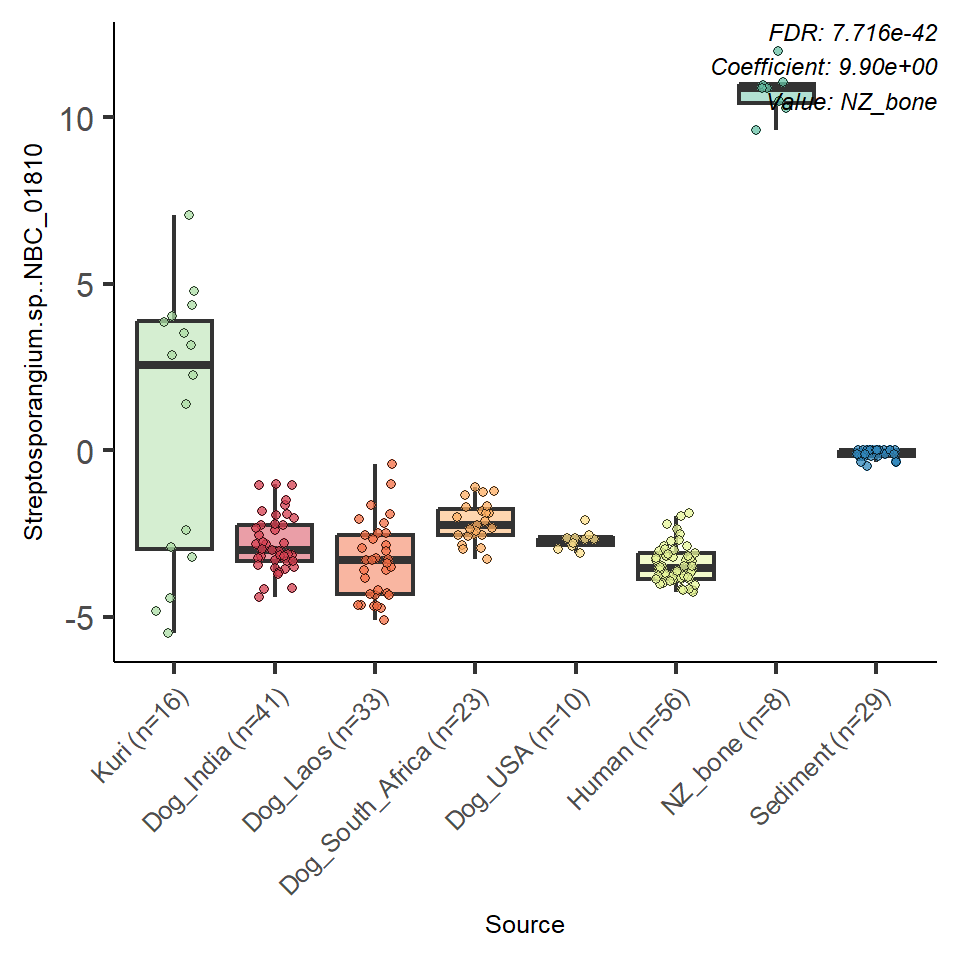


**Figure 1. continued**

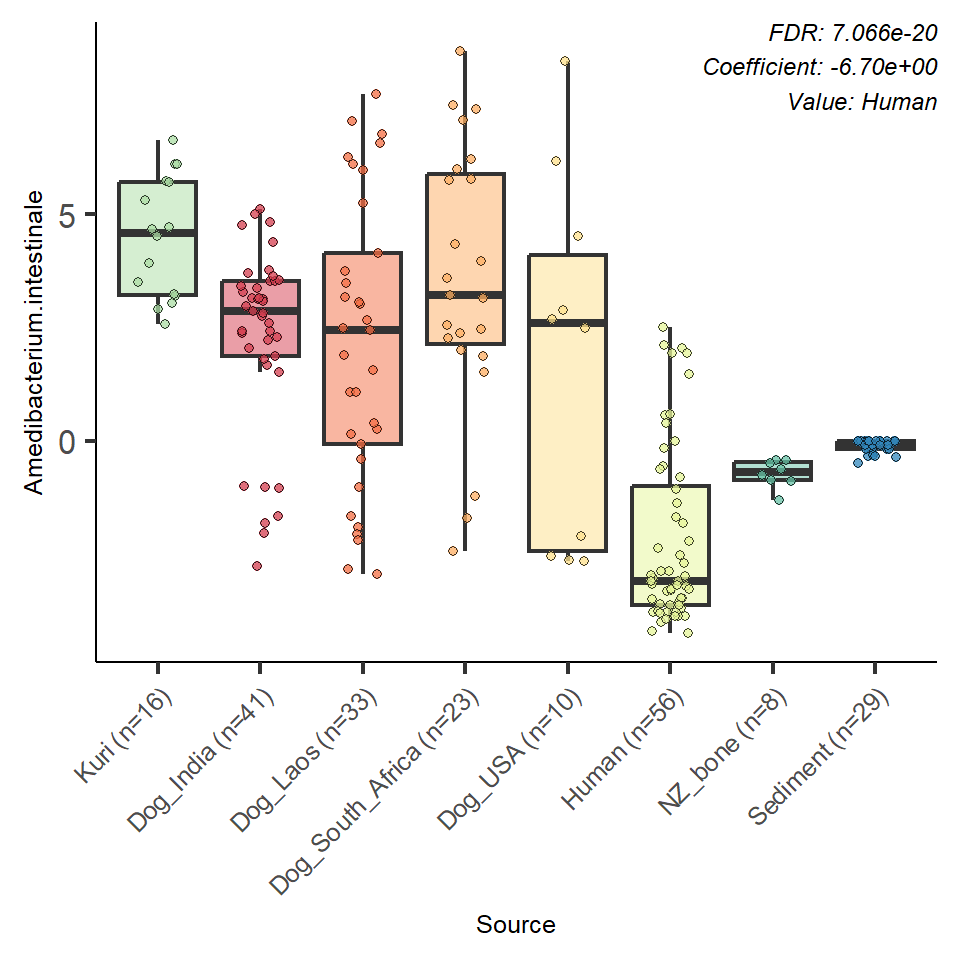




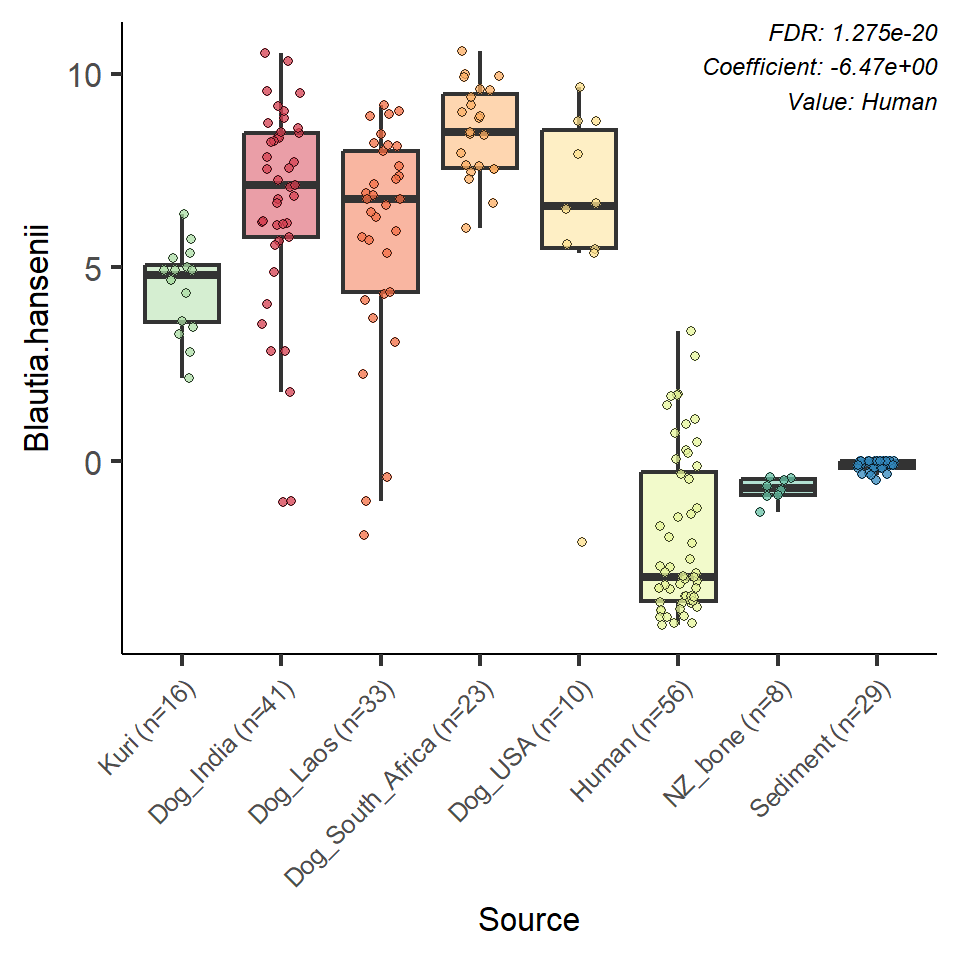
**Figure 1. continued**

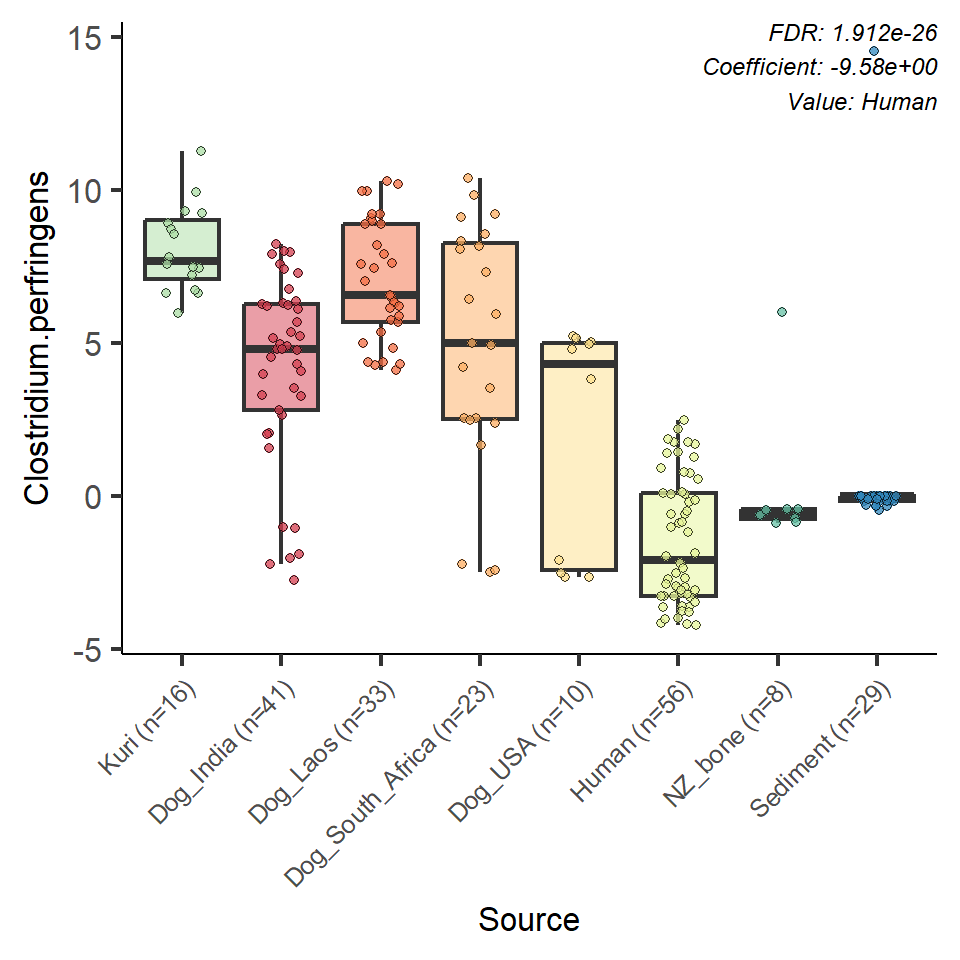


**Figure 2. MaAsLin2 results showing boxplots of shared microbiome species (based on CLR transformed data)**

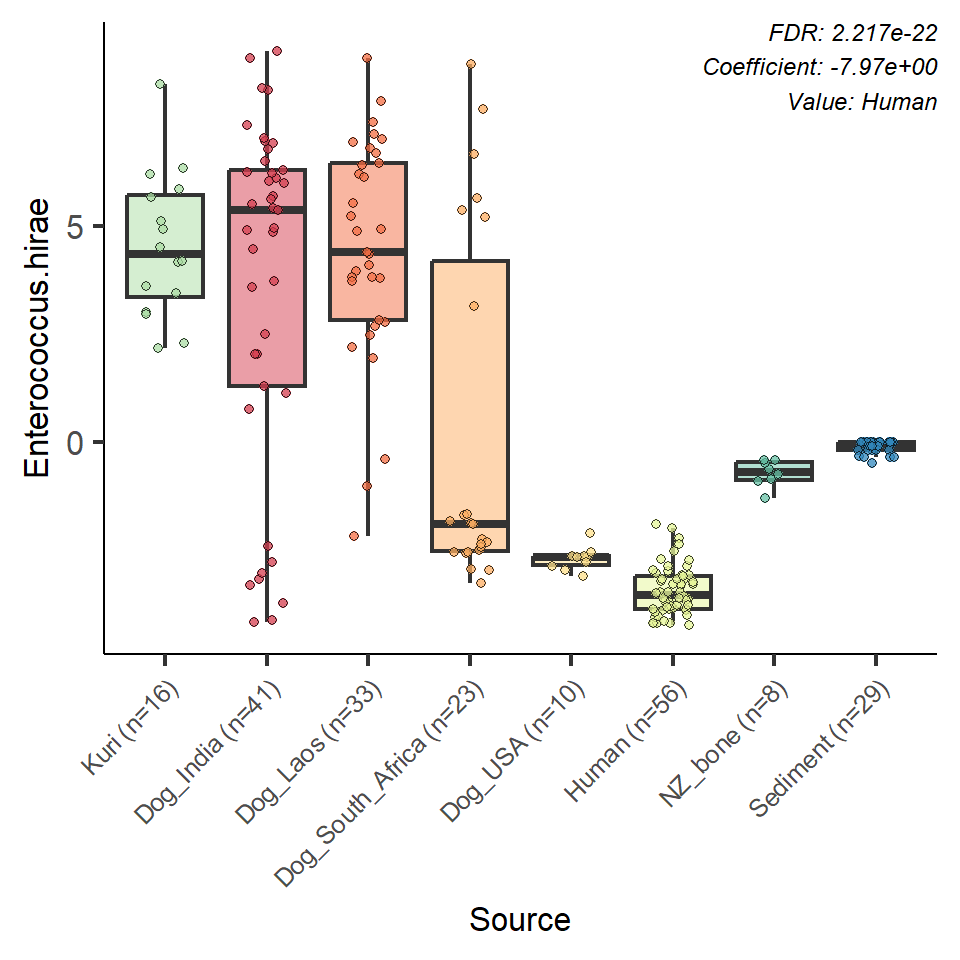


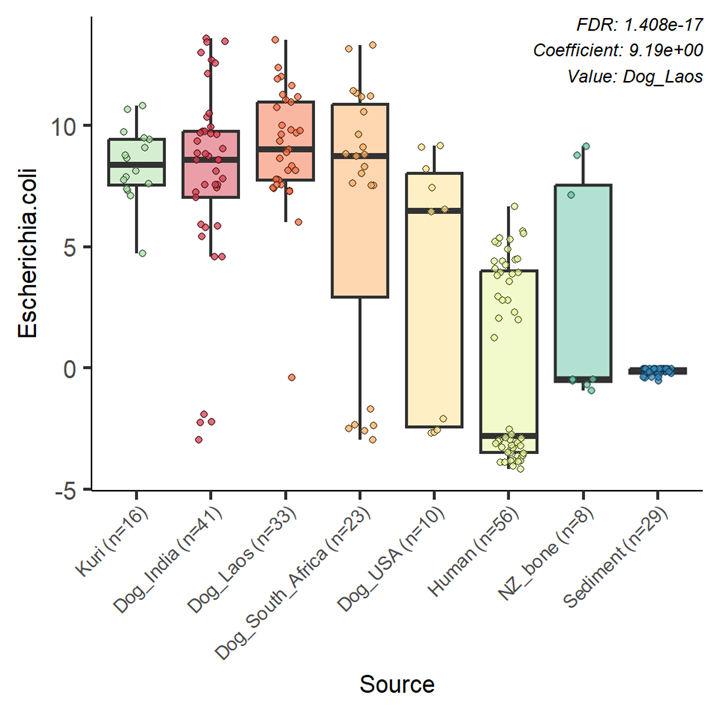
**Figure 2. Continued**



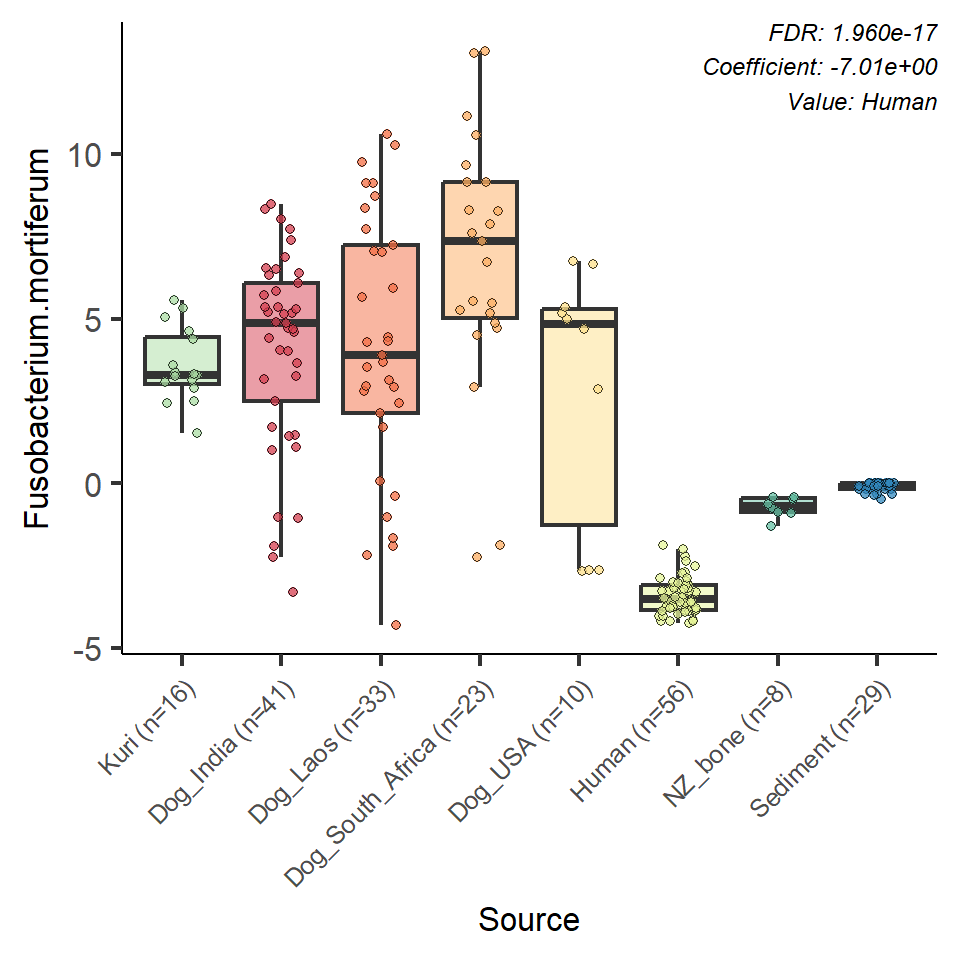


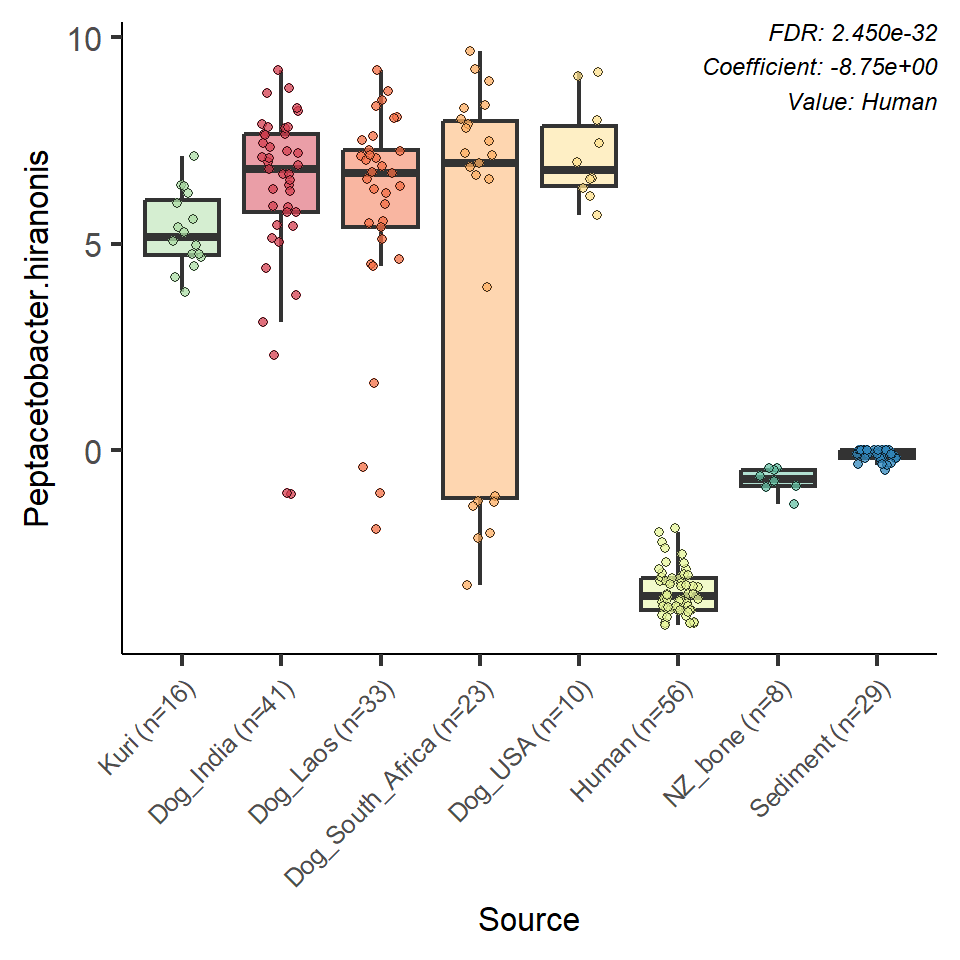
**Figure 2. Continued**





**Figure 2. Continued**





**Figure 3. MaAsLin2 results showing boxplots of species common in palaeofaecal species, but rare in other sources (based on CLR transformed data)**

A graph of different colored boxes

AI-generated content may be incorrect. A graph of different colored squares

AI-generated content may be incorrect.

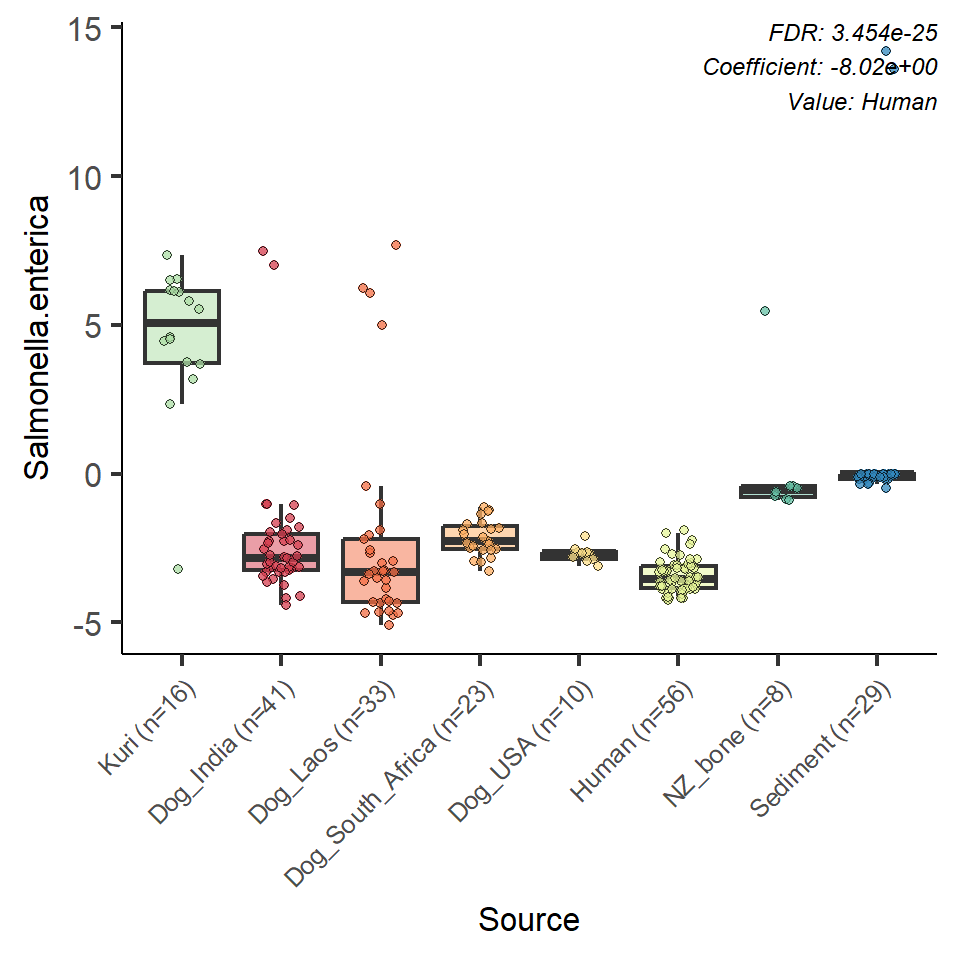
**Figure 3. Continued**

A graph with different colored squares

AI-generated content may be incorrect.A graph with different colored squares and numbers

AI-generated content may be incorrect.

**Figure 3. Continued**

A chart with different colored squares

AI-generated content may be incorrect.