Figure 2

The figure shows the distribution of read counts across various bacterial phyla for two species: C. porcellus and H. sapiens. The x-axis represents different bacterial phyla, and the y-axis represents the log10 read count. Each bar represents the median read count, with the error bars showing the interquartile range. The red and black bars indicate the median read counts for C. porcellus and H. sapiens, respectively, with the number of asterisks indicating statistical significance.

Phyla such as Firmicutes, Bacteroidetes, Proteobacteria, Actinobacteria, and others are shown with their respective read counts. The data suggests that C. porcellus and H. sapiens have different bacterial profiles, with some phyla being more abundant in one species than the other.

For example, Firmicutes and Bacteroidetes are more abundant in H. sapiens, while Proteobacteria and Actinobacteria are more abundant in C. porcellus. The statistical significance is indicated by the number of asterisks next to each bar, with more asterisks indicating a higher degree of significance.

The figure provides a visual representation of the relative abundance of bacterial phyla in the two species, allowing for a comparison of their microbial communities.