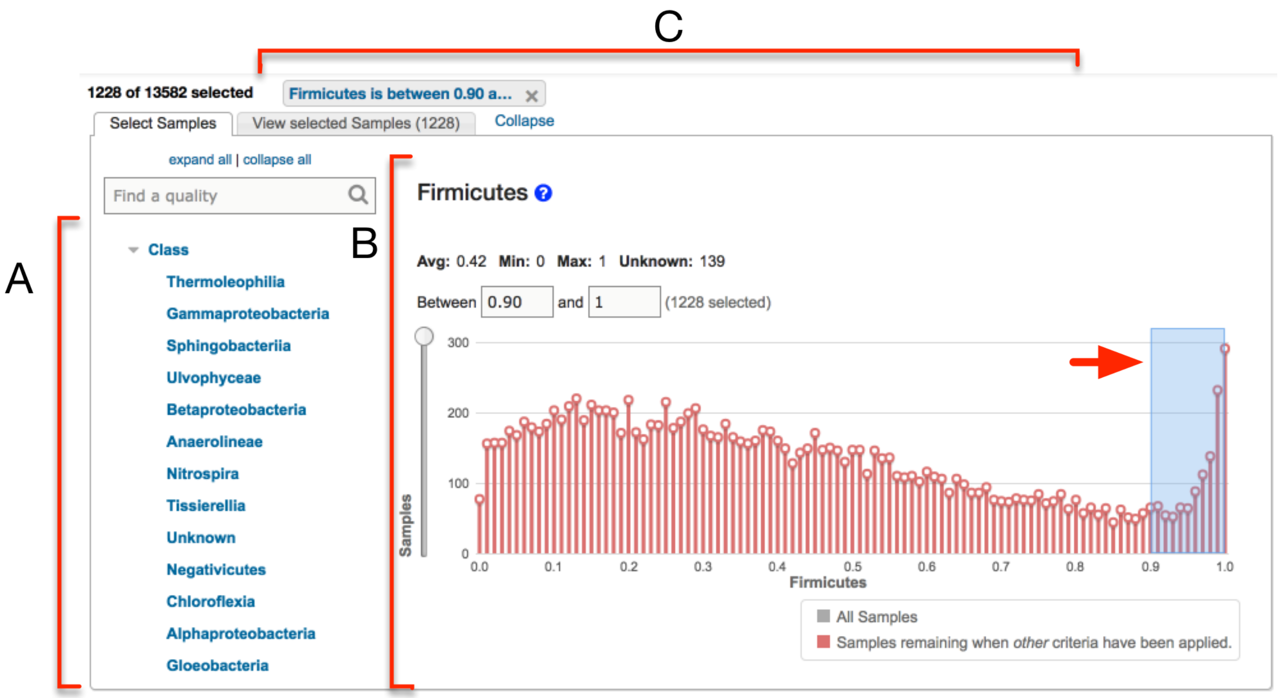

1228 of 13582 selected

Firmicutes is between 0.90 a...

Avg: 0.42 **Min:** 0 **Max:** 1 **Unknown:** 139

Between 0.90 and 1 (1228 selected)

Figure S1: Screenshot of the filter page for searching by taxon abundance. (A) A searchable filter list shows all taxa at the phylum, class, family, order, genus and species level, across all samples in the database. (B) Selecting any taxon from the filter list shows the distribution of relative abundance for all samples in the database. Selecting any relative abundance value, or a range of values, applies a filter to the database that returns only samples that contain that taxon at the specified relative abundance value(s). (C) Any filter applied by the user remains accessible through filter history at the top of the page.

Measure(s)

☑ Shannon ☐ Simpson ☐ Chao1 ☐ ACE ☐ Fisher

Visualization type

● Boxplot ○ Dot plot

Download

Enter one or more sample details to facet the plot

host body habitat (5)

```
> Kruskal-Wallis rank sum test:
  [Shannon]: chi-squared = 5882.795688, df = 5846.000000, p-value = 0.36476773
```

Distance Method: Bray-Curtis

Color by: host body habitat (5)

Shape by: Select sample details

Figure S2: Screenshot of the alpha and beta diversity apps. (A) The analysis tab of the results page provides access to a suite of interactive web apps for visualization and analysis of microbial community diversity and composition. (B) Launching the alpha diversity app allows users to choose between Shannon, Simpson, Chao1, ACE and Fisher diversity metrics, and to display the data as either a box plot or a dot plot. Selecting the ‘Explore Sample Details’ tab of the alpha diversity app (black arrow) lets users facet the plot using any available sample details. (C) Similarly, launching the beta diversity app presents users with drop down menus to choose distance method, and to color and shape points based on sample details. In the example shown in panels B and C, alpha and beta diversity were analyzed by host body habitat for over 6000 samples from the Human Microbiome Project.