

Analysis Settings

Choose how Peaks are Retained for Analyses

(Effects all protein analysis)

Select Samples

Choose Clustering Settings

Optional Settings

[Adjust the Dendrogram](#)

Insert Samples from Another Experiment

PCA, PCoA, t-SNE

Save Dendrogram

Suggestions for Reporting Protein Analysis:

This dendrogram was created by analyzing 8 samples, and retaining peaks with a signal to noise ratio above 4 and occurring in greater than 70 % of replicate spectra. Peaks occurring below 3000 m/z or above 15000 m/z were removed from the analyses. For clustering spectra, distance and algorithms were used.

Mirror Plots

Dendrogram

Mirror Plots

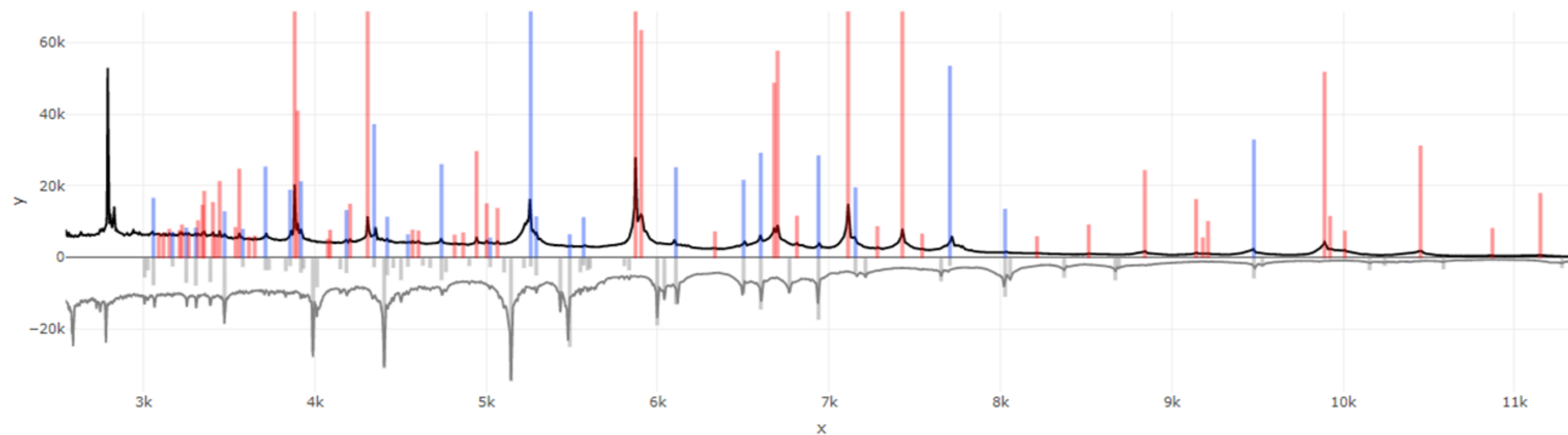
Choose two samples to compare in the mirror plots below. Matching peaks will be colored blue and non-matching peaks will be colored red.

Spectrum 1 (positive y-axis)

Bacillus-3610

Spectrum 2 (negative y-axis)

Micromonospora-B011



Download SVG