

### Analysis Settings

#### Choose how Peaks are Retained for Analyses

(Effects all protein analysis)

Percent Presence

70

Signal to Noise Cutoff

4

Lower Mass Cutoff

3000

Upper Mass Cutoff

15000

Select Samples

Choose Clustering Settings

### Optional Settings

Mirror Plots

Dendrogram

## Mirror Plots

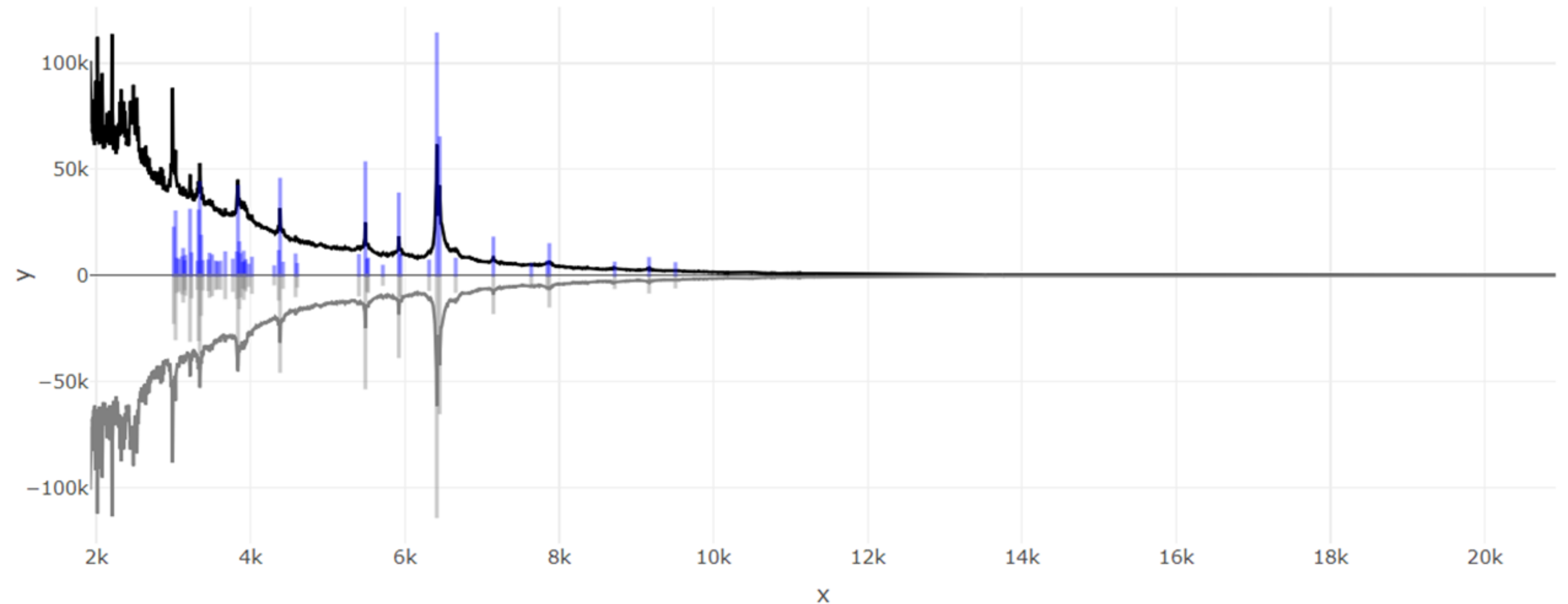
Choose two samples to compare in the mirror plots below. Matching peaks will be colored blue and non-matching peaks will be colored red.

Spectrum 1 (positive y-axis)

172-1

Spectrum 2 (negative y-axis)

172-1



Download SVG