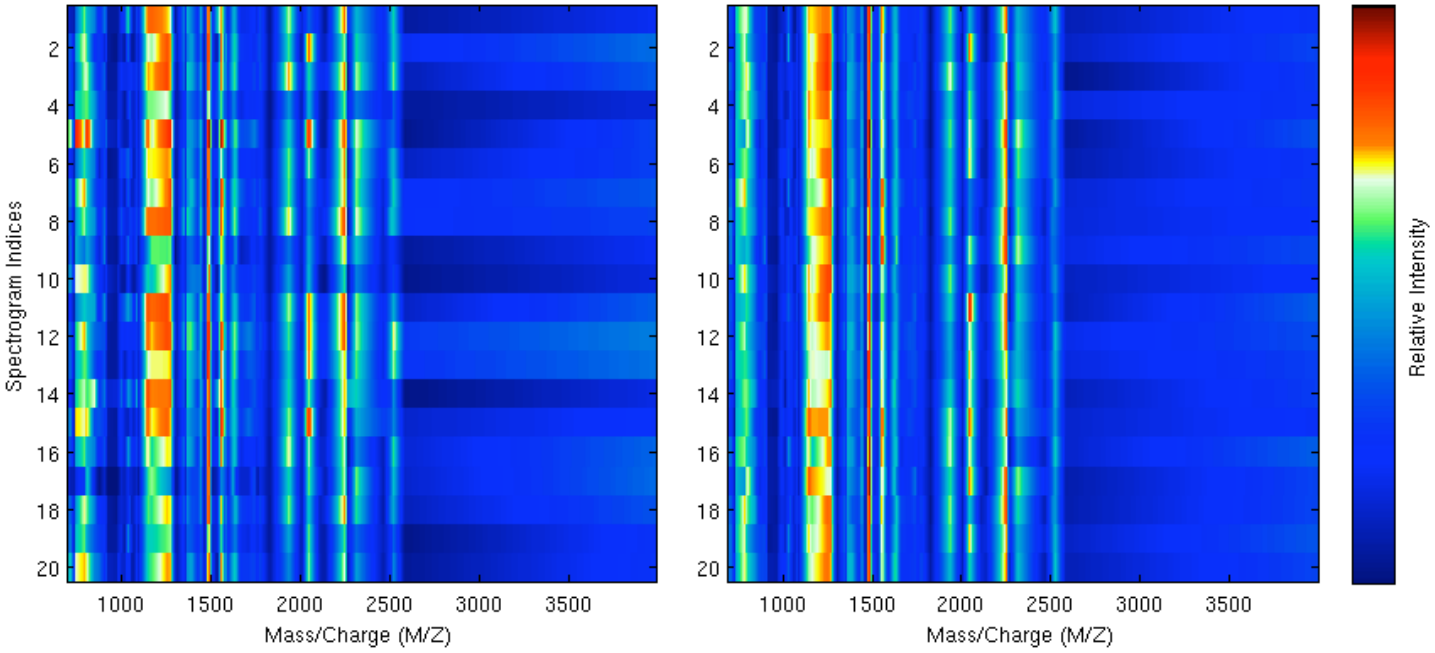

Figure 5: Heatmaps of peak intensities for raw (left) and EigenMS-normalized QC peptides (right) from the calibration data. Note that horizontal darker bands are apparent for batches 4 and 5, similar to those seen for the *Salmonella* peptides in Figure 1 of the main manuscript.

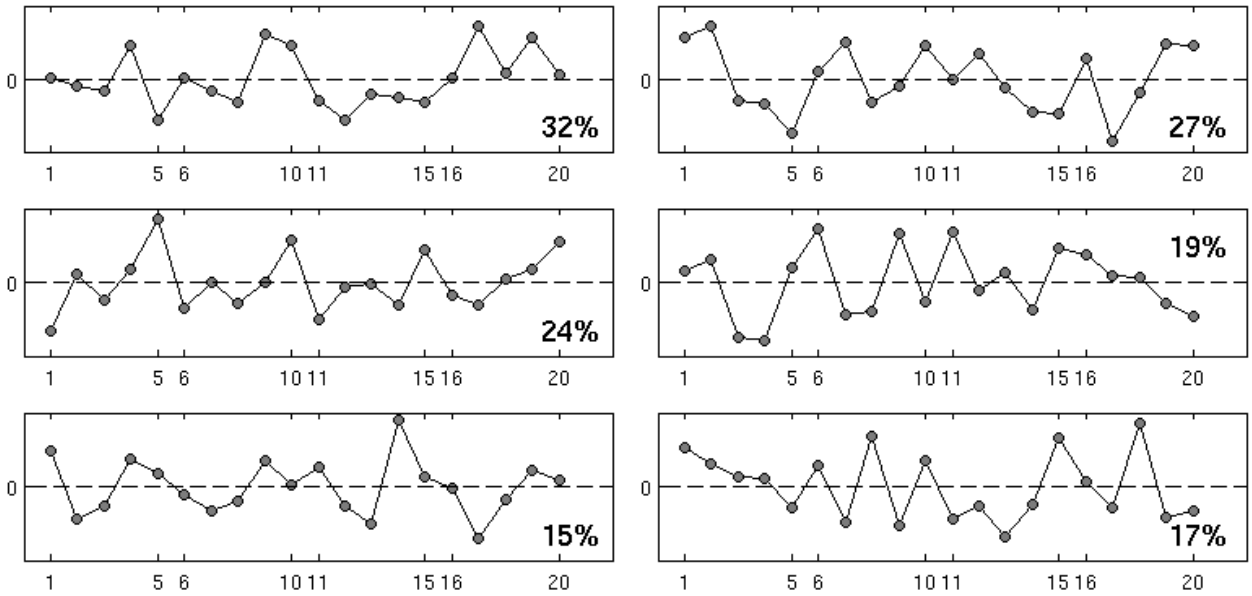

Figure 6: Visual representation of the eigenpeptides from the raw (left) and EigenMS-normalized QC peptides (right) from the calibration data. Top three eigenpeptides with first one at the top, second in the middle and 3rd at the bottom of the panel. Spectral order is shown on the x-axis and corresponds to the spectral order in the heatmaps. On the x-axis is spectral index, with the 20 ticks corresponding to the 20 replicated experiments. The first 5 ticks correspond to batches 1?5 of concentration 1, and so on. Percentages show percent explained by each eigenpeptide.

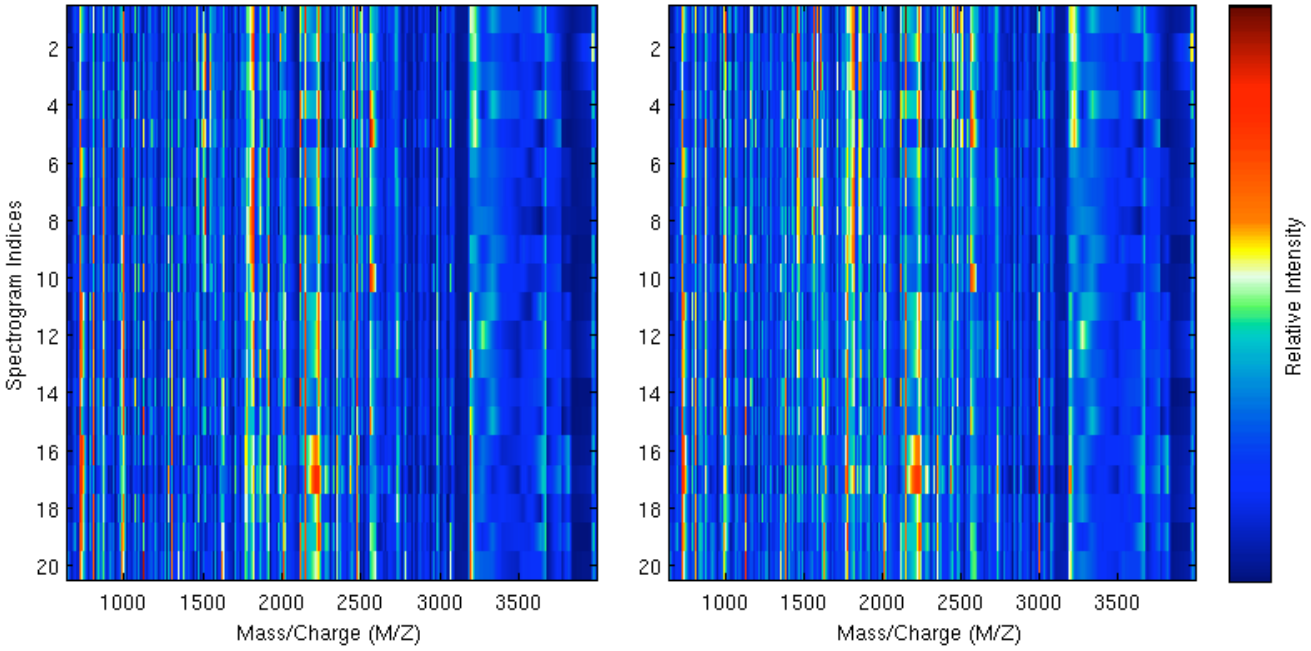

Figure 7: Heatmaps of peak intensities for the *Salmonella* peptides from the calibration data, after normalization by scatterplot smoothing (left) and global scaling (right). Note that that some horizontal banding is still apparent.

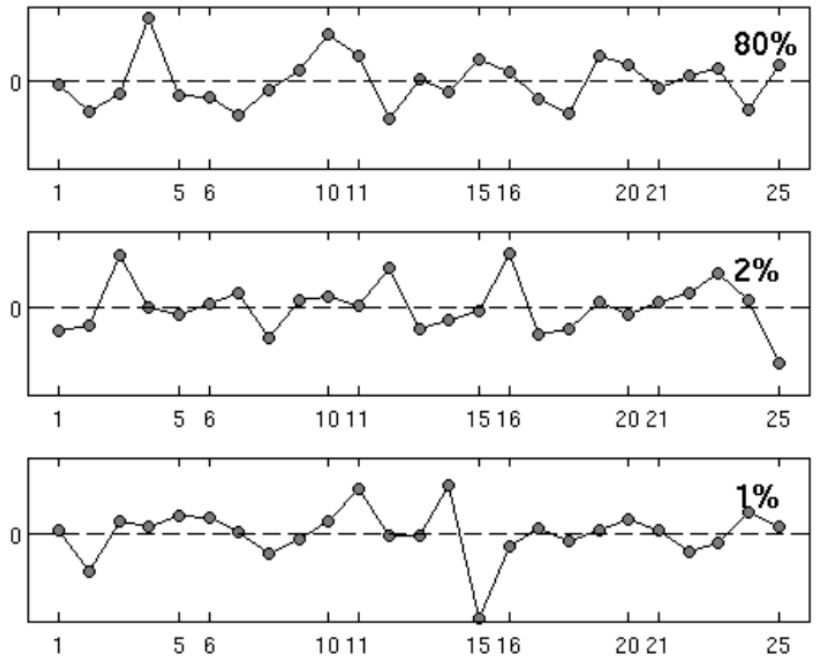

Figure 8: Visual representation of the residual eigenpeptides from the simulated data.

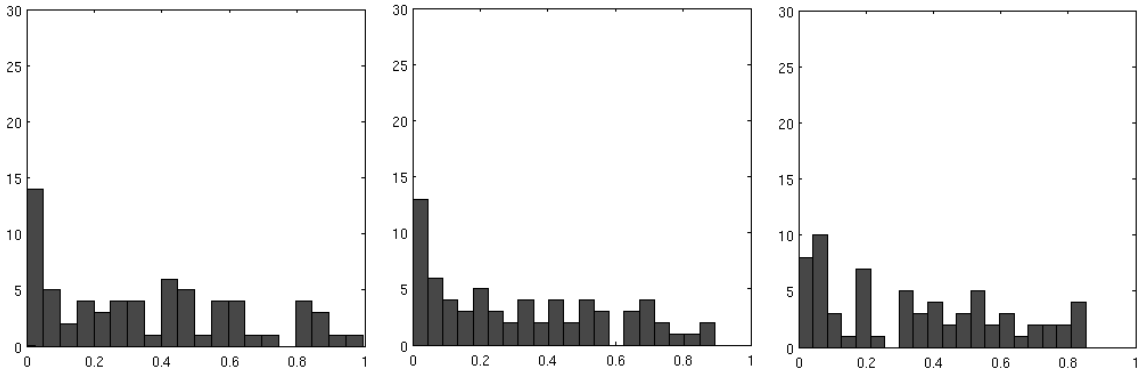

Figure 9: Histograms of null p-values for raw (left), EigenMS before rescaling (middle), and EigenMS after rescaling (right) QC peptides from the calibration data. Rescaling shifts the null p-value distribution in the correct direction, toward uniformity. Imperfect pipetting that resulted in nonconstant QC concentrations across groups and/or the use of technical replication may be responsible for the non-uniformity that persists after normalization by EigenMS. Under the assumptions of our model, EigenMS achieves uniform null p-values (Table 3 in the main document).