BASIS: High-performance bioinformatics platform for processing of large-scale mass spectrometry imaging data in chemically augmented histology

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SUPPLEMENTARY INFORMATION

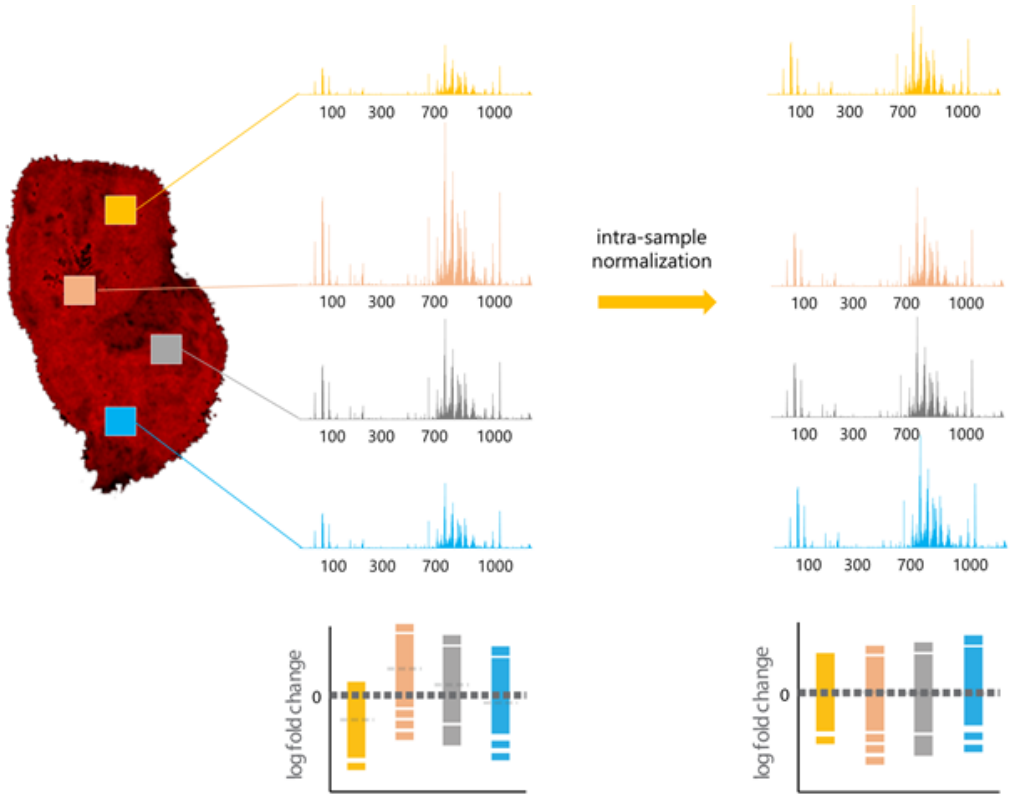

Figure S1. Intra-sample normalization strategy. Spectra with different median log fold changes are zero-centred in order to account for the difference in total ion intensities between spectra within the same sample (intra-sample normalization).

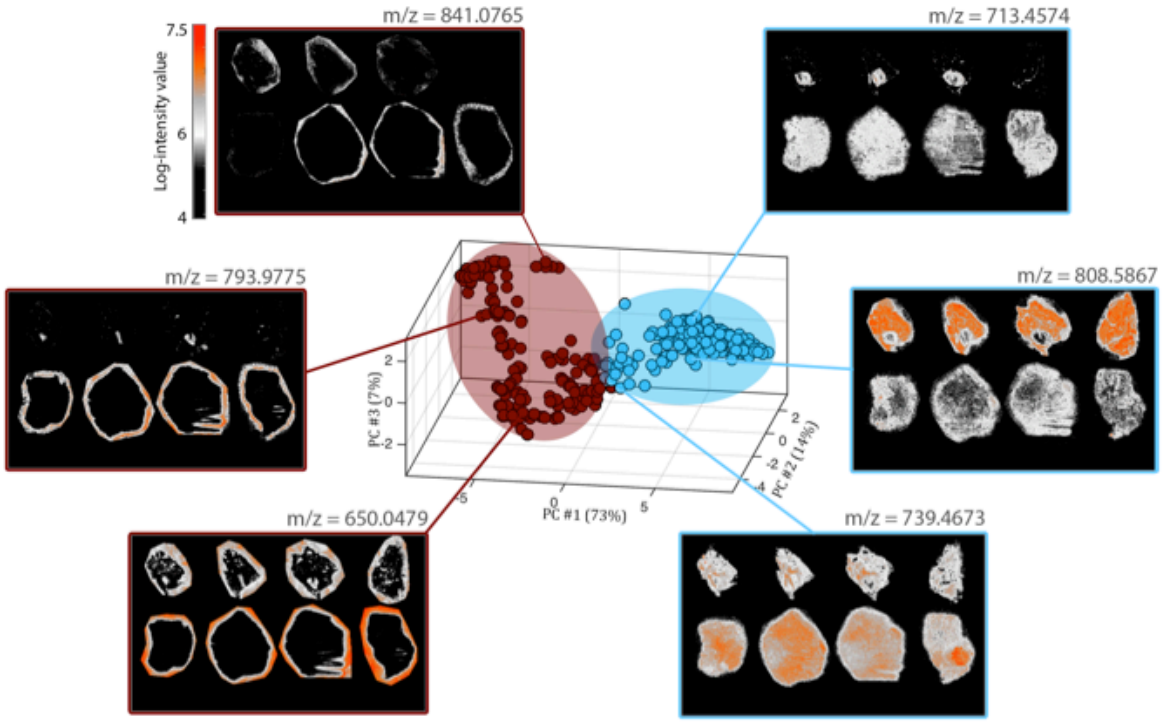

Figure S2. Cluster-driven matrix/solvent removal strategy for large-scale MSI data. The negative intensity correlation between tissue (matrix) and solvent is utilized to perform clustering and subsequent separation of tissue- and background-related signals. The differentiability of such clusters is also visualized by a PCA plot.