

Comparative Analysis of Quantitative Mass Spectrometric Methods for Subcellular Proteomics

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SUPPLEMENTAL FIGURES

Fig. S1. Distribution of precursors with weighted idotp.

Fig. S2-S4. PCA analysis of peptides using all four quantitative proteomics methods.

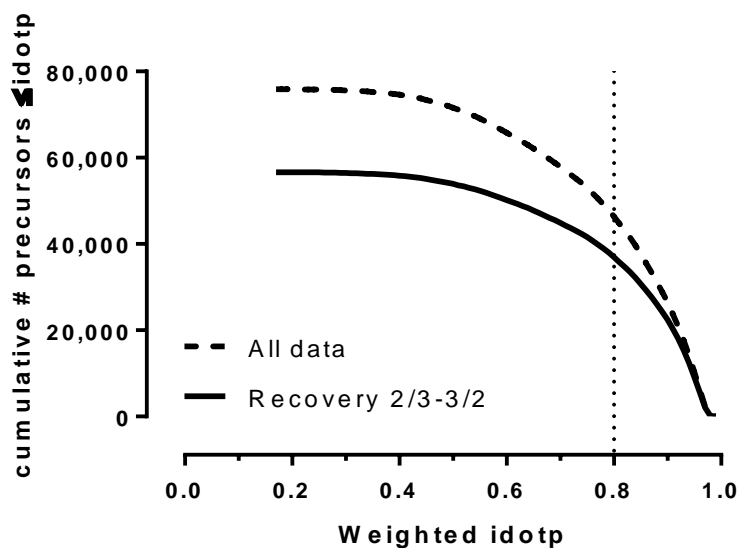


Fig. S1. Distribution of precursors with weighted idotp. Weighted idotp is defined as: $\frac{\sum (\text{idotp} \times \text{intensity})}{\sum (\text{precursor intensities in all runs})}$ of precursor per run. Solid line plot represents precursors with acceptable recoveries while dashed line plot includes all recoveries. Vertical dashed line represents the acceptable weighted idotp threshold of 0.8.

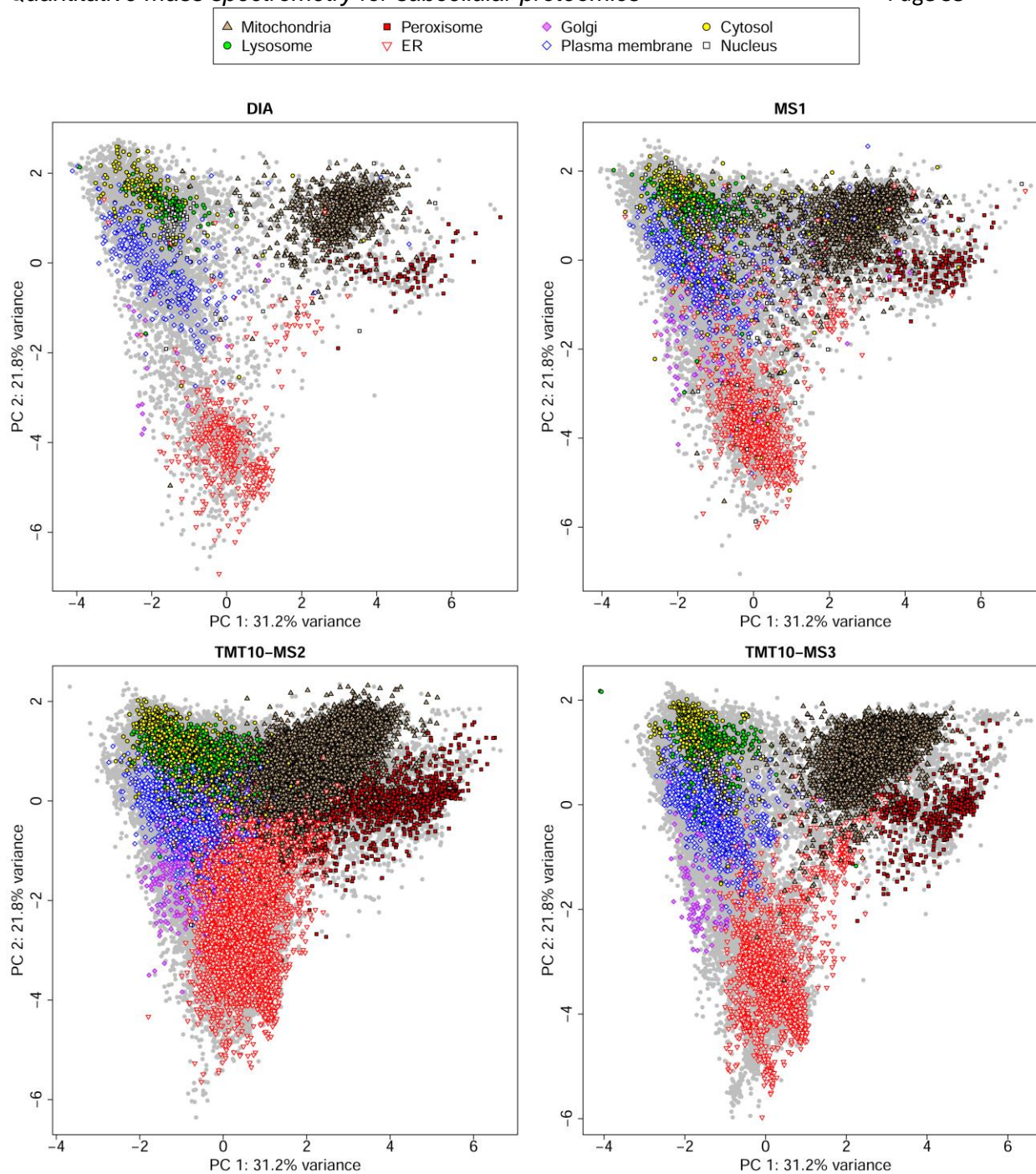


Fig. S2. Principal component 1 versus 2 of peptides obtained using the four different quantitative MS approaches. Peptides are assigned to organelles as indicated by color – unassigned peptides are indicated in grey.

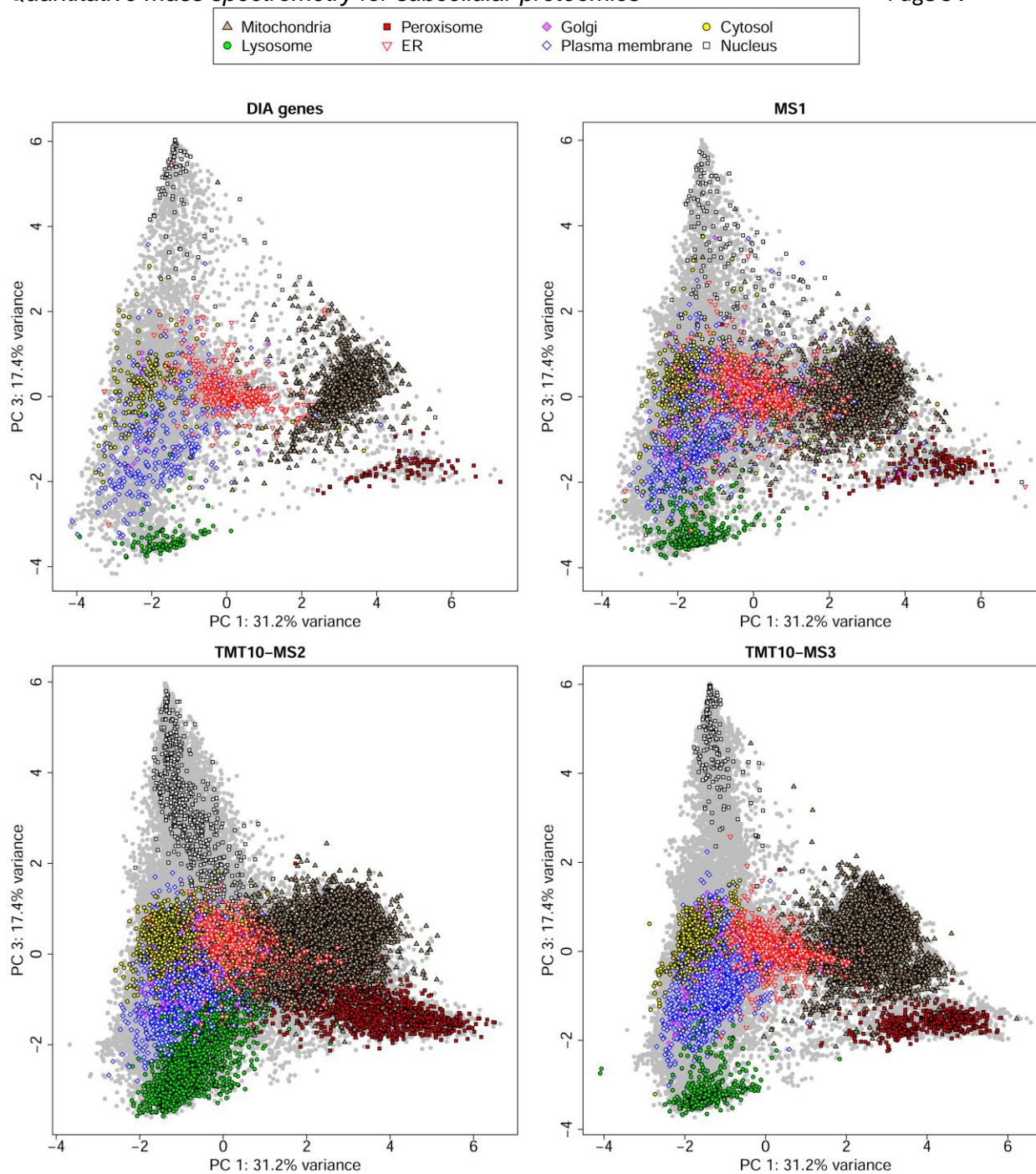


Fig. S3. Principal component 1 versus 3 of peptides obtained using the four different quantitative MS approaches. Peptides are assigned to organelles as indicated by color – unassigned peptides are indicated in grey.

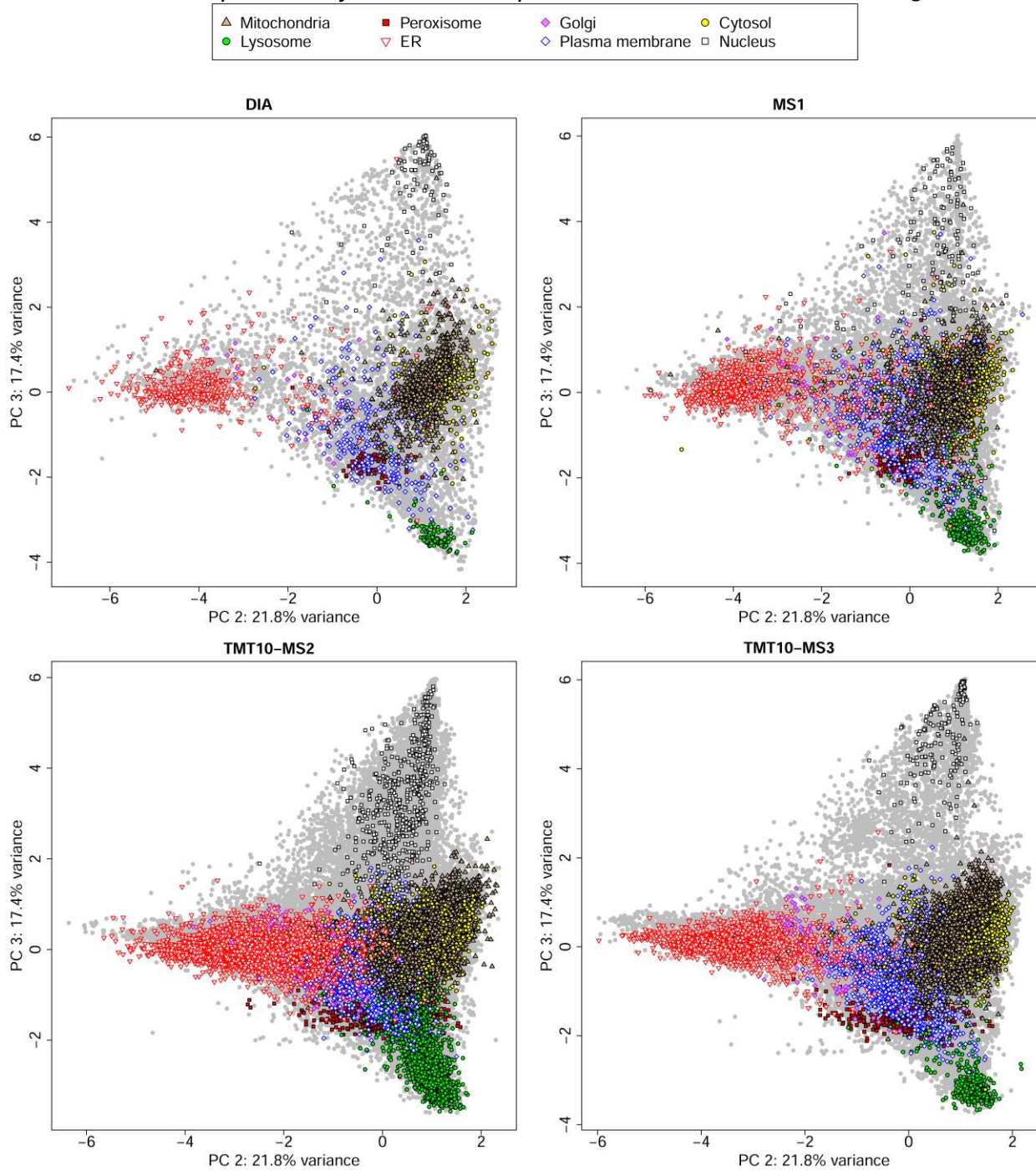


Fig. S4. Principal component 2 versus 3 of peptides obtained using the four different quantitative MS approaches. Peptides are assigned to organelles as indicated by color – unassigned peptides are indicated in grey.