Supplementary Material

Targeted Quantification of the Lysosomal Proteome in Complex Samples

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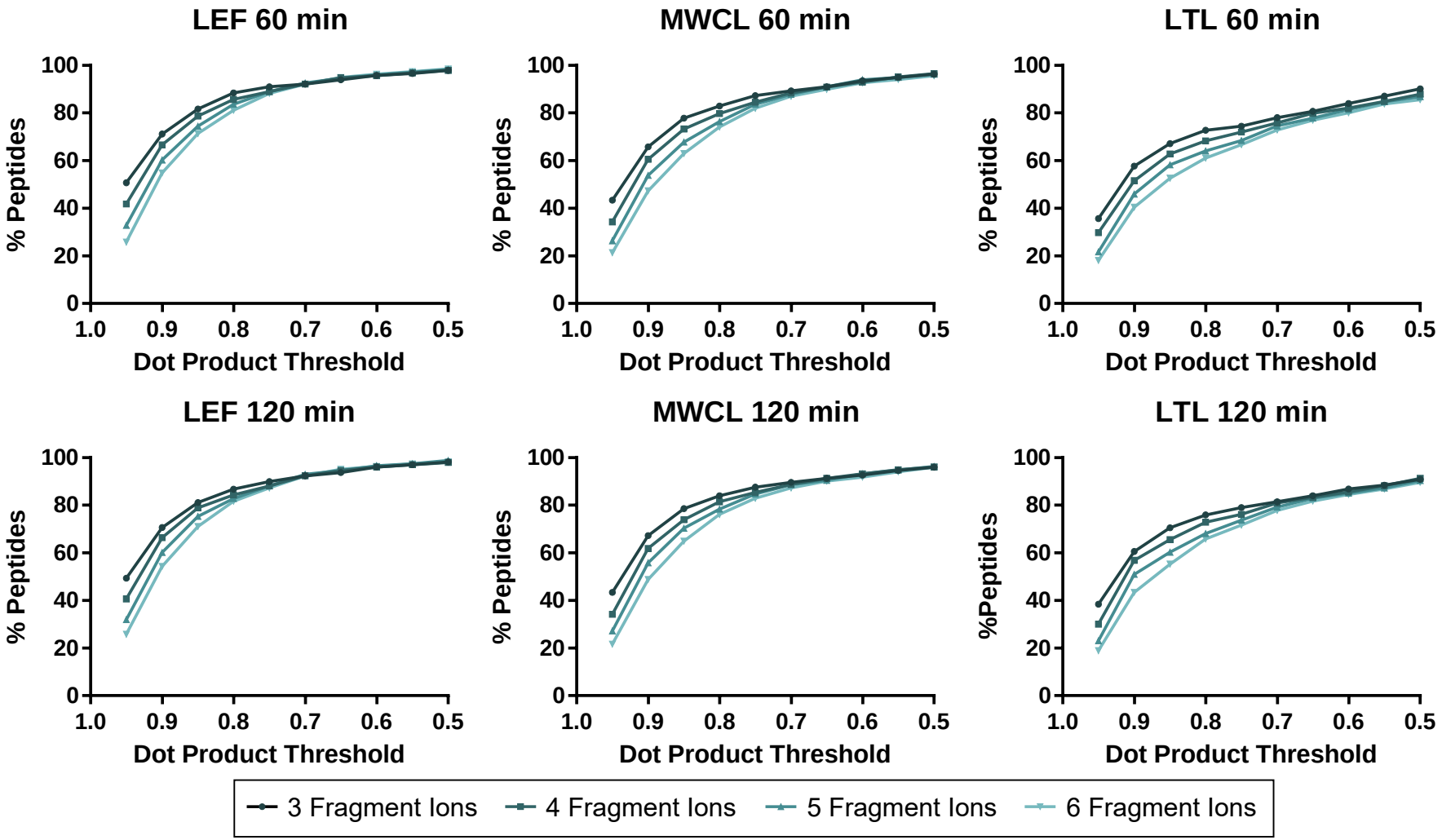
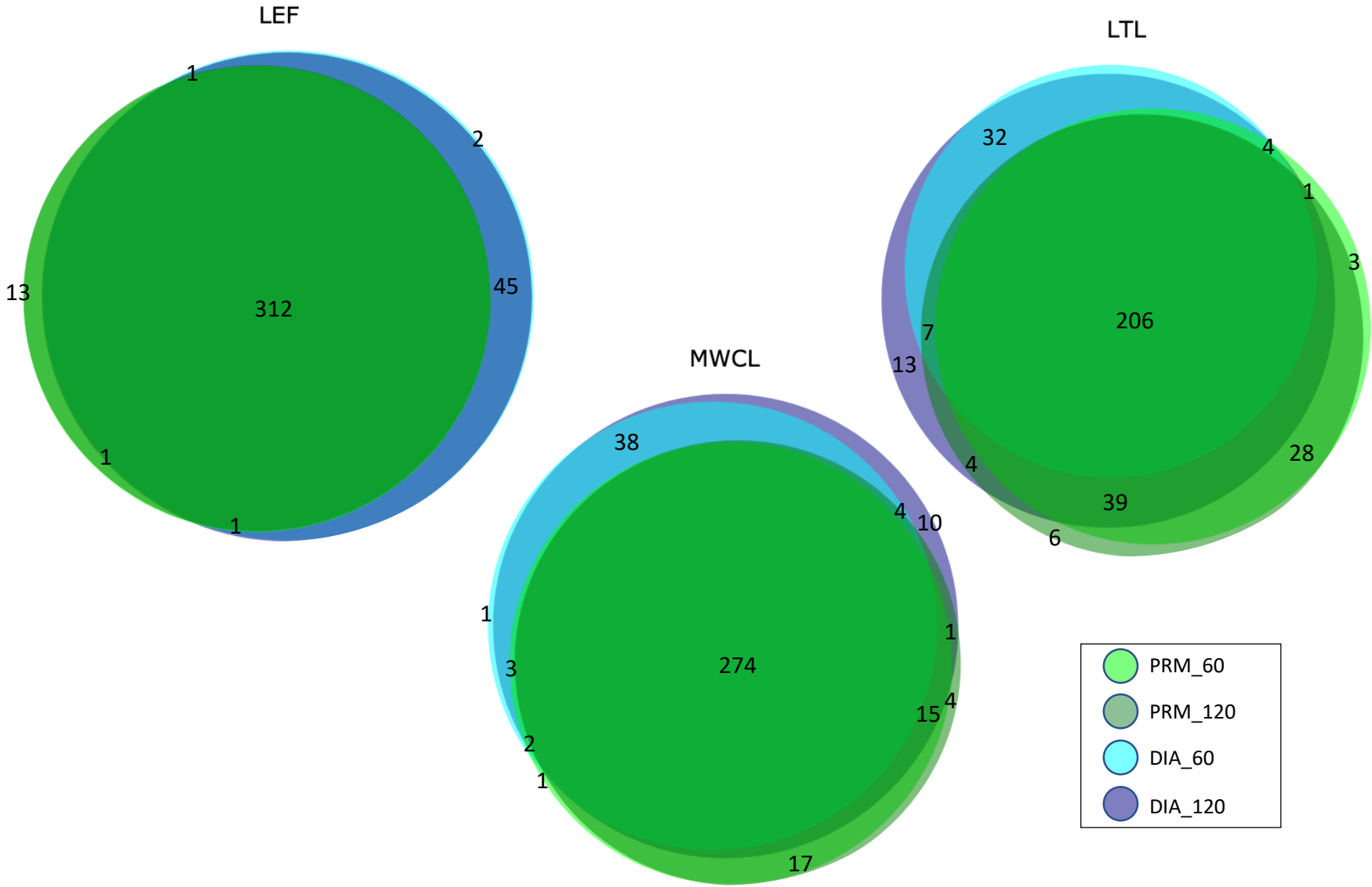
Supplementary Figure 1: Dot product threshold determination for the acceptance of PRM data.
Supplementary Figure 2: Overlap of identified proteins from PRM and DIA runs

Supplementary Reference

1. Hulsen, T., J. de Vlieg, and W. Alkema, BioVenn - a web application for the comparison and visualization of biological lists using area-proportional Venn diagrams. Bmc Genomics, 2008. 9(488).



Supplementary Figure 1: Dot product threshold determination for the acceptance of PRM data. Shown are threshold determination graphs for 60 min and 120 min gradients for the lysosome-enriched fraction (LEF), mouse embryonic fibroblast whole cell lysate (MWCL), and liver tissue lysate (LTL). Data were analyzed with Skyline Daily using three, four, five, or six fragment ions. In each plot, the percentage of peptides passing the applied dot product threshold, which is indicated on the X axis, is displayed. Each line represents a different number of fragment ions utilized for peptide quantification.



Supplementary Figure 2: Overlap of identified proteins from PRM and DIA runs. PRM data were analyzed using Skyline Daily, DIA data using Spectronaut. Proteins which were quantified in individual MS runs were extracted and compared. Each Venn diagram represents one sample type: lysosome-enriched fraction (LEF), mouse embryonic fibroblast whole cell lysate (MWCL), and liver tissue lysate (LTL). Compared are data from four different triplicate analyses conducted with PRM and DIA, each with 60 min and 120 min gradients. Venn diagrams were created using DeepVenn [1].