File Name: Supplementary Data 1

Description: Protein groups and peptides identified using Evosep-Astral and Neo-EV1107-Astral methods.

File Name: Supplementary Data 2

Description: Protein groups and peptides identified using different MS2 maximum injection time (IT) from 1 to 3.5 ms.

File Name: Supplementary Data 3

Description: Protein groups and peptides identified using different mass ranges.

File Name: Supplementary Data 4

Description: Protein groups and peptides identified using different isolation windows from 0.8 to 2 Da.

File Name: Supplementary Data 5

Description: Protein groups and peptides identified using different AGC values from 100 to 600.

File Name: Supplementary Data 6

Description: Evaluation of the high-throughput nDIA method with one to five minutes LC gradients.

File Name: Supplementary Data 7

Description: Evaluation of the quantitative performance of the high-throughput nDIA method with three-species samples mixed in various ratios.

File Name: Supplementary Data 8

Description: Comparison of the protein and peptide identifications using different digestion durations from 30 min to 15 h. To check the missed cleavage percentage, up to three missed cleavage sites were allowed for this analysis.

File Name: Supplementary Data 9

Description: Protein groups and peptides identified using the standard and high-throughput sample preparation workflows.

File Name: Supplementary Data 10

Description: Proteins identified in the large-scale mouse tissue proteomics datasets including 507 tissue samples. Statistical analyses for all pairwise comparisons were performed using two-tailed Student's t-tests. No adjustments for multiple comparisons were applied. Dataset available on Figshare: https://doi.org/10.6084/m9.figshare.31143709.

File Name: Supplementary Data 11

Description: Differentially regulated proteins in each tissue following treatment of ASNase for 1 to 8 days. For each protein, the fold change of the median intensity from ASNase treated and PBS treated sample groups was calculated. Only proteins with a fold change >2 or <0.5 and p-value <0.05 were selected as differential proteins.

File Name: Supplementary Data 12

Description: Functional clustering analysis of the differentially regulated proteins in the SQWAT. Pathway enrichment analysis was performed using DAVID (https://davidbioinformatics.nih.gov/) with default settings. P-values were calculated using the modified Fisher's exact test (EASE score). No adjustments for multiple comparisons were applied.

File Name: Supplementary Data 13

Description: Functional clustering analysis of the differentially regulated proteins in the GAT. Pathway enrichment analysis was performed using DAVID (https://davidbioinformatics.nih.gov/) with default settings. P-values were calculated using the modified Fisher's exact test (EASE score). No adjustments for multiple comparisons were applied.

File Name: Supplementary Data 14

Description: Functional clustering analysis of the differentially regulated proteins in the lung. Pathway enrichment analysis was performed using DAVID (https://davidbioinformatics.nih.gov/) with default settings. P-values were calculated using the modified Fisher's exact test (EASE score). No adjustments for multiple comparisons were applied.

File Name: Supplementary Data 15

Description: Functional clustering analysis of the differentially regulated proteins in the spleen. Pathway enrichment analysis was performed using DAVID (https://davidbioinformatics.nih.gov/) with default settings. P-values were calculated

using the modified Fisher's exact test (EASE score). No adjustments for multiple comparisons were applied.

File Name: Supplementary Data 16

Description: Functional clustering analysis of the differentially regulated proteins in the stomach. Pathway enrichment analysis was performed using DAVID (https://davidbioinformatics.nih.gov/) with default settings. P-values were calculated using the modified Fisher's exact test (EASE score). No adjustments for multiple comparisons were applied.

File Name: Supplementary Data 17

Description: Functional clustering analysis of the differentially regulated proteins in the small intestine. Pathway enrichment analysis was performed using DAVID (https://davidbioinformatics.nih.gov/) with default settings. P-values were calculated using the modified Fisher's exact test (EASE score). No adjustments for multiple comparisons were applied.

File Name: Supplementary Data 18

Description: Functional clustering analysis of the differentially regulated proteins in the large intestine. Pathway enrichment analysis was performed using DAVID (https://davidbioinformatics.nih.gov/) with default settings. P-values were calculated using the modified Fisher's exact test (EASE score). No adjustments for multiple comparisons were applied.

File Name: Supplementary Data 19

Description: Functional clustering analysis of the differentially regulated proteins in the liver. Pathway enrichment analysis was performed using DAVID (https://davidbioinformatics.nih.gov/) with default settings. P-values were calculated using the modified Fisher's exact test (EASE score). No adjustments for multiple comparisons were applied.

File Name: Supplementary Data 20

Description: Functional clustering analysis of the differentially regulated proteins in the kidney. Pathway enrichment analysis was performed using DAVID (https://davidbioinformatics.nih.gov/) with default settings. P-values were calculated using the modified Fisher's exact test (EASE score). No adjustments for multiple comparisons were applied.

File Name: Supplementary Data 21

Description: Functional clustering analysis of the differentially regulated proteins in the heart. Pathway enrichment analysis was performed using DAVID (https://davidbioinformatics.nih.gov/) with default settings. P-values were calculated using the modified Fisher's exact test (EASE score). No adjustments for multiple comparisons were applied.

File Name: Supplementary Data 22

Description: Functional clustering analysis of the differentially regulated proteins in the muscle. Pathway enrichment analysis was performed using DAVID (https://davidbioinformatics.nih.gov/) with default settings. P-values were calculated using the modified Fisher's exact test (EASE score). No adjustments for multiple comparisons were applied.

File Name: Supplementary Data 23

Description: Functional clustering analysis of the differentially regulated proteins in the brain. Pathway enrichment analysis was performed using DAVID (https://davidbioinformatics.nih.gov/) with default settings. P-values were calculated using the modified Fisher's exact test (EASE score). No adjustments for multiple comparisons were applied.

File Name: Supplementary Data 24

Description: Functional clustering analysis of the differentially regulated proteins in the bone marrow. Pathway enrichment analysis was performed using DAVID (https://davidbioinformatics.nih.gov/) with default settings. P-values were calculated using the modified Fisher's exact test (EASE score). No adjustments for multiple comparisons were applied.

File Name: Supplementary Data 25

Description: Number of shared tissues for differential proteins. The differential proteins identified in different time points (1 day, 3 days, 5 days, and 8 days) were merged for each tissue type. The number of shared tissues means certain proteins were identified to be differentially regulated in a certain number of tissues.

File Name: Supplementary Data 26

Description: Metabolomics analysis of amino acid in the tissues. Statistical analyses for all pairwise comparisons were performed using two-tailed Student's t-tests. No adjustments for multiple comparisons were applied.

File Name: Supplementary Data 27

Description: Metabolomics analysis of polar metabolites in the tissues. Statistical analyses for all pairwise comparisons were performed using two-tailed Student's t-tests. No adjustments for multiple comparisons were applied.

File Name: Supplementary Data 28

Description: Dysregulated metabolites and proteins and co-regulated pathways. Joint pathway enrichment analysis was performed using MetaboAnalyst (https://www.metaboanalyst.ca) with default settings. P-values were calculated using Fisher's exact test. No adjustments for multiple comparisons were applied.