SUPPLEMENTAL DATA

NATURAL GENETIC VARIATION DIFFERENTIALLY AFFECTS THE PROTEOME AND TRANSCRIPTOME IN *C. ELEGANS*

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Supplemental data consist of 5 Figures and 8 Tables

FIG. S1. **Protein abundance value correction for arginine-to-proline conversion.** *A,* The intensity contribution of heavy proline to the heavy arginine or heavy lysine peaks is proportional to the number of prolines. (y-axis: number of peptides with 1 - 4 prolines). *B,* The proportion of the intensity contribution of heavy proline to the heavy arginine or lysine peak is independent of the signal intensity. *C,* Proline corrected CB4856/N2 iBAQ ratios correlate with the uncorrected iBAQ ratios. *D,* Proline corrected CB4856/N2 protein abundance ratios correlate with the uncorrected protein abundance ratios. The 129 differentially expressed proteins are shown as violet dots. The other quantified proteins are shown in grey. r^2_{129} - is the regression coefficient for the 129 differentially expressed proteins. r^2_T - is the regression coefficient for all quantified proteins. The protein abundance and iBAQ ratio regression coefficient is higher for the differentially expressed proteins.

FIG. S2. **Peptide intensity correlations between the three biological replicates.** *A,* log2 light peptide intensity correlations. *B,* log2 heavy peptide intensity correlations. r - is the Pearson correlation coefficient for all quantified peptides.

FIG. S3. **The annotated MS/MS spectra of single peptide matches quantified in the first biological replicate.** For all proteins with a single peptide match the annotated MS/MS spectrum with the lowest posterior error probability (PEP) value is plotted. In total, 377 MS/MS spectra were extracted from the corresponding RAW files. Annotation of the spectra was done with matching b- and y-ions (within 0.6 Dalton error tolerance). The dotted blue lines indicate a matching y-ion, a dotted black line indicates a matching b-ion. For precursor masses higher than doubly charged, the multiply charged fragment ions are also plotted. The plots were generated using the R package protViz.

FIG. S4. **The annotated MS/MS spectra of single peptide matches quantified in the second biological replicate.** For all proteins with a single peptide match the annotated MS/MS spectrum with the lowest posterior error probability (PEP) value is plotted. In total, 414 MS/MS spectra were extracted from the corresponding RAW files. Annotation of the spectra was done with matching b- and y-ions (within 0.6 Dalton error tolerance). The dotted blue lines indicate a matching y-ion, a dotted black line indicates a matching b-ion. For precursor masses higher than doubly charged, the multiply charged fragment ions are also plotted. The plots were generated using the R package protViz.

FIG. S5. **The annotated MS/MS spectra of single peptide matches quantified in the third biological replicate.** For all proteins with a single peptide match the annotated MS/MS spectrum with the lowest posterior error probability (PEP) value is plotted. In total, 442 MS/MS spectra were extracted from the corresponding RAW files. Annotation of the spectra was done with matching b- and y-ions (within 0.6 Dalton error tolerance). The dotted blue lines indicate a matching y-ion, a dotted black line indicates a matching b-ion. For precursor masses higher than doubly charged, the multiply charged fragment ions are also plotted. The plots were generated using the R package protViz.

TABLE S1**. Number of proteins identified and quantified in the three different SILAC experiments**.

TABLE S2**. Proteins, peptide sequences, percentage coverage for each protein and number of peptides with and without proline quantified in the three biological replicates.**

TABLE S3. **Gene features.** Transcript and protein levels, and corresponding ratios of the genes quantified in the three biological replicates are listed for each individual sample as well as the mean-values per genotype.

TABLE S4. **Gene enrichments of GO-terms, gene classes, KEGG, protein domains.** WormBook chapters and eQTLs in protein and transcript datasets.

TABLE S5. **Characterization of the 129 differentially expressed proteins.**

TABLE S6. **List of 377 single peptide matches quantified in the first biological replicate with the lowest posterior error probability (PEP) and the corresponding MS/MS information.**

TABLE S7. **List of 414 single peptide matches quantified in the second biological replicate with the lowest posterior error probability (PEP) and the corresponding MS/MS information.**

TABLE S8. **List of 442 single peptide matches quantified in the third biological replicate with the lowest posterior error probability (PEP) and the corresponding MS/MS information**.