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**Manuscript: A previously uncharacterized Factor Associated with Metabolism and Energy (FAME/C14orf105/CCDC198/1700011H14Rik) is related to evolutionary adaptation, energy balance, and kidney physiology**

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10226981/>

The proteinGroups.txt file, the resulting output from MaxQuant, was further processed in R, v. 4.1.1. using the Differential Enrichment of Proteomics Data (DEP) R package[76](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10226981/#CR76). In the workflow, firstly contaminant hits were filtered out and protein intensities were log2 transformed. Only proteins with intensity > 0 in more than 4/6 samples of at least one condition were retained. Intensities were normalized using LoessF normalization, and missing values were imputed using minimal value. Finally, limma test with Benjamini-Hochberg adjustment for multiple comparison was used to test for the differentially expressed proteins. Proteins were denoted as upregulated when passing the threshold of log2 fold change > 1 and adjusted p-value < 0.05. Corresponding cellular localizations of upregulated proteins were visualized using the Human Cell Map resource[77](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10226981/#CR77) (Supplementary Fig. [23c](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10226981/#MOESM1))