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Data Article

Proteomic dataset of wolframín-deficient mouse heart and skeletal muscles

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ABSTRACT

The data presented in this article are related to the research article entitled "Increased Mitochondrial Protein Levels and Bioenergetics in the *musculus rectus femoris* of Wfs1-Deficient mice" (Eimre et al., accepted for publication). This dataset reports the analysis of Wfs1-deficient mouse heart, *musculus soleus*, and white part of *musculus rectus femoris* by liquid chromatography/tandem mass spectrometry. Label-free quantitative analysis of the mass spectrometry data identified 4056 proteins, with 114, 212, and 1290 proteins differentially expressed (t -test; $p < 0.05$) in the heart, *m. soleus*, and *m. rectus femoris*, respectively, between the Wfs1-deficient and wild-type groups. Eight proteins were found to be differentially expressed in all mentioned muscles, with 1 protein differently expressed in oxidative (*m. soleus* and heart) and 88 in skeletal muscles. This dataset supports the cited study and can be used to extend additional analyses. Data are available via ProteomeXchange with identifier PXD011019.

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Specifications table

Subject area	Biology
More specific subject area	Proteomics, pathophysiology
Type of data	Figure, tables
How data was acquired	LC-MS/MS was performed on an Q Exactive Plus tandem mass spectrometer coupled to an Ultimate 3000 RSLCnano system
Data format	Raw and analyzed
Experimental factors	WFS1 deficiency
Experimental features	Proteins of WFS1 deficient mouse muscles were precipitated, resuspended and analyzed by label free LC-MS/MS. Label-free quantitation on the mass spectrometer data files was performed with MaxQuant
Data source location	Tartu, Estonia
Data accessibility	The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PXD011019.

Value of the data

- This is the first proteomic dataset of Wfs1 deficient muscles.
- The data may be a valuable starting point for studying the direct and indirect mechanisms of Wfs1 deficiency on mouse muscles.
- These data and further experiments based on these data may provide valuable information for understanding the mechanisms of Wolfram syndrome and type 1 diabetes.

1. Data

Proteins found to be differentially expressed in all studied Wfs1-deficient muscles are presented in Fig. 1 and at the beginning of Table S4. The level of Bcl2-associated agonist of the cell death protein was decreased in both oxidative muscles (Table S4). Protein expression in wolframin-deficient skeletal muscle was compared to that in wild-type, which showed that the expression of 35 proteins was decreased, while 61 proteins were increased (Table 1). Data of differentially expressed proteins in the wolframin-deficient heart are in Table S1, wolframin-deficient *musculus soleus* in Table S2, and wolframin-deficient *musculus rectus femoris* in Table S3. Label-free quantitative (LFQ) intensities and other information for all proteins identified by liquid chromatography (LC)/tandem mass spectrometry (MS/MS) analysis of muscles are in Tables S4 and S5 (P3; P5; P6; P8; P17; P21; P23; P25: *m. rectus femoris* in wild-type mice; P1; P19; P22; P24; P26: *m. rectus femoris* in Wfs1-deficient mice; P4; P7; P18: *m. soleus* in wild-type mice; P2; P20: *m. soleus* of Wfs1-deficient mice; P9; P11; P12; P14: heart in wild-type mice; P10; P13; P15; P16: heart in Wfs1-deficient mice). All peptides identified and quantified are shown in Table S6.

2. Experimental design, materials and methods

2.1. Animals and proteomics sample preparation

The heart, *m. soleus*, and white glycolytic part of the *m. rectus femoris* from 9–12-month-old Wfs1 KO male mice and their wild-type littermates were used for LC/MS/MS analysis. The animals were housed under standard laboratory conditions on a 12-h light-dark cycle (lights on at 07:00) with free access to food and water. Experiments in this study were performed in accordance with the European Parliament Directive 2010/63/EU and permit (No. 86, May 4, 2016) from the Estonian National Board

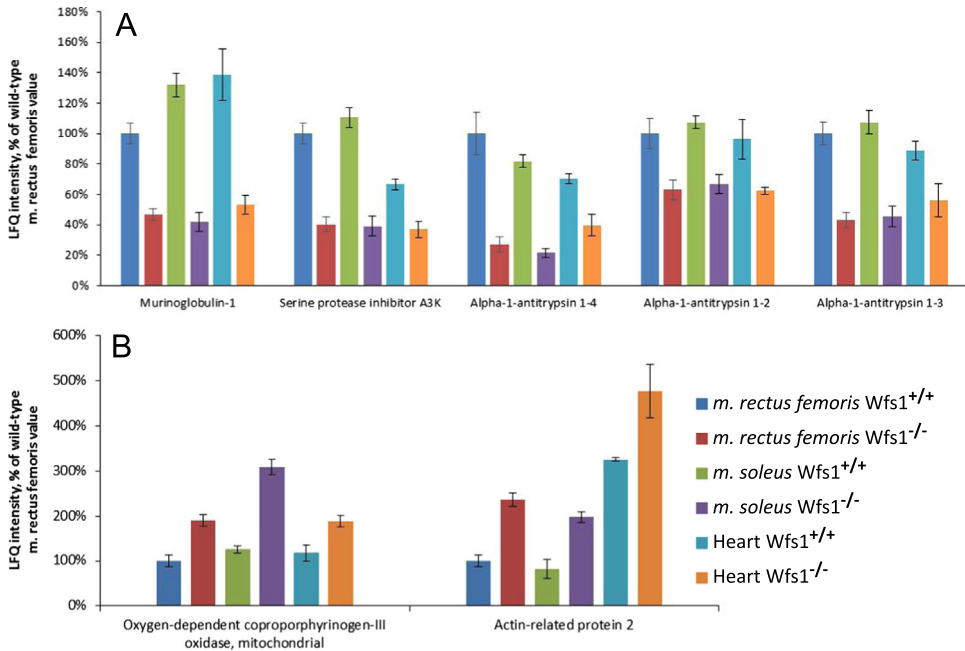


Fig. 1. Proteins showing higher (A) and lower (B) expression proteins in all studied *Wfs1*-deficient muscles. Data are presented as mean \pm SEM, $p < 0.5$ compared to wild-type.

of Animal Experiments. Muscle tissues were homogenized by sonication (Bandelin Sonopuls HD 2200, Sigma-Aldrich, St. Louis, MO, USA) on ice. Proteins in the homogenates were precipitated, suspended, and digested with trypsin. The obtained peptides were desalted and reconstituted in 0.5% trifluoroacetic acid [1].

2.2. Proteomics data analysis

LC/MS/MS analysis was performed using an Ultimate 3000 RSLCnano system (Dionex, Sunnyvale, CA, USA) and Q Exactive Plus (Thermo Fisher Scientific, Waltham, MA, USA) tandem mass spectrometer.

Mass spectrometric raw data were processed using the MaxQuant 1.5.3.17 software package [2]. LFQ was conducted using the MaxQuant LFQ algorithm [3]. A search was performed against the UniProt (www.uniprot.org) *Mus musculus* reference proteome database (downloaded on November 11, 2015; 57,320 entries). The peptide-spectrum match and protein false discovery rate was kept below 1% using a target-decoy approach [1]. Statistical analysis of LFQ intensities of proteins was performed by Student's *t*-test. Data are given as the mean \pm standard error of the mean. A value of $p < 0.05$ was considered statistically significant.

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Transparency document. Supporting information

Transparency data associated with this article can be found in the online version at <https://doi.org/10.1016/j.dib.2018.10.015>.

Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at <https://doi.org/10.1016/j.dib.2018.10.015>.

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