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 spec-
trometry 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 Proteo-
meXchange 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
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 ± standard error of the mean. A value of \( p < 0.05 \) was considered statistically significant.

Acknowledgements

This work was supported by Institutional Research Funding IUT20-46 of the Estonian Ministry of Education and Research.
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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