

Description of Additional supplementary files

Supplementary Dataset 1. Raw UMI counts matrix of 1000 fiber transcriptomics dataset.

Supplementary Dataset 2. Raw LFQ intensity matrix of the 1000 fiber proteomics dataset.

Supplementary Dataset 3. Quantified transcripts (raw UMI counts) within the 1000 fiber transcriptomics dataset after filtering.

Supplementary Dataset 4. Quantified proteins (log2 LFQ intensity) within the 1000 fiber proteomics dataset after filtering and imputation.

Supplementary Dataset 5. PC1 and PC2 drivers within the 1000 fiber transcriptomics study.

Supplementary Dataset 6. PC1 and PC2 drivers within the 1000 fiber proteomics study.

Supplementary Dataset 7. Over-representation analysis of the top drivers (top 5%) in PC1 and PC2 within the 1000 fiber transcriptomics and proteomics datasets.

Supplementary Dataset 8. Protein abundance of proteins within the GO term "Cytosolic Ribosome" in the 1000 fiber proteomics dataset.

Supplementary Dataset 9. Pseudobulked transcript expression within slow and fast skeletal muscle fibers in the 1000 fiber transcriptomics dataset.

Supplementary Dataset 10. Pseudobulked protein abundance within slow and fast skeletal muscle fibers in the 1000 fiber proteomics dataset.

Supplementary Dataset 11. Differential expression results between slow and fast skeletal muscle fibers in the 1000 fiber transcriptomics dataset.

Supplementary Dataset 12. Differential abundance results between slow and fast skeletal muscle fibers in the 1000 fiber proteomics dataset.

Supplementary Dataset 13. Over-representation analysis of the differentially regulated transcripts and proteins between slow and fast skeletal muscle fibers in the 1000 fiber transcriptomics and proteomics datasets.

Supplementary Dataset 14. Transcription factor activity inference via SCENIC for slow versus fast fibers in the 1000 fiber transcriptomics dataset.

Supplementary Dataset 15. Differential expression results between slow and fast skeletal muscle fibers in non-coding transcripts the 1000 fiber transcriptomics dataset.

Supplementary Dataset 16. Differential expression results between slow and fast skeletal muscle fibers in the microprotein dataset.

Supplementary Dataset 17. Detected proteins within the nemaline myopathy proteomics dataset.

Supplementary Dataset 18. Quantified proteins within the nemaline myopathy proteomics dataset after filtering and imputation.

Supplementary Dataset 19. Log2 transformed LFQ intensities of identified microproteins within the nemaline myopathy dataset

Supplementary Dataset 20. Pseudobulked protein abundance within the nemaline myopathy proteomics dataset.

Supplementary Dataset 21. Differential protein abundance within ACTA1- and TNNT1-nemaline myopathies.

Supplementary Dataset 22. Gene set enrichment analysis of the differential regulation within ACTA1- and TNNT1-nemaline myopathies.

Supplementary Dataset 23. Differential protein abundance within ACTA1- and TNNT1-nemaline myopathies by MYH-based fiber type.

Supplementary Dataset 24. Differentially abundant microproteins within ACTA1- and TNNT1- nemaline myopathies.

Supplementary Dataset 25. Detected proteins within the bulk nemaline myopathy proteomics dataset.

Supplementary Dataset 26. Differential protein abundance within TNNT1-nemaline myopathy in the bulk dataset.

Supplementary Dataset 27. Gene set enrichment analysis of the differentially abundant proteins within TNNT1-nemaline myopathy in the bulk dataset.

Supplementary Dataset 28. Metadata for the 1000 fiber transcriptomics dataset.

Supplementary Dataset 29. Metadata for the 1000 fiber proteomics dataset.

Supplementary Dataset 30. Metadata for the nemaline myopathy proteomics dataset.