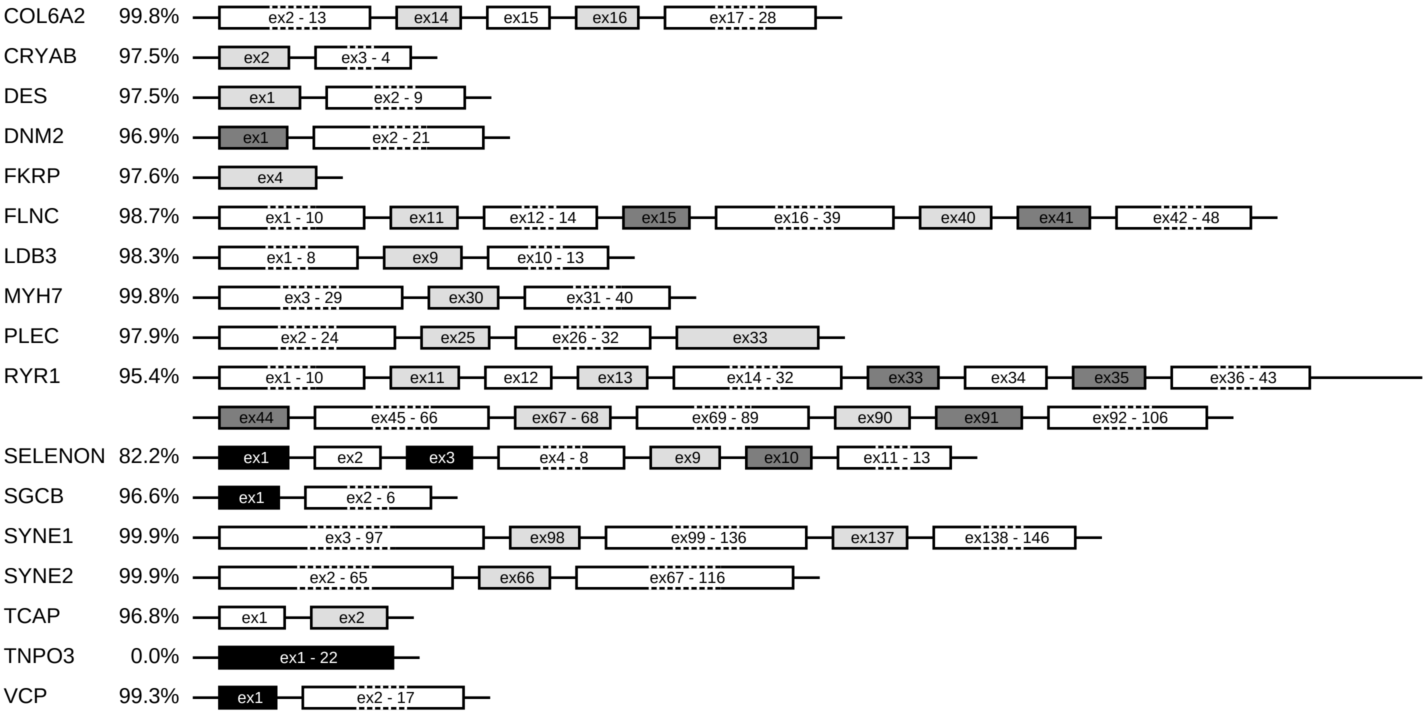
Appendix 1. Coverage of target sequences

Patient name: Demo Patient

The following genes are 100% covered (with a depth of at least 20x):
ANO5, BAG3, CAPN3, CAV3, CAVIN1, COL6A1, COL6A3, DAG1, DMD, DNAJB6, DPM3, DYSF, EMD, FHL1, FKTN, GNE, LMNA, MATR3, MYOT, NEB, POMGNT1, POMT1, POMT2, SGCA, SGCD, SGCG, TRIM32, TTN

Some parts of the following genes are not 100% covered (see details below)

Legend:
☐ exons covered to 100% (with a depth of at least 20x)
░ exons covered at 90-100% (with a depth of at least 20x)
▒ exons covered at <90% (with a depth of at least 20x)
■ exons not covered (with a depth of at least 20x)



Comments could be added here.

Analysis statistics:

- genes count: 45
- transcripts count: 45
- transcripts covered to 100% (with a depth of at least 20x): 62.3%
- transcripts covered to 90-100% (with a depth of at least 20x): 33.3%
- transcripts covered to <90% (with a depth of at least 20x): 2.2%
- transcripts not covered (with a depth of at least 20x): 2.2%