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**Supplementary figure 1.** Sequence matches in Ensembl v87 for the qRT-PCR primers used for DTU validation by Deng et al. (Deng et al., 2013). The primers were designed based on Ensembl v60. Despite being well designed within the context of Ensembl v60, it is clear in the new annotation that the primers target more transcripts than originally expected, in a way that makes it impossible to interpret the measurements from CMTM4 and TOM1L1. The red brackets indicate the pairs of forward and reverse primers. The dark blue vertical lines indicate portions of the sequence that have been hidden for convenient viewing of the relevant segments. The sequence in black background is the genomic sequence. The primer matches in the isoforms are highlighted in light blue. The alignments were visualized with Jalview (Waterhouse et al., 2009).

# References

Deng,N. *et al.* (2013) Detecting Splicing Variants in Idiopathic Pulmonary Fibrosis from Non-Differentially Expressed Genes. *PLoS One*, **8**, e68352.

Waterhouse,A.M. *et al.* (2009) Jalview Version 2-A multiple sequence alignment editor and analysis workbench. *Bioinformatics*, **25**, 1189–1191.