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Corrigendum

C7orf30 is necessary for biogenesis of the large subunit of the mitochondrial ribosome

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The authors wish to make the following corrections to their article:

In Figure 4 A, MRPL3 panel, the authors have erroneously inserted a different exposure image of the Complex II blot instead of the MRPL3 western blot. A corrected Figure is provided below.

The results and conclusion of the article are not affected and remain valid. The authors apologise to the readers for the inconvenience caused.

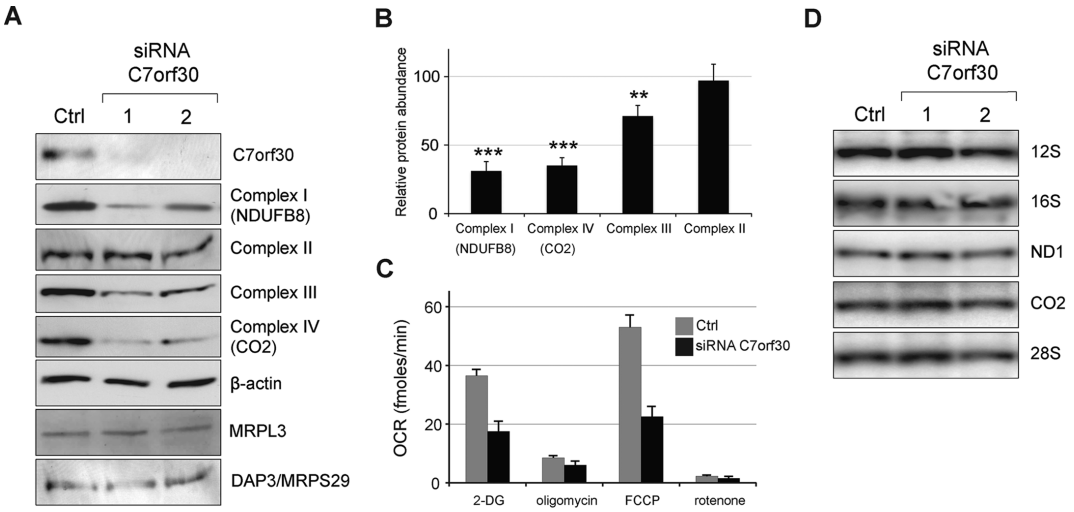

Figure 4. Inactivation of C7orf30 perturbs OXPHOS function without affecting mitochondrial transcripts. (A) Steady-state level of the OXPHOS subunits in cells transfected with siRNA to C7orf30. Steady-state protein levels of the endogenous C7orf30 protein, subunits of respiratory chain complexes and components of the mitoribosome (DAP3/MRPS29 and MRPL3) were analysed by western blotting in control cells transfected with an unrelated siRNA (Ctrl) or cells transfected with two siRNAs specific for C7orf30 for 6 days. β-actin was used as a loading control. (B) Quantification of steady-state levels of OXPHOS components in C7orf30-depleted cells. Western blot signals from the experiments as per (A) for 'siRNA 1' were quantified for C7orf30-depleted cells using ImageQuant software. Relative abundance is presented as a percentage of the steady-state level for control cells transfected with an unrelated siRNA. n = 3, $^{**}P<0.01$, $^{***}P<0.001$; two-tailed unpaired Student's t-test error bars = 1 SD. (C) OCR in C7orf30-depleted cells. OCR measured in an extracellular flux Seahorse instrument in control cells transfected with an unrelated siRNA or cells treated with siRNA to C7orf30 for 6 days. The wells containing cells were sequentially injected with 20 mM 2-DG to inhibit glycolysis, 100 nM oligomycin to inhibit ATP-synthase, 1 μM FCCP to uncouple the respiratory chain and 200 nM rotenone to inhibit complex I. n = 6, error bars = 1 SD. (D) Steady-state levels of mitochondrial transcripts upon inactivation of C7orf30. Total RNA from control cells (Ctrl) and cells transfected with two siRNAs specific for C7orf30 were analysed by northern blots using radioactive probes specific for the indicated mitochondrial transcripts. Nuclear-encoded 28S rRNA was used as a loading control.

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