

**Cell Metabolism, Volume 21**

**Supplemental Information**

**Opa1 Overexpression Ameliorates the Phenotype**

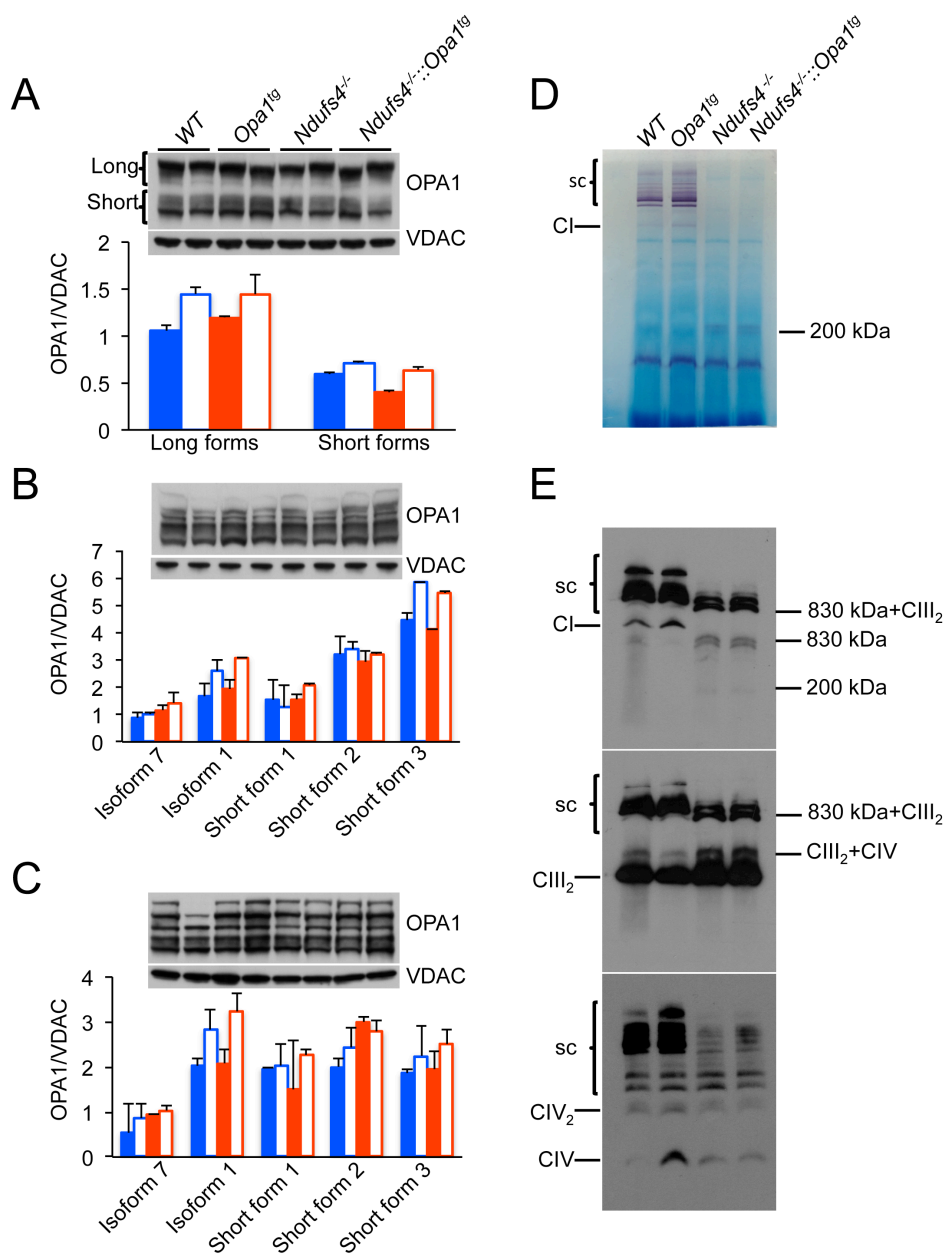
**of Two Mitochondrial Disease Mouse Models**

**Gabriele Civiletto, Tatiana Varanita, Raffaele Cerutti, Tatiana Gorletta, Serena Barbaro, Silvia Marchet, Costanza Lamperti, Carlo Viscomi, Luca Scorrano, and Massimo Zeviani**

Supplemental Material Online

Figure S1, related to figure 1.

Analysis of the *Ndufs4*<sup>-/-</sup> and *Ndufs4*<sup>-/-</sup>::*Opa1*<sup>Tg</sup> mouse models.



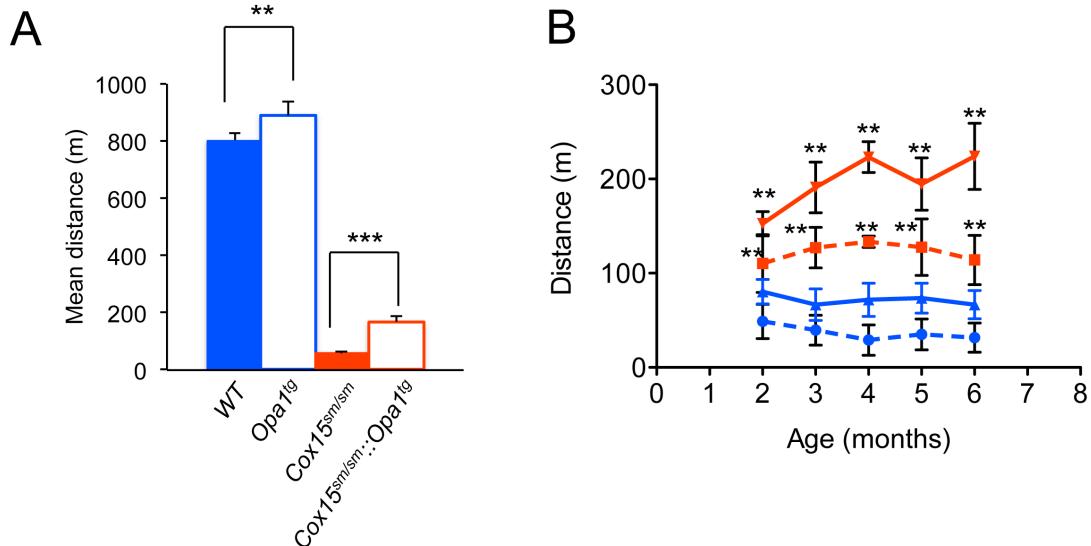
A) Western blot immunovisualization (upper panel) and densitometric analysis (lower panel) of OPA1 long (L) and Short (S) isoforms in brain mitochondria. Solid blue: *WT*; blue outline: *Opa1*<sup>Tg</sup>; solid red: *Cox15*<sup>sm/sm</sup>; red outline: *Cox15*<sup>sm/sm</sup>::*Opa1*<sup>Tg</sup>. Error bars represent SEM. VDAC was used as a loading control.

B) Western blot immunovisualization (upper panel) and densitometric analysis (lower panel) of OPA1 forms in skeletal muscle mitochondria of *WT*, *Opa1*<sup>Tg</sup>, *Ndufs4*<sup>-/-</sup>, *Ndufs4*<sup>-/-</sup>::*Opa1*<sup>Tg</sup> mice. Solid blue: *WT*; blue outline: *Opa1*<sup>Tg</sup>; solid

- red: *Cox15<sup>sm/sm</sup>*; red outline: *Cox15<sup>sm/sm</sup>::Opa1<sup>Tg</sup>*. Error bars represent SEM. VDAC was used as a loading control.
- C) Western blot immunovisualization (upper panel) and densitometric analysis (lower panel) of OPA1 forms in heart mitochondria of *WT*, *Opa<sup>Tg</sup>*, *Ndufs4<sup>-/-</sup>*, *Ndufs4<sup>-/-</sup>::Opa<sup>Tg</sup>* mice. Solid blue: *WT*; blue outline: *Opa1<sup>Tg</sup>*; solid red: *Cox15<sup>sm/sm</sup>*; red outline: *Cox15<sup>sm/sm</sup>::Opa1<sup>Tg</sup>*. Error bars represent SEM. VDAC was used as a loading control.
- D) BNGE-in-gel activities of MRC CI from BNGE of digitonin-treated isolated mitochondria of *WT*, *Opa<sup>Tg</sup>*, *Ndufs4<sup>-/-</sup>*, *Ndufs4<sup>-/-</sup>::Opa<sup>Tg</sup>* samples. See main text for details.
- E) Western-blot immunovisualization of MRC CI, CIII, and CIV from BNGE of digitonin-treated isolated mitochondria of *WT*, *Opa<sup>Tg</sup>*, *Ndufs4<sup>-/-</sup>*, *Ndufs4<sup>-/-</sup>::Opa<sup>Tg</sup>* samples. See main text for details. Anti-COX1, anti-NDUFB8 and anti-UQCRC1 antibodies were used for CIV, CI, and CIII.

Figure S2, related to figure 2.

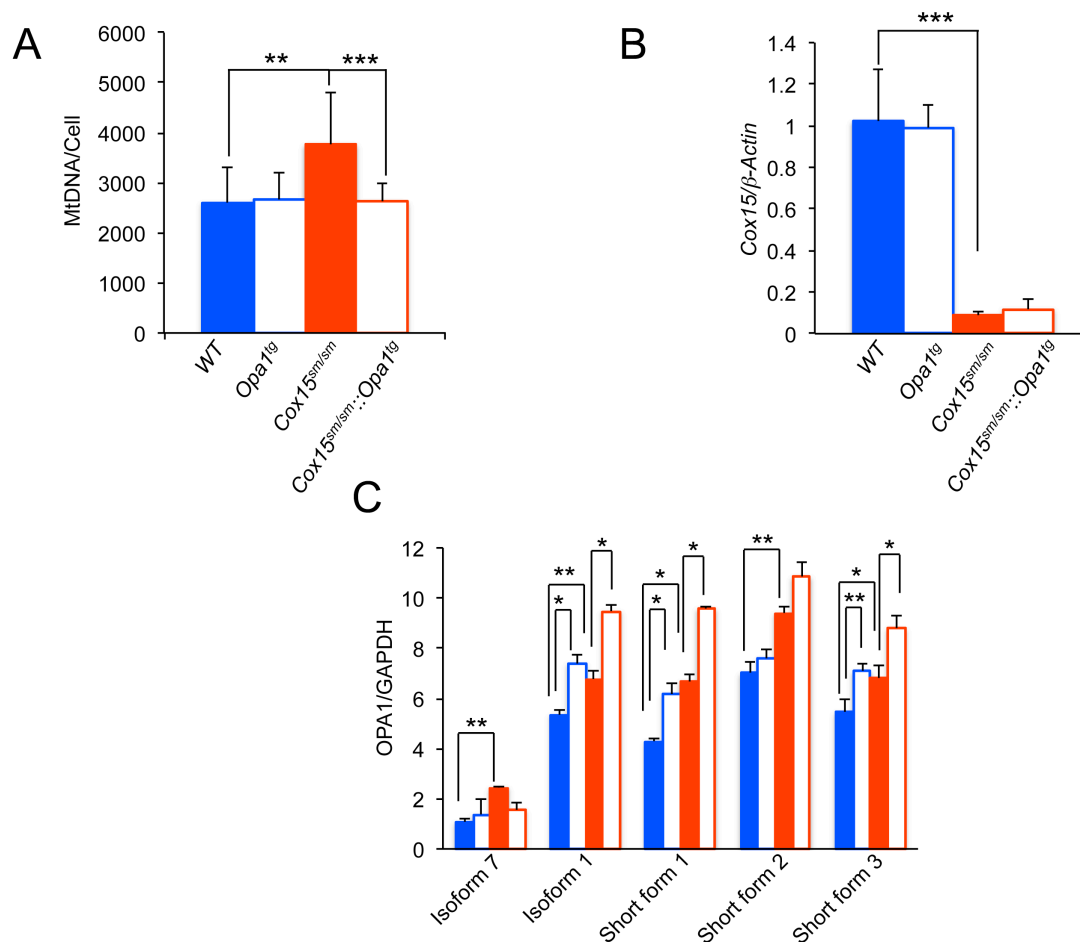
**In vivo phenotypic characterization of  $Cox15^{sm/sm}$  and  $Cox15^{sm/sm}::Opa1^{Tg}$  mouse models**



A) Means of weekly-performed treadmill tests over 5 weeks. Solid blue:  $WT$  (n=8); blue outline:  $Opa1^{tg}$  (n=9); solid red:  $Cox15^{sm/sm}$  (n=9); red outline:  $Cox15^{sm/sm}::Opa1^{Tg}$  (n=10). Error bars represent SEM. Statistical significance was calculated by unpaired, 2-tail Student's t test: \*\*p<0.01: \*\*\*p<0.005.

B) Motor performance by treadmill tests in males (continuous lines) and females (dashed lines). Red lines:  $Cox15^{sm/sm}::Opa1^{Tg}$ ; blue lines:  $Cox15^{sm/sm}$  individuals. Asterisks refer to significant differences between  $Cox15^{sm/sm}::Opa1^{Tg}$  vs  $Cox15^{sm/sm}$  calculated by unpaired, 2-tail Student's t test: \*\*p<0.01. Values between genders were not significantly different for either genotype. Error bars represent SEM.

**Figure S3, related to figure 6.**  
**Quantitative analyses in skeletal muscle**



A) Quantification of Cox15 transcript. Solid blue: *WT* (n=4); blue outline: *Opa1<sup>tg</sup>* (n=4); solid red: *Cox15<sup>sm/sm</sup>* (n=4); red outline: *Cox15<sup>sm/sm</sup>::Opa1<sup>tg</sup>* (n=4). Error bars represent SEM. Statistical significance was calculated by unpaired, 2-tail Student's t test: \*\*\*p<0.005.

B) Quantification of mtDNA copy number. Solid blue: *WT* (n=4); blue outline: *Opa1<sup>tg</sup>* (n=4); solid red: *Cox15<sup>sm/sm</sup>* (n=4); red outline: *Cox15<sup>sm/sm</sup>::Opa1<sup>tg</sup>* (n=4). Error bars represent SEM. Statistical significance was calculated by unpaired, 2-tail Student's t test: \*\*p<0.01; \*\*\*p<0.005.

C) Densitometric analysis of *Opa1* isoforms in skeletal muscle on n=4 samples for each genotype. Error bars represent SEM. Statistical significance was calculated by unpaired, 2-tail Student's t test: \*p<0.05; \*\*p<0.01; \*\*\*p<0.005.