



**Supplemental Fig S4. Soleus muscle from heterozygous mice displays normal metabolic gene expression when compared to wildtype mice.** (a) Heatmap showing the pattern of expression of fatty acid oxidation and glucose metabolism enzymes in the soleus muscle of 15-week-old *Nr1d1*<sup>+/+</sup> *Nr1d1*<sup>+/-</sup> and *Nr1d1*<sup>-/-</sup> mice (c-d) glycolytic gene expression in the soleus muscle of 15 weeks old *Nr1d1*<sup>-/-</sup> and *Nr1d1*<sup>+/-</sup> mice (n = 6). Mean expression of *Nr1d1*, *Nr1d2* and *Rora* and *Bmal* 1 in soleus muscle. (c) Mean expression of the fatty acid oxidation genes *Eno1* and *Tpi1*. (d) Average gene expression of the glucose metabolism factors *Cpt1a*, *Cpt1b*, *Hk1*, *Hk2*, *Pfk1*, *Ucp1*, *Ucp2* and *Ucp3*. Gene expression quantified using RT-qPCR. \*p<0.05 and \*\*p<0.01 were determined by One-Way ANOVA. Data represented as a mean ± s.e.m (n = 6)