SUPPLEMENTARY FILE

Gene expression profiling reveals fundamental sex-specific differences in SIRT3-mediated redox and metabolic signaling in mouse embryonic fibroblasts

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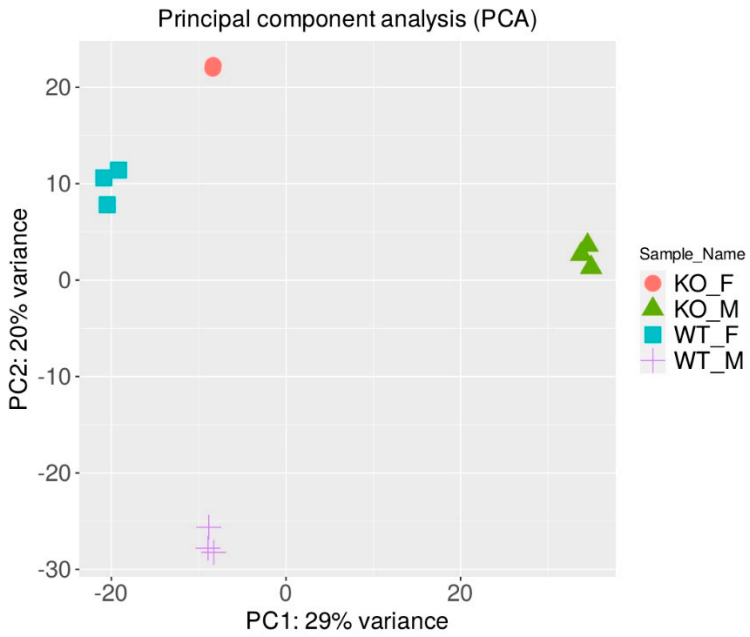

Figure S1. Principal component analysis was performed using IDEP (1) with TPM matrix as input. KO - knockout; WT – wild type; M - male; F-female.

Table S1. TPM values of main ISR regulators and effectors.

	TPM (WT_M)	TPM (KO_M)	P_{adj}_males	TPM (WT_F)	TPM (KO_F)	P_{adj}_females
Hif1a	57.67	83.72	[a]6.80E-27	57.58	60.47	0.244
Atf4	210.72	372.88	[a]4.90E-95	284.00	260.00	[c]0.041
Atf5	208.14	323.73	[a]8.20E-41	206.00	200.00	0.874
Gadd34	38.67	37.98	0.984	42.72	32.51	[a]6.10E-4
Nfe2l1	114.15	134.15	[a]3.20E-11	125.00	132.00	1
Nfe2l2	48.86	55.28	[c]0.01	44.20	45.36	0.896
Xbp1	65.86	90.53	[a]1.40E-13	59.30	84.20	[a]3.80E-14
Chop/Ddit 3	81.31	102.72	[b]0.001	82.09	74.59	0.791
Ddit4	40.07	62.39	[a]2.50E-14	44.70	56.20	[a]1.60E-4

P_{adj} – the marks [a, b, c] are shown in Fig. 5 and 6

Original unedited Western blot images (Figure 2S, 3S, 4S, 5S, 6S)

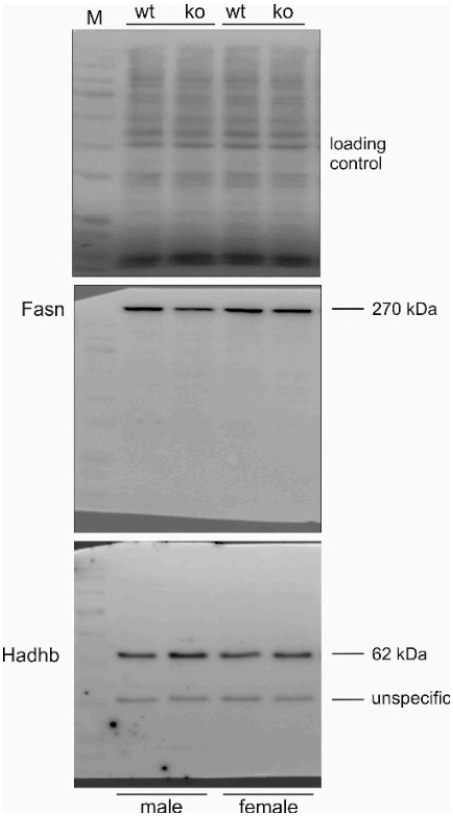

Figure S2. Western blot of Fasn and Hadhb in Sirt3 WT and Sirt3 KO MEF of both sexes. Amidoblack was used as a loading control; 20 micrograms of proteins per lane.

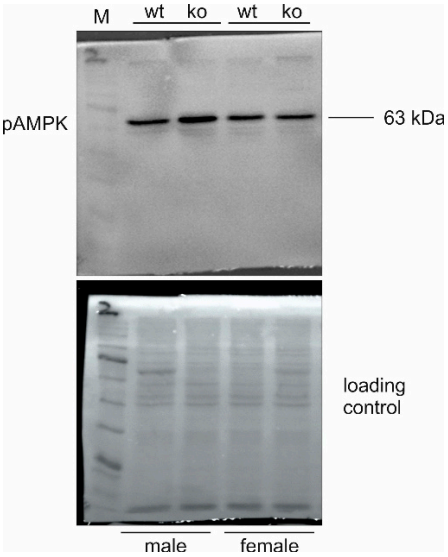

Figure S3. Western blot of pAMPK in Sirt3 WT and Sirt3 KO MEF of both sexes. Amidoblack was used as a loading control; 20 micrograms of proteins per lane.

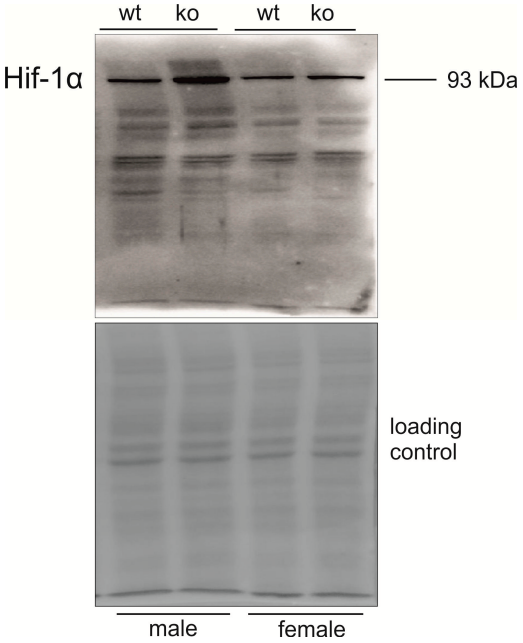

Figure S4. Western blot of Hif-1α in Sirt3 WT and Sirt3 KO MEF of both sexes. Amidoblack was used as a loading control; 20 micrograms of proteins per lane.

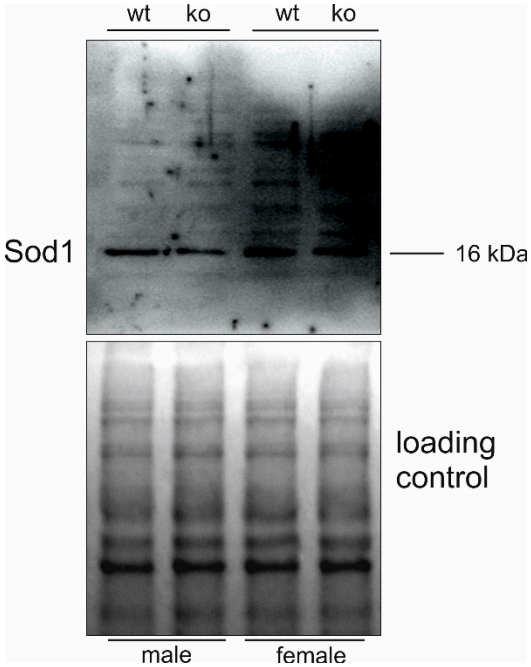

Figure S5. Western blot of Sod1 in Sirt3 WT and Sirt3 KO MEF of both sexes. Amidoblack was used as a loading control; 20 micrograms of proteins per lane.

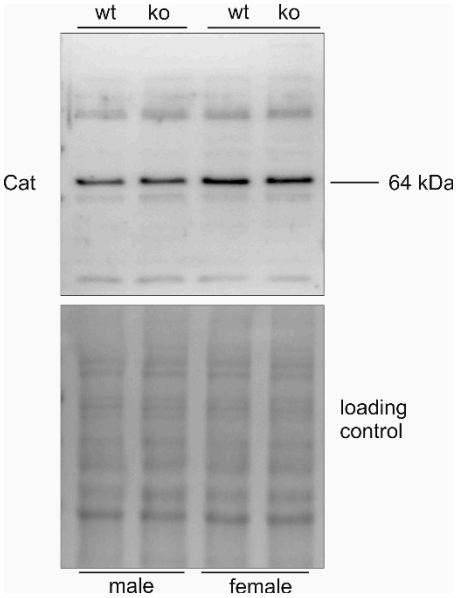

Figure S6. Western blot of Cat in Sirt3 WT and Sirt3 KO MEF of both sexes. Amidoblack was used as a loading control; 20 micrograms of proteins per lane.

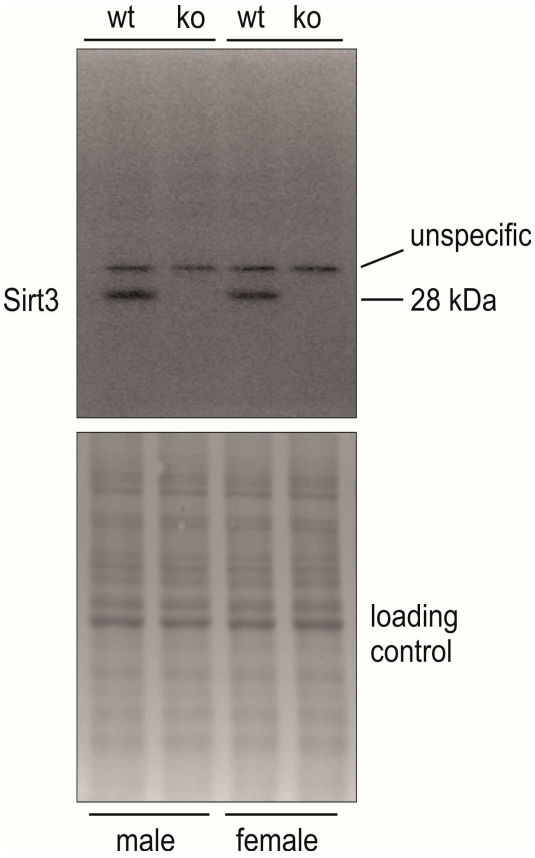

Figure S7. Western blot of Sirt in Sirt3 WT and Sirt3 KO MEF of both sexes. Amidoblack was used as a loading control; 20 micrograms of proteins per lane.

References:

1. Ge S.X.; Son, E.W.; Yao, R. iDEP: An integrated web application for differential expression and pathway analysis of RNA-Seq data. *BMC Bioinform.* **2018**, *19*, 534.