

Supporting Information

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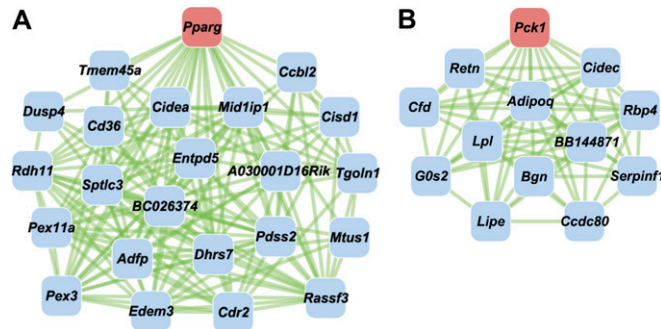


Fig. S1. Skin gene networks of *Pparg* and *Pck1*. (A) Peroxisome proliferative activated receptor gamma, coactivator 1 alpha (*Pparg*) (red) correlation subnetwork ($\rho > \pm 0.70$) in *Mus spretus*/*Mus musculus* backcross mice (FVBBX) epidermis. (B) *Pck1* (red) correlation subnetwork ($\rho \geq \pm 0.65$) in FVBBX epidermis.

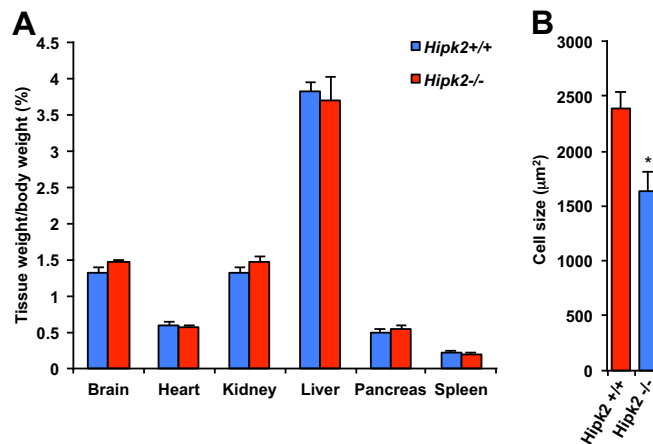


Fig. S2. (A) Weights of the brain, heart, kidney, liver, pancreas, and spleen remain essentially unchanged in *homeodomain-interacting protein kinase 2* (*Hipk2*) knockout mice compared with *Hipk2* wild-type mice. Weights of the indicated tissues from 8-wk-old female *Hipk2*^{+/+} ($n = 8$) and *Hipk2*^{-/-} ($n = 8$) mice after normalization to body weight. Data are presented as mean \pm SEM. (B) Adipocyte cell size is significantly reduced in *Hipk2* knockout mice compared with *Hipk2* wild-type mice. Adipocyte size of ovarian white adipose tissue from 8- to 10-wk-old female *Hipk2*^{+/+} ($n = 4$) and *Hipk2*^{-/-} mice ($n = 4$). * $P < 0.05$ for *Hipk2*^{+/+} versus *Hipk2*^{-/-} mice. Data are presented as mean \pm SEM.

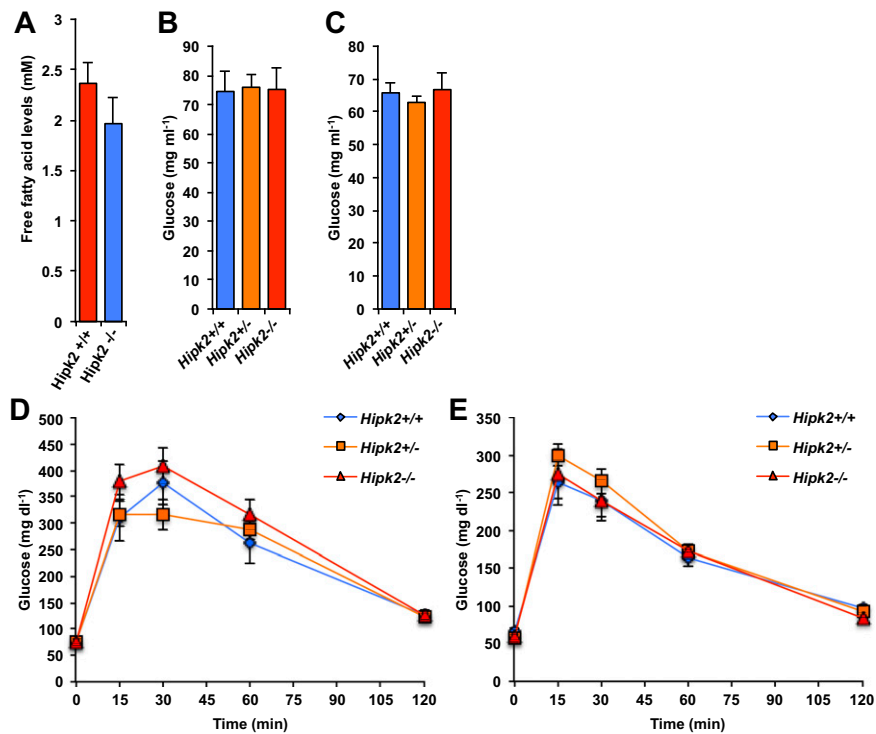


Fig. S5. Free fatty acid levels, glucose levels, and glucose clearance in *Hipk2*-null mice are comparable to wild-type littermates. (A) Free fatty acid concentrations were determined in fasted (6 h) female *Hipk2*^{+/+} ($n = 3$) and *Hipk2*^{-/-} ($n = 6$) mice. (B and C) Blood glucose levels of male (B) and female (C) *Hipk2*^{+/+}, *Hipk2*^{+/-}, and *Hipk2*^{-/-} mice ($n = 7-14$, *Hipk2*^{+/+}; $n = 14-16$, *Hipk2*^{+/-}; $n = 7-10$, *Hipk2*^{-/-}). (D and E) Glucose tolerance tests on male (D) and female (E) *Hipk2*^{+/+}, *Hipk2*^{+/-}, and *Hipk2*^{-/-} mice ($n = 6-14$, *Hipk2*^{+/+}; $n = 17$, *Hipk2*^{+/-}; $n = 6-8$, *Hipk2*^{-/-}). Data are presented as mean \pm SEM.

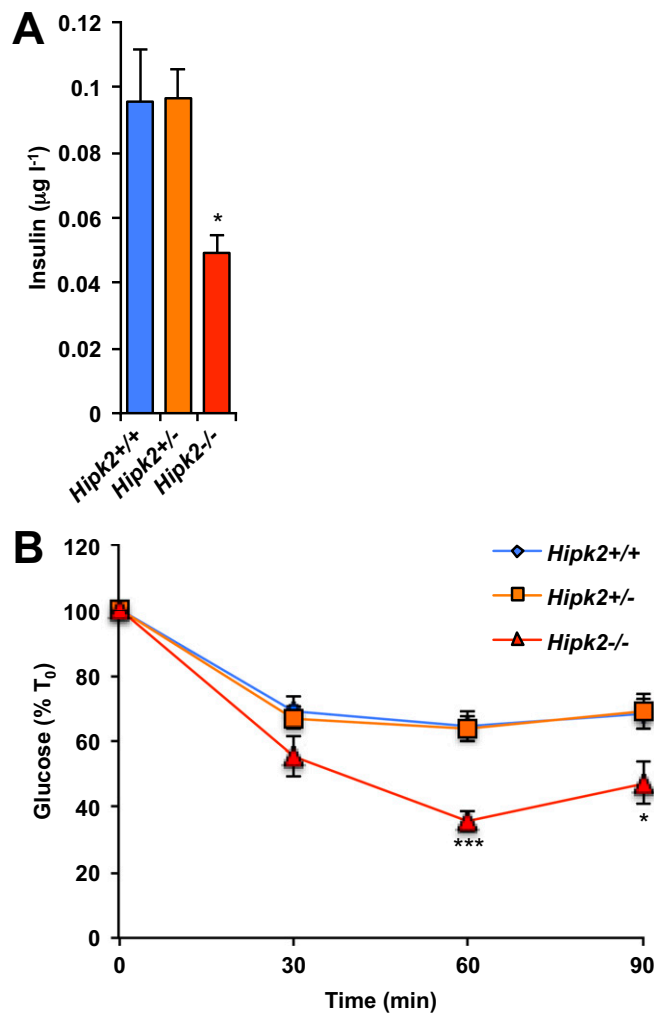


Fig. S6. Loss of *Hipk2* reduces basal insulin levels and increases insulin sensitivity. (A) Plasma insulin levels of 8- to 10-wk-old male *Hipk2*^{+/+}, *Hipk2*^{+/-}, and *Hipk2*^{-/-} mice (n = 7, *Hipk2*^{+/+}; n = 14, *Hipk2*^{+/-}; n = 7, *Hipk2*^{-/-}). (B) Insulin tolerance tests on 8- to 10-wk-old male *Hipk2*^{+/+}, *Hipk2*^{+/-}, and *Hipk2*^{-/-} mice (n = 6, *Hipk2*^{+/+}; n = 17, *Hipk2*^{+/-}; n = 6, *Hipk2*^{-/-}). T₀, time zero (start of the experiment, i.e., the basal level when insulin was injected). *P < 0.05 and ***P < 0.001 for *Hipk2*^{+/+} versus *Hipk2*^{+/-} or *Hipk2*^{-/-} mice. Data are presented as mean ± SEM.

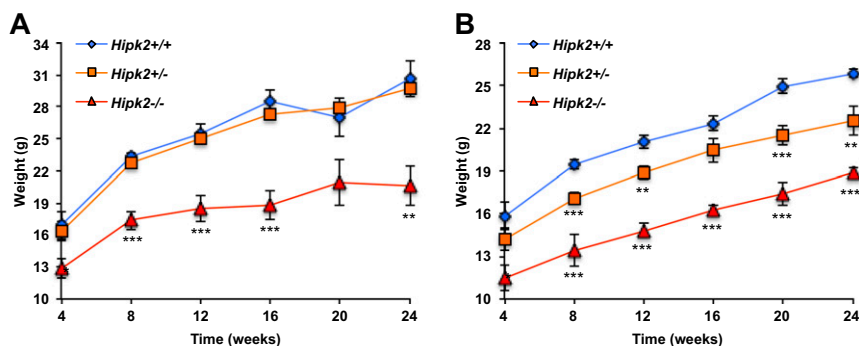


Fig. S7. *Hipk2* knockout mice weigh less than control group littermates. Body weights of male (A) and female (B) *Hipk2*^{+/+}, *Hipk2*^{+/-}, and *Hipk2*^{-/-} mice (n = 12–26, *Hipk2*^{+/+}; n = 8–30, *Hipk2*^{+/-}; n = 6–17, *Hipk2*^{-/-}). *P < 0.05, **P < 0.01, and ***P < 0.001 for *Hipk2*^{+/+} versus *Hipk2*^{+/-} or *Hipk2*^{-/-} mice. Data are presented as mean ± SEM.

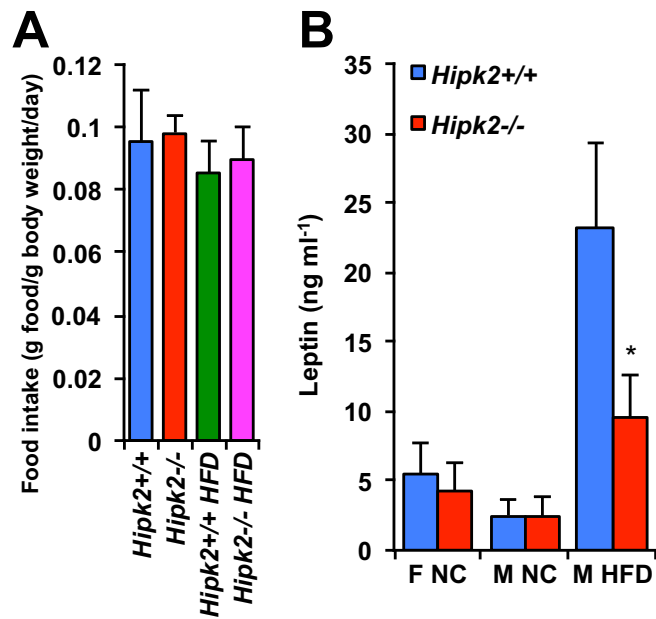


Fig. S8. (A) Food intake is indistinguishable between *Hipk2*-null mice and *Hipk2* wild-type mice. Daily food intake normalized to body weight of *Hipk2*^{+/+} ($n = 7$) and *Hipk2*^{-/-} ($n = 7$) mice on normal chow or a high-fat diet (HFD). Data are presented as mean \pm SEM. (B) There are significantly lower circulating levels of leptin in male *Hipk2*-null mice compared with *Hipk2* WT mice on a high-fat diet. Plasma leptin levels in normal chow-fed (NC) female (F) and male (M) mice or HFD-fed male mice ($n = 4-8$). * $P < 0.05$ for *Hipk2*^{+/+} versus *Hipk2*^{-/-} mice. Data are presented as mean \pm SEM.

Table S1. Hipk2 correlations to adipocyte-associated genes are more pronounced in female mice

Top 40 Hipk2 correlations in female FVBBX mice	rho	Top 40 Hipk2 correlations in male FVBBX mice	rho
Scd1	0.81	<i>Hoxd10</i>	0.76
<i>Rassf3</i>	0.80	<i>Gse1</i>	0.76
<i>A030001D16Rik</i>	0.80	<i>Rab3ip</i>	0.76
Fa2h	0.80	<i>Tpm1</i>	0.76
Ptplb	0.79	<i>Palld</i>	0.76
Mid1ip1	0.79	Elovl4	0.75
<i>Pank1</i>	0.77	<i>Tmem62</i>	0.75
Mgll	0.77	Far2	0.74
<i>3110001I20Rik</i>	0.77	<i>Al646023</i>	0.74
Crat	0.76	<i>Tmem139</i>	0.73
Dhcr24	0.76	<i>Pdzrn3</i>	0.73
Soat1	0.76	<i>D630004K10Rik</i>	0.73
<i>2610019F03Rik</i>	0.76	<i>Col4a5</i>	0.73
Far2	0.75	<i>Mark1</i>	0.72
<i>Pxmp4</i>	0.75	<i>Enc1</i>	0.72
<i>Gnmt</i>	0.75	<i>Rassf3</i>	0.71
Hsd3b2	0.74	<i>Gpr125</i>	0.71
Pdss2	0.73	<i>Lbh</i>	0.71
<i>Dock3</i>	0.73	<i>E430014L09Rik</i>	0.71
<i>Mgst1</i>	0.73	<i>Frm4a</i>	0.71
Acot1	0.73	<i>Sardh</i>	0.71
<i>Arl6ip2</i>	0.73	<i>Cpe</i>	0.70
<i>2310001A20Rik</i>	0.73	<i>Nfe2l3</i>	0.70
<i>Edem3</i>	0.72	<i>Gli1</i>	0.70
Pparg	0.72	<i>Marcks1</i>	0.70
<i>2010305C02Rik</i>	0.72	<i>Nrp2</i>	0.70
<i>Brp44</i>	0.72	<i>1200009O22Rik</i>	0.69
Leng4	0.72	<i>Krtap3-3</i>	0.69
<i>Zcd1</i>	0.72	<i>Slc39a10</i>	0.69
Slc27a1	0.72	<i>Pcp4</i>	0.69
<i>Hoxb2</i>	0.71	Acsm3	0.69
Elovl4	0.71	<i>BC024479</i>	0.69
<i>1200015F23Rik</i>	0.71	<i>Odz3</i>	0.68
Cat	0.71	<i>Sh3d19</i>	0.68
Pnpla5	0.71	<i>Echdc1</i>	0.68
<i>Tmem164</i>	0.71	<i>2610019P18Rik</i>	0.68
Acsm3	0.71	<i>9130213B05Rik</i>	0.68
<i>Panx3</i>	0.71	<i>Scrg1</i>	0.68
<i>Ccbl2</i>	0.71	<i>Pitrm1</i>	0.67
<i>Ppa1</i>	0.71	<i>Hnrpa2b1</i>	0.67

Hipk2 correlations in epidermis from female ($n = 40$) and male ($n = 31$) FVBBX mice. Genes in bold are directly annotated to the Gene Ontology (GO) term "lipid metabolic process" (GO ID code 0006629).

Table S2. TaqMan probes used for quantitative PCR analysis

Gene	TaqMan probe
<i>Adfp</i>	Mm00475794_m1
<i>Adipoq</i>	Mm00456425_m1
<i>Cebpa</i>	Mm00514283_s1
<i>Cebpb</i>	Mm00843434_s1
<i>CD36</i>	Mm01135198_m1
<i>Cfd</i>	Mm01143935_g1
<i>Cidea</i>	Mm00432554_m1
<i>Fabp4</i>	Mm00445878_m1
<i>Fa2h</i>	Mm00626259_m1
<i>Hipk2</i>	Mm00439329_m1
<i>Mest</i>	Mm00484993_m1
<i>Lipe</i>	Mm00495359_m1
<i>Pank1</i>	Mm00458408_m1
<i>Pck1</i>	Mm01247058_m1
<i>Pparg1/2</i>	Mm00440945_m1
<i>Pparg2</i>	Mm00440940_m1
<i>Ppargc1a</i>	Mm01208835_m1
<i>Rbp4</i>	Mm00803264_g1
<i>Scd1</i>	Mm00772290_m1
<i>Ucp1</i>	Mm0494069_m1