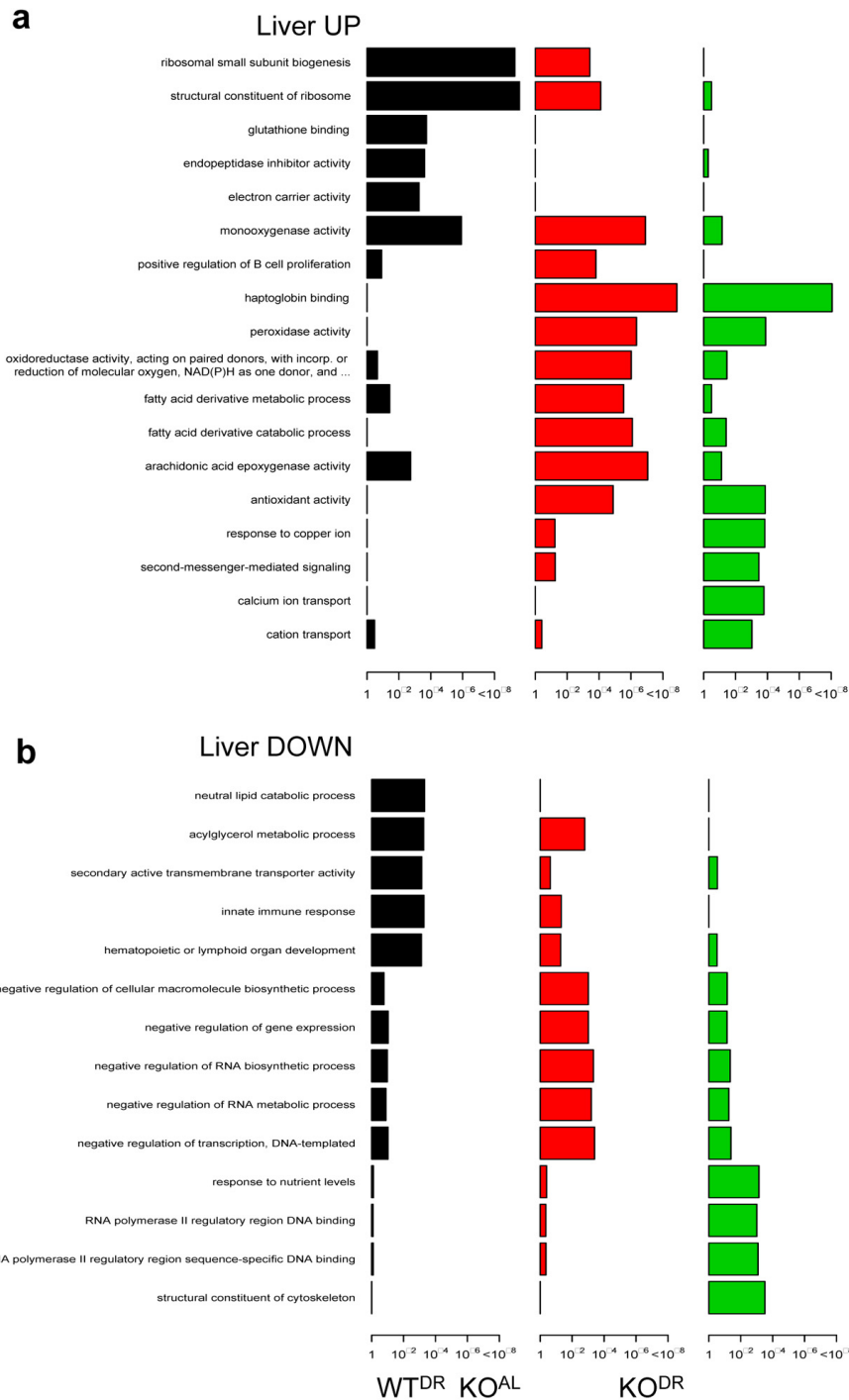
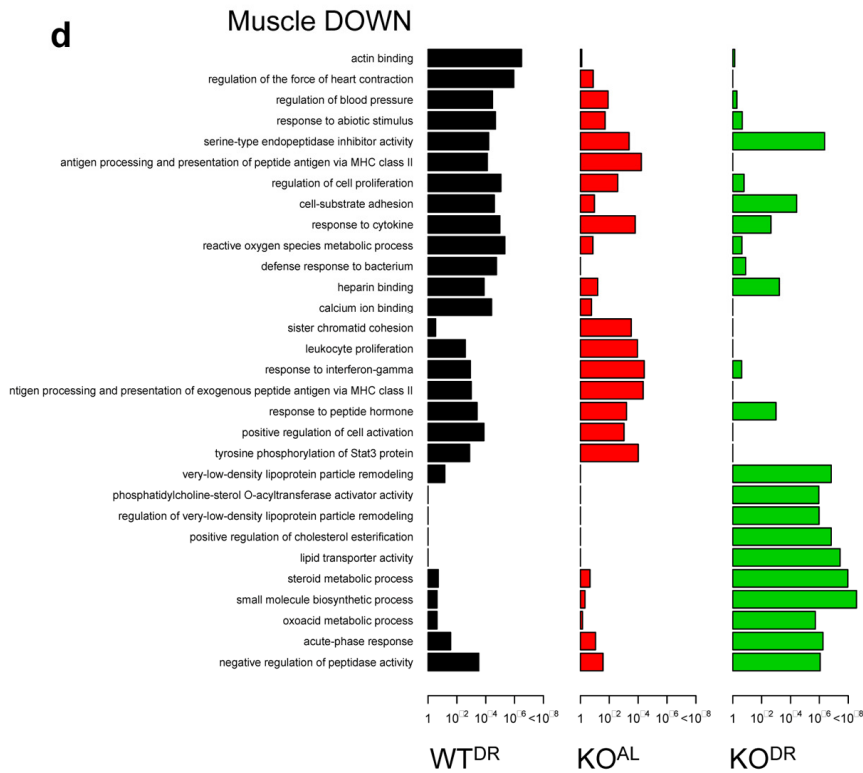
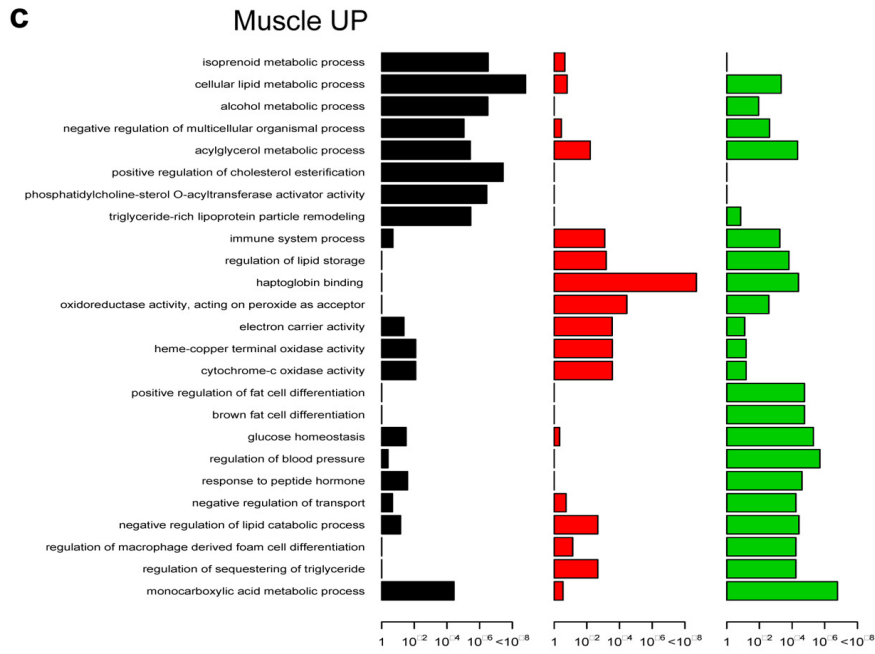


SUPPLEMENTARY MATERIAL

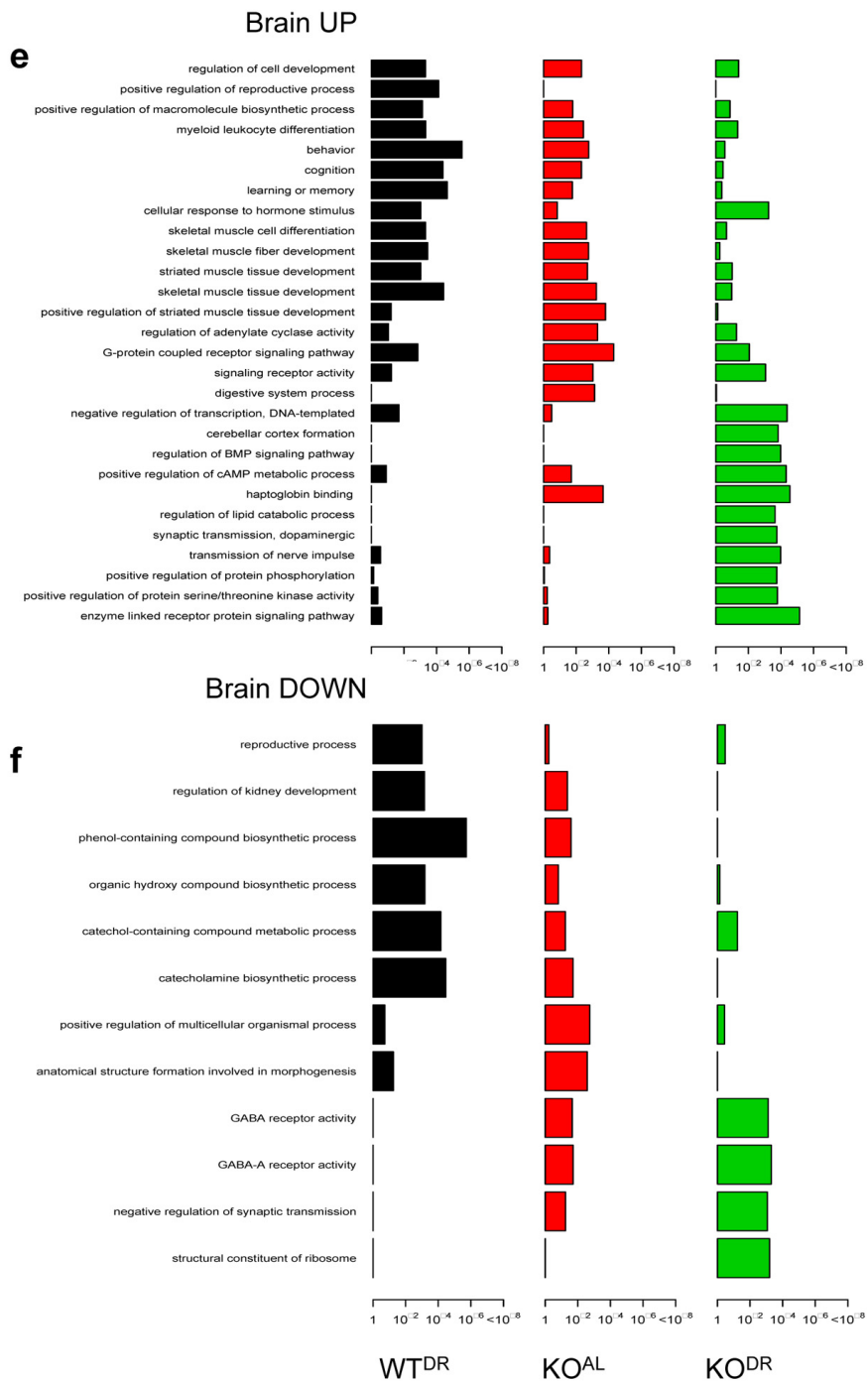
Supplementary Figures



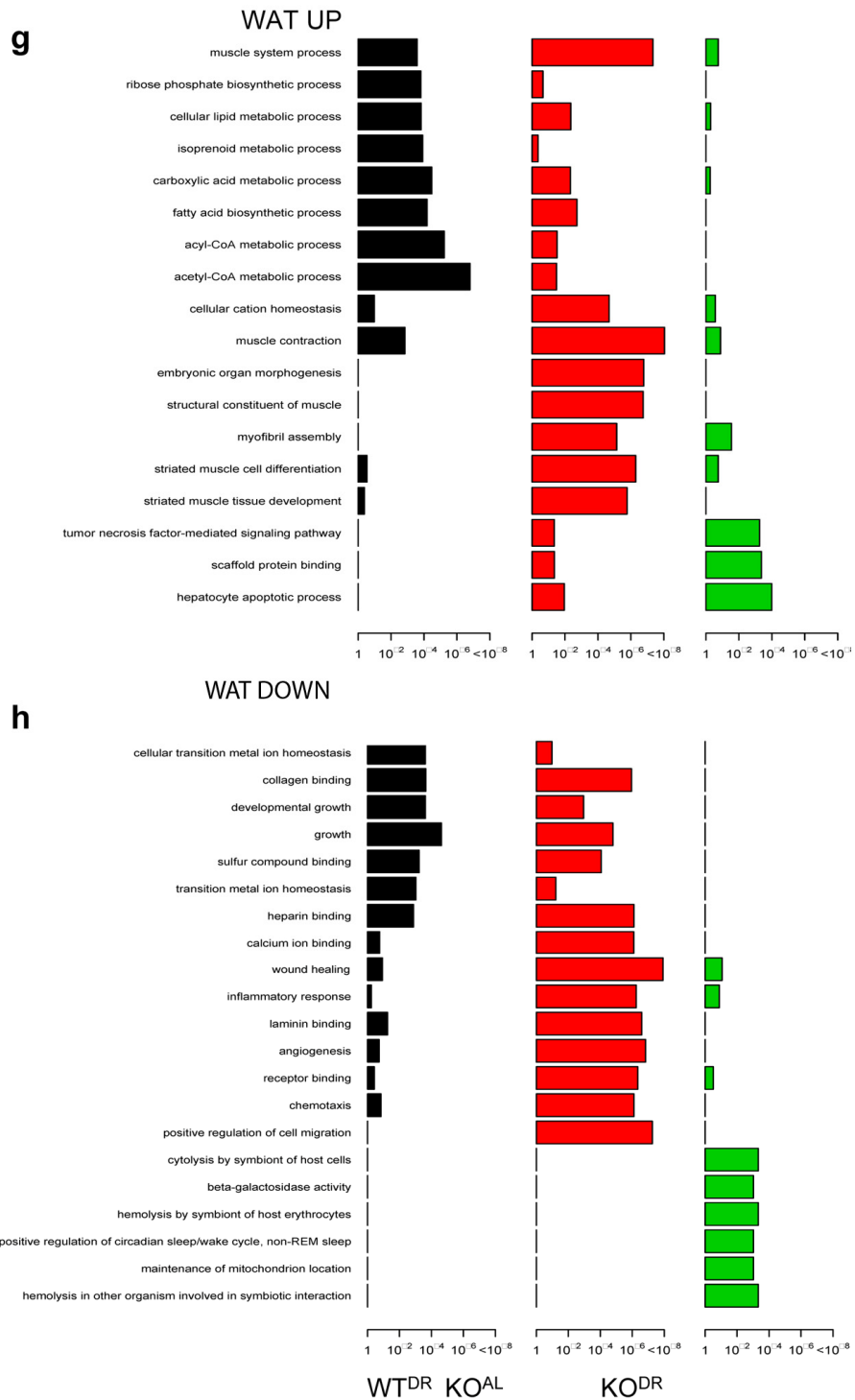
Supplementary Figure S1a, b. Up- and down-regulated gene ontology in four tissues of KO^{AL}, KO^{DR} and WT^{DR}. (a) Up-regulated gene ontology (GO) terms in liver tissue of KO^{AL}, KO^{DR} and WT^{DR} mice. (b) Down-regulated GO terms in liver tissue of KO^{AL}, KO^{DR} and WT^{DR} mice.



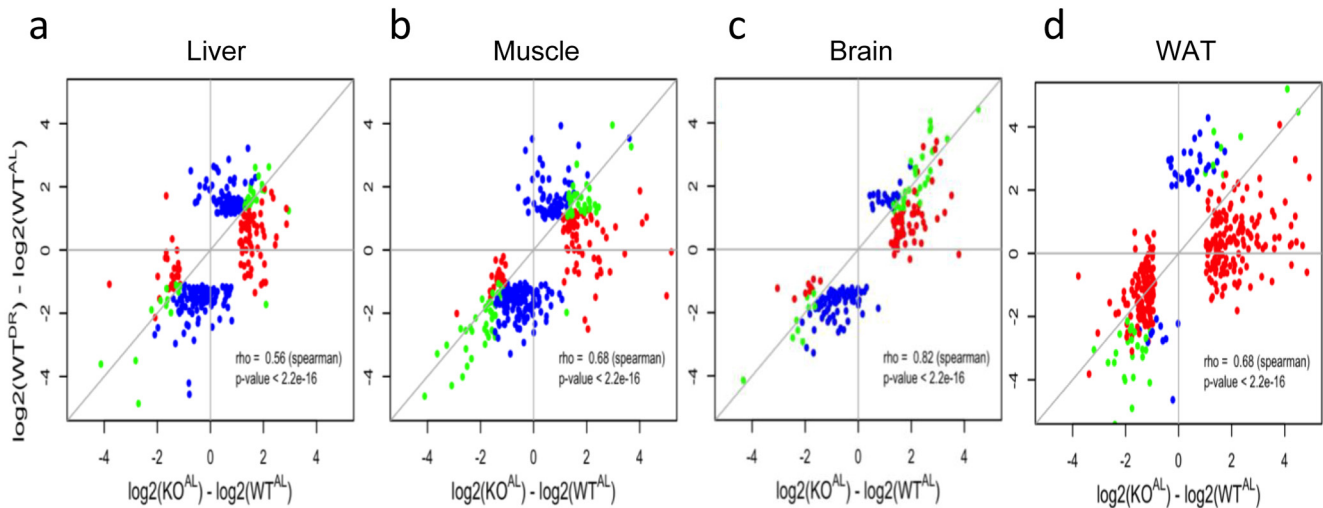
Supplementary Figure S1c, d. Up- and down-regulated gene ontology in four tissues of KO^{AL}, KO^{DR} and WT^{DR}. (c) Up-regulated gene ontology (GO) terms in whole brain tissue of KO^{AL}, KO^{DR} and WT^{DR} mice. (d) Down-regulated GO terms in skeletal muscle tissue of KO^{AL}, KO^{DR} and WT^{DR} mice.



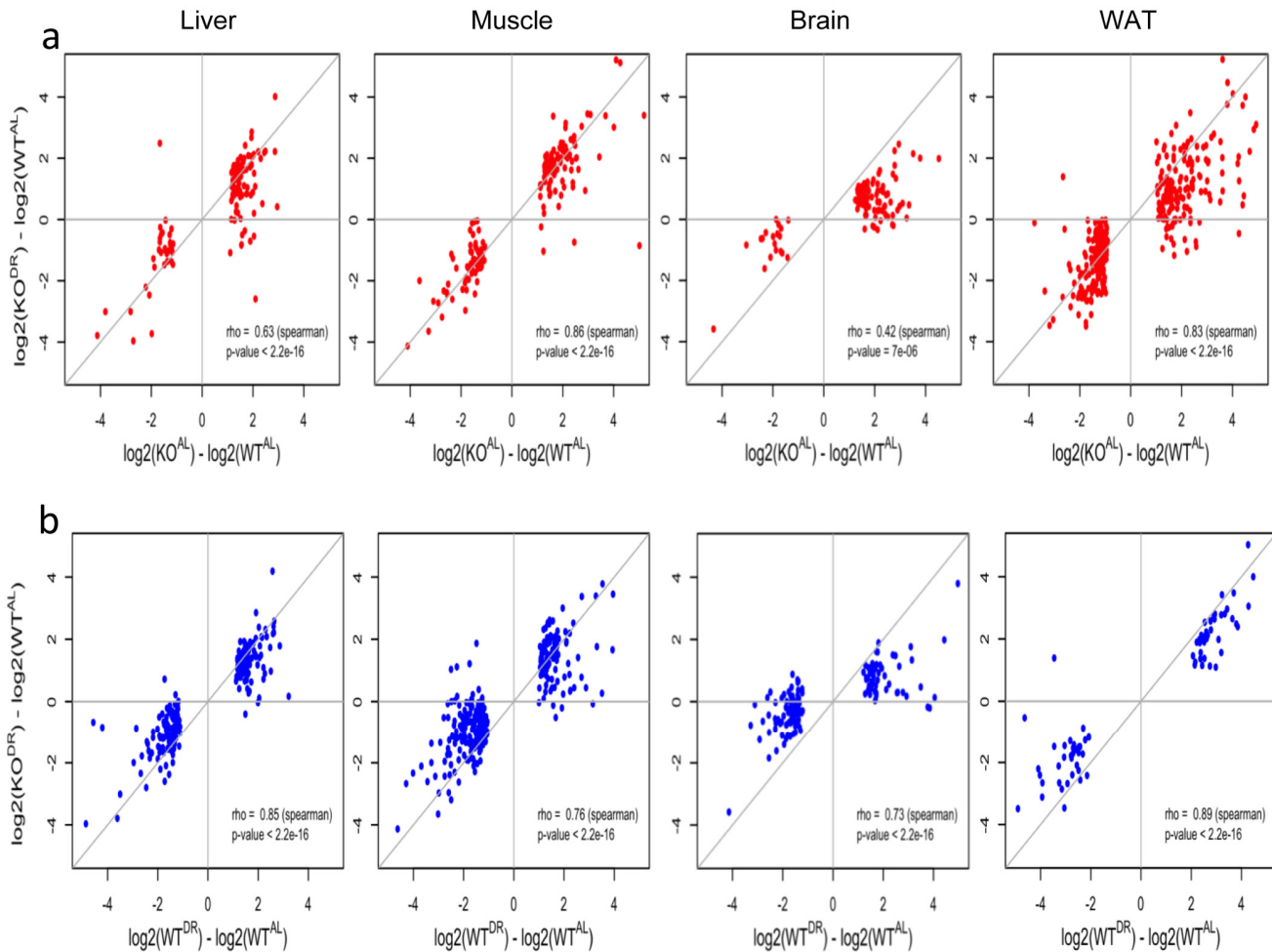
Supplementary Figure S1e, f. Up- and down-regulated gene ontology in four tissues of KO^{AL}, KO^{DR} and WT^{DR}. (e) Up-regulated gene ontology (GO) terms in skeletal muscle of KO^{AL}, KO^{DR} and WT^{DR} mice. (f) Down-regulated GO terms in brain of KO^{AL}, KO^{DR} and WT^{DR} mice.



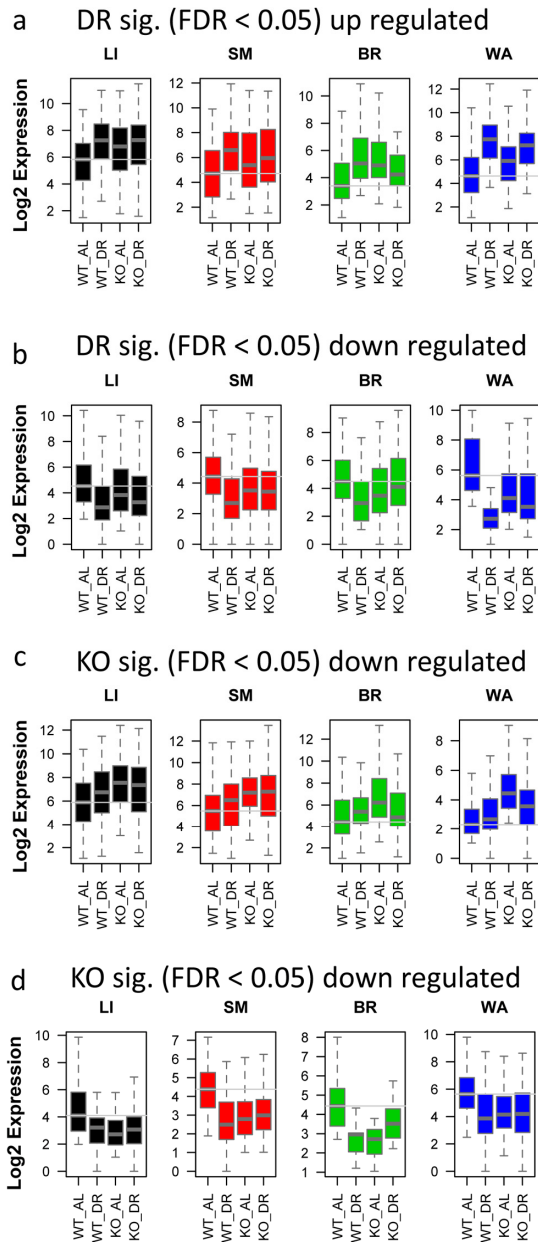
Supplementary Figure S1g, h. Up- and down-regulated gene ontology in four tissues of KO^{AL}, KO^{DR} and WT^{DR}. (g) Up-regulated gene ontology (GO) terms in WAT of KO^{AL}, KO^{DR} and WT^{DR} mice. (h) Down-regulated GO terms in WAT of KO^{AL}, KO^{DR} and WT^{DR} mice.



Supplementary Figure S2. Correlation between WT^{DR} and KO^{AL} conditions. The log₂ fold change correlation between genes in (a) liver, (b) skeletal muscle, (c) brain, and (d) WAT which are significantly (FDR < 10%) differentially expressed (q value < 0.10) in WT^{DR} (blue) and KO^{AL} (red) compared to WT^{AL}. Genes differentially expressed in both conditions are green.



Supplementary Figure S3. Gene expression correlation between WT^{AL} and KO^{AL} to the extreme conditions of WT^{AL} and KO^{DR}. (a) The log₂ fold change of genes significantly (FDR < 10%) differentially expressed (q value < 0.10) when comparing WT^{AL} and KO^{AL} (red). (b) The log₂ fold change of genes significantly (FDR < 10%) differentially expressed (q value < 0.10) when comparing AL and DR conditions in an *Irs1*^{WT} background (blue).



Supplementary Figure S4. Boxplot showing the distribution of expression for genes significantly (FDR < 10%) up (a) or down (b) in WT^{DR} compared to WT^{AL} and significantly up (c) or down (d) in KO^{AL} compared to WT^{AL} for all tissues analysed (liver-LI, smooth muscle – SM, brain – BR and WA – white adipose tissue).

Supplementary Tables

Please browse the Full Text version to see the data of Supplementary Tables related to this manuscript:

Table S1. Complete gene expression profile among four tissues in KO^{AL} mice compared to WT^{AL} mice as control.

Table S2. Complete up-regulated gene ontology (GO) terms among four tissues in KO^{AL} mice.

Table S3. Complete down-regulated gene ontology (GO) terms among four tissues in KO^{AL} mice.

Table S4. Complete gene expression profile among four tissues in WT^{DR} mice compared to WT^{AL} mice as control.

Table S5. Complete up-regulated gene ontology (GO) terms among four tissues in WT^{DR} mice.

Table S6. Complete down-regulated gene ontology (GO) terms among four tissues in WT^{DR} mice.

Table S7. Complete gene expression profile among four tissues in KO^{AL} and WT^{DR} mice.