Supplementary Figure 1

Metadata corresponding to figure 2. Shown are blood glucose, weight, sex, age, RNA-seq batch, and genetic background as they correspond to each sample in the dendrogram.

Supplementary Figure 2

Comparison of differentially expressed genes between the present work and Ref. 41 (Neelankal John *et al.*, 2018). Distributions of gene expression of those genes found to be differentially expressed by Neelankal John *et al.*, (2018) **(A)** Genes more highly expressed in WT than in *LepR*$^{db/+}$. **(B)** Genes more highly expressed in *LepR*$^{db/+}$ than WT. **(C)** Genes more highly expressed in *LepR*$^{db/db}$ than *LepR*$^{db/+}$. **(D)** Genes more highly expressed in *LepR*$^{db/+}$ than *LepR*$^{db/db}$. **(E)** Genes more highly expressed in WT than *LepR*$^{db/db}$. **(F)** Genes more highly expressed in *LepR*$^{db/db}$ than WT. For each comparison, the distribution of gene expression between analogous mouse strains in the two studies is shown. The gene name labels along the x-axes are colored if the gene was also found to be differentially expressed in our data (FDR <0.1). Differentially expressed gene labels are colored according to the condition in which the gene is more highly expressed.

Supplementary Figure 3

Differentially expressed genes between groups of NOD samples. (A) Genes whose expression increased from T1ND samples that clustered with healthy adult samples (ND(HA)) to T1ND samples that clustered with diabetic samples (ND(D)) and increased from ND(D) to T1D samples. (**B**) Genes whose expression decreased from ND(HA) samples ND(D) samples and decreased from ND(D) samples to T1D samples.