SUPPLEMENTARY DATA

Supplementary Table 1. Variants with the strongest association with 24-h EE in Pima Indians.

Position is based on human genome Build 37. Variant identification number (rs#) is based on dbSNP version 141. Risk allele is defined as the allele associated with lower 24-h EE. RAF: Risk allele frequency as calculated in full-heritage Pima Indians. SE: Standard Error. Beta coefficient is expressed per copy of the risk allele in kcal/day. Results are adjusted for age, sex, FM, FFM, SPA and the first 5 genetic principal components in a mixed model that accounted for genetic relationships among individuals. Variants are sorted by their *p*-value for the association with 24-h EE (all $p<0.01$).

Supplementary Table 2. Variants with the strongest association with RMR in Pima Indians.

Position is based on human genome Build 37. Variant identification number (rs#) is based on dbSNP version 141. Risk allele is defined as the allele associated with lower RMR. RAF: Risk allele frequency as calculated in full-heritage Pima Indians. SE: Standard Error. Beta coefficient is expressed per copy of the risk allele in kcal/day. Results are adjusted for age, sex, FM, FFM and the first 5 genetic principal components in a mixed model that accounted for genetic relationships among individuals. Variants are sorted by their *p*-value for the association with RMR (all $p<0.01$).

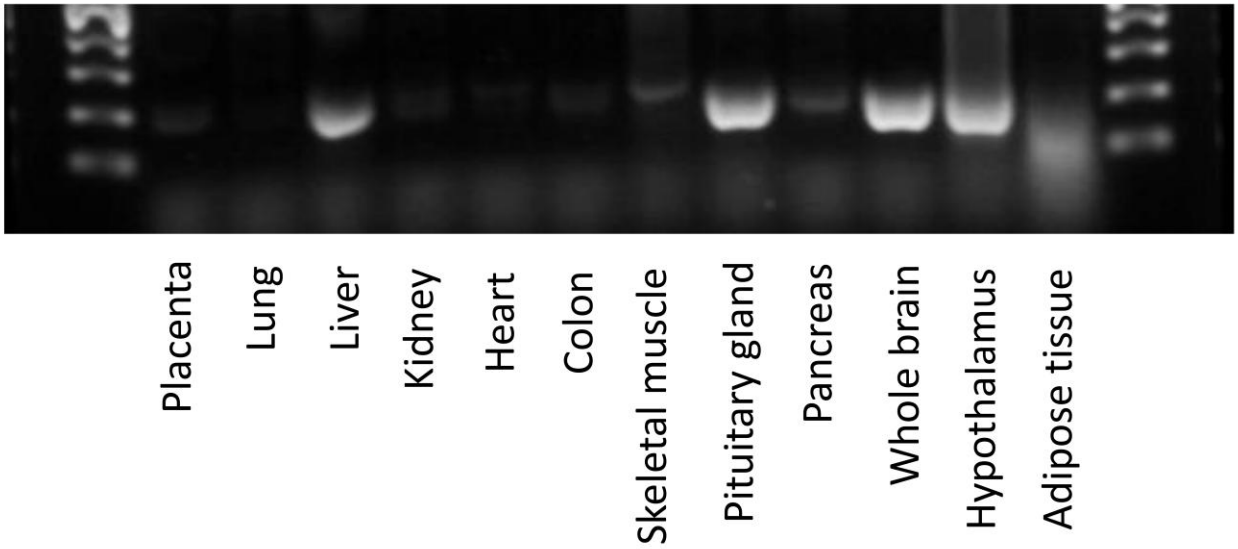
Supplementary Table 3. Associations of variants consistently associated with lower 24-h EE and RMR with maximum BMI and PFAT in Pima Indians.

Position is based on human genome Build 37. Variant identification number (rs#) is based on dbSNP version 141. Risk allele is defined as the allele associated with lower 24-h EE and lower RMR. RAF: Risk allele frequency as calculated in full-heritage Pima Indians. SE: Standard Error. Beta coefficients are expressed per copy of the risk allele in kcal/day (24-h EE and RMR), logarithmic BMI units (maximum BMI) and percent body fat (PFAT). Results are adjusted for age, sex, body composition measures (FM and FFM, only for EE analyses), SPA (only for 24-h EE analysis), birth year (only for BMI analysis) and the first 5 genetic principal components in a mixed model that accounted for genetic relationships among individuals. Variants are sorted by their p-value for the association with maximum BMI and they all show concordant associations with 24-h EE and RMR with both $p<0.01$.

SUPPLEMENTARY DATA

Supplementary Figure 1. Tissue distribution of human *GPR158* RNA.

Human tissue cDNA panel was obtained from Clontech (Mountain View, CA). PCR shows that *GPR158* RNA is predominately expressed in whole brain, hypothalamus, pituitary gland and liver.



SUPPLEMENTARY DATA

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