

Figure S1. Validation of selected eQTLs by qRT-PCR in adipose tissue of relevant BN.GK congenic strains (A) and transcription analysis of genes containing sequence variants between GK and BN in illumina oligonucleotides (B). Significant differential expression of genes that validated eQTLs is indicated in red. Details of oligonucleotides used for qRT-PCR are given in S9 Table. *P<0.05 significantly different to the BN control.

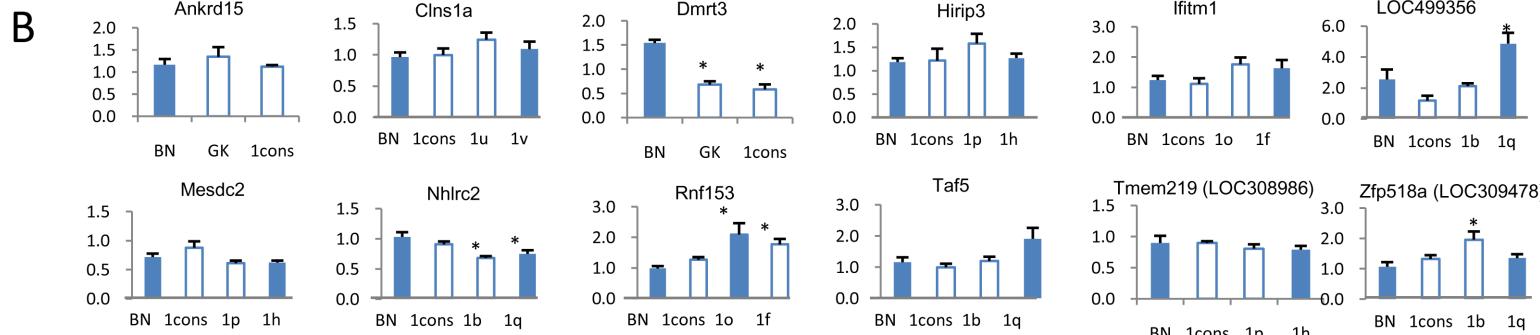
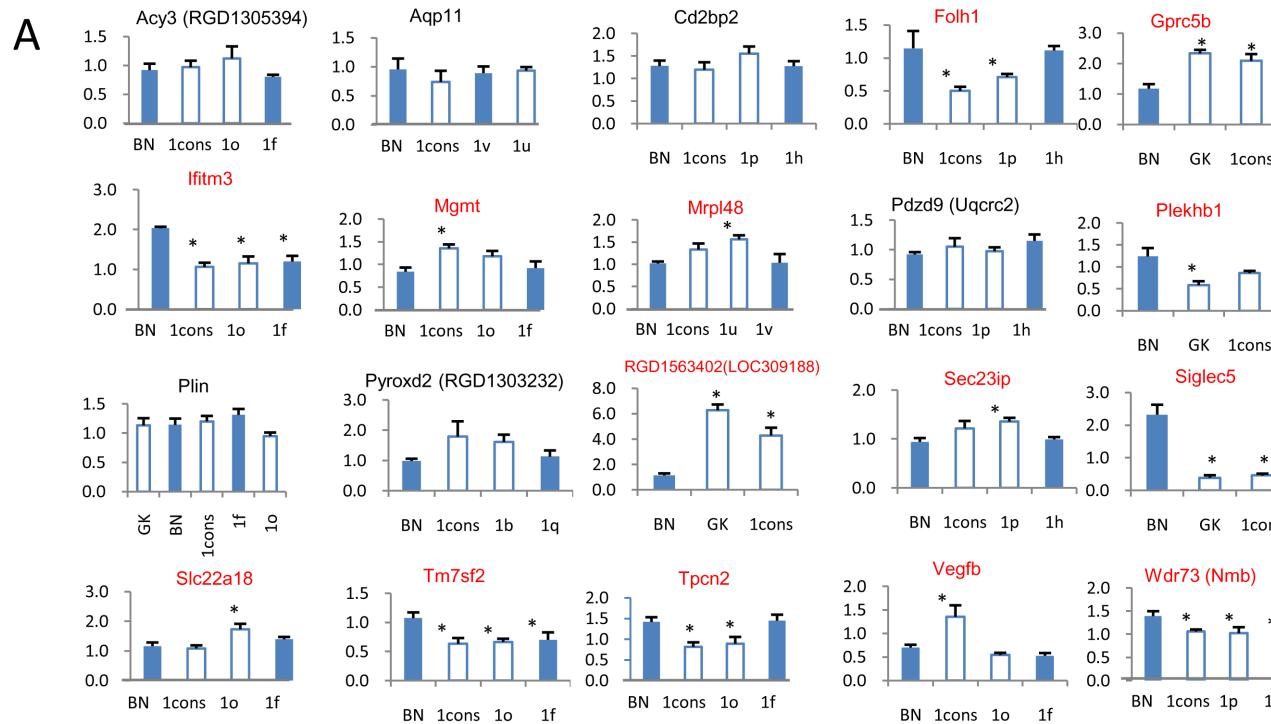
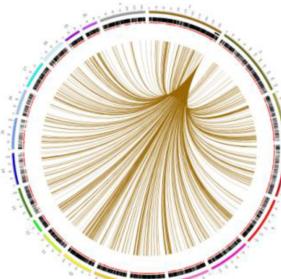


Figure S2. Effects of introgressed haplotypes in congenic strains on trans-regulated fat gene transcription.

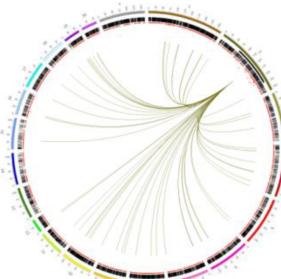
Distant effects of GK/BN polymorphisms in congenic strains on gene transcription is illustrated by the chromosomal location of genes that are found differentially expressed ($P<0.05$) between congenics and controls and map outside the introgressed genomic region in the congenics. Examples are given for BN.GK congenics carrying GK haplotypes of chromosomes 1, 2, 4, 5 and 7 on a BN genetic background (A) and for reciprocal congenics (B,C) carrying GK or BN alleles of chromosome 7 (C), 8 (B) or 10 (C) transferred onto the genetic background of the BN (BN.GK congenics) or GK (GK.BN congenics) strain, respectively (B,C). The colour of the lines illustrates the transcriptional effects of genes mapped to the congenic interval on distant genes as in Figure 5E. Full details of differentially expressed genes are given in S1 Table.

A

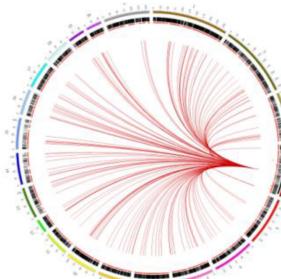
BN.GK-1b



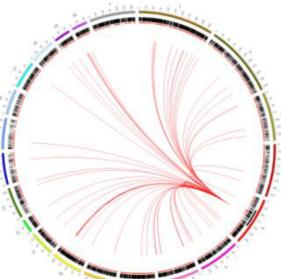
BN.GK-2c



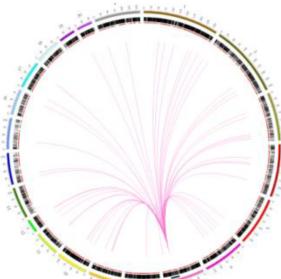
BN.GK-4b



BN.GK-5a



BN.GK-7d



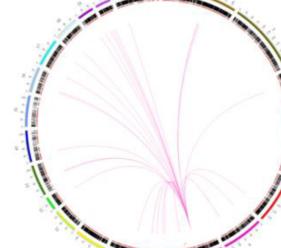
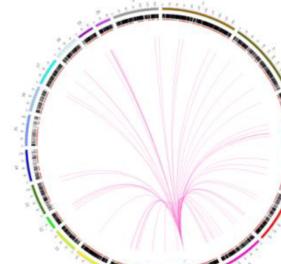
B

BN.GK-8b

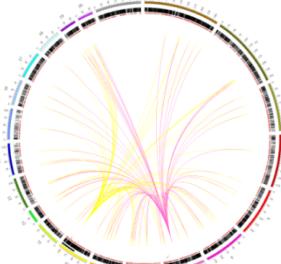


C

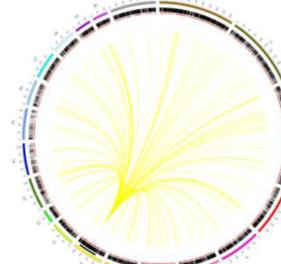
BN.GK-7a



GK.BN-10_7a



BN.GK-10a



GK.BN-8a

GK.BN-7a

Figure S3. Correlation analysis of the effects of GK alleles on the genetic control of gene expression in F2 hybrids and congenic strains. The effect of GK alleles at statistically significant cis-acting (A,B) and trans-acting (C,D) eQTLs (P -adjusted <0.05) in the GKxBN F2 cross are plotted against expression ratio of corresponding genes significantly differentially expressed (P -adjusted <0.05) between congenics derived from GK and BN strains and controls mapped either across the genome (A,C) or in congenic intervals (B,D). Full details of eQTLs and differentially expressed genes are given in S1 Table.

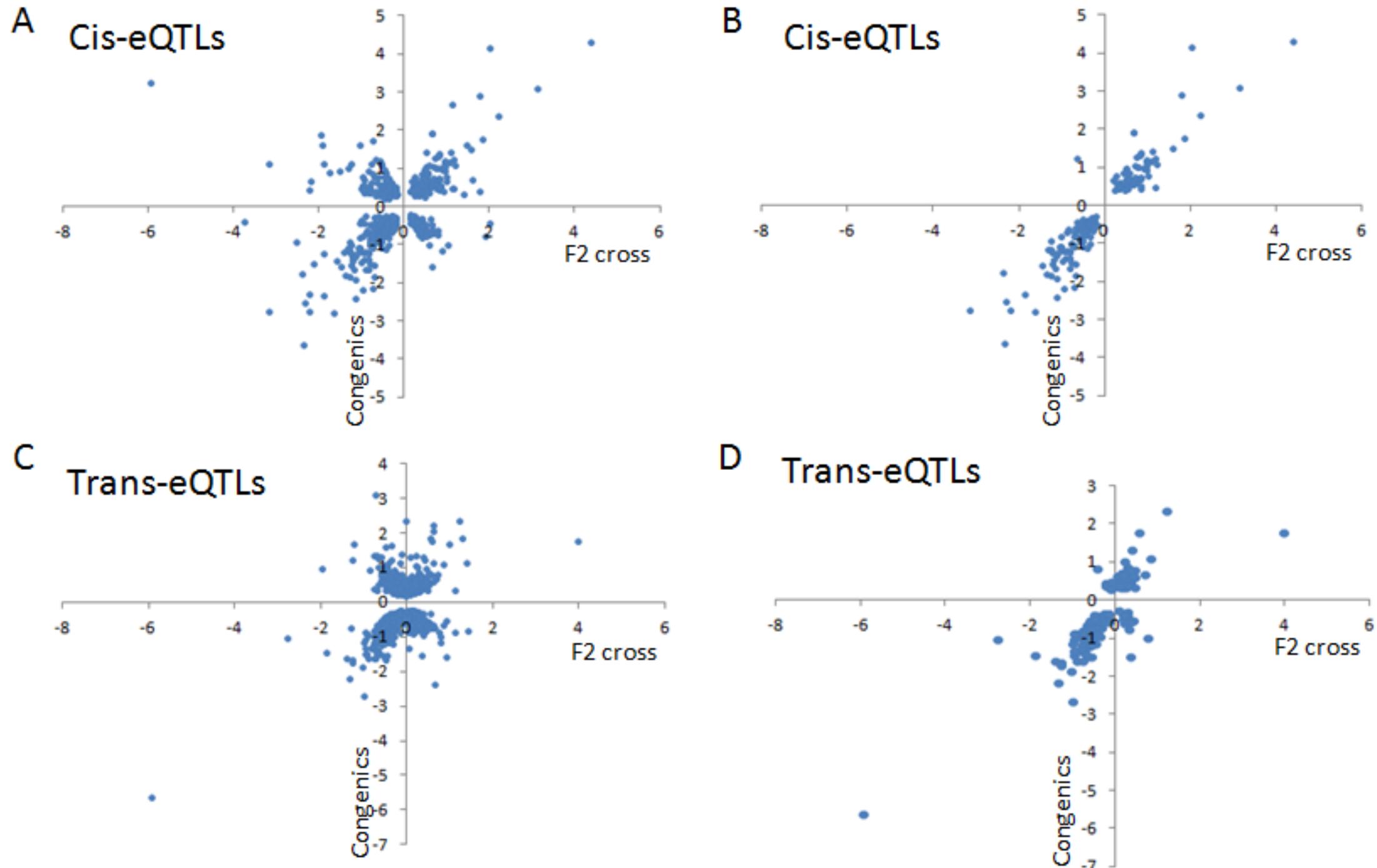


Figure S4. Phenotype analyses in BN.GK congenic strains. Body weight (A) and fasting glycemia (B) were measured in 24 week-old congenic and control BN and GK rats. *P<0.01; **P<0.001 significant differences between BN.GK congenic rats and BN controls.

