

Legends for Supplementary Figures and Tables:

Supplementary Figure 1: SNP mapping in BKS

This figure contains 19 pages, one each for chromosomes 2-19 plus the X-chromosome. On each page, horizontal lines indicate the location, in bp, of SNPs along the chromosome (centromere at the top). The center set of lines indicates the positions of all SNPs tested that were informative between B6 and DBA on the chromosome. Lines that extend to the right-hand side indicate those informative SNPs having the DBA allele. Lines in the left-hand column indicate SNPs that are unique to BKS. That is, the SNP has the same allele for B6 and DBA and yet, for BKS, the SNP shows the alternate allele indicating a genetic origin other than B6 or DBA.

Supplementary Figure 2: SNP mapping in B6 and DBA

This figure contains 20 pages, one each for chromosomes 1-19 plus the X-chromosome. On each page, horizontal lines indicate the location, in bp, of SNPs along the chromosome (centromere at the top). The left-hand set of lines indicates the positions of all SNPs tested on the chromosome. Lines that extend to the right-hand side indicate those SNPs that were informative between B6 and DBA.

Supplementary Figure 3: Comparison of BKS-unique SNP-alleles among common inbred strains.

The graph shows the number of allele-matches for all 144 BKS-unique SNPs with a set of 57 inbred strains. As expected all 144 alleles match for BKS and no alleles match for B6 or DBA. BKS-*db* matches perfectly except for SNPs altered by congenic replacement on chromosome 4 (See Fig.3 in main manuscript). While the 129 strains showed the next best overall match with BKS, at least a third of BKS-unique SNPs failed to match in these strains, suggesting that the NonB6-NonDBA blocks were contributed by a less common inbred strain or by an outbred or wild strain.

Supplementary Table 1: SNP Genotype Data in B6, DBA, BKS and BKS-db.

SNP ID numbers use standard notation with “rs” (RefSNP) as a prefix on SNPs from the public databases and with “mCV” (mouse Celera Variant) as a prefix for SNPs identified by Celera. The second column gives the chromosome location for the SNP and the third column gives the SNP location in bases as shown in Build 32 of the public genome database. The next two columns (Allele A and Allele B) give the alternate nucleotide allele for each SNP. The last four columns (B6, DBA, BKS, BKS-db) give the allele (A

or B) carried by the corresponding strain. Data is shown for 10,517 SNPs where Build 32 locations are known and where all four strains gave homozygous genotypes.

Supplementary Table 4: *Cis*-Regulated Genes in DBA blocks of C57BLKS/J

The first column gives locus link ID numbers or Genbank ID numbers for genes showing *cis*-regulation in the B6 X DBA F2 cross (See Reference 12). The second and third columns give the corresponding gene symbol and full gene name, respectively. Genes whose expression showed significant correlation with diabetes-related phenotypes in the same cross are shown in bold. For these genes, the fourth column indicates which phenotypes showed this correlation. The table shows phenotype codes for various measures of plasma lipids, obesity and atherosclerosis. Definitions of these phenotype codes are given in Supplementary Table 5. The fifth and sixth columns indicate the gene position on the chromosome in nucleotides (Build 32 of the public database) and in recombination units (morgans), respectively. The seventh, eighth and ninth columns indicate the nucleotide position of the corresponding eQTL, its LOD score and r-square value (fraction of the gene's expression variation explained by the eQTL).

Supplementary Table 5: Phenotype Code Definitions

This table defines the correlated phenotypes listed by code in Supplementary Table 4. The first column gives the correlated phenotype code as shown in Supplementary Table 4, Column 4. The second column gives the abbreviated phenotype name. The third column gives the phenotype description.