

SUPPLEMENTARY DATA

Supplementary Table 1. Candidate loci that were associated with diabetes- and/or obesity-related traits.

All	With Fst in the top 5% bracket	With long haplotypes	With SNP(s) at the 5' regulatory region
<i>ACE</i>	<i>ADAMTS9</i>	<i>ARHGEF12</i>	<i>CDKAL1</i>
<i>ACLY</i>	<i>ADCY5</i>	<i>BCL11A</i>	rs9368197
<i>ADAMTS9</i>	<i>ARHGEF12</i>	<i>CDKAL1</i>	
<i>ADCY5</i>	<i>ATP2A3</i>	<i>CYB5R4</i>	<i>CYB5R4</i>
<i>ADIPOQ</i>	<i>ATP8A1</i>	<i>DGKB</i>	rs1325471
<i>ADRA2A</i>	<i>BCL11A</i>	<i>ENPP1</i>	
<i>ADRB1</i>	<i>CDKAL1</i>	<i>GAD2</i>	<i>GAD2</i>
<i>ADRB2</i>	<i>CAMK1D</i>	<i>GIP</i>	rs2839670
<i>ADRB3</i>	<i>CTNNBL1</i>	<i>GLIS3</i>	
<i>AGRP</i>	<i>CYB5R4</i>	<i>IL6</i>	<i>GIP</i>
<i>ALDH3A2</i>	<i>DGKB</i>	<i>INSR</i>	rs3895874
<i>APOA1</i>	<i>DLK1</i>	<i>JAZF1</i>	rs3848460
<i>APOA4</i>	<i>ENPP1</i>	<i>KCNQ1</i>	rs937301
<i>APOC3</i>	<i>ETV5</i>	<i>LEPR</i>	
<i>ARHGEF12</i>	<i>FTO</i>	<i>MCHR2</i>	<i>PPARG</i>
<i>ARRB1</i>	<i>G6PC2</i>	<i>MYO1C</i>	rs2920502
<i>ASM</i>	<i>GAD2</i>	<i>NEGR1</i>	
<i>ATP2A1</i>	<i>GIP</i>	<i>PARD3</i>	
<i>ATP2A3</i>	<i>GLIS3</i>	<i>PLCB1</i>	
<i>ATP8A1</i>	<i>HMGA2</i>	<i>PPARA</i>	
<i>BCDIN3D</i>	<i>HNF1B</i>	<i>PPARD</i>	
<i>BCL11A</i>	<i>HTR2C</i>	<i>PPARG</i>	
<i>BDNF</i>	<i>HTR3A</i>	<i>PTPRA</i>	
<i>C2CD4B</i>	<i>IL4</i>	<i>PTPRD</i>	
<i>CAPN10</i>	<i>IL6</i>	<i>PYY</i>	
<i>CART</i>	<i>INSR</i>	<i>RAPGEF4</i>	
<i>CBL</i>	<i>ITGB2</i>	<i>SLC6A4</i>	
<i>CCKAR</i>	<i>JAZF1</i>	<i>TCF7L2</i>	
<i>CCL2</i>	<i>KATNAL1</i>	<i>THADA</i>	
<i>CCL5</i>	<i>KCNQ1</i>		
<i>CAMK1D</i>	<i>KCTD15</i>		
<i>CDKAL1</i>	<i>LEPR</i>		
<i>CDKN2A/2B</i>	<i>MCHR1</i>		
<i>CENTD2</i>	<i>MCHR2</i>		
<i>CHCHD9</i>	<i>MTMR9</i>		
<i>CNR1</i>	<i>MYO1C</i>		
<i>CPT2</i>	<i>NEGR1</i>		
<i>CRHR1</i>	<i>NOS1AP</i>		
<i>CRK</i>	<i>NTRK2</i>		
<i>CRY2</i>	<i>PARD3</i>		
<i>CTNNBL1</i>	<i>PLCB1</i>		
<i>CYB5R4</i>	<i>PPARA</i>		
<i>CYP17A1</i>	<i>PPARD</i>		
<i>DGKB</i>	<i>PPARG</i>		
<i>DIO2</i>	<i>PTPRA</i>		
<i>DLK1</i>	<i>PTPRD</i>		
<i>DPP4</i>	<i>PYY</i>		
<i>DRD2</i>	<i>RAPGEF4</i>		
<i>DUSP9</i>	<i>SEC16B</i>		
<i>ENPP1</i>	<i>SLC6A4</i>		

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<i>ERRalpha</i>	<i>SREBF1</i>		
<i>ETV5</i>	<i>STAT3</i>		
<i>EXT2</i>	<i>TBC1D1</i>		
<i>FAAH</i>	<i>TCF7L2</i>		
<i>FADS1</i>	<i>THADA</i>		
<i>FAIM2</i>	<i>TP53</i>		
<i>FAS</i>	<i>TUB</i>		
<i>FOXA2</i>	<i>WFS1</i>		
<i>FTO</i>	<i>WWOX</i>		
<i>G6PC2</i>			
<i>GAD2</i>			
<i>GCG</i>			
<i>GCGR</i>			
<i>GCK</i>			
<i>GCKR</i>			
<i>GH1</i>			
<i>GHSR</i>			
<i>GIP</i>			
<i>GIPR</i>			
<i>GLIS3</i>			
<i>GPAM</i>			
<i>GRB14</i>			
<i>GRL</i>			
<i>GRXCR1</i>			
<i>HHEX/IDE</i>			
<i>HMGA2</i>			
<i>HNF1B</i>			
<i>HTR1A</i>			
<i>HTR1B</i>			
<i>HTR2A</i>			
<i>HTR2C</i>			
<i>HTR3A</i>			
<i>HYOU1</i>			
<i>IGF2</i>			
<i>IGF2BP2</i>			
<i>IL4</i>			
<i>IL6</i>			
<i>INPPL1</i>			
<i>INS</i>			
<i>INSR</i>			
<i>IRS1</i>			
<i>ITGA2B</i>			
<i>ITGB2</i>			
<i>JAZF1</i>			
<i>KATNAL1</i>			
<i>KCNJ11</i>			
<i>KCNQ1</i>			
<i>KCTD15</i>			
<i>KIF3A</i>			
<i>KLF14</i>			
<i>KLF7</i>			
<i>LEPR</i>			
<i>LGR5</i>			
<i>LTA</i>			
<i>LYPLAL1</i>			
<i>LYZL1</i>			

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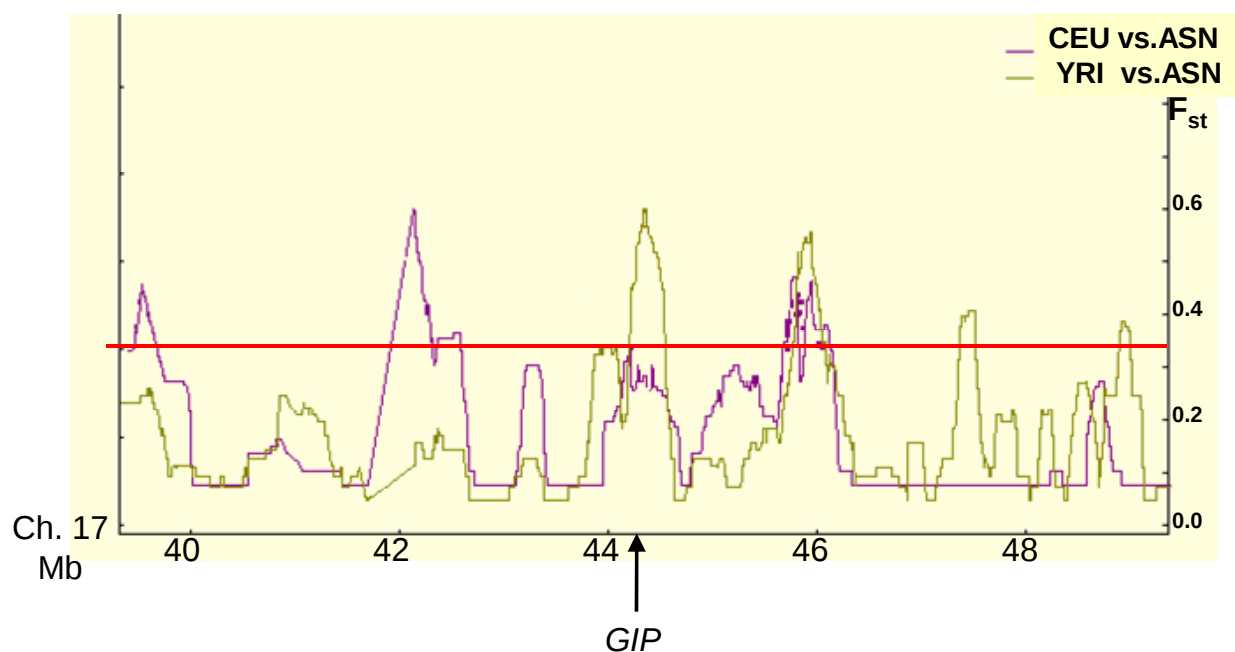
MADD			
MAF			
MAOA			
MAPK9			
MC3R			
MC4R			
MC5R			
MCHR1			
MCHR2			
MGEA5			
MSRA			
MTCH2			
MTMR9			
MTNR1B			
MYO1C			
NCOA6			
NEGR1			
NEU3			
NMB			
NMU			
NOS1AP			
NOS2			
NOTCH2			
NOX4			
NPC1			
NPY			
NPY1R			
NPY2R			
NPY5R			
NTRK2			
PARD3			
PCSK1			
PDK1			
PIK3R1			
PKLR			
PLCB1			
POMC			
PPARA			
PPARD			
PPARG			
PPARGC1B			
PPP2CA			
PPY			
PRC1			
PRKAA2			
PRKCA			
PROX1			
PTEN			
PTER			
PTPRA			
PTPRD			
PTPRF			
PYY			
RAPGEF4			
RBP4			
RORC			

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<i>RPS6KB1</i>			
<i>SCD1</i>			
<i>SCG3</i>			
<i>SCG5</i>			
<i>SEC16B</i>			
<i>SH2B1</i>			
<i>SHBG</i>			
<i>SLC25A12</i>			
<i>SLC2A2</i>			
<i>SLC2A4</i>			
<i>SLC30A8</i>			
<i>SLC6A14</i>			
<i>SLC6A4</i>			
<i>SNAP25</i>			
<i>SOCS1</i>			
<i>SOCS3</i>			
<i>SOCS7</i>			
<i>SORBS1</i>			
<i>SOX6</i>			
<i>SREBF1</i>			
<i>SRR</i>			
<i>SSTR2</i>			
<i>STAT3</i>			
<i>STXBP4</i>			
<i>SVIL</i>			
<i>TBC1D1</i>			
<i>TCF7L2</i>			
<i>TFAP2B</i>			
<i>THADA</i>			
<i>TMEM18</i>			
<i>TMEM5</i>			
<i>TP53</i>			
<i>TRIB3</i>			
<i>TRPV1</i>			
<i>TUB</i>			
<i>UBL5</i>			
<i>UCP2</i>			
<i>UCP3</i>			
<i>UTS2R</i>			
<i>VPS13C</i>			
<i>VTN</i>			
<i>WFS1</i>			
<i>WWOX</i>			
<i>ZBED3</i>			
<i>ZFAND6</i>			

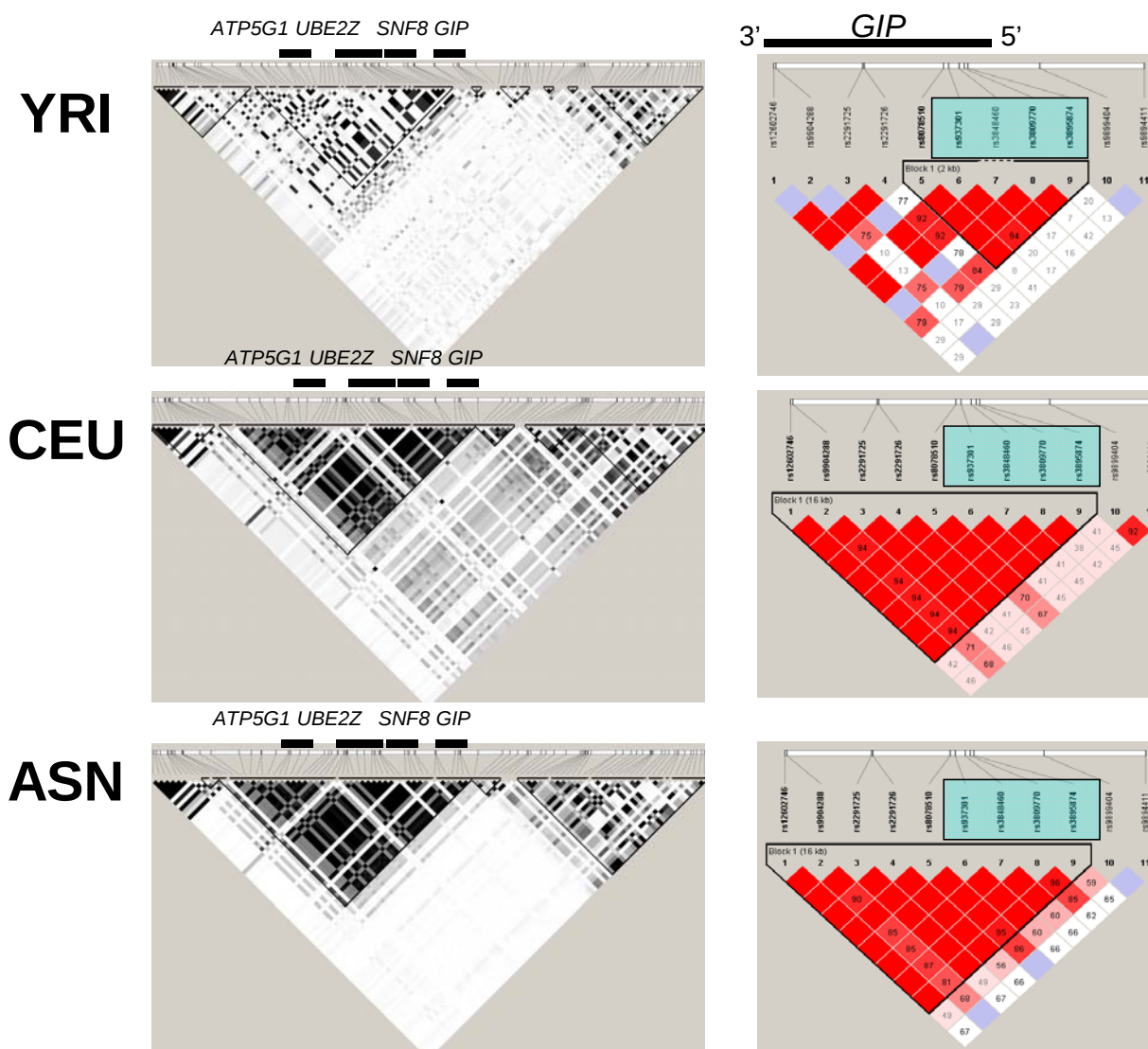
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Supplementary Figure 1. F_{ST} values across position 40-50 Mb of human chromosome 17 (Genome Build 36.3). The F_{ST} plot consists of pairwise comparisons of CEU–ASN and YRI–ASN populations and was generated using Haplotter (52). The position of GIP is indicated by an arrow. The top 5% of F_{ST} for comparisons between CEU and ASN, and between YRI and ASN are 0.2055 and 0.3374, respectively. The 5% cutoff of F_{ST} for comparisons between YRI and ASN is indicated by a red horizontal line.



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Supplementary Figure 2. Variants in the *GIP* locus are highly linked in CEU and ASN—but not in YRI—chromosomes. **Left panel:** Plots of the degree of linkage disequilibrium (LD) between each pair of genotyped SNPs in a 200-kb region surrounding the *GIP* locus (chr17:44,295 kb – 44,495 kb) in YRI, CEU, and ASN populations. Neighboring genes, including *ATP5G1*, *UBE2Z*, and *SNF8*, are indicated by black bars above LD plots. In CEU and ASN, the 91-kb LD block extended beyond the genic region of *GIP* and covered *ATP5G1*, *UBE2Z*, and *SNF8*. In YRI, LD was minimal at the same genomic region. The color scheme was based on r^2 values. White areas represent LD with $r^2 = 0$. Grey areas represent LD with $0 < r^2 < 1$. Black areas represent LD with $r^2 = 1$. **Right panel:** Plots of the degree of LD between 11 pairs of genotyped SNPs in the genic region of *GIP* (rs12602746 to rs9894411). Red areas represent regions with a high degree of LD and a high likelihood of odds (LOD) ($D' = 1$, LOD scores > 2). Blue areas represent regions with low LOD ($D' = 1$, LOD < 2). The four linked SNPs at the 5' gene region of *GIP* are indicated by a blue shade.



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Supplementary Figure 3. Plots of the haplotype structure of genotyped SNPs in a 91-kb LD block surrounding *GIP* in HapMap II populations: YRI, CEU, and ASN. The 44 SNPs in this region were highly linked and displayed a low haplotype diversity in CEU and ASN (SNP No. 36-79). By contrast, the same region in YRI chromosomes exhibited a high frequency of recombination compared to CEU and ASN. Four SNPs at the 5' gene region of *GIP* (rs3895874, rs3809770, rs3848460, and rs937301; SNP No. 76-79) were positioned in a haploblock in all three populations (26). These SNPs are indicated by a blue, shaded background.

