Fig.3

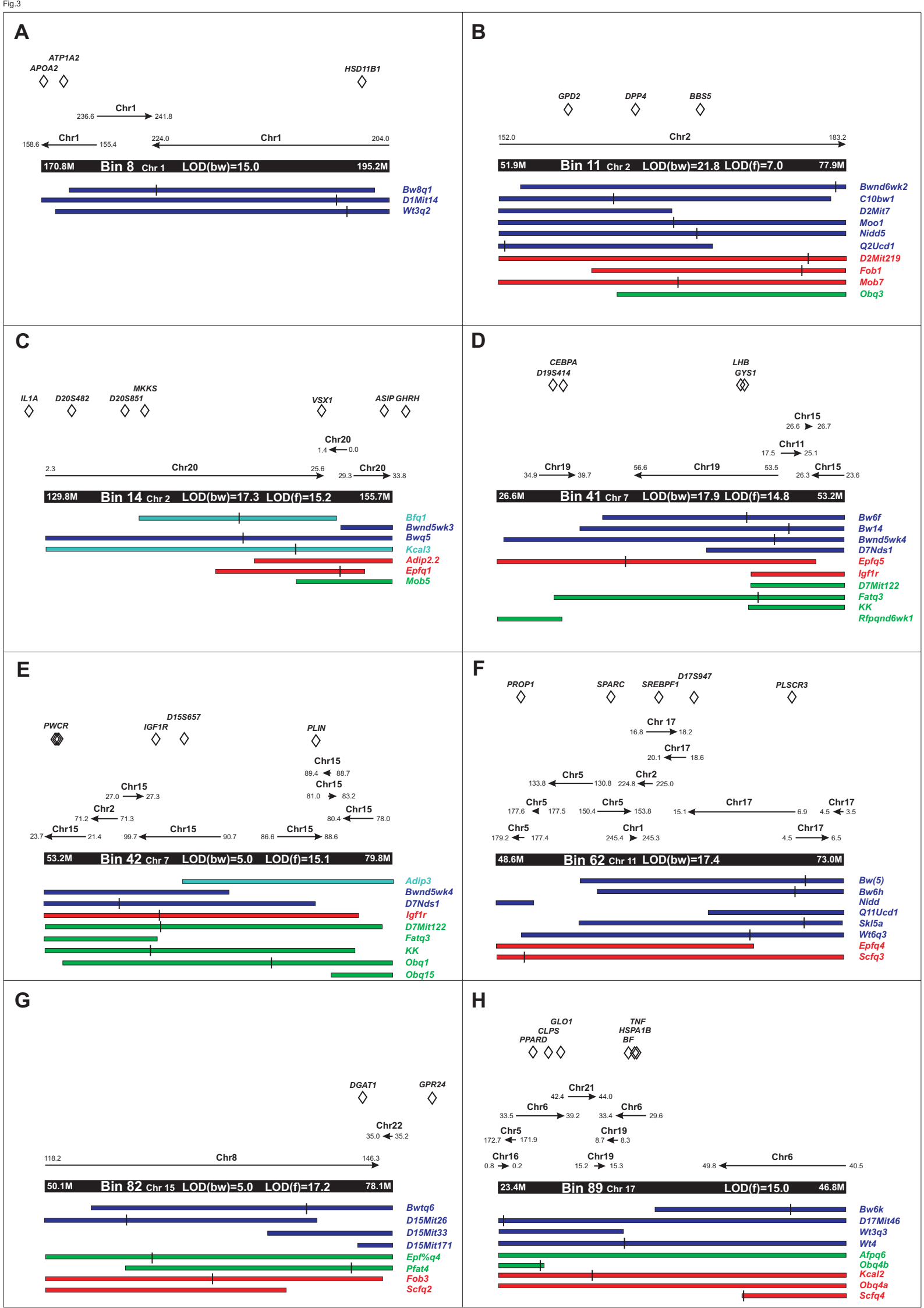
A
ATP1A2
APOA2
HSD11B1
Chr1
236.6
241.8
Chr1
158.6
155.4
224.0
Chr1
204.0
170.8M
Bin 8 Chr 1 LOD(bw)=15.0
195.2M
Bw8q1
D1Mit14
Wt3q2
B
GPD2
DPP4
BBS5
152.0
Chr2
183.2
51.9M
Bin 11 Chr 2 LOD(bw)=21.8 LOD(f)=7.0
77.9M
Bwnd6wk2
C10bw1
D2Mit7
Moo1
Nidd5
Q2Ucd1
D2Mit219
Fob1
Mob7
Obq3
C
IL1A
D20S482
MKKS
D20S851
VSX1
ASIP GHRH
Chr20
1.4
0.0
2.3
Chr20
25.6
Chr20
29.3
33.8
129.8M
Bin 14 Chr 2 LOD(bw)=17.3 LOD(f)=15.2
155.7M
Bfq1
Bwnd5wk3
Bwq5
Kcal3
Adip2.2
Epfq1
Mob5
D
CEBPA
D19S414
LHB
GYS1
Chr15
26.6
26.7
Chr11
17.5
25.1
Chr19
34.9
39.7
56.6
Chr19
53.5
Chr15
26.3
23.6
26.6M
Bin 41 Chr 7 LOD(bw)=17.9 LOD(f)=14.8
53.2M
Bw6f
Bw14
Bwnd5wk4
D7Nds1
Epfq5
Igf1r
D7Mit122
Fatq3
KK
Rfpqnd6wk1
E
PWCR
IGF1R
D15S657
PLIN
Chr15
89.4
88.7
Chr15
27.0
27.3
Chr15
81.0
83.2
Chr2
71.2
71.3
Chr15
80.4
78.0
Chr15
23.7
21.4
Chr15
99.7
90.7
Chr15
86.6
88.6
53.2M
Bin 42 Chr 7 LOD(bw)=5.0 LOD(f)=15.1
79.8M
Adip3
Bwnd5wk4
D7Nds1
Igf1r
D7Mit122
Fatq3
KK
Obq1
Obq15
F
PROP1
SPARC
SREBPF1
D17S947
PLSCR3
Chr 17
16.8
18.2
Chr17
20.1
18.6
Chr5
133.8
130.8
Chr2
224.8
225.0
Chr5
177.6
177.5
Chr5
150.4
153.8
Chr17
15.1
6.9
Chr17
4.5
3.5
Chr5
179.2
177.4
Chr1
245.4
245.3
Chr17
4.5
6.5
48.6M
Bin 62 Chr 11 LOD(bw)=17.4
73.0M
Bw(5)
Bw6h
Nidd
Q11Ucd1
Skl5a
Wt6q3
Epfq4
Scfq3
G
DGAT1
GPR24
Chr22
35.0
35.2
118.2
Chr8
146.3
50.1M
Bin 82 Chr 15 LOD(bw)=5.0 LOD(f)=17.2
78.1M
Bwtq6
D15Mit26
D15Mit33
D15Mit171
Epf%q4
Pfat4
Fob3
Scfq2
H
GLO1
CLPS
PPARD
TNF
HSPA1B
BF
Chr21
42.4
44.0
Chr6
33.5
39.2
Chr6
33.4
29.6
Chr5
172.7
171.9
Chr19
8.7
8.3
Chr16
0.8
0.2
Chr19
15.2
15.3
Chr6
49.8
40.5
23.4M
Bin 89 Chr 17 LOD(f)=15.0
46.8M
Bw6k
D17Mit46
Wt3q3
Wt4
Afpq6
Obq4b
Kcal2
Obq4a
Scfq4

Figure 3: Candidate genes and syntenic regions of human chromosomes in the eight bins with highest significance.

Black horizontal bars represent genomic regions of mouse chromosomes where the bin number and boundaries (in Mbp, M) as well as LOD score values (>4.3) for body weight (bw) and body fat (fat weight and fat percentage; fw, f%) from the meta-analysis are indicated. Arrows denote corresponding syntenic regions on human chromosomes with physical positions in Mbp. Indicated are QTL for body weight (blue), fat weight (red), body fat percentage (green) and both body weight and body fat (cyan), respectively, which map into the bins. Ticks indicate the position of peak markers. Diamonds represent physical positions of candidate genes and genetic loci which have been implicated in regulation of body weight and body composition in rodents and/or humans. *APOA2*, apolipoprotein A-II; *ASIP*, agouti signaling protein; *ATP1A2*, Na^+,K^+-ATPase alpha2 subunit; *BBS5*, Bardet-Biedl syndrome 5; *BF*, complement factor B; *C/EBPA*, CCAAT/enhancer binding protein alpha; *CLPS*, pancreatic colipase; *DGAT1*, diacylglycerol O-acyltransferase 1; *GPD2*, glycerol-3-phosphate dehydrogenase 2; *DPP4*, dipeptidylpeptidase 4; *GLO1*, glyoxalase I; *GHRH*, growth hormone releasing hormone; *GPR24*, G protein-coupled receptor 24 (Melanin conentrating hormone receptor 1); *GYS1*, glycogen synthase 1; *HSD11B1*, hydroxysteroid 11-beta dehydrogenase 1; *HSPA1*, heat shock 70kDa protein 1A; *IGF1R*, insulin-like growth factor 1 receptor; *IL1A*, interleukin 1 alpha; *LHB*, luteinizing hormone beta polypeptide; *MKKS/BBS6*, McKusick-Kaufman syndrome protein; *PLIN*, perilipin; *PLSCR3*, phospholipid scramblase 3; *PPARD*, peroxisome proliferator activator receptor delta; *PROP1*, prophet of Pit1, paired-like homeodomain transcription factor; PWCR, Prader-Willi syndrome chromosome region; *SPARC*, secreted protein acidic and rich in cysteine/osteonectin/BM40; *SREBP-1*, sterol regulatory element binding transcription factor 1; *TNF*, tumor necrosis factor; *VSX1*, visual system homeobox 1 homolog (see paper for details and references).