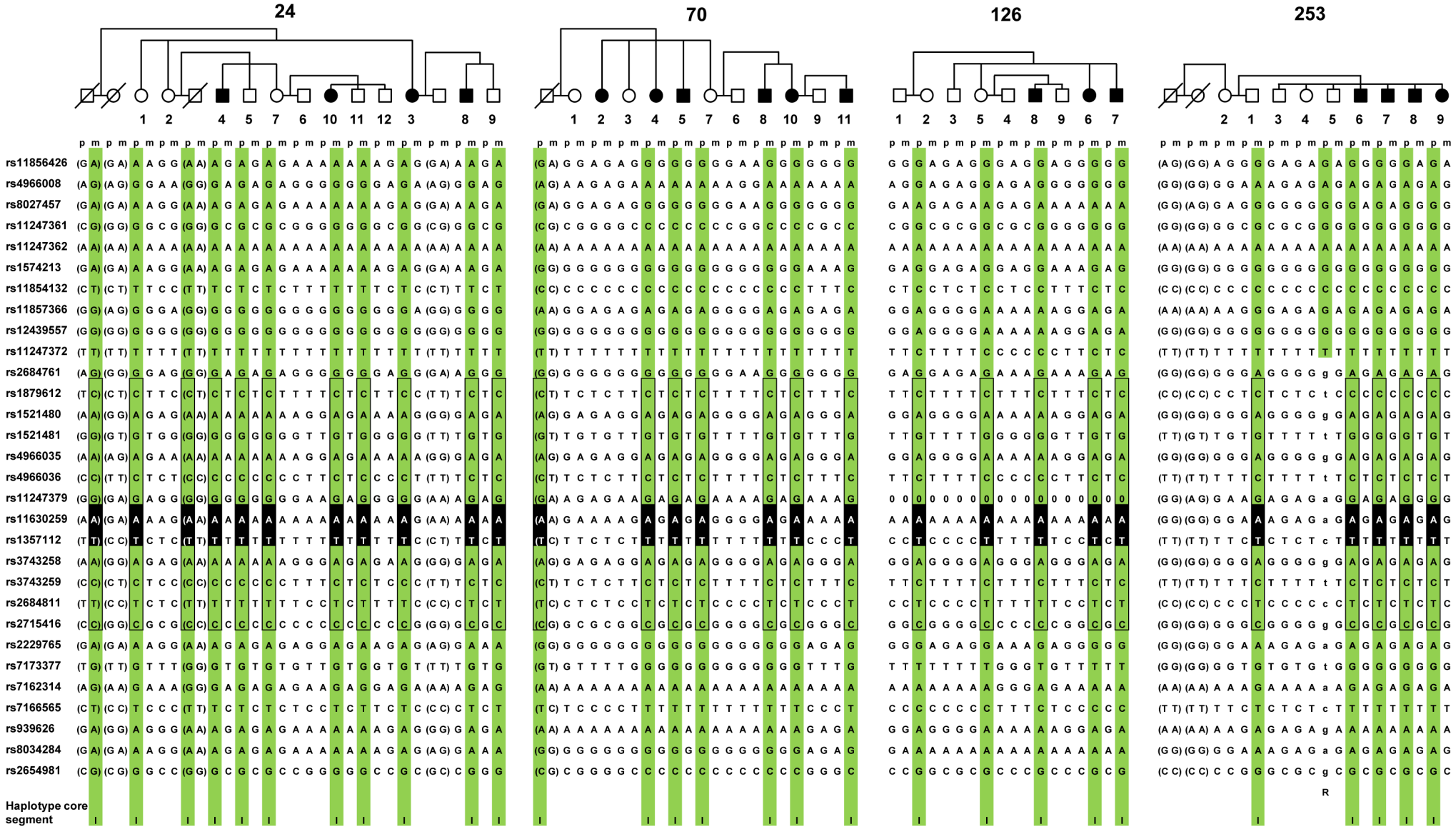
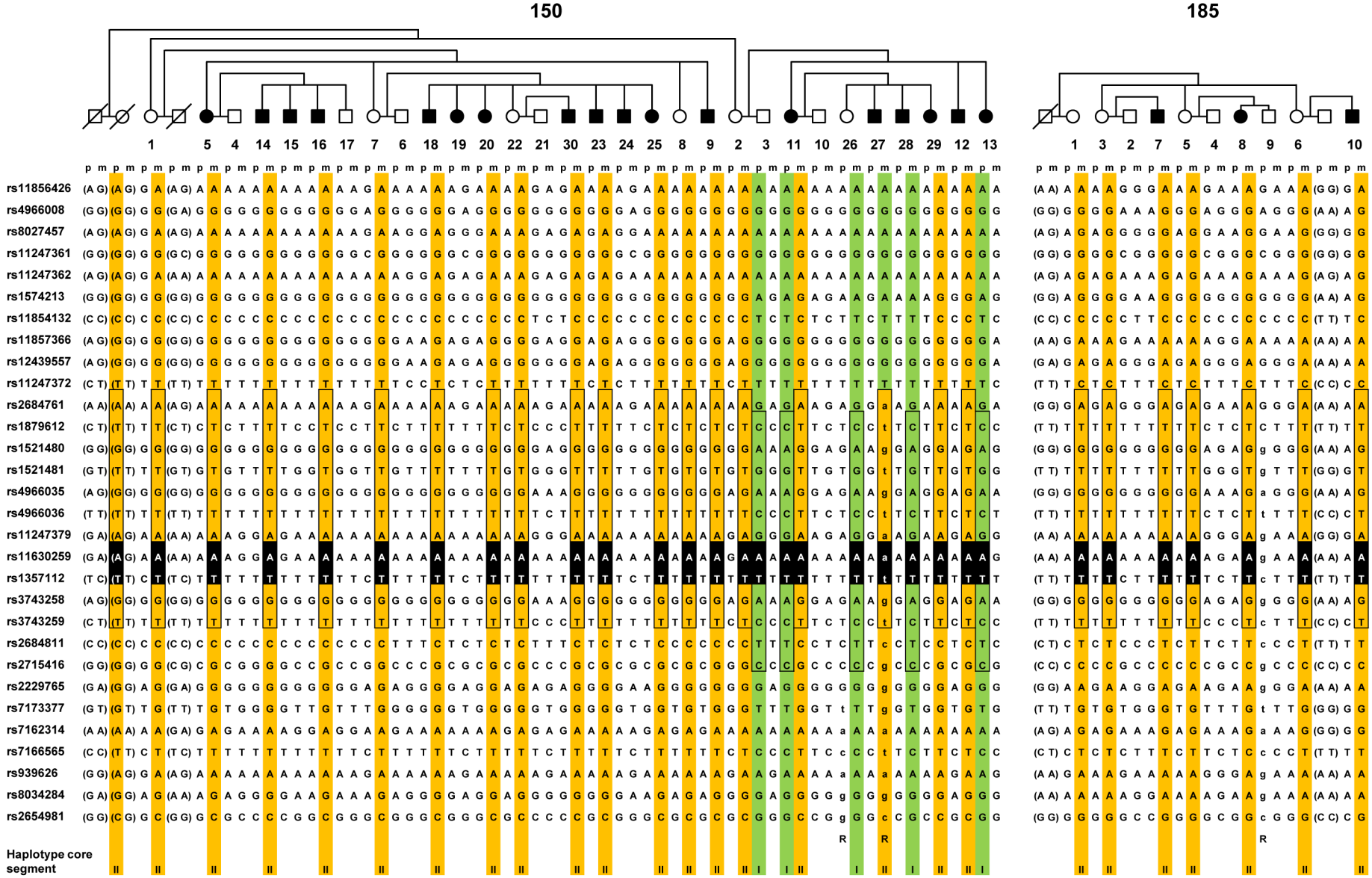
Figure S2. *IGF1R* haplotype segregation in the linked families.

Each successive column represents a single chromosome, with the paternal (p) and maternal (m) origin indicated above the haplotype. The individuals genotyped are indicated by the same numbers as in Figure S1. The bracketed () haplotypes are imputed for untyped individuals. Recombinations are indicated by R below the haplotypes, with noncapital letter allele coding distal to the predicted crossover breakpoint. Green- and orange-shaded areas indicate within-family haplotype sharing, with haplotypes carrying core segments I (55 kb) and II (79 kb) that were shared IBS between families shown by green and orange, respectively. Core segments I and II are further indicated by solid boxes, with the core I haplotype shared by families 24, 70, 126, 253 and 150 and the core II haplotype by families 150 and 185. The location of maximal haplotype sharing (rs11630259–rs1357112 haplotype AT) in all disease-cosegregating chromosomes in all families is shown by white letters on a black background. See text for details.


24
70
126
253
rs11856426
rs4966008
rs8027457
rs11247361
rs11247362
rs1574213
rs11854132
rs11857366
rs12439557
rs11247372
rs2684761
rs1879612
rs1521480
rs1521481
rs4966035
rs4966036
rs11247379
rs11630259
rs1357112
rs3743258
rs3743259
rs2684811
rs2715416
rs2229765
rs7173377
rs7162314
rs7166565
rs939626
rs8034284
rs2654981
Haplotype core segment


150
185
1 5 4 14 15 16 17 7 6 18 19 20 22 21 30 23 24 25 8 9 2 3 11 10 26 27 28 29 12 13
1 3 2 7 5 4 8 9 6 10
rs11856426
rs4966008
rs8027457
rs11247361
rs11247362
rs1574213
rs11854132
rs11857366
rs12439557
rs11247372
rs2684761
rs1879612
rs1521480
rs1521481
rs4966035
rs4966036
rs11247379
rs11630259
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rs3743259
rs2684811
rs2715416
rs2229765
rs7173377
rs7162314
rs7166565
rs939626
rs8034284
rs2654981
Haplotype core segment