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.