Figure EV1. Schematic representation of genome-wide LOD score calculations.
LOD scores calculated with ALLEGRO are given along the y-axis relative to genomic position cM (centiMorgan) on the x-axis. Note the highest peak (LOD score 2.4) in the region on chromosome 10 and a second lower peak in the XY PAR1 (LOD score 1.7).
Figure EV2. Haplotype reconstruction for the PAR1 region.
Pedigree of the family with associated SNPs in the pseudoautosomal region 1 (PAR1) of chromosome X is represented. A total LOD score of 1.7 was identified between the flanking markers rs3995646 and rs5939344 and covered a 2.02 Mb sequence (chrX:706800–2735491; hg19). Filled symbol, LWD-affected individual; symbol with a slash, deceased individual; slash, divorced; arrow, index patient. Colored chromosomal regions show traceable inheritance: red color regions, common haplotype co-segregating with LWD; black lines, regions affected by a crossing over of unknown location.

Figure EV3. Haplotype reconstruction for chromosome 10.
Pedigree of the family with associated SNPs co-segregating with the disease phenotype on chromosome 10 is represented. A total LOD score of 2.4 was identified between the flanking markers rs10509480 and rs10509758 and covered a 19.2 Mb region (chr10:85477515–104681710; hg19). Filled symbol, LWD-affected individual; symbol with a slash, deceased individual; slash, divorced; arrow, index patient. Colored chromosomal regions show traceable inheritance: red color regions, common haplotype co-segregating with LWD; black lines, regions affected by a crossing over of unknown location.
CYP26C1 genetic modifier in SHOX deficiency

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