



Figure S1. Exclusion of a heterozygous deletion involving *ZNF445* in patient 1.

A. Genomewide array comparative genomic hybridization analysis.

B. Exome sequencing-based CNV calling developed by Nord et al.¹

C. Quantitative real-time PCR analysis for three positions on *ZNF445*.

Reference

1. Nord AS, Lee M, King MC, Walsh T. Accurate and exact CNV identification from targeted high-throughput sequence data. *BMC Genomics*. 2011;12:184.