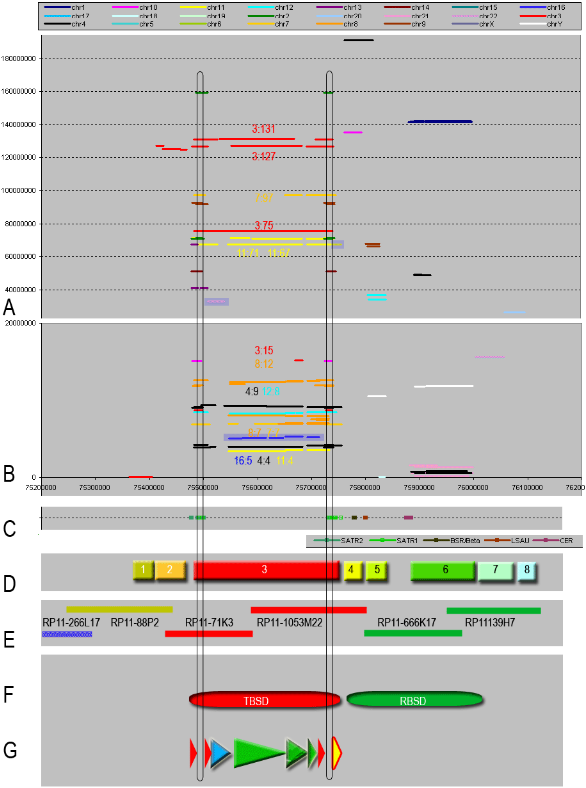

Supplementary material 7. Sequence analysis of the TBR1 between base pair positions 75200000 and 76200000 (horizontal dimension, scale is shown at the bottom of B). Vertical empty bars show positions of SATR/HERVE elements.

A-B. Dot-plot alignment of long SDs (> 10kb in size) to different human chromosomes (see color description at the top of the figure); with Mb positions 20 to 180 (A) and 0 to 20 (B) in vertical dimension.

C. Positions of satellite repeats.

D. Eight multicopy regions identified, based on the alignment data, of which 4 (1, 2, 7 and 8) were duplicated and 4 (3-6) were present in more than 2 copies, amplified, in the human genome. The amplified regions were associated with satellite repeats (see C).

E. Positions of BAC clones used for FISH.

F. Two "SD-amplicons" identified based on the sequence alignments and FISH results.

G. Schematic representation of TBSD composition. Parts shown by different triangles have different "amplification pattern" as identified by comparison to all homologous sequences.