



Supplementary Figure S4: (a) Phylogenetic tree of the 24 haplotypes from 12 CEU fathers which are heterozygous regarding the 730Kb wide region under TD in Chr6p (715 SNPs, Fig. 3). NA-codes identify the 12 subjects according to the HapMap nomenclature (www.hapmap.org). Transmitted haplotypes are marked with a green triangle (▲), while a red square (■) marks the non-transmitted ones. The bootstrap consensus tree inferred from 10,000 replicates¹ is taken to represent the phylogenetic distances among the haplotypes analyzed. The phylogenetic tree was inferred using the neighbor-joining method². The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test are shown next to the two major branches. Phylogenetic analyses were conducted in MEGA4³. (b) Alignment of the central region of the SNP sequences that originated the phylogenetic analysis. Transmitted and non-transmitted haplotypes are marked as in panel a.

1. Felsenstein J (1985) Confidence limits on phylogenies: An approach using the bootstrap. *Evolution* 39:783-791.
 2. Saitou N & Nei M (1987) The neighbor-joining method: A new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution* 4:406-425.
 3. Tamura K, Dudley J, Nei M & Kumar S (2007) MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. *Molecular Biology and Evolution* 24:1596-1599.