Figure S7 **The level of amino acid substitutions at the PBR ($K_{B(m)}$) among *HLA-DRB1* allele pairs that share the same coalescence time ($m = K_S + K_N$) in 45 non-recombinant alleles.** The ordinate axis represents the mean number of nonsynonymous substitutions at the non-PBR among allele pairs ($K_{B(m)}$). The abscissa axis represents the number of putative synonymous substitutions ($m = K_S + K_N$). Error bars indicate the standard deviation from the mean. The $K_{B(m)}$ and m values were calculated by using 45 non-recombinant alleles which were not showed as a recombinant by both of the method described in Satta (1992) and GENECONV program.