Additional file 5: Scatterplots of pairwise distances and LD estimated by $r^2$ between all SNPs (MAF>5%) in eleven candidate genes (for all and for individual genes) in five populations (for all and for individual populations). The non-linear fitting curve of the mutation-recombination-drift model is shown. Thresholds for LD are indicated by horizontal solid lines which are 0.16 (over all populations), 0.33 (PR), 0.28 (EKO), 0.46 (SMH), 0.28 (ROM), and 0.25 (Petkus).