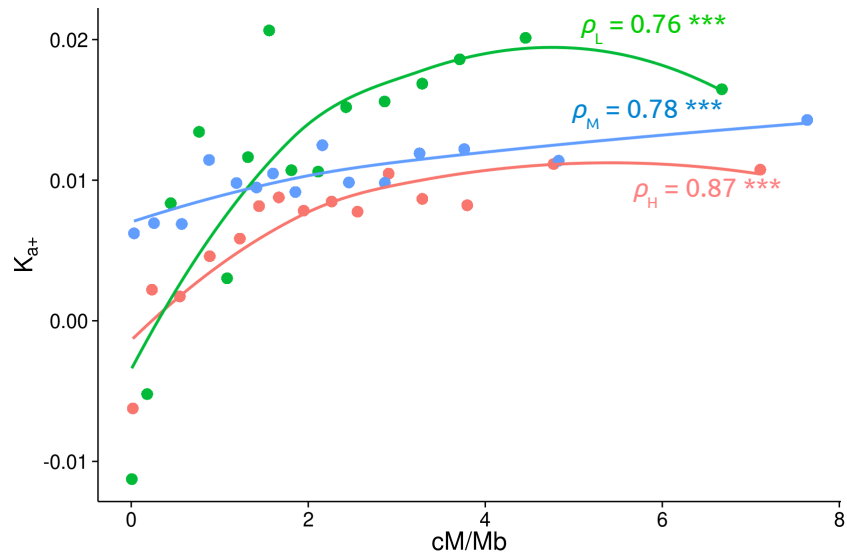
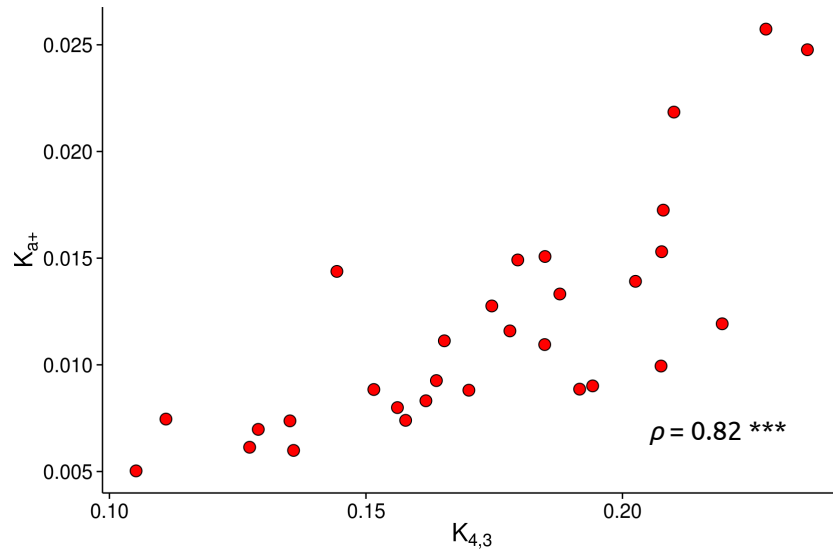


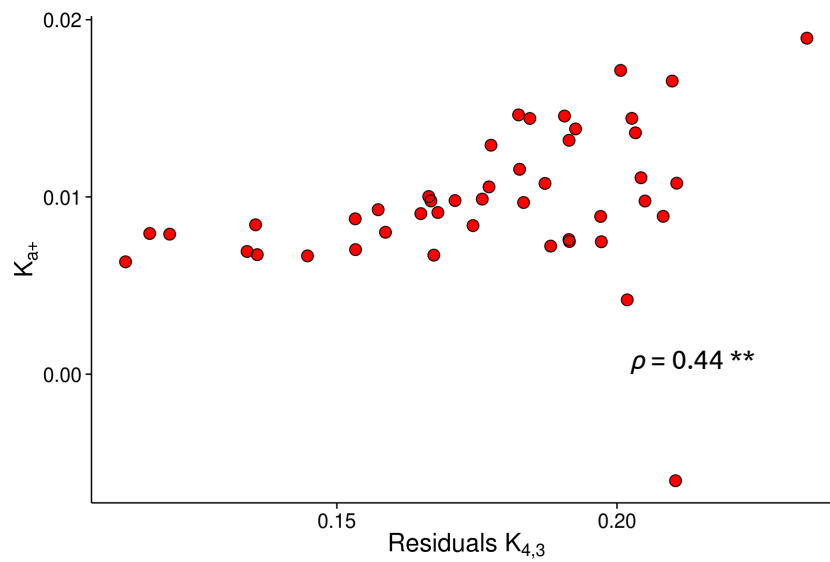
Supplementary Fig. 1. Relations between ω_A in the y axis and the rate of recombination (cM/Mb) in the x axis: (A) using DGRP data, North Carolina population, (B) using DPGP2 data, Rwanda population, (C) excluding immune response and testes related genes and (D) using as neutral reference short intron sites (< 66 nt, bases from 8 to 30). Each data point has been estimated binning 136 genes according to their recombination rate levels. The recombination rate ranks can be consulted in the supplementary table 1. ρ : Spearman's rank correlation coefficient, with significance denoted by asterisks (***<0.001; **<0.01; *<0.05).



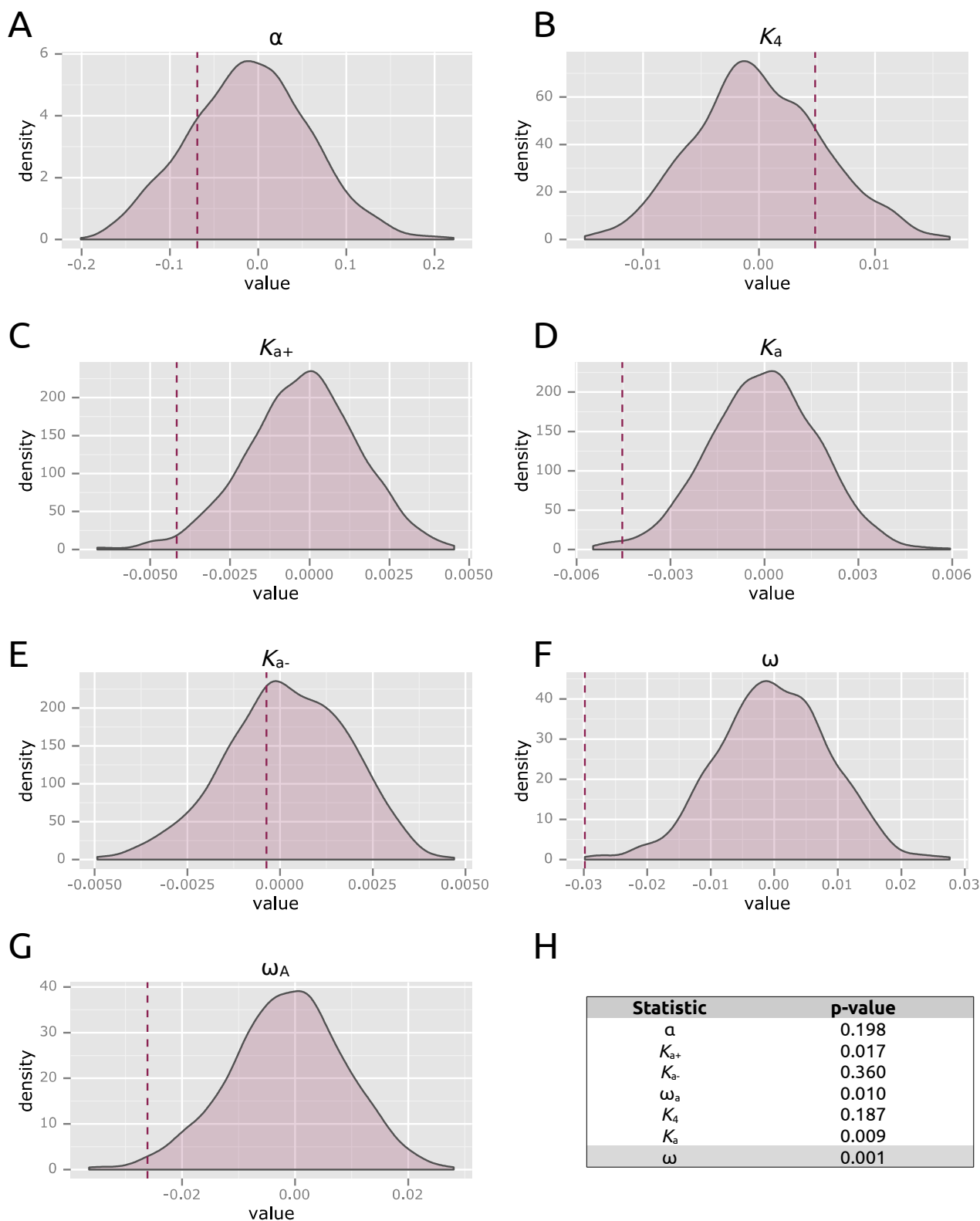
Supplementary Fig. 2. Relationship between K_{a+} in the y axis and the rate of recombination (cM/Mb) in the x axis for three *Fop* groups; genes belonging to the high *Fop* (H) group are in red, medium *Fop* (M) genes are in blue and low *Fop* (L) genes are in green. Each data point has been estimated binning 136 genes according to their recombination rate levels. The recombination rate ranks can be consulted in the supplementary table 3. ρ : Spearman's rank correlation coefficient, with significance denoted by asterisks (***<0.001; **<0.01; *<0.05). The lines are LOESS regressions.



Supplementary Fig. 3. Relationship between K_{a+} in the y axis and an estimate of the mutation rate ($K_{4,3}$) in the x axis after excluding genes with low recombination rates (< 1.32 cM/Mb). Each data point has been estimated binning 136 genes according to their mutation rate ($K_{4,1}$). The mutation rate ranks can be consulted in the supplementary table 2 C. ρ : Spearman's rank correlation coefficient, with significance denoted by asterisks (*** <0.001 ; ** <0.01 ; * <0.05).



Supplementary Fig. 4. Relationship between K_{a+} in the y axis and the residuals of the multiple linear regression: $K_{4,3} \sim \text{Recombination Rate} + \text{Fop}$ at the gene level as an alternative estimate of the mutation rate in the x axis. Each data point has been estimated binning 136 genes according to their mutation rate ($K_{4,1}$). The mutation rate ranks are the same than those showed in Figure 1 and they can be consulted as well in the supplementary table 2 A. ρ : Spearman's rank correlation coefficient, with significance denoted by asterisks ($*** < 0.001$; $** < 0.01$; $* < 0.05$).



Supplementary Fig. 5. Permutation test null distributions and observed differences (red dashed vertical lines) between “Control genes” and “Immune&Testes genes” based on several statistics: (A) α , the proportion of adaptive nonsynonymous substitutions, (B) K_4 , the number of 4-fold synonymous substitutions per site, (C) K_{a+} , the number of adaptive non-synonymous substitutions per site, (D) K_a , the number of non-synonymous substitutions per site, (E) K_{a-} , the number of non-adaptive non-synonymous substitutions per site, (F) ω (K_a/K_4), (G) ω_A (K_{a+}/K_4) and (H) the one-tailed p-value for the different statistics.