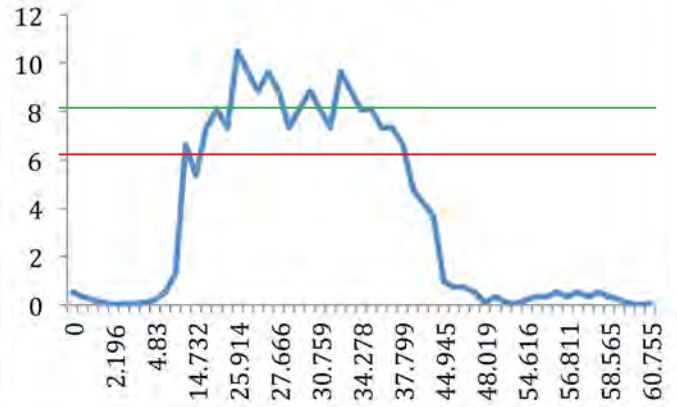
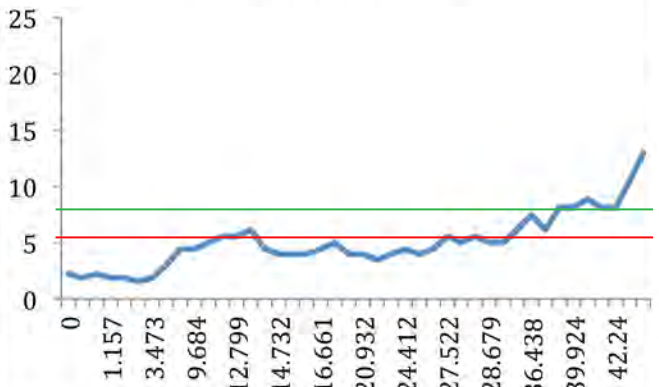
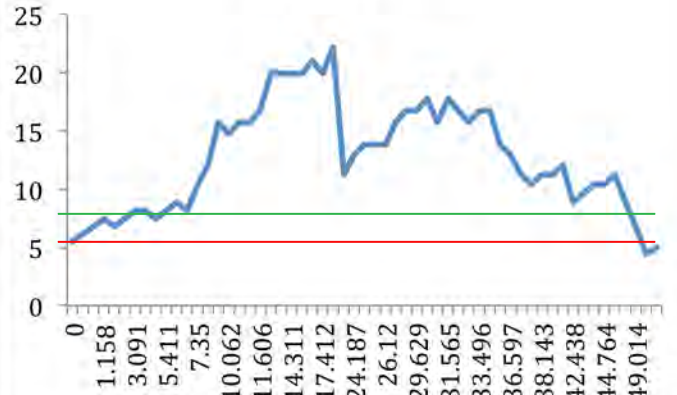
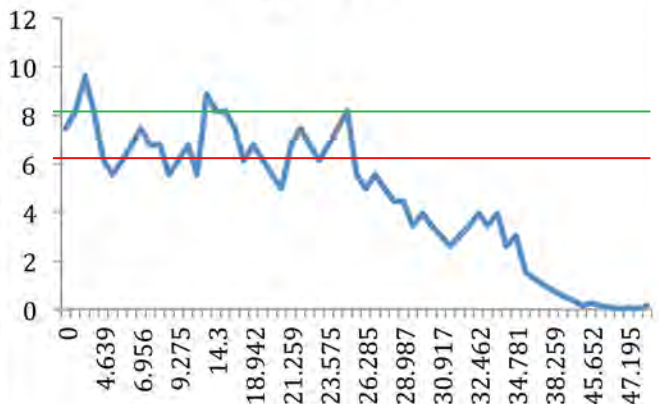
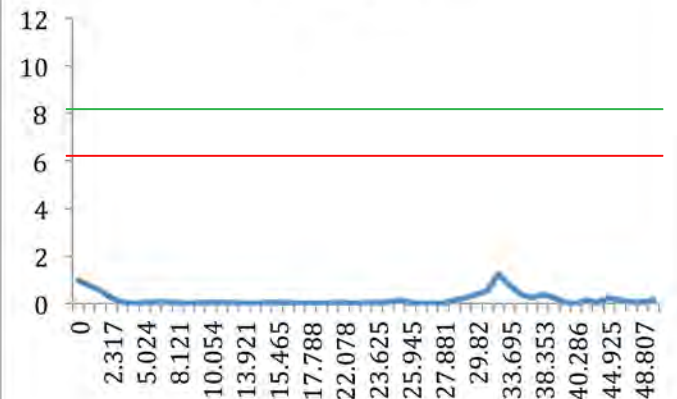
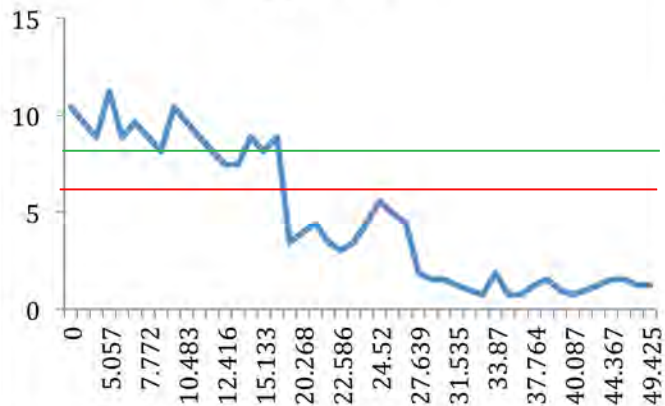
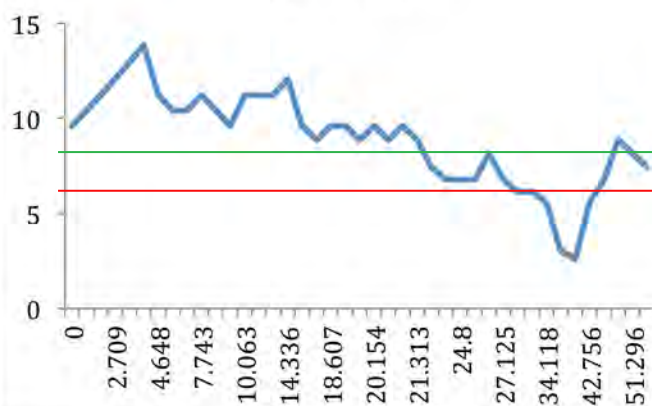
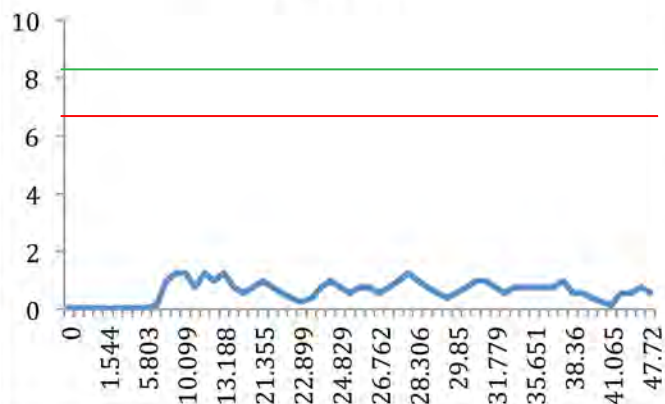
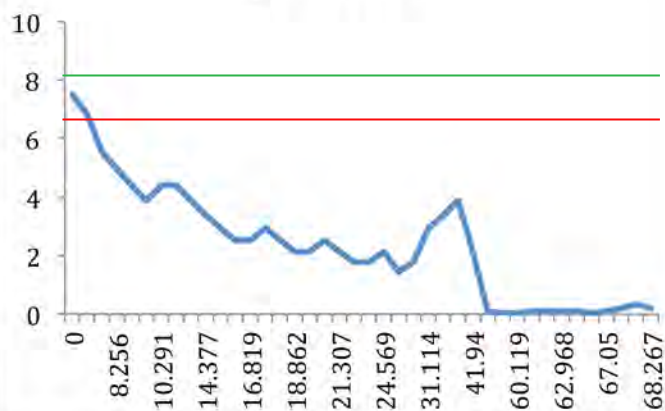
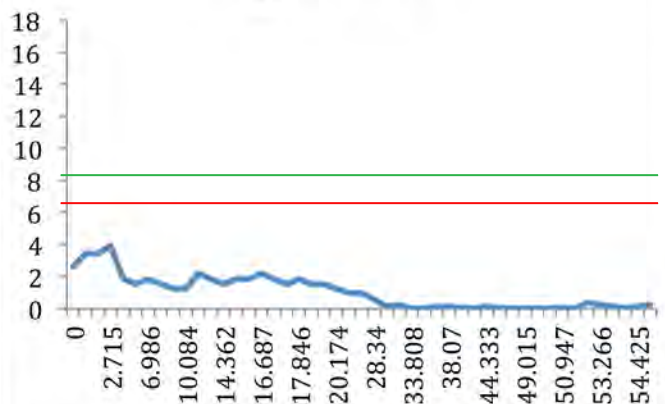
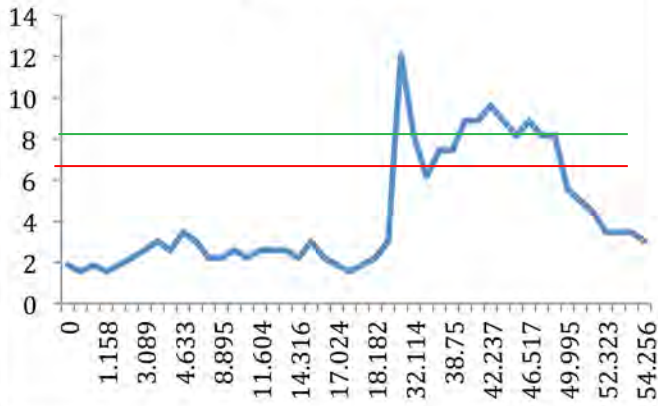


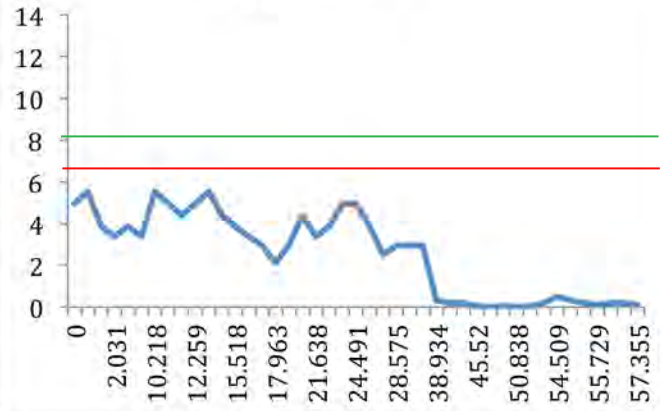
χ^2 LG1 χ^2 LG2 χ^2 LG3 χ^2 LG4 χ^2 LG5 χ^2 LG6

χ^2 LG7 χ^2 LG8 χ^2 LG9 χ^2 LG10 χ^2 LG11 χ^2 LG12

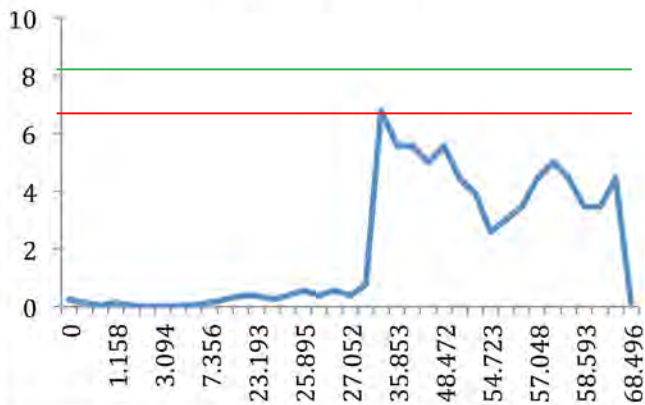
χ^2 LG13



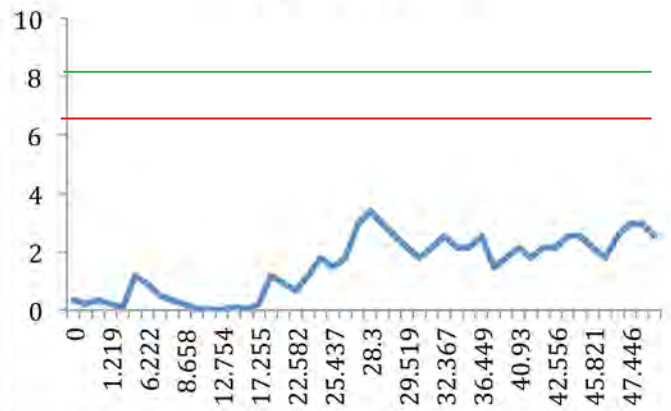
χ^2 LG14



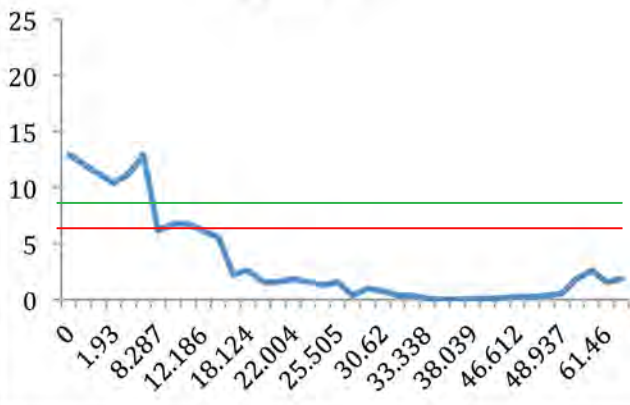
χ^2 LG15



χ^2 LG16



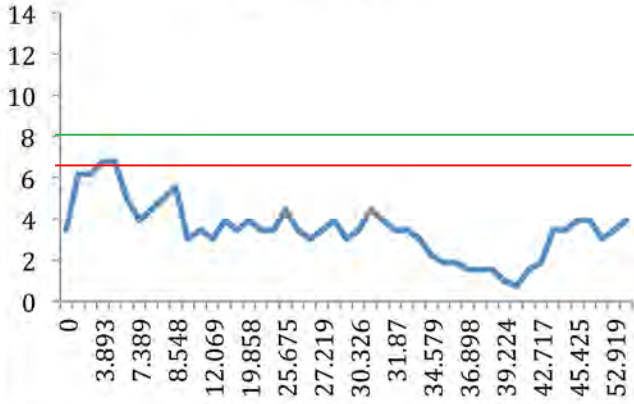
χ^2 LG17



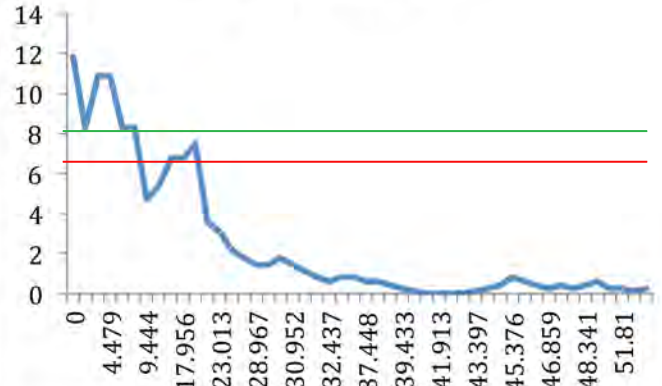
χ^2 LG18



χ^2 LG19



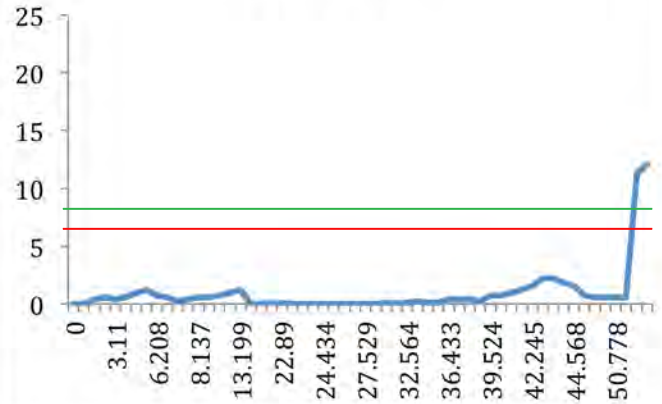
χ^2 LG20



χ^2 LG21



χ^2 LG22



χ^2 LG23



χ^2 LG24

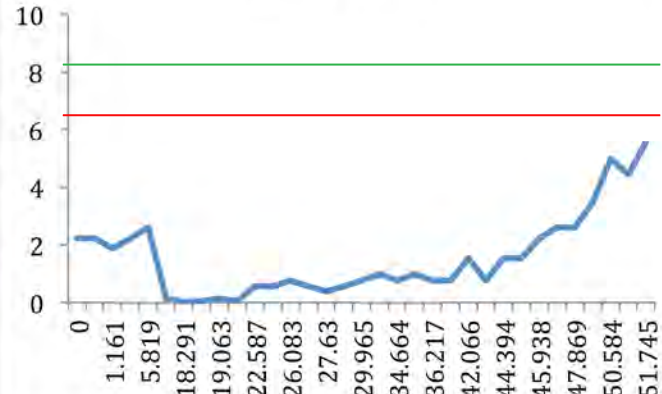


Figure S2 Genome-wide patterns of marker segregation distortion plotted as a function of Chi-square values against marker position along each linkage group. Horizontal lines indicate Chi-squared significance values of $P=0.01$ (red) and $P=0.005$ (green).