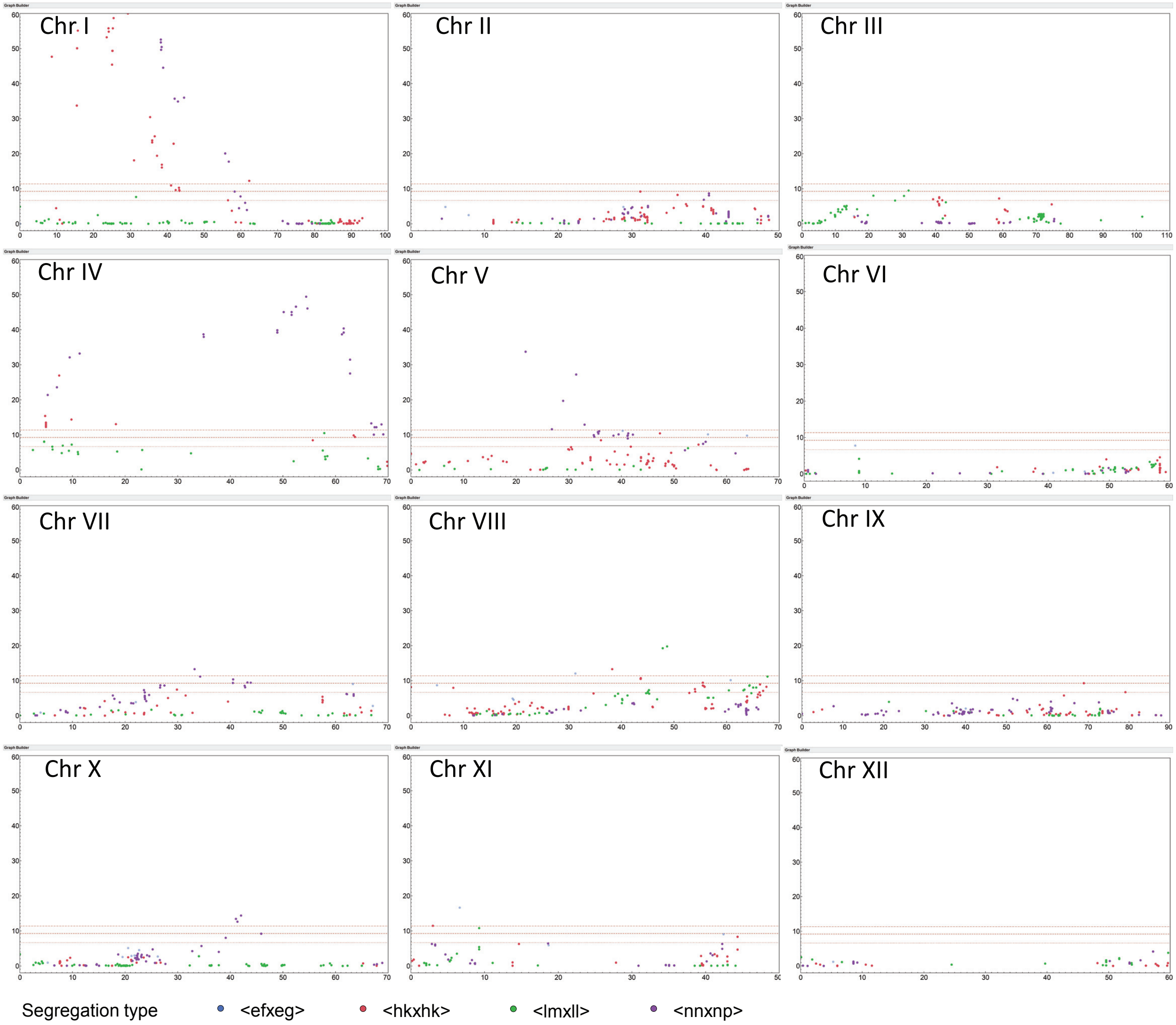

Figure S1 Genome-wide patterns of marker segregation distortion in DMDD population for 1830 STS markers from different segregation categories plotted as a function of Chi-square value (y-axis) against marker physical position (x-axis) on each of the 12 potato chromosomes. Dotted, dashed and dotted-dashed lines represent Chi-square significance values at p = 0.01 for marker segregation categories with two, three and four genotypic classes, respectively.