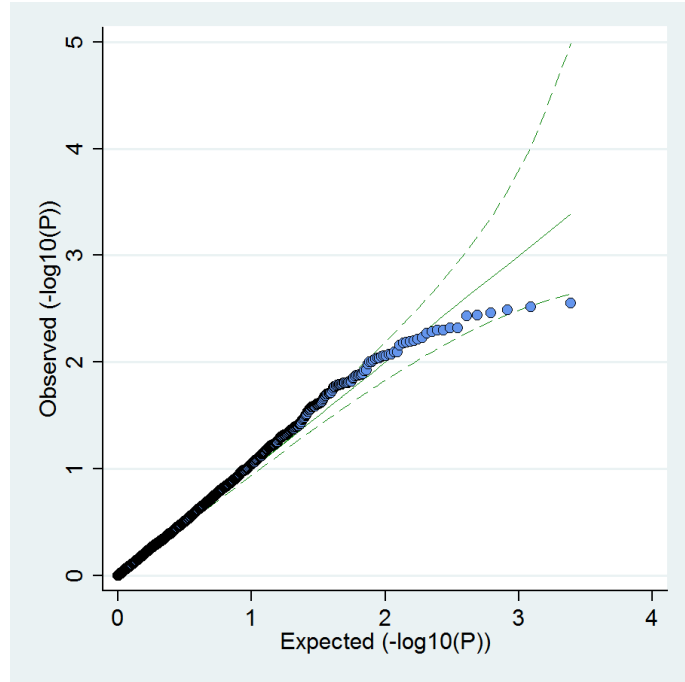
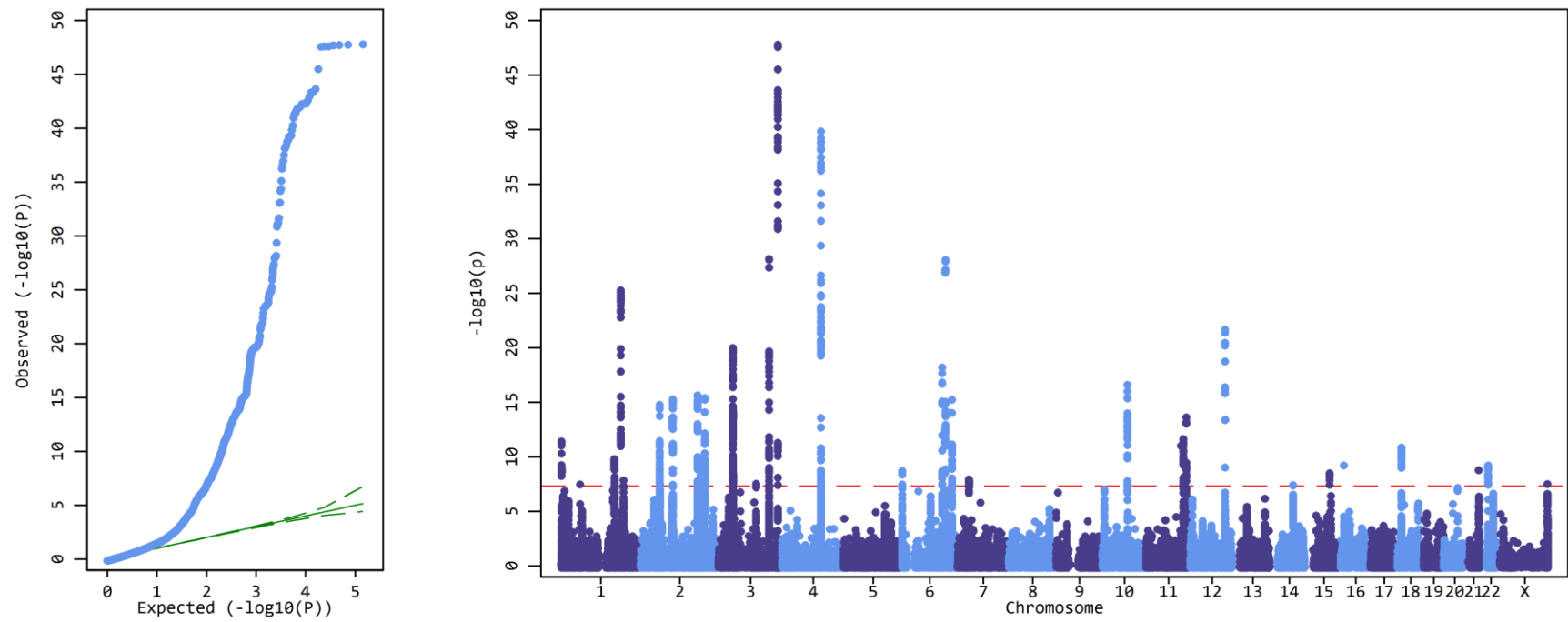


Supplementary Figure 1(a): QQ and Manhattan plots for all SNPs.



Supplementary Figure 1(b): QQ plot of the “null” SNPs not associated with autoimmune diseases ($\lambda = 1.02$)



Supplementary Figure 2: QQ and Manhattan plots from the Meta-analysis of the Irish and Trynka *et al* datasets excluding the HLA/MHC locus (chr6:20-40Mb)

Supplementary Figures (i)-(viii): Distribution of polygene scores across all SNPs for Coeliac disease individuals (affected) and controls(unaffected) for p values of <0.5 (fig(i)) to $<5e-8$ (fig(viii)) . The median score, along with the upper and lower quartiles, are represented by vertical dark red, blue and orange lines respectively. At each threshold, the polygene scores were significantly higher for individuals with CD when compared to controls.

Figure i

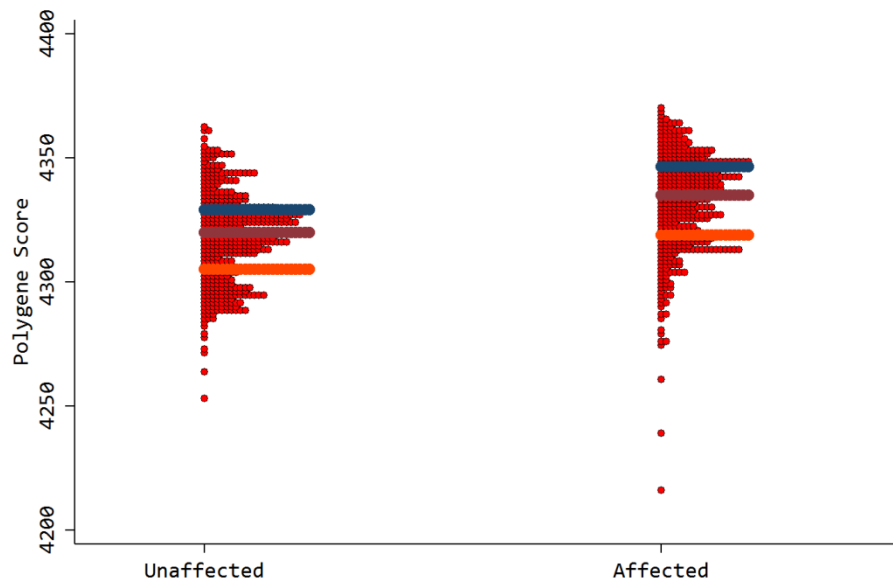


Figure ii

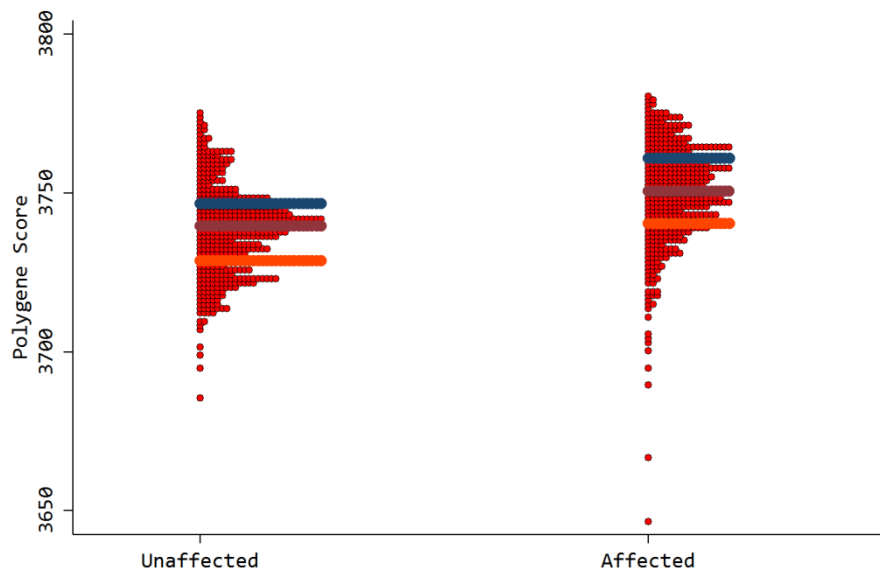


Figure iii

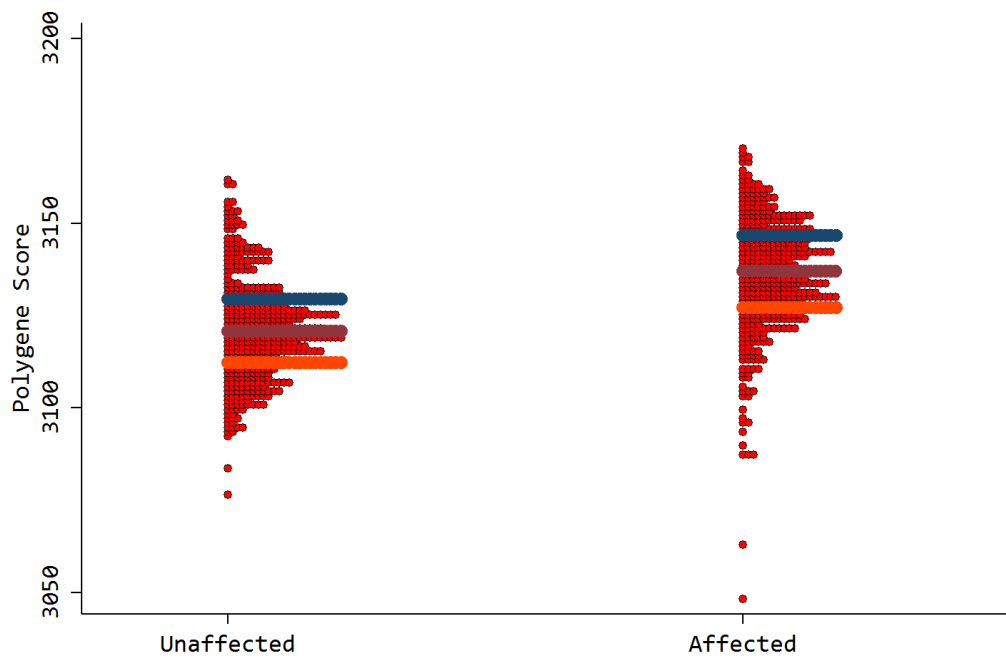


Figure iv

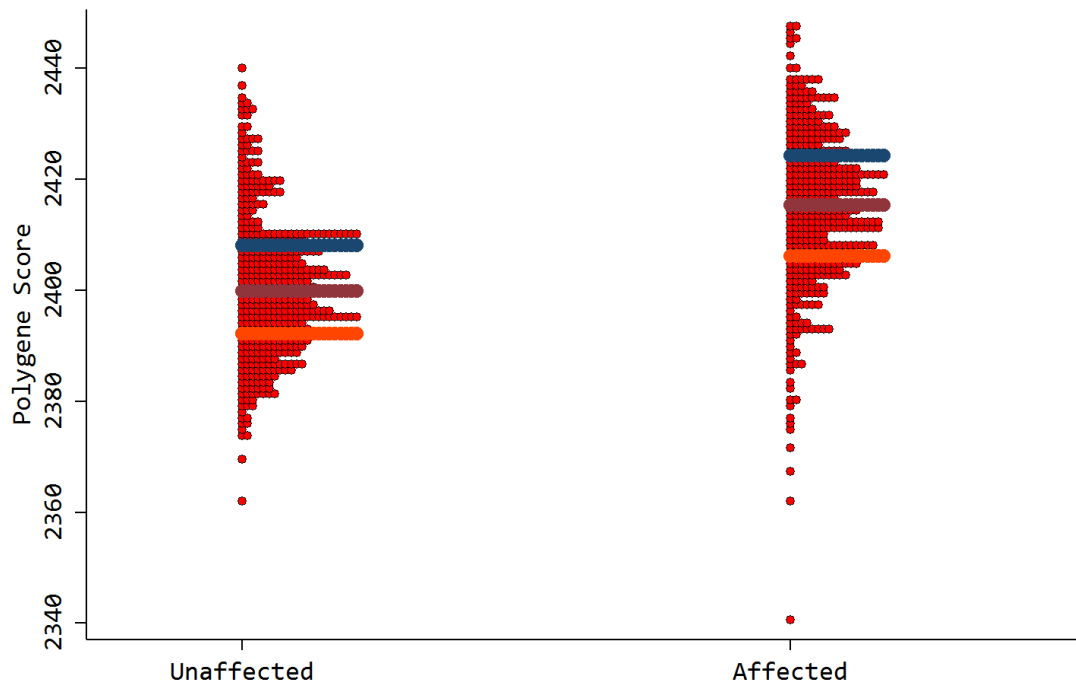


Figure v

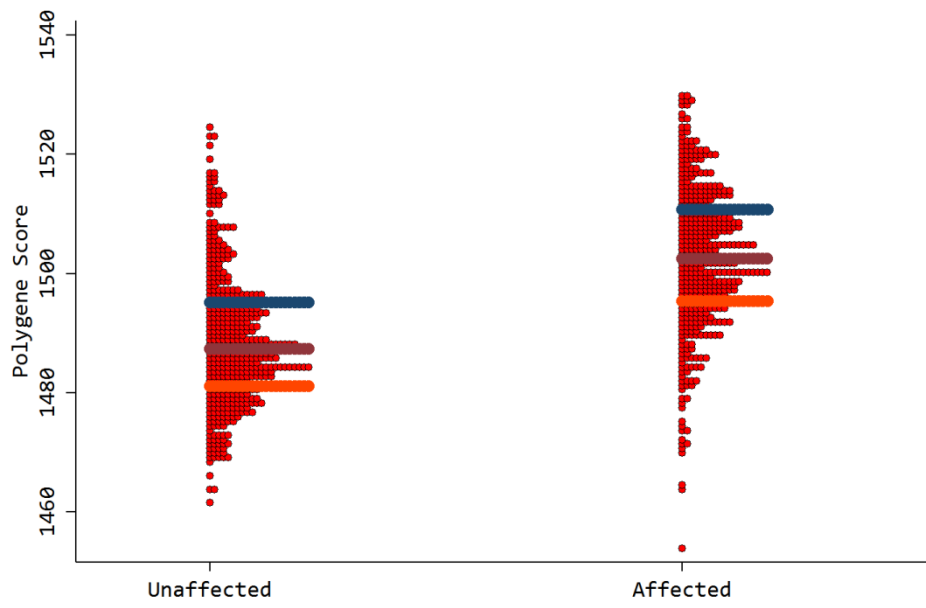


Figure vi

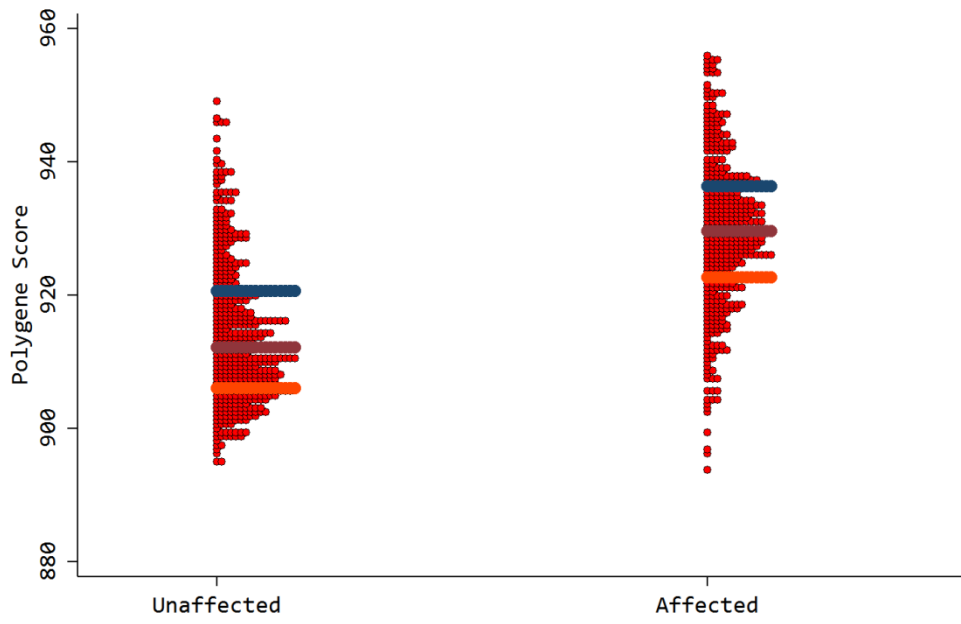


Figure vii

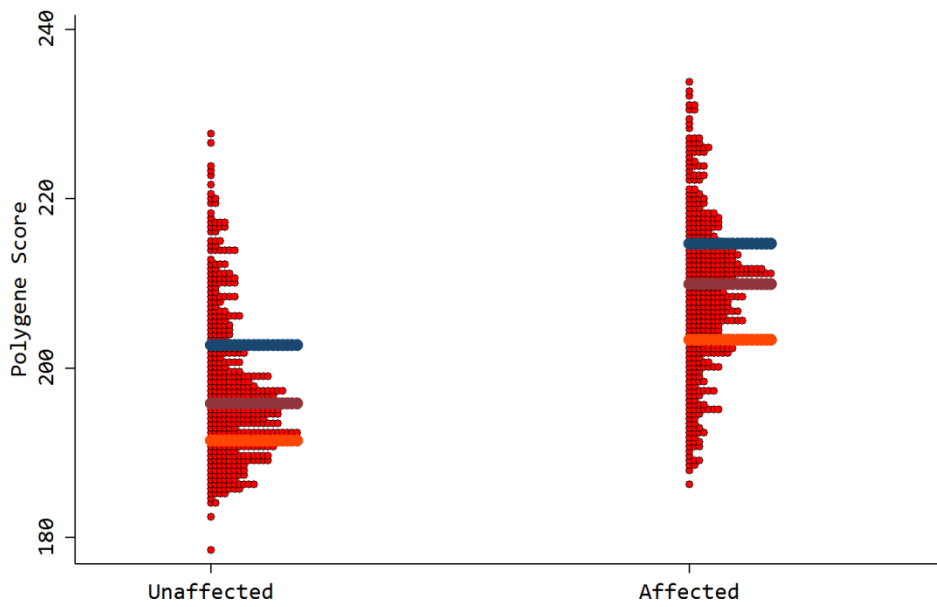
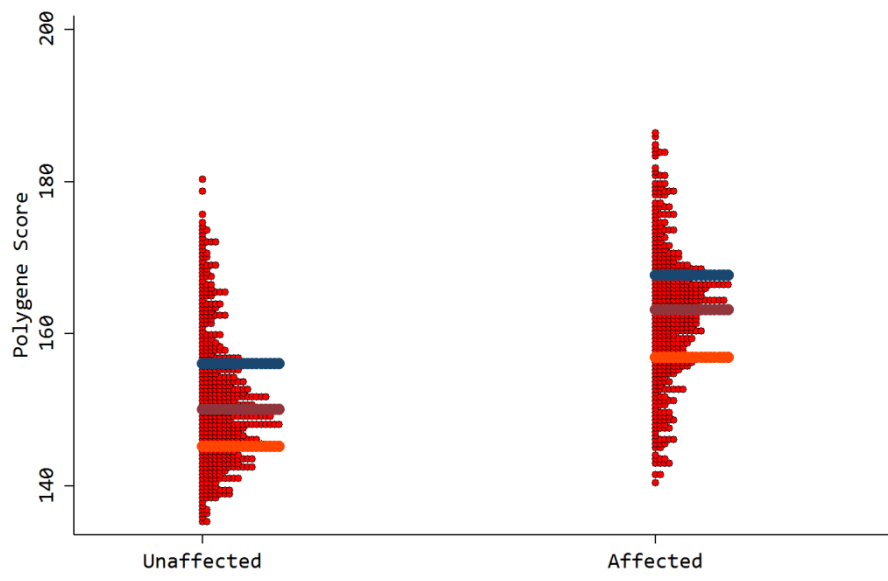


Figure viii



Supplementary Figures (ix)-(xvi): Distribution of polygene scores across non-HLA SNPs for Coeliac disease individuals (affected) and controls(unaffected) for p values of <0.5 (fig(i)) to $<5e-8$ (fig(viii)) . The median score, along with the upper and lower quartiles, are represented by vertical dark red, blue and orange lines respectively. At each threshold, the polygene scores were significantly higher for individuals with CD when compared to controls.

Figure ix

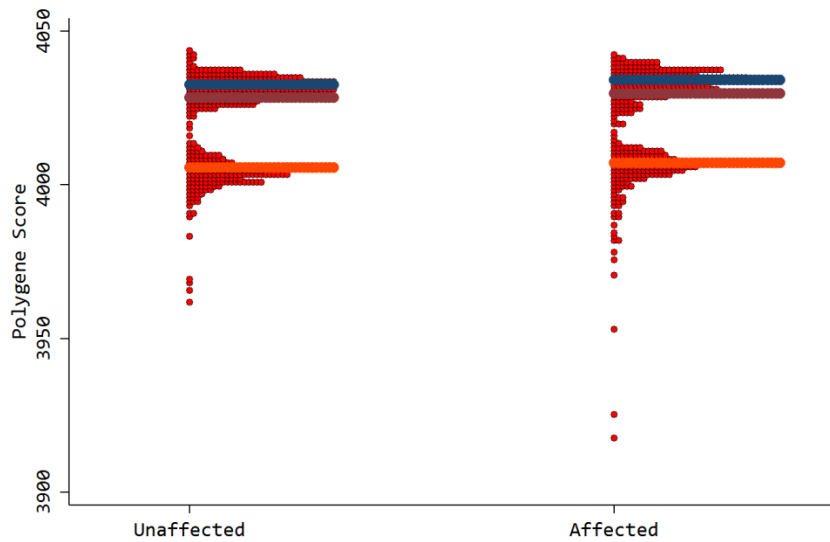


Figure x

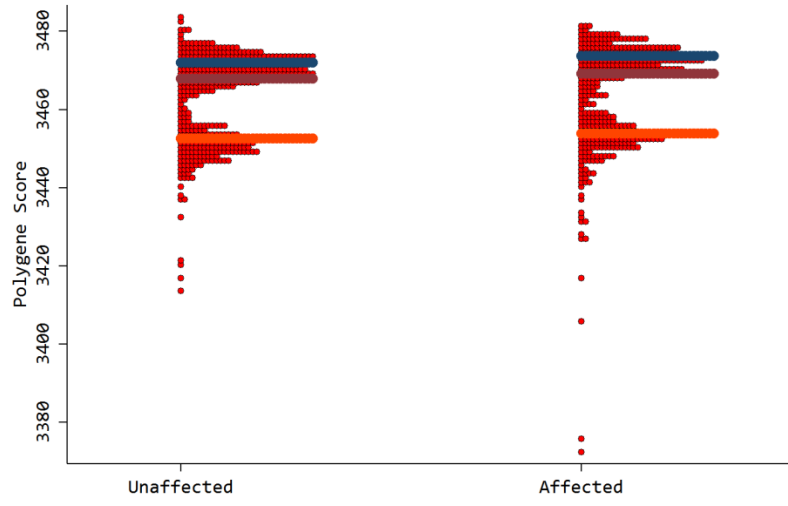


Figure xi

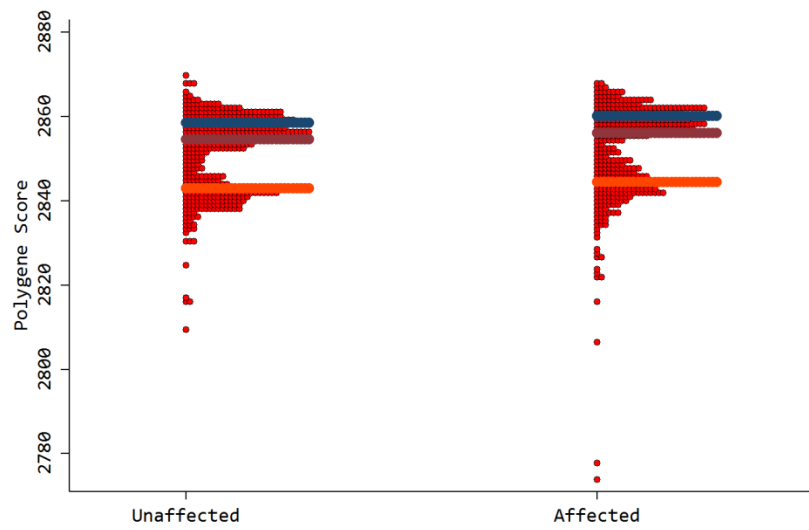


Figure xii

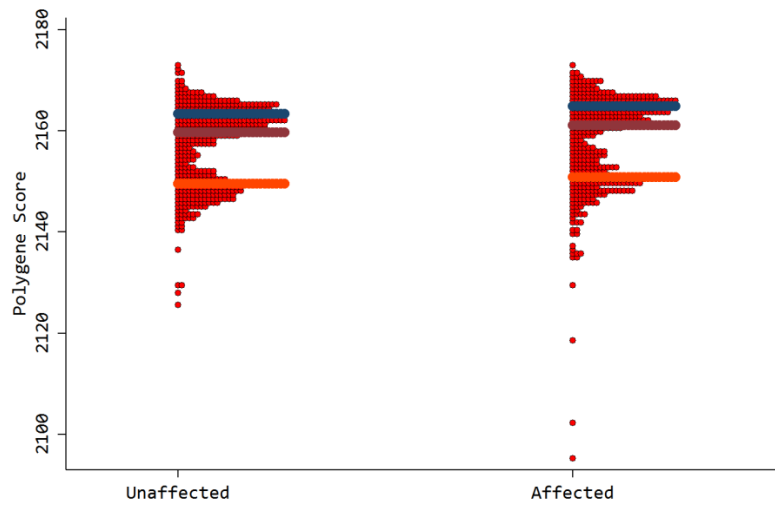


Figure xiii

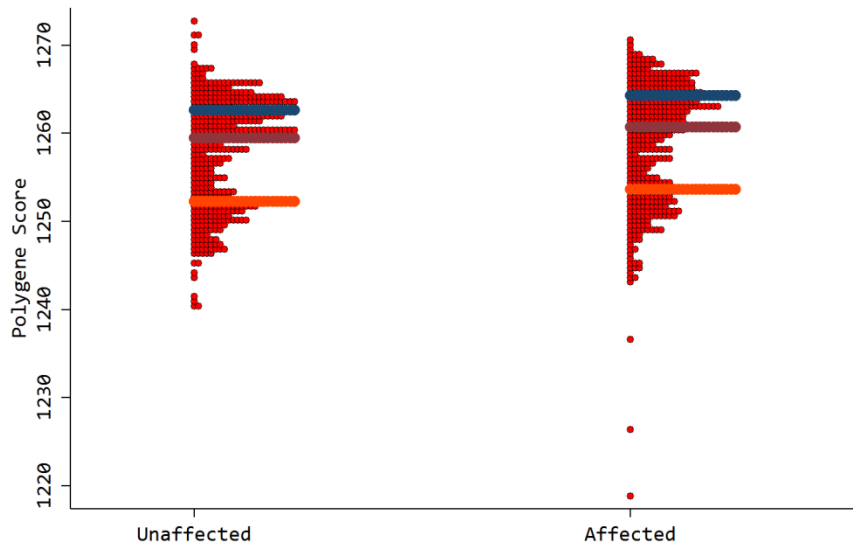


Figure xiv

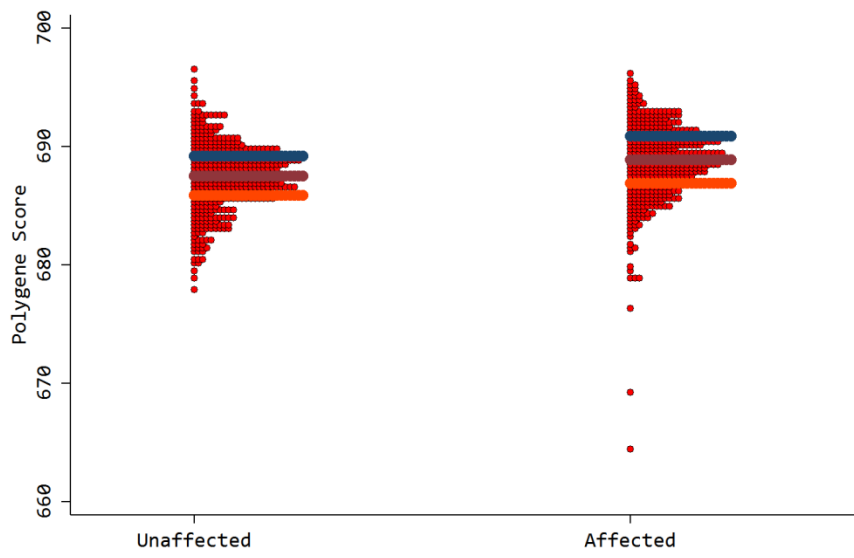


Figure xv

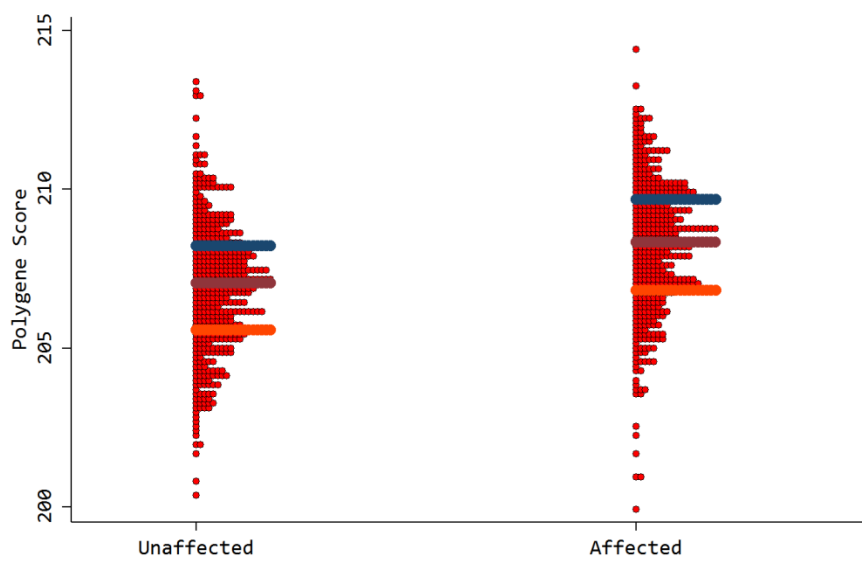


Figure xvi

