



Figure S15. Crossovers (COs) associated with sequence features. A) CO rates (black) in comparison with Col/Ler SNP counts (gray shading) in 100-kb windows along the chromosomes and disease resistance genes (red ticks). CO rates are tallied as the number of COs per window divided by the total number of individuals. Horizontal dashed grey line indicates the genome-wide mean CO rate. B) Percentage of AT (red) and GC (blue) content across the genome. The green shading shows the CO rates presented in (A) and the same axis scale applies. Black ticks show disease resistance genes. The horizontal dashed red line indicates the genome-wide mean %AT content and the horizontal dashed blue line indicates the genome-wide mean %GC content. The position information shown in (B) also applies to (A). Solid vertical lines indicate chromosome boundaries and dashed vertical lines represent the mid-points of the centromeres in both A and B.