Figure S 1 : Enrichment of association signal around the gene for CD.
The percentage of SNPs with $p < \alpha$ (red circles) is plotted for their distance to the closest gene and values have been smoothed using a 50 kb sliding window (blue line). The light blue area represents the distribution expected by chance (95% confidence intervals) based on 100,000 permutations of the disease status. The purple triangle represents the proportion of SNPs with $p < \alpha$ in coding exons. For the plots on the right we excluded SNPs and genes in the MHC region.
Figure S2: Enrichment of association signal around the gene for T1D.
The percentage of SNPs with $p < \alpha$ (red circles) is plotted for their distance to the closest gene and values have been smoothed using a 50 kb sliding window (blue line). The light blue area represents the distribution expected by chance (95% confidence intervals) based on 100,000 permutations of the disease status. The purple triangle represents the proportion of SNPs with $p < \alpha$ in coding exons. For the plots on the right we excluded SNPs and genes in the MHC region.
Figure S 3 : Enrichment of association signal around the gene for RA.
The percentage of SNPs with $p < \alpha$ (red circles) is plotted for their distance to the closest gene and values have been smoothed using a 50 kb sliding window (blue line). The light blue area represents the distribution expected by chance (95% confidence intervals) based on 100,000 permutations of the disease status. The purple triangle represents the proportion of SNPs with $p < \alpha$ in coding exons. For the plots on the right we excluded SNPs and genes in the MHC region.
Figure S 4: Enrichment of association signal around the gene for BD.
The percentage of SNPs with \( p < \alpha \) (red circles) is plotted for their distance to the closest gene and values have been smoothed using a 50 kb sliding window (blue line). The light blue area represents the distribution expected by chance (95% confidence intervals) based on 100,000 permutations of the disease status. The purple triangle represents the proportion of SNPs with \( p < \alpha \) in coding exons. For the plots on the right we excluded SNPs and genes in the MHC region.
Figure S 5: Enrichment of association signal around the gene for HT.
The percentage of SNPs with $p < \alpha$ (red circles) is plotted for their distance to the closest gene and values have been smoothed using a 50 kb sliding window (blue line). The light blue area represents the distribution expected by chance (95% confidence intervals) based on 100,000 permutations of the disease status. The purple triangle represents the proportion of SNPs with $p < \alpha$ in coding exons. For the plots on the right we excluded SNPs and genes in the MHC region.
Figure S 6: Enrichment of association signal around the gene for CAD.
The percentage of SNPs with $p < \alpha$ (red circles) is plotted for their distance to the closest gene and values have been smoothed using a 50 kb sliding window (blue line). The light blue area represents the distribution expected by chance (95% confidence intervals) based on 100,000 permutations of the disease status. The purple triangle represents the proportion of SNPs with $p < \alpha$ in coding exons. For the plots on the right we excluded SNPs and genes in the MHC region.
Figure S 7: Enrichment of association signal around the gene for T2D.
The percentage of SNPs with \( p < \alpha \) (red circles) is plotted for their distance to the closest gene and values have been smoothed using a 50 kb sliding window (blue line). The light blue area represents the distribution expected by chance (95% confidence intervals) based on 100,000 permutations of the disease status. The purple triangle represents the proportion of SNPs with \( p < \alpha \) in coding exons. For the plots on the right we excluded SNPs and genes in the MHC region.
Figure S 8 : Combined Enrichment of association signal around the gene for seven diseases. The percentage of SNPs with $p < \alpha$ (red circles) is plotted for their distance to the closest gene and values have been smoothed using a 50 kb sliding window (blue line). The light blue area represents the distribution expected by chance (95% confidence intervals) based on 100,000 permutations of the disease status. The purple triangle represents the proportion of SNPs with $p < \alpha$ in coding exons.
Figure S 9: Combined enrichment of association signal around the gene for seven diseases after removal of the MHC region.

The percentage of SNPs with $p < \alpha$ (red circles) is plotted for their distance to the closest gene and values have been smoothed using a 50 kb sliding window (blue line). The light blue area represents the distribution expected by chance (95% confidence intervals) based on 100,000 permutations of the disease status. The purple triangle represents the proportion of SNPs with $p < \alpha$ in coding exons. The MHC region was excluded for all plots. The plots on the left and the right side show the same data at different scaling.