



Supplemental Figure 1. A. Quantile-quantile plot for genome-wide association analysis of ACL and PCL injury. The expected versus observed log transformed values for 9,086,322 p-values from the meta-analysis are graphed. The y-axis shows the observed p-values and the x-axis shows the p-values expected by chance. The black dots represent the SNPs arranged by their observed p-values and the red line shows the expected trajectory if the SNPs had p-values expected by chance. B. Manhattan plot for genome-wide association analysis of ACL and PCL injury. The $-\log_{10}$ p-values for association with ACL and PCL injuries for SNPs from the meta-analysis are plotted by genomic position with chromosome number listed across the bottom. The y-axis shows the $-\log_{10}$ p-value for association with ACL and PCL injury. The red line indicates the threshold for genome-wide significance