

Supplementary Figure 1. Principal Component Analyses in CeD and RA datasets. The panels show that the populations corresponding to A. the CeD and B. the RA datasets cluster properly, without the presence of significant outliers that might introduce bias in the analysis.

Supplementary Figure 2. QQ plots for each of the populations analysed in A. the CeD and B. the RA datasets. The distribution of the p-values adjusted to its theoretical distributions per population. In the UK cohort, despite the deviation observed, the λ value suggested no inflation in the results. The distributions were calculated using a set of independent SNPs ($r^2 < 0.2$) across the genome.







