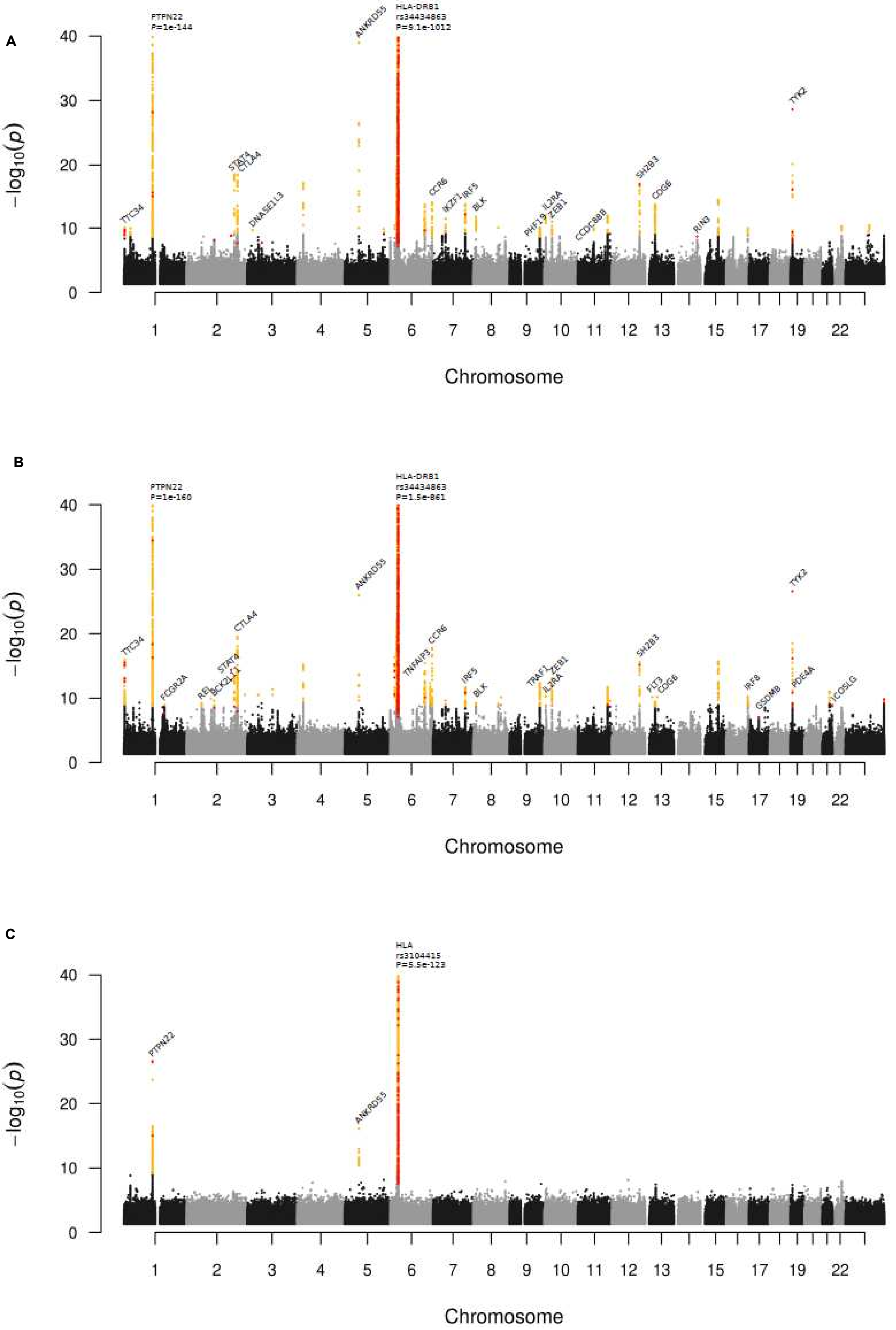

Supplemental Figure 1. Manhattan plots for the genome-wide association meta-analysis of rheumatoid arthritis in Northwestern Europe, separately in (A) RA overall (31,313 cases and 1,067,659 controls), (B) seropositive (18,019 cases and 991,604 controls) and (C) seronegative (8,515 cases and 1,015,471 controls). We used logistic regression in the Icelandic, Swedish, Danish, Norwegian and UK datasets separately and Finnish summary data to test for association of sequence variants with RA overall, seropositive and seronegative RA, and a fixed-effects inverse variance meta-analysis to combine results from the six study groups (see detailed methods in Supplementary Information 2). Significant associations for high and moderate impact variants are shown in red and that of other variants in yellow. Lead signals with P<10^{-40} are shown in the graphs (for the *HLA*-locus and *PTPN22* rs2476601).