Supplemental Data

Dense Genotyping of Immune-Related Regions Identifies Loci for Rheumatoid Arthritis Risk and Damage in African Americans

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Supplementary Figure S1. Distribution of modified total radiographic scores for our study population using kernel density estimates. Estimates were calculated according to the density R package. Vertical marks are individual subject’s overall total modified total Sharp scores on which the density estimates are based.

Supplementary Figure S2. Quantile-quantile plots of p values for the iChip study. P values are from logistic regression (A and B), and from a zero-inflated negative binomial model for radiographic severity of RA (C). (A) is with the HLA region excluded (chr6:26,000,000-34,000,000), (B) is with all markers. (C) includes markers from the zero and count portions of the model zero-inflated negative binomial model.
Supplementary Figure S3. Locus zoom plots of suggestively associated genomic loci. For each zoom plot, the x-axis indicates genomic position and the y-axis indicates association strength –log(p). The color bar indicates the strength of LD with the index SNP in purple and is based on LD patterns from persons of African ancestry from the March 2012 release of the 1000 Genomes project. (A) Locus zoom plot showing the association of AFF3 to RA radiographic severity, according to the count portion of the zero-inflated negative binomial model. (B) Locus zoom plot showing the association of TNFRSF9 to RA radiographic severity, according to the count portion of the zero-inflated negative binomial model. (C) The association of CTLA4 to RA radiographic severity according to the zero portion of the zero-inflated negative binomial model. (D) Locus zoom plot showing the association of IL2RA to RA radiographic severity according to the zero portion of the zero-inflated negative binomial model. (E) Locus zoom plot showing the association of TRAF1-C5 found to be associated with RA radiographic severity according to the zero portion of the zero-inflated negative binomial model. (F) Locus zoom plot showing the association of NALCN/ITGBL1 to RA radiographic severity. The marker density in this region is low, making it difficult to assess how much support this SNP has from surrounding SNPs in LD.