

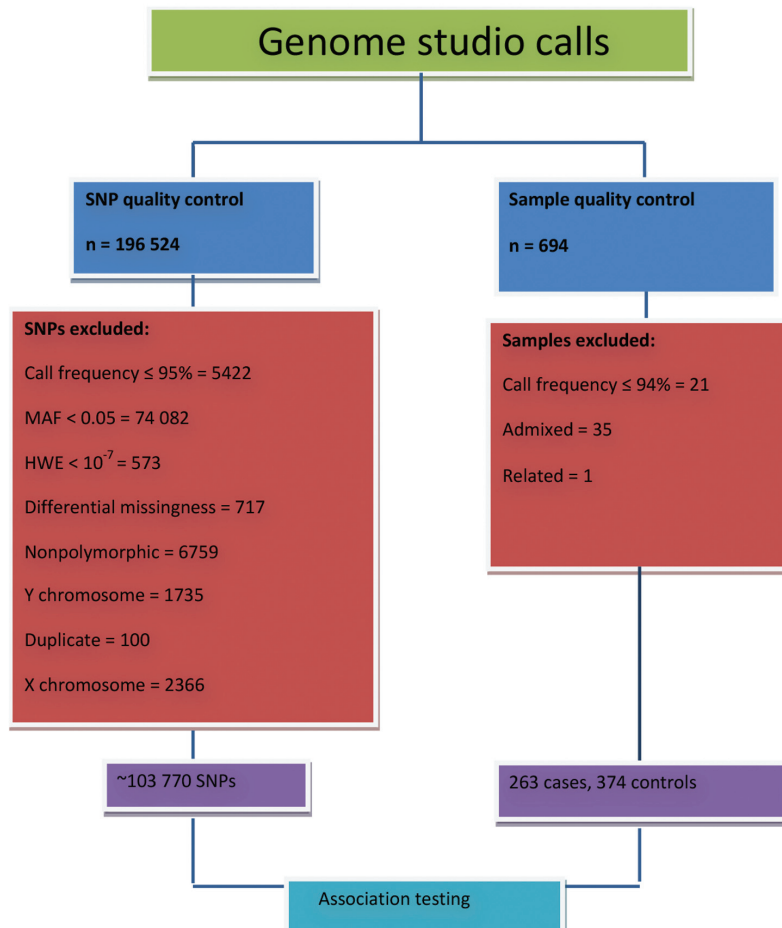
Supplemental Data

ImmunoChip Identifies Novel, and Replicates Known, Genetic Risk Loci for Rheumatoid Arthritis in Black South Africans

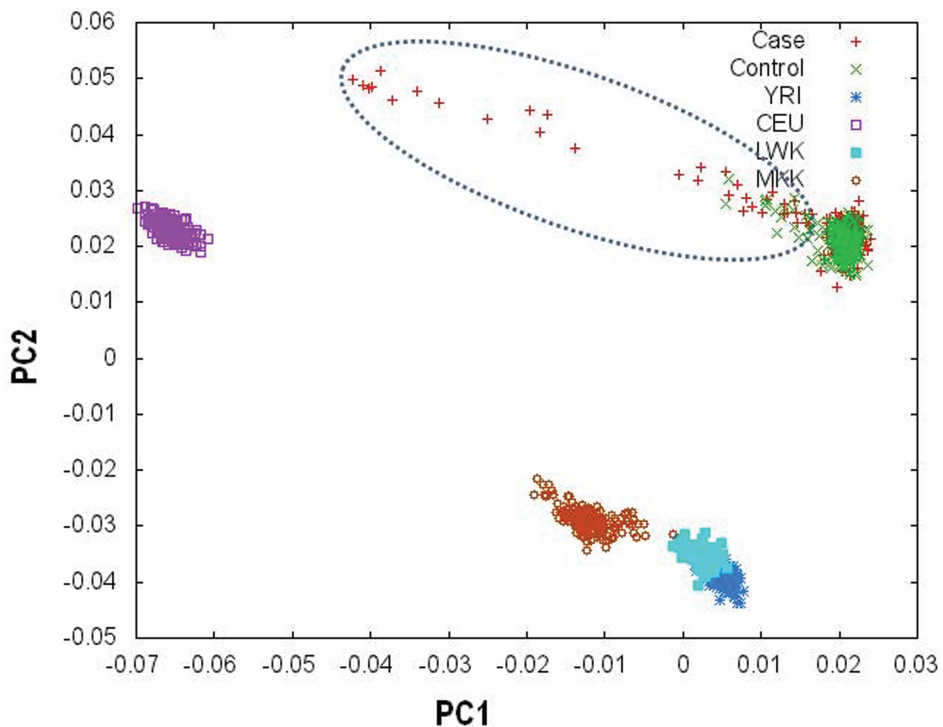
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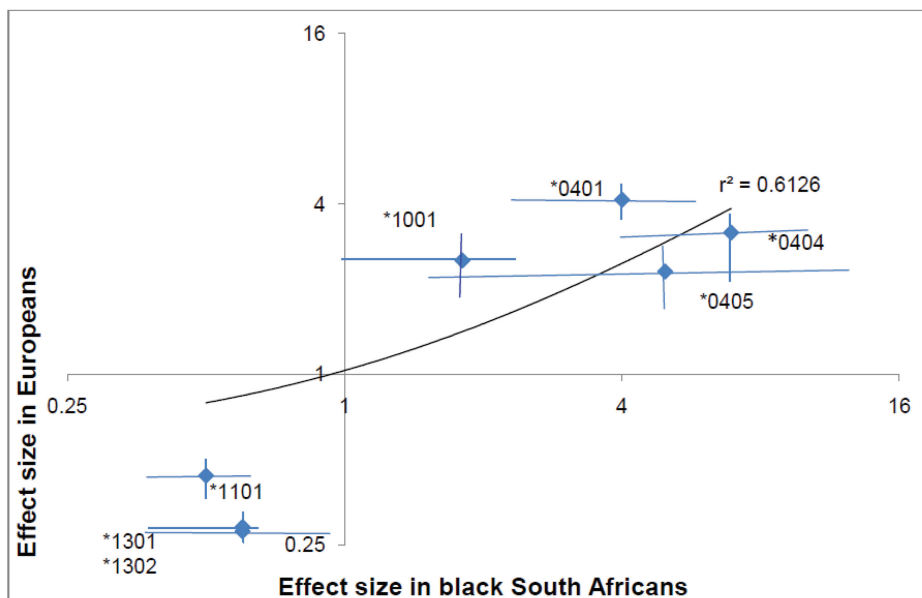
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Supplementary Figure S1. Flow diagram of quality control summarizing the SNPs and samples that survived the QC procedures.



**Supplementary Figure S2.** Principle component (PC) analyses plot showing the structure of black South African RA cases and controls in relation to CEU, YRI, LWK, MKK populations. The individuals with significant European admixture are circled. A total of 13 355 SNPs were used for the analysis.



**Supplementary Figure S3.** Comparison of classical *HLA-DRB1* allele effect sizes in Europeans and black South Africans. The odds ratios (OR) (and 95% confidence intervals) of only the significantly associated classical *HLA-DRB1* alleles in our study are plotted as a function of the reported odds ratios (and 95% confidence intervals) in Europeans (see van der Woude D, *et al.* (2010) Protection Against Anti-Citrullinated Protein Antibody-Positive Rheumatoid Arthritis Is Predominantly Associated With *HLA-DRB1*\*1301: A Meta-Analysis of *HLA-DRB1* Associations With Anti-Citrullinated Protein Antibody-Positive and Anti-Citrullinated Protein Antibody-Negative Rheumatoid Arthritis in Four European Populations. *Arthritis Rheum.* 62:1236–45).



A STUDY OF GENETIC VARIANTS ASSOCIATED WITH RA IN AN AFRICAN POPULATION

Supplementary Table S1. Significantly associated SNPs.

Gene	Number of significantly associated SNPs	Range of P values		Range of OR (95% CI)	Region
		Before*	After*		
<i>HLA-DQB1   DQA2</i>	39	2.33E-18 - 8.35E-8	<b>0.79 - 0.04</b>	3.90 - 0.49	Intergenic
<i>HLA-DRB1   DQA1</i>	14	4.08E-22 - 3.29E-8	<b>0.98 - 0.06</b>	4.18 - 0.47	Intergenic
<i>HLA-DRA   DRB5</i>	10	1.49E-20 - 1.49E-20	<b>0.38 - 0.007</b>	3.11 - 0.53	Intergenic
<i>HLA-DRA</i>	3	8.27E-9 - 1.18E-9	<b>0.94 - 0.17</b>	2.21 - 1.77	Intron
<i>BTNL2   HLA DRA</i>	7	4.55E-09 - 2.30E-9	<b>0.75 - 0.89</b>	0.52 - 0.50	Intergenic
<i>CCHCR1</i>	1	8.69E-8	<b>0.03</b>	1.80	Coding
<i>HLA-DRB5</i>	1	1.31E-25	<b>0.21</b>	6.15	Intron
<i>LOC442175   ZNF165</i>	1	1.64E-8	<b>0.19</b>	2.23	Intergenic
<i>PSMB9   HLA-DMB</i>	1	7.98E-10	<b>0.32</b>	7.79	Intergenic

OR=odds ratio, CI= confidence interval, \*Before and after conditioning on the HLA DRB1 alleles

Supplementary Table S2. SNPs that reached  $p < 5 \times 10^{-4}$ .

Chr	SNP	A1	MAF in cases	MAF in controls	A2	P value	OR (95% CI)	Gene	Region
1	rs6588249	A	0.15	0.22	G	0.00075	0.60 (0.45-0.81)	<i>IL23R</i>	Intron
2	rs36049530	G	0.27	0.37	A	0.000766	0.66 (0.51-0.84)	<i>IL18RAP   SLC9A4</i>	Intergenic
2	rs3917267	A	0.13	0.08	G	0.001066	1.82 (1.27-2.63)	<i>IL1R1</i>	Intron
2	rs871658	G	0.38	0.47	C	0.000461	0.67 (0.53-0.84)	<i>IL1R1</i>	Intron
2	rs13035227	G	0.37	0.48	A	0.000261	0.66 (0.52-0.82)	<i>LOC100131131   IL1R1</i>	Intergenic
2	rs6754776	G	0.37	0.48	C	0.000261	0.65 (0.52-0.82)	<i>LOC100131131   IL1R1</i>	Intergenic
2	rs13012334	G	0.22	0.32	A	0.000484	0.63 (0.48-0.81)	<i>IL1R2   LOC100131131</i>	Intergenic
2	rs62182630	A	0.19	0.27	G	0.000623	0.62 (0.45-0.80)	<i>CTLA4   ICOS</i>	Intergenic
2	rs13421616	A	0.09	0.15	G	0.000725	0.54 (0.48-0.68)	<i>CTLA4   ICOS</i>	Intergenic
4	rs6825116	A	0.45	0.35	C	0.000157	1.55 (1.23-1.95)	<i>LOC389203   RBPJ</i>	Intergenic
4	rs34185821	G	0.48	0.37	A	0.000158	1.55 (1.23-1.95)	<i>LOC389203   RBPJ</i>	Intergenic
4	rs10517086	A	0.48	0.38	G	0.000172	1.54 (1.23-1.94)	<i>LOC389203   RBPJ</i>	Intergenic
4	rs6448432	A	0.52	0.41	G	0.000176	1.54 (1.23-1.94)	<i>LOC389203   RBPJ</i>	Intergenic
4	rs7668577	C	0.53	0.42	A	0.000194	1.53 (1.22-1.92)	<i>LOC389203   RBPJ</i>	Intergenic
4	rs35944082	G	0.46	0.36	A	0.000223	1.54 (1.22-1.93)	<i>LOC389203   RBPJ</i>	Intergenic
4	rs17630466	G	0.467	0.37	A	0.000342	1.51 (1.22-1.68)	<i>LOC389203   RBPJ</i>	Intergenic
4	rs6822921	A	0.42	0.52	G	0.000512	0.67 (0.52-0.88)	<i>LOC389203   RBPJ</i>	Intergenic
6	rs62434218	A	0.51	0.42	G	0.000866	1.46 (1.28-1.58)	<i>TNFAIP3   PERP</i>	Intergenic
6	rs73778221	A	0.09	0.15	G	0.001034	0.55 (0.38-0.79)	<i>TNFAIP3   PERP</i>	Intergenic
6	rs73796835	A	0.24	0.17	G	0.000995	1.59 (1.44-1.69)	<i>RSPH3   TAGAP</i>	Intergenic

MAF=Minor allele frequency, OR=Odds Ratio