SUPPLEMENTARY DATA

SUPLLEMENTARY TABLE

	01	02	03	04	05	06	07	08	60	10	11	12	13	14	15	16	17	18	19	20	21	22	23	
Bantu	0 0 0 0 0 0 0 0 1 0 0 1 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	A A A G A A A G A A A G G A A A G G A A A G A A A G A A A G A A A G A A A G A A A G A A A G A A A G A A A G A A A G A A A G A A A G A A A G A A A G A A A G A A A A G A	T T T T T T T T T T T T T G G T T T T T	0 0 0 0 4 0 0 0 4 0 0 0 0 4 4 0 0 0 4 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	G G G G A G G G G G G G A G G G G A G	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	A A A A A A A A A A A A A A A A A A A	A A A A C A A A A A A A A A A A A A A A	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	G G G G G G G G G G G G G G G G G G G	A A A A A A A A A A A A A A A A A A A	ТТТТТТТТТСТТТТТТСТТТТТТ			G A G G A A A A A A A A A A A A A A A A	ТТТТТТТТТТТТТТТТТТТТТТТ	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	.302 .236 .083 .033 .031 .031 .021 .021 .021 .021 .012 .010 .010 .01
European	С С С Т С С С С С С С С С С С С С	T T T C T T T T T	G G G G A G G G G	00000000000000	0 0 0 0 0 0 0 0 0	T T T T T C T T T	T T T T T T C T T	G G G G G G A G	G A G G G G G G G	С С С С С С С С Т	G T G G G G G G G G													.854 .052 .021 .010 .010 .010 .010 .010 .010 .01

Supplementary Table 1. Predicted frequency of *IL23A* haplotypes detected within the Southern African Bantu and European populations.

SUPPELEMENTARY FIGURE



Figure S1. Intra-species sequence comparison of *IL23A*. Within the transcribed region of *IL23A*, the exonic regions are most highly conserved across the species. Eleven of the 44 vertebrates did not reveal a homologue for this gene. The UCSC Genome Browser (<u>http://genome.ucsc.edu</u>) was used to determine the sequence similarity of *IL23A* coding regions across 44 vertebrates, including 31 placental mammals, eight of which were primates.