Supplementary text

DNA sample populations

DNA samples were obtained from the NIGMS Human Genetic Cell Repository (CEU) or the NHGRI collection (all other samples) at the Coriell Institute for Medical Research. Samples were from the 1000 Genomes Project populations as follows: 61 African ancestry in Southwest USA (ASW), 85 Utah residents with Northern and Western European Ancestry from the CEPH collection (CEU), 97 Han Chinese in Beijing, China (CHB), 100 Han Chinese South (CHS), 60 Colombian in Medellin, Colombia (CLM), 93 Finnish in Finland (FIN), 89 British from England and Scotland, (GBR), 14 Iberian populations in Spain (IBS), 89 Japanese in Tokyo, Japan (JPT), 97 Luhya in Webuye, Kenya (LWK), 66 Mexican ancestry in Los Angeles, California (MXL), 55 Puerto Rican in Puerto Rico (PUR), 98 Toscans in Italy (TSI) and 88 Yoruba in Ibadan, Nigeria (YRI). An additional 113 International HapMap Project samples were genotyped, comprising of 53 CEU, 4 CHB, 5 JPT and 51 YRI samples not represented in the 1000 Genomes Project cohort.

FCGR3A-Sanger, FCGR3B-Sanger and FCGR3(A+B)-Sanger assays

Primers listed in Supplementary Table 1 (Supplementary digital content 4) were designed as follows: primers 1 and 4(FCGR3A-Sanger) were taken from Quartuccio *et al.*[3]. For primer 4(FCGR3B-Sanger), two base pairs at the 3' end of primer 4(FCGR3A-Sanger) were altered to match the *FCGR3B* sequence. Primers 2, 3 and 5 were designed using PrimerQuest software (Integrated DNA Technologies, San Diego, California, USA). PCR was performed on an Eppendorf Mastercycler ep 96 thermal cycler (Eppendorf, Hamburg, Germany). For the FCGR3A-Sanger and FCGR3B-Sanger assays, the PCR amplification programme initiated with 2 min of denaturation at 94°C followed by 10 cycles: 20 s at 94°C, 40 s gradient from 62°C to 57.5°C, 0.5°C decrement at each cycle, 1 min at 72°C, then 29 cycles as follows: 20 s at 94°C, 40 s at 57°C, 1 min at 72°C. Finally there was 5 min of elongation at 72°C. For the FCGR3(A+B)-Sanger assay, the PCR amplification programme was as follows: 10 min of denaturation at 95°C followed by 40 cycles: 15 s at 95°C and 1 min at 60°C.

The PCR reaction mix contained 25ng genomic DNA for the FCGR3A-Sanger and FCGR3(A+B)-Sanger assays, 50ng genomic DNA for the FCGR3B-Sanger assay, and 1U GoTaq polymerase (Promega, Madison, Wisconsin, USA), 0.25mM dNTPs, and 2.5pmol of each primer. Following PCR, direct Sanger sequencing was performed according to the manufacturer's protocol for BigDye Terminator Cycle Sequencing Kit v3.1 (Applied Biosystems, Foster City, California, USA) on an ABI 3730xl DNA Analyzer (Applied Biosystems). Data was analysed using Sequencher software (Gene Codes Corporation, Ann Arbor, Michigan, USA).

TaqMan genotyping

Five µl TaqMan reactions contained 1-20ng genomic DNA and were run on an Eppendorf MasterCycler ep 384; Life Technologies ViiA™ 7 Real-Time PCR System according to the manufacturer's instructions. The following cycling conditions were used: 95°C for 10 min followed by 40 cycles: 15 s at 95°C and 1 min at 60°C. Data was analyzed using ViiA™ 7 Software v1.2.1.