Table S1 Quality control criteria implemented on genotype data and the number of SNPs discarded at each step. This quality control was carried out as part of a larger study involving a total of 1342 samples.

Metric examined	**Purpose of metric applied**	**Threshold applied**	**Number of SNP removed at this stage**
Cluster separation[I]	Removal of SNPs with inadequately defined clusters	<0.25 discarded	1319
Call frequency	Removal of SNPs which were not called in a minimum number of samples	<98% call rate discarded	2380
AB R Mean[II]	Removal of SNPs with low intensity data	<0.15 discarded	7
AB T Mean[III]	Removal of SNPs for which the heterozygote cluster was not well separated from the homozygote clusters	<0.2 and >0.8 discarded	20
Heterozygote excess	Removal of SNPs which deviate significantly from Hardy-Weinberg equilibrium	Heterozygosity of <-0.3 and >0.1 discarded	149
ECAX markers	Removal of X chromosome markers for which the males were called heterozygous	Each marker assessed individually	20

[I]Measures the separation between the three genotype clusters and varies from 0 to 1

[II]Mean normalized intensity of the heterozygote cluster, with values increasing from 0

[III]Mean of the normalized theta values of the heterozygote cluster, with values ranging from 0-1. Values of <0.2 and >0.8 indicate that the heterozygote cluster has shifted towards the homozygotes.