	Number of patients	Number of markers
	537	655 216
Step 0. Remove poorly mapped markers and those w/o agreement between v1.0 and v1.1 and Will Rayner and Illumina	537	573 502
Step 1. Removal of individuals/SNPs with low call rate Keep individuals with call rate ≥ 90% and SNPs ≥ 90%	478	549 466
Step 2. Removal of individuals with discordant sex information Keep individuals with chromosome X homozygosity rate ≤ 20%	475	549 466
Step 3. Removal of individuals with excessive heterozygosity rate Keep individuals with heterozygosity rate ≤ 4 x S.D.	472	549 466
Step 4. Removal of related individuals Keep individuals with identity-by-descent ≤ 0.25	444	549 466
Step 5. Removal of population outliers Keep individuals within 4 x S.D. from the population structure cluster center mean	444	549 466
Step 6. Removal of rare and non-HWE markers Keep SNPs with MAF ≥ 1% and follow Hardy-Weinberg Equilibrium (p-value < 5 x 10^{-6})	444	528 461