|  |  |  |  |
| --- | --- | --- | --- |
| StepNumber | Criteria |  | SNP Failure Determination  |
| 1 | Illumina GenTrain Score |  | < 0.6  |
| 2 | Illumina Cluster Separation Score |  | < 0.4  |
| 3 | Call Rate |  | < 0.95  |
| 4 | Mendelian Errors in YRI |  | > 1 (out of 30 trios)  |
| 5 | Replication Errors |  | > 2  |
| 6 | Hardy-Weinberg Equilibrium p-value |  | < 1 × 10-6  |
| 7 | Discordant calls from GWAS arrays on overlapping samples |  | > 10% |
| 8 | Discordant calls on YRI: across studies |  | > 3 (out of 90 samples)  |
| 9 | Discordant calls from GenoSNP |  | > 3.3%  |
| 10 | Discordant calls on YRI:PAGE consensus versus HapMap database |  | > 3 (out of 90 samples)  |
|  |

**Supporting Information Table S3:** SNP quality control criteria. GenTrain and cluster separation scores are Illumina-provided genotype metrics. SNPs that failed only for GenTrain or cluster separation scores at only one site and passed a manual inspection were classified as passing. Otherwise, SNPs failing any criterion for any one study were classified as failed across PAGE.