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| --- | --- | --- | --- |
| Step  Number | 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.