**Table S1.** SNP Exclusions and Number of Analyzed SNPs

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Affymetrix 10K 2.0 Array** | | **Illumina Infinium Linkage 12 Bead Array** | |
|  | **Excluded** | **Remaining** | **Excluded** | **Remaining** |
| Total N on array | --- | 10,204 | --- | 6,090 |
| Unknown genetic positiona | 114 | 10,090 | 33 | 6,057 |
| Call rate < 95% | 686 | 9,404 | 390 | 5,667 |
| MAFb < 1% | 366 | 9,038 | 11 | 5,656 |
| HWEc p-value < 0.001 | 13 | 9,025 | 4 | 5,652 |
| Duplicate concordance < 95% | 6 | 9,019 | 4 | 5,648 |
| Mendelian errors in 2% of families | 4 | 9,015 | 0 | 5,648 |
| LDd at r2 ≥ 0.1 | 3,435 | 5,580 | 1,057 | 4,591 |
| **Final Unique SNPs combined** e**: 10,091** |  |  |  |  |

a NCBI Build 36.3

b Minor allele frequency

c Hardy-Weinberg equilibrium

d Linkage disequilibrium

e An overlapping 80 SNPs in both arrays were included regardless of LD, thus the total of unique SNPs is 80 less than the sum of SNPs remaining in each array.