

Table S3. The MAF for SNPs selected for genotyping in each region based on HapMap R27 CHB.

| | Coding, 3' UTR and Promoter | Intron |
|---------|--------------------------------|--------|
| MAF >5 | 331 | 323 |
| MAF <5 | 129 | 74 |
| MAF =0 | 201 | 2 |
| Unknown | 467 | 23 |