## Results of re-genotyping of flagged SNPs

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| --- | --- | --- | --- | --- | --- |
| SNP | Maj/Min | MAF\* | FST(SL-STU) | Re-genotyping | Action |
| Sinha | Tamils | Moors | STU | Method | Total n†(n successful) | Result |
| rs12233719  | A/C | 0 | 0 | 0 | 0.995 | 0.993 | Seq | 10 (10) | All GG | Amend genotypes to CC  |
| rs6824108  | G/A | 0 | 0 | 0 | 0.908 | 0.948 | Seq | 10 (9) | Discordant(2 CT, 7 TT) | Exclude  |
| rs4148434  | A/G | 0 | 0 | 0 | 0.691 | 0.627 | Taqman | 125 (118) | Discordant(55CC, 53CT, 10TT) | Exclude original data but use MAF from Taqman  |
| rs1292096  | G/A | 0 | 0 | 0 | 0.221 | 0.175 | Taqman | 125 (117) | Discordant(69GG, 36GA, 10AA) | Exclude original data but use MAF from Taqman |
| rs429358  | A/G | 0 | 0 | 0 | 0.132 | 0.102 | Taqman | 125 (115) | Discordant(95TT, 18CT, 2CC) | Exclude original data but use MAF from Taqman  |
| rs609290  | G/A | 0.102 | 0.097 | 0.039 | 0.270 | 0.066 | Taqman | 125 (119) | Concordant | Keep  |

Maj: major allele, Min: minor allele, MAF: minor allele frequency, Sinha: Sinhalese, Seq: Sanger sequencing

\*MAF from dataset after merging, †rs12233719 and rs6824108 were suspected to be allele flips and thus only 10 random Sri Lankan (SL) samples were chosen for sequencing. The other 4 SNPs were genotyped by Taqman in 125 SL samples with DNA remaining. rs6824108 was excluded from all analyses. rs4148434, rs1292096 and rs429358 were excluded from PCA and STRUCTURE analyses but MAF from Taqman genotyping included for FST analyses (see Supplemental Digital Content 1).