



**Concordance between MAF in SGVP CHS and 1000 genomes CHS after merging SGVP and 1000 genomes datasets**

This plot shows the correlation of minor allele frequencies (MAF) in SGVP CHS and 1000 genomes CHS, who are expected to be genetically similar to SGVP CHS. 7 SNPs with substantially different MAFs (circled in red) were removed (see Supplemental Digital Content 1).