

Identification and characterization of *SEC24D* as a susceptibility gene for hepatitis B virus infection

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Code and parameter setting for bioinformatics analysis:

In the replication stage, association of SNPs with HBV infection was performed under an additive genetic model using PLINK (v.1.07) with age, sex and the first five PCs as covariates. The input parameters used in current study as following:

```
nohup plink --bfile HBV_infection_file --pheno HBV_phenotype --pheno-name  
HBV_infection --geno 0.05 --mind 0.05 --noweb --logistic --covar  
covariate_phenotype_file --covar-name age, sex, PC1, PC2, PC3, PC4, PC5  
--nonfounders --maf 0.05 --hwe 0.000001 --adjust --out results_HBV_infections &
```

The population admixture of samples was assessed by PC analysis (PCA) as implemented in EIGENSTRAT. The input parameters used in current study as following:

```
nohup smartpca.perl -i HBV_infection_file.bed -a HBV_infection_file.bim -b  
HBV_infection_file.fam -o HBV_infection_file.pca -p HBV_infection_file.pca.plot -e  
HBV_infection_file.pca.eval -l HBV_infection_file.pca.log -k 10 -s 10 -m 0 &
```