

Figure S1

Step	1st	2nd		3rd
Variant type	SNP	indel, SNP, STR	indel, SNP, STR	indel, SNP, STR
Data type	cross-sectional	cross-sectional	cross-sectional	longitudinal
Phenotype	dichotomous traits	means of proportions	dichotomous traits	dichotomous traits, quantitative traits
Statistical tool	chi-square test	descriptive statistics	Fisher's exact test	quasipoisson regression model
Program	PLINK ¹	NA	R ²	R ²
Use given in the present study	extensive exploratory method used for subphenotype selection	exploratory method to detect statistical tendencies	exploratory method to detect statistical tendencies	offered higher statistical power than allowed by the analysis of dichotomous traits and allowed the prediction of correlated dependent variables

¹ Open-source whole genome association analysis toolset PLINK v1.07 program (Purcell et al., 2007).

² R Core Team. R: A language and environment for statistical computing (Team, R.C., 2013).