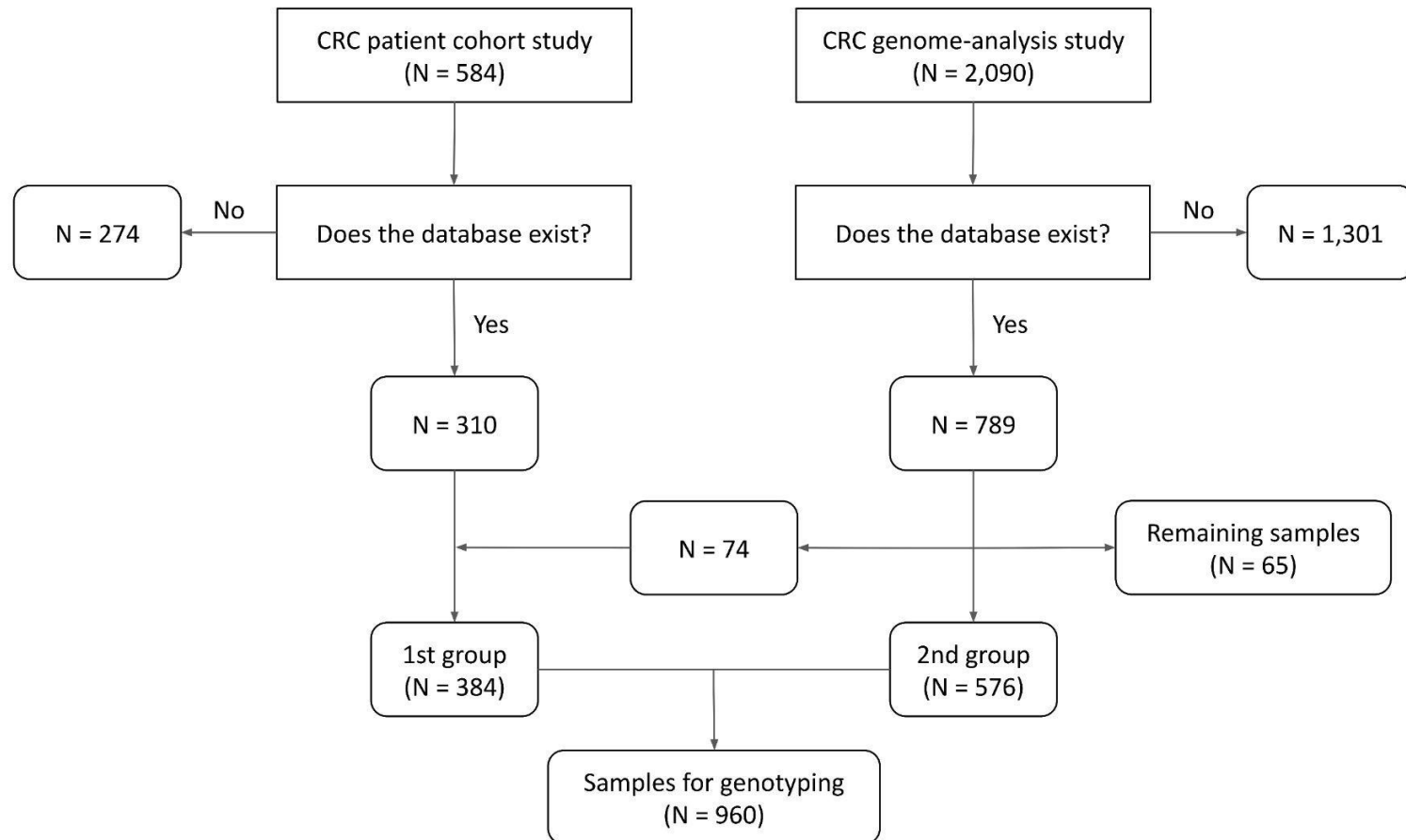


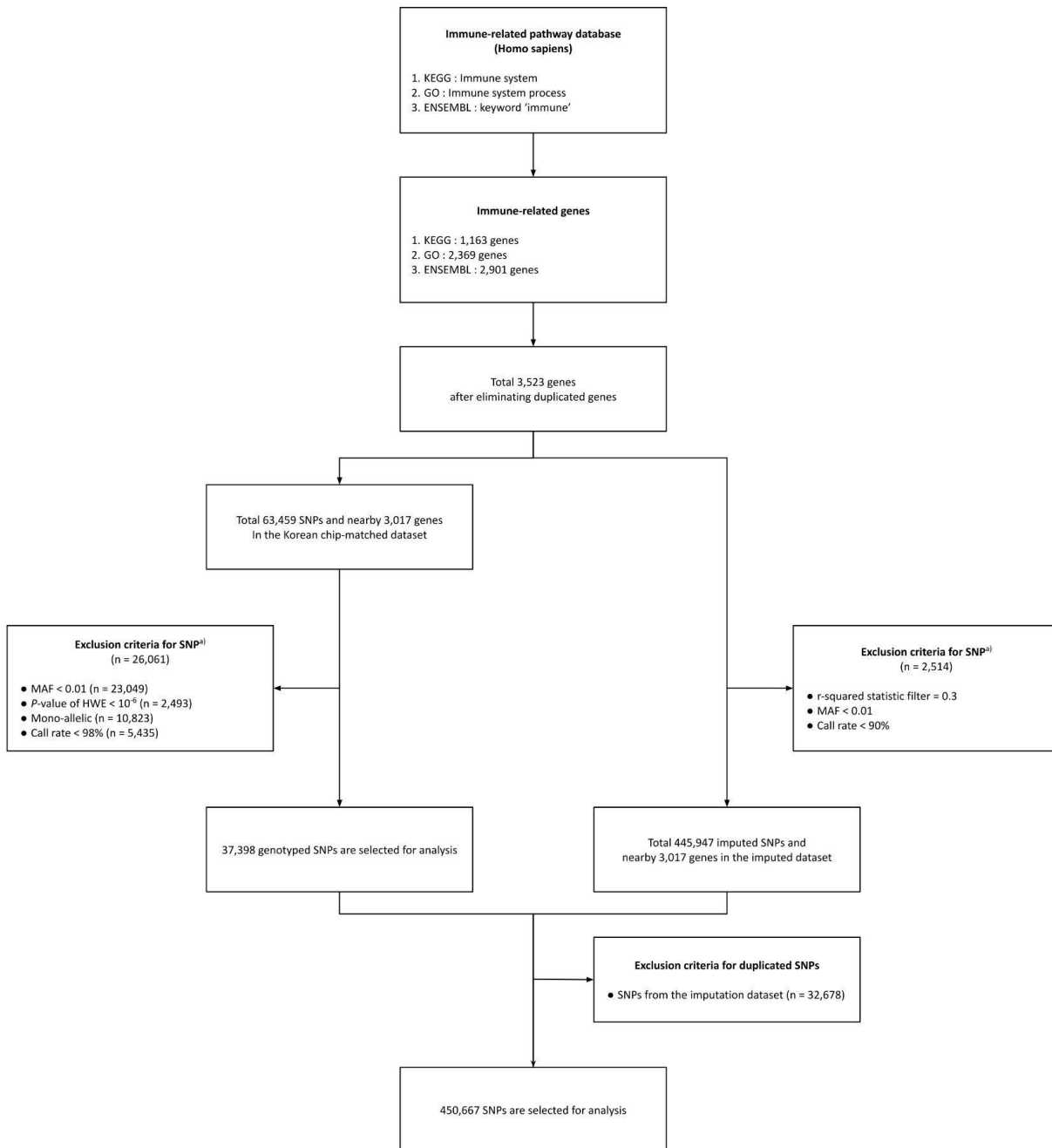
Supplementary figure 1. Flowchart of study population selection.



Supplementary figure 2. VIF estimation to detect multicollinearity of potential confoundings.

Histologic grade					1.350784
Tumor location				1.035217	1.035217
BMI			1.006136	1.039823	1.036032
Age		1.012955	1.006139	1.039838	1.049150
Sex	1.002695	1.013152	1.006602	1.040305	1.050939
	Age	BMI	Tumor location	Histologic grade	Stage

Supplementary figure 3. Flowchart of gene and SNP selection.



a) Total numbers of excluded SNPs are not mutually exclusive for each criteria.

Supplementary figure 4. The formula to calculate PRS.

$$\text{PRS}_j = \frac{\sum_{i=1}^N \beta_i \times \text{dosage}_{ij}}{P \times M_j}$$

β_i : the effect size of SNP i ($i \in 1, 2, 3, \dots, N$),

dosage_{ij} : the allelic dosage of the effect allele in SNP i for individual j ,

P : the ploidy (2 for humans; diploid),

M_j : the number of non-missing SNPs in individual j)