GWAS summary statistics and SNP weights for polygenic score calculation

From *Wu et al. 150 risk variants for diverticular disease of intestine prioritise cell-types and enable polygenic prediction of disease susceptibility. Cell Genomics, 2023*

Below is a description of the GWAS summary statistics for the diverticular disease (DivD) of intestine and corresponding age of onset (AgeO) and SNP weights of DivD for polygenic score calculation.

The GWAS summary statistics for DivD and AgeO were generated based on individuals of European ancestry (short as **DivD-EUR** and **AgeO-EUR**). Please refer to the original study above for detailed information.

The GWAS summary statistics are in COJO format:
1. SNP: rsID or positional SNP identifier
2. A1: Effect allele
3. A2: Other allele
4. freq: Allele frequency of A1
5. b: Effect size for A1
6. se: standard error for A1
7. p: P-value from association test
8. N: Number of individuals

The SNP weights of DivD-EUR for polygenic score calculation are in the following format (Please refer to the original study above for detailed information):
1. SNP: rsID
2. CHR: Chromosome
3. BP: Base pair position
4. A1: Effect allele
5. A1Freq: Allele frequency of A1
6. A1Efect: Weights for A1

Any query please email Yeda Wu (yeda.wu@uq.connect.edu.au).

Below is a graphic abstract from the study above created by Yeda Wu for your pleasure.