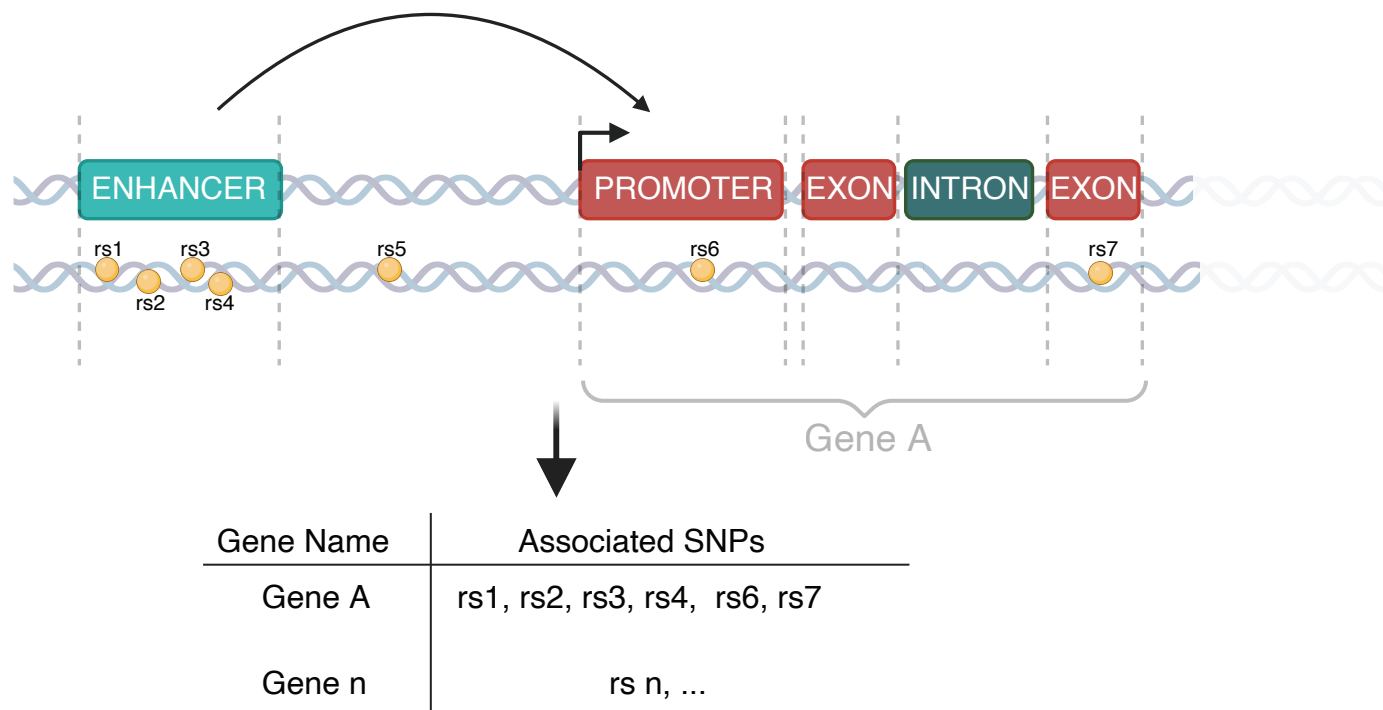


**H-MAGMA (HiC - Multi-marker Analysis of GenoMic Annotation) workflow:**

**STEP 1. Annotation: cell type-derived chromatin interaction data.**  
(in this case promoter-enhancer interaction data)



**STEP 2: Gene analysis using MAGMA software:** Testing association of genes with phenotype by using SNP-wise Mean model using SNP-level p-values from **GWAS summary statistics**

Gene Name	Gene-level P-value
Gene A	p-value
Gene n	p-value