A list of RSIDs was extracted from each GWAS study and saved in unique CSVs. These files are inputted into the program and data from dbSNP and Ensemble are retrieved. For each input RSID the following data was retrieved from dbSNP: Merged RSIDs, Merged Dates, Locus, Name, Orientation, Sequence Ontology, and Clinical Significance.

Gene Length, GRCh37 position, and GRCh38 position.