Acquired aplastic anemia (AA) is an autoimmune disorder characterized by bone marrow failure and the potential for progression to myelodysplastic syndromes (MDS) or acute myeloid leukemia (AML) in ~15% of patients. Although rare genetic variants in AA have not been extensively studied in the past, evidence suggests they could play a role in the disease's pathogenesis. This study developed a robust pipeline for analyzing whole exome sequencing data with public controls (gnomAD summary counts). Variant calling, variant quality control and filtering procedures are based on GATK best practices. Ethnicity-stratified rare variant association tests were implemented though accurate estimating inflation factors and modeling linkage disequilibrium. We identified FLG2, GPRC6A, and ABCB5 as the top three genes in our preliminary list of rare variant associations with AA. While the pipeline was effective in processing raw sequencing data and performing association analysis, the study's conclusions are limited by the small dataset and the lack of in-depth genetic analyses, which are planned for future research. Moving forward, expanding the dataset, and performing functional studies will be crucial for validating these variants and exploring their roles in AA.