

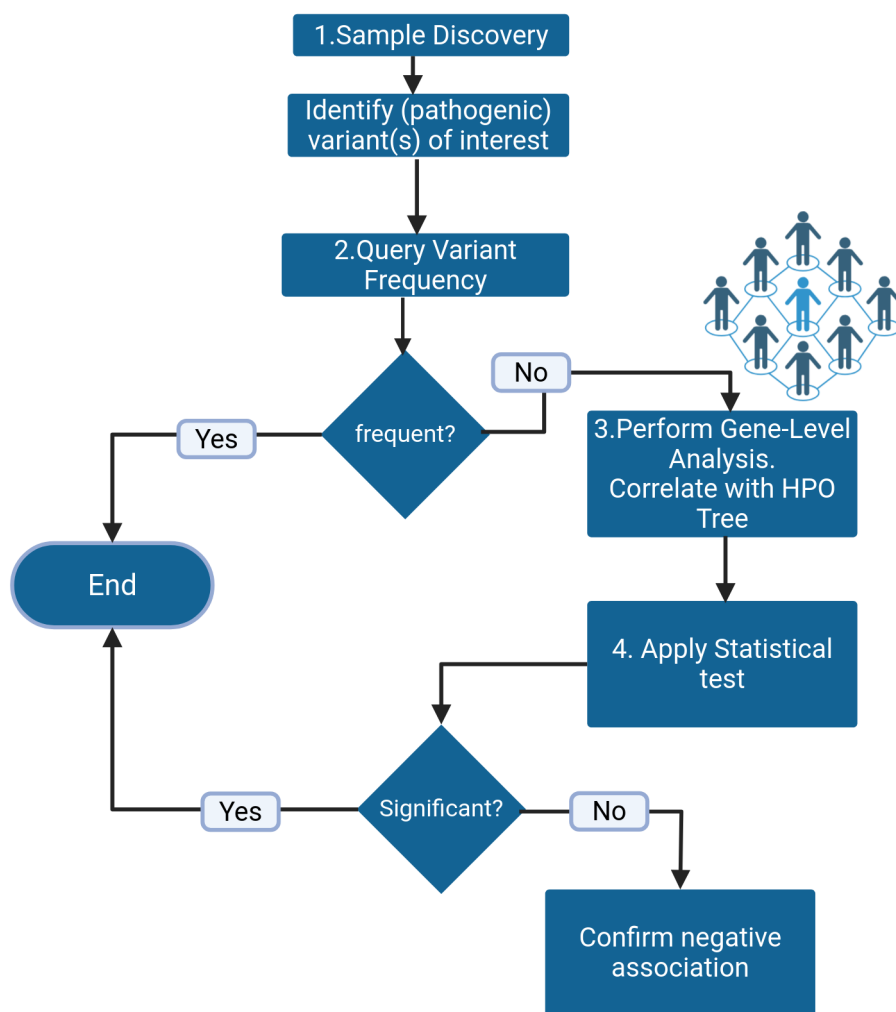


Fig. S3. Workflow for the use case - (Multi-Center) Data Analysis to assign VUS as benign

Description of the variant analysis workflow. 1. sample-level filtering to identify candidate pathogenic variants. 2. variant frequency 3. genotype–phenotype association on the *PUF60* variant to evaluate correlation with intellectual disability. 4. statistical test to assess significance.