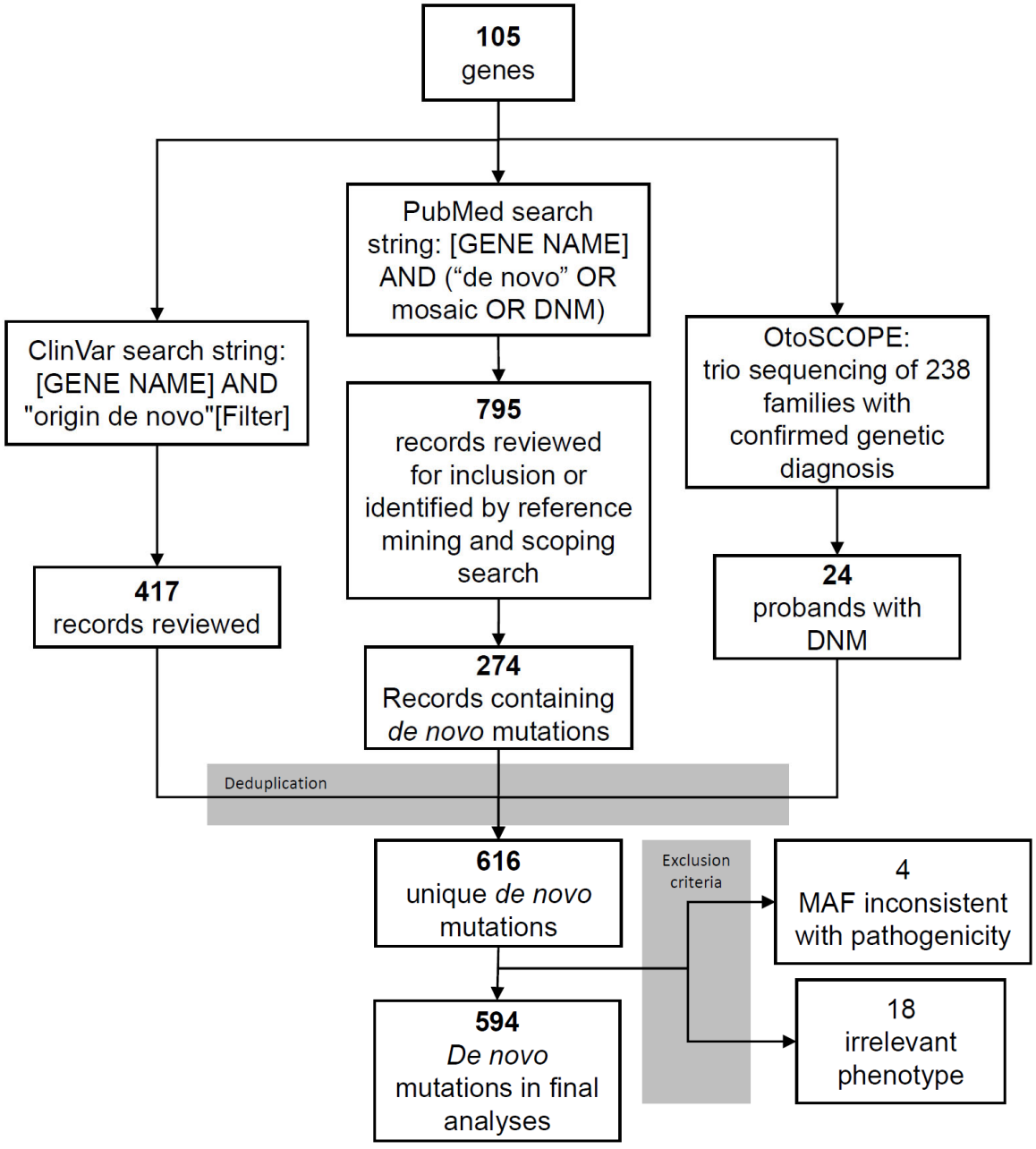

Supplementary Figure S1. Summary of the review strategy. 105 genes encompassing common and rare ARNSHL, ARSHL, ADNSHL, ADSHL, and XLHL genes were selected for comprehensive review of *de novo* mutations (DNMs) reported in the PubMed and ClinVar databases. A systematic search string was created for the PubMed and ClinVar databases. Large genomic deletions encompassing multiple genes, DNMs with clearly irrelevant phenotypes, and DNMs with MAF inconsistent with pathogenicity were excluded from analysis.