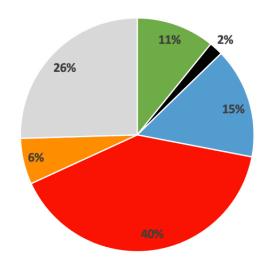
Supplementary Figure 1

A B

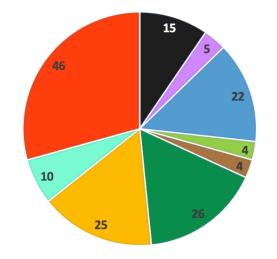
DISTRIBUTION OF ALL 157 HL VARIANTS IN THIS STUDY





DISTRIBUTION OF VARIANTS BY GENE

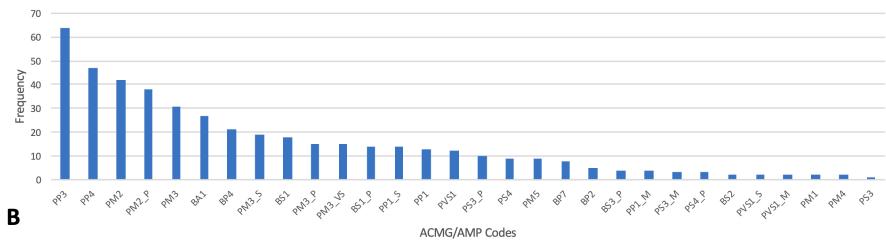




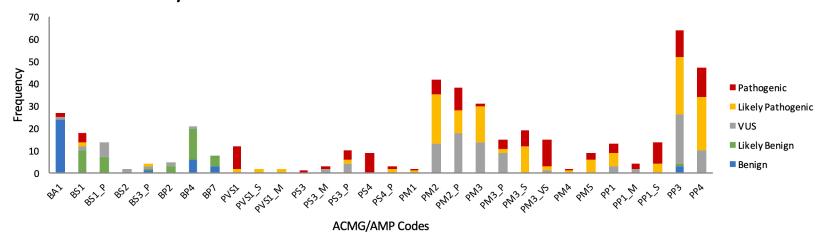
Supplementary Figure 2



Α



ACMG/AMP Code Contribution Towards the HL VCEP Final Classification



Supplementary Figure 1. *A*, Distribution of all 157 variants by conflict type. *B*, Distribution of variant by gene. VUS, Variant of Uncertain Significance; B, Benign; LB, Likely Benign; P, Pathogenic; LP, Likely Pathogenic.

Supplementary Figure 2. Usage (A) and contribution (B) of the different ACMG/AMP codes, specified by the HL EP, to the final variant classification.