



**Figure S1.** Distribution of Unique and Reported MEVs based on MAF. Compared to the reported coding variants, a larger proportion of the unique variants were singletons. Unique coding variants = Variants not reported in gnomAD 2.1.1 Exomes. Reported coding variants = Variants reported at least once gnomAD 2.1.1 Exomes. Singletons = single alleles observed in only one individual in the MEV dataset.