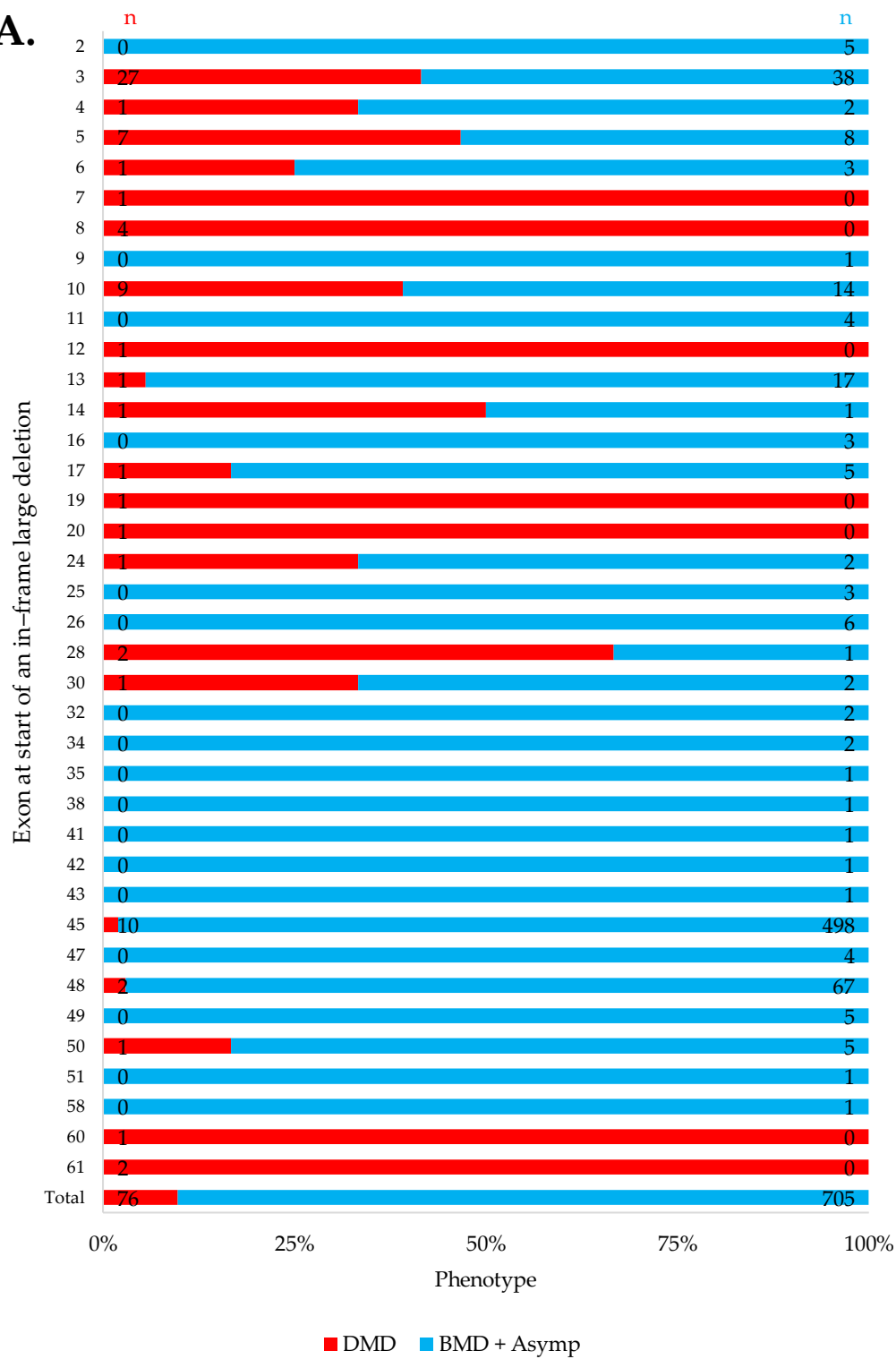
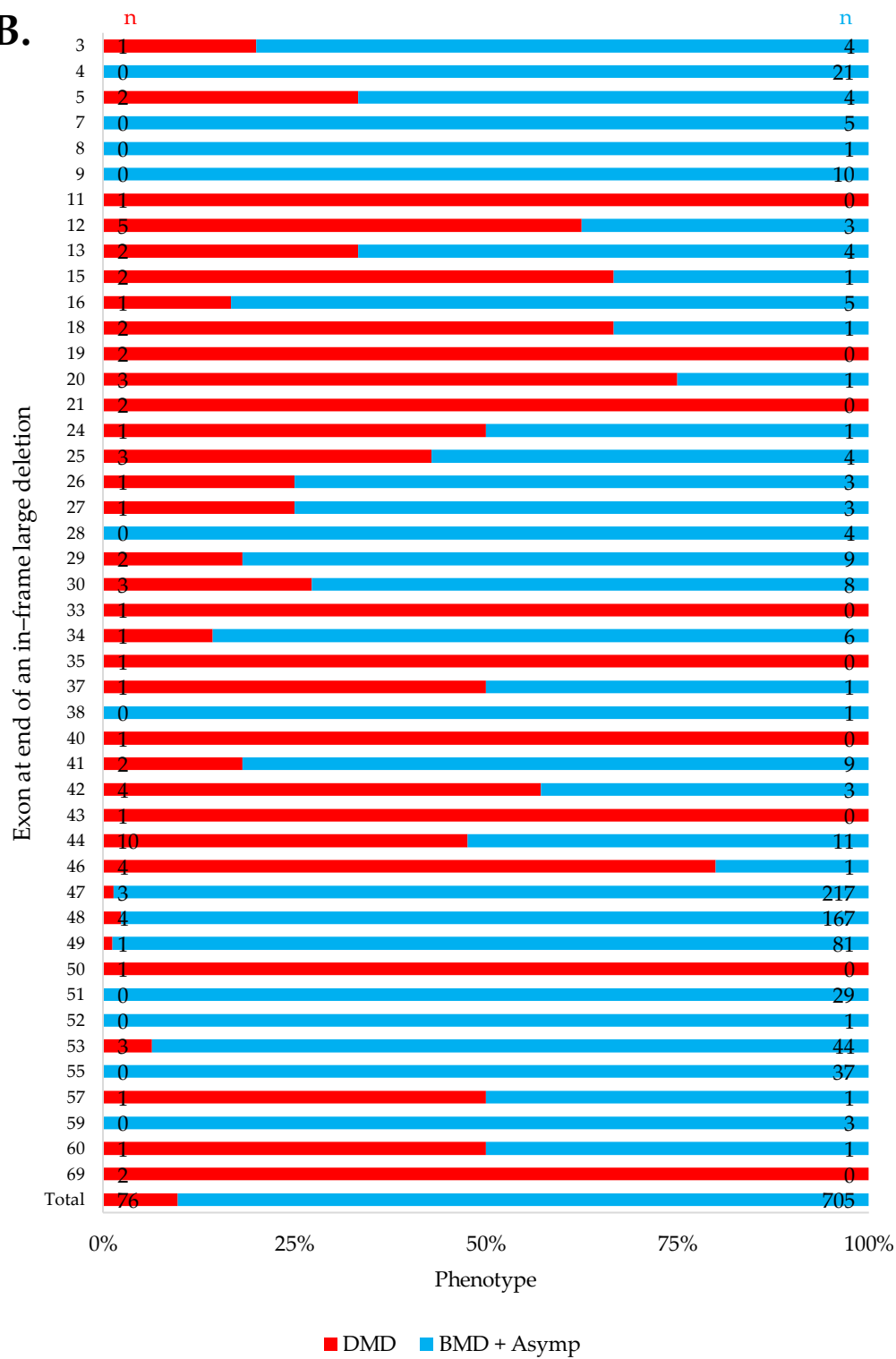
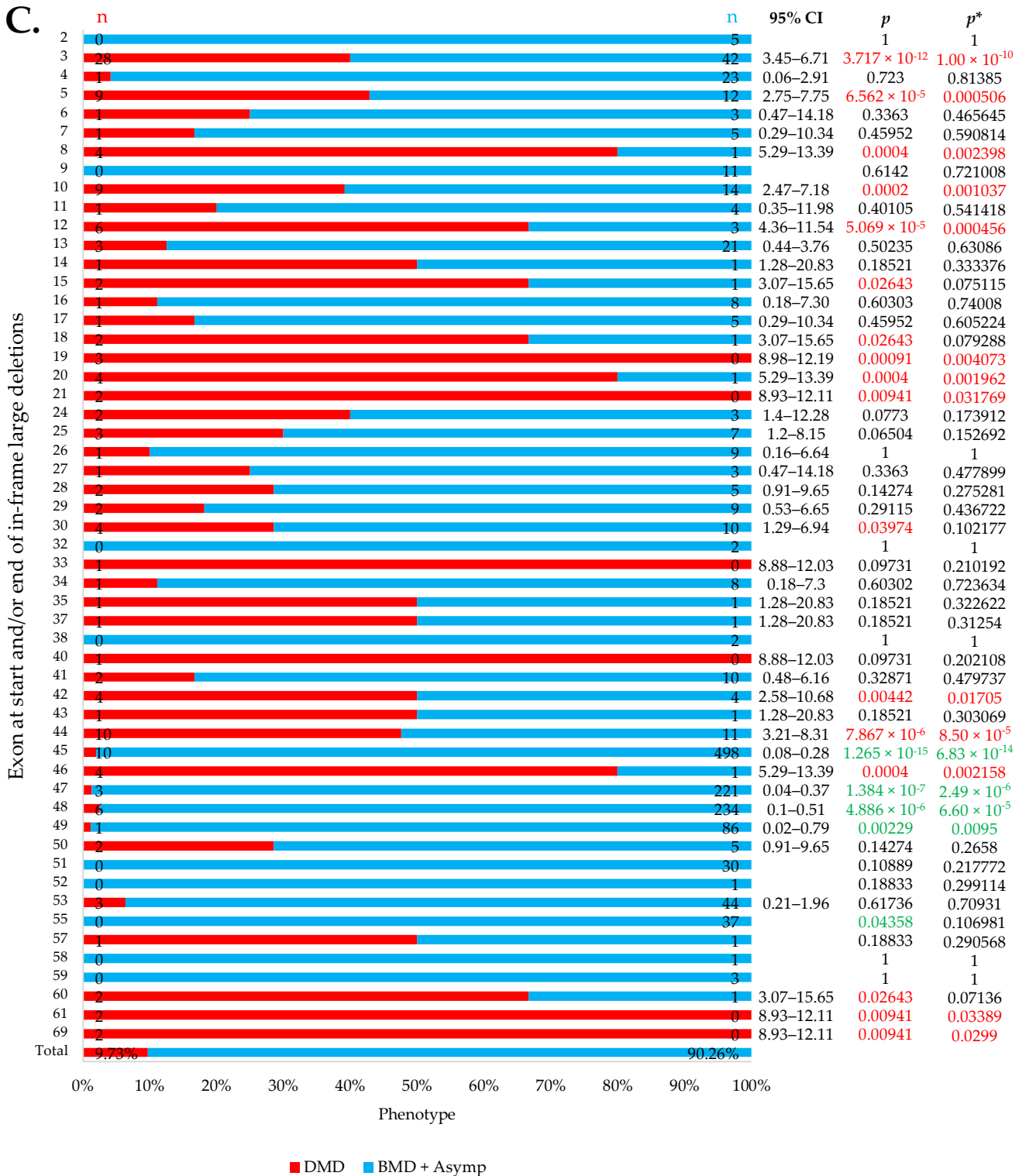


A.



B.





**Figure S4.** Association between in-frame deletions (A) starting, (B) ending, and (C) starting and/or ending at each exon and consequent phenotypes in the eDystrophin database. Phenotypic ratios associated with in-frame deletions starting and/or ending at a given exon and all other exons were compared using a two-tailed Fisher's exact test. n indicates the number of individuals with DMD (red) and milder (blue; BMD and asymptomatic) phenotypes. Green and red asterisks indicate a significantly lower and higher incidence of DMD phenotype, respectively.  $p$  =  $p$ -value, as calculated by Fisher's exact test;  $p^*$  = Benjamini–Hochberg adjusted  $p$ -value.