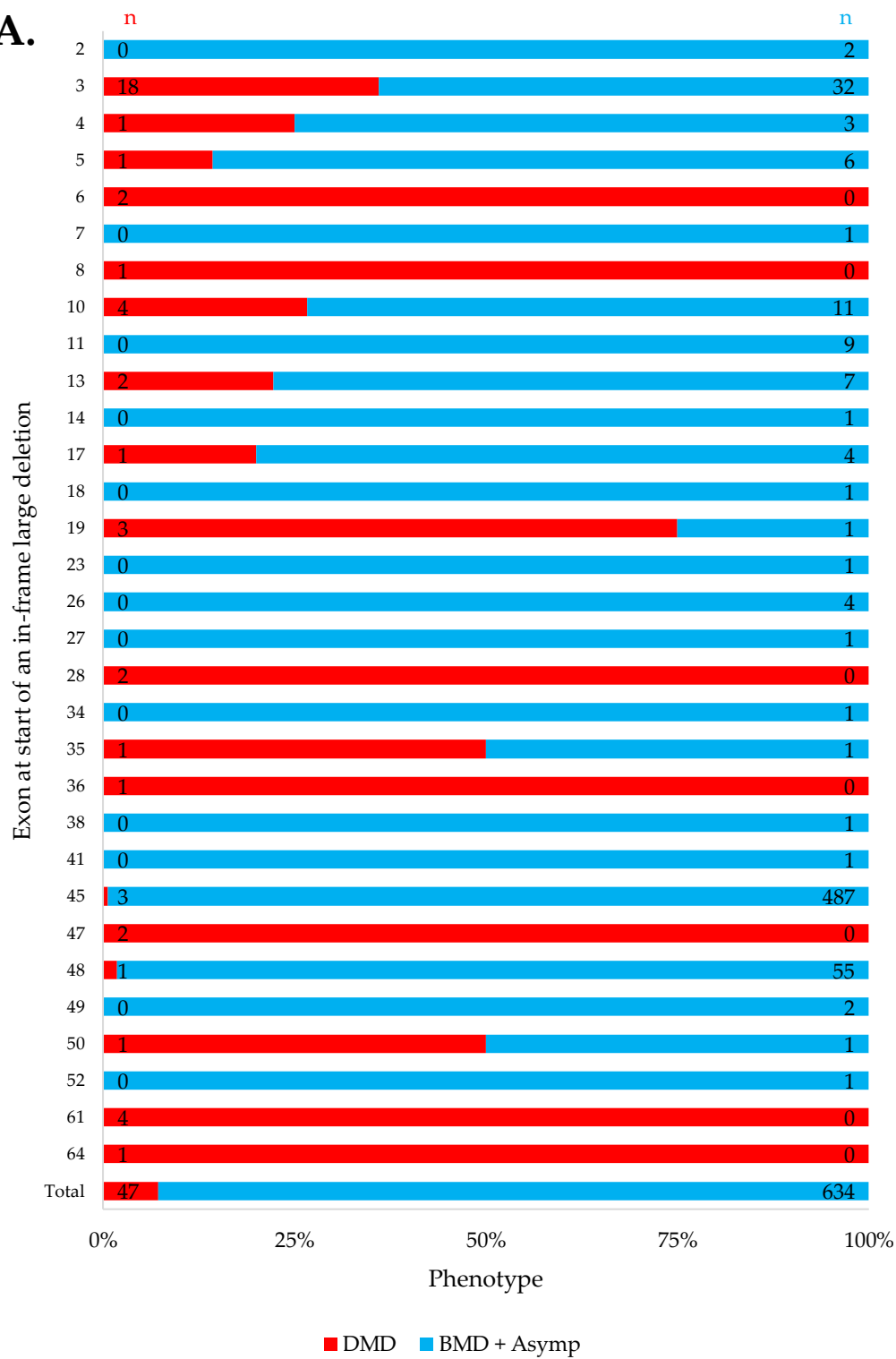
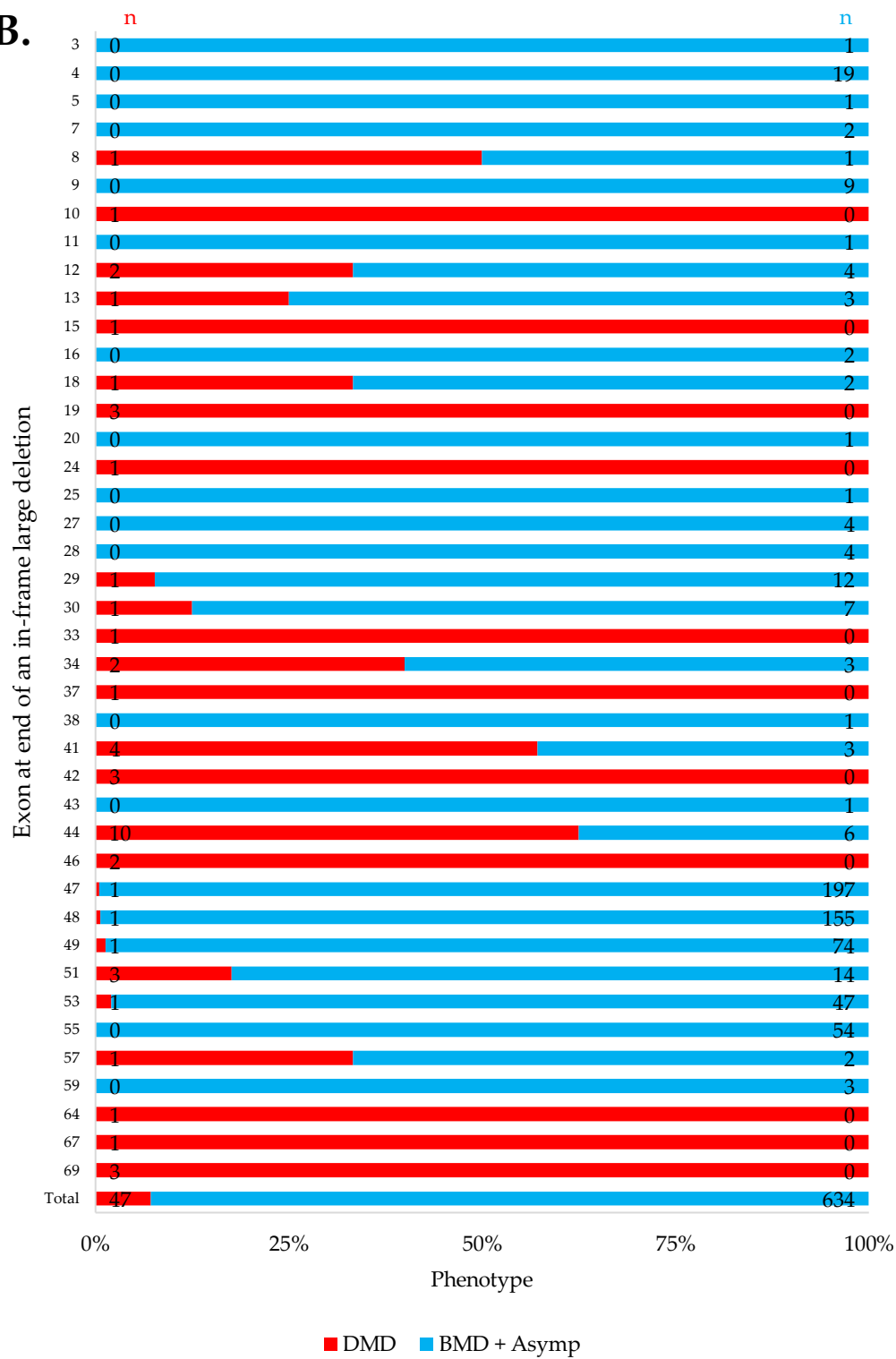


A.



B.



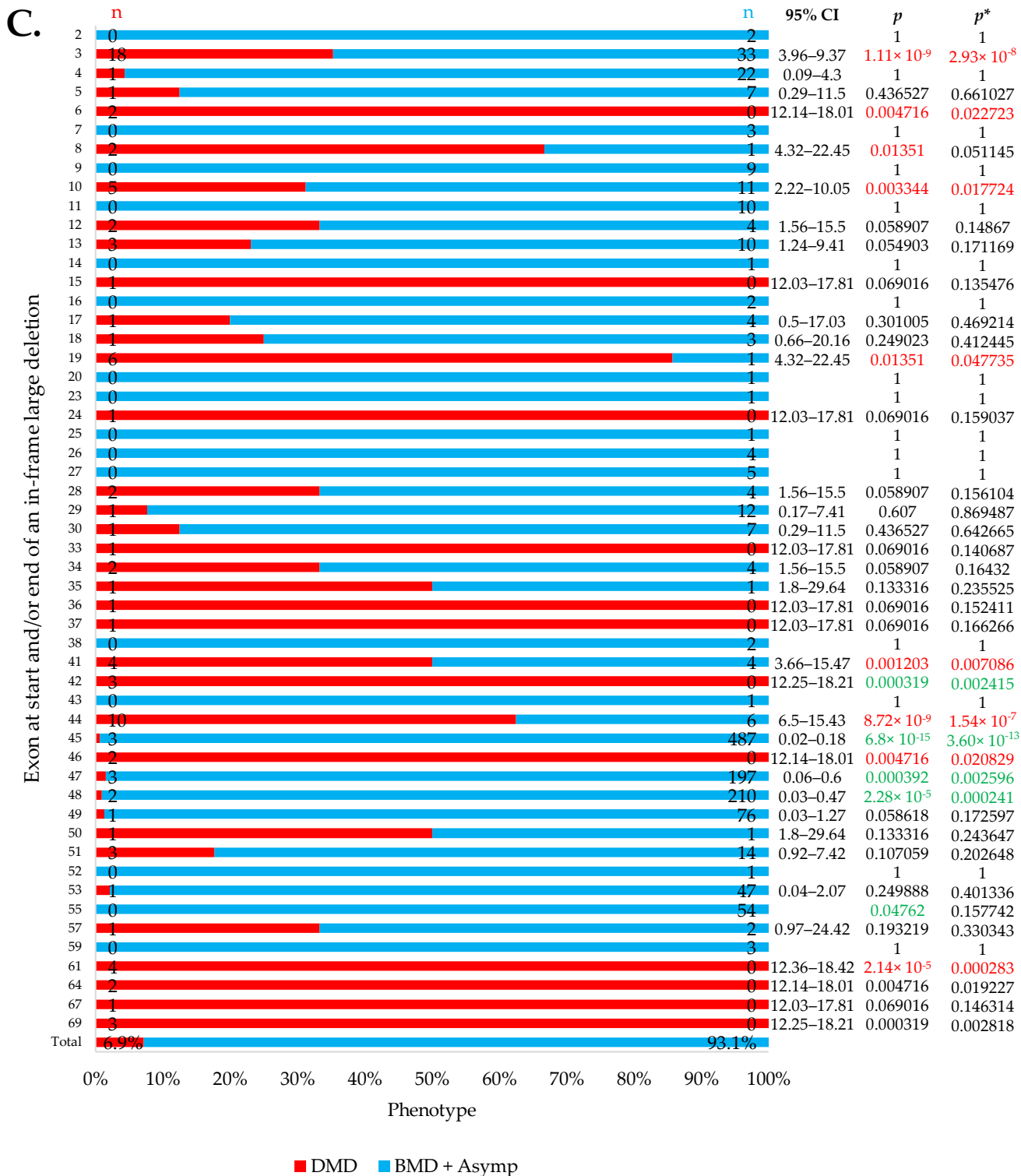


Figure S5. Association between in-frame deletions (A) starting, (B) ending, and (C) starting and/or ending at each exon and consequent phenotypes in the UMD-DMD France database. Phenotypic ratios associated with in-frame deletions starting and/or ending at a given exon and all other exons were compared 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.