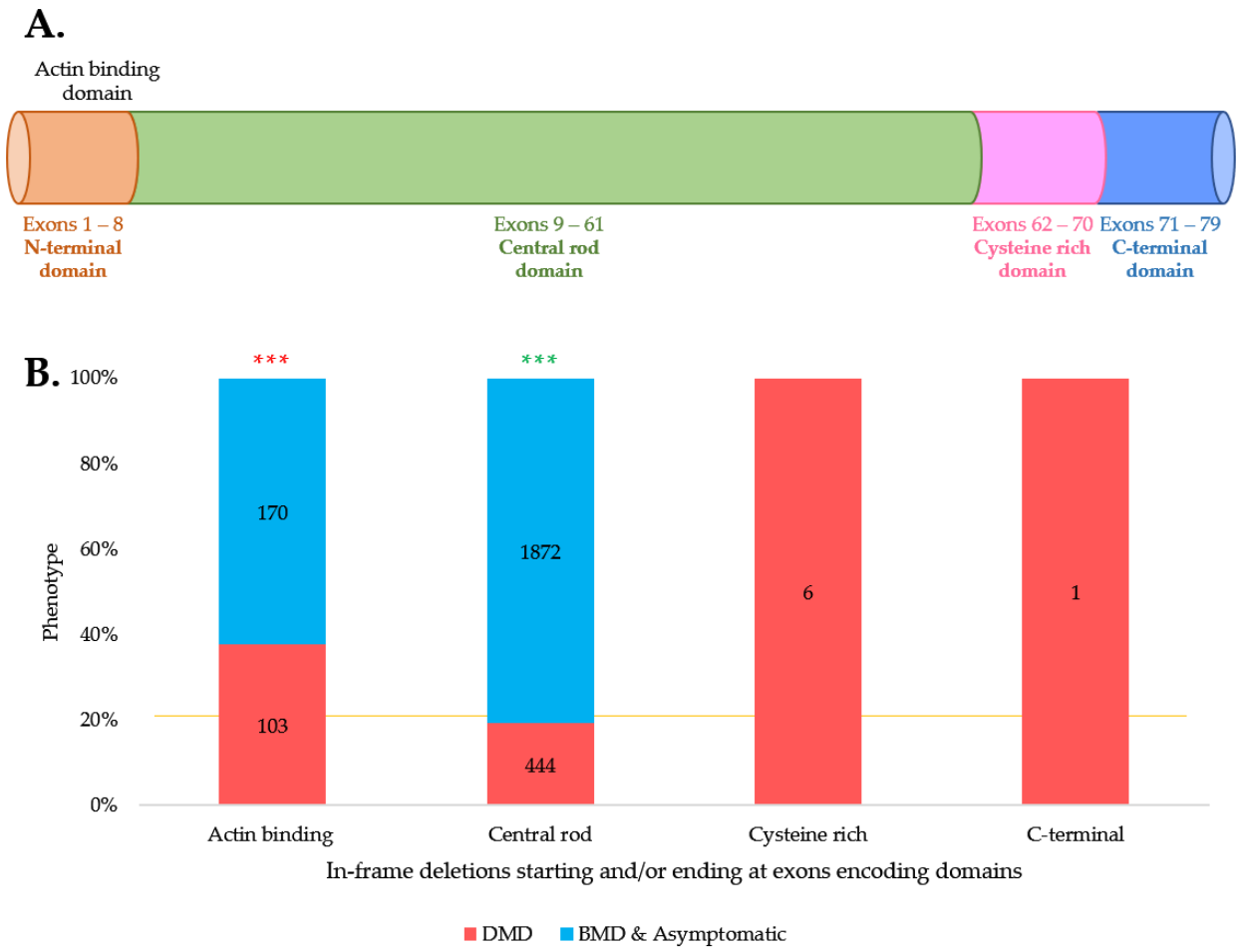

Figure S7. Overview of clinical phenotypes associated with in-frame deletions starting and/or ending at different exons and their corresponding dystrophin domains. **(A)** Schematic illustration of dystrophin of domains and the exons encoding those domains [1]. **(B)** Clinical phenotypes of in-frame deletions starting and/or ending at exons encoding different domains of dystrophin. Green and red asterisks indicate a significantly lower and higher incidence of DMD phenotype for a given domain, respectively, as compared to the overall incidence rate. Data on the in-frame large deletions' phenotypic outcomes were collected from the UMD-DMD France Knowledgebase, eDystrophin database, and the existing literature. The yellow line indicates the overall incidence rate of DMD phenotype (**Figure 2**). We compared the phenotypic ratios associated with in-frame deletions starting and/or ending at the exons coding for a given domain and all other exons. The statistical significance was determined using a two-tailed Fisher's Exact test. (*** = $p <$ 0.0001).

References:

1. Le Rumeur, E. Dystrophin and the two related genetic diseases, Duchenne and Becker muscular dystrophies. *Bosn. J. Basic Med. Sci.* 2015, 15, doi:10.17305/bjbms.2015.636.