SI:Structural Basis for the Distinct Membrane Binding Activity of the Homologous C2A domains of Myoferlin and Dysferlin

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Supporting Information (SI)

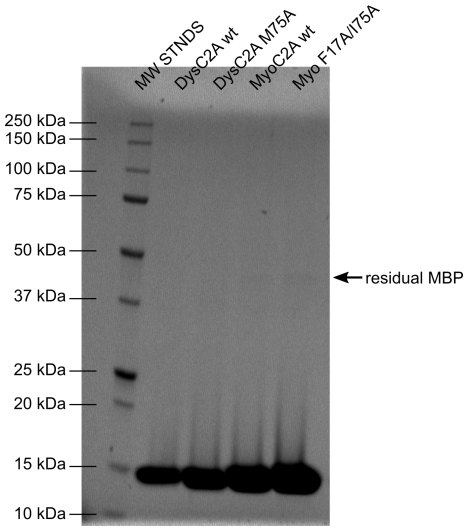

Fig. S1. 15-25% PAGE-SDS gel of C2A domain purification. Molecular weight ladder is annotated in the far-left lane. Dysferlin WT, Dysferlin C2A M75A, Myoferlin WT, and Myoferlin F17A-I75A C2 domains are listed from left to right. A minor maltose-binding protein (MBP) contamination is noted in the myoferlin double-mutant preparation.

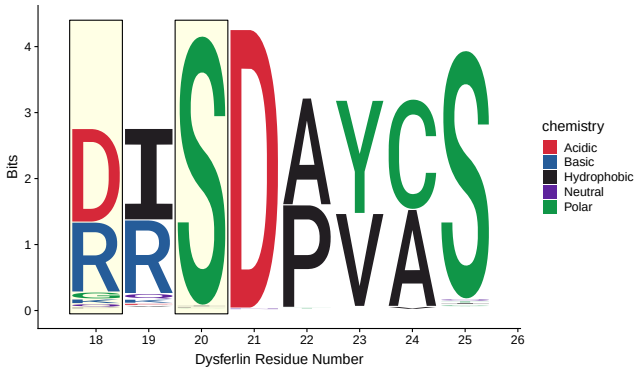

Fig. S2. Dysferlin sequence logo constructed from 1780 aligned dysferlin C2A sequences. The columns highlighted with yellow boxes are the residues that are referenced in this manuscript. In the first column there is a clear preference for 'D' and 'R' residues. In the second column, there is a preference for 'I' and 'R' residues. These two columns likely emit from the prevalence of canonical vs. variant 1 isoforms of dysferlin present in the NCBI protein database.

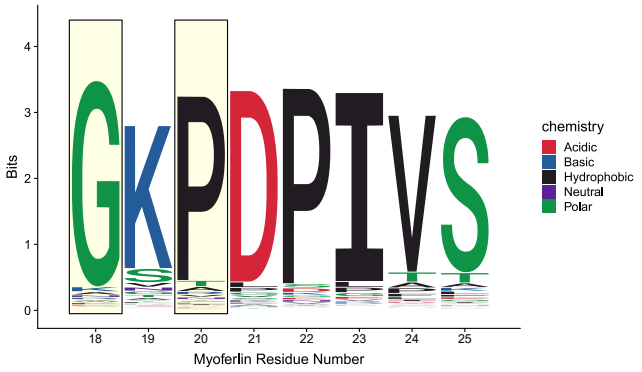

Fig. S3. Myoferlin sequence logo constructed from 565 aligned myoferlin C2A sequences. The columns highlighted with yellow boxes are the residues that are referenced with this manuscript.

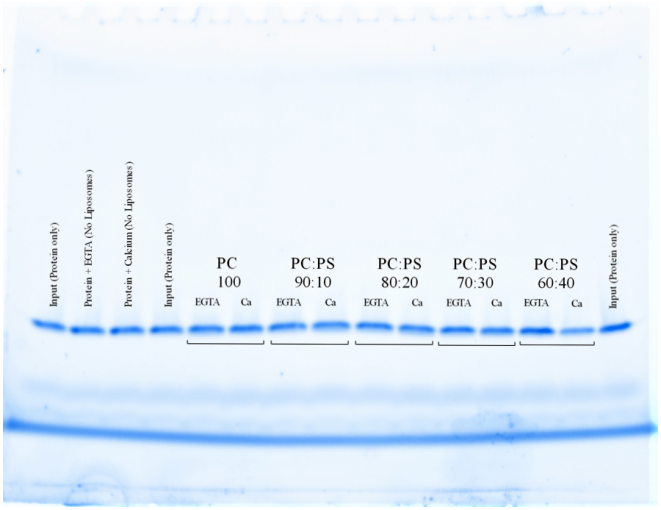

Fig. S4. Example of a Co-sedimentation gel using a 10-15% SDS PAGE gel stained using the Bio-Rad stain-free system. Positive controls and experimental lanes are labeled.

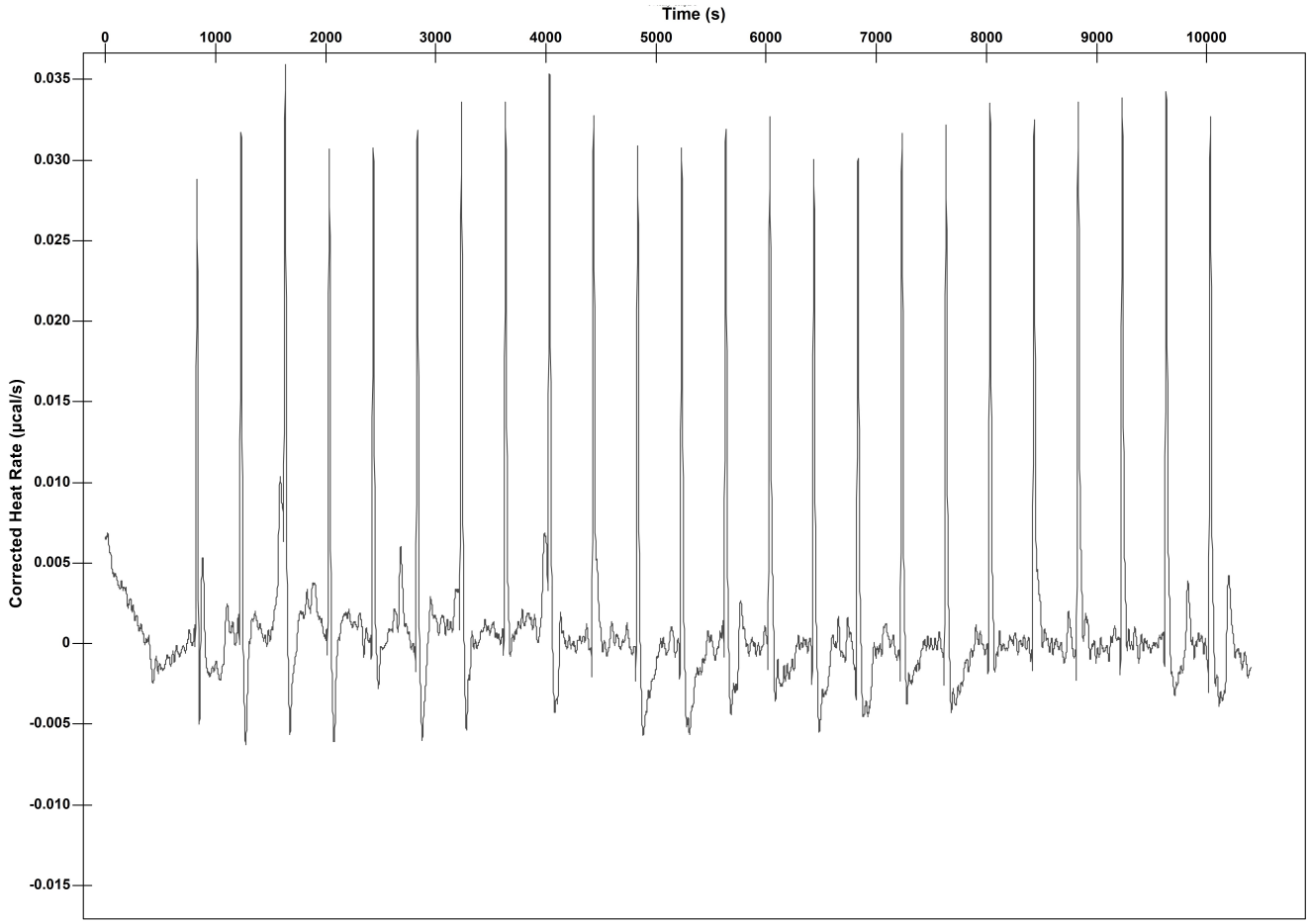

Fig. S5. ITC thermogram of dysferlin I19A M75A C2A