



Figure S1: Comparison of individual and global m-value fit results. A) Global RMSD vs. m-value for simultaneous fits across all protein variants and calcium conditions. A value of 0.95 kcal/mol/M minimizes the RMSD. B and C) Unfolding curves at 0 mM and 5 mM CaCl_2 fit with a floating m-value rather than a global m-value. (These curves correspond to those shown in Fig 5A and B). D) Comparison of estimated ΔG for each protein/calcium condition for a fixed m-value versus floating m-values. E) Comparison of the estimated m-value for each protein/calcium condition for a fixed m-value versus floating m-values. F) Comparison of the estimated C_m for each protein/calcium condition for a fixed m-value versus floating m-values.