

Supplementary information for:

Structural preferences shape the entropic force of disordered protein ensembles

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Figure S1

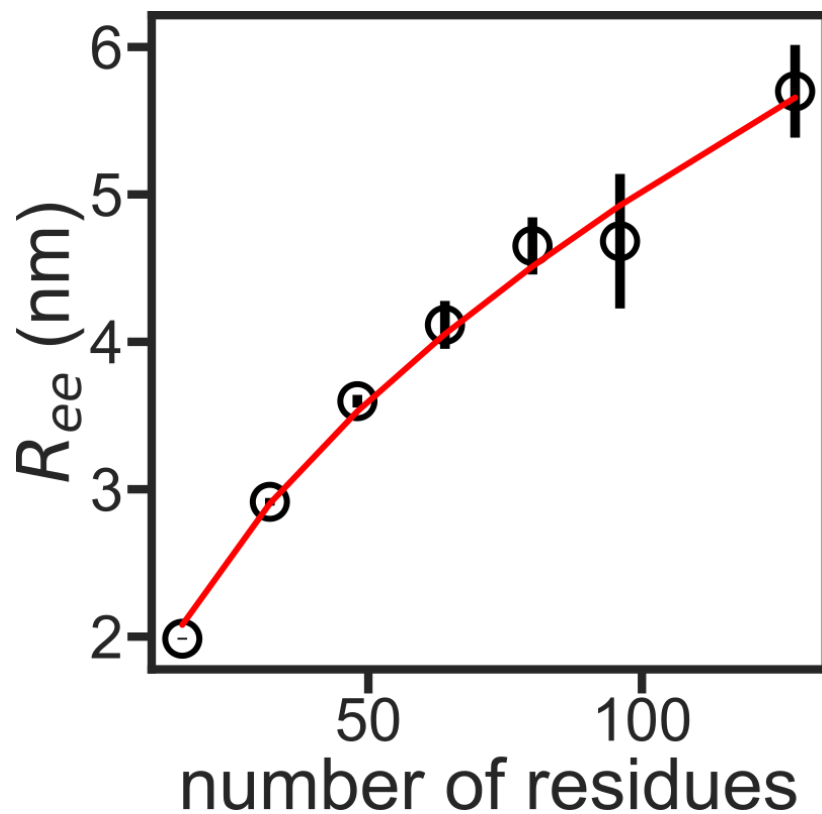


Figure S1. GS repeats match homopolymer scaling law under buffer conditions. The average end-to-end distance from five repeats vs the total number of residues for a series of Gly-Ser repeats, The error bars are the standard deviation of the five repeats. The red curve is the result of fitting to $R_{ee} = R_0 N^\nu$, with $R_0 = 0.55 \pm 0.06$ nm and $\nu = 0.48 \pm 0.03$. Errors are obtained from the fit.

Figure S2

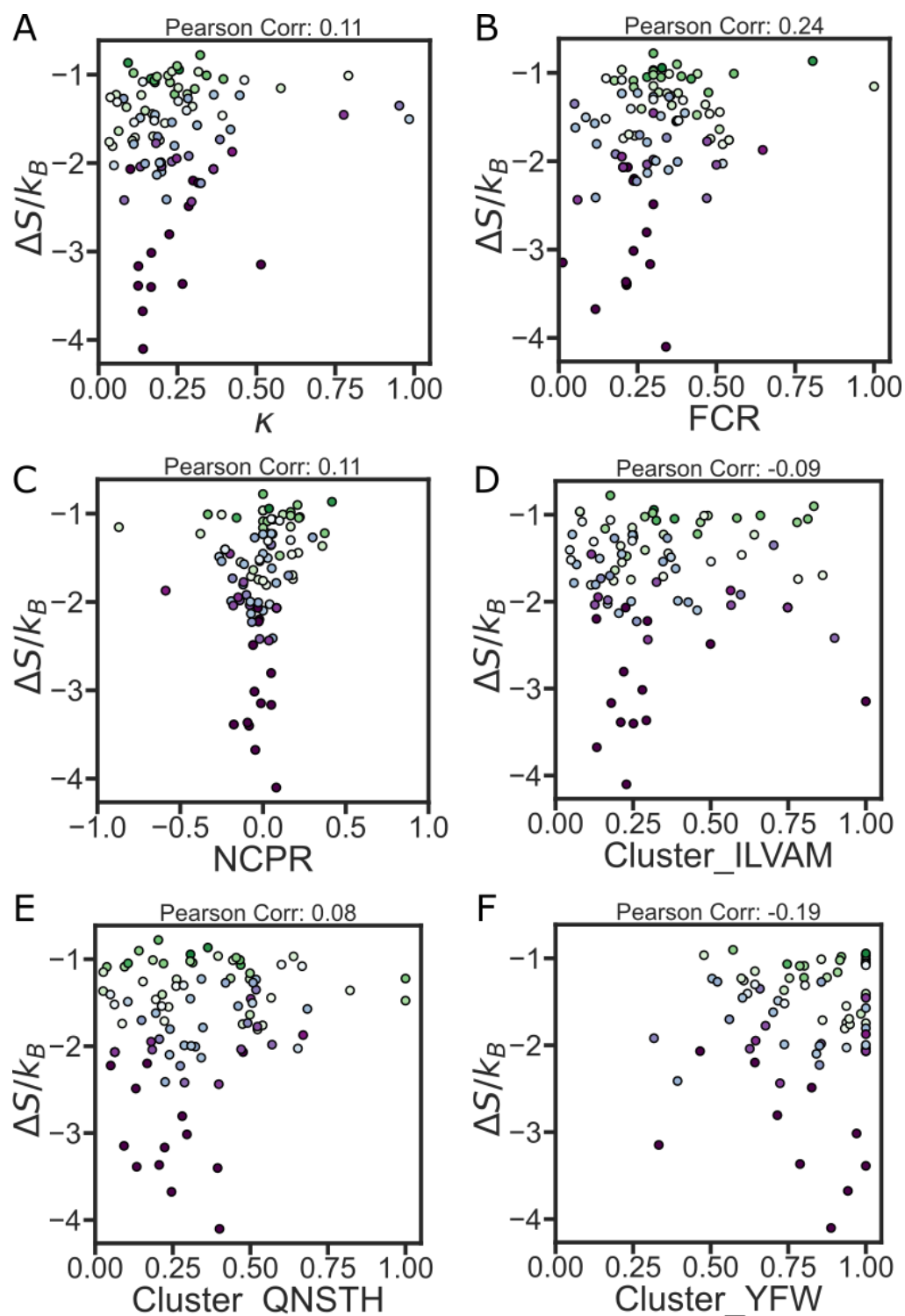


Figure S2. Sequence features are not correlated with the entropic force strength. The entropic force strength is plotted vs several sequence features calculated using the localCIDER python package. **(A)** κ : a metric for mixing of charged amino acids¹⁹, **(B)** FCR: fraction of charged residues, **(C)** NPCR: net charge per residue, **(D)** Cluster_ILVAM: hydrophobic amino acid mixing calculated using the same algorithm as κ , **(E)** Cluster_QNSTH: polar amino acid mixing calculated using the same algorithm as κ , **(F)** Cluster_YFW, aromatic amino acid mixing calculated using the same algorithm as κ .

Figure S3

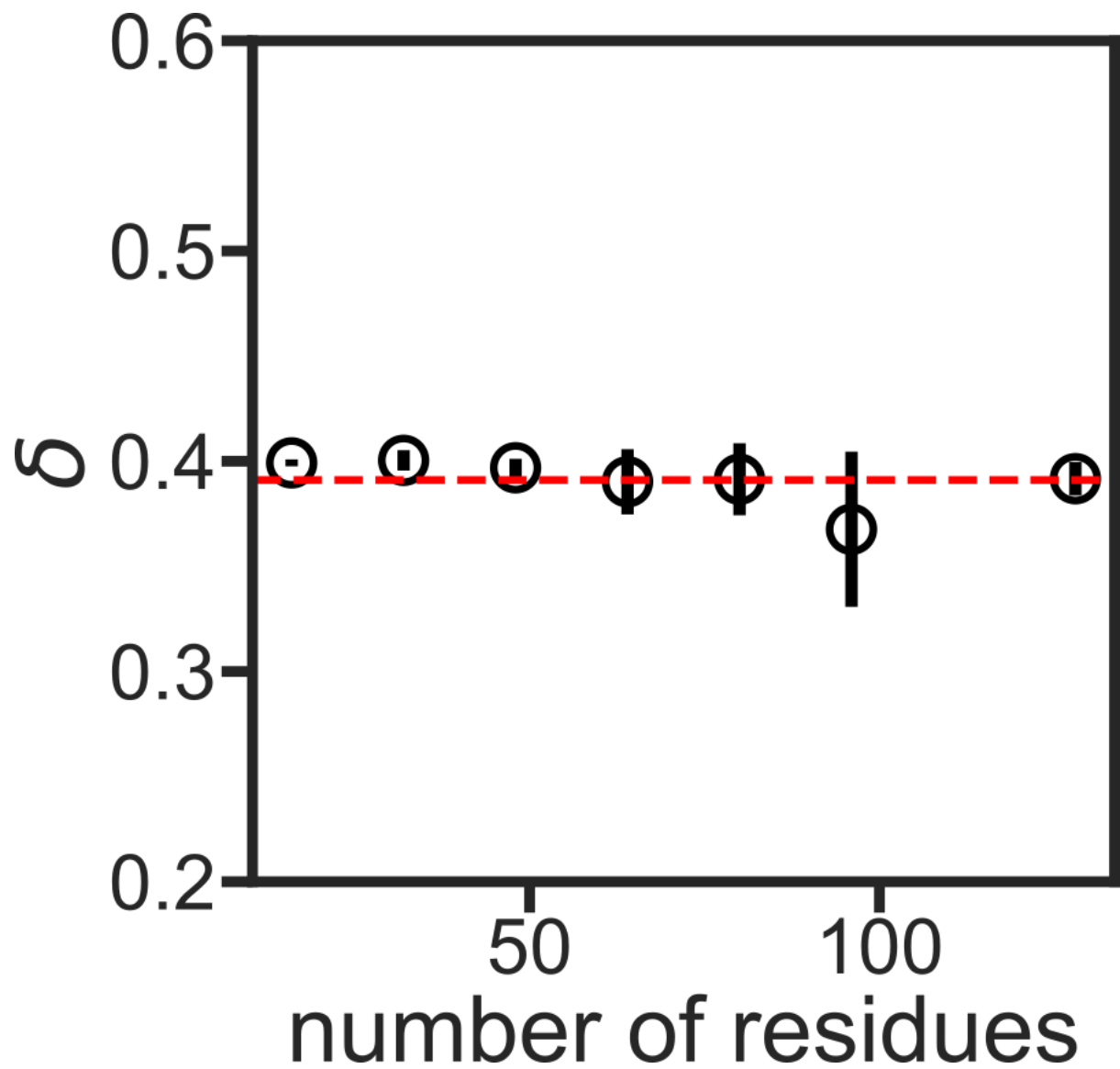


Figure S3. GS repeat asphericity is independent of length. The average asphericity of GS repeats vs the number of residues in the sequence. The mean of all seven data points is shown by the red line, with $\delta = 0.39 \pm 0.01$.

Figure S4

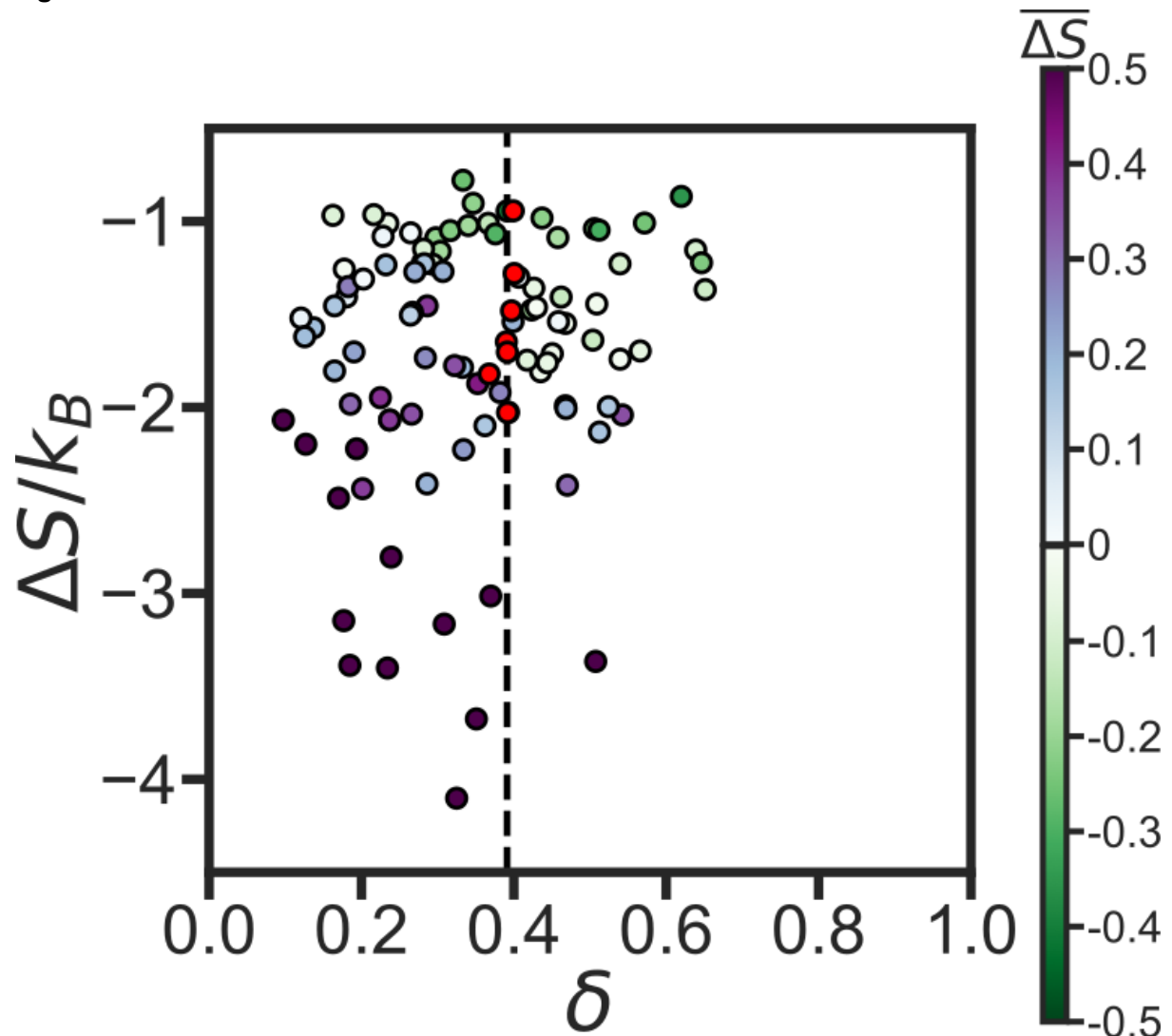


Figure S4. Entropic force as a function of average asphericity. The black line represents the length-independent asphericity of GS-repeats shown in **Fig. S3**. Each marker represents a single IDR, color-coded as in **Fig. 5A**, with stronger purple (green) markers showing a stronger (weaker) entropic force compared to the GS repeat of the same size.