**Distinct types of disorder in the human proteome: functional implications for alternative splicing**

**Supplement**

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**Text S2. A note on results of Buljan et al.** [6]

Recently Buljan et al. reported that tissue specific alternative exons are enriched more with binding motifs compared to both general and constitutive A exons [6]. However, we would like to point out that what they measured is the percentage of A exons that have at least one binding site, which is different than ratio of amino acids in distinct exon types that fall into a binding motif (See Fig 4B). When we performed the same analysis as Buljan et al., namely measured the percentage of A exons with at least one binding site, we realized complete agreement with their finding using both their binding motif dataset and our internal ELM dataset (P< 0.001586 and P<0.12 respectively). Note however that, we deliberately chose to report our findings in terms of binding motif density as we believe it better reflects the real amount of regulatory activity.

References

6. Buljan M, Chalancon G, Eustermann S, Wagner GP, Fuxreiter M, et al. (2012) Tissue-Specific Splicing of Disordered Segments that Embed Binding Motifs Rewires Protein Interaction Networks. Molecular Cell 46: 871–883. doi:10.1016/j.molcel.2012.05.039.