

Figure S1: Performance of state-of-the art methods on biomolecular condensate localization prediction

(A-H) ROC curves calculated with the predictions by catGranule, DeepPhase, FuzDrop, MaGS, MaGSeq, ParSe, PSAP, PScore, PSPred and LLPhyScore, as well as with simple protein features calculated by the methods RBPPred, DisProt, MetaPred, IUPred, and Disopred3. Curves are calculated using all proteins of indicated cellular condensates as positives and NS1 (A, C, E, G) or NS2 (B, D, F, H) as negative set. AUC values are provided for each method in the legend.

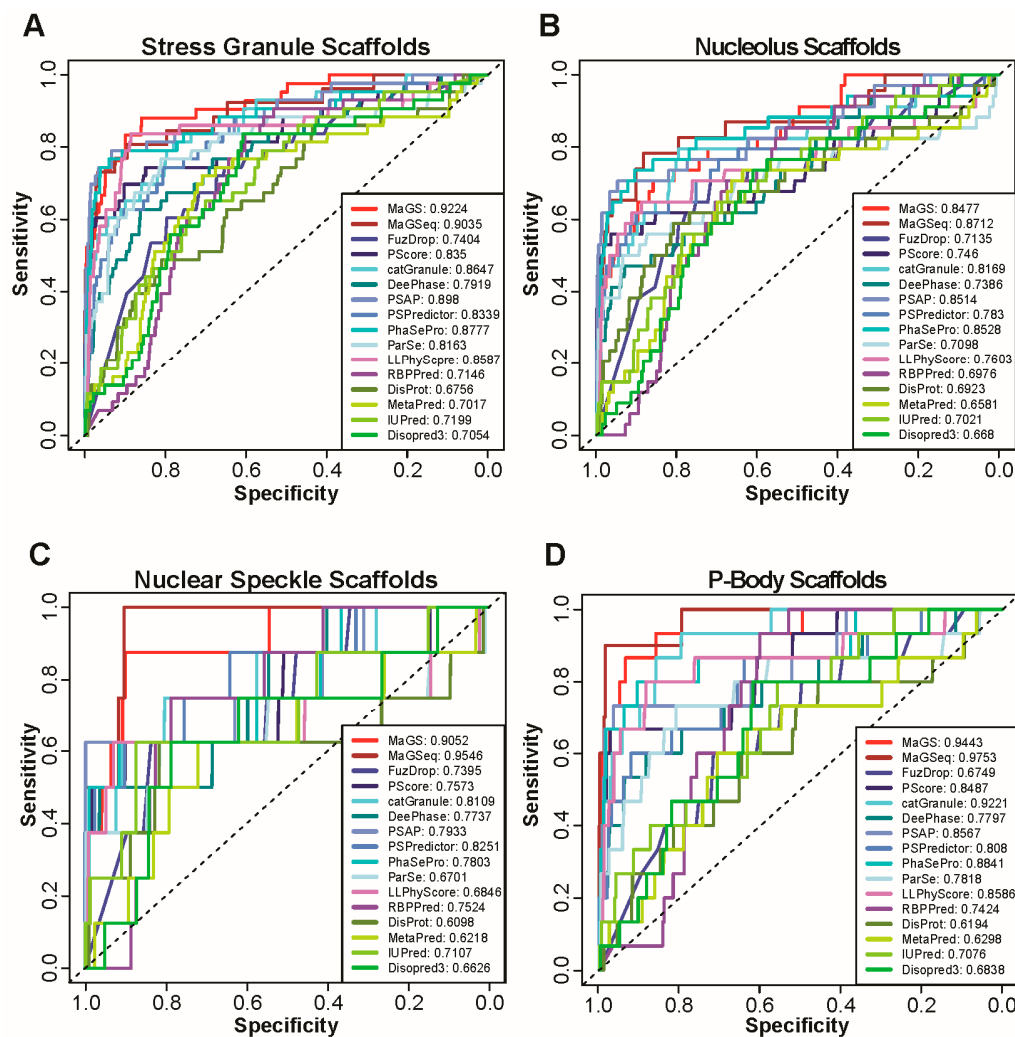


Figure S2: Performance of state-of-the art methods on prediction of scaffold localization in biomolecular condensates

(A to D) ROC curves calculated with predictions by the same methods used as Supplementary Figure S1. Curves are calculated using known scaffolds of stress granules (A), nucleolar condensates (B), nuclear speckles (C), or P-bodies (D) as positives, while NS1 is used as negative set. AUC values are provided for each method in the legend.

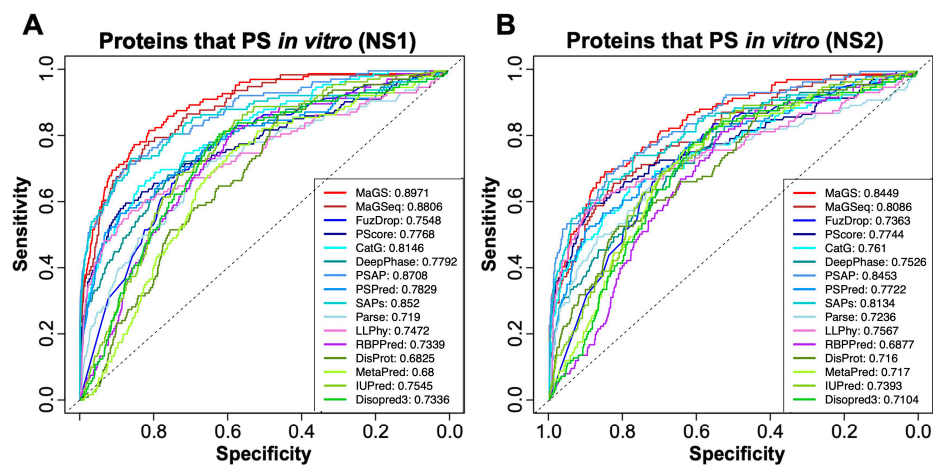


Figure S3: Performance of state-of-the art methods and simple protein features for *in vitro* phase separation prediction

(A and B) ROC curves calculated with predictions by the same methods used for Supplementary Figure S1. Curves are calculated using proteins known to phase separate *in vitro* as positives and NS1 (A) or NS2 (B) as negative set. AUC values are provided for each method in the legend