Atomic Resolution Interactions Regulating Partitioning of a FUS Folded RRM Domain into Model CAPRIN1 Condensates

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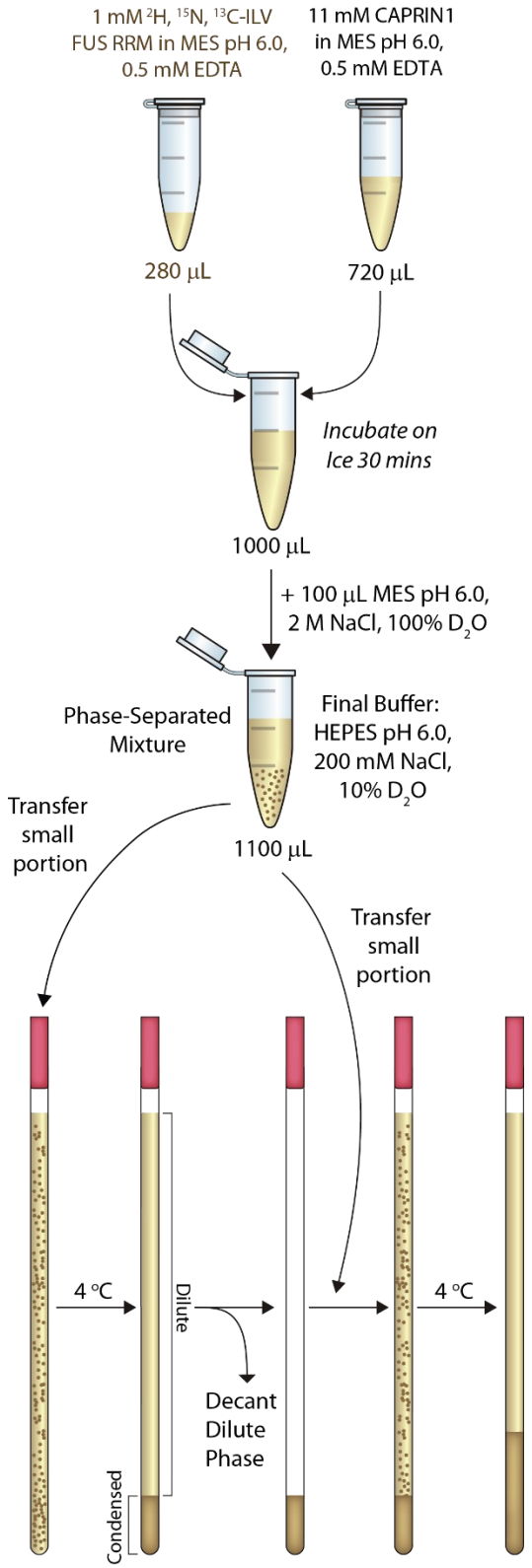

Figure S1 – Schematic illustrating the protocol for preparation of the phase-separated NMR sample.

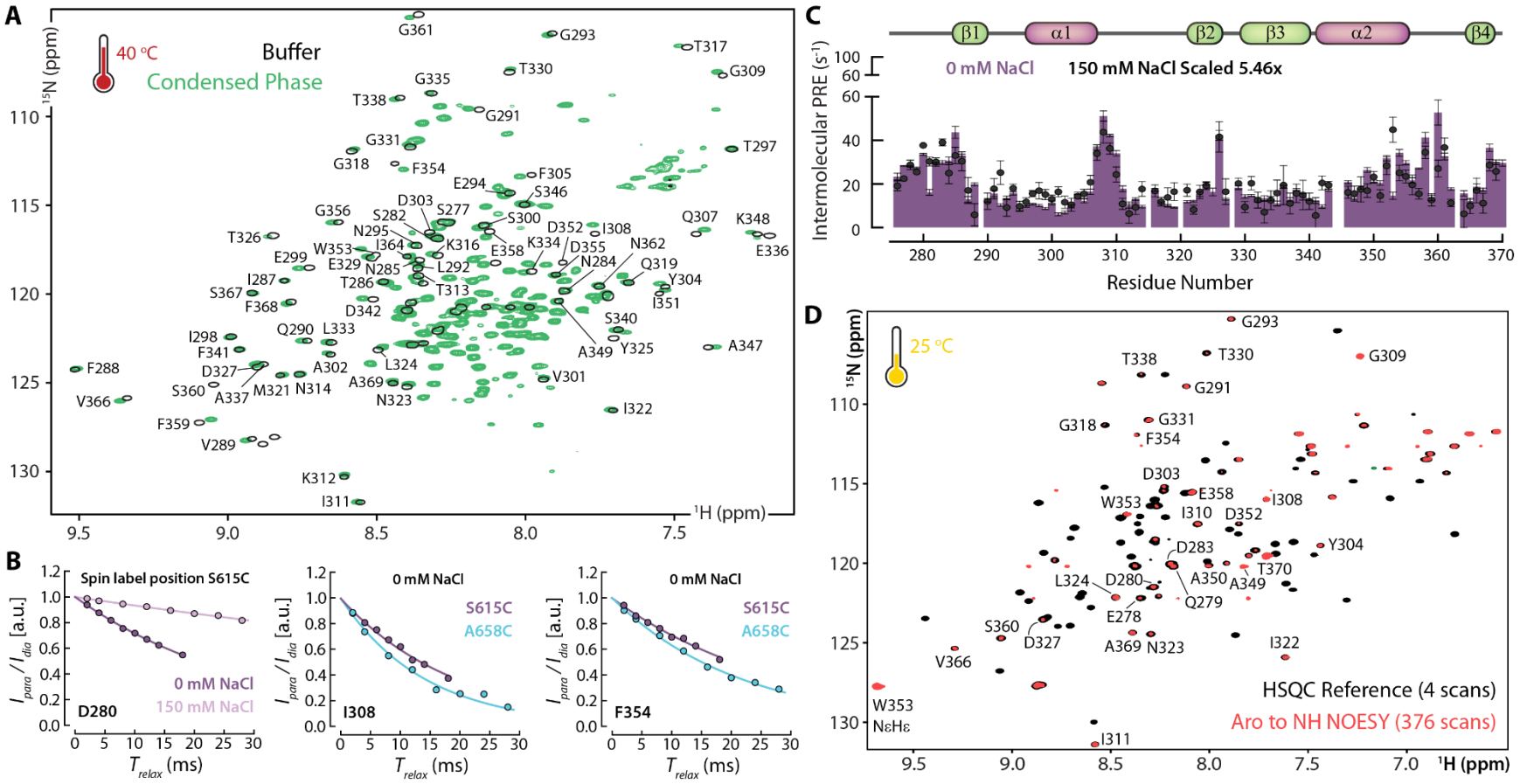

Figure S2 – Supporting data for client-scaffold interactions maps based on intermolecular NOE, PRE and chemical shift perturbation measurements. (**A**) Overlay of [^{1}H,^{15}N]-HSQC-TROSY spectra of ^{2}H, ^{15}N FUS RRM in buffer (*black* single contours) and in the condensed phase of ^{2}H, ^{15}N FUS RRM:^{1}H, ^{14}N CAPRIN1 (*light green*). FUS RRM folded resonances are annotated. Spectra were recorded at 800 MHz, 40 °C. (**B**) I_{para} / I_{dia} *vs.* T_{relax} profiles for representative FUS RRM residues under low and high salt conditions (*left*, *pink vs. purple*) and with spin labels introduced in the N-terminal arginine-rich region (S615C, *purple*) and in between the two aromatic-rich (A658C, *blue*) regions of CAPRIN1. (**C**) Intermolecular PRE profiles for 200 µM ^{15}N, ^{13}C FUS RRM in the presence of 200 µM ^{14}N CAPRIN1 S615C-maleimide-DOTA coordinated with either gadolinium (paramagnetic) or lutetium (diamagnetic) both without (*purple bars*) and with (*black circles*) 150 mM NaCl. The 150 mM NaCl intermolecular PRE profile is scaled up 5.46 fold. (**D**) NOESY spectrum (*red*) showing intermolecular NOEs from CAPRIN1 aromatic protons to FUS RRM backbone amides. The corresponding region from a [^{1}H,^{15}N]-HSQC spectrum is also shown (*black*). The NOESY and HSQC experiments were recorded at 800 MHz, 25 °C with 376 and 4 scans, respectively.

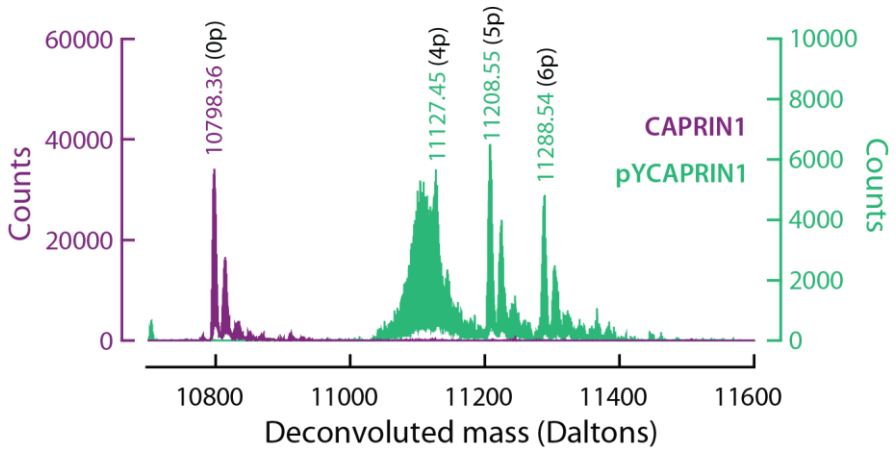

Figure S3 – Characterization of the number of phosphorylated CAPRIN1 tyrosine sidechains (#p) *via* mass spectrometry.