**Paragraph for interactome paper**

Additionally, the YTH-domain protein contain protein mRNA CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR 30 (AtCPSF30) was identified in the At-RBP set, and is known to function in mRNA 3’-end formation and polyadenylation site choice (Thomas et al., 2012). AtCPSF30 is thought to bind RNA via its N-terminal CCCH zinc finger domains (Hunt, 2014), but the presence of a C-terminal YTH domain, which is a unique feature of AtCPSF30, has led to speculation that it might also contact m6A in pre-mRNA (Chakrabarti et al., 2015), possibly linking RNA methylation to alternative mRNA 3’ end cleavage and polyadenylation.

To investigate this possibility, we analysed publicly available transcriptome-wide datasets of Arabidopsis m6A methylation (Luo et al., 2015) as well as cleavage and polyadenylation sites (Wu et al., 2011; Sherstrev et al., 2013). When comparing m6A peaks to polyadenylation sites, we found a 47% overlap of these signals in the 3’UTR. Similarly, a 36% overlap was found between m6A and cleavage sites in the 3’UTR. This further supports a possible functional connection between m6A methylation and 3’end formation in plants.