**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 performed a meta-gene analysis involving the two publicly available dataset of transcriptome-wide m6A methylation (Luo et al., 2014; Wan et al., 2015), and two datasets of polpolyadenylation sites (Wu et al., 2011; Sherstrev et al., 2013). Both m6A datasets consistently show an enrichment of m6A sites in the 3’UTR relative to other transcript sections, and a localisation of m6A sites near the stop codon.

Following a RRACH motif-guided search within m6A peaks from Wan et al. to identify m6A candidate sites at single-nucleotide resolution, we investigated a spatial co-localisation of m6A sites with polyadenylation sites using the R package RNAModR [Evers et al., 2016, submitted to Bioinformatics]. Results suggest an enrichment of 3’UTR m6A sites within a 100 nt window *upstream* of polyadenylation sites, while the 100 nt region *downstream* of polyadenylation sites is significantly depleted in m6A sites.

An equivalent analysis based on m6A data from Luo et al. gives consistent results. Additionally we found a large overlap of m6A peaks from Luo et al. with polyadenylation sites in the 3’UTR (47% of the m6A peaks overlap with polyadenylation sites from Wu et al., and 36% of the m6A peaks overlap with cleavage sites from Sherstnev et al., respectively).

In summary, the enrichment/depletion of m6A sites upstream/downstream of polyadenylation sites supports a possible functional connection between m6A methylation and 3’end formation in plants.