

# Modification Specificity of m<sup>6</sup>A Methylation in Mammalian Cells

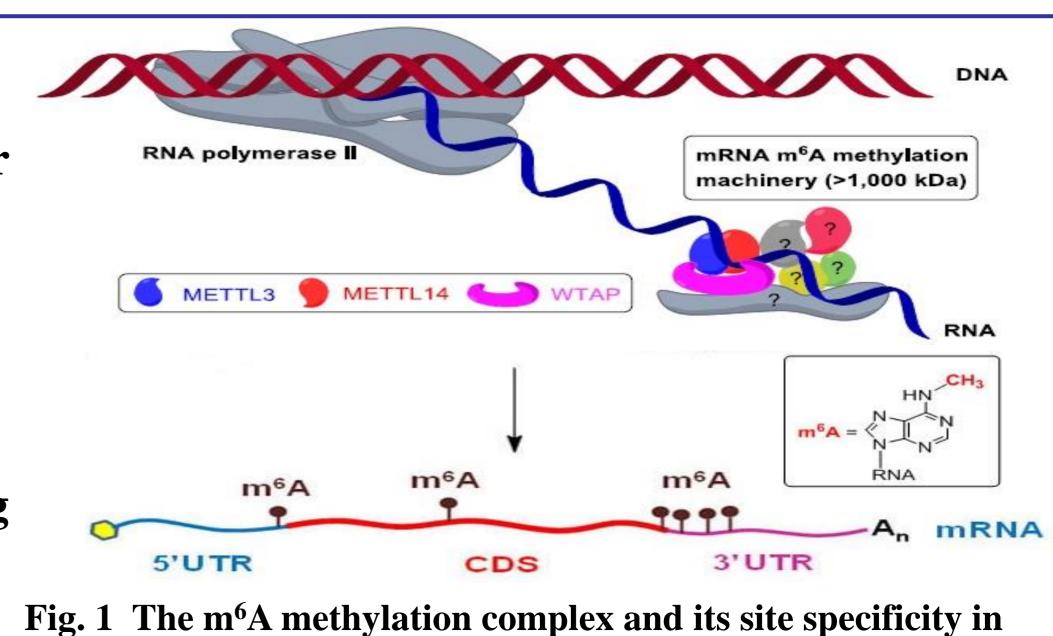
21629031. Jie Cao and Jianzhao Liu

Department of Polymer Science and Engineering, Zhejiang University, Hangzhou 310027, China

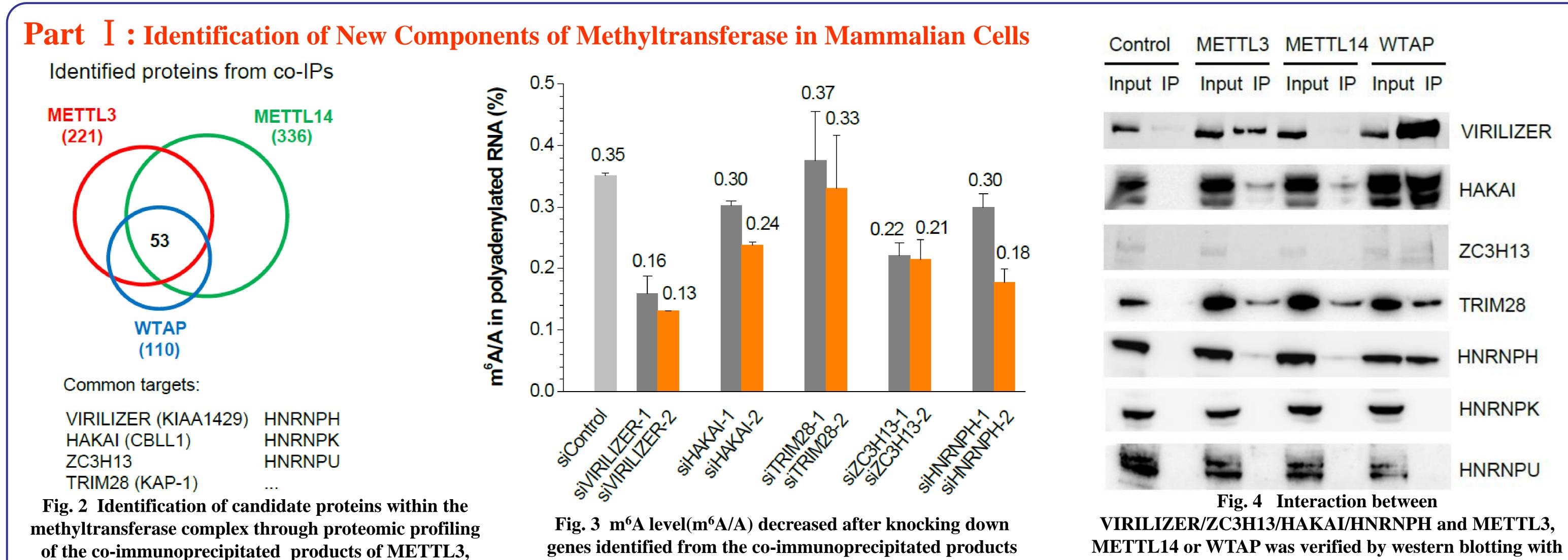


## **Introduction** :

*N*<sup>6</sup>-methyladenosine (m<sup>6</sup>A) is the most prevalent modification in messenger RNA (mRNA) of higher eukaryotes, and it plays an important role in the regulation of biological processes. Transcriptomewide mapping has revealed that m<sup>6</sup>A is favorably enriched in 3'UTR(3' untranslated Region) and stop codon of mRNA in mammalian systems. The METTL3/METTL14/WTAP complex has been identified as the core component of human methyltransferase complex. But the whole methyltransferase complex has yet to be fully identified and the mechanism of the enrichment of m<sup>6</sup>A in 3'UTR of mammalian mRNA remains unknown. Here we report new components including VIRILIZER, ZC3H13, HAKAI, and HNRNPH as candidates of the methyltransferase complex and among them, VIRILIZER can regulate m<sup>6</sup>A modification specificity in Hela cells.

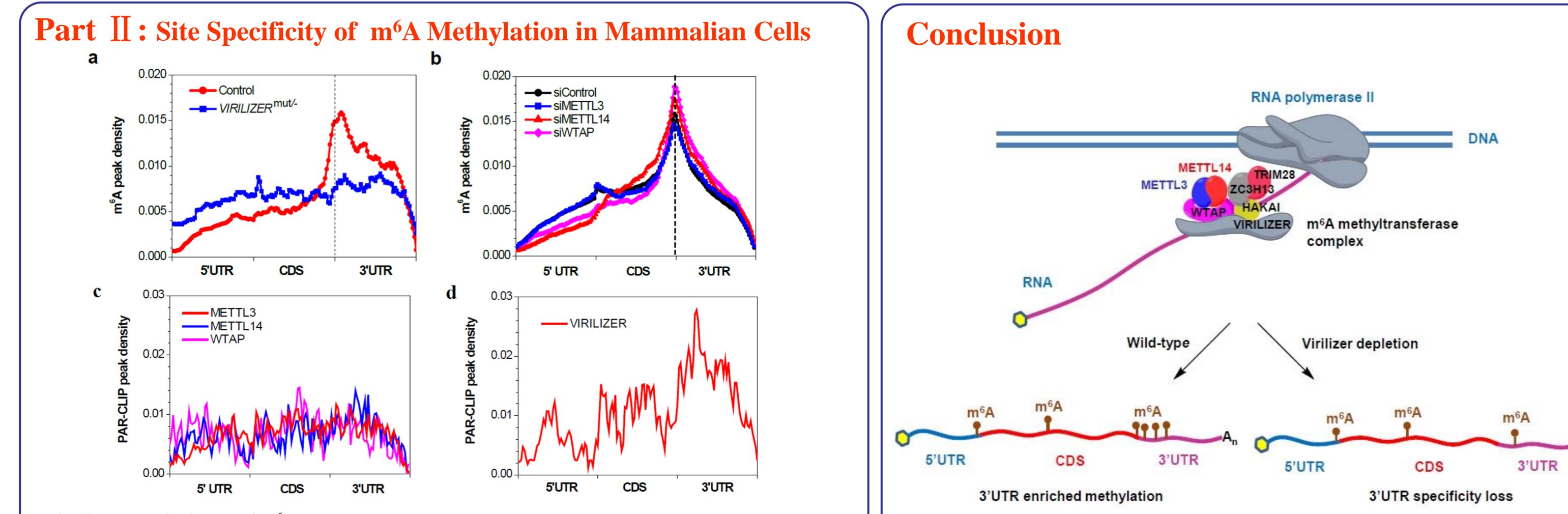


mammalian systems



**METTL14 and WTAP** 

the co-immunoprecipitated products



of METTL3/METTL14/WTAP

5); in Fig. 6 VIRILIZER/HAKAI/ZC3H13 are identified as new components of m<sup>6</sup>A methyltransferase complex, among them VIRILIZER can regulate m<sup>6</sup>A methylation specificity

Fig. 5 The enrichiment of m<sup>6</sup>A in 3'UTR disappeared in VIRILIZER stably knocked down cell line VIRILIZER<sup>mut/-</sup>(a); while knock down of METTL3 or METTL14 didn't effect its site specificity(b); PAR-CLIP manifested that the binding site of METTL3/METTL14/WTAP distribute averagely in mRNA(C); while the major binding sites of VIRILIZER are located in 3'UTR(d)

#### Summary :

Our study focused on characterization of the full methyltransferase complex besides previously identified components of METTL3, METTL14, and WTAP in order to decipher the mechanism for m<sup>6</sup>A modification specificity. Based on proteomic search and biochemical validation, we found out new components of m<sup>6</sup>A methyltransferase complex including VIRILIZER, HAKAI and ZC3H13. We chose VIRILIZER as our focus due to its huge effect on m<sup>6</sup>A modification. In the m<sup>6</sup>A methylome of *VIRILIZER*<sup>+/-</sup> cell line, the signature pattern of m<sup>6</sup>A enrichment in 3'UTR and near stop codon disappeared, indicative of loss of m<sup>6</sup>A modification specificity. PAR-CLIP data further manifested that the major binding sites of VIRILIZER are located in 3'UTR. Together we propose a model that VIRILIZER may serve as a scaffold, target 3'UTR of specific set of mRNAs, and recruit METTL3/METTL14 mainly through WTAP.

### Acknowledgements

We thank the National Natural Science Foundation of China (21642015) and National Key Research and Development Program of China (2017YFA0506800). J. L. thanks the Thousand Young Talents Plan of China and Hundred Talents Program of Zhejiang University.

#### References

[1] Liu, J. Z.; Yue, Y. et al. *Nat. Chem. Biol.* 2014, *10*, 93.
[2] Zhao, B.S., et al. *Nat. Rev. Mol. Cell Biol.* 2016, *18*, 31.