



**Supplementary information, Fig. S6. Comparison of homologous sequences of the WTAP H1-H4 and ZC3H13 Barding domains. a** Alignment of sequences (*Hs*, *Homo sapiens*; *Dr*, *Danio rerio*; *Xl*, *Xenopus laevis*; *Dm*, *Drosophila melanogaster*; *At*, *Arabidopsis thaliana*) of WTAP H1-H4. The up-triangles with (WTAP-a) or without black-border (WTAP-b) indicate the residues that interact with VIRMA, colored by the corresponding domain of VIRMA. **b** Alignment of sequences (*Hs*, *Homo sapiens*; *Dr*, *Danio rerio*; *Xl*, *Xenopus laevis*; *Dm*, *Drosophila melanogaster*; *At*, *Arabidopsis thaliana*) of the ZC3H13 Barding domain. The up-triangles indicate the residues that interact with VIRMA, colored by the corresponding domain of VIRMA.