### A

**ΔS2-G17**

| Sequence          | Prediction | Confidence  |
|-------------------|------------|-------------|
| T.brucei_Trm140   | SFSSDEKK   | 9           |
| T.brucei_MTase37  | SFSSDEKK   | 0           |
| S.cerevisiae_Trm140 | SFSSDEKK   | 300         |
| H.sapiens_METTL6  | SFSSDEKK   | 0           |
| M.musculus_METTL6 | SFSSDEKK   | 0           |

### B

**ΔS2-G17**

| Sequence          | Prediction | Confidence  |
|-------------------|------------|-------------|
| T.brucei_Trm140   | PTRTRGCCAL-TDPHAV---KL----HGNDFSLDEKLGGLA-----PEER | 46           |
| T.brucei_MTase37  | MPDK1ENNTRKRPREEPFVVEDYRPYT | 26           |
| S.cerevisiae_Trm140 | ENIAHEGRDNTEGQNAVEKSDFEKSDTEGSRSIRGDLIPFEFGKRNLTEESDVWDHNAWDN | 360          |
| H.sapiens_METTL6  | MASLQR     | 6           |
| M.musculus_METTL6 | MASFQR     | 6           |
Supplementary Figure 2. Predicted RNA-binding residues of TbTrm140. (A) Output from BindN predicting RNA-binding residues in the 341 amino acid sequence of Trm140 (Wang and Brown 2006). The + symbols denote likely RNA binding residues. (B) Clustal 2.1 multiple sequence alignment of S. cerevisiae and T. brucei Trm140. Putative motifs (I-VI) characteristic of class 1 Rossmann-fold methyltransferases are indicated above the sequence and key conserved residues are highlighted in black. Gray highlighted regions in both the BindN and alignment correspond to the N-terminal and C-terminal deletion mutants, ∆S2-G17 and ∆l320-S340, respectively.