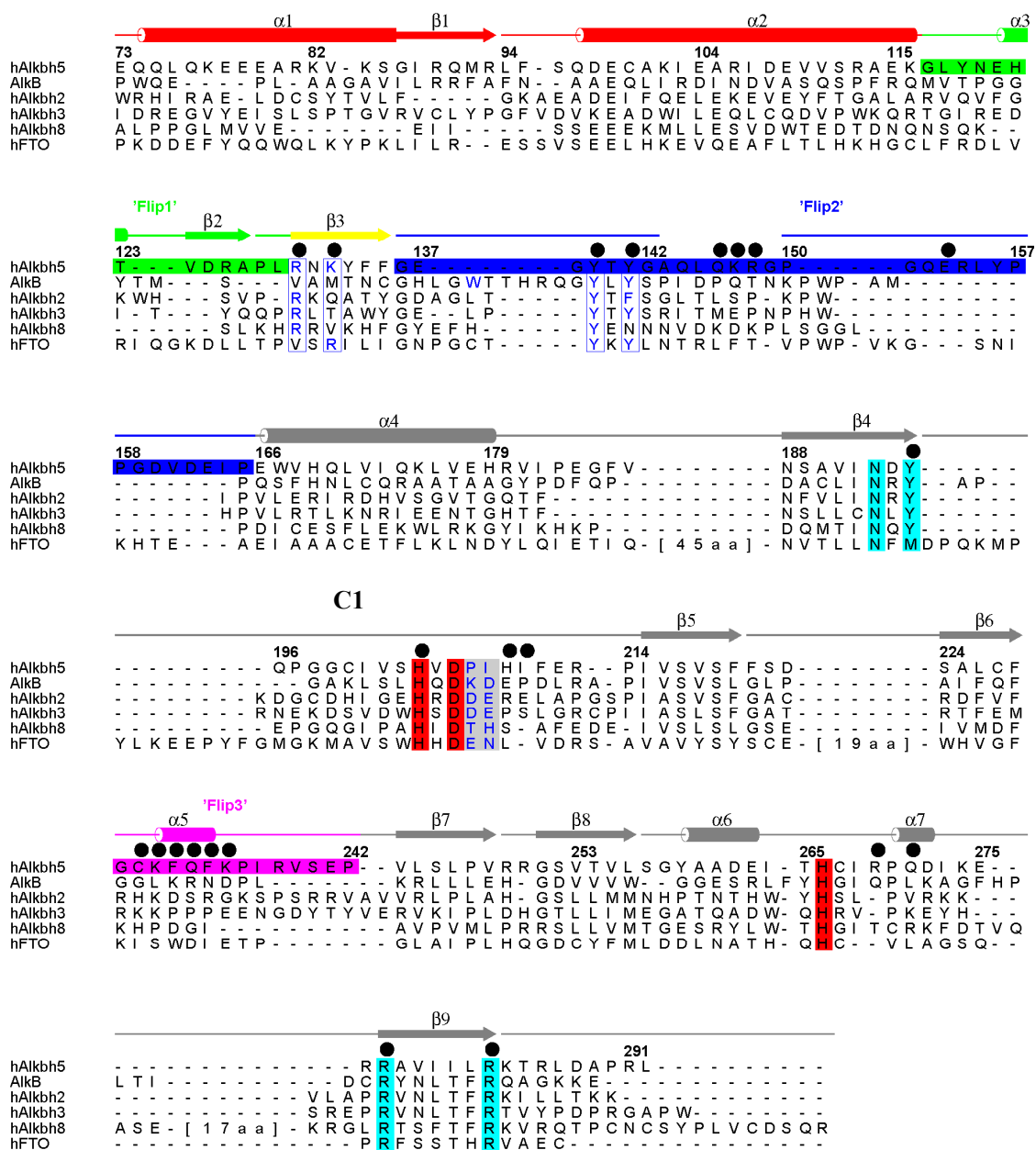


## Supplementary Figure 1



**Figure S1.** Structure-based sequence alignment of Alkbh5 and AlkB family proteins. The sequences were aligned using the program T-Coffee (1). The ALSCRIPT program (2) was used to prepare the figure. Secondary structure elements of Alkbh5 are shown. The “Flip1”, “Flip2” and “Flip3” motifs in Alkbh5 are colored in green, blue and magenta, respectively. The residues involved in binding of  $\text{Fe}^{2+}$  and  $\alpha$ -KG are highlighted in red and cyan, respectively. Residues selected for site-directed mutation analysis are indicated by black filled circles. The two residues following the conserved H-X-D/E motif are shown in gray shadow and colored in blue. The mutated residues that are the candidate determinants for the m6A recognition and catalysis of Alkbh5 are relatively conserved among the AlkB family, which are colored blue and

highlighted within the blue frame. The sequences are used as follows: *hAlkbh5*, NP\_060228/AK301107; *AlkB*, NP\_416716/U00008; *hAlkbh2*, NP\_001001655/AB277859; *hAlkbh3*, NP\_631917/DQ196343; *hAlkbh8*, NP\_620130/AK095523; *hFTO*, NP\_001073901/AC007347.

### Supplementary References

1. Poirot, O., O'Toole, E., and Notredame, C. (2003) Tcoffee@igs: A web server for computing, evaluating and combining multiple sequence alignments, *Nucleic Acids Res.* **31**, 3503-3506
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