

Supplementary material:

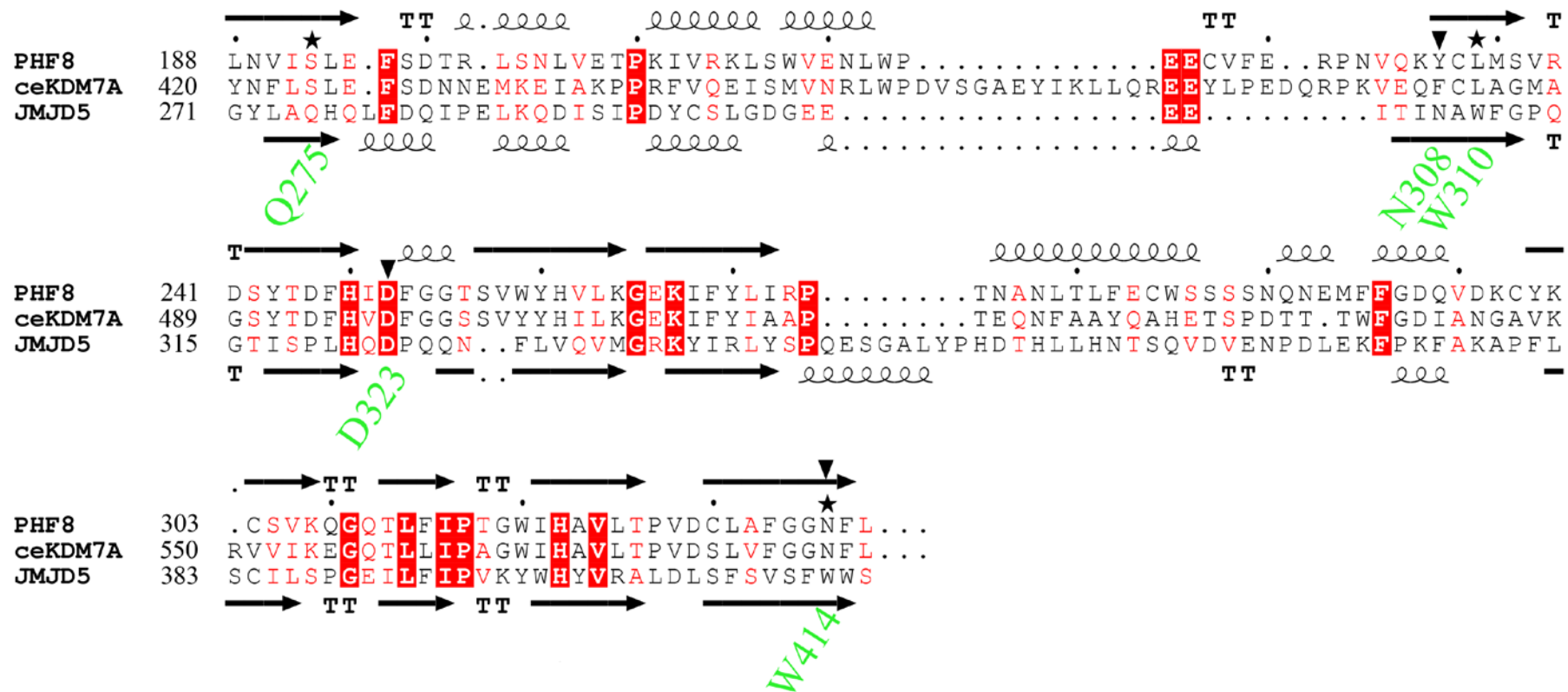


Figure S1. Structure based sequence alignment of PHF8, ceKDM7A and JMJD5^{176-C}. The residues responsible for blocking the entrance of methylated lysine residue in JMJD5^{176-C} and residues involved in methylated lysine binding in PHF8 and ceKDM7A are marked by stars and triangle, respectively.