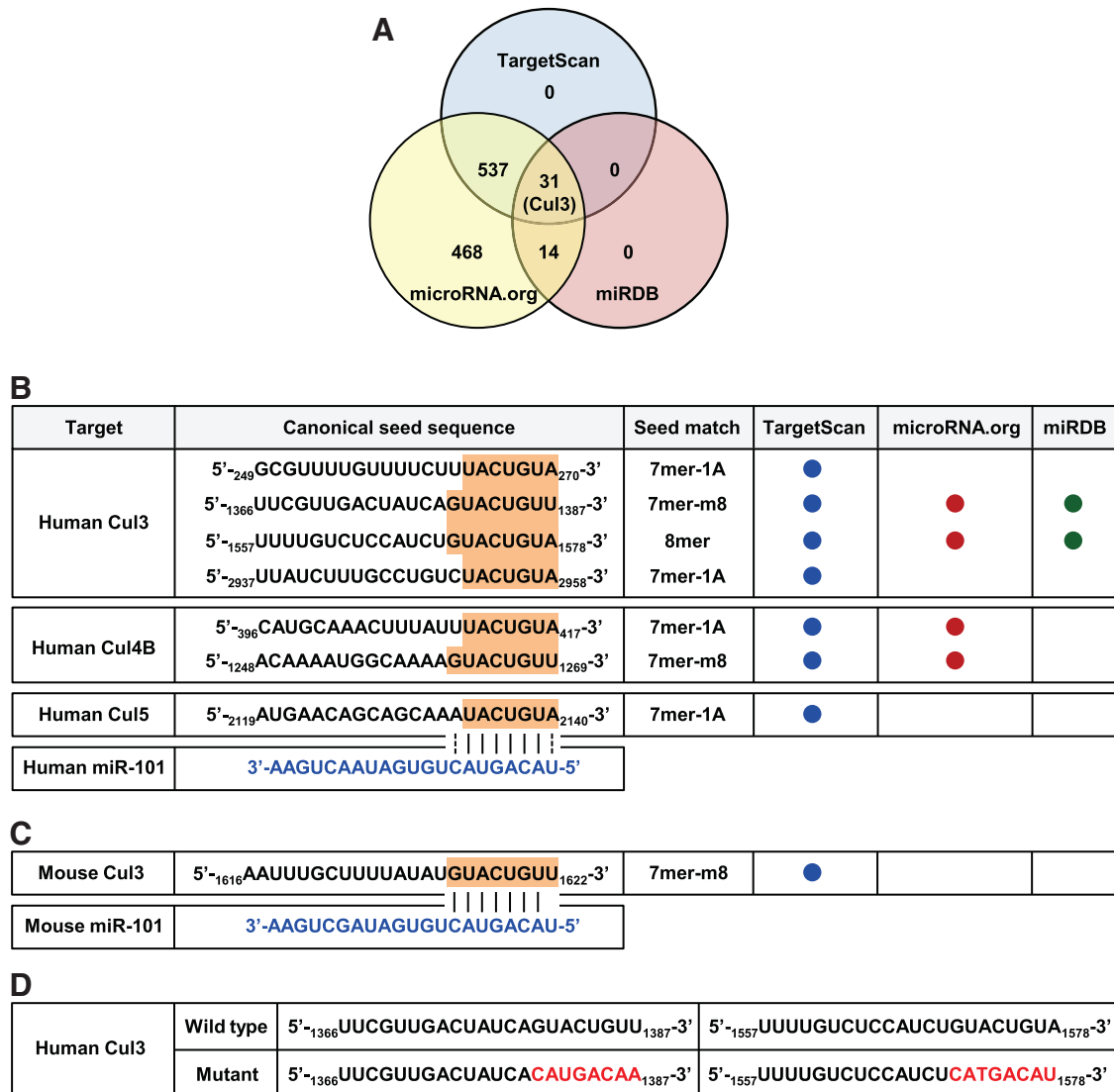


Supplementary Data



SUPPLEMENTARY FIG. S1. Computational prediction of miR-101 targets. (A) Venn diagram displaying mRNAs computationally predicted to targets Cul3 by TargetScan, microRNA.org, and miRDB. Highly reliable targets were selected using cutoff scores of ≤ 0.1 for TargetScan and miRDB and ≥ 60 for microRNA.org. (B) Alignment of potential binding sites of human in the 3'UTRs of human cullin gene family. (C) Alignment of potential binding site of mouse miR-101 in the 3'UTR of mouse Cul3. (D) The sequence of Cul3 3'UTR mutants used for the reporter assay. 3'UTR, 3'untranslated region; Cul, cullin; miRNA, miR, microRNA.