

Figure S1. A schematic view of the analysis steps of the sRNA-seq profiles to identify miRNAs and their editing sites in *Macaca mulatta*. The arrows indicate the steps and the related algorithms of the corresponding steps are provided beside the arrows. (a) The computational steps for identifying conserved miRNAs. (b) The computational steps for analyzing the distributions of sRNA sequencing reads that are aligned to different categories of molecules. (c) The computational steps for identifying species specific miRNAs from the 12 self-generated sRNA-seq profiles. (d) The computational steps for identifying mutation and/or editing sites in miRNAs of *Macaca mulatta* from the 12 self-generated and 58 public sRNA-seq profiles. ①, ②, and ③ represent the prediction of putative targets for conserved, species specific and edited miRNAs, respectively, with the HitSensor algorithm. The enriched KEGG pathways and enriched GO terms of the predicted miRNA targets were calculated with KOBAS (v3.0).

samples selected (SRR1048283). (f) The details of hsa-mir-1260b_18_A_g in a brain embryonal tumor sample (SRR531707).

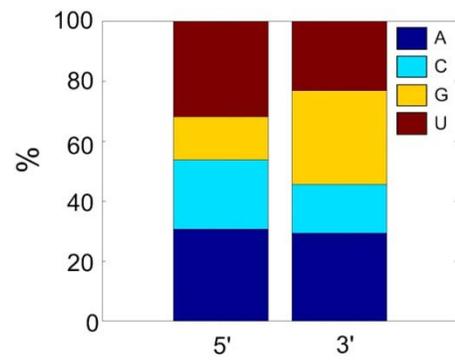


Figure S3. The percentages of nucleotides around the 32 A-to-I editing sites in miRNAs of *Macaca mulatta*.

The details of mml-mir-219-1_35_C_u in one of the brain samples selected (SRR553577). (f)
The details of hsa-mir-219-1_35_C_u in a frontal lobe sample (SRR448330). (g) The details of
mml-mir-219-2_33_C_u in one of the brain samples selected (SRR1955935). (h) The details of
hsa-mir-219-2_33_C_u in a prefrontal cortex sample (SRR1103939).

numbers of G-to-U sites at different positions of mature miRNAs. (c) The MiRME map of mml-let-7e in one of the brain samples selected (SRR553578). (d) The MiRME map of mml-mir-388 in one of the brain samples selected (SRR553577). (e) The MiRME map of mml-mir-424 in one of the kidney samples selected (SRR553606). (f) The details of mml-let-7e_19_G_u in SRR553578. (g) The details of mml-mir-338_46_G_u in SRR553577. (h) The details of mml-mir-424_25_G_u in SRR553606.

Reference

- [1] Zheng, Y.; Ji, B.; Song, R.; Wang, S.; Li, T.; Zhang, X.; Chen, K.; Li, T.; Li, J. Accurate detection for a wide range of mutation and editing sites of microRNAs from small RNA high-throughput sequencing profiles. *Nucleic Acids Research* 2016, 44, e123.