

## Supplementary Information

### **Influence of the DNA sequence/length and pH on deaminase activity, as well as the roles of the amino acid residues around the catalytic center of APOBEC3F**

**Li Wan**<sup>1,2</sup>, **Takashi Nagata**<sup>1,2</sup>, **Masato Katahira**<sup>1,2</sup>

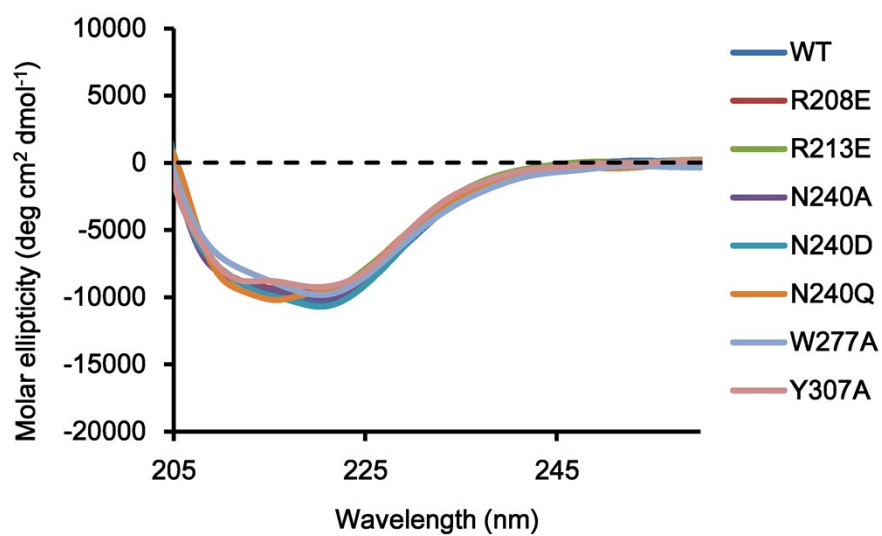
<sup>1</sup>Institute of Advanced Energy, Kyoto University, Gokasho, Uji, Kyoto 611-0011, Japan

<sup>2</sup>Graduate School of Energy Science, Kyoto University, Gokasho, Uji, Kyoto 611-0011, Japan

## Materials and Methods

### **Circular dichroism (CD) spectroscopy**

Wild type and mutant A3F-CTDs (2-6  $\mu\text{M}$ ) were individually dissolved in the 20 mM Tris-HCl (pH 7.5) solution containing 300 mM NaCl, 0.05 % CHAPS and 1 mM DTT. CD spectra were recorded with a Jasco J-720A spectrometer (Japan Spectroscopic Co., Japan) at 25°C using a cell of the optical path of 1 mm. Each spectrum was background-corrected, smoothed, and converted to molar ellipticity  $[\theta]$  ( $\text{deg}\cdot\text{cm}^2\cdot\text{dmol}^{-1}$ ). The protein concentration was determined by the procedure described by Greenfield.<sup>1</sup>



**Figure S1** CD spectra of wild type and mutant A3F-CTDs whose deaminase activities were significantly low

#### Reference

1. N. J. Greenfield, *Nat Protoc*, 2006, **1**, 2876-2890.