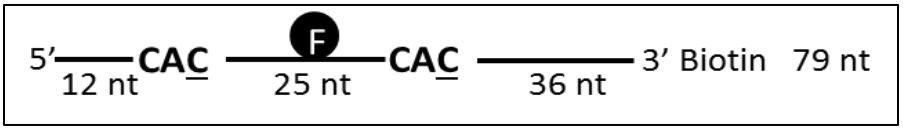
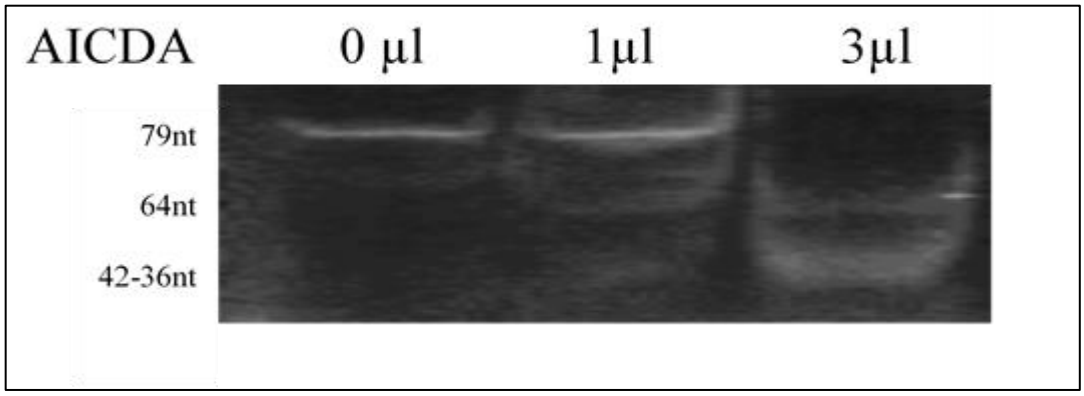
Supplementary Figure 5. Uracil-DNA glycosylase (UDG) hydrolysis assay. A) EGFR oligomer sequence where the teal and red regions represent exact replicates of the EGFR sequence around c.2369 position (highlighted C). B) Representation of the designed oligomer. C) UDG hydrolysis assay in alkaline environment causes the degradation of EGFR oligomer (79nt) into its components (64nt) and (36nt) upon exposure to AICDA enzyme.

A) 5'CGTGCAGCTCATCACGCAGCTCATGCCCCGTGCAGCTCATCACGCAGCTCATGC CCTTCGGCTGCCTCCTGGACTATGT-3'Biotin

B)



C)



We then evaluated the ability of AICDA to deaminate cytosine in EGFR gene. To this end, we tested cytosine deamination of an EGFR oligomer, designed to contain the cytosine of interest twice, by purified AICDA protein. (Supplementary Figure 2 A, B). AICDA deaminates preferentially Cs in WRC (W=A/T, R=A/G) motif, but can also recognize and deaminate the third C in the CAC motif (28). Thus, cytosine in the EGFR oligomer will undergo deamination to uracil and uracil-DNA glycosylase (UDG) would cause hydrolysis of the glycosylic bond between uracil and its ribose sugar (29). As shown in supplementary Figure 2C, AICDA does recognize EGFR sequence and induces deamination of cytosine at both CAC motifs leading to the hydrolysis of the oligomer at these nucleotides.

28. Chelico L, Pham P, Goodman MF. Stochastic properties of processive cytidine DNA deaminases AID and APOBEC3G. Philosophical transactions of the Royal Society of London. Series B, Biological sciences. 2009;364:583-93.

29. Chelico L, Pham P, Calabrese P, Goodman MF. APOBEC3G DNA deaminase acts processively 3' --> 5' on single-stranded DNA. Nat Struct Mol Biol. 2006;13:392-9.