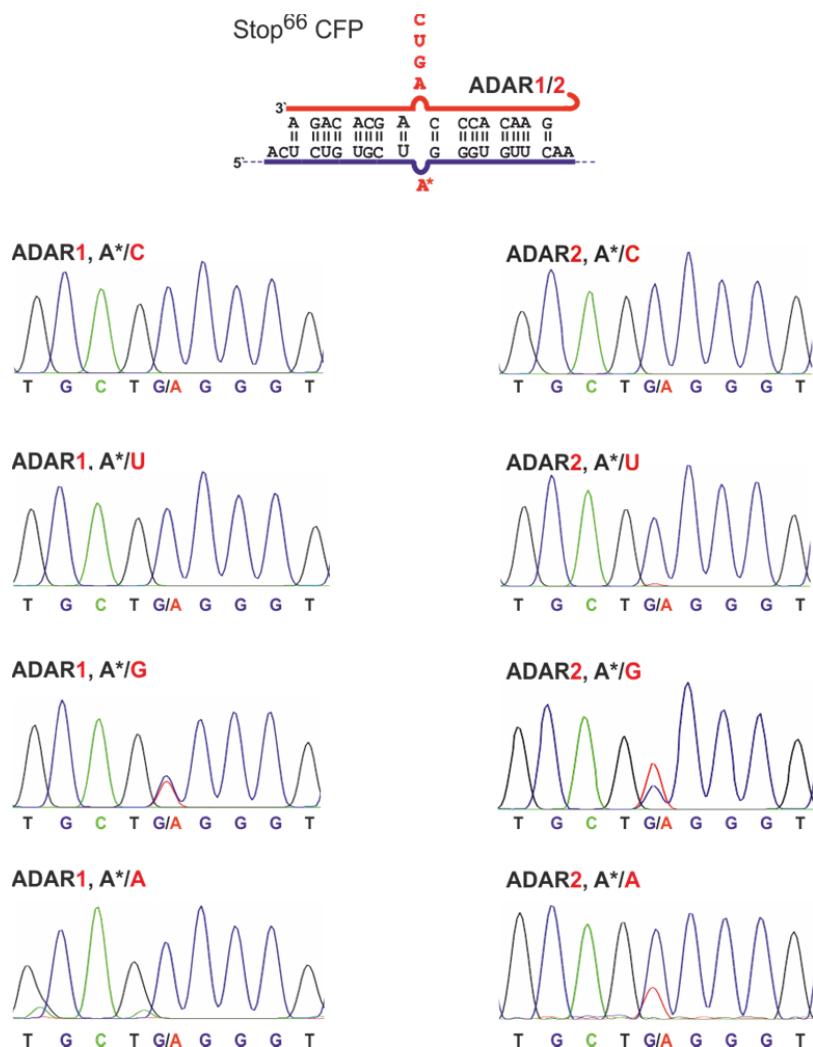


## Supporting Information

### Optimal guideRNAs for Re-directing Deaminase Activity of hADAR1 and hADAR2 in trans

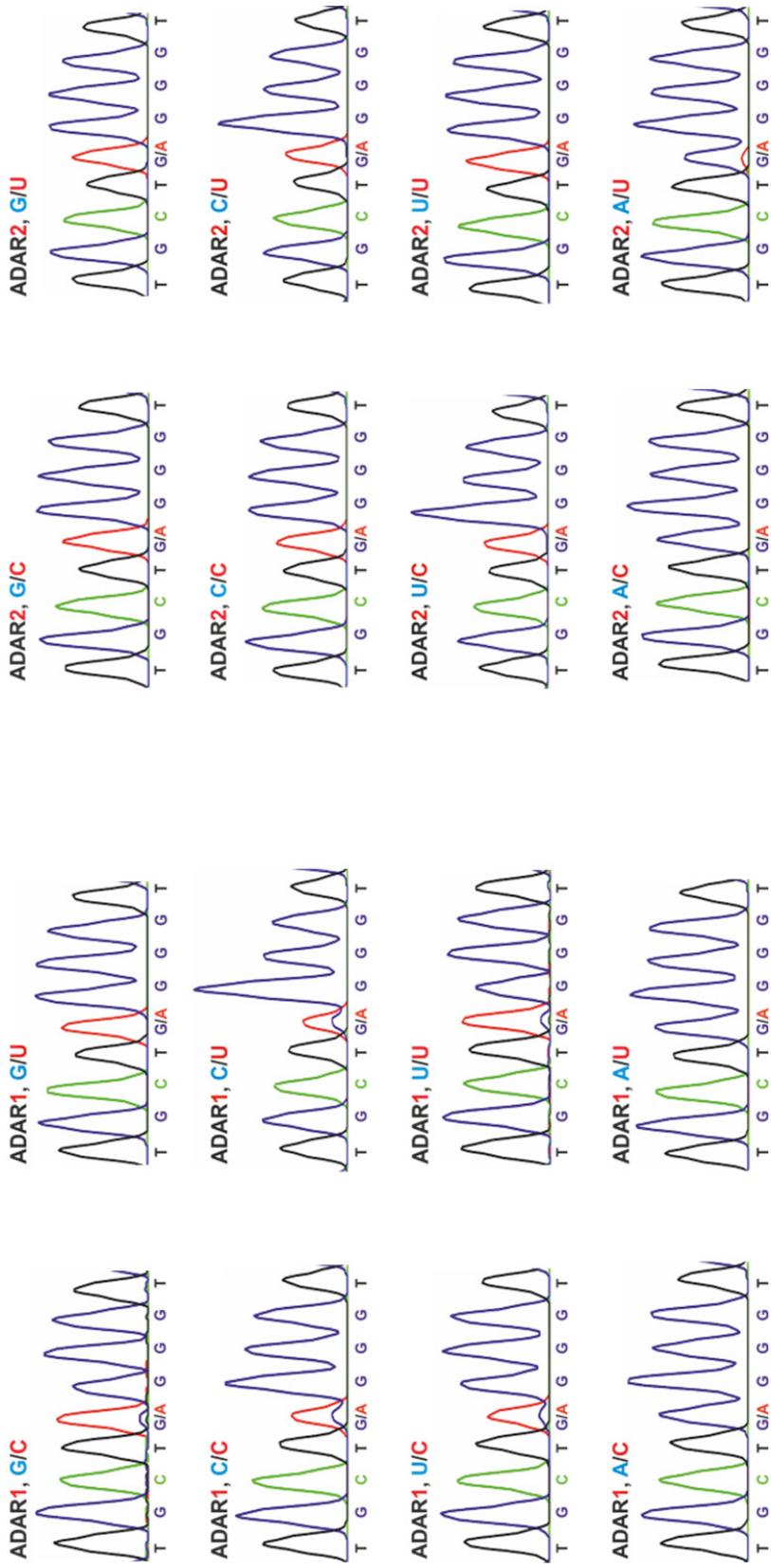
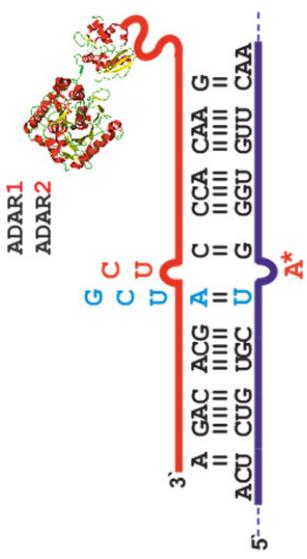
Marius F. Schneider, Jacqueline Wettenkel, Patrick C. Hoffmann and Thorsten Stafforst

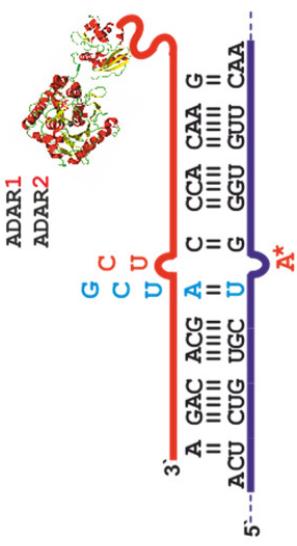
## Sequencing results



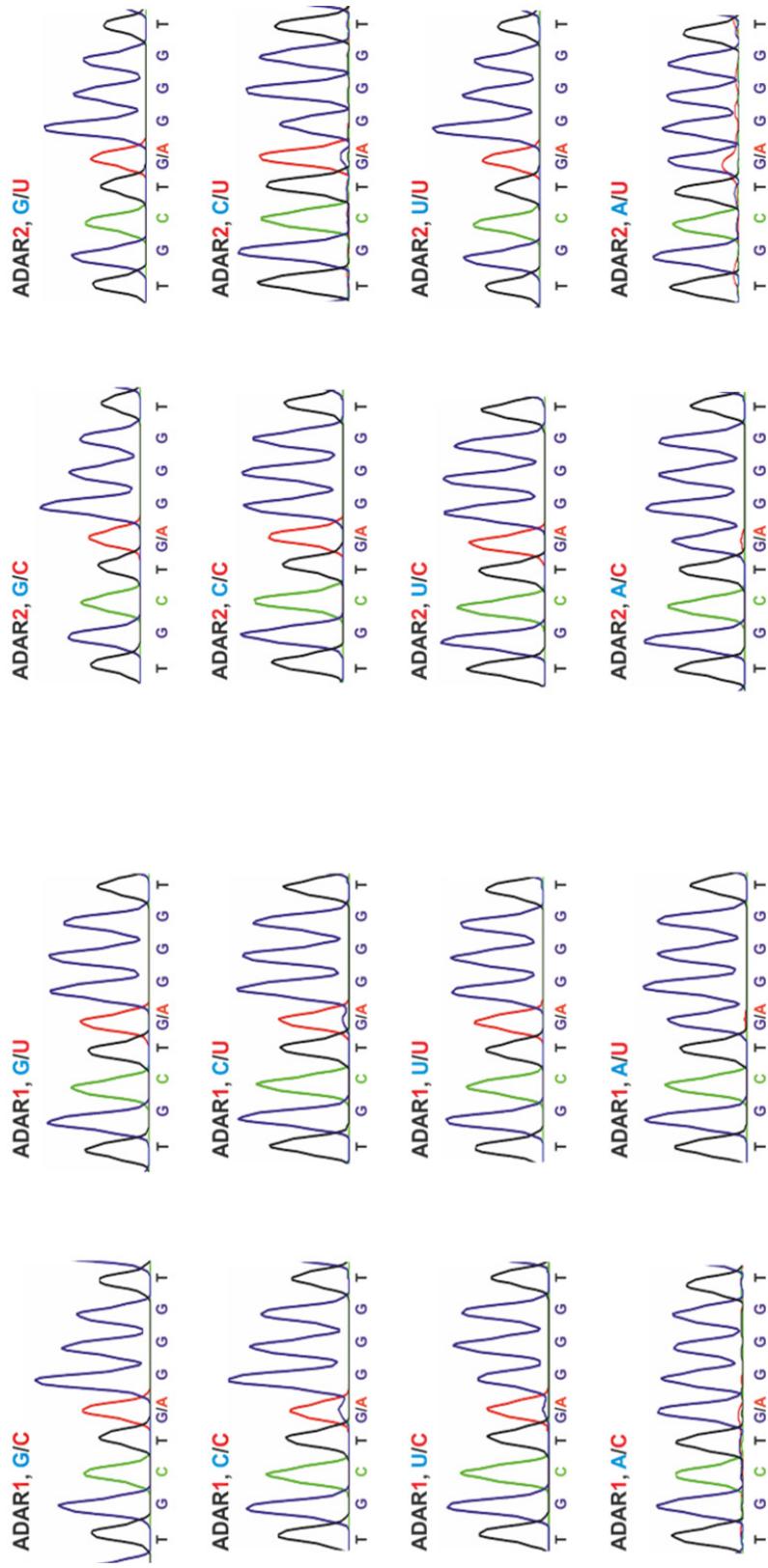
**Figure S1.** Effect of the counter base in our standard Stop66 CFP transcript. The adenine base (A\*) of the Stop66 codon (UA\*G) was either paired with uridine or mismatched with cytosine, guanosine or adenosine by incubating the mRNA with one of the four BG-modified guideRNAs 5'-BG-r(UCG GAA CAC CC~~X~~ AGC ACA GA), with X = C, U, G, or A. The standard editing conditions (concentrations, editing times, etc.) including 0.75 mM magnesium have applied as described in the method part of the manuscript.

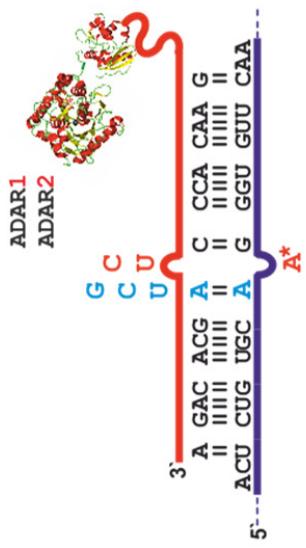
**Figure S2.1** Sequencing traces for the editing of the **UAG codon** under standard conditions including 0.75 mM magnesium as described in the method part of the manuscript.



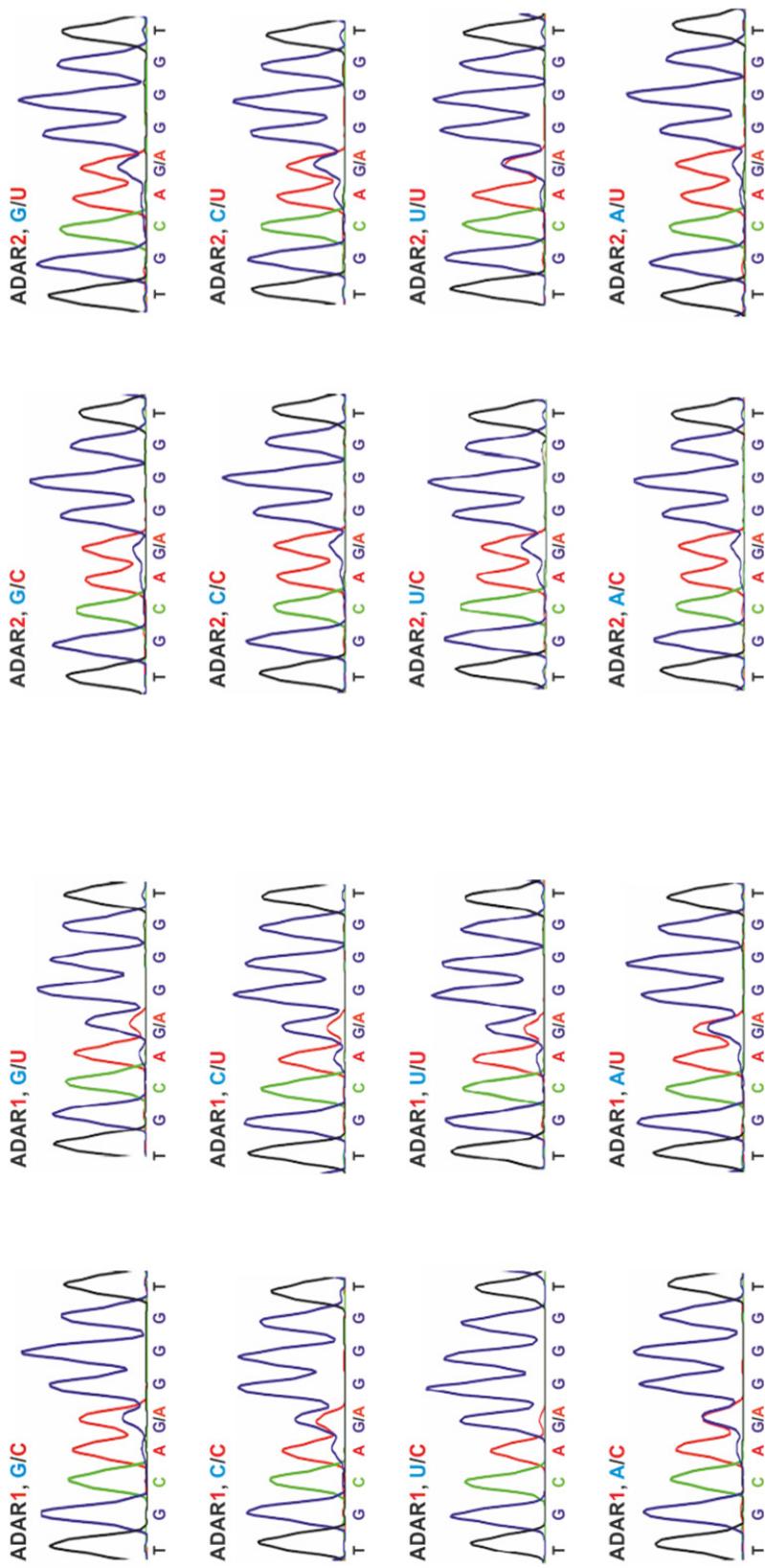


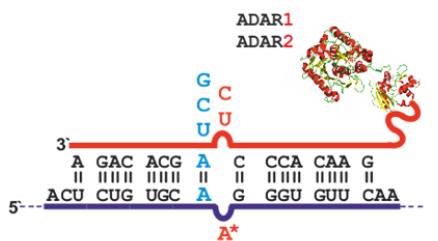
**Figure S2.2** Replicate of experiments shown in Figure S2.1, editing of the **UAG codon** under standard conditions including 0.75 mM magnesium.





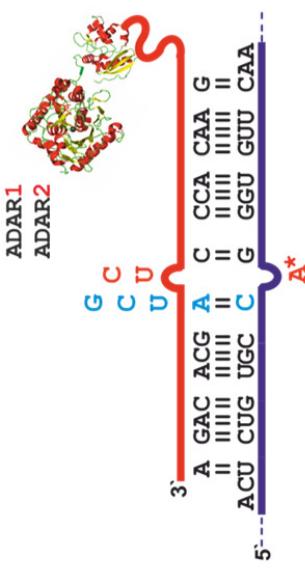
**Figure S3.1.** Sequencing traces for the editing of the **AAG codon** under standard conditions including 0.75 mM magnesium as described in the method part of the manuscript.



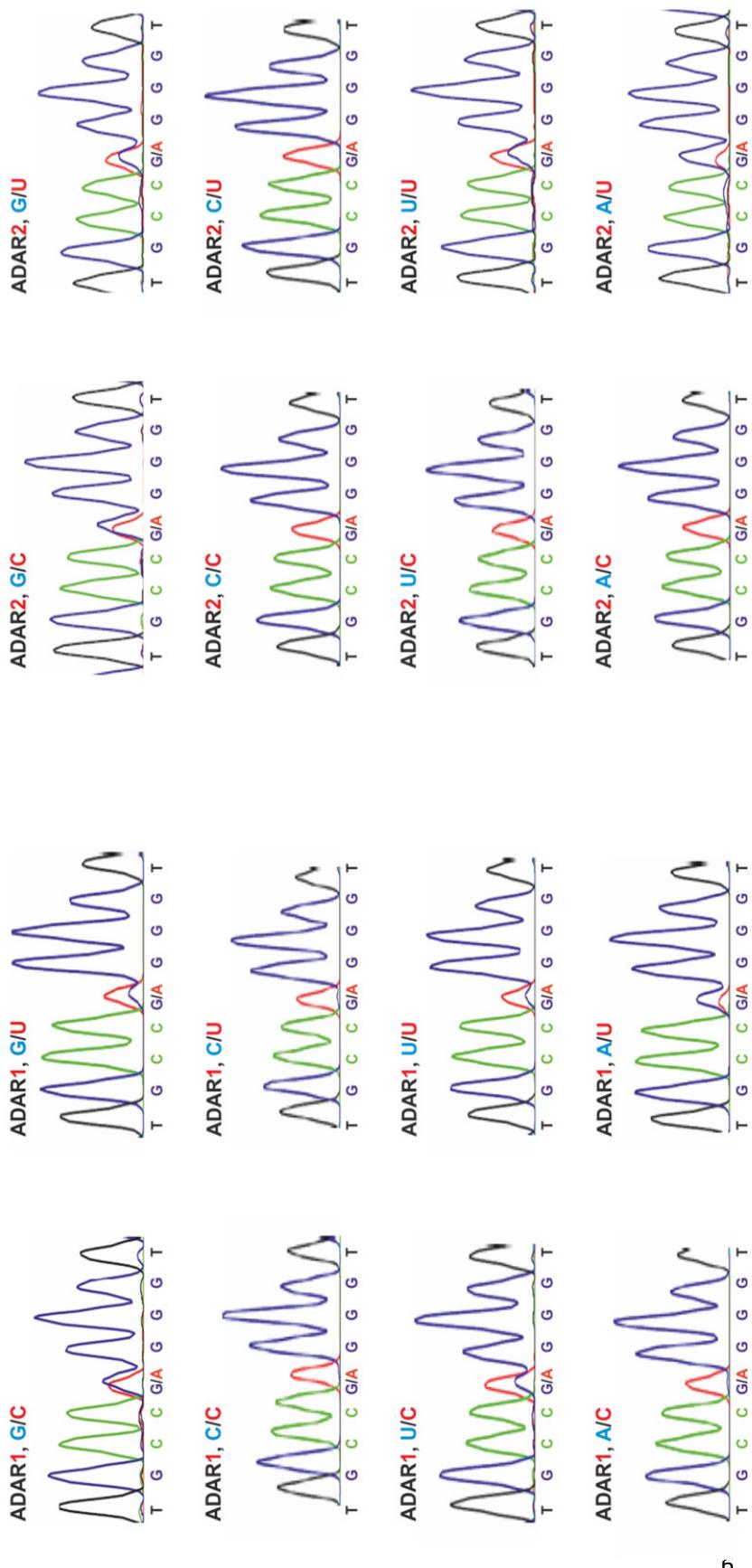


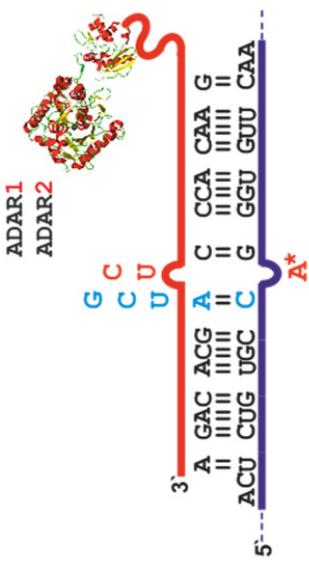
**Figure S3.2.** Replicate of the editing of the **AAG codon** with 0.75 mM magnesium as in Figure S3.



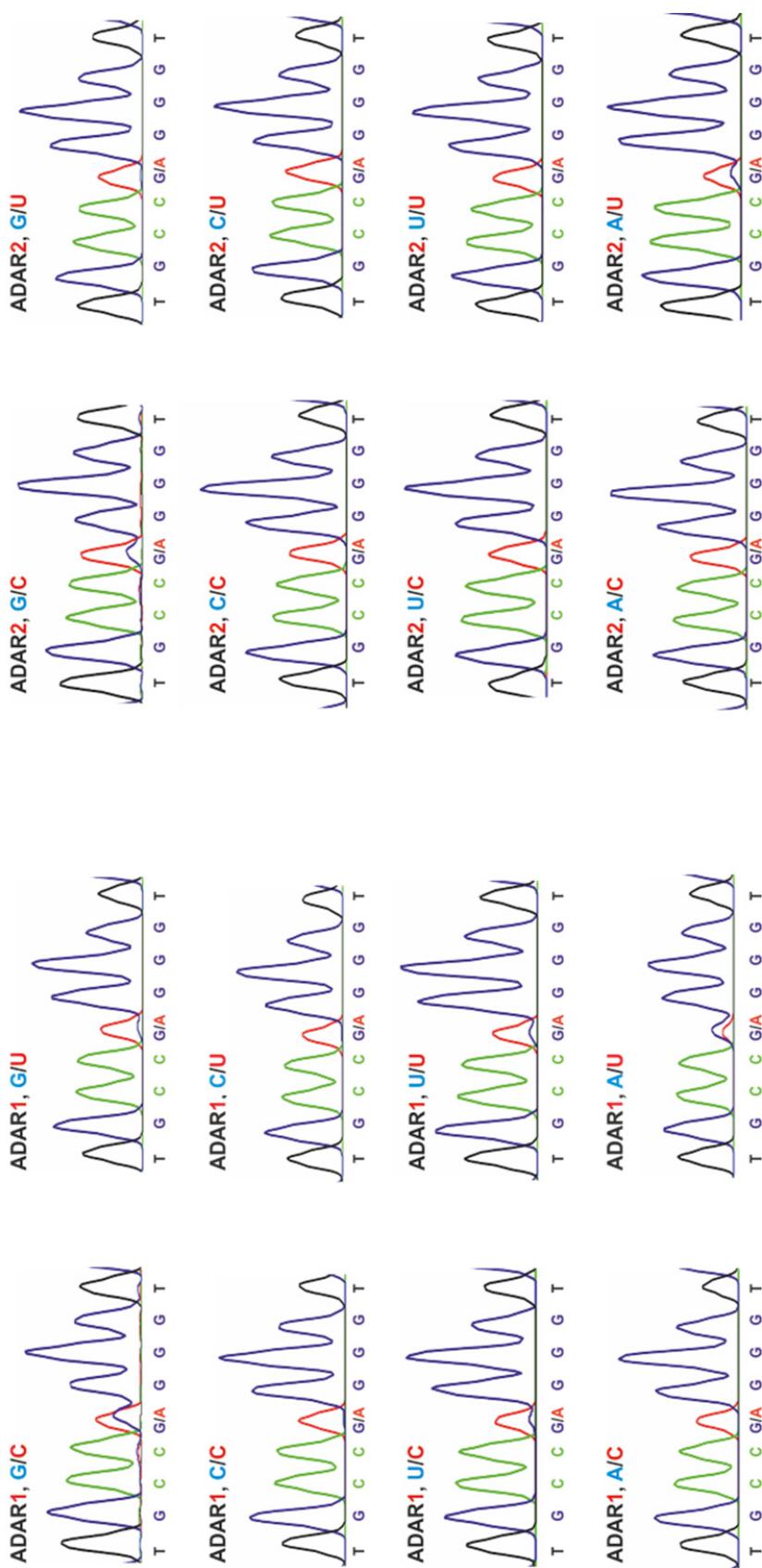


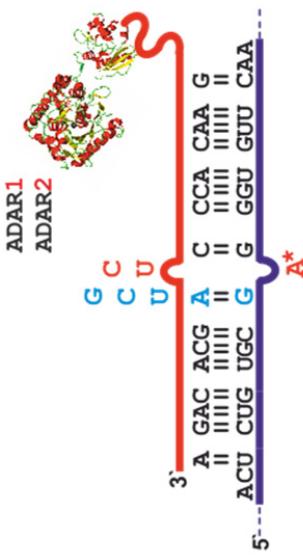
**Figure S4.1.** Sequencing traces for the editing of the **CAG codon** under standard conditions including 0.75 mM magnesium as described in the method part of the manuscript.



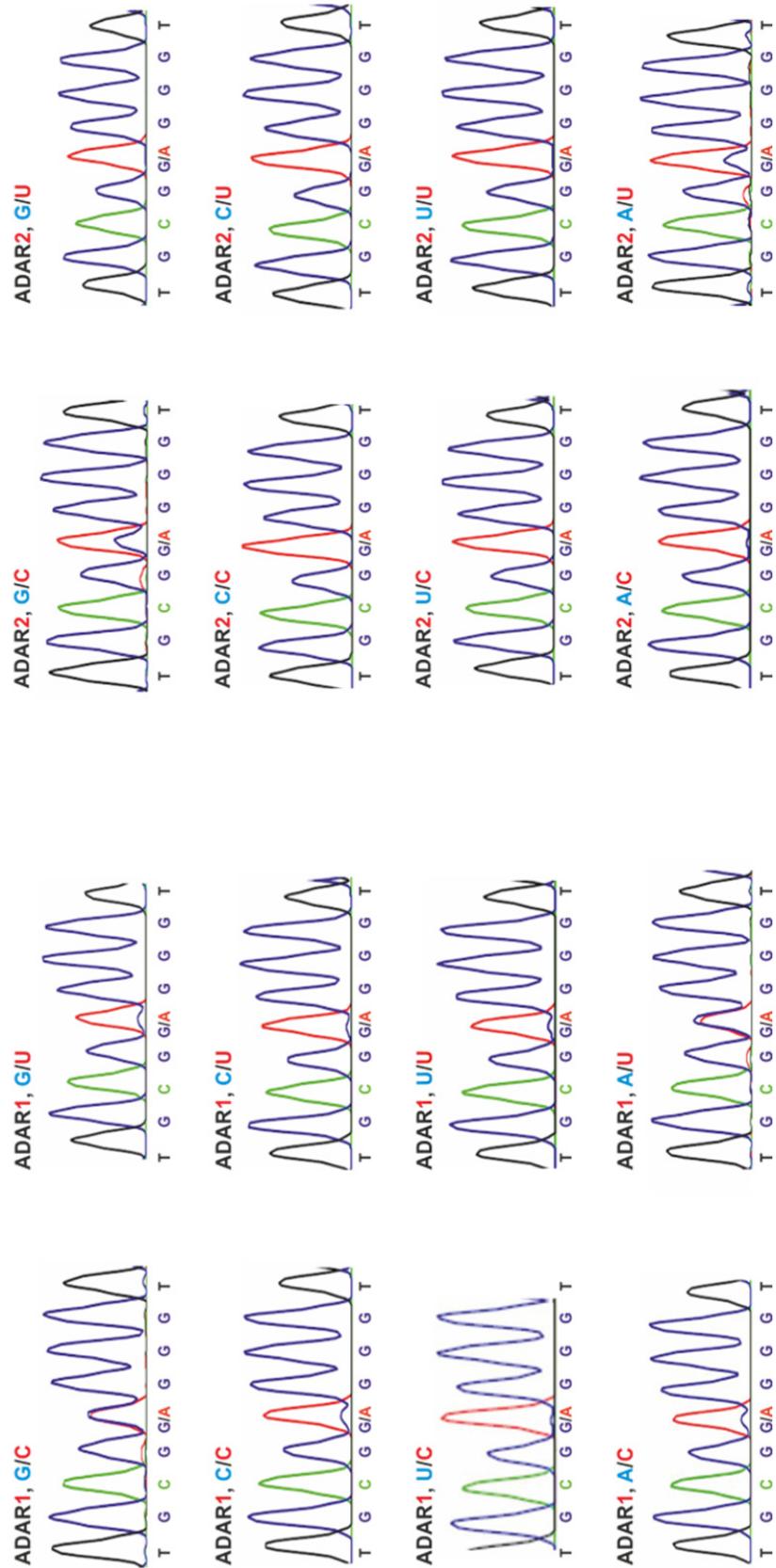


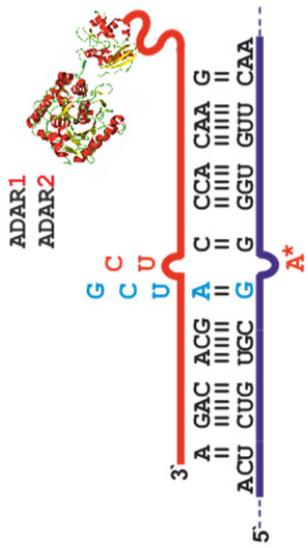
**Figure S4.2.** Replicate for the editing of the CAG codon with Mg as described in Figure S4.1.



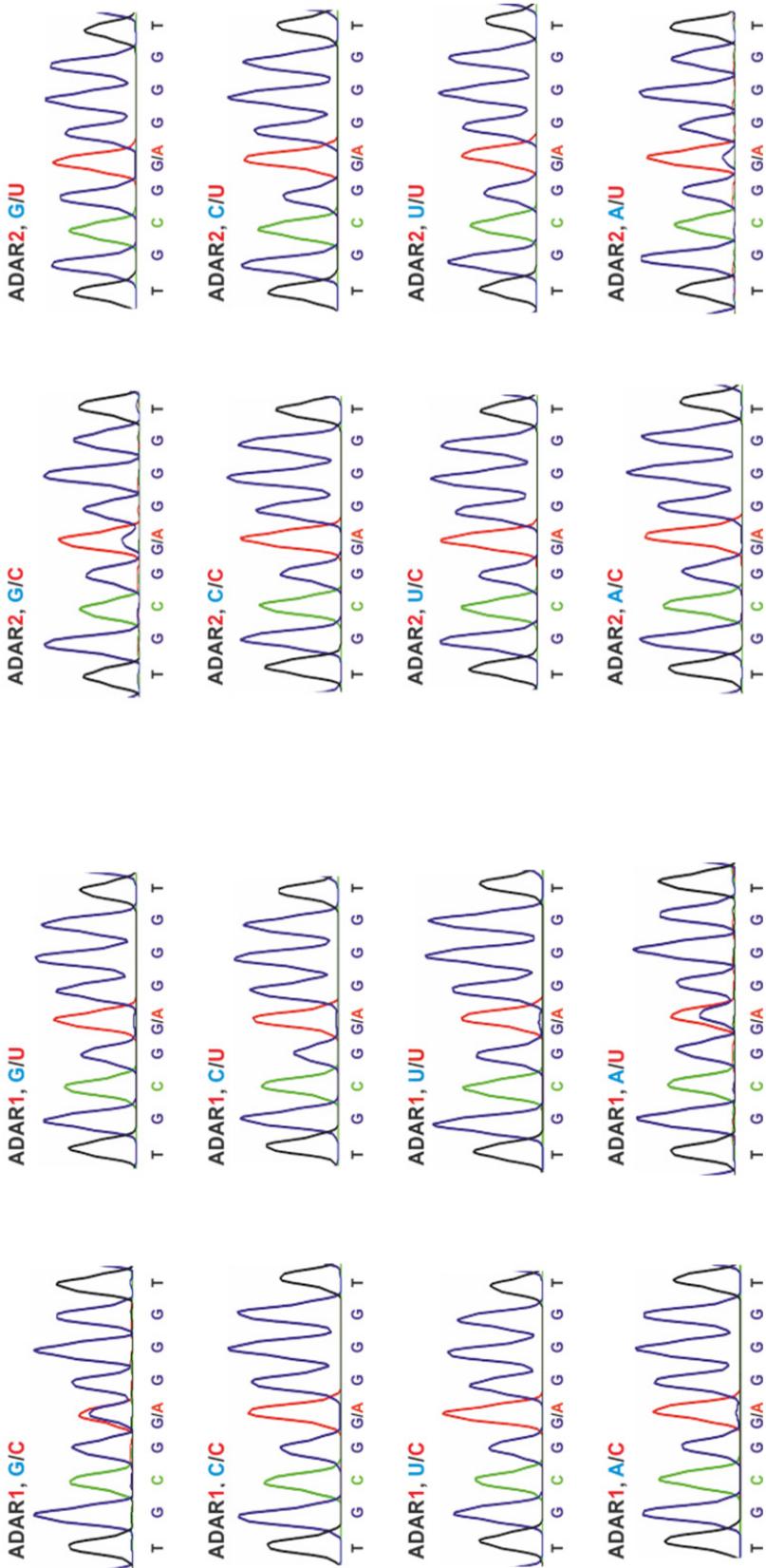


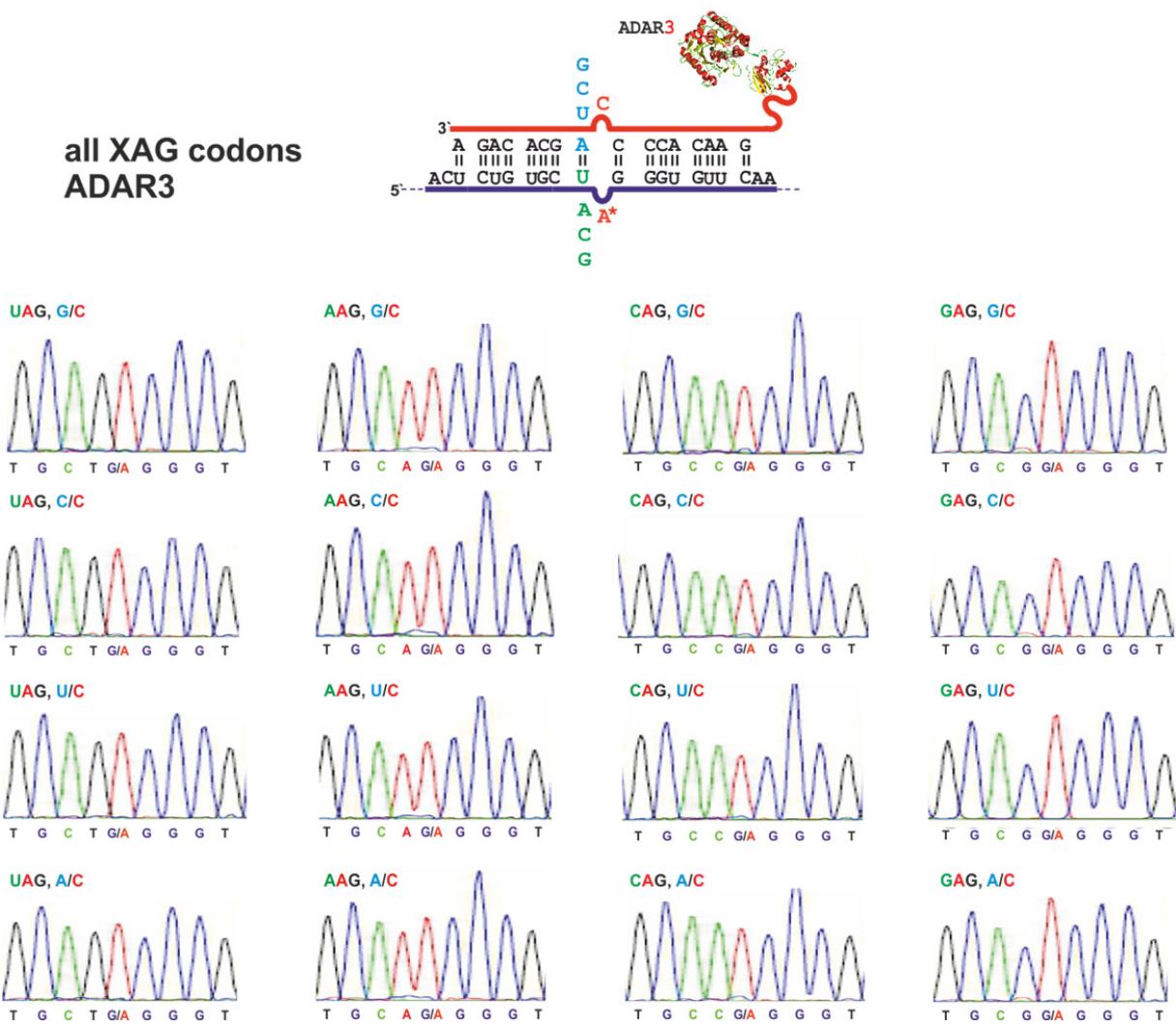
**Figure S5.1.** Sequencing traces for the editing of the **GAG codon** under standard conditions including 0.75 mM magnesium as described in the method part of the manuscript.





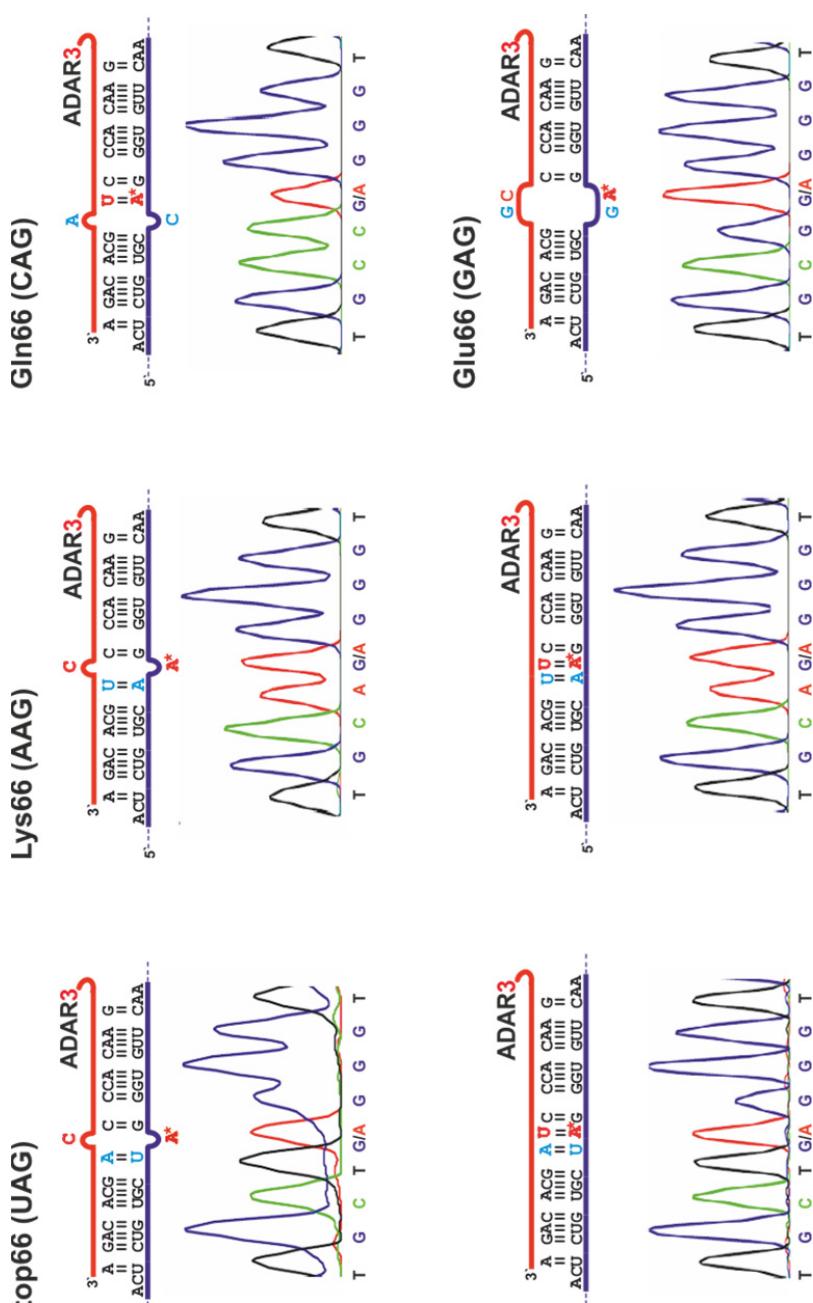
**Figure S5.2.** Replication of the editing of the **GAG codon** shown in Figure S5 under standard conditions including 0.75 mM magnesium.

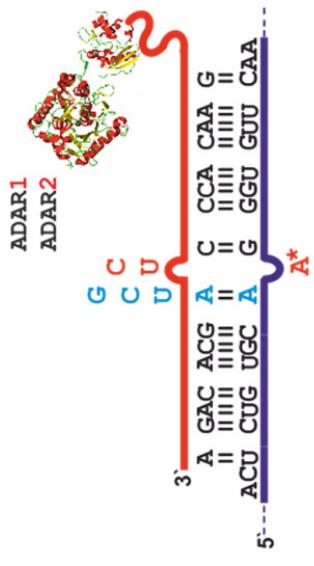




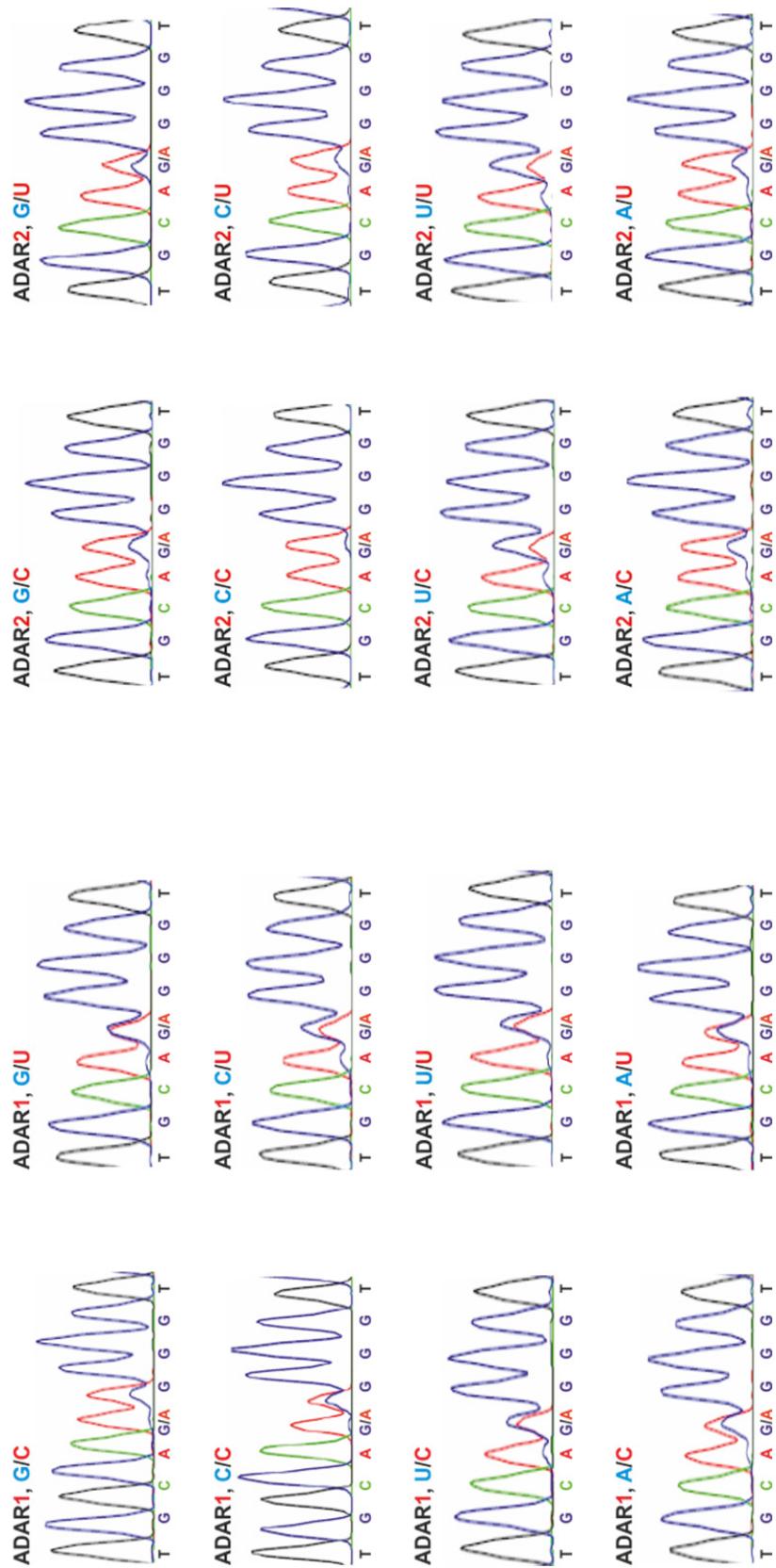
**Figure S6.** Sequencing traces for the editing of all four **XAG codons** ( $X = U, A, C, G$ ) with SNAP-ADAR3 in presence of one of the four guideRNAs putting the targeted adenosine into A/C mismatch. Editing was done under standard conditions but in the absence of magnesium as described in the method part of the manuscript.

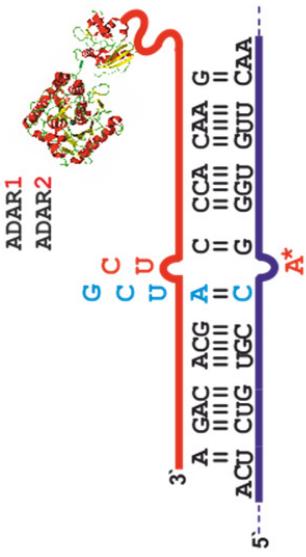
**Figure S7.** Sequencing traces for the editing of all four **XAG codons** ( $X = U, A, G, C$ ) with **SNAP-ADAR3** and a few selected guideRNAs under standard conditions including 0.75 mM magnesium as described in the method part of the manuscript.



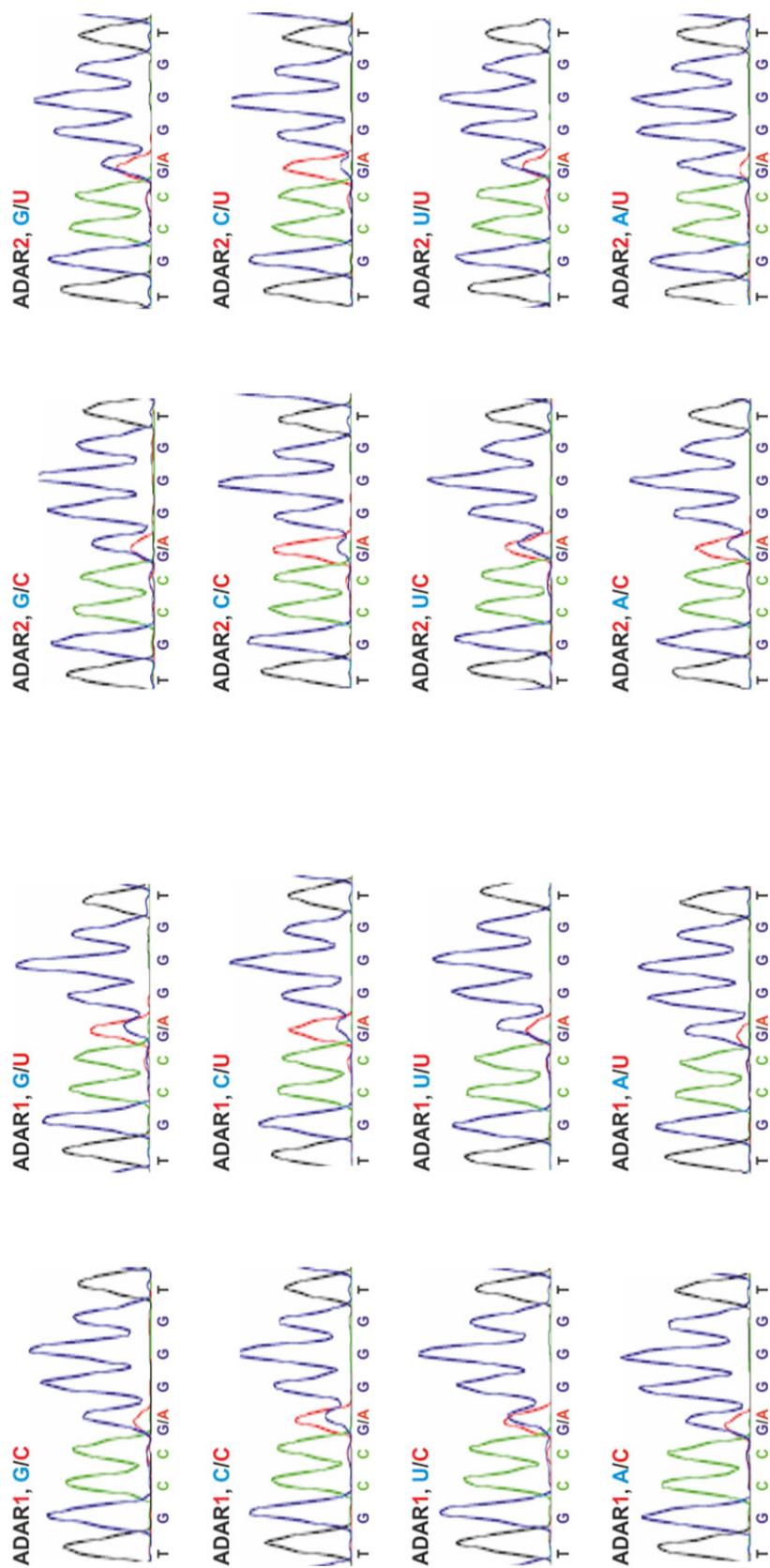


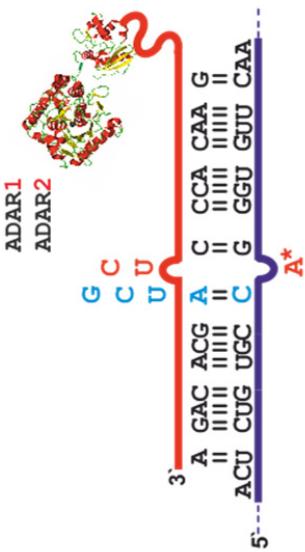
**Figure S8.** Sequencing traces for the editing of the AAG codon under standard conditions in the absence of magnesium as described in the method part of the manuscript. All other conditions were kept constant compared to the experiments shown in Figure S3.



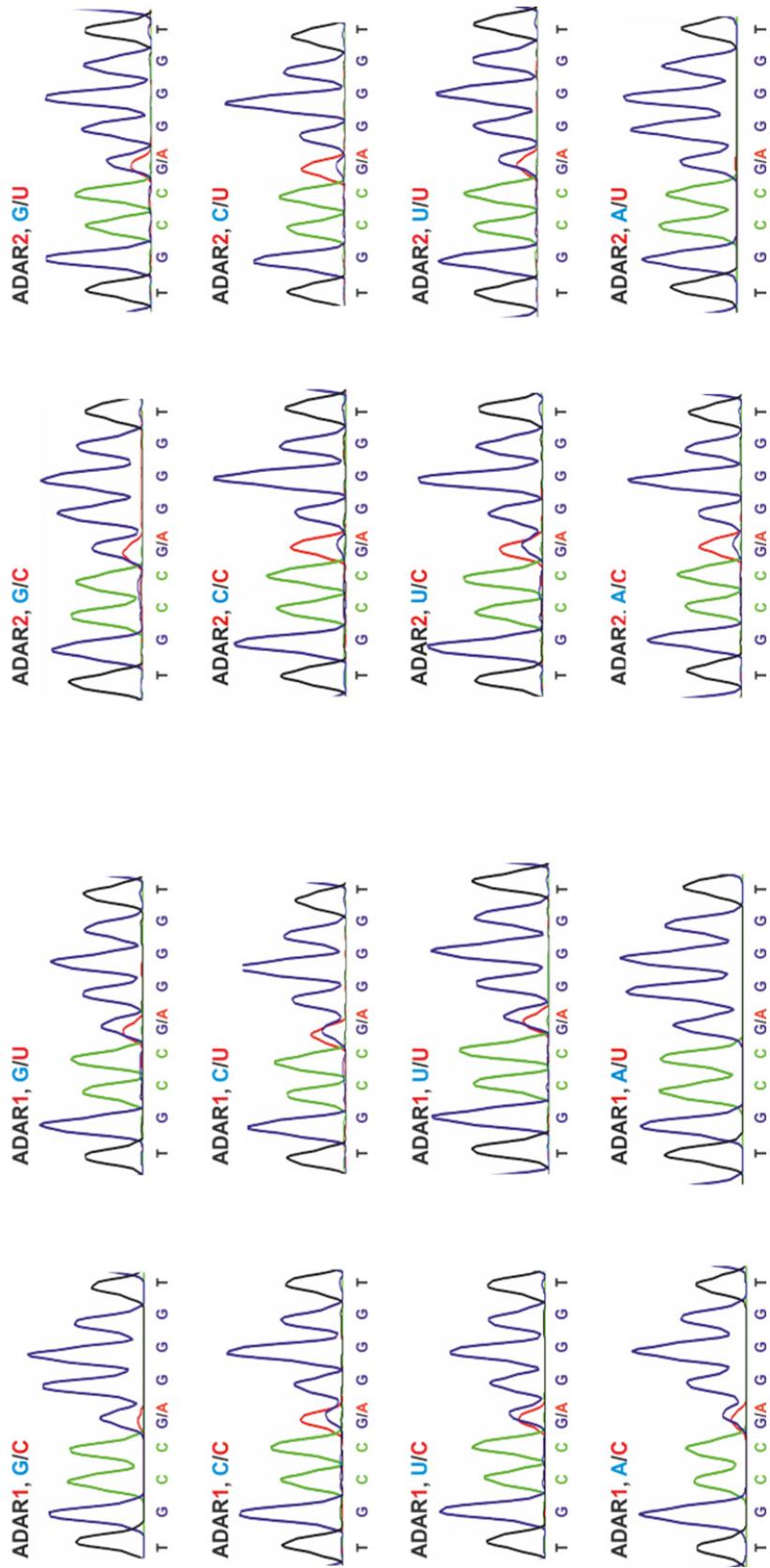


**Figure S9.1.** Sequencing traces for the editing of the CAG codon under standard conditions in **absence** of magnesium as described in the method part of the manuscript. All other conditions were kept constant compared to the experiments shown in Figure S4.





**Figure S9.2.** Replicate of editing of the **CAG codon** under standard conditions in **absence** of magnesium as described Figure S9.1



**Figure S10.** Sequencing traces for the editing of the **GAG codon** under standard conditions in **absence** of magnesium as described in the method part of the manuscript. All other conditions were kept constant compared to the experiments shown in Figure S5.

