Supplementary figure 1

**A**

Supplementary figure 1 Building the single-copy EGFP<sup><i>fluor</i></sup> / EGFP<sup><i>Y66S</i></sup> reporter HAP1 cell lines (A)

Schematic of the human AAVS1 locus and two homologous arms (HA-L and HA-R) used to build the donor plasmids. The AAVS1-T2 spacer spanned the border between HA-L and HA-R regions on the genome. The corresponding single guide RNA (sgRNA) targeting the AAVS1-T2 spacer sequence together with SpCas9 protein and donor plasmid were electroporated into HAP1 cells. SpCas9-induced DNA DSB facilitated the HDR using the donor plasmid as repair template. The correctly targeted allele contained a UCOE (Ubiquitous Chromatin Opening Element) sequence, a human EF1alpha promoter, an EGFP<sup><i>fluor</i></sup> or EGFP<sup><i>Y66S</i></sup> reporter gene, an IRES (Internal Ribosome Entry Site) sequence and a puromycin resistant gene, which were flanked by two homologous arms. (B) To verify the correct single
allele targeting, we utilized a PCR based strategy. First, the PCR product across the HA-L border (using the primer pair L-Fw/L-Rv) verified the correct homologous recombination of HA-L, which resulted in a 1127-bp band on the gel image (black arrows represented the positive integrations). The HA-L-integrated clones were selected to proceed with the HA-R border PCR analysis using the primer pair R-Fw/R-Rv, and a 1178-bp band indicated a correct integration of HA-R. Subsequently, the double positive clones from the border PCR analysis were further screened by another round of PCR using the primer set W-Fw and W-Rv, which selected the clones containing a non-integrated allele (a 1090-bp band on the gel image). Finally, two primer sets, Fw1/Rv1 and Fw2/Rv2, targeting two small regions located on the donor plasmid outside the ‘HA-L-reporter-HA-R’ region were used to exclude the random integration of the donor plasmid. The 392-bp and 194-bp bands indicated the corresponding plasmid regions were randomly integrated in the genome, whereas the double negative clones (red arrows) from this analysis were finally selected as the correct single-copy reporter clones. The gel images shown here were selected to represent the principle. (C) Clone screening. * Survived clones from a full 96-well plate of single cells from single-cell sorting, ** Double positive clones from a border PCR screen, *** Single-copy reporter clones from a PCR-based zygosity screen. PCR primers were listed in Supplementary table 1.
Supplementary figure 2

(A) Verifying CAPR by Sanger sequencing

To confirm the repair of EGFP_{\text{\textsuperscript{\textit{\textit{\textit{fluor}}}}}} reporter cells by CAPR (including ‘single-cut’ controls), EGFP positive cells were FACS-sorted in both bulk and single cells. Genomic DNA was isolated from both bulk EGFP positive cells and from 20 EGFP-positive clones respectively. The target locus on the genomic DNA then was amplified by PCR, and the PCR products were further analyzed by Sanger sequencing. Chromatograms, from top to bottom, exhibited unrepaired fluorophore-removal locus of the EGFP_{\text{\textsuperscript{\textit{\textit{\textit{fluor}}}}}} reporter gene, the EGFP fluorophore restored by the homologous repair insert with dual or single cut.
AsCas12a cleavage and the repair using a non-homologous repair insert. In the chromatograms showing the repaired EGFP\textsuperscript{\Deltafluor} reporter genes, the recovered EGFP fluorophore coding region was covered by green shadow. Because all the sequencing data did not show mutations, we only present one chromatogram from each group.

**B) Indel efficiencies of AsCas12a-created ‘left cut’ and ‘right cut’ on the EGFP\textsuperscript{\Deltafluor} reporter gene**

To assess the indel efficiencies of two AsCas12a cleavage sites, ‘left cut’ and ‘right cut’, on the EGFP\textsuperscript{\Deltafluor} reporter gene (we used these two sites in CAPR studies. Figure 1). AsCas12a protein and crRNA targeting each site were respectively transduced into the single-copy EGFP\textsuperscript{\Deltafluor} reporter cells. Following genomic DNA isolation, the PCR amplified targeting locus was used to perform T7E1 assay. The schematic displays the predicted cleavage patterns of uncut, left-cut and right-cut PCR products after T7 endonuclease treatment. The agarose gel showed T7 endonuclease-resulting fragments. Band sizes are indicated at the right side of the gel image. The indel efficiencies were quantified using ImageJ analysis of the gel image.
Supplementary figure 3

(A) To examine how AsCas12a protein concentration influenced the LAHR efficiency, we tested an AsCas12a protein gradient using the EGFP$^{Y66S}$ mutant reporter cells. At a final concentration of 15 µM
AsCas12a, LAHR efficiency plateaued. Error bars correspond to the standard deviation of the average of n = 3 parallel samples. The experiment was repeated three times and a representative dataset is presented here. (B) With different molar ratios between AsCas12 protein and crRNA, LAHR was performed to repair the EGFP<sup>Y66S</sup> mutation. The experiment demonstrates that 1:4 is the optimized ratio. Error bars corresponded to the standard deviation of the average of n = 3 parallel samples. The experiment was repeated three times and a representative dataset was presented here. (C) The repair efficiency showed a positive correlation with the increasing amount of LAHR template. Error bars corresponded to the standard deviation of the average of n = 3 parallel samples. The experiment was repeated three times and a representative dataset was presented here.
Supplementary figure 4

Cell viability assessment following iTOP transduction of LAHR components

The post-iTOP cell viabilities of different cell lines were assessed by MTS assay. The MTS assay was performed 24 hours after iTOP transduction. The bar graphs show the viabilities of different cell lines that performed iTOP deliveries of 80-bp LAHR or 100-nt ssODN template in different quantities, together with AsCas12a protein and crRNA. We observed no significant difference in cell viability between the empty iTOP and the no-template DNA controls and any of the tested template samples. Error bars corresponded to the standard deviation of the average of n = 3 parallel samples. The experiment was repeated three times and a representative dataset was presented here. Statistical test: two-tailed unpaired t-test, ns P > 0.05.
Here, we examined HDR efficiency using reverse complementary ssODN templates (ssODN1 and ssODN2) in the EGFP<sup>Y66S</sup> reporter cell line. Since the AsCas12a PAM (green arrow) and SpCas9 PAM (orange arrow) had the same orientation, for both, the top strand was the ‘non-target strand’ and the bottom strand was a ‘target strand’. The ssODN1 from the ‘target strand’ favored the Cas9-mediated HDR, while the ssODN2 from the ‘non-target strand’ favored Cas12a-mediated HDR. This result is consistent with the previously published data (1,2). Error bars corresponded to the standard deviation of the average of n = 3 parallel samples. The experiment was repeated three times and a representative dataset is presented here.
Supplementary figure 6

The ‘A200C’ mutation that turned EGFP off in the EGFP<sup>Y66S</sup> reporter cells is indicated as a red C/G pair. LAHR templates I to VIII contained base substitutions (blue base pairs) to introduce silent mutations. FACS data (Green bars) showed the percentages of EGFP positive cells after LAHR. The gray bars indicate the repair efficiency of the A200C mutation using the indicated templates. Error bars correspond to the standard deviation of the average of n = 3 parallel samples.

Supplementary figure 6 FACS and NGS analyses for LAHR in repairing the ‘A200C’ mutation
Supplementary figure 7 Improving LAHR efficiency by PAM sequence or seed region disruption

(A) In this study, we used the EGFP<sup>Y66S</sup> reporter cell line described above. The targeting locus is indicated as a stretch of gray-shadowed dsDNA, and the A200C mutation is shown as a red C/G pair. The AsCas12a PAM sequence is indicated by a green arrow on top, and the seed region is green-
underlined. To examine the effects of PAM sequence or seed region disruption on LAHR editing efficiency, we designed different LAHR templates containing silent mutations to destroy PAM sequence (Mut 1), seed region (Mut 2) and both (Mut 3) as indicated. The ‘Control 1’ template was a LAHR template with unchanged PAM and seed sequences. In addition, for comparison, we also included ssODN templates containing same mutations as those in the LAHR templates, which were ‘Mut 4’ with mutated PAM, ‘Mut 5’ with mutated seed and ‘Mut 6’ with both. The ‘Control 2’ template was an unmutated ssODN template. (B) The corresponding A200C repair efficiencies are indicated by the percentage of EGFP positive cells based on FACS analysis. Error bars correspond to the standard deviation of the average of n = 3 parallel samples.
Supplementary figure 8 Delivering Cas12a RNP and LAHR template with electroporation

To examine the applicability of LAHR with a non-iTOP delivery method, we electroporated AsCas12a RNP and LAHR template into the single-copy EGFP<sup>Y66S</sup> cells. We tested the LAHR efficiency in two quantity setups, 50 pmol and 500 pmol, and the molar ratio between components is 1:1. The graph depicts the percentage of EGFP-positive cells from the FACS analysis. Error bars correspond to the standard deviation of the average of n = 3 parallel samples. The experiment was repeated three times and a representative dataset is presented here.
Supplementary figure 9

Introducing single nucleotide substitutions in endogenous genes by LAHR and HDR

Supplementary figure 9 Introducing single nucleotide substitutions in endogenous genes by LAHR and HDR
(A) A single nucleotide substitution, C698874T, was introduced in human ALK by LAHR or Cas9-mediated HDR. The editing locus, between 698861 and 698898, was in the intron 19 of the ALK gene, and is shown as double-stranded DNA. The AsCas12a PAM is indicated by a green arrow. Green arrow heads indicate the AsCas12a cleavage sites. The yellow-shadowed base pair is the base substitution target. The SpCas9 PAM is indicated by a blue arrow. The alignments below the schematic are the NGS results. Guide RNA targeting sequences are underlined by grey bars. The C698874T substitution is highlighted by a blue box. The percentage of the total reads and the number of reads (in brackets) is shown at the end of each edited sequence. (B) A single nucleotide substitution, A474580G, was introduced in human CACNA1D by LAHR or Cas9-mediated HDR. The editing locus, between 474555 and 474591, was in the exon 43 of the CACNA1D gene, and is shown as double-stranded DNA. The AsCas12a PAM is indicated by a green arrow. Green arrow heads indicate the AsCas12a cleavage sites. The yellow-shadowed base pair is the base substitution target. The SpCas9 PAM is indicated by a blue arrow. The alignments below the scheme are the NGS results. Guide RNA targeting sequences are underlined by grey bars. The A474580G substitution is highlighted by a blue box. The percentage of the total reads and the number of reads (in brackets) is shown at the end of each edited sequence.
Supplementary figure 10

A

|       | PARP1 | RAD52 | POLQ | RAD51 | 53BP1 | XRCC5 |
|-------|-------|-------|------|-------|-------|-------|
| mRNA relative expression level (%) |
| WT    | #1    | #2    | #1   | #2    | #1    | #2    |

B

Day -1: cell preparation
Day 0: siRNA transfection
Day 1-2: medium change and passage
Day 3: cell seeding for ITOP
Day 4: ITOP delivery of A5Cas12a, cRNA and LAHR template
Day 6: culture on dish

RNA isolation and qPCR

Day 6: harvest

FITC intensity FACS analysis

C

|       | PARP1 | RAD52 | POLQ | RAD51 | 53BP1 | XRCC5 |
|-------|-------|-------|------|-------|-------|-------|
| mRNA relative expression level (%) |
| WT    | #2    | WT    | #2   | WT    | #2    | WT    | #1    |

15
Supplementary figure 10

(A) Selection of the siRNA achieving efficient knockdown
For each target gene, two siRNAs (#1 and #2) were tested. The bar graphs show the expression level of each target gene 48 hours after transfection. ‘WT’ indicates the expression level of the target gene in an siRNA-free control transfection sample. Error bars correspond to the standard deviation of the average of 3 biological replicate groups, in each of which 3 technical replicates were included. Statistical test: two-tailed unpaired t-test, ns P > 0.05, * P < 0.05, ** P < 0.01, *** P < 0.001.

(B) Experimental setup of LAHR under siRNA knockdown conditions
Schematic representation of the experimental setup. In brief, siRNA transfections (using selected siRNAs from (A)) were performed on day 0. Two days after, each siRNA-transfected sample was split into two plates. One group of plates was prepared for the iTOP transduction on day 4, followed by FACS analysis on day 6 to determine the repair efficiencies under different knockdown conditions, while cells on the other group of plates were cultured till day 6 for RNA isolation and the qPCR analysis to examine the knockdown efficacies of the target genes at the time point when LAHR were applied.

(C) Confirmation of the siRNA-knockdown efficacy by qPCR
Analysis of the knockdown efficacies of target genes at the time point of LAHR editing by qPCR. The bar graphs demonstrate the gene expression level. ‘WT’ indicated the expression level of the target gene in an siRNA-free control transfection sample. Error bars correspond to the standard deviation of the average of 3 technical replicates. Statistical test: two-tailed unpaired t-test, * P < 0.05, *** P < 0.001.
Supplementary figure 11

Supplementary figure 11 Repairing the EGFP$^{Y66S}$ mutant by LAHR following a classic-MMEJ pathway
(A) Schematic representation of a LAHR template containing a 3’ homologous overhang, which forces the ligation step of LAHR to follow a classic MMEJ pathway. The targeting locus is presented as a stretch of dsDNA containing a mutation (red dots on both strands), the AsCas12a cut site is indicated by purple arrow heads and a homologous region is indicated with brown blocks. The LAHR template (with a 3’ overhang) contains a base substitution (green dots on both strands) and a 3’ homologous overhang (a brown block). After AsCas12a cleavage, the homologous region on the editing locus was double-stranded, which only matched the 3’ homologous overhang on the repair if a compatible 3’ homologous overhang is created by resection. In the green box, the classic MMEJ pathway is shown.

(B) An LAHR template containing a 3’ homologous overhang was used to repair the EGFP<sup>Y66S</sup> mutation. A standard LAHR template (containing a 5’ overhang) was used as control. The bar chart shows the comparison of the repair efficiencies as percentage of the EGFP-positive cells determined by flow-cytometry analysis. Error bars correspond to the standard deviation of the average of n = 3 parallel samples. The experiment was repeated three times and a representative dataset is presented here. Statistical test: two-tailed unpaired t-test, *** P < 0.001.
Supplementary figure 12

Figure 2B

Figure 2C

Figure 3A

Figure 4B

Supplementary figure 6

Supplementary figure 12 FACS plots of Figure 2, 3, 4 and Supplementary figure 6
Supplementary Table 1 Border-PCR primers

| Name | Sequence (5’ to 3’) |
|------|---------------------|
| L-Fw | TGGACTTGTCTCCTTCCCTG |
| L-Rv | GTGGATGAATACTGCACATTGTG |
| R-Fw | ATGATCGTGTCGTTTGTTT |
| R-Rv | AGACCTGACCCAAACCAG |
| W-Fw | TGGACTTTGTCTCCTTCCCTG |
| W-Rv | TGGGGCTTTTCTGCAACCAT |
| Fw1  | GAAGAATCGCAAAAACCAGAAG |
| Rv1  | ATCGAATTGCTGCTCAGT |
| Fw2  | ATTGCCACCCCTGTCAGC |
| Rv2  | GCAGAATCCAGGTTGGCAAC |

Supplementary Table 2 gBlock fragments of EGFP mutants

| Name | Sequence (5’ to 3’) |
|------|---------------------|
| EGFP<sup>Δfluor</sup> | GTGAAGCGGCCGCGCCACATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTG |
|           | CCCATCTGGTCTGAGCTGACGGCGACGTAAACGGCACAAGTTTACGCTGCTCGG |
|           | CGAGGGCGAGGGCGATGCCCATCGAGCGCGACACTGAAATTTCCTCGACCAC |
|           | CGGCAAGCCTGGCCGGCTCCGACCACCTGTTAACGCTGCTGCTG |
|           | CCGCTACCCCGACCACATAGAAGAGCAAGCATCTTCTTCTCAAGTGGCACCTG |
|           | CTACGTCCAGAGGCACCACCATCTTCTTCTCAAGAGCAAGGCAACTACAAGACCC |
|           | CGGAGTGAAGTGGCTCCGAGACCGCAGCGTGCAGCTCGCCGACCACTAC |
|           | ATTTCAAGAGGAGCCCAAAACATCTGCTGGGCACAAAGCTGACGAGGCAAG |
|           | ACAACGTCTATATCATGCGCCGACAAGCAGAGAAGAGGCAACTACAAGACCC |
|           | CGGCAACTACAGGGCGACCGACGCTCGCGGACCAACTACAGGAGGCAAC |
|           | CCGCCATCGGCGAGGCCCCGTGGTCGCCGACAAACCACCTACGAGGCAAG |
|           | TCCGCCCTGAGCAAAGCACCACAGAGAGGCGCGATCACAGTGGCTGCGTAC |
|           | GTGACCGCCGGGGGATCCTCCTCGGCATGGAGGAGCTGCTGACTAAAGTAA |
| EGFP<sup>Y66S</sup> | GTGAAGCGGCCGCGCCACATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTG |
|           | CCCATCTGGTCTGAGCTGACGGCGACGTAAACGGCACAAGTTTACGCTGCTCGG |
|           | CGAGGGCGAGGGCGATGCCCATCGAGCGCGACACTGAAATTTCCTCGACCAC |
|           | CGGCAAGCCTGGCCGGCTCCGACCACCTGTTAACGCTGCTGCTG |
|           | CCGCTACCCCGACCACATAGAAGAGCAAGCATCTTCTTCTCAAGTGGCACCTG |
|           | CTACGTCCAGAGGCACCACCATCTTCTTCTCAAGAGCAAGGCAACTACAAGACCC |
|           | CGGAGTGAAGTGGCTCCGAGACCGCAGCGTGCAGCTCGCCGACCACTAC |
|           | ATTTCAAGAGGAGCCCAAAACATCTGCTGGGCACAAAGCTGACGAGGCAAG |
|           | ACAACGTCTATATCATGCGCCGACAAGCAGAGAAGAGGCAACTACAAGACCC |
|           | CGGCAACTACAGGGCGACCGACGCTCGCGGACCAACTACAGGAGGCAAC |
|           | CCGCCATCGGCGAGGCCCCGTGGTCGCCGACAAACCACCTACGAGGCAAG |
|           | TCCGCCCTGAGCAAAGCACCACAGAGAGGCGCGATCACAGTGGCTGCGTAC |
|           | GTGACCGCCGGGGGATCCTCCTCGGCATGGAGGAGCTGCTGACTAAAGTAA |
Supplementary Table 3 Guide RNAs used in this study

| Name | Sequence (5' to 3') |
|------|---------------------|
| AAVS1 targeting (SpCas9) | GGGGCCACUAGGACAGGAGUUGUUAAGCATUCGAAUAUGCAAGUUAAA AUAAGGCUGACUGCGUUUAUCAUCUGAAAAGUGGCACCGAGUCGGGUC |
| CAPR-left (AsCas12a) | UAAUUUCACUCUUGUAAGAUAGGGUCAGCUUCGCUAGGUUGGC |
| CAPR-right (AsCas12a) | UAAUUUCACUCUUGUAAGAUAGCCGCUACCCCGACCACAUGAA |
| EGFPY66S (AsCas12a) | UAAUUUCACUCUUGUAAGAUAGUGACCACCCUGACCUCCGGCU |
| B2M (AsCas12a) | UAAUUUCACUUCUUGUAAGAUAGUGGACAAACACGAGAGCGGG |
| ALK (AsCas12a) | UAAUUUCACUCUUGUAAGAUAGUGGACAAACACGAGAGCGGG |
| CACNA1D (AsCas12a) | UAAUUUCACUCUUGUAAGAUAGUGGACAAACACGAGAGCGGG |
| PAM1 (SpCas9) | UUGGTGAACACCCUGACCUUGUUUAGAGCUAAUAUAGCAAGUUAAA AUAAGGCUGACUGCGUUUAUCAUCUGAAAAGUGGCACCGAGUCGGGUC |
| PAM2 (SpCas9) | GCUGAAGCAUGACGACCGGCUUUUAGAGCUAAUAUAGCAAGUUAAA AUAAGGCUGACUGCGUUUAUCAUCUGAAAAGUGGCACCGAGUCGGGUC |
| PAM3 (SpCas9) | GCGGCUGAAGCAUGACGACCGGCUUUUAGAGCUAAUAUAGCAAGUUAAA AUAAGGCUGACUGCGUUUAUCAUCUGAAAAGUGGCACCGAGUCGGGUC |
| B2M-PAM1 (SpCas9) | GAAGUGAACUUAUGAGAAAGUUGAAGGUAAUAGCAAGGUAAA AUAAGGCUGACUGCGUUUAUCAUCUGAAAAGUGGCACCGAGUCGGGUC |
| B2M-PAM2 (SpCas9) | CAGTAAAGTCCTTAAATGTGUUUUAGAGCUAAUAUAGCAAGUUAAA AUAAGGCUGACUGCGUUUAUCAUCUGAAAAGUGGCACCGAGUCGGGUC |
| B2M-PAM3 (SpCas9) | AAGTCACTTAAATGTGUUUUAGAGCUAAUAUAGCAAGUUAAA AUAAGGCUGACUGCGUUUAUCAUCUGAAAAGUGGCACCGAGUCGGGUC |
| ALK (SpCas9) | UGGACAAACACGAGAGGCUGUUGUUAAGAGCUAAUAUAGCAAGUUAAA AUAAGGCUGACUGCGUUUAUCAUCUGAAAAGUGGCACCGAGUCGGGUC |
| CACNA1D (SpCas9) | CAGUAGUAAAGGAUAGCUACGGGCUUUUAGAGCUAAUAUAGCAAGUUAAA AUAAGGCUGACUGCGUUUAUCAUCUGAAAAGUGGCACCGAGUCGGGUC |
### Supplementary Table 4 Repair inserts used in Figure 1

**EGFP fluorophore coding sequence**

| Name       | Sequence (5’ to 3’)                                                                 |
|------------|--------------------------------------------------------------------------------------|
| **sticky-ended** | GCCACCTACGGCAAGCTGCCCTTGAAATTCTGCACCACCGGGCAAGCTTGCAGTGTTCACGGCTACCCCGAGCACAC   |
|            | GCCCGTGCCCTGGCCACCCACCTCTGACCACCCCTGACCTACGGCTGTCAGTGGTTCACGGCTACCCCGAGCACAC   |
|            | GCCTACGGCTGACCTACGGCTGTCAGTGGTTCACGGCTACCCCGAGCACAC                             |
|            | TGCAGTGGTTCACGGCTACCCCGAGCACAC                                                 |
|            | GCCACCTACGGCAAGCTGCCCTTGAAATTCTGCACCACCGGGCAAGCTTGCAGTGTTCACGGCTACCCCGAGCACAC   |
|            | GCCCGTGCCCTGGCCACCCACCTCTGACCACCCCTGACCTACGGCTGTCAGTGGTTCACGGCTACCCCGAGCACAC   |
|            | GCCTACGGCTGACCTACGGCTGTCAGTGGTTCACGGCTACCCCGAGCACAC                             |
|            | TGCAGTGGTTCACGGCTACCCCGAGCACAC                                                 |
| **blunt-ended** | GCCACCTACGGCAAGCTGCCCTTGAAATTCTGCACCACCGGGCAAGCTTGCAGTGTTCACGGCTACCCCGAGCACAC   |
|            | GCCCGTGCCCTGGCCACCCACCTCTGACCACCCCTGACCTACGGCTGTCAGTGGTTCACGGCTACCCCGAGCACAC   |
|            | GCCTACGGCTGACCTACGGCTGTCAGTGGTTCACGGCTACCCCGAGCACAC                             |
|            | TGCAGTGGTTCACGGCTACCCCGAGCACAC                                                 |
|            | GCCACCTACGGCAAGCTGCCCTTGAAATTCTGCACCACCGGGCAAGCTTGCAGTGTTCACGGCTACCCCGAGCACAC   |
|            | GCCCGTGCCCTGGCCACCCACCTCTGACCACCCCTGACCTACGGCTGTCAGTGGTTCACGGCTACCCCGAGCACAC   |
|            | GCCTACGGCTGACCTACGGCTGTCAGTGGTTCACGGCTACCCCGAGCACAC                             |
|            | TGCAGTGGTTCACGGCTACCCCGAGCACAC                                                 |
| **sticky-ended (non-homologous)** | GCCACGTATGGGAAATTAACATTAAAGTTTATATGTACGACGGGAAAATTAACCATATCGCCGTGCACCACCTCTG    |
|            | GCCCTAAGGTCAGGGTAGGTGCCACACCGGGCGAGGGTAGGTGCCACACCGGGCGAGGGTAGGTGCCACACCTCTG    |
|            | GCCTAAGGTCAGGGTAGGTGCCACACCGGGCGAGGGTAGGTGCCACACCTCTG                            |
|            | TGCAGTGGTTCACGGCTACCCCGAGCACAC                                                 |

### Supplementary Table 5 Repair templates used in Figure 2

**Mutation site**

| Name | Sequence (5’ to 3’)                                                                 |
|------|--------------------------------------------------------------------------------------|
| 20 bp | GGTGACCACCTGACCTCTCAG                                                               |
|      | ACGCCGGTAGTCAGGGGCTGGTCCACC                                                       |
| 40 bp | CCCGTCACCTGGCCATTTTGACCACCCCTGAGCTCG                                               |
|      | ACGCCGGTAGTCAGGGGCTGGTCCACC                                                       |
| 60 bp | TCTGACCACCGCAAGCTGCCCCTGGCCTGGCCACCTTTGACCACCCCTGACCTCG                             |
|      | CGTAGGGCGGGGAGCTGGTGCGACGAGCTTGGGAGCAGGGGAGCTGGTGCAAG                                 |
| 80 bp | CAAGGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG |
|      | ACGCCGGTAGTCAGGGGCTGGTCCACC                                                       |

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### 100 bp

| Sequence | Description |
|----------|-------------|
| GAGGGGGATGCGACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACGGCAAGCTGCCCGTGCCCTGGCCCACTTTGGTGACCACCCTGACCT | |
| ACGCCGAGGTCAAGGGTCTGACCAAATGGGCCAGGGCAGGGCAGCTTGGCG | |
| GTTGTGACAGATGAACTTCCAAGGTCAGCTTGACCTCCCTCGCGCTCCCTCGCGCCGGACACGCTGA | |

### 120 bp

| Sequence | Description |
|----------|-------------|
| TCAGCGTGTCGCCGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACGGCAAGCTGCCCGTGCCCTGGCCCACTTTGGTGACCACCCTGACCT | |
| ACGCCGAGGTCAAGGGTCTGACCAAATGGGCCAGGGCAGGGCAGCTTGGCG | |
| GTTGTGACAGATGAACTTCCAAGGTCAGCTTGACCTCCCTCGCGCTCCCTCGCGCCGGACACGCTGA | |

### 160 bp

| Sequence | Description |
|----------|-------------|
| ATCCCTGGTGTCAGCTGAGCGGAGGCTAAAGGCAAACTGACGTGCTGGGCG | |
| ACGCCGAGGTCAAGGGTCTGACCAAATGGGCCAGGGCAGGGCAGCTTGGCG | |
| GTTGTGACAGATGAACTTCCAAGGTCAGCTTGACCTCCCTCGCGCTCCCTCGCGCCGGACACGCTGA | |

### 200 bp

| Sequence | Description |
|----------|-------------|
| GTTGAAGGAGGGCGAGGGTCTGACCAAATGGGCCAGGGCAGGGCAGCTTGGCG | |
| ACGCCGAGGTCAAGGGTCTGACCAAATGGGCCAGGGCAGGGCAGCTTGGCG | |
| GTTGTGACAGATGAACTTCCAAGGTCAGCTTGACCTCCCTCGCGCTCCCTCGCGCCGGACACGCTGA | |

### 4-nt 5’ overhang

| Sequence | Description |
|----------|-------------|
| CAAGCTGACCTGAAGTTCCAACCGGGCAAGCTGCCCTCCCTGGCCCG | |
| ACGCCGAGGTCAAGGGTCTGACCAAATGGGCCAGGGCAGGGCAGCTTGGCG | |
| GTTGTGACAGATGAACTTCCAAGGTCAGCTTGACCTCCCTCGCGCTCCCTCGCGCCGGACACGCTGA | |

### 5-nt 5’ overhang

| Sequence | Description |
|----------|-------------|
| CAAGCTGACCTGAAGTTCCAACCGGGCAAGCTGCCCTCCCTGGCCCG | |
| ACGCCGAGGTCAAGGGTCTGACCAAATGGGCCAGGGCAGGGCAGCTTGGCG | |
| GTTGTGACAGATGAACTTCCAAGGTCAGCTTGACCTCCCTCGCGCTCCCTCGCGCCGGACACGCTGA | |

### 3-nt 5’ overhang

| Sequence | Description |
|----------|-------------|
| CAAGCTGACCTGAAGTTCCAACCGGGCAAGCTGCCCTCCCTGGCCCG | |
| ACGCCGAGGTCAAGGGTCTGACCAAATGGGCCAGGGCAGGGCAGCTTGGCG | |
| GTTGTGACAGATGAACTTCCAAGGTCAGCTTGACCTCCCTCGCGCTCCCTCGCGCCGGACACGCTGA | |

### 4-nt 5’ overhang (one silent mutation)

| Sequence | Description |
|----------|-------------|
| CAAGCTGACCTGAAGTTCCAACCGGGCAAGCTGCCCTCCCTGGCCCG | |
| ACGCCGAGGTCAAGGGTCTGACCAAATGGGCCAGGGCAGGGCAGCTTGGCG | |
| GTTGTGACAGATGAACTTCCAAGGTCAGCTTGACCTCCCTCGCGCTCCCTCGCGCCGGACACGCTGA | |
### Supplementary Table 6 Repair templates used in Figure 3

| Mutation site | Name | Sequence (5’ to 3’) |
|---------------|------|---------------------|
| 4-nt 3’ overhang | a | CAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | b | CGGCAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | c | CGGCAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | d | CGGCAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | e/g/h | CACCGCGAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | f | AGTTCAGGTCACCACCGGCAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | g/h | AGTTCAGGTCACCACCGGCAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | h | AGTTCAGGTCACCACCGGCAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | i | AGTTCAGGTCACCACCGGCAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | j | AGTTCAGGTCACCACCGGCAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | k | AGTTCAGGTCACCACCGGCAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | l | AGTTCAGGTCACCACCGGCAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | m | AGTTCAGGTCACCACCGGCAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | n | AGTTCAGGTCACCACCGGCAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | o | AGTTCAGGTCACCACCGGCAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | p | AGTTCAGGTCACCACCGGCAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | q | AGTTCAGGTCACCACCGGCAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | r | AGTTCAGGTCACCACCGGCAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | s | AGTTCAGGTCACCACCGGCAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | t | AGTTCAGGTCACCACCGGCAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | u | AGTTCAGGTCACCACCGGCAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | v | AGTTCAGGTCACCACCGGCAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | w | AGTTCAGGTCACCACCGGCAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | x | AGTTCAGGTCACCACCGGCAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | y | AGTTCAGGTCACCACCGGCAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | z | AGTTCAGGTCACCACCGGCAAGCTGACCCTGAAGTTCATCTGCAACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
| | | AGTTCAGGTCACCACCGGCAAGCTGCCCCGTGCCCTTGCCCGCTTTGGTGACCACCCTGACCT |
Supplementary Table 7 Repair templates used in Figure 4

| Mutation site | Name | Sequence (5' to 3') |
|---------------|------|---------------------|
| LAHR template (B2M) | TCACGTCATCCACGCAAGAATGGAAGATTTCCTGAAATTTCCTGGTATG | TCACGTCATCCACGCAAGAATGGAAGATTTCCTGAAATTTCCTGGTATG |
|                |      | GTGAGGTTTCATCCACGCAAGAATGGAAGATTTCCTGAAATTTCCTGGTATG |
|                |      | GTCAACTTAAATGCGAGGTAGATCTGAAACCAGACATAGCAATTCAGG |
|                |      | AAATTTGACTTTCCATCTGCTGGATGACGTA |
ssODN1 (B2M) AGTCAAAATTCTCGAATTGCTATGTTGTCTGGTTTCATCCGACATTCAATTGGAGATGGAGCATT
ssODN2 (B2M) GAAATGCTCCACTTTTCTCAATTTCCATCTTCTGATGTTACATTTTAACTTTGGACT
LAHR template (ALK) CCCCGCTCTCGTGTTTGTCCACTAAATGTGAGCAGCGTCTGAGGACCCAGCAGCTGATTTTTCAATTCTCTCTCCATTCTTCAGTAAGTCAATC
LAHR template (ALK) AGCTCAATTTTAGTGAGAAACACGAGA
ssODN (ALK) AGCAAAGCCATGTTGAGGGTATTACTCCTGAGTGTGTATGTTACCCCCGCTCTG
ssODN (ALK) TCTCGTGTTTGTCCACTAAATGTGACGCCCAGGCTCAGGACCCCCAGCTGCCTCATTATTGTGGCCTGTTTGACTCT
LAHR template (CACNA1D) AGACCCAGAGATACATGGCTATTTCAGGGACCCCCACTGCTTGGGGGAGCCAGGAGTATTTCAGTAGTGAGGAATGCTG
LAHR template (CACNA1D) AGGAGCCAGAGCAGCTCACCTGCTCCAGGTGGGCGAGCTGTCATCCTCGCAGCATTCCTCACTACTGAAATACTCCTGCTCCCCCAAGCAGTGGGGGTC
ssODN (CACNA1D) AGGAGCCAGAGCAGCTCACCTGCTCCAGGTGGGCGAGCTGTCATCCTCGCAGCATTCCTCACTACTGAAATACTCCTGCTCCCCCAAGCAGTGGGGGTC

Supplementary Table 8 siRNA target sequences and qPCR primers

| Name         | Sequence (5’ to 3’)          |
|--------------|-----------------------------|
| T-53BP1#1    | GCCAGGUUCUAGAGGAUGA          |
| T-53BP1#2    | GCAACAAGAACCTATTGGAAGAGU     |
| T-XRCC5#1    | GAAGUUCUGUCACAGCUGA          |
| T-XRCC5#2    | GCUUCAGGGUGUCUGUC            |
| T-POLQ#1     | CCUUAAGACUGUAGGUAC           |
| T-POLQ#2     | CAACCACACCCUUACUGAAA         |
| T-PARP1#1    | AAGCUCUCGCUCCUGAACAUA        |
| T-PARP1#2    | AAGAUAGACGCGUAGGCGA          |
| T-RAD51#1    | GGGAAGUAGAGAAGCCAAA          |
| T-RAD51#2    | GAAUUGAGACUGAGGAUCUA         |
| T-RAD52#1    | GGGAUUAGAGAGCCAAA            |
| T-RAD52#2    | AGUCCAAGGCUUUAAUCUU         |
| 53BP1#1-Fw   | AGATGGACCCTACTGGAGATC        |
| 53BP1#1-Rv   | TGTTATTGGAACCCACTATTACCAGTC |
| 53BP1#2-Fw   | AGCAAGACATCCCTGGTACA        |
| 53BP1#2-Rv   | ACCTCTGACCAGAGCAGCTGCA      |
| XRCC5#1-Fw   | TCAGAAGAGCAGCCTTTAACA       |
| XRCC5#1-Rv   | TCGTCCACATCACCACCTTC        |
| Name   | Sequence (5’ to 3’)                           |
|--------|----------------------------------------------|
| XRCC5#2-Fw | AAGACTTGCGGCAATACATG                        |
| XRCC5#2-Rv | CAGCATATTCCAAATATGCTGC                     |
| POLQ#1-Fw | CAACAGATGGCAACTGAAAATG                     |
| POLQ#1-Rv | CTTGTTCAGGAACCTGGAAGAC                    |
| POLQ#2-Fw | CATGACAGAGACAGTGAAAGATTC                  |
| POLQ#2-Rv | ACTTTGGAGCATAAAGCCAC                    |
| PARP1#1-Fw | ATACTCCATCTCAGTGGGTC                    |
| PARP1#1-Rv | ATGGAATCCCTGCTGACATC                |
| PARP1#2-Fw | GAGATTCTGAAGAAGCCGAGA               |
| PARP1#2-Rv | CAACTTCTCCCCAACAGGATTA                 |
| RAD51#1-Fw | AGTGTCAGTAAATGCCAA                   |
| RAD51#1-Rv | GTGAAACCATTGGAACT                     |
| RAD51#2-Fw | AGTCCAATGGTTTCC                  |
| RAD51#2-Rv | TGGCAGGTGACAGCTA                        |
| RAD52#1-Fw | ACAGCACTCTGTAACTGCT                      |
| RAD52#1-Rv | TGGTGTGCGTGGTCAGCG                 |
| RAD52#2-Fw | GGGACCTCACAATACC            |
| RAD52#2-Rv | CTGGCAGTGGAGCTTAATT                   |
| GAPDH-Fw | ACAACTTTGATGTCAGGAAGG                 |
| GAPDH-Rv | GCCATCAGCCACAGTTTC                |

| Name          | Sequence (5’ to 3’)                           |
|---------------|----------------------------------------------|
| EGFP-Fw       | GCCTCAGACAGTGGTTCAAAAG                       |
| EGFP-Rv       | TAACATATAGACAAACGCACACCG                    |
| EGFP-seq      | TGAGCAAGGCGAGG                                |
| B2M-Fw        | GAGGGAAAGATACAAAGTCACCG                     |
| B2M-Rv        | CATCAATATCCACACAGGTCGCCAC                  |
| B2M-seq       | TGGAAATGGAAATTGGGAG                        |

Supplementary Table 9 Genomic PCR primers and sequencing primers

Supplementary Table 10 Next generation sequencing primers

| Name          | Sequence (5’ to 3’)                           |
|---------------|----------------------------------------------|
| Miseq EGFP-Fw | GATGTGATTAAGAGACAGGACCTGAAAGATACGAC        |
| Miseq EGFP-Rv | CGTGTGCTCTCAGTCTAGCTGGACAGGCGCT             |
| Miseq ALK-Fw  | GATGTGATTAAGAGACAGGACACGACTGGAAGCCCGA     |
### Supplementary Table 11 Protein sequence of recombinant proteins

| Name           | Sequence                                                                 |
|----------------|--------------------------------------------------------------------------|
| SpCas9         | MDKKYSIGLDIGTN&SVGAWA8TVTDEYKVPSSKKFKVVLGNTDRHSI8KNNIGALLFDGSGETEAAGTRLKRTARRRYYTRRRNKRICYLQIEFSNEMAVKVDSSFHRLEESFLVEEDKHERHPIFGNI VDEVAYHEKYPTIHYRKLKVLDSTDKALRLYLYHALMIKFRGHFLIEGDLNPDNSVDKFLIGQYVQNYLFEENPASVGDAIKALSARLSKSRRLNIAQLPGEKKNGLFGNLIAL GLGLTNPFXSFNLDAEDAKLQSLKDYDDLLNLAQLDIQGAYDLAFLAACNSDALSLDLSDILRVRNTEITKAPLSMIRKLYLHDLSTLLKALVRQPLYKEFIDDSKNGYAGYID GASQEEFYKFLKPIKLEDMDGTELWKLNRDILLRKRQTFDNGSHPQIHLGELHARRQ EDFYFLKLDKRENEKILEKLFYRFYPPVPLRGNSRFAMTRKSETEITPWNFEVEVDKGA SAQSFIERMTNFKDLNPNEKVLPHSLYYEFVYNLTEKVKYVTMEGRKPAFLSIEQKO KAVIDLFLKTNKVTQKLUKDYFKKIECFDSIEVISGVEDRPNASLGTYHDLLLHKIKDKDFL DNEENJELIDIVLTLFREDREMERTLYKHLDFFKVKMKLKRRRTTYGWRGLSRLKIN GIRDKQSGTKEFKLSDKFDGAFNRNMQLIHDSSLTDFEDIQKCAQVSQGDSLHEIANLA GSPAIFKQGILQVFQKVDLKVSMGRHKPHENIVEMARENQTTQKQKNRSMERKMYREEGI KELQGSQLKEHPVENTQLQNEKLYLYLYLQNGRDMDYVQEDLINRSLDYDVHPQSFLL DDSIDKLVRSDLKRNQSGDNSVPEEVKKMKNYWRQNLNAKLRQFDNLTKAEROGLSELDKAGFIRQVLQVTRQITKHVAIQILDSRMNTKDYENDKILEVKVLKSVLSDFR KDFQFYKVREINNYHHAHAYNAHDKLVNAGTVALTNKYPKLESEFYVDKMYVRDIAKIAESEQ EIGKATAKYFFYSINNNMFKTEITLNLANGEIRKRPLIEGNETGEIWSDKGRDFATVRKVLSP MQVNIKVETQTVGGFSKEILPKRNSDKLARIKKWDPKKYYGDSFSTPAYSVLVAKVEK GKSKKLKSVKELTLLTFSREEMSSEKFNAPIFDLEAGKYEVKVDKLLKPYKLSFELNGRSK RMLASAGELQKGNELALPSLYVNYFLASHYELKLGSPDENEQKQLFVHQHKYHELDIEI EQISEFSCRVLADANLKDVLASYKHKDRHPKIREQAEKNIIIHLFRTLNLGAPAFAKYFDI TIDRKRKYSTKEVLDATLQHISGITYRDLSQLGDDGGGSGTRELKKRRKVGGSHHHHH IIH Stop |
| AsCas12a       | MTQFEFGTNLYQVSÝKLRLFELIPQGTLKHIQEGQFIEEDKARNDHYKELPKIIDRYKTYADQCQLQLVKQDLWENLSAAIDSYKREKEETENALIEEQATYRINAIHYDFGRTDNLTDAINKRHAEIYKGLKAEFLNGVKKQLQGTVTYTHENALLRSFDKFTTYFSGFYENRNKVSÆDISTAPIPHRIVDNFPQFKN chocolateselnthtLVAPSRLREHFENVKKAGIFFVSTSIEEVFSFFPYNQIT QTQIDLYNQLLQGGSISREAGTEKIKGLNVLNLAIQNDTAHIAISSLPHFROFLPKQLSDRNTLSFLILEEFSDESIQFSCKYKTLLRNENALTERAEFLNENSDILTHIFISFHHKLETISSALCDH WDTLRINALYERRISLGTGKISAKEVESKLKHIHONLQEEISAGKELSEAKQKTEILSAHAHALDOQPLPPLTLKQOEELKILSOQLSDLGLYHLDWAVFEDSVEIPFESARKLTIGKLE MEPLSFYNKARNYATKQPSVEFKLFNMQMPTLASGDWNKENGAGICGKNNLFGKNGLYLG |
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