

Supplementary information, Figure S2 Visual-plus-quantitative assay systems for homologous recombination (HR), non-homologous end joining (NHEJ) and single-strand annealing (SSA) repairs. The contents of this figure are reproduced from our previous publication(Liu et al., 39:489-502, 2012, Journal of Genetics and Genomics), to facilitate a review of our work. (A) Structures of the HR, SSA and NHEJ constructs. Plasmid 5'-Egfp containing the 1st to 444th base pairs (bp) of wild-type (WT) Egfp was used as a repair donor. Two I-SceI sites in opposing orientations were used to replace the 198th to 201st bp of Egfp to generate the mutant *Egfp*. The two opposite I-SceI recognition sequences are blue; the inter-space sequence between the two I-SceI sequences are black; the new start codon ATG is red; and the red arrows indicate the I-SceI recognition sites. HR: the mutant Egfp is expressed by the CMV promoter and terminated by the SV40 polyA sequence; the yellow triangle indicates the I-SceI recognition site; and 198-201 is the 4 bp sequence of WT Egfp. SSA: 5'-Egfp is expressed by the CMV promoter and terminated by the SV40 polyA sequence and the mutant *Egfp* has no promoter. NHEJ: the distance between the two opposite I-SceI sites and the start codon of Egfp is 20 bp. (B) The three pairs of primers used in quantitative real-time PCR (qPCR) to quantitatively measure the HR, NHEJ and SSA repair frequencies. The normalizing primers, forward 457-481 and reverse 666-685, of *Egfp* are brown. HR and SSA repair primers: the forward primer 185-202 of WT Egfp is green and covers the mutation site in the mutant Egfp, such as the substitution of 4 bp (198-201) of the WT Egfp sequence in red with 50 bp DNA (two I-SceI sites) in black, and the reverse primer 471-492 in dark green. NHEJ repair primers: the forward primer -133 to -110 is orange and the reverse primer is the same as the one used in the HR and SSA repair systems.