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Site-specific strand bias in gene correction using single-stranded oligonucleotides

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In the Material and Methods section entitled “Cell culture and transfections” the ssODN concentration should be 0.25 μ M instead of 0.25 mM.

An error occurred in the top panel of Fig. 2. The corrected part of Fig. 2 is given below.

An error occurred in the plotting of data for the top panels of Fig. 4. The corrected versions of Fig. 4A and B are given below.

Fig. 2 ssODN sequences used for correction of the episomal *E. coli* β -galactosidase gene. Upper, lower case DNA and 2'-O-methyl uracil residues, respectively. The targeted bases in the target sequence and the corresponding complementary or mismatched bases in the ssODNs are underlined

	659
β -gal 659G>A	5' - -TTCATCTGTGGTGCAACGGGCGCTAGGTTCGGTTACGGCCAGGACAGTCGT - -3' 3' - -AAGTAGACACCACGTTGCCCGCGATCCAGCCAATGCCGGTCCTGTCTAGCA - -5'
β -gal 25 AS+	3' - TuuuuCGTTGCCCGCGA <u>CC</u> CAGCCAATGCCuuuu - 5'
β -gal 25 S+	5' - uuuuGCAACGGGCGCTGGTTCGGTTACGGuuuuA - 3'
β -gal 25 AS-	3' - TuuuuCGTTGCCCGCGA <u>TCC</u> AGCCAATGCCuuuu - 5'
β -gal 25 S-	5' - uuuuGCAACGGGCGCTAGGTTCGGTTACGGuuuuA - 3'
β -gal 35 AS+	3' - TuuuuCACCACGTTGCCCGCGA <u>CC</u> CAGCCAATGCCGGTCCuuuu - 5'
β -gal 35 S+	5' - uuuuGTGGTGCAACGGGCGCTGGTTCGGTTACGGCCAGGuuuuA - 3'
β -gal 35 AS-	3' - TuuuuCACCACGTTGCCCGCGA <u>TCC</u> AGCCAATGCCGGTCCuuuu - 5'
β -gal 35 S-	5' - uuuuGTGGTGCAACGGGCGCTAGGTTCGGTTACGGCCAGGuuuuA - 3'
β -gal 45 AS+	3' - TuuuuGTAGACACCACGTTGCCCGCGA <u>CC</u> CAGCCAATGCCGGTCCTGTCAuuuu - 5'
β -gal 45 S+	5' - uuuuCATCTGTGGTGCAACGGGCGCTGGTTCGGTTACGGCCAGGACAGTuuuuA - 3'
β -gal 45 AS-	3' - TuuuuGTAGACACCACGTTGCCCGCGA <u>TCC</u> AGCCAATGCCGGTCCTGTCAuuuu - 5'
β -gal 45 S-	5' - uuuuCATCTGTGGTGCAACGGGCGCTAGGTTCGGTTACGGCCAGGACAGTuuuuA - 3'

Fig. 4 Correction of the *E. coli* β -galactosidase 659G>A mutation in CHO-K1 cells. The correction frequencies were calculated as the number of blue cells divided by the total number of cells. Data are given as mean + SD. Comparison of the correction frequencies obtained by treatment with: **A** ssODNs β -gal 25 AS+, β -gal 25 S+,

β -gal 35 AS+, β -gal 35 S+, β -gal 45 AS+, and β -gal 45 S+ ($n=8$ for all samples); **B** ssODNs β -gal 25 AS-, β -gal 25 S-, β -gal 35 AS-, β -gal 35 S-, β -gal 45 AS-, β -gal 45 S-, and the mutant plasmid pCH110 659G>A alone ($n=3$ for all samples). $P \leq 0.05$ (see text for details)