



Suppl. Fig. 1

**Fig. S1.** Introduction of S769(AGT)→A769(GCA) and F771(TTC)→A771(GCA) mutations into chromosomal *polA* gene of *E. coli* MG1655. **A.** Codon replacement within the chromosomal *polA* gene done in two recombineering steps. First, the 3' *polA* region (codon 769 to the ochre stop codon) was replaced with a Zeo<sup>R</sup> cassette. In a second recombineering step, the *polA*<sub>SD<sup>-</sup></sub> ::*cat* allele replaced the Zeo<sup>R</sup> cassette and introduced the altered S769A (AGT → GCA) and F771A (TTC → GCA) codons into the *polA* locus. **B.** PCR-amplification of genomic fragments from MG1655 *polA*<sub>SD<sup>-</sup></sub> ::*cat* with primers cp8 and cp92 and cp61 and cp11 (Table 3) respectively, yielded fragments of 2418 bp and 687 bp characteristic for a successful *polA*<sub>SD<sup>-</sup></sub> ::*cat* insertion. M, DNA size markers. **C.** Trace DNA sequencing file displaying the intended AGT →GCA (Ser769) and TTC→GCA (F771) *polA* mutations in the genome of *E. coli* MG1655 *polA*<sub>SD<sup>-</sup></sub> ::*cat*.

**Supplementary Table 1: Plasmids used in this study**

<b>Strain</b>	<b>Relevant Characteristics</b>	<b>Source or Reference</b>
pRed/ET	Red/ET expression plasmid; pSC101 based; Ap <sup>R</sup>	Gene Bridges
pSKpolAint	pBluescript derivative with 3'-end of the wild-type <i>polA</i> gene and closely linked <i>cat</i> gene; Ap <sup>R</sup> , Cm <sup>R</sup>	[1]
pJM993	pSKpolAint derivative: 3'- end of <i>polA</i> encodes S769(AGT)→A769 (GCA) and F771(TTC) → A771(GCA) point mutations and closely linked <i>cat</i> gene; Ap <sup>R</sup> , Cm <sup>R</sup>	This work
pGB2	low-copy-number, pSC101-derived vector: Spc <sup>R</sup>	[2]
pRW134	pGB2 derivative expressing <i>umuD'</i> C from the native <i>umuDC</i> promoter; Spc <sup>R</sup>	[3]
pJM963	pRW134 derivative expressing <i>umuD'</i> and <i>umuC_Y11A</i> from the native <i>umuDC</i> promoter: Spc <sup>R</sup>	[4]

**Supplementary Table 2: Oligonucleotides used in this study**

<b>Name</b>	<b>Sequence</b>	<b>Source and Reference</b>
cp6	5'-CAGATGTCACCTTGCAGTTGC	BioSpring
cp8	5'-AATGGCAGCGAAGCTCGAGC	BioSpring
cp11	5'-GGCGGTAGACAGCAATATCG	BioSpring
cp61	5'-GGCTTCCATGTCGGCAGAATG	BioSpring
cp92	5'-TATCAACGGTGGTATATCCAG	BioSpring
p2	5'-GTGACAGCTTATGTTGCTTACTTACGAAAAAAGGCAT GTTTCAGGCGAATCTTACGCCCCGCCCTGCCACTC	BioSpring
p3	5'-AGCAACGCCGTAGCGCGAAAGCGATCAACTTTGGTCT GATTTATGGCATGAATTAACCCTCACTAAAGGGCG	BioSpring
P4	5'-GTGACAGCTTATGTTGCTTACTTACGAAAAAAGGCAT GTTTCAGGCGAATCTAGCACGGAGTTCATTAGGGCTC	BioSpring
polA-FD424	5'-CGGACTGGATACGCTGTATGC	Lofstrand/[1]
polA-RD424	5'- CTTCCAGTACCTCTTCCGACG	Lofstrand/[1]
polA-RBamHI	5'-GCTCGGATCCTTTAGTGCGCCTGATCCCAGT	Lofstrand
polA_F2105	5'-GCCAGAGGATTATGTGATTGT	Lofstrand
SSP1	5'-ATGGTACGGACGTGCTT	Lofstrand
SSP1-27	5'-ATGGTACGGACGTGCTTTAGTCGTAA	Lofstrand
FLAPU	5'-UAGTCGTTAATCATTAGTACCAGTATCGACAG	Lofstrand
XAG49 <sup>a</sup>	5'-CTGTCGATACTGGTACTAATGAXTAACGACTAAAGCA CGTCCGTACCAT	Lofstrand

<sup>a</sup>:X denotes the location of the synthetic abasic site

## References

- [1] K. Makiela-Dzbenska, M. Jaszczur, M. Banach-Orlowska, P. Jonczyk, R.M. Schaaper, I.J. Fijalkowska, Role of *Escherichia coli* DNA polymerase I in chromosomal DNA replication fidelity, *Mol. Microbiol.* 74 (2009) 1114-1127.
- [2] G. Churchward, D. Belin, Y. Nagamine, A pSC101-derived plasmid which shows no sequence homology to other commonly used cloning vectors, *Gene* 31 (1984) 165-171.
- [3] E.S. Szekeres, R. Woodgate, C.W. Lawrence, Substitution of *mucAB* or *rumAB* for *umuDC* alters the relative frequencies of the two classes of mutations induced by a site-specific T-T cyclobutane dimer and the efficiency of translesion DNA synthesis, *J.Bacteriol.* 178 (1996) 2559-2563.
- [4] A. Vaisman, W. Kuban, J.P. McDonald, K. Karata, W. Yang, M.F. Goodman, R. Woodgate, Critical amino acids in *Escherichia coli* responsible for sugar discrimination and base-substitution fidelity, *Nucleic Acids Res.* 40 (2012) 6144-6157.