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Supplemental Information

**DNA ADP-Ribosylation Stalls Replication
and Is Reversed by RecF-Mediated Homologous
Recombination and Nucleotide Excision Repair**

Emeline Lawarée, Gytis Jankevicius, Charles Cooper, Ivan Ahel, Stephan Uphoff, and Christoph M. Tang

A

DarT

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EPEC:  YDYSASLNPKALIWRIVHRDNIPIWLDNGLHCGNSLVQAEINININPELIGKRAGHPVE
      . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . |
T. aquaticus: MPQOGLAYFPVTLIYHITHLNNLQGIQRGGLLPYS-QRPPTQQNVAYGHIQAHRAQVVVE

EPEC:  VGTGGTLHDVVFYFFTFPSPMLMNIHSGRGGIKRRPNEEIIVLVSNLRNVAAHDVFPVFTD
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
T. aquaticus: VGRGKLDHVVFYFCPRSPMLYAIHTQTDY-QGDQRPLHLVSSAQKVAEARIPFVFTD

EPEC:  SHAYNWNYYTSLNSLDQIDWPILQARFRDPPDPAKFEFYQAALIWQHCPISLLDGI
      | | . . . | . | . | . | . | . | . | . | . | . | . | . | . | . | . |
T. aquaticus: RHARVQYVCFHKLKALDWQAIOA-SYWA---N--VREKKQAEFLVKDFFPWLVEEI

EPEC:  ICYSEEVRLQLEQWL--FQRNLTMSVHTRSGWYFS
      . . | | | | . | . | . | . | . | . |
T. aquaticus: GVVDKTIQAQVESILAQFPDLHHPFVRBRSSWYK
  
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DarG

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EPEC:  MEALVNTVNTVGMKGIALMFKERFENMKVYALACKQKQVITGKMFITETGELMSPRWI
      . | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
T. aquaticus: VEALVNTVNTVGMKGVVALQFKRAFPPNYQAVYKACERGOVQIGRIFFVYDRGPLAQPRYI

EPEC:  VNFPTKQHWRRDRSMEWIEDGLQDRRFLIEENVQSIAPPLGAGNGGLNWPVRAQIESA
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
T. aquaticus: FNFPTKQHWRRHPSMEYVEEGLKDLVCRIQELRVRSIALPPLGAGNGGLNWPVEVKQRIQEA

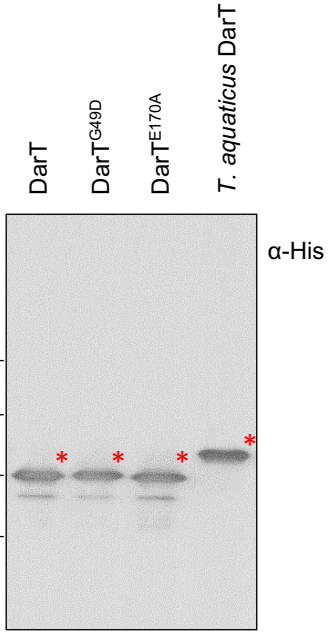
EPEC:  LGDLQDQVDILIQPTE--KYQNVAKSTGVKRLTPARAATAELVRRYVWVLMGECSLLEIQKL
      | | . . . | . | . | . | . | . | . | . | . | . | . | . | . | . |
T. aquaticus: LEALEGVEVWVYFVENVPKAHSIVPLKTKPRLTPARAALLKFLGYLALGEPGLRLEAQKL

EPEC:  AMLLQRAIEHQDQDDILKLRFEAHYIGPYAPNLNHLNLDGTYLKAERKIPDSQPLDVIW
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
T. aquaticus: AYFLQEA-----GLD-LKLDLFAKQKFGPYAEPLNHVLARLEGHYIQG---FGDRITGSIQR

EPEC:  FNDQKKEHVNAVNLNEAREWLPALQVQSQIDGFESPFGLLELATVWLLSRGECQPLDS
      . . | . . | . . . | . . . | . . . | | | | | | | | | | | | | |
T. aquaticus: LKPKALDEAVLFLADYPKA-DEAATRAADWVKGFTPYGLELLATVHWAV-RHEGARWAS

EPEC:  VKEGLHQWFAGERWASRKLRLFDNNLQFAINRVMEFHC
      . . | . . | . . | . . | . . | . . | . . | . . | . . | . . |
T. aquaticus: LQKRL-----QAW-NPRKATFPKTHLQVALDALLKRG
  
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B



C

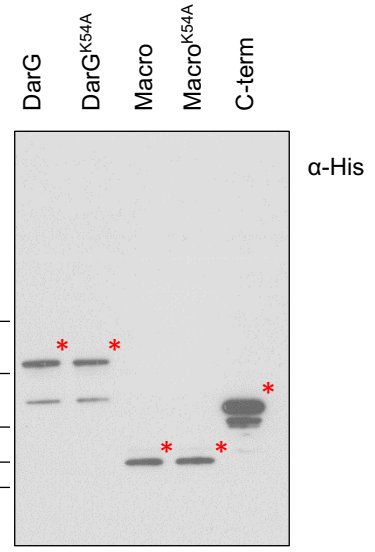


Figure S1: Alignment of DarTG from *T. aquaticus* and EPEC, and the corresponding purified proteins after *in vitro* transcription/translation, related to Figures 1 and 2. (A) The amino acid similarity between *T. aquaticus* and EPEC DarT or DarG is 47% and 59%, respectively. Identical residues are shown with a line, similar residues are shown with a dot. The mutated glycine in EPEC DarT (G49D) is shown in purple while the mutated glutamic acid residues (DarT^{E160A} in *T. aquaticus* and DarT^{E170A} in EPEC) are marked in green. The macrodomain of DarG is highlighted in yellow while the C-terminal domain of DarG is showed in blue. The catalytic lysine residues of DarG (K80A in *T. aquaticus* and K54A in EPEC) are marked in red. Alignment was performed by Clustal O with JalView software. Levels of His-tagged (B) DarT and (C) DarG variants (indicated with red asterisks) obtained after *in vitro* transcription/translation determined by Western blot analysis using an anti-His antibody.

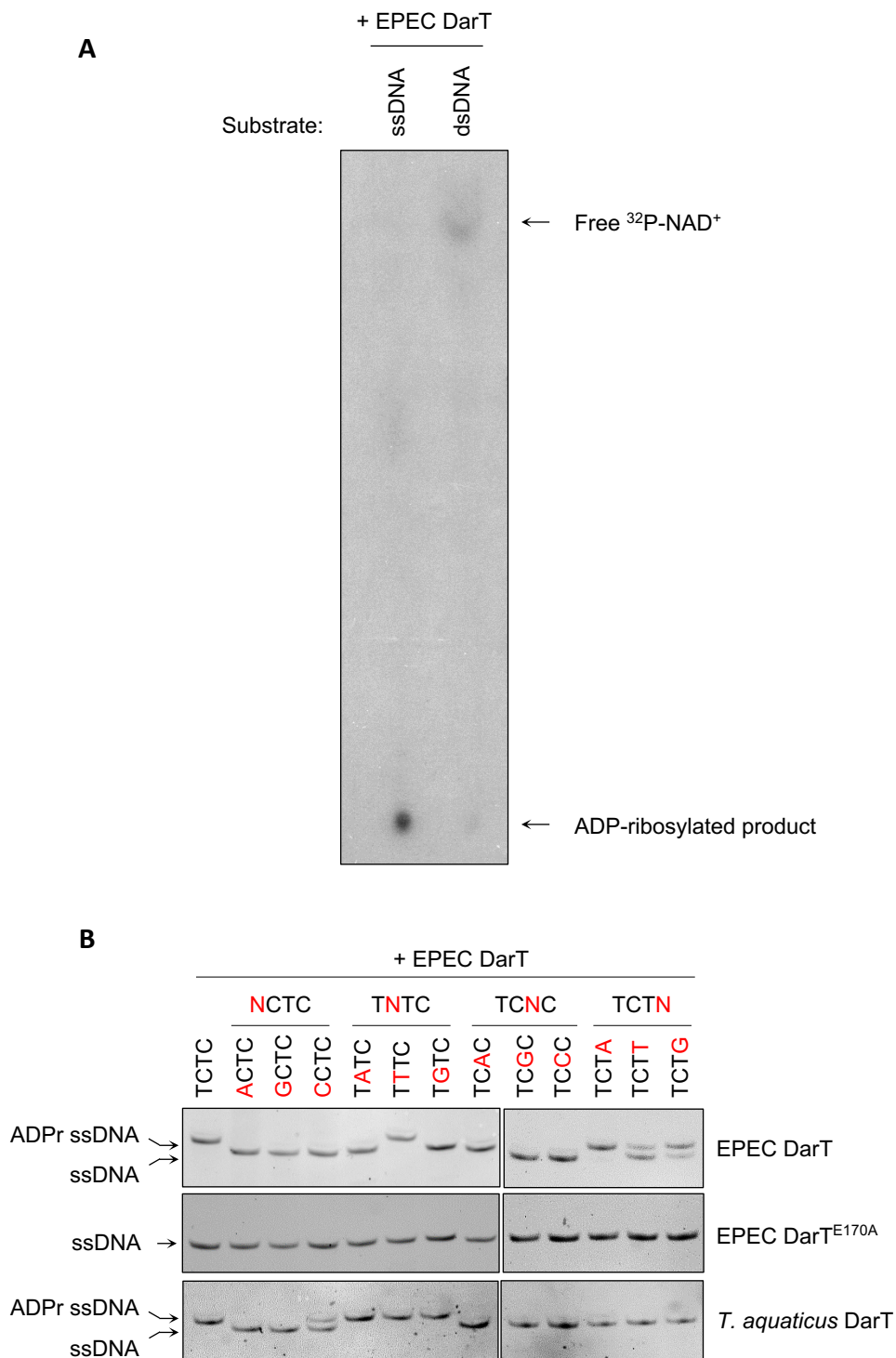


Figure S2: EPEC DarT only ADP-ribosylates ssDNA, on a different DNA sequence than *T. aquaticus* DarT, related to Figure 1. (A) ADP-ribosylation of 13-mer ssDNA or dsDNA oligonucleotides incubated with EPEC DarT with $^{32}\text{P-NAD}^+$ and separated by thin-layer chromatography. Sequences of the oligonucleotides are provided in the Star methods. **(B)** ADP-ribosylation of 27-mer ssDNA oligonucleotides incubated with purified EPEC DarT or DarT^{E170A} or *T. aquaticus* DarT. The region with different sequence is shown above each lane. ADPr ssDNA: ADP-ribosylated ssDNA. All oligonucleotides are listed in Table S1. n = 3, representative data from one experiment shown.

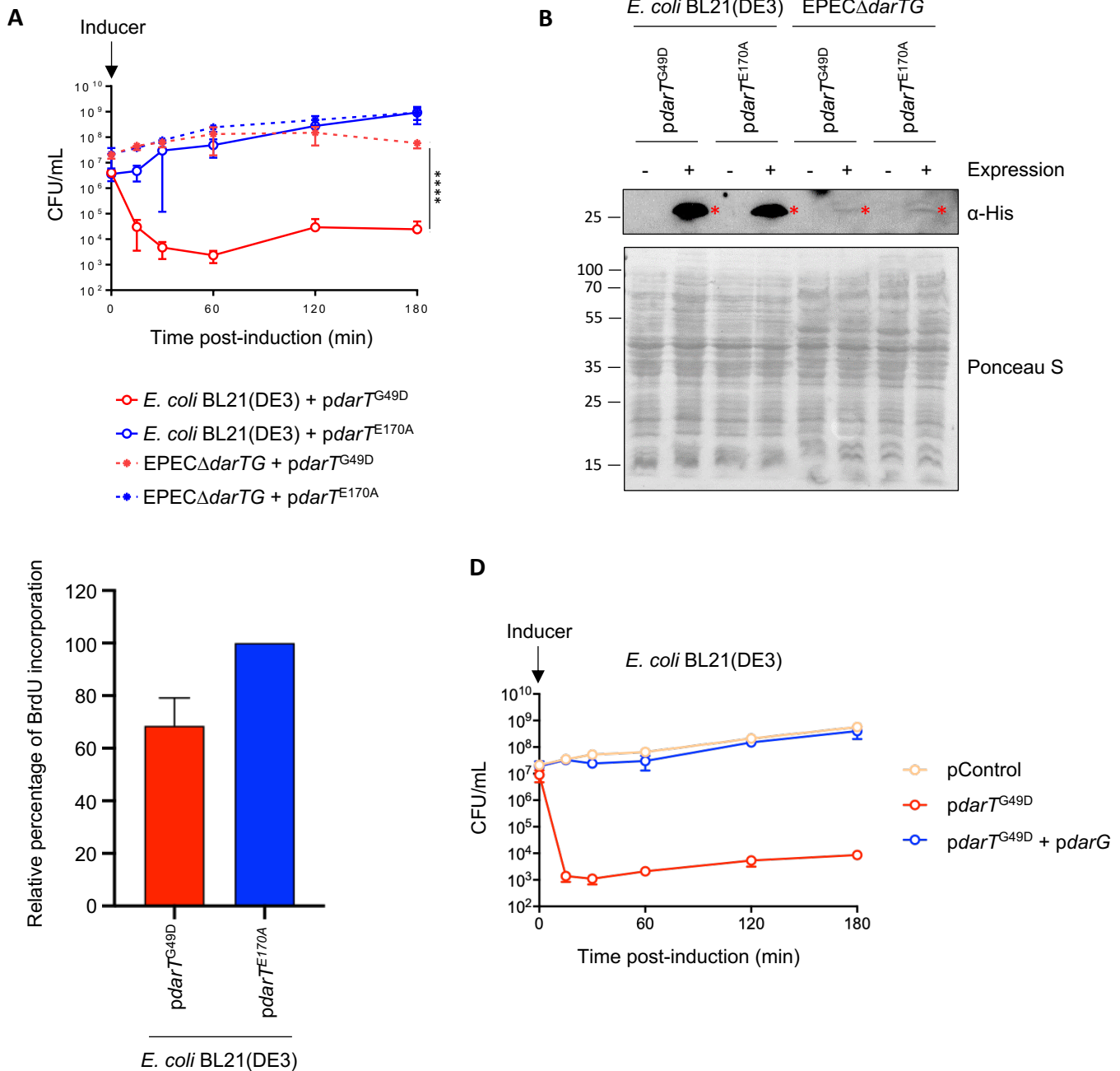


Figure S3: Differential DarT^{G49D}/DarT^{E170A} toxicity and expression levels in *E. coli* BL21(DE3) and EPEC, where DarT^{G49D} inhibits DNA replication in *E. coli* BL21(DE3) within 5 min of expression, related to Figures 1 and 5. (A) Viability of *E. coli* BL21(DE3) and EPEC $\Delta darTG$ following expression of $darT^{G49D}$ or $darT^{E170A}$. $n = 3 \pm$ s. d., ** $p < 0.0001$ by two-way ANOVA between *E. coli* BL21(DE3) + $pdarT^{G49D}$ and EPEC $\Delta darTG$ + $pdarT^{G49D}$. (B) Levels of His-tagged DarT^{G49D} or DarT^{E170A} (red asterisks) in cell lysates of *E. coli* BL21(DE3) and EPEC $\Delta darTG$ using an anti-His antibody. Expression of His-DarT^{G49D}/His-DarT^{E170A} is repressed by addition of 0.8% glucose or expressed by the addition 0.8% arabinose for 3 hrs. Ponceau S staining is shown as the loading control. $n = 3$, representative data from one experiment shown. (C) Relative values were obtained by calculating the ratio of the amount of BrdU incorporated following expression of $darT^{G49D}$ vs. $darT^{E170A}$. $n = 2 \pm$ s. d. (D) Viability of *E. coli* BL21(DE3) grown in M9 medium following expression of $darT^{G49D}$ with or without DarG. pControl, empty plasmid; $n = 2 \pm$ s. d.**

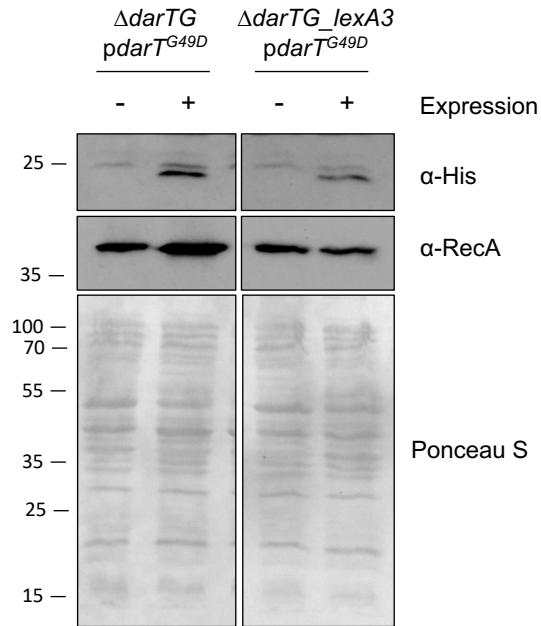


Figure S4: Cellular RecA levels do not increase in the absence of an SOS response, related to Figure 3. Western blot analysis of RecA expression levels in cell lysates of $EPEC\Delta darTG$ and $EPEC\Delta darTG_lexA3$ using an anti-His (to detect levels of His tagged $DarT^{G49D}$ or $DarT^{E170A}$) and anti-RecA antibody after 3 hours of $darT^{G49D}$ expression. Ponceau S staining is shown as the loading control. n = 3, representative data from one experiment shown.

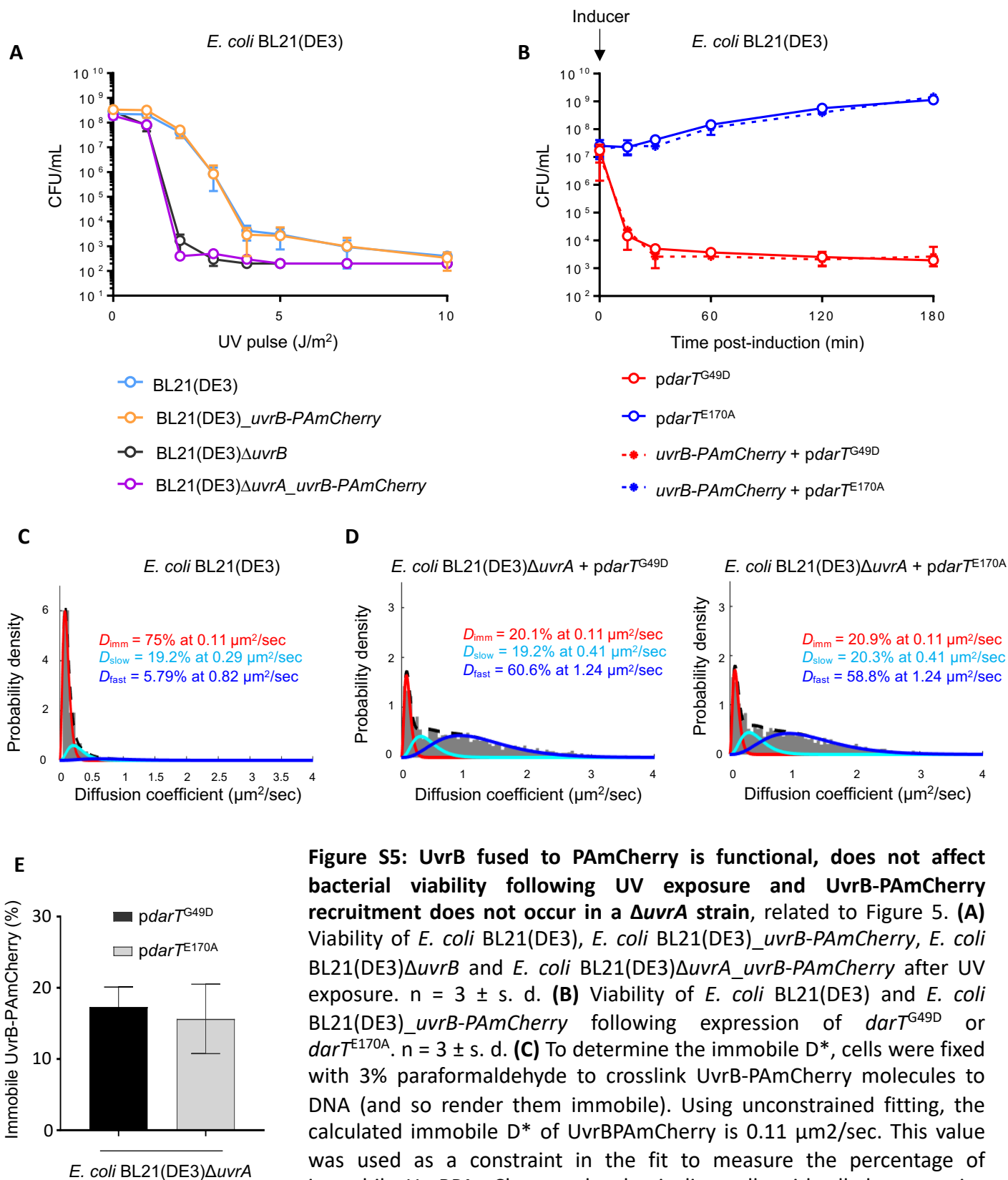


Figure S5: UvrB fused to PAMCherry is functional, does not affect bacterial viability following UV exposure and UvrB-PAMCherry recruitment does not occur in a Δ uvrA strain, related to Figure 5. (A) Viability of *E. coli* BL21(DE3), *E. coli* BL21(DE3)_{uvrB-PAMCherry}, *E. coli* BL21(DE3) Δ uvrB and *E. coli* BL21(DE3) Δ uvrA_{uvrB-PAMCherry} after UV exposure. $n = 3 \pm$ s. d. **(B)** Viability of *E. coli* BL21(DE3) and *E. coli* BL21(DE3)_{uvrB-PAMCherry} following expression of *darT*^{G49D} or *darT*^{E170A}. $n = 3 \pm$ s. d. **(C)** To determine the immobile D^* , cells were fixed with 3% paraformaldehyde to crosslink UvrB-PAMCherry molecules to DNA (and so render them immobile). Using unconstrained fitting, the calculated immobile D^* of UvrBPAMCherry is 0.11μ m²/sec. This value was used as a constraint in the fit to measure the percentage of immobile UvrBPAMCherry molecules in live cells with all three species (immobile, slow, fast) present. **(D)** Determination of D^* values of UvrB-PAMCherry in *E. coli* BL21(DE3) Δ uvrA, fitted with a three constrained species model following 15 min expression of *darT*^{G49D} or *darT*^{E170A}. **(E)** Percentage of immobile UvrB-PAMCherry in *E. coli* BL21(DE3) Δ uvrA after 15 min expression of *darT*^{G49D} or *darT*^{E170A}. $n = 2$ biological replicates \pm s. d.; total number of cells = 3,698; total number of tracks = 38,918.

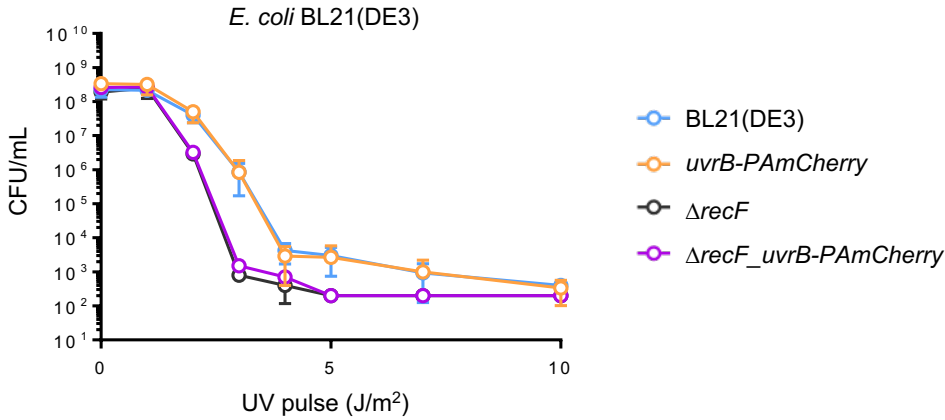
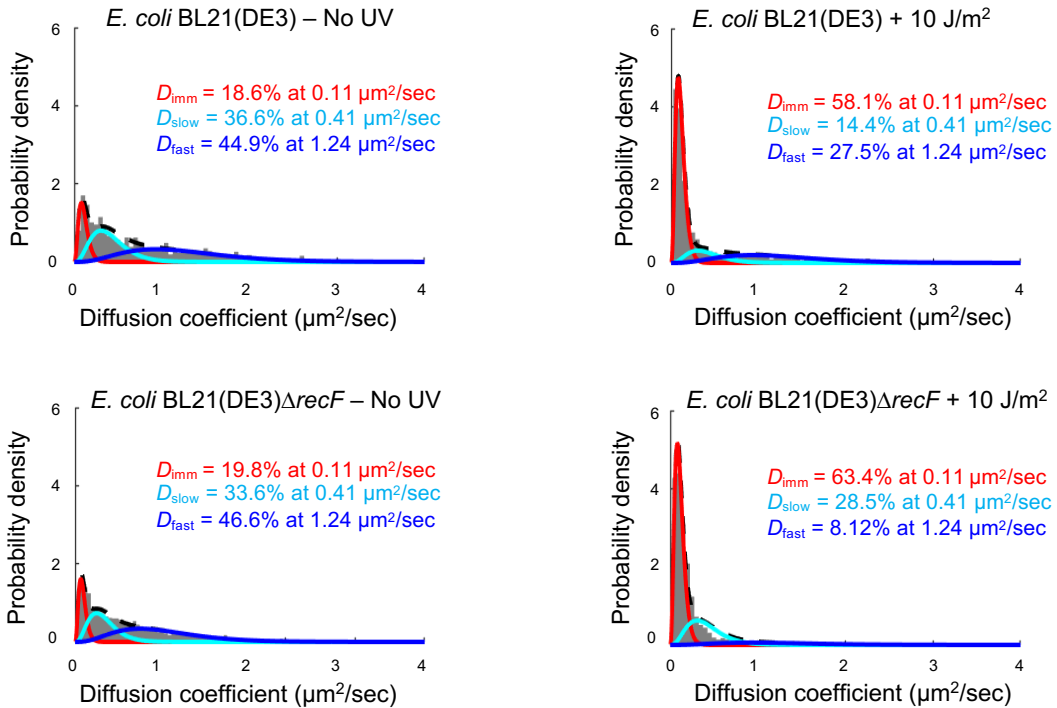
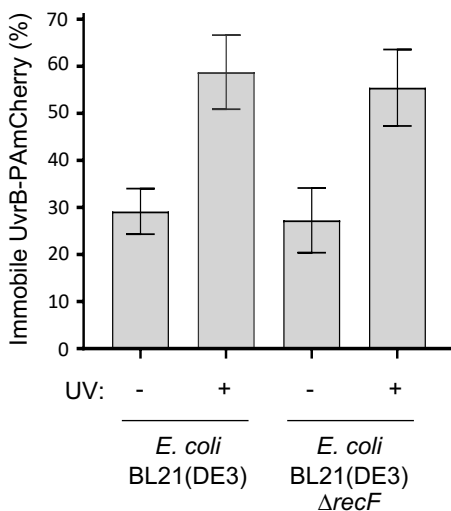
A**B****C**

Figure S6: NER is functional in a ΔrecF strain, related to Figure 6. (A) Viability of BL21(DE3), BL21(DE3)*uvrB*-PAmCherry, BL21(DE3) ΔrecF and BL21(DE3) ΔrecF *uvrB*-PAmCherry after exposure to different UV doses. $n = 3 \pm \text{s. d.}$ **(B)** Determination of D^* values of UvrB-PAmCherry in *E. coli* BL21(DE3) and BL21(DE3) ΔrecF , fitted with a three species model (three constraints fit) with or without UV exposure. **(C)** Percentage of immobile UvrB-PAmCherry in *E. coli* BL21(DE3) and *E. coli* BL21(DE3) ΔrecF after UV exposure. $n = 3$ biological replicates $\pm \text{s. d.}$; total number of cells = 12,976; total number of tracks = 126,225.

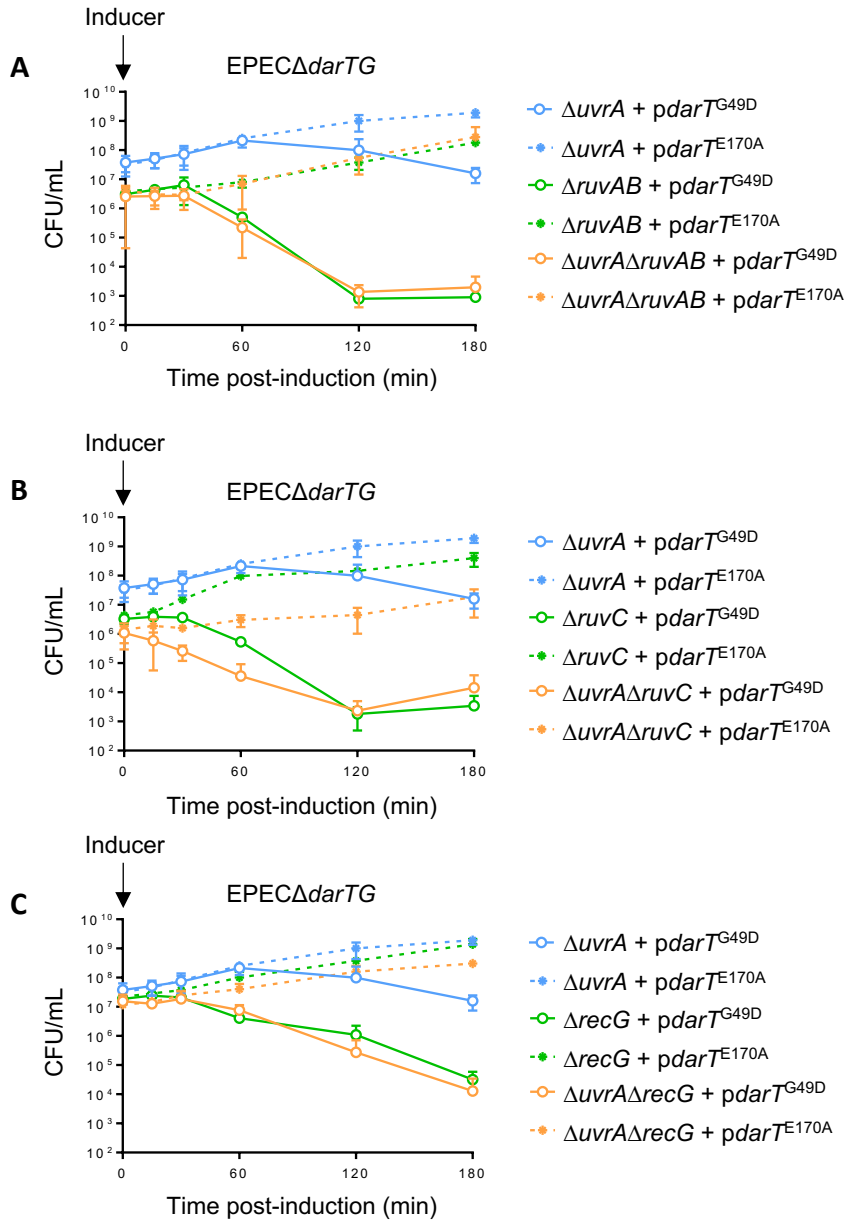


Figure S7: Investigation of the sequentiality between RecF-mediated HR and NER pathways, related to Figure 6. Viability of strains following expression of *darT*^{G49D} or *darT*^{E170A} in EPEC Δ darTG lacking RecF-mediated HR and/or NER **(A)** EPEC Δ darTG Δ ruvAB and EPEC Δ darTG Δ uvrA Δ ruvAB, **(B)** EPEC Δ darTG Δ ruvC and EPEC Δ darTG Δ uvrA Δ ruvC, **(C)** EPEC Δ darTG Δ recG and EPEC Δ darTG Δ uvrA Δ recG. n = 3 \pm s. d. NS = p > 0.9999 by two-way ANOVA between EPEC Δ darTG Δ ruvAB/ Δ ruvC/ Δ recG + pdarT^{G49D} and EPEC Δ darTG Δ uvrA Δ ruvAB/ Δ ruvC/ Δ recG + pdarT^{G49D}.

Name	Sequence
ADPr-EL1	GAGCTGTACAAGTCAGAT <u>TCTC</u> GAGCTC
ADPr-EL2	GAGCTGTACAAGTCAGA <u>ACTC</u> GAGCTC
ADPr-EL3	GAGCTGTACAAGTCAGAG <u>CTC</u> GAGCTC
ADPr-EL4	GAGCTGTACAAGTCAGAC <u>CTC</u> GAGCTC
ADPr-EL5	GAGCTGTACAAGTCAGAT <u>TATC</u> GAGCTC
ADPr-EL6	GAGCTGTACAAGTCAGAT <u>TTTC</u> GAGCTC
ADPr-EL7	GAGCTGTACAAGTCAGAT <u>GTTC</u> GAGCTC
ADPr-EL8	GAGCTGTACAAGTCAGAT <u>CACG</u> GAGCTC
ADPr-EL9	GAGCTGTACAAGTCAGAT <u>CGCG</u> GAGCTC
ADPr-EL10	GAGCTGTACAAGTCAGAT <u>CCCC</u> GAGCTC
ADPr-EL11	GAGCTGTACAAGTCAGAT <u>CTA</u> GAGCTC
ADPr-EL12	GAGCTGTACAAGTCAGAT <u>CTT</u> GAGCTC
ADPr-EL13	GAGCTGTACAAGTCAGAT <u>CTGG</u> GAGCTC
ADPr-EL14	GAGCTGTACAAGTCAGT <u>TCTC</u> GAGCTC
ADPr-EL15	GAGCTGTACAAGTCAGG <u>TCTC</u> GAGCTC
ADPr-EL16	GAGCTGTACAAGTCAGCT <u>TCTC</u> GAGCTC
ADPr-EL17	GAGCTGTACAAGTCAGAT <u>TCTCT</u> AGCTC
ADPr-EL18	GAGCTGTACAAGTCAGAT <u>TCTC</u> GAGCTC
ADPr-EL19	GAGCTGTACAAGTCAGAT <u>TCTC</u> CAGCTC
ADPr-EL20	CTCGACATGATCAGTCG <u>TCTC</u> TCTCGAG
ADPr-EL21	CTCGACATGATCAGTCG <u>TTTCTC</u> TCTCGAG

Table S1, related to STAR method: Oligonucleotides used for ADP-ribosylation assays

Name	Strain	Relevant genotype or description	Reference
EL131	Dh5 α	<i>fhuA2</i> Δ (<i>argF-lacZ</i>) <i>U169</i> <i>phoA</i> <i>glnV44</i> Φ 80 Δ (<i>lacZ</i>)M15 <i>gyrA96</i> <i>recA1</i> <i>relA1</i> <i>endA1</i> <i>thi-1</i> <i>hsdR17</i>	(Hanahan, 1983)
EL183	SM10	<i>thi</i> <i>thr</i> <i>leu</i> <i>tonA</i> <i>lacy</i> <i>supE</i> <i>recA::RP4-2-Tc::Mu</i> λ pir; <i>kan</i> ^R	(Simon, 1983)
EL615	<i>E. coli</i> λ pir	λ pir Δ <i>dapA</i> Δ <i>recA</i> ; <i>apra</i> ^R <i>erm</i> ^R <i>zeo</i> ^R	(Herrero et al., 1990)
EL270	BTH101	<i>F-</i> <i>cya-99</i> <i>araD139</i> <i>galE15</i> <i>galk16</i> <i>rpsL1</i> (<i>Strr</i>) <i>hsdR2</i> <i>mcrA1</i> <i>mcrB1</i>	(Karimova et al., 2000)
EL67	BL21(DE3)	<i>E. coli</i> expression strain: <i>F</i> ⁻ <i>ompT</i> <i>hsdS</i> (<i>r_B</i> ⁻ <i>m_B</i> ⁻) <i>dcm</i> ⁺ <i>Tet</i> ^r <i>gal</i> λ (DE3) <i>endA</i> [<i>argU</i> <i>proL</i>]	Stratagene
EL572	BL21(DE3) Δ <i>recF</i>	BL21(DE3) Δ <i>recF</i>	This study
EL646	BL21(DE3) Δ <i>uvrA</i> <i>uvrB</i> - <i>PAmCherry</i>	BL21(DE3) Δ <i>uvrA</i> with chromosomal <i>uvrB</i> fused to <i>PAmCherry</i> ; <i>Kan</i> ^R	This study
EL653	BL21(DE3) Δ <i>uvrB</i>	BL21(DE3) Δ <i>uvrB</i>	This study
EL325	BL21(DE3) <i>uvrB</i> - <i>PAmCherry</i>	BL21(DE3) with chromosomal <i>uvrB</i> fused to <i>PAmCherry</i> ; <i>Kan</i> ^R	This study
EL614	BL21(DE3) Δ <i>recF</i> <i>uvrB</i> - <i>PAmCherry</i>	BL21(DE3) Δ <i>recF</i> with chromosomal <i>uvrB</i> fused to <i>PAmCherry</i> ; <i>kan</i> ^R	This study
EL1	EPEC	Enteropathogenic <i>E. coli</i> isolate O127:H6 str. E2348/69; <i>Str</i> ^R	(Knutton et al., 1987)
EL2	EPEC Δ <i>darTG</i>	EPEC E2348/69 Δ <i>darTG</i> ; <i>Str</i> ^R	This study
EL268	EPEC Δ <i>darTG</i> Δ <i>dinB</i>	EPEC E2348/69 Δ <i>darTG</i> Δ <i>dinB</i> ; <i>Str</i> ^R	This study
EL326	EPEC Δ <i>darTG</i> Δ <i>dinB</i> Δ <i>polB</i> Δ <i>umuD</i>	EPEC E2348/69 Δ <i>darTG</i> Δ <i>dinB</i> Δ <i>polB</i> Δ <i>umuD</i> ; <i>Str</i> ^R	This study
EL377	EPEC Δ <i>darTG</i> Δ <i>fpg</i>	EPEC E2348/69 Δ <i>darTG</i> Δ <i>fpg</i> ; <i>Str</i> ^R	This study
EL415	EPEC Δ <i>darTG</i> <i>lexA3</i>	EPEC E2348/69 containing a point mutation (G85D) in chromosomal <i>lexA</i> ; <i>Str</i> ^R	This study
EL226	EPEC Δ <i>darTG</i> Δ <i>mutH</i>	EPEC E2348/69 Δ <i>darTG</i> Δ <i>mutH</i> ; <i>Str</i> ^R	This study
EL228	EPEC Δ <i>darTG</i> Δ <i>mutS</i>	EPEC E2348/69 Δ <i>darTG</i> Δ <i>mutS</i> ; <i>Str</i> ^R	This study
EL378	EPEC Δ <i>darTG</i> Δ <i>nei</i>	EPEC E2348/69 Δ <i>darTG</i> Δ <i>nei</i> ; <i>Str</i> ^R	This study
EL379	EPEC Δ <i>darTG</i> Δ <i>nfo</i>	EPEC E2348/69 Δ <i>darTG</i> Δ <i>nfo</i> ; <i>Str</i> ^R	This study
EL269	EPEC Δ <i>darTG</i> Δ <i>polB</i>	EPEC E2348/69 Δ <i>darTG</i> Δ <i>polB</i> ; <i>Str</i> ^R	This study
EL203	EPEC Δ <i>darTG</i> Δ <i>recA</i>	EPEC E2348/69 Δ <i>darTG</i> Δ <i>recA</i> ; <i>Str</i> ^R	This study
EL588	EPEC Δ <i>darTG</i> Δ <i>recD</i>	EPEC E2348/69 Δ <i>darTG</i> Δ <i>recD</i> ; <i>Str</i> ^R	This study
EL526	EPEC Δ <i>darTG</i> Δ <i>recF</i>	EPEC E2348/69 Δ <i>darTG</i> Δ <i>recF</i> ; <i>Str</i> ^R	This study
EL527	EPEC Δ <i>darTG</i> Δ <i>recG</i>	EPEC E2348/69 Δ <i>darTG</i> Δ <i>recG</i> ; <i>Str</i> ^R	This study
EL468	EPEC Δ <i>darTG</i> Δ <i>ruvAB</i>	EPEC E2348/69 Δ <i>darTG</i> Δ <i>ruvAB</i> ; <i>Str</i> ^R	This study
EL528	EPEC Δ <i>darTG</i> Δ <i>ruvC</i>	EPEC E2348/69 Δ <i>darTG</i> Δ <i>ruvC</i> ; <i>Str</i> ^R	This study
EL307	EPEC Δ <i>darTG</i> Δ <i>umuD</i>	EPEC E2348/69 Δ <i>darTG</i> Δ <i>umuD</i> ; <i>Str</i> ^R	This study
EL224	EPEC Δ <i>darTG</i> Δ <i>uvrA</i>	EPEC E2348/69 Δ <i>darTG</i> Δ <i>uvrA</i> ; <i>Str</i> ^R	This study
EL530	EPEC Δ <i>darTG</i> Δ <i>uvrA</i> Δ <i>recF</i>	EPEC E2348/69 Δ <i>darTG</i> Δ <i>uvrA</i> Δ <i>recF</i> ; <i>Str</i> ^R	This study
EL531	EPEC Δ <i>darTG</i> Δ <i>uvrA</i> Δ <i>recG</i>	EPEC E2348/69 Δ <i>darTG</i> Δ <i>uvrA</i> Δ <i>recG</i> ; <i>Str</i> ^R	This study
EL533	EPEC Δ <i>darTG</i> Δ <i>uvrA</i> Δ <i>ruvAB</i>	EPEC E2348/69 Δ <i>darTG</i> Δ <i>uvrA</i> Δ <i>ruvAB</i> ; <i>Str</i> ^R	This study
EL532	EPEC Δ <i>darTG</i> Δ <i>uvrA</i> Δ <i>ruvC</i>	EPEC E2348/69 Δ <i>darTG</i> Δ <i>uvrA</i> Δ <i>ruvC</i> ; <i>Str</i> ^R	This study
EL412	EPEC Δ <i>darTG</i> Δ <i>xth</i>	EPEC E2348/69 Δ <i>darTG</i> Δ <i>xth</i> ; <i>Str</i> ^R	This study

Table S2, related to STAR method : Strains used in this study