CORRECTION

Correction: A Single *parS* Sequence from the Cluster of Four Sites Closest to *oriC* Is Necessary and Sufficient for Proper Chromosome Segregation in *Pseudomonas aeruginosa*

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In Fig 1, the table in panel B is incorrect. Please see the corrected Fig 1 here.

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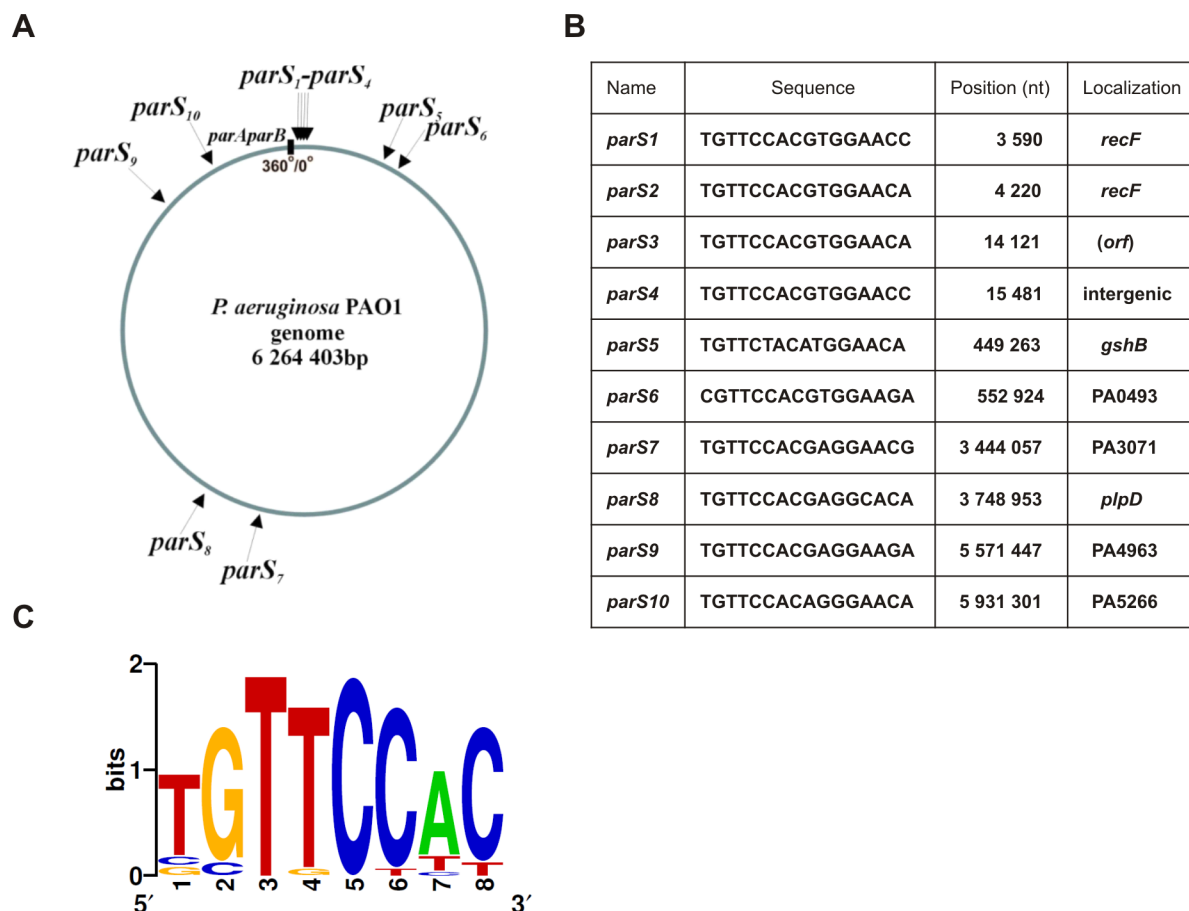click for updates

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A

B

Name	Sequence	Position (nt)	Localization
parS1	TGTTCCACGTGGAACC	3 590	*recF*
parS2	TGTTCCACGTGGAACA	4 220	*recF*
parS3	TGTTCCACGTGGAACA	14 121	(*orf*)
parS4	TGTTCCACGTGGAACC	15 481	intergenic
parS5	TGTTCTACATGGAACA	449 263	*gshB*
parS6	CGTTCCACGTGGAAGA	552 924	PA0493
parS7	TGTTCCACGAGGAACG	3 444 057	PA3071
parS8	TGTTCCACGAGGCACA	3 748 953	*plpD*
parS9	TGTTCCACGAGGAAGA	5 571 447	PA4963
parS10	TGTTCCACAGGGAACA	5 931 301	PA5266

C

Fig 1. The *parS* sites and their localization in the *Pseudomonas aeruginosa* genome. (A) Circular map of the *P. aeruginosa* genome with locations of putative ParB binding sequences [9]. Position of the *parAparB* operon is shown as black rectangle, grey arrow marks *oriC*, black arrows indicate predicted *parS* sites. **(B)** Nucleotide sequences, genomic coordinates and gene locations of the *parS* sites. The sequences are presented in a clockwise configuration. The coordinates are given according to the genomic sequence of the PAO1-UW strain [69]. **(C)** Sequence logo for all twenty 8-bp half-sites in the *P. aeruginosa* PAO1-UW genome (weblogo.berkeley.edu/logo.cgi). Nucleotides at positions 2 and 5 are invariant in all half-sites.

Reference

1. Jecz P, Bartosik AA, Glabski K, Jagura-Burdzy G (2015) A Single *parS* Sequence from the Cluster of Four Sites Closest to *oriC* Is Necessary and Sufficient for Proper Chromosome Segregation in *Pseudomonas aeruginosa*. PLoS ONE 10(3): e0120867. doi:10.1371/journal.pone.0120867 PMID: 25794281