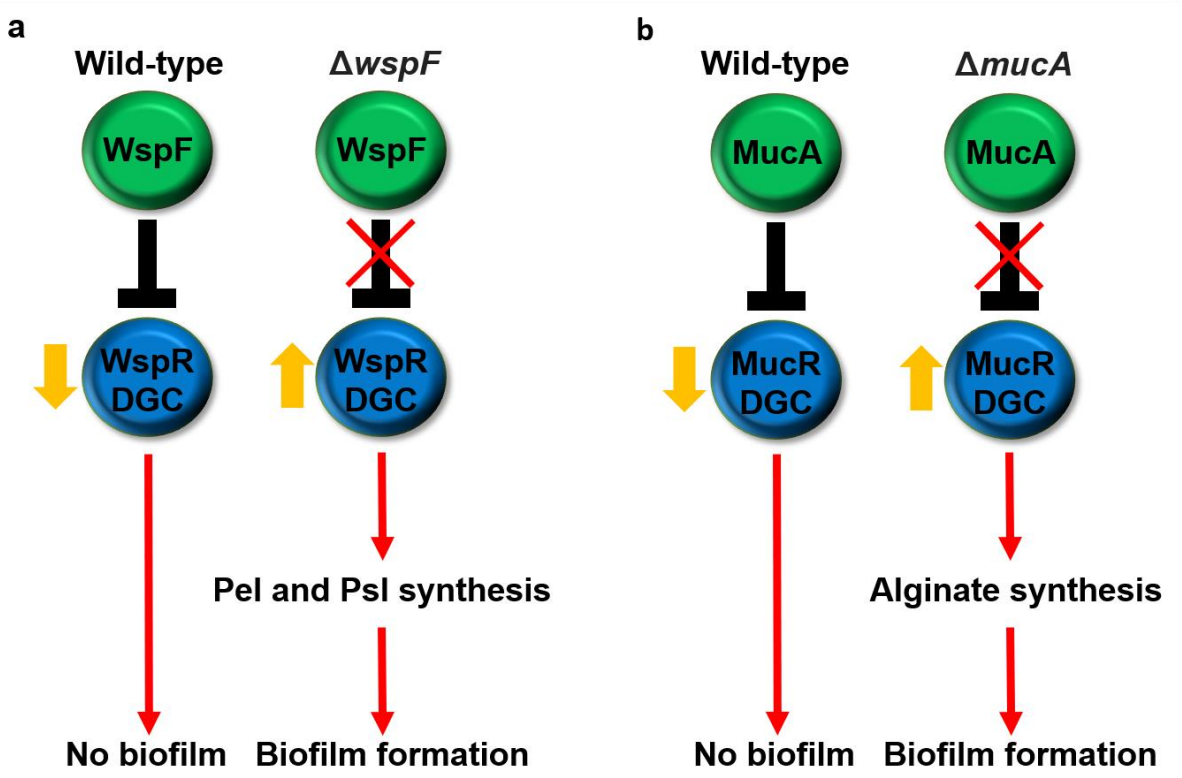
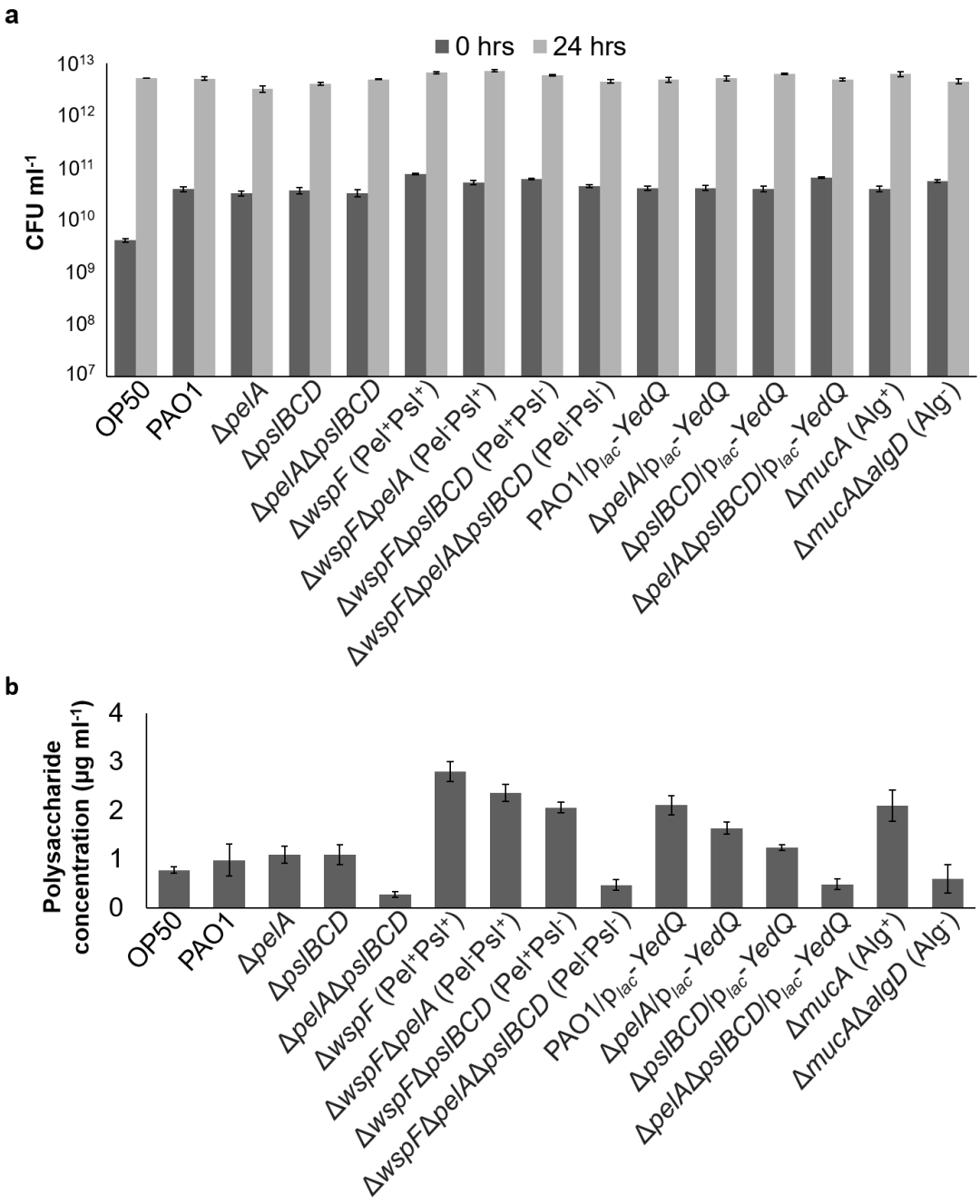
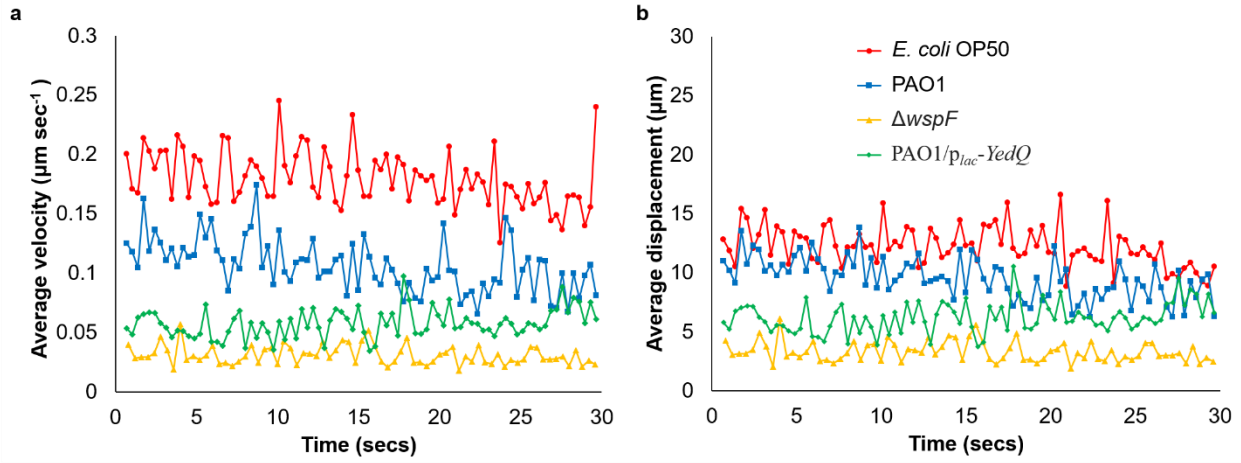


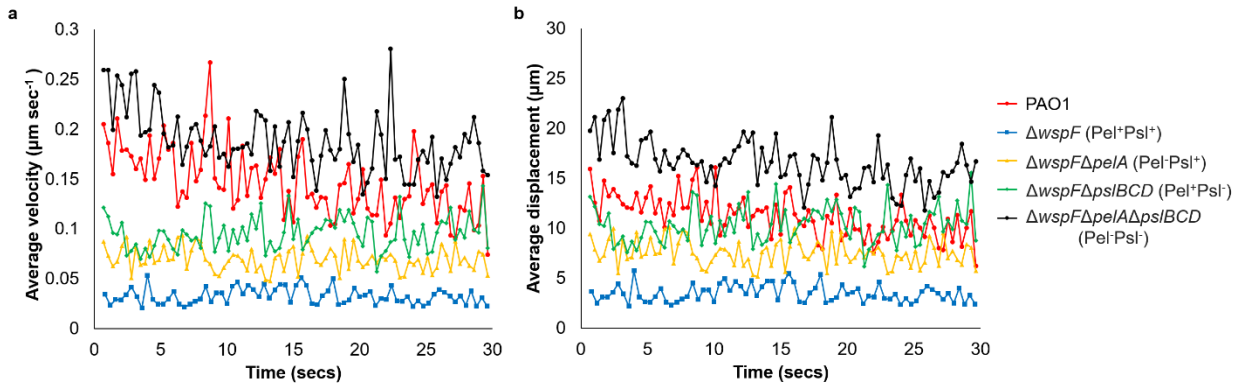
Supplementary Figure S1. Schematic diagram of the (a) *wsp* and (b) *muc* operons which regulate exopolysaccharide production and biofilm formation.



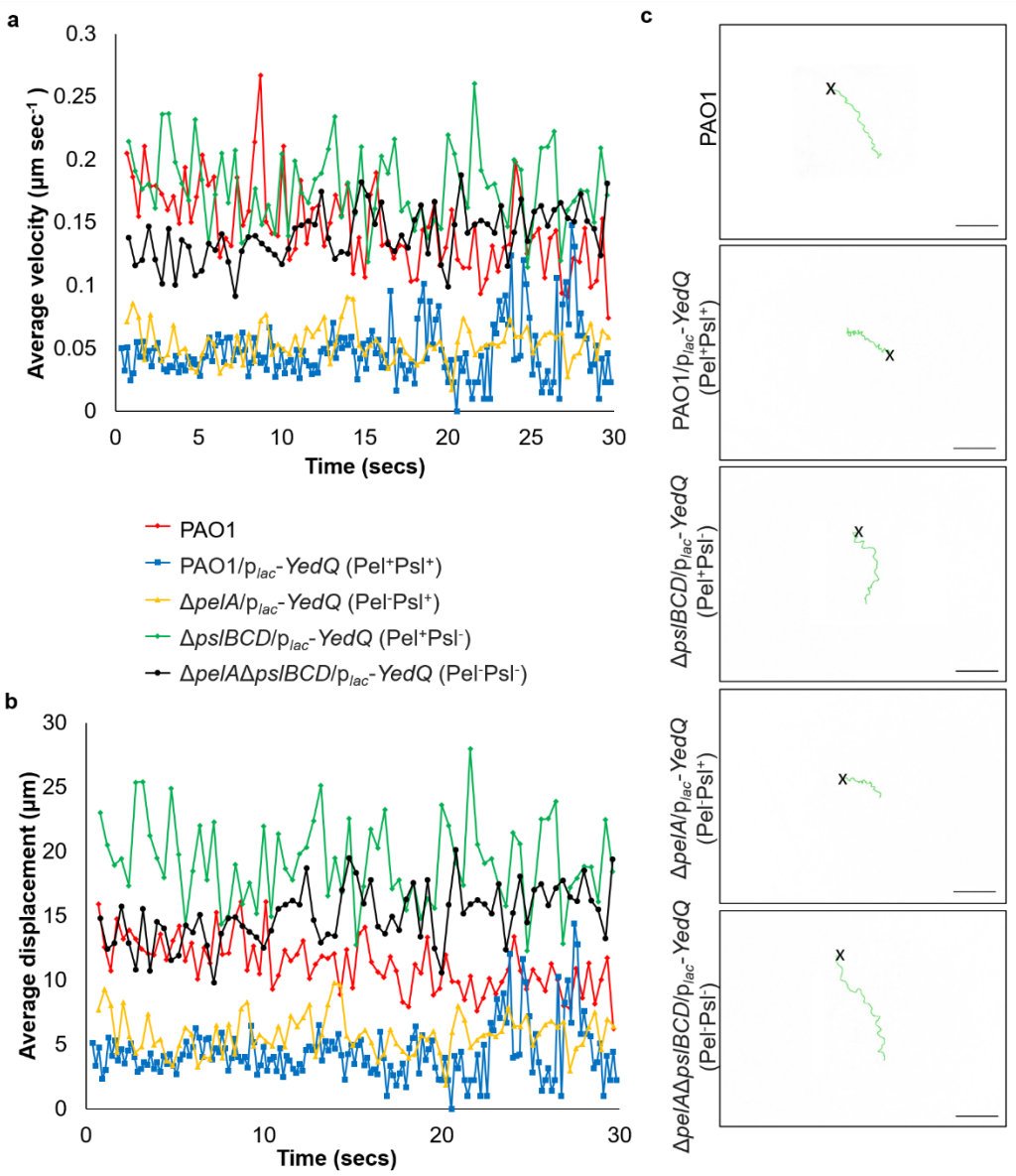
Supplementary Figure S2. Cell number and associated exopolysaccharide production on bacterial lawns. (a) CFU ml^{-1} and (b) concentration of exopolysaccharides. Means and s.d. from triplicate experiments are shown.



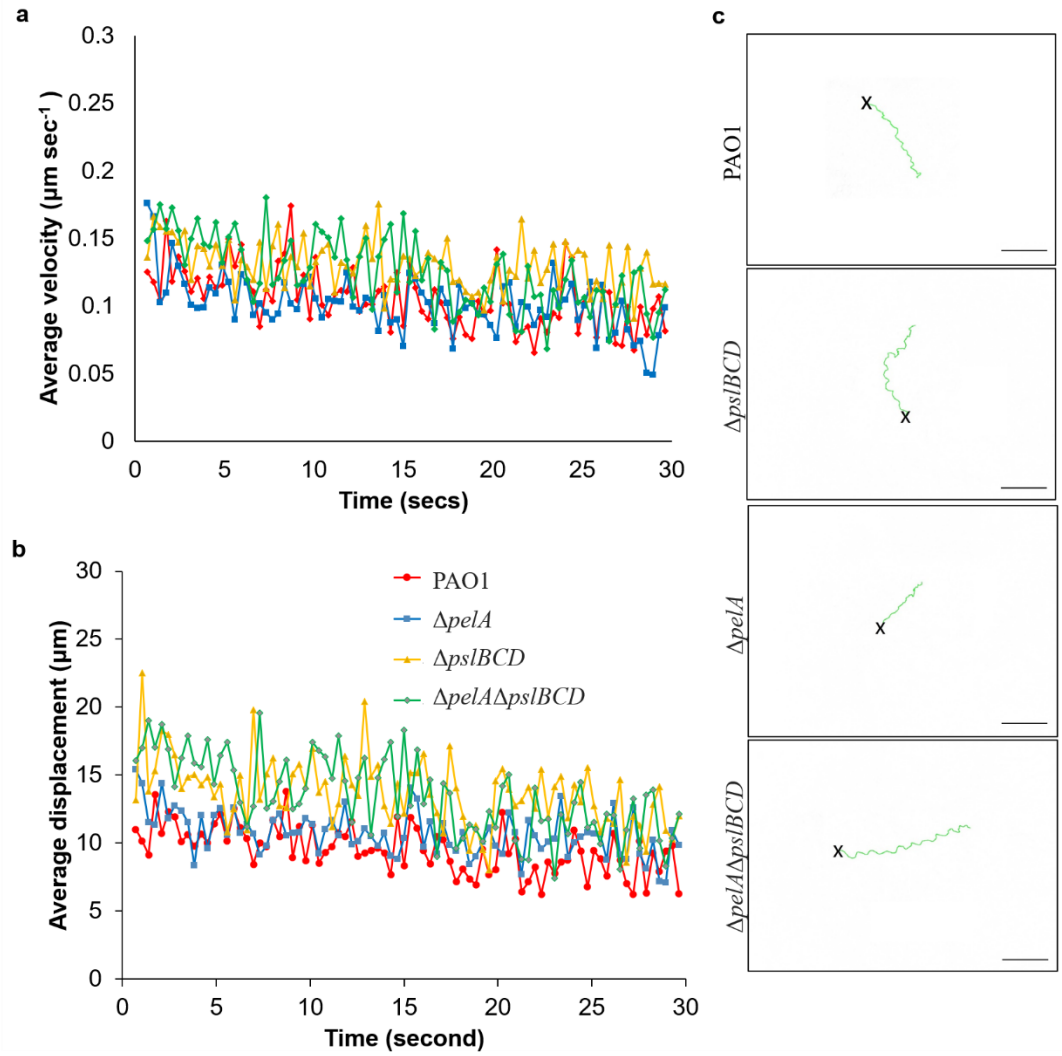
Supplementary Figure S3. Biofilms impede locomotion and restrict roaming of *C. elegans*. (a) Average velocity and (b) average displacement travelled by *C. elegans* on OP50, PAO1, Δ*wspF* and PAO1/p_{lac}-*YedQ* lawns over 30 secs. Means and s.d. from triplicate experiments are shown.



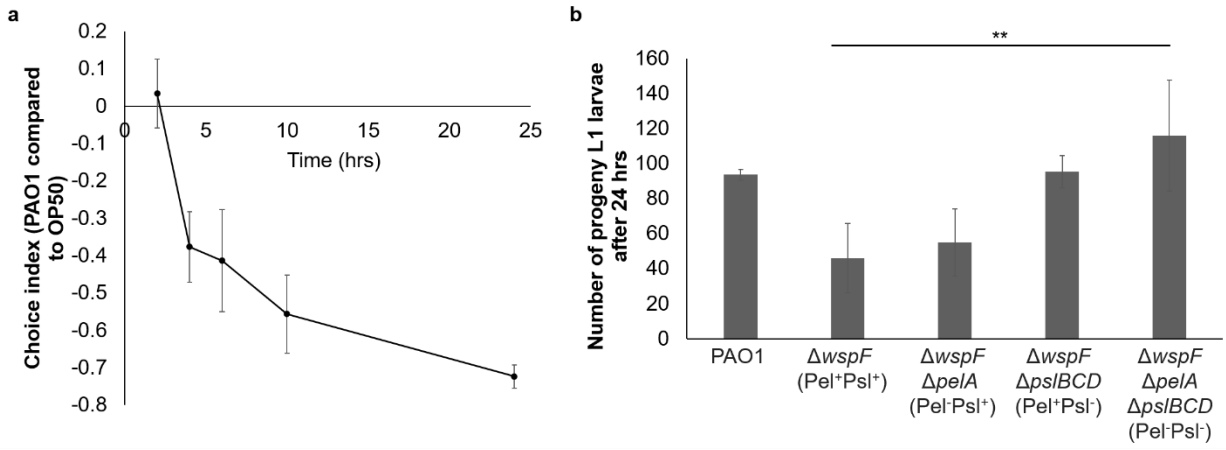
Supplementary Figure S4. Psl is more important than Pel at impeding nematode locomotion under influence by *wsp* operon. (a) Average velocity and (b) average displacement travelled by *C. elegans* on EPS mutant lawns over 30 secs. Means and s.d. from triplicate experiments are shown.



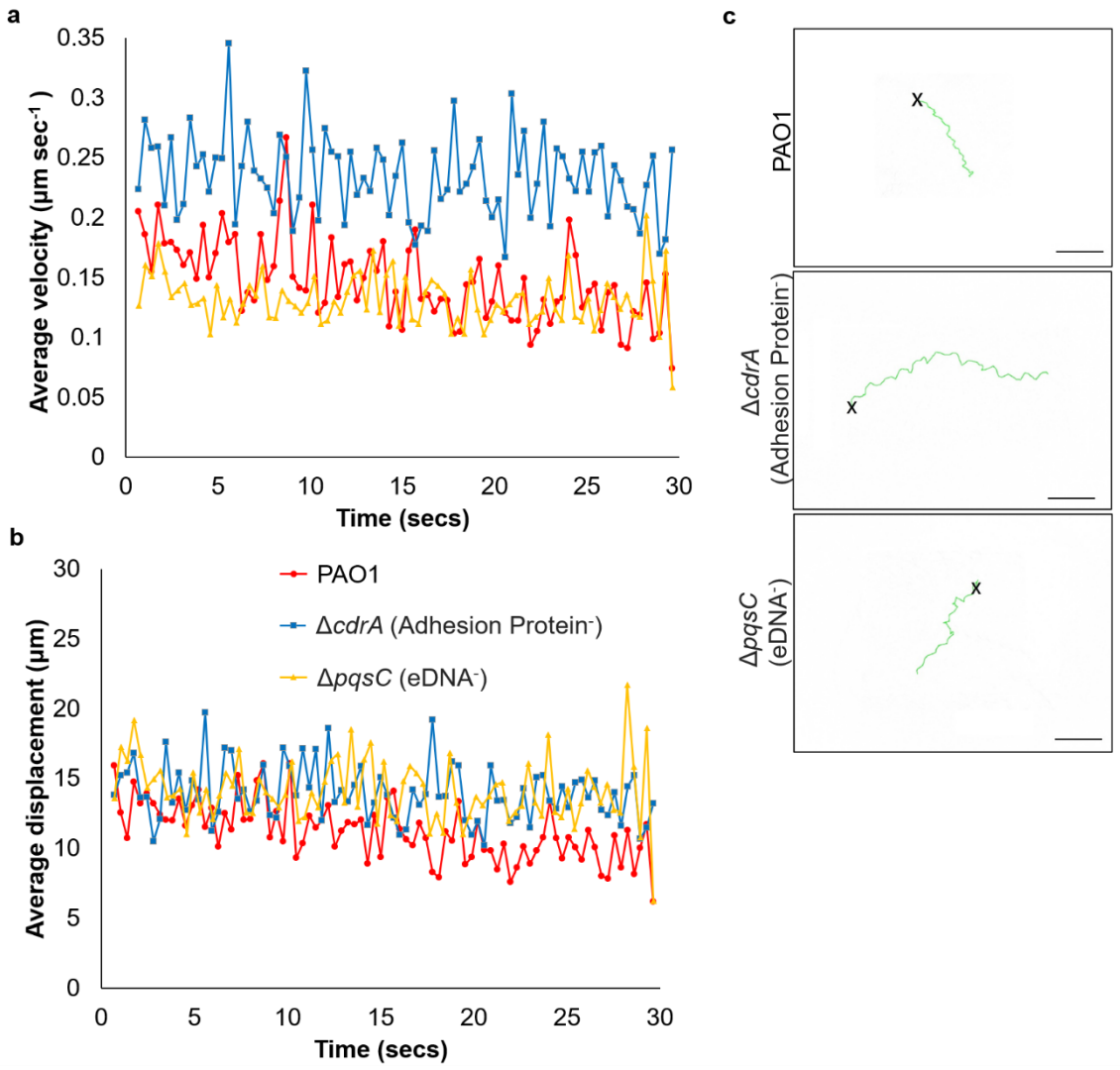
Supplementary Figure S5. Psl is more important than Pel at impeding nematode locomotion under influence by p_{lac}-*YedQ*. (a) Average velocity, (b) average displacement, and (c) representative tracks travelled by *C. elegans* on EPS mutants/p_{lac}-*YedQ* lawns over 30 secs. Means and s.d. from triplicate experiments are shown.



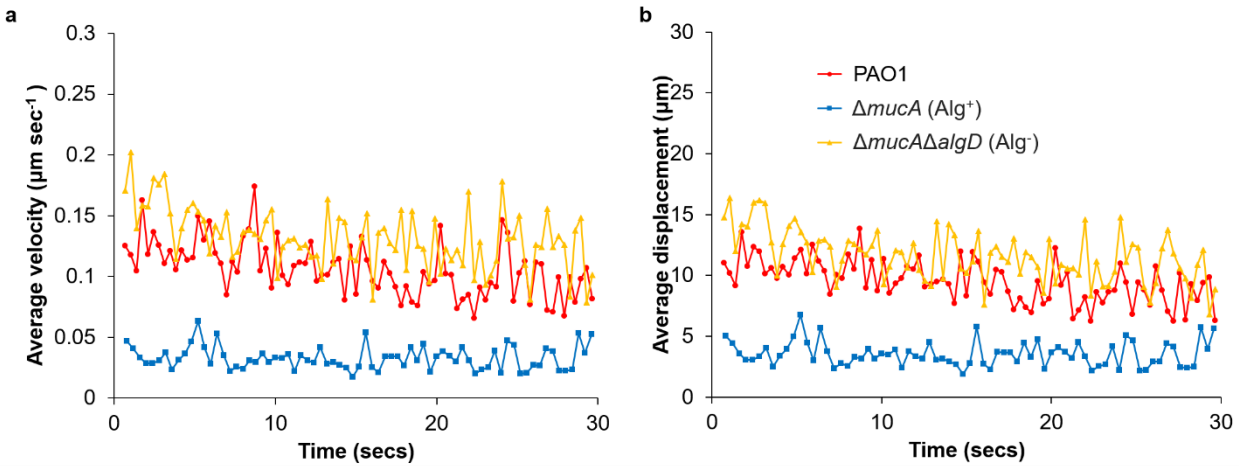
Supplementary Figure S6. Psl is more important than Pel at impeding nematode locomotion. (a) Average velocity, (b) average displacement, and (c) representative tracks travelled by *C. elegans* on EPS mutants lawns over 30 secs. Means and s.d. from triplicate experiments are shown.



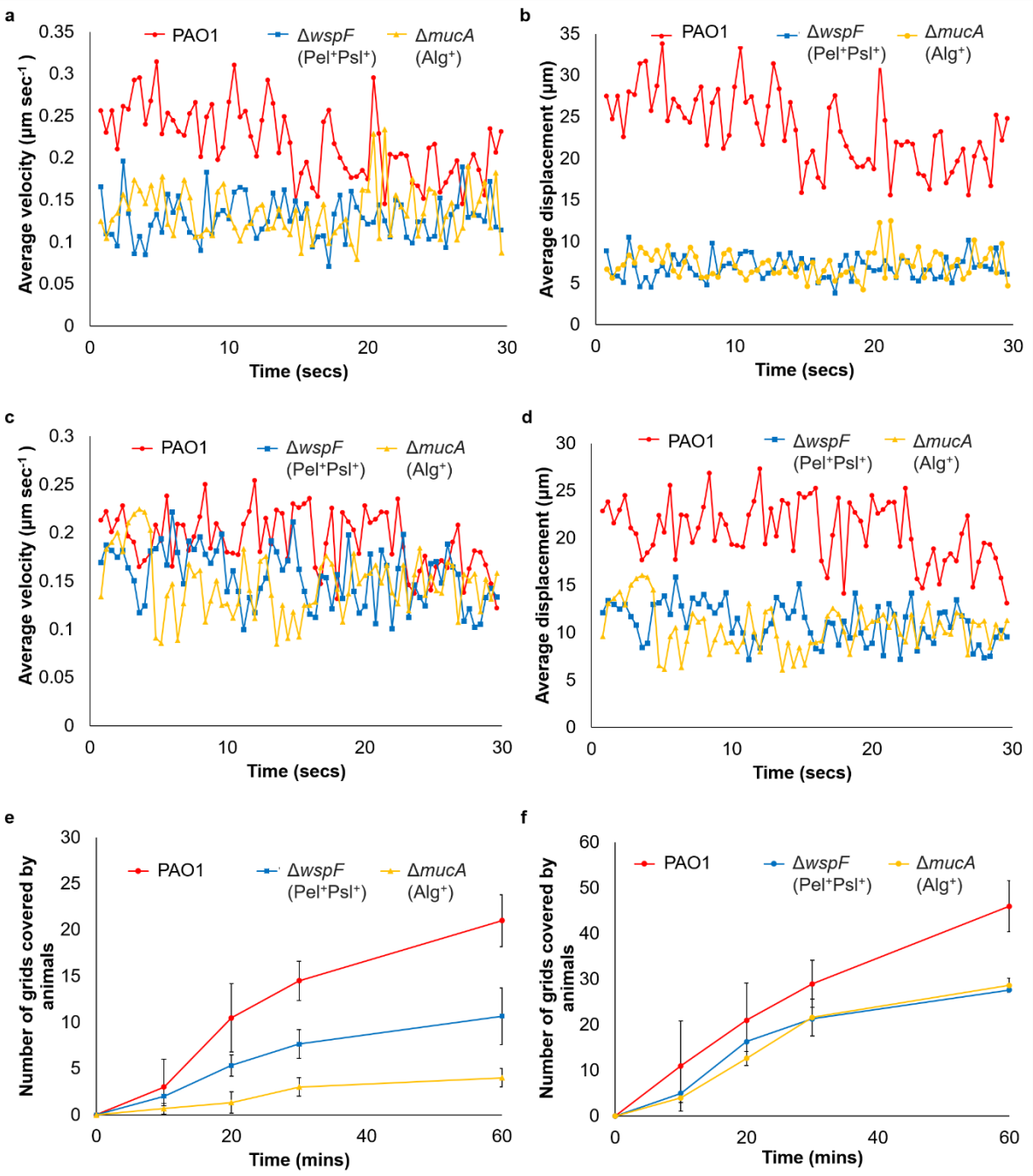
Supplementary Figure S7. *E. coli* OP50 is a preferential choice of *C. elegans* for food and reproduction. (a) Food choice index of PAO1 as compared to OP50. (b) Number of progeny L1 larvae hatched from adult nematodes which had escaped from *P. aeruginosa* biofilm trap and reached susceptible OP50 lawns after 24 hrs incubation. Means and s.d. from triplicate experiments are shown. **P < 0.01, ***P < 0.001, One-Way ANOVA.



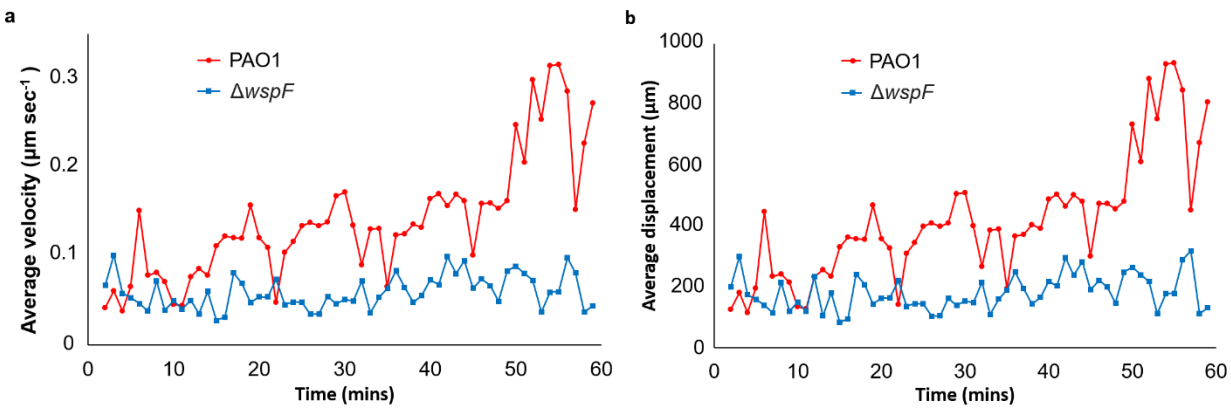
Supplementary Figure S8. CdrA adhesion proteins and eDNA are less involved in quagmire phenotype. (a) Average velocity, (b) average displacement, and (c) representative tracks travelled by C. elegans on PAO1, ΔcdrA and ΔpqsC lawns over 30 secs. Means and s.d from triplicate experiments are shown.



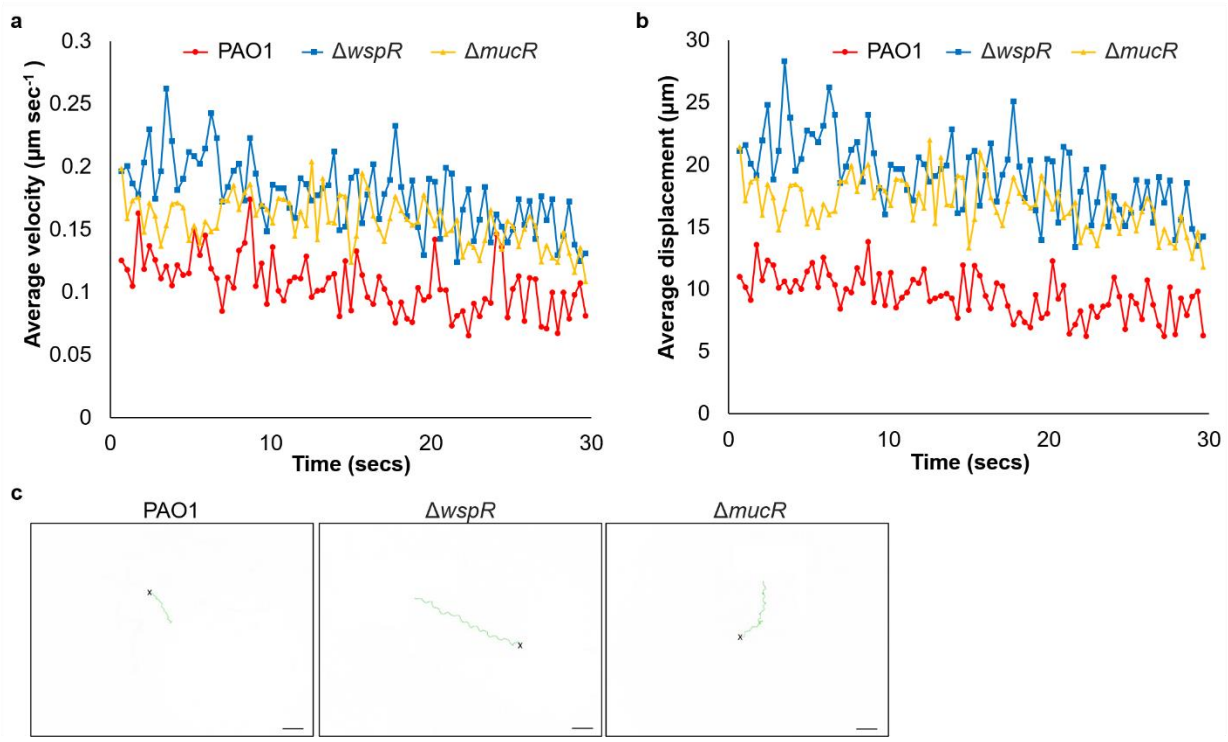
Supplementary Figure S9. Role of alginate in the quagmire phenotype. (a) Average velocity and (b) average displacement travelled by *C. elegans* on PAO1, Alg^+ and Alg^- lawns over 30 secs. Means and s.d. from triplicate experiments are shown.



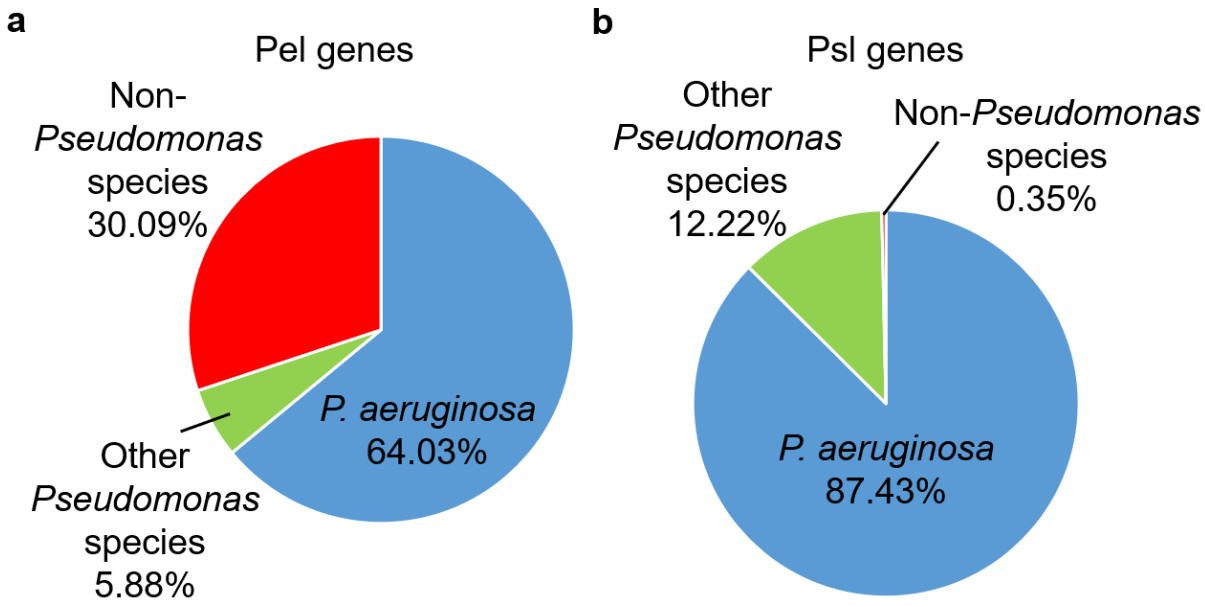
Supplementary Figure S10. Biofilms could impede *C. elegans* at L1 larvae and adult stages. (a) Average velocity and (b) average displacement of L1 *C. elegans* larvae on biofilms. (c) Average velocity and (d) average displacement of adult *C. elegans* on biofilms. Extent of roaming of (e) L1 larvae and (f) adult *C. elegans* on bait biofilm after leaving the trap biofilm. Means and s.d. from triplicate experiments are shown.



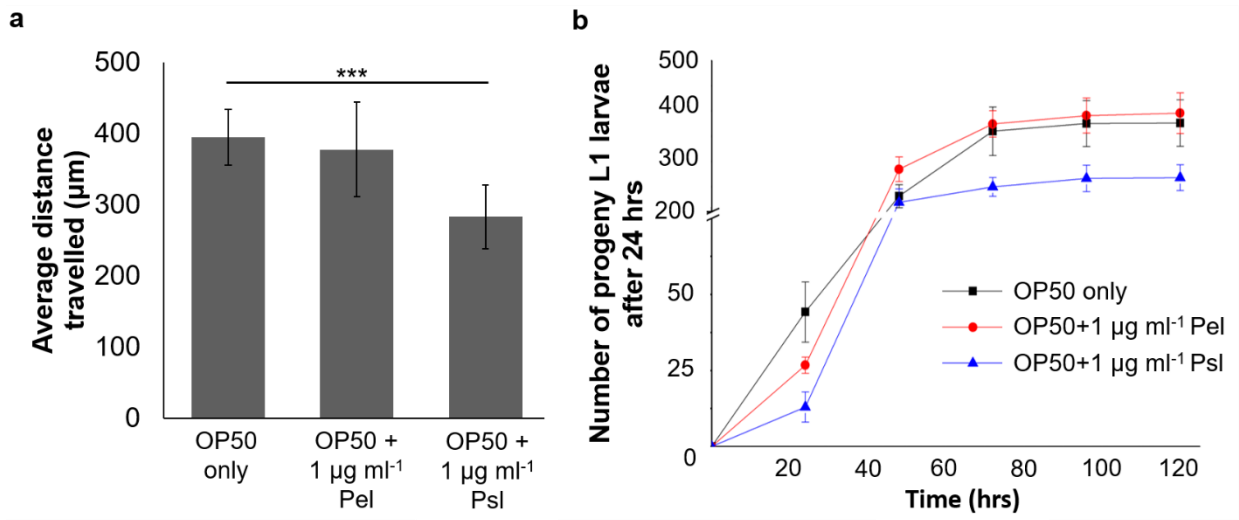
Supplementary Figure S11. Biofilms could impede *C. elegans* over prolonged duration of 1 hr. (a) Average velocity and (b) average displacement of *C. elegans* on biofilms over 1 hr of measurement. Means and s.d. from triplicate experiments are shown.



Supplementary Figure S12. WspR and MucR are involved in the quagmire phenotype. (a) Average velocity, (b) average displacement and (c) representative tracks travelled by *C. elegans* on PAO1, Δ*wspR* and Δ*mucR* over 30 secs. Means and s.d from triplicates experiments are shown.



Supplementary Figure S13. Presence of (a) Pel and (b) Psl synthesis genes in sequenced microbial species (*P. aeruginosa*, other *Pseudomonas* species and non-*Pseudomonas* species).



Supplementary Figure S14. Exogenous addition of 1 µg ml^{-1} Pel or Psl to OP50 strain resulted in (a) reduced average distance and (b) delayed reproduction of progeny of *C. elegans*. **P < 0.01, ***P < 0.001, n.s (not significant), One-Way ANOVA.

Supplementary Table S1. Bacterial strains and plasmids used in this study.

Strain/ plasmid	Description	Source/ Reference
	P. aeruginosa	
PAO1	Prototypic nonmucoid wild-type strain	[1]
Δ*pelA*	Pel exopolysaccharide defective *pelA* mutant in PAO1	[2]
Δ*pslBCD*	Psl exopolysaccharide defective *pelBCD* mutant in PAO1	[2]
Δ*pelA*Δ*pslBCD*	Pel and Psl exopolysaccharides defective *pelA* and *pslBCD* mutant in PAO1	[2]
Δ*wspF*	*wspF* knockout of PAO1 constructed by allelic exchange	[3]
Δ*wspF*Δ*pelA*	Pel exopolysaccharide defective *pelA* mutant in Δ*wspF* mutant	This study
Δ*wspF*Δ*pslBCD*	Psl exopolysaccharide defective *pelBCD* mutant in Δ*wspF* mutant	This study
Δ*wspF*Δ*pelA*Δ*pslBCD*	Pel and Psl exopolysaccharides defective *pelA* and *pslBCD* mutant in Δ*wspF* mutant	[3]
PAO1/p_{lac}-*YedQ*	Gm^r; PAO1 containing the plac-yedQ vector	[4]
Δ*pelA*/p_{lac}-*YedQ*	Gm^r; PAO1/ΔpelA containing the plac-yedQ vector	[4]
Δ*pslBCD*/p_{lac}-*YedQ*	Gm^r; PAO1/ΔpslBCD containing the plac-yedQ	[4]

Δ*pelA*Δ*pslBCD*/p$_{lac}$-*YedQ*	Gm^r; PAO1/ΔpelAΔpslBCD containing the plac-yedQ vector	[4]
Δ*mucA*	*mucA* knockout of PAO1 constructed by allelic exchange	[5]
Δ*mucA*Δ*algT*	Alginate exopolysaccharide defective *algT* mutant in Δ*mucA* mutant	[5]
Δ*cdrA*	*cdrA* knockout of PAO1 constructed by allelic exchange	This study
Δ*pqsC*	*pqsC* knockout of PAO1 constructed by allelic exchange	[6]
Δ*wspR*	*wspR* knockout of PAO1 constructed by allelic exchange	This study
Δ*mucR*	*mucR* knockout of PAO1 constructed by allelic exchange	This study
E. coli		
OP50	Used for maintenance of *C. elegans*	Laboratory collection
DH5α	F$^-$, ø80d*lacZ*ΔM15, Δ(*lacZYA*-*argF*)U169, *deo*R, *recA*1, *endA*1, *hsdR*17(rK$^-$, mK$^+$), *phoA*, *supE*44, λ–, *thi*-1, *gyrA*96, *relA*1	Laboratory collection
Plasmid		
pUCp22	Ap^r and Gm^r; broad-host-range cloning vector	[7]
p$_{lac}$-*YedQ*	Gm^r; pUCP22 carrying the yedQ gene	[4]

Supplementary Videos:

Supplementary Video 1. *C. elegans* locomotion on *E. coli* OP50.

Supplementary Video 2. *C. elegans* locomotion on *P. aeruginosa* PAO1.

Supplementary Video 3. *C. elegans* locomotion on Δ*wspF* (Pel^+Psl^+).

Supplementary Video 4. *C. elegans* locomotion on PAO1/p_{lac}-*YedQ* (Pel^+Psl^+).

Supplementary Video 5. *C. elegans* locomotion on Δ*wspF*Δ*pelA*Δ*pslBCD* (Pel^-Psl^-).

Supplementary Video 6. *C. elegans* locomotion on Δ*wspF*Δ*pelA* (Pel^-Psl^+).

Supplementary Video 7. *C. elegans* locomotion on Δ*wspF*Δ*pslBCD* (Pel^+Psl^-).

Supplementary Video 8. *C. elegans* locomotion on Δ*pelA*/p_{lac}-*YedQ* (Pel^-Psl^+).

Supplementary Video 9. *C. elegans* locomotion on Δ*pslBCD*/p_{lac}-*YedQ* (Pel^+Psl^-).

Supplementary Video 10. *C. elegans* locomotion on Δ*pelA*Δ*pslBCD*/p_{lac}-*YedQ* (Pel^-Psl^-).

Supplementary Video 11. *C. elegans* locomotion on Δ*pelA*.

Supplementary Video 12. *C. elegans* locomotion on Δ*pslBCD*.

Supplementary Video 13. *C. elegans* locomotion on Δ*pelA*Δ*pslBCD*.

Supplementary Video 14. *C. elegans* locomotion on Δ*mucA* (Alg^+).

Supplementary Video 15. *C. elegans* locomotion on Δ*mucA*Δ*algD*(Alg^-).

Supplementary Data:

Supplementary Data S1. List of *P. aeruginosa* sequenced isolates containing mutations in *wspF* gene and WspF protein.

Supplementary Data S2. List of sequenced bacterial species found in *C. elegans* native microbiome, which contain *pel* and *psl* genes.

Supplementary Data S3. List of all sequenced bacterial species containing *pel* and *psl* genes.

References:

1. B W Holloway, a. and A.F. Morgan, *Genome Organization in Pseudomonas.* Annual Review of Microbiology, 1986. **40**(1): p. 79-105.
2. Yang, L., Y. Hu, Y. Liu, J. Zhang, J. Ulstrup, and S. Molin, *Distinct roles of extracellular polymeric substances in Pseudomonas aeruginosa biofilm development.* Environmental Microbiology, 2011. **13**(7): p. 1705-1717.
3. Rybtke, M.T., B.R. Borlee, K. Murakami, Y. Irie, M. Hentzer, T.E. Nielsen, et al., *Fluorescence-Based Reporter for Gauging Cyclic Di-GMP Levels in Pseudomonas aeruginosa.* Applied and Environmental Microbiology, 2012. **78**(15): p. 5060-5069.
4. Chen, Y., M. Yuan, A. Mohanty, J.K.H. Yam, Y. Liu, S.L. Chua, et al., *Multiple diguanylate cyclase-coordinated regulation of pyoverdine synthesis in Pseudomonas aeruginosa.* Environmental Microbiology Reports, 2015. **7**(3): p. 498-507.
5. Yang, L., Y. Liu, T. Markussen, N. Høiby, T. Tolker-Nielsen, and S. Molin, *Pattern differentiation in co-culture biofilms formed by Staphylococcus aureus and Pseudomonas aeruginosa.* FEMS Immunology & Medical Microbiology, 2011. **62**(3): p. 339-347.
6. Wang, V.B., S.-L. Chua, B. Cao, T. Seviour, V.J. Nesatyy, E. Marsili, et al., *Engineering PQS Biosynthesis Pathway for Enhancement of Bioelectricity Production in Pseudomonas aeruginosa Microbial Fuel Cells.* PLOS ONE, 2013. **8**(5): p. e63129.
7. Chua, S.L., Y. Ding, Y. Liu, Z. Cai, J. Zhou, S. Swarup, et al., *Reactive oxygen species drive evolution of pro-biofilm variants in pathogens by modulating cyclic-di-GMP levels.* Open Biology, 2016. **6**(11): p. 160162.