

Supplementary Information

Genome-Wide Identification of Genes Necessary for Biofilm Formation of Nosocomial Pathogen *Stenotrophomonas maltophilia* Reveals Orphan Response Regulator FsnR is a Critical Modulator

Xiu-Min Kang^{1,2§}, Fang-Fang Wang^{1§}, Huan Zhang^{1,3}, Qi Zhang^{2*}, Wei Qian^{1*}

¹ State Key Laboratory of Plant Genomics, Institute of Microbiology, Chinese Academy of Sciences, Beijing 100101, China. ² School of Chemical Engineering & Environment, Beijing Institute of Technology, Beijing 100081, China. ³ College of Life Sciences, University of Chinese Academy of Sciences, Beijing 100049, China.

§ These authors contributed equally to this work

* Corresponding authors. Wei Qian, Tel: +86-10-64806063; Fax: +86-10-64858245; Email: qianw@im.ac.cn. Qi Zhang, Tel: 86-10-68918012; Email: zhangqi@bit.edu.cn

Keywords: *Stenotrophomonas maltophilia*, biofilm, transposon mutagenesis, response regulator, flagella assembly

Table S1. TAIL-PCR identification of genes associated with biofilm formation of *Stenotrophomonas maltophilia*

| Library ID | Gene name | Gene code ¹ | Insertion site | Putative function or description | Relative production of biofilm ² |
|---------------------------|-------------|------------------------|----------------|--|---|
| Flagellar and pili | | | | | |
| SMA21-B18 | <i>flgE</i> | Smlt2314 | 2356638 | flagellar hook protein FlgE | 0.09 ± 0.02 |
| SMA24-K12 | <i>flgE</i> | Smlt2314 | 2357167 | flagellar hook protein FlgE | 0.06 ± 0.02 |
| SMA23-F7 | <i>flgK</i> | Smlt2308 | 2351423 | flagellar hook-associated protein FlgK | 0.20 ± 0.02 |
| SMA22-P5 | <i>flgK</i> | Smlt2308 | 2350254 | flagellar hook-associated protein FlgK | 0.24 ± 0.02 |
| SMA7-D19 | <i>flgG</i> | Smlt2312 | 2355626 | flagellar basal body rod protein FlgG | 0.16 ± 0.02 |
| SMA3-A22 | <i>flgH</i> | Smlt2311 | 2354349 | flagellar basal body L-ring protein | 0.29 ± 0.02 |
| SMA12-E14 | <i>flhF</i> | Smlt2272 | 2314389 | flagellar biosynthesis regulator FlhF | 0.10 ± 0.02 |
| SMA33-M8 | <i>flgI</i> | Smlt2310 | 2354014 | flagellar basal body P-ring protein | 0.09 ± 0.02 |
| SMA36-A20 | <i>flhA</i> | Smlt2273 | 2315325 | flagellar biosynthesis protein FlhA | 0.04 ± 0.02 |
| SMA24-L1 | <i>fliI</i> | Smlt2286 | 2329126 | flagellum-specific ATP synthase | 0.04 ± 0.02 |
| SMA5-N23 | <i>fliI</i> | Smlt2286 | 2329375 | flagellum-specific ATP synthase | 0.15 ± 0.02 |
| SMA1-O11 | <i>fliN</i> | Smlt2281 | 2325341 | flagellar motor switch protein | 0.02 ± 0.02 |
| SMA7-L17 | <i>fliN</i> | Smlt2281 | 2325099 | flagellar motor switch protein | 0.04 ± 0.02 |
| SMA5-B13 | <i>fliD</i> | Smlt2303 | 2344144 | flagellar hook-associated protein 2 | 0.29 ± 0.02 |
| SMA8-H1 | <i>fliD</i> | Smlt2303 | 2343369 | flagellar hook-associated protein 2 | 0.22 ± 0.02 |
| SMA20-O1 | <i>fliD</i> | Smlt2303 | 2343922 | flagellar hook-associated protein 2 | 0.11 ± 0.02 |
| SMA29-J9 | <i>fliO</i> | Smlt2280 | 2324844 | flagellar protein FliO | 0.03 ± 0.02 |
| SMA27-G19 | <i>fliF</i> | Smlt2289 | 2332513 | flagellar MS-ring protein | 0.48 ± 0.02 |
| SMA22-G16 | <i>fliF</i> | Smlt2289 | 2332351 | flagellar MS-ring protein | 0.13 ± 0.02 |
| SMA33-D16 | <i>fliM</i> | Smlt2282 | 2325508 | flagellar motor switch protein FliM | 0.08 ± 0.02 |
| SMA29-N19 | <i>fliK</i> | Smlt2284 | 2327270 | flagellar hook-length control protein | 0.06 ± 0.02 |
| SMA37-A8 | | Smlt0709 | 739626 | fimbria adhesin protein | 0.06 ± 0.02 |

| | | | | | |
|--|-------------|----------|---------|---|-------------|
| SMA10-I4 | | Smlt0707 | 736153 | pili chaperone protein | 0.00 ± 0.02 |
| SMA26-D10 | | Smlt0707 | 736381 | pili chaperone protein | 0.05 ± 0.02 |
| SMA21-J12 | | Smlt0707 | 735772 | pili chaperone protein | 0.03 ± 0.02 |
| SMA1-D14 | <i>fimV</i> | Smlt3426 | 3467204 | fimV protein | 0.40 ± 0.02 |
| Polysaccharide biosynthesis and carbohydrate metabolism | | | | | |
| SMA11-N24 | <i>xanA</i> | Smlt0653 | 670657 | phosphohexosemutase | 0.00 ± 0.02 |
| SMA24-K24 ³ | | Smlt3804 | 3885560 | glyceraldehyde 3-phosphate dehydrogenase | 1.19 ± 0.02 |
| SMA6-A2 | | Smlt4259 | 4372983 | uracil-DNA glycosylase | 1.21 ± 0.02 |
| SMA26-B22 | | Smlt0490 | 500892 | pyruvate dehydrogenase subunit E1 | 2.08 ± 0.02 |
| Purine biosynthesis | | | | | |
| SMA34-L13 | <i>purE</i> | Smlt1613 | 1676463 | phosphoribosylaminoimidazole carboxylase | 0.47 ± 0.02 |
| SMA2-D12 | <i>purK</i> | Smlt1614 | 1677627 | phosphoribosylaminoimidazole carboxylase ATPase subunit | 0.40 ± 0.02 |
| SMA5-E20 | <i>purK</i> | Smlt1614 | 1677333 | phosphoribosylaminoimidazole carboxylase ATPase subunit | 0.56 ± 0.02 |
| SMA28-I22 | <i>purD</i> | Smlt4254 | 4369733 | phosphoribosylamine--glycine ligase | 0.41 ± 0.02 |
| SMA28-E14 | <i>purC</i> | Smlt4318 | 4434102 | phosphoribosylaminoimidazolesuccinocarboxamide synthase | 0.52 ± 0.02 |
| SMA25-F12 | <i>purC</i> | Smlt4318 | 4434385 | phosphoribosylaminoimidazolesuccinocarboxamide synthase | 0.52 ± 0.02 |
| SMA34-D21 | <i>purL</i> | Smlt0684 | 708539 | phosphoribosylformylglycinamide synthase | 0.28 ± 0.02 |
| SMA14-N11 | <i>guaA</i> | Smlt2072 | 2098217 | GMP synthase | 0.01 ± 0.02 |
| Transportation | | | | | |
| SMA21-I12 | <i>mrkC</i> | Smlt0708 | 738300 | outer membrane usher protein mrkc precursor | 0.06 ± 0.02 |
| SMA25-J1 | <i>mrkC</i> | Smlt0708 | 738264 | outer membrane usher protein mrkc precursor | 0.05 ± 0.02 |
| SMA1-M13 | <i>mrkC</i> | Smlt0708 | 737324 | outer membrane usher protein mrkc precursor | 0.03 ± 0.02 |
| SMA23-L17 | <i>mrkC</i> | Smlt0708 | 739000 | outer membrane usher protein mrkc precursor | 0.04 ± 0.02 |
| SMA2-C16 | <i>mrkC</i> | Smlt0708 | 737190 | outer membrane usher protein mrkc precursor | 0.13 ± 0.02 |
| SMA20-H21 | | Smlt4552 | 4672328 | glutathione-regulated cation-efflux system | 0.06 ± 0.02 |
| SMA26-E2 | | Smlt0845 | 887435 | transmembrane transport protein | 0.12 ± 0.02 |
| Gene regulation | | | | | |
| SMA4-B6 | | Smlt2299 | 2340975 | response regulator protein LuxR family | 0.03 ± 0.02 |

| | | | | | |
|---------------------------------------|-------------|-------------------|---------------|---|--------------------|
| SMA7-F19 | | Smlt2297 | 2340048 | RNA polymerase sigma-54 factor (sigma-N) | 0.03 ± 0.02 |
| SMA31-L10 | <i>fliA</i> | Smlt2270 | 2311509 | RNA polymerase sigma factor for flagellar | 0.04 ± 0.02 |
| SMA32-N20 | <i>ravS</i> | Smlt2324 | 2366132 | PAS domain sensor histidine kinase | 0.16 ± 0.02 |
| SMA27-H15 | <i>glnL</i> | Smlt0158 | 172801 | nitrogen regulation protein NR(II) | 0.55 ± 0.02 |
| Peptide and lipid biosynthesis | | | | | |
| SMA26-C23 | | Smlt0208 | 222379 | peptide synthase | 0.35 ± 0.02 |
| SMA11-F15 | | Smlt0208 | 222773 | peptide synthase | 0.39 ± 0.02 |
| SMA26-F10 | | Smlt0208 | 223044 | peptide synthase | 0.56 ± 0.02 |
| SMA23-C6 | | Smlt0208 | 222148 | peptide synthase | 0.56 ± 0.02 |
| SMA15-G14 | | Smlt0208 | 221659 | peptide synthase | 0.56 ± 0.02 |
| SMA27-O8 | | Smlt0208 | 222499 | peptide synthase | 0.51 ± 0.02 |
| SMA18-J16 | | Smlt0418 | 427771 | aminopeptidase | 0.16 ± 0.02 |
| SMA30-B20 | | Smlt0625 | 641485 | lipase | 1.32 ± 0.02 |
| Oxidoreduction | | | | | |
| SMA25-G12 | | Smlt0209 | 223554 | NAD(P)H dehydrogenase | 0.40 ± 0.02 |
| SMA36-C6 | | Smlt0209 | 223158 | NAD(P)H dehydrogenase | 0.38 ± 0.02 |
| SMA20-E12 | | Smlt0209 | 223345 | NAD(P)H dehydrogenase | 0.59 ± 0.02 |
| SMA3-K17 | <i>pntB</i> | Smlt0857 | 897800 | NAD(P) transhydrogenase subunit beta PntB | 0.32 ± 0.02 |
| SMA14-L15 | | Smlt3167 | 3208008 | NAD-dependent glutamate dehydrogenase | 0.51 ± 0.02 |
| Function unknown | | | | | |
| SMA30-E7 | | Smlt0276 | 293008 | hypothetical protein | 0.27 ± 0.02 |
| SMA31-C20 | | Smlt3195 | 3236474 | hypothetical protein | 0.44 ± 0.02 |
| SMA28-M23 | | Smlt0416 | 393052 | hypothetical protein | 1.44 ± 0.02 |
| SMA34-E19 | | Smlt0639 | 656017 | hypothetical protein | 0.10 ± 0.02 |
| Transposable elements | | | | | |
| SMA14-I22 | | Smlt0518 | 526451 | transposase | 0.47 ± 0.02 |
| Intergenic region | | | | | |
| SMA10-P7 | | Smlt0704-Smlt0706 | | Intergenic region | 0.12 ± 0.02 |

| | | | |
|---|---|-------------------|--------------------|
| SMA13-I9 | Smlt0417-Smlt0418 | Intergenic region | 0.50 ± 0.02 |
| SMA35-A20 | Smlt0722-Smlt0723 | Intergenic region | 0.42 ± 0.02 |
| SMA37-D2 | Smlt4645-Smlt4647 | Intergenic region | 0.06 ± 0.02 |
| Undefined (inserted in multi-copy locus) | | | |
| SMA31-H5 | 416255、421919、 4792803、4787139 | ND | 0.10 ± 0.02 |
| SMA21-O22 | 416470、422134、 4786924、4792588 | ND | 1.70 ± 0.02 |

1. Gene code and names are according to the genomic annotation of *S. maltophilia* K279a
2. Relative production of biofilm of mutants are compared to that of the wild-type (set as unit). Standard deviations are shown (n = 3)
3. Mutants in red highlighted that mutation of these genes caused increase in biofilm formation.

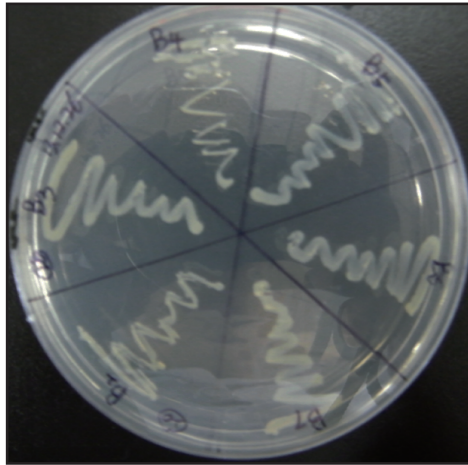


FIG S1. Stability of the EZ::TN transposon inserted mutants. Six transformants from the mutant library were randomly selected. The bacterial progenies were grown in NYG agar without any antibiotics for 20 rounds of subcultures under 28°C. After subculture, bacterial strains were inoculated onto a NYG agar containing kanamycin (50 µg/ml) and cultured for 48 hours under 28°C.

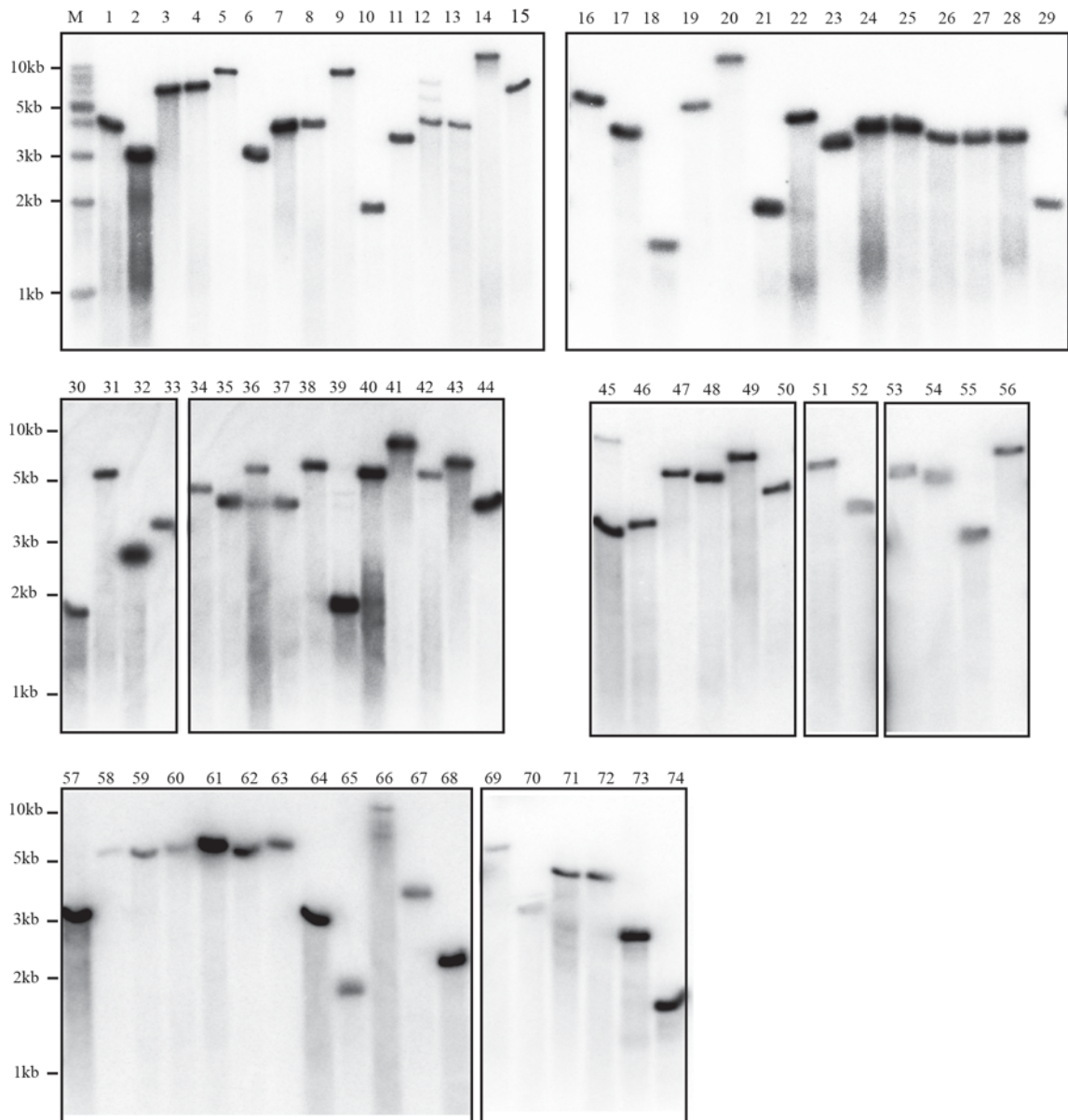


FIG. S2. Determination of insertional copy numbers of identified mutants. Transposon insertion numbers were analyzed by Southern blotting. Total DNA of the bacterial strains were digested by *Sma*I and separated in 1% agarose gel. A PCR product of EZ::TN transposon was labeled by [α - 32 P]-dCTP and used as DNA probe in hybridization. M: 1 kb DNA ladder. The numbers of lanes are according to the codes of mutant library and Table S1, as follows:

1: SMA11-F15, 2: SMA7-F19, 3: SMA5-N23, 4: SMA33-M8, 5: SMA31-L10, 6: SMA4-B6
7: SMA15-G14, 8: SMA20-E12, 9: SMA12-E14, 10: SMA3-A22, 11: SMA23-C6, 12: SMA8-H1
13: SMA20-O1, 14: SMA28-I22, 15: SMA24-L1, 16: SMA33-D16, 17: SMA25-G12, 18: SMA34-D21
19: SMA24-K12, 20: SMA31-H5, 21: SMA28-E14, 22: SMA5-B13, 23: SMA23-L17, 24: SMA27-O8
25: SMA26-F10, 26: SMA1-M13, 27: SMA25-J1, 28: SMA21-I12, 29: SMA27-H15, 30: SMA25-F12
31: SMA5-E20, 32: SMA10-P7, 33: SMA35-A20, 34: SMA21-B18, 35: SMA26-D10, 36: SMA18-J16
37: SMA21-J12, 38: SMA3-K17, 39: SMA13-I9, 40: SMA14-I22, 41: SMA1-D14, 42: SMA37-A8
43: SMA34-E19, 44: SMA36-C6, 45: SMA2-C16, 46: SMA26-C23, 47: SMA32-N20, 48: SMA29-N19
49: SMA36-A20, 50: SMA29-J9, 51: SMA27-G19, 52: SMA10-I4, 53: SMA34-L13, 54: SMA22-G16
55: SMA7-D19, 56: SMA14-L15, 57: SMA14-N11, 58: SMA37-D2, 59: SMA7-L17, 60: SMA23-F7
61: SMA22-P5, 62: SMA2-D12, 63: SMA1-O11, 64: SMA11-N24, 65: SMA31-C20, 66: SMA 26-E2
67: SMA30-E7, 68: SMA20-H21, 69: SMA30-B20, 70: SMA26-B22, 71: SMA6-A2, 72: SMA28-M23
73: SMA21-O22, 74: SMA24-K24