



Escherichia coli SPFH membrane microdomain proteins HflKC contribute to aminoglycoside and oxidative stress tolerance

Aimee K Wessel, Yutaka Yoshii, Alexander Reder, Rym Boudjemaa, Magdalena Szczesna, Jean-Michel Betton, Joaquin Bernal-Bayard, Christophe Beloin, Daniel Lopez, Uwe Völker, et al.

► To cite this version:

Aimee K Wessel, Yutaka Yoshii, Alexander Reder, Rym Boudjemaa, Magdalena Szczesna, et al.. Escherichia coli SPFH membrane microdomain proteins HflKC contribute to aminoglycoside and oxidative stress tolerance. 2023. [pasteur-04118332](#)

HAL Id: [pasteur-04118332](#)

<https://pasteur.hal.science/pasteur-04118332>

Preprint submitted on 6 Jun 2023

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution - NonCommercial - NoDerivatives 4.0 International License

1 ***Escherichia coli* SPFH membrane microdomain proteins HflKC**
2 **contribute to aminoglycoside and oxidative stress tolerance**

3
4
5 Aimee K. WESSEL^{1†}, Yutaka YOSHII^{1†}, Alexander REDER², Rym BOUDJEMAA³,
6 Magdalena SZCZESNA^{1,6}, Jean-Michel BETTON⁴, Joaquin BERNAL-BAYARD^{1,7},
7 Christophe BELOIN¹, Daniel LOPEZ⁵, Uwe VÖLKER², Jean-Marc GHIGO^{1*}

8
9
10 ¹ *Institut Pasteur, Université de Paris-Cité, CNRS UMR6047, Genetics of Biofilms Laboratory F-*
11 *75015 Paris, France.*

12
13 ² *Department of Functional Genomics, Interfaculty Institute for Genetics and Functional*
14 *Genomics, University Medicine Greifswald, 17487 Greifswald, Germany.*

15
16 ³ *Abbelight, 191 avenue Aristide Briand, 94230 Cachan*

17
18 ⁴ *Institut Pasteur, Université de Paris-Cité, UMR UMR6047, Stress adaptation and metabolism*
19 *in enterobacteria 75015 Paris, France.*

20
21 ⁵ *Universidad Autonoma de Madrid, Centro Nacional de Biotecnologia, Campus de*
22 *Cantoblanco, Calle Darwin 3, 28049 Madrid, España*

23
24 ⁶ *Centre for Bacteriology Resistance Biology, Imperial College London, London, SW7 2AZ, UK*

25
26 ⁷ *Departamento de Genética, Facultad de Biología, Universidad de Sevilla, Apartado 1095,*
27 *41080 Sevilla, Spain*

29 † AW and YY equally contributed to this work. Author order was determined both alphabetically and in
30 order of increasing seniority.

32
33 ***Corresponding author:** Jean-Marc Ghigo (jean-marc.ghigo@pasteur.fr)

34
35 **Running Title:** *E. coli* SPFH proteins contribute to stress tolerance

36
37 **Keywords**

38 Membrane microdomains; SPFH proteins; Flotillin; Lipid raft; Stress tolerance;
39 *Escherichia coli*

41 **ABSTRACT**

42
43 Many eukaryotic membrane-dependent functions are often spatially and temporally
44 regulated by membrane microdomains (FMMs) also known as lipid rafts. These domains
45 are enriched in polyisoprenoid lipids and scaffolding proteins belonging to the Stomatin,
46 Prohibitin, Flotillin, and HflK/C (SPFH) protein superfamily that was also identified in
47 Gram-positive bacteria. By contrast, little is still known about FMMs in Gram-negative
48 bacteria. In *Escherichia coli* K12, 4 SPFH proteins, YqiK, QmcA, HflK, and HflC, were
49 shown to localize in discrete polar or lateral inner-membrane locations, raising the
50 possibility that *E. coli* SPFH proteins could contribute to the assembly of inner-membrane
51 FMMs and the regulation of cellular processes.

52 Here we studied the determinant of the localization of QmcA and HflC and showed that
53 FMM-associated cardiolipin lipid biosynthesis is required for their native localization
54 pattern. Using Biolog phenotypic arrays, we showed that a mutant lacking all SPFH genes
55 displayed increased sensitivity to aminoglycosides and oxidative stress that is due to the
56 absence of HflKC. Our study therefore provides further insights into the contribution of
57 SPFH proteins to stress tolerance in *E. coli*.

58

59 **IMPORTANCE**

60
61 Eukaryotic cells often segregate physiological processes in cholesterol-rich functional
62 membrane micro-domains. These domains are also called lipid rafts and contain proteins
63 of the Stomatin, Prohibitin, Flotillin, and HflK/C (SPFH) superfamily, which are also
64 present in prokaryotes but were mostly studied in Gram-positive bacteria. Here, we
65 showed that the cell localization of the SPFH proteins QmcA and HflKC in the Gram-
66 negative bacteria *E. coli* is altered in absence of cardiolipin lipid synthesis. This suggests
67 that cardiolipins contribute to *E. coli* membrane microdomain assembly. Using a broad
68 phenotypic analysis, we also showed that HflKC contribute to *E. coli* tolerance to
69 aminoglycosides and oxidative stress. Our study, therefore, provides new insights into the
70 cellular processes associated with SPFH proteins in *E. coli*.

71 **INTRODUCTION**

72

73 In addition to separating the intracellular content of cells from the environment, lipid
74 bilayer membranes also contribute to specialized functions, including cross-membrane
75 transport, enzymatic activity, signaling as well as anchoring of cytoskeletal and
76 extracellular structures (1, 2). In eukaryotes, these membrane-dependent functions are
77 often spatially and temporally regulated by functional membrane microdomains (FMMs)
78 called lipid rafts (3-5). FMMs compartmentalize membrane cellular processes in
79 cholesterol- and sphingolipid-enriched membrane regions formed upon lipid-lipid, lipid-
80 protein and protein-protein interactions (5-7). A family of membrane proteins called
81 SPFH proteins (for Stomatin/Prohibitin/Flotillin/HflK/C) has been shown to localize in
82 eukaryotic lipid rafts and to recruit and provide a stabilizing scaffold to other raft-
83 associated proteins (8-13).

84

85 Whereas most prokaryotes lack sphingolipids and cholesterol (14), the Gram-positive
86 bacteria *Bacillus subtilis* and *Staphylococcus aureus* can also compartmentalize cellular
87 processes in functional membrane microdomains (FMMs) (14-16). Although whether
88 bacterial FMMs display a distinct lipidic composition still needs to be established, they
89 have been reported to be potentially enriched in polyisoprenoid lipids as well as in
90 cardiolipins at the cell poles (14-16)

91

92 FMMs also contain SPFH proteins, including flotillins, and a pool of proteins involved
93 in diverse cellular processes (17) (14, 16). In *B. subtilis*, flotillins FloT and FloA
94 colocalize in membrane foci and contribute to the assembly of membrane protein
95 complexes (18) (15). Lack of flotillins impairs biofilm formation, sporulation, protease
96 secretion, motility, and natural competence, indicating that the formation of FMMs also
97 plays critical cellular roles in *B. subtilis* (15, 18-22).

98 SPFH proteins are also present in Gram-negative bacteria, and *Escherichia coli* K12 even
99 possesses four genes, *yqiK*, *qmcA*, *hflK*, and *hflC*, which encode proteins with an SPFH
100 domain and a N-terminal transmembrane segment (23). QmcA and YqiK are predicted to
101 face the cytoplasmic compartment, while HflK and HflC are predicted to be exposed in
102 the periplasm, forming the HflKC complex negatively regulating the protease activity of

103 FtsH against membrane proteins (24-27). HflC and QmcA are detected Fluorescent
104 microscopy also showed that *E. coli* SPFH proteins HflC and QmcA are localized in
105 discrete polar or lateral membrane foci (28), raising the possibility that *E. coli* SPFH
106 proteins could localize in inner-membrane FMMs and regulate specific cellular processes
107 (29). However, apart from the functional and structural description of HflKC as a
108 regulator of the FtsH membrane protease (24, 27, 30) and a recent study suggesting that
109 YqiK is involved in cell motility and resistance to ampicillin (31), the functions of FMM
110 in *E. coli* and other Gram-negative bacteria are still poorly understood.

111 In this study, we used fluorescent and super-resolution microscopy to perform a detailed
112 analysis of QmcA and HflC membrane localization signals. We then showed that the
113 integrity of QmcA and HflC protein domains is required for their inner membrane
114 localization, and that the lack of cardiolipin and isoprenoid lipids known to associate with
115 FMMs alters their localization. Moreover, using single and multiple SPFH gene mutants,
116 we showed that HflKC SPFH proteins contribute to aminoglycosides and oxidative stress
117 resistance. Our study therefore provides new insights into the determinants of cellular
118 localization and the function associated with *E. coli* SPFH proteins.

119 **RESULTS**

120

121 **Chromosomal *E. coli* SPFH fluorescent fusion proteins show distinct localization**
122 **patterns.**

123

124 To investigate the determinant of cell localization of *E. coli* SPFH proteins, we first
125 tagged YqiK and QmcA, which C-termini are predicted to be in the cytoplasm (26), with
126 a C-terminal monomeric super folder green fluorescent protein (msfGFP). We then
127 tagged HflC and HflK, which C-termini are predicted to be in the periplasm (26), with
128 the C-terminal monomeric red fluorescent protein mCherry. All these fusions were
129 expressed under their own promoter from their native chromosomal location (Sup. Fig.
130 S1). Epifluorescence and super-resolution microscopy confirmed the previously reported
131 polar localization of HflK and HflC (28), with 94% and 91% polar localization pattern
132 for HflC-mCherry and HflK-mCherry, respectively (n=150) (Fig. 1B and Sup. Fig. S2).
133 By contrast, C-terminally tagged QmcA-GFP showed punctate foci distributed
134 throughout the cell body, with 96% of the cells harboring 5 foci or more (n=150) (Fig.
135 1A). However, we could not detect YqiK-GFP, possibly due to its low native
136 chromosomal expression level. We then used anti-GFP or mCherry antibodies to perform
137 immunodetection on cytoplasmic as well as inner and outer membrane fractions of *E. coli*
138 strains expressing either HflC-mCherry or QmcA-GFP. In agreement with previous
139 results (26, 29), both fusion proteins were detected in the inner membrane fraction and
140 showed minimal degradation profile (Fig. 2 and Sup. Fig. S3 and S4). Moreover, the
141 functionality of the HflKC fusion could be demonstrated (see result sections below).

142

143 **Domain swap analysis shows that protein integrity is essential for QmcA-GFP and**
144 **HflC-mCherry localization.**

145

146 To identify HflC and QmcA membrane localization signals, we constructed multiple
147 fluorescently tagged truncated versions of both proteins. We tagged with msfGFP a
148 QmcA protein reduced to its transmembrane region and SPFH domain (QmcA-GFP is
149 therefore now named TM^{QmcA}-SPFH^{QmcA}-GFP in Figure 3) and, separately, one reduced
150 to the QmcA transmembrane region only (TM^{QmcA}-GFP) (Fig. 3A). To test the role of the
151 QmcA transmembrane region, we also swapped TM^{QmcA} in the three constructs by the
152 single-spanning TM domain of the phage coat protein Pf3 (TM^{Pf3}), which orients
153 subsequent amino acids to the cytosol (38) (Fig. 3A). Similarly, in addition to the full

length HflC-mCherry, we tagged with mCherry the HflC transmembrane region and SPFH domain (HflC-mCherry is therefore now named TM^{HflC}-SPFH^{HflC}-mCherry in Figure 3) and, separately, only its TM region (TM^{HflC}-mCherry) (Fig. 3B). We also swapped the HflC TM region with the single-spanning TM region of colistin M immunity protein (TM^{Cmi}), which orients subsequent amino acids to the periplasm (39) (Fig. 3B). Epifluorescence microscopy of HflC and QmcA derivative fusions showed that in addition to native full-length constructs only full-length constructs with swapped TM (TM^{Pf3}-QmcA-GFP and TM^{Cmi}-HflC-mCherry) displayed significant punctate foci or polar localization, respectively (Fig. 3AB), although at reduced frequency compared to native QmcA-GFP and HflC-mCherry (Sup. Fig. S5). Finally, we prepared inner and outer membrane fractions of *E. coli* strains expressing each QmcA and HflC derivative, and we observed that all these constructs were still mainly located in the inner membrane fraction. This indicates that, while we observed that QmcA-GFP and HflC-mCherry derivatives exhibit altered cell localization, they do not exhibit significant mis-localization and remain located in the inner membrane (Sup. Fig. S3 and Fig S4). These results therefore indicated that specific QmcA and HflC localization requires the combination of a transmembrane and full cytoplasmic (QmcA) or periplasmic (HflC) domain.

Lack of cardiolipin and isoprenoid lipid synthesis alters the cell localization of QmcA and HflC.

FMMs were proposed to be enriched with negatively charged cardiolipins and isoprenoids, which promote the localization of polar proteins and modulation of membrane lipid fluidity (15, 18, 32-37). We first tested whether alteration of cardiolipin synthesis could cause mis-localization of *E. coli* SPFH proteins QmcA or HflKC in a mutant lacking the major cardiolipin synthases *clsABC* (38). Whereas a super-resolution microscopy analysis only showed an alteration of the number of QmcA-GFP punctates (1-5 cluster per bacterium) compared to WT (10-15 cluster per bacterium) (Fig. 4A and Sup. Fig. S6), the localization of HflC-mCherry showed a drastic loss of polar localization pattern (Fig. 4B and Supp. Fig. S4). We then used an *idi* mutant with reduced isoprenoid lipid synthesis due to the lack of isomerization of isopentenyl diphosphate (IPP) into dimethylallyl diphosphate (DMAPP) (39, 40). Whereas QmcA-GFP punctate localization was not affected, HflC-mCherry polar localization was abolished in the Δid mutant (Fig.

188 4A and Sup. Fig. S6). These results demonstrated that the alteration of cardiolipin and, in
189 a lesser extent, isoprenoid lipid synthesis pathway affects HflC fusion protein localization
190 in *E. coli*.

191

192 **Phenotypic analysis of *E. coli* SPFH mutant shows that only the absence of HflKC**
193 **increases *E. coli* sensitivity to aminoglycosides and oxidative stress.**

194

195 To identify potential phenotypes and functions associated with the *E. coli* SPFH proteins
196 YqiK, QmcA, HflK and HflC, we introduced single and multiple deletions of the
197 corresponding SPFH genes. We observed that neither single mutants nor the quadruple
198 $\Delta hflK$, $\Delta hflC$, $\Delta qmcA$, and $\Delta yqiK$ (hereafter referred to $\Delta SPFH$ mutant) displayed any
199 significant growth defects in rich or minimal media (Fig. 5A and Sup. Fig. S7A).
200 Considering the role of SPFH proteins in the activation of inner-membrane kinases
201 involved in *B. subtilis* biofilm formation (15), we tested adhesion and biofilm capacity of
202 WT and $\Delta SPFH$ strains but could not detect any significant differences between these two
203 strains. We then used BiologTM phenotypic microarrays to perform a large-scale
204 phenotypic assay comparing an *E. coli* WT and $\Delta SPFH$ mutant (Sup. Table S1). This
205 analysis revealed that the $\Delta SPFH$ mutant is metabolically less active when grown in the
206 presence of various aminoglycosides (tobramycin, capreomycin, sisomicin and
207 paromomycin) or when exposed to paraquat (Fig. 5B and Sup. Fig. S7BC). Consistently,
208 the minimal inhibitory concentration (MIC) for tobramycin of the $\Delta SPFH$ mutant was 3-
209 fold lower than that of the WT MIC (Fig. 5C), and the sensitivity of the $\Delta SPFH$ mutant to
210 paraquat was increased compared to the WT (Fig. 5D and Sup. Fig. S7D). Test of
211 individual SPFH-gene mutants for their sensitivity to tobramycin and paraquat showed
212 that the HflKC complex is the sole responsible for both phenotypes, as both single *hflK*
213 and *hflC* or a double *hflKC* mutants displayed increased sensitivity to tobramycin and
214 oxidative stress (Fig. 5CD and Sup. Fig. S5E). This phenotype could be complemented
215 upon the introduction of a plasmid expressing *hflKC* genes in the double *hflKC* mutant
216 and C-terminally tagged HflC-mCherry and HflK-mCherry displayed wildtype MIC for
217 tobramycin and paraquat, indicating that both fusions were functional and relevant
218 proxies for the bacterial localization of the HflKC complex (Sup. Fig. S8).

219

220

221 **Contribution of HflC localization to tobramycin and paraquat tolerance**

222

223 Whereas the MIC determination for tobramycin and paraquat of an Δidi mutant showed
224 no significant difference compared to the WT, the MIC for tobramycin and paraquat of a
225 Δ clsABC mutant was reduced by 2 to 3-fold (Fig.5CD). Considering the scaffolding role
226 of HflKC and the importance of cell localization, we tested the localization and
227 contribution to aminoglycoside and stress tolerance of AcrA, a protein previously
228 identified in *E. coli* inner-membrane potentially associated with FMM (28). AcrA is an
229 efflux pump involved in the transport of a wide range of substrates including
230 aminoglycosides (41). However, while an *acrA* deletion did not alter *E. coli* MIC
231 profile to tobramycin and paraquat as much as a $\Delta hflC$ mutant (Fig.5CD), the expression
232 of AcrA-GFP from their native chromosomal context did not lead to any distinct polar
233 co-localization with HflC in exponential or stationary phase conditions (Sup. Fig. S9).

234

235 Taken together, these results indicate that the HflKC SPFH protein complex contributes
236 to oxidative and antibiotic stress resistance.

237

238

239 **DISCUSSION**

240

241 SPFH-domain proteins have been identified in most organisms (16, 42) and extensively
242 studied in eukaryotes (3, 5, 43). By contrast, prokaryotic SPFH proteins and proteins
243 associated with functional membrane microdomains (FMMs) are much less understood.
244 This is particularly the case for Gram-negative bacteria, in which potential FMMs
245 functions are mostly inferred from studies performed in *B. subtilis* and *S. aureus*. In this
246 study, we investigated the functions and the localization determinants of *E. coli* SPFH
247 proteins. Focusing on QmcA and HflKC SPFH proteins, we used a domain deletion and
248 replacement approach and showed that most of the tested domain replacement variants
249 correctly localized to the inner membrane but failed to display WT protein localization
250 patterns. This indicates that inner-membrane localization alone is not sufficient for the
251 correct subcellular distribution of HflC and QmcA, whose localization signals likely rely
252 on oligomerization for focal flotillin cluster formation (44), which could be abolished in
253 the domain deletion constructs, potentially explaining the observed localization defects.

254

255 QmcA and HflKC SPFH proteins display different localization patterns and could be part
256 of different FMMs, potentially using different localization signals. The punctate
257 localization pattern displayed by QmcA-GFP fusion was also observed in the case of *E.*
258 *coli* YqiK expressed from plasmid and other Gram-positive bacteria flotillin
259 homologues(15, 16, 36, 45, 46). Interestingly, *B. subtilis*, *B. anthracis* and *S. aureus*
260 flotillin genes are physically associated with a gene encoding a NfeD protein, which could
261 contribute to protein-protein interactions within flotillin assemblies (47, 48). Consistently,
262 *E. coli* *qmcA* gene is located upstream of the NfeD-like *ybbJ* gene, like NfeD-like *yqiJ*
263 gene is located upstream of *yqiK* (see Supplementary Figure S1). This further supports
264 the notion that QmcA and YqiK could be considered as *E. coli* FloA/FloT homologs.

265

266 By contrast, the *hflKC* transcription unit is not closely associated with a *nfeD*-like gene,
267 suggesting that HflKC may not be a flotillin. However, while QmcA and YqiK have an
268 opposite orientation to HflK and HflC, they are structurally similar proteins and the four
269 *E. coli* SPFH proteins could therefore share some degrees of functionalities. The
270 topological similarity between HflK and HflC might contribute to HflKC complex

271 formation, and its interaction with FtsH protease, resulting in a large periplasmic FtsH-
272 HflKC complex localized at the cell pole (24, 25, 49-52)
273 Along with phosphatidylethanolamine and phosphatidylglycerol, cardiolipins are the
274 primary constituent components of *E. coli* membranes that concentrate into cell poles and
275 dividing septum (53-56). It was indeed observed that the composition of *E. coli* membrane
276 lipids at cell poles is altered in a *clsABC* cardiolipin deficient mutant, compensated by an
277 increased amount of phosphatidylglycerol (32, 57). Several studies also reported that
278 cardiolipin-enriched composition in membranes at cell poles influences both the
279 localization and activity of inner membrane proteins, such as respiratory chain protein
280 complexes and the osmosensory transporter ProP (33, 34, 58-60). We showed here that,
281 similarly to ProP, HflC and QmcA localization patterns are affected in a Δ *clsABC* mutant,
282 suggesting that HflKC and QmcA complexes could act as scaffolds for cardiolipin-
283 enriched FMM cargo proteins. Isoprenoid lipids such as farnesol, carotenoids, and
284 hopanoids have been proposed to be constituents of bacterial FMMs or to interact with
285 SPFH proteins and FMM-associated proteins (14). Consistently, blocking the *S. aureus*
286 carotenoid synthetic pathway by zaragozic acid leads to flotillin mis-localization (15),
287 and the inactivation of farnesol synthesis in a *B. subtilis* *yisP* mutant impairs focal
288 localization of the FMM-associated sensor kinase KinC (15). We showed that interfering
289 with the *E. coli* *idi* isoprenoid biosynthesis pathway also strongly alters the localization
290 of HflC. This further indicates that isoprenoid lipids contribute to the formation or
291 integrity of FMMs, possibly by altering isoprenoid-dependent membrane fluidity, as
292 shown in *S. aureus* and *B. subtilis* FMMs (14, 61).

293

294 Our investigation of the phenotypes displayed by an *E. coli* mutant lacking all SPFH
295 protein genes showed that the absence of HflKC leads to an increased susceptibility to
296 oxidative stress and aminoglycosides. The HflKC complex was previously shown to
297 modulate the quality control proteolytic activity of FtsH by regulating the access of
298 misfolded membrane protein products to FtsH (24, 25, 62). *E. coli* Δ *hflK* and Δ *hflC*
299 mutant strains were also shown to accumulate increased amounts of hydroxyl radical,
300 suggesting that HflK and HflC could influence tolerance to aminoglycosides and
301 oxidative stress by suppressing excessive hydroxyl radical production. Alternatively,
302 HflK and HflC could contribute to tobramycin resistance via FtsH-dependent proteolytic

303 activity (63) or favoring FMM formation and the assembly of membrane proteins and
304 lipids, such as cardiolipin, involved in the transport and movement of aminoglycosides
305 within cells and cell membranes. Consistently, several proteins associated with
306 aminoglycosides transport potentially associated with FMMs composition, including
307 transporters and several components of the AcrAB-TolC efflux pump (28), suggesting
308 that deletion of *hflK* or *hflC* could reduce the activity of these proteins in FMMs and
309 enhance entry of aminoglycosides. Whereas the susceptibility to aminoglycosides indeed
310 partly relies on the AcrAB-TolC efflux pump (41, 64-66), we found that lack of the AcrA
311 only moderately decreases the MIC to tobramycin, compared to a *hflKC* mutation. We
312 also showed that the alteration of the cardiolipin pathway in a Δ *clsABC* mutant altered
313 both the localization and sensitivity to tobramycin and paraquat of a HflC-GFP fusion.
314 This suggests that cardiolipin could be required for the correct localization of HflKC to
315 FMMs at cell poles. However, we observed that, although an *idi* isoprenoid pathway
316 mutant affects HflC localization, it does not show altered sensitivity. We cannot rule out
317 that the effect of Δ *clsABC* mutant on resistance to aminoglycosides and oxidative
318 stress could be unrelated to its impact on HflKC polar localization. Alternatively, the lack
319 of effect of Δ *idi* mutant may be due to an incomplete inactivation of the pathway since
320 lycopene production in a Δ *idi* mutant is reduced by 1/3 but not totally abolished, due to
321 the fact that the *idi* protein is a reversible isomerase.(39).

322 In conclusion, the present study provides new insights into the functions of *E. coli* SPFH
323 proteins and some of their interacting partners and further experiments will be needed to
324 fully uncover the roles played by this intriguing family of membrane proteins in Gram-
325 negative bacteria.

326

327 **MATERIALS & METHODS**

328

329 **Bacterial strains and growth conditions**

330 Bacterial strains and plasmids used in this study are described in Sup. Table S2, and
331 further explained in Sup. Fig. S1 and Figure 3. Unless stated otherwise, all experiments
332 were performed in lysogeny broth (LB) or M63B1 minimal medium supplemented with
333 0.4% glucose (M63B1.G) at 37 °C. Antibiotics were used as follows: kanamycin (50
334 µg/mL); chloramphenicol (25 µg/mL); ampicillin (100 µg/mL); and zeocin (50 µg/mL).
335 All compounds were purchased from Sigma-Aldrich (St Louis, MO, USA) except for
336 Zeocin (InvivoGen, Santa Cruz, CA, USA).

337

338 **Mutant construction**

339 *Generation of mutants in E. coli:* Briefly, *E. coli* deletion or insertion mutants used in this
340 study originated either from the *E. coli* Keio collection of mutants (67) or were generated
341 by λ-red linear recombination using pKOBEG (Cm^R) or pKOBEGA (Amp^R) plasmids
342 (68) using primers listed in Sup. Table S3. P1vir transduction was used to transfer
343 mutations between different strains. When required, antibiotic resistance markers flanked
344 by two FRT sites were removed using the Flp recombinase (69). Plasmids used in this
345 study were constructed using an isothermal assembly method, Gibson assembly (New
346 England Biolabs, Ipswich, MA, USA) using primers listed in Sup. Table S3. The integrity
347 of all cloned fragments, mutations, and plasmids was verified by PCR with specific
348 primers and DNA sequencing

349

350 *Construction of deletion mutants*

351 Δ*yqiK*, Δ*qmca*, Δ*hf1K*, Δ*hf1C*, Δ*clsA*, Δ*clsB*, Δ*clsC*, Δ*idi*, Δ*acrA*, deletions were
352 transferred into *E. coli* MG1655strep by P1vir phage transduction from the corresponding
353 mutants in the *E. coli* BW25113 background of the Keio collection (67). The associated
354 kanamycin marker was then removed using the Flp recombinase expressed from the
355 plasmid pCP20 (69). (Details regarding the construction of all other strains used in this
356 study are presented in Sup.Table S2).

357

358 *Construction of GFP and mCherry fusions*

359 See Supplementary Methods section in Supplementary Materials

360

361 *Construction of complemented strains*

362 The *hflKC* genes were amplified from MG1655*strep* using primers listed in
363 Supplementary Table S3 and cloned at the downstream of the IPTG-inducible promoter
364 of a pZS*12 vector using the Gibson assembly to generate plasmids pZS*12-HflKC Then,
365 these plasmids were introduced into $\Delta hflKC$ mutants, respectively, to construct
366 complemented mutants (Sup. Table S2). A pZS*12 empty vector was also introduced into
367 wildtype and $\Delta hflKC$ mutants. Mutants harbouring these pZS*12 plasmids were
368 incubated and used for the below experiments in the presence of IPTG (1 mM) and
369 ampicillin.

370

371 **Epifluorescence microscopy**

372 Bacteria were incubated into 5 mL of fresh LB medium and harvested at OD₆₀₀ 0.4 for
373 samples in exponential phase or OD₆₀₀ 2.0 for stationary phase. After washing twice with
374 M63B1 medium, cells corresponding to 1 mL of the bacterial culture were pelleted by
375 centrifugation and resuspended into 0.1 mL of M63B1 medium for exponential samples,
376 or 1 mL of the medium for stationary samples. Ten μ L aliquots of the cell suspension
377 were immobilized on glass slides previously covered with freshly made M63B1 medium
378 0.8% agarose pads. Cells were observed using a ZEISS Definite focus fluorescent
379 microscope (Carl Zeiss, Oberkochen, Germany), equipped with an oil-immersion
380 objective lens microscope (Pln-Apo 63X/1.4 oil Ph3). GFP or mCherry fluorescence was
381 exited with a ZEISS Colibri LED illumination system and the fluorescence signal was
382 detected with Zeiss FS38 HE (Carl Zeiss) or Semrock HcRed filters (Semrock, Rochester,
383 NY, USA). GFP, and mCherry fluorescence images were taken at 1000, and 2000 msec.
384 exposure, respectively. Image processing was performed using ImageJ and Adobe
385 Photoshop. For each tested strain, the subcellular localization patterns of 50 randomly
386 selected bacteria were evaluated four times (a total of 200 cells), and each frequency was
387 expressed as percentiles.

388

389 **Super-resolution microscopy**

390 Bacteria were imaged using single-molecule localization microscopy and stochastic

optical reconstruction microscopy (SMLM-STORM), using a previously described method (70). Overnight cultures were fixed with PFA 4%, permeabilized with Triton 0,05%, and labeled with either GFP monoclonal FluoTag®-Q — Sulfo-Cyanine 5 (Cy5), or RFP monoclonal FluoTag®-Q – Cy5, which are single-domain antibodies (sdAb) conjugated to Cy5. Labeling was performed at 1:250 (concentration), and washing steps were carried out three times using Abbelight's SMART kit buffer. For imaging, Abbelight's imaging system was used with NEO software. Abbelight's module was added to an Olympus IX83 with 100x TIRF objective, N.A. 1.49. We used Hamamatsu's sCMOS Flash 4 camera and a 647nm 500mW Oxxius laser, with an astigmatic lens, to allow for 3D imaging of the sample (71).

401

402 **Inner membrane separation**

403 *E. coli* overnight cultures were diluted into 1 L of fresh LB medium to OD₆₀₀ of 0.02 and
404 incubated at 37°C and 180 rpm until reaching OD₆₀₀ 0.4. Cells were harvested and washed
405 once with 10 mM HEPES (pH 7.4) and stored at -20°C for at least 1 h. Bacteria were then
406 resuspended in 10 mL of 10 mM HEPES (pH 7.4) containing 100 µL of Benzonase (3.10⁴
407 U/mL) and were passed through a FRENCH press (Thermo) at 20,000 psi. The lysate was
408 centrifuged at 15,000 g for 15 min at 4 °C to remove cell debris, and aliquots of the
409 suspension were stored at 4 °C as the whole extract. Then, the suspension was centrifuged
410 at 100,000 g for 45 min at 4 °C to separate supernatant and pellets, and aliquots of the
411 supernatant were stored at 4 °C as the cytosolic and periplasmic fractions. The pellets
412 were suspended into 600 µL of cold 10 mM HEPES (pH 7.4) and homogenized by using
413 2 mL tissue grinder (Kontes Glass, Vineland, NJ, USA). Discontinuous sucrose gradients
414 with the following composition were placed into ultracentrifugation tube: bottom to top
415 0.5 mL of 2 M sucrose, 2.0 mL of 1.5 M sucrose, and 1.0 mL of 0.8 M sucrose, and 500
416 µL of the homogenized samples were placed on the top of sucrose gradients. The
417 gradients were centrifuged at 100,000 g for 17.5 h at 4 °C. Subsequently, 400 µL of
418 aliquots were collected into 11 microtubes from top to bottom, and the samples were
419 proceeded to the immunodetection method, as described below.

420

421 **Immunodetection of inner membrane proteins**

422 Aliquots of samples were suspended in 4× Laemmli buffer (BioRad) with 2-
423 Mercaptoethanol (Sigma) and incubated for 5 min at 98 °C. The protein samples (10 µL
424 each) were run on 4-20 % Mini-PROTEAN TGX Stain-FreeTM precast Gels (BioRad)
425 in 1× TGX buffer and then transferred to nitrocellulose membrane using a Trans-Blot®
426 Turbo™ Transfer System (BioRad). Subsequently, the membranes were blocked using
427 blocking buffer consisting of 5% skim milk in PBS with 0.05% Tween 20 (PBST) for 2
428 h at 4 °C with agitation. The membranes were then incubated in PBST containing 1%
429 skim milk with first antibodies, polyclonal rabbit antiserum raised against ExbB and TolC
430 (kindly given by Dr. Philippe Delepelaire), GFP (Invitrogen, A6455, Thermo Fisher
431 Scientific, Indianapolis, IN, USA) and mCherry (Invitrogen, PA5-34974) at 1:20,000
432 overnight at 4 °C with agitation. The membranes were washed in PBST and incubated in
433 PBST containing 1% skim milk with a secondary antibody, anti-rabbit IgG conjugated
434 with horseradish peroxidase (Cell signaling, 7074S), at 1:10,000 for 2 h at 25 °C with
435 agitation. After washing the excess secondary antibody, specific bands were visualized
436 using the ECL prime detection method (GE Healthcare) and imaged with an imaging
437 system, iBright™ CL1500 (Invitrogen).

438

439 **Microbial growth phenotypic analysis**

440 A high-throughput analysis for microbial growth phenotypes using a colorimetric reaction,
441 Phenotype MicroArrays (Biolog Inc., Hayward, CA, USA), was performed in accordance
442 with the manufacturer's protocol. Briefly, several colonies of *E. coli* grown on LB agar
443 were transferred in 10 mL of a mixture of Biolog IF-0a media (BioLog) and sterilized
444 water into a sterile capped test tube. The suspension was mixed gently, and the turbidity
445 was adjusted to achieve the appropriate transmittance using the Biolog turbidimeter
446 (BioLog). The cell suspension was diluted with the IF-0a plus dye mix, as mentioned in
447 the manufacturer's protocol. 100 µL of the mixture suspension was inoculated into PM
448 plates 1-3 and 9-20 and incubated for 72 h at 37 °C. The absorbance of each well was
449 taken every 15 min. The OmniLog software (BioLog) was used to view and edit data, to
450 compare data lists, and to generate reports.

451

452 **Monitoring of bacterial growth**

453 An overnight culture of *E. coli* was diluted into fresh LB and M63B1 supplemented with
454 0.4% glucose medium to OD₆₀₀ of 0.05, and 200 µL aliquots were cultured in the presence
455 or absence of paraquat (Methyl viologen dichloride hydrate, Sigma-Aldrich) in 96-well
456 microplates at 37 °C for 24 h with shaking. The absorbance of each culture at 600 nm was
457 measured every 15 min for 24 h using a microplate reader (Tecan Infinite, Mannedorf,
458 Switzerland).

459

460 **Susceptibility of *E. coli* against Tobramycin and Paraquat**

461 The broth microdilution method was used to determine the MIC (minimum inhibitory
462 concentration) values of Tobramycin (Sigma-Aldrich) and Paraquat (Sigma-Aldrich) in
463 96-well microtiter plates. Briefly, 100 µL of LB medium was distributed into each well
464 of the microtiter plates. Tobramycin was 2-fold serially diluted in each well. Five µL of
465 approximately 1 × 10⁷ CFU/mL of *E. coli* was inoculated into each well, and the plates
466 were incubated at 37°C for 24 h. The lowest concentration that visibly inhibited bacterial
467 growth was defined as the MIC. All strains were evaluated in biological and technical
468 triplicates.

469 The spot assay was performed to evaluate the susceptibility of *E. coli* against
470 paraquat. Briefly, an overnight culture of *E. coli* was diluted into fresh LB medium to
471 OD₆₀₀ of 0.05. Ten µL of the diluted culture was spotted on LB plates containing either
472 no or 100 µM paraquat. The plates were incubated at 37°C for 24 h, and the photographs
473 were taken. All strains were evaluated in triplicate.

474

475 **Statistical analysis**

476 Data analysis was performed using GraphPad Prism 9.5 software (GraphPad, La Jolla,
477 CA, USA). All data are expressed as mean (\pm standard deviation, SD) in figures.
478 Statistical analysis was performed using unpaired non-parametric Mann-Whitney test.
479 Differences were considered statistically significant for *P* values of <0.05.

480 **ACKNOWLEDGMENTS**

481

482 We thank Philippe Delepelaire for insightful comments and material support. We thank
483 Uwe Sauer and Philip Warmer for initial assessment of lipid composition of some of the
484 strains used in this study. We are grateful to Eva Wolrab and Sven van Teeffelen for their
485 initial interest in the project and for providing the strains for msfGFP and mCherry
486 constructions. This work was supported by EU Horizon 2020 Rafts4Biotech grant 720776
487 (to JMG, DL, AKW, YY, AR, UV and MS), the French government's Investissement
488 d'Avenir Program, Laboratoire d'Excellence "Integrative Biology of Emerging
489 Infectious Diseases" (grant n°ANR-10-LABX-62-IBEID) and the *Fondation pour la*
490 *Recherche Médicale* (grant no. DEQ20180339185). This work benefited from the
491 facilities and expertise of Add Photonic BioImaging platform (UTechS PBI, Institut
492 Pasteur). A.K.W. was supported by a Pasteur-Roux-Cantarini postdoctoral and a grant
493 from the Philippe Foundation.

494

495 **AUTHOR CONTRIBUTIONS:**

496 A.K.W., Y.Y., and J.-M.G. designed the experiments. A.K.W., Y.Y., A.R., R.B.; M.S.,
497 J.B-B. performed the experiments. A.K.W., Y.Y., A.R., U.V. M.S., R.B., J.-M.B., C.B.,
498 D.L. and J.-M.G. analyzed the data. Y.Y., A.K.W. and J.-M.G. wrote the paper with
499 significant contribution from all authors.

500 **DATA AVAILABILITY**

501 The data that support the findings of this study are presented in the paper and/or the
502 Supplementary Materials. Strains and plasmids are available from the corresponding
503 author, JMG, upon reasonable request.

504 **COMPETING INTERESTS**

505 The authors declare no competing financial or non-financial interests.

506

507 **REFERENCES**

- 509 1. Alberts B, Johnson A, Lewis J, Raff M, Roberts K, Walter P. 2002. Molecular
510 biology of the cell 6th edition ed. Garland Science., New York.
- 511 2. Cho W, Stahelin RV. 2005. Membrane-protein interactions in cell signaling and
512 membrane trafficking. *Annu Rev Biophys Biomol Struct* 34:119-51.
- 513 3. Simons K, Ikonen E. 1997. Functional rafts in cell membranes. *Nature* 387:569-
514 72.
- 515 4. Rajendran L, Simons K. 2005. Lipid rafts and membrane dynamics. *J Cell Sci*
516 118:1099-102.
- 517 5. Simons K, Sampaio JL. 2011. Membrane organization and lipid rafts. *Cold
518 Spring Harb Perspect Biol* 3:a004697.
- 519 6. Pike LJ. 2006. Rafts defined: a report on the Keystone Symposium on Lipid
520 Rafts and Cell Function. *J Lipid Res* 47:1597-8.
- 521 7. Sezgin E, Levental I, Mayor S, Eggeling C. 2017. The mystery of membrane
522 organization: composition, regulation and roles of lipid rafts. *Nat Rev Mol Cell
523 Biol* 18:361-374.
- 524 8. Langhorst MF, Reuter A, Stuermer CA. 2005. Scaffolding microdomains and
525 beyond: the function of reggie/flotillin proteins. *Cell Mol Life Sci* 62:2228-40.
- 526 9. Morrow IC, Parton RG. 2005. Flotillins and the PHB domain protein family:
527 rafts, worms and anaesthetics. *Traffic* 6:725-40.
- 528 10. Stuermer CA, Plattner H. 2005. The 'lipid raft' microdomain proteins reggie-1
529 and reggie-2 (flotillins) are scaffolds for protein interaction and signalling.
530 *Biochem Soc Symp* doi:10.1042/bss0720109:109-18.
- 531 11. Browman DT, Hoegg MB, Robbins SM. 2007. The SPFH domain-containing
532 proteins: more than lipid raft markers. *Trends Cell Biol* 17:394-402.
- 533 12. Zeke A, Lukács M, Lim WA, Reményi A. 2009. Scaffolds: interaction platforms
534 for cellular signalling circuits. *Trends Cell Biol* 19:364-74.
- 535 13. Zhao F, Zhang J, Liu YS, Li L, He YL. 2011. Research advances on flotillins.
536 *Virol J* 8:479.
- 537 14. Lopez D, Koch G. 2017. Exploring functional membrane microdomains in
538 bacteria: an overview. *Curr Opin Microbiol* 36:76-84.
- 539 15. Lopez D, Kolter R. 2010. Functional microdomains in bacterial membranes.
540 *Genes Dev* 24:1893-902.
- 541 16. Bramkamp M, Lopez D. 2015. Exploring the existence of lipid rafts in bacteria.
542 *Microbiol Mol Biol Rev* 79:81-100.
- 543 17. Bach JN, Bramkamp M. 2013. Flotillins functionally organize the bacterial
544 membrane. *Mol Microbiol* 88:1205-17.
- 545 18. Donovan C, Bramkamp M. 2009. Characterization and subcellular localization
546 of a bacterial flotillin homologue. *Microbiology* 155:1786-1799.
- 547 19. Dempwolff F, Möller HM, Graumann PL. 2012. Synthetic motility and cell
548 shape defects associated with deletions of flotillin/reggie paralogs in *Bacillus
549 subtilis* and interplay of these proteins with NfeD proteins. *J Bacteriol* 194:4652-
550 61.
- 551 20. Yepes A, Schneider J, Mielich B, Koch G, García-Betancur JC, Ramamurthi
552 KS, Vlamakis H, López D. 2012. The biofilm formation defect of a *Bacillus
553 subtilis* flotillin-defective mutant involves the protease FtsH. *Mol Microbiol*
554 86:457-71.

- 555 21. Mielich-Süss B, Schneider J, Lopez D. 2013. Overproduction of flotillin
 556 influences cell differentiation and shape in *Bacillus subtilis*. *mBio* 4:e00719-13.
 557 22. Schneider J, Mielich-Süss B, Böhme R, Lopez D. 2015. In vivo characterization
 558 of the scaffold activity of flotillin on the membrane kinase KinC of *Bacillus*
 559 *subtilis*. *Microbiology* 161:1871-1887.
- 560 23. Hinderhofer M, Walker CA, Friemel A, Stuermer CA, Möller HM, Reuter A.
 561 2009. Evolution of prokaryotic SPFH proteins. *BMC Evol Biol* 9:10.
- 562 24. Kihara A, Akiyama Y, Ito K. 1996. A protease complex in the *Escherichia coli*
 563 plasma membrane: HflKC (HflA) forms a complex with FtsH (HflB), regulating
 564 its proteolytic activity against SecY. *Embo j* 15:6122-31.
- 565 25. Saikawa N, Akiyama Y, Ito K. 2004. FtsH exists as an exceptionally large
 566 complex containing HflKC in the plasma membrane of *Escherichia coli*. *J Struct*
 567 *Biol* 146:123-9.
- 568 26. Chiba S, Ito K, Akiyama Y. 2006. The *Escherichia coli* plasma membrane
 569 contains two PHB (prohibitin homology) domain protein complexes of opposite
 570 orientations. *Mol Microbiol* 60:448-57.
- 571 27. Ma C, Wang C, Luo D, Yan L, Yang W, Li N, Gao N. 2022. Structural insights
 572 into the membrane microdomain organization by SPFH family proteins. *Cell*
 573 *Res* 32:176-189.
- 574 28. Guzmán-Flores JE, Steinemann-Hernández L, González de la Vara LE,
 575 Gavilanes-Ruiz M, Romeo T, Alvarez AF, Georgellis D. 2019. Proteomic
 576 analysis of *Escherichia coli* detergent-resistant membranes (DRM). *PLoS One*
 577 14:e0223794.
- 578 29. Guzman-Flores JE, Alvarez AF, Poggio S, Gavilanes-Ruiz M, Georgellis D.
 579 2017. Isolation of detergent-resistant membranes (DRMs) from *Escherichia coli*.
 580 *Anal Biochem* 518:1-8.
- 581 30. Ito K, Akiyama Y. 2005. Cellular functions, mechanism of action, and
 582 regulation of FtsH protease. *Annu Rev Microbiol* 59:211-31.
- 583 31. Padilla-Vaca F, Vargas-Maya NI, Elizarrarás-Vargas NU, Rangel-Serrano Á,
 584 Cardoso-Reyes LR, Razo-Soria T, Membrillo-Hernández J, Franco B. 2019.
 585 Flotillin homologue is involved in the swimming behavior of *Escherichia coli*.
 586 *Arch Microbiol* 201:999-1008.
- 587 32. Koppelman CM, Den Blaauwen T, Duursma MC, Heeren RM, Nanninga N.
 588 2001. *Escherichia coli* minicell membranes are enriched in cardiolipin. *J*
 589 *Bacteriol* 183:6144-7.
- 590 33. Romantsov T, Helbig S, Culham DE, Gill C, Stalker L, Wood JM. 2007.
 591 Cardiolipin promotes polar localization of osmosensory transporter ProP in
 592 *Escherichia coli*. *Mol Microbiol* 64:1455-65.
- 593 34. Mileykovskaya E, Dowhan W. 2009. Cardiolipin membrane domains in
 594 prokaryotes and eukaryotes. *Biochim Biophys Acta* 1788:2084-91.
- 595 35. Feng X, Hu Y, Zheng Y, Zhu W, Li K, Huang CH, Ko TP, Ren F, Chan HC,
 596 Nega M, Bogue S, López D, Kolter R, Götz F, Guo RT, Oldfield E. 2014.
 597 Structural and functional analysis of *Bacillus subtilis* YisP reveals a role of its
 598 product in biofilm production. *Chem Biol* 21:1557-63.
- 599 36. García-Fernández E, Koch G, Wagner RM, Fekete A, Stengel ST, Schneider J,
 600 Mielich-Süss B, Geibel S, Markert SM, Stigloher C, Lopez D. 2017. Membrane
 601 Microdomain Disassembly Inhibits MRSA Antibiotic Resistance. *Cell*
 602 171:1354-1367.e20.

- 603 37. Zielińska A, Savietto A, de Sousa Borges A, Martinez D, Berbon M, Roelofsen
 604 JR, Hartman AM, de Boer R, van der Klei IJ, Hirsch AKH, Habenstein B,
 605 Bramkamp M, Scheffers D-J. 2020. Flotillin mediated membrane fluidity
 606 controls peptidoglycan synthesis and MreB movement. *bioRxiv*
 607 doi:10.1101/736819:736819.
- 608 38. Nishijima S, Asami Y, Uetake N, Yamagoe S, Ohta A, Shibuya I. 1988.
 609 Disruption of the *Escherichia coli* *cls* gene responsible for cardiolipin synthesis.
 610 *J Bacteriol* 170:775-80.
- 611 39. Hemmi H, Ohnuma S, Nagaoka K, Nishino T. 1998. Identification of genes
 612 affecting lycopene formation in *Escherichia coli* transformed with carotenoid
 613 biosynthetic genes: candidates for early genes in isoprenoid biosynthesis. *J*
 614 *Biochem* 123:1088-96.
- 615 40. Hahn FM, Hurlburt AP, Poulter CD. 1999. *Escherichia coli* open reading frame
 616 696 is *idi*, a nonessential gene encoding isopentenyl diphosphate isomerase. *J*
 617 *Bacteriol* 181:4499-504.
- 618 41. Aires JR, Nikaido H. 2005. Aminoglycosides are captured from both periplasm
 619 and cytoplasm by the *AcrD* multidrug efflux transporter of *Escherichia coli*. *J*
 620 *Bacteriol* 187:1923-9.
- 621 42. Tavernarakis N, Driscoll M, Kyrides NC. 1999. The SPFH domain: implicated
 622 in regulating targeted protein turnover in stomatin and other membrane-
 623 associated proteins. *Trends Biochem Sci* 24:425-7.
- 624 43. Morrow IC, Rea S, Martin S, Prior IA, Prohaska R, Hancock JF, James DE,
 625 Parton RG. 2002. Flotillin-1/reggie-2 traffics to surface raft domains via a novel
 626 golgi-independent pathway. Identification of a novel membrane targeting
 627 domain and a role for palmitoylation. *J Biol Chem* 277:48834-41.
- 628 44. Bach JN, Bramkamp M. 2015. Dissecting the molecular properties of
 629 prokaryotic flotillins. *PLoS One* 10:e0116750.
- 630 45. Dempwolff F, Schmidt FK, Hervás AB, Stroh A, Rösch TC, Riese CN, Dersch
 631 S, Heimerl T, Lucena D, Hülsbusch N, Stuermer CA, Takeshita N, Fischer R,
 632 Eckhardt B, Graumann PL. 2016. Super Resolution Fluorescence Microscopy
 633 and Tracking of Bacterial Flotillin (Reggie) Paralogs Provide Evidence for
 634 Defined-Sized Protein Microdomains within the Bacterial Membrane but
 635 Absence of Clusters Containing Detergent-Resistant Proteins. *PLoS Genet*
 636 12:e1006116.
- 637 46. Somani VK, Aggarwal S, Singh D, Prasad T, Bhatnagar R. 2016. Identification
 638 of Novel Raft Marker Protein, FlotP in *Bacillus anthracis*. *Front Microbiol*
 639 7:169.
- 640 47. Dempwolff F, Wischhusen HM, Specht M, Graumann PL. 2012. The deletion of
 641 bacterial dynamin and flotillin genes results in pleiotrophic effects on cell
 642 division, cell growth and in cell shape maintenance. *BMC Microbiol* 12:298.
- 643 48. Yokoyama H, Matsui I. 2020. The lipid raft markers stomatin, prohibitin,
 644 flotillin, and HflK/C (SPFH)-domain proteins form an operon with NfeD
 645 proteins and function with apolar polyisoprenoid lipids. *Crit Rev Microbiol*
 646 46:38-48.
- 647 49. Kihara A, Ito K. 1998. Translocation, folding, and stability of the HflKC
 648 complex with signal anchor topogenic sequences. *J Biol Chem* 273:29770-5.

- 649 50. Edgar R, Rokney A, Feeney M, Semsey S, Kessel M, Goldberg MB, Adhya S,
650 Oppenheim AB. 2008. Bacteriophage infection is targeted to cellular poles. *Mol
651 Microbiol* 68:1107-16.
- 652 51. Bandyopadhyay K, Parua PK, Datta AB, Parrack P. 2010. *Escherichia coli* HflK
653 and HflC can individually inhibit the HflB (FtsH)-mediated proteolysis of
654 lambdaCII in vitro. *Arch Biochem Biophys* 501:239-43.
- 655 52. Qiao Z, Yokoyama T, Yan XF, Beh IT, Shi J, Basak S, Akiyama Y, Gao YG.
656 2022. Cryo-EM structure of the entire FtsH-HflKC AAA protease complex. *Cell
657 Rep* 39:110890.
- 658 53. Raetz CR, Dowhan W. 1990. Biosynthesis and function of phospholipids in
659 *Escherichia coli*. *J Biol Chem* 265:1235-8.
- 660 54. Lin TY, Weibel DB. 2016. Organization and function of anionic phospholipids
661 in bacteria. *Appl Microbiol Biotechnol* 100:4255-67.
- 662 55. Sohlenkamp C, Geiger O. 2016. Bacterial membrane lipids: diversity in
663 structures and pathways. *FEMS Microbiol Rev* 40:133-59.
- 664 56. El Khoury M, Swain J, Sautrey G, Zimmermann L, Van Der Smissen P, Décout
665 JL, Mingeot-Leclercq MP. 2017. Targeting Bacterial Cardiolipin Enriched
666 Microdomains: An Antimicrobial Strategy Used by Amphiphilic
667 Aminoglycoside Antibiotics. *Sci Rep* 7:10697.
- 668 57. Oliver PM, Crooks JA, Leidl M, Yoon EJ, Saghatelian A, Weibel DB. 2014.
669 Localization of anionic phospholipids in *Escherichia coli* cells. *J Bacteriol*
670 196:3386-98.
- 671 58. Romantsov T, Stalker L, Culham DE, Wood JM. 2008. Cardiolipin controls the
672 osmotic stress response and the subcellular location of transporter ProP in
673 *Escherichia coli*. *J Biol Chem* 283:12314-23.
- 674 59. Arias-Cartin R, Grimaldi S, Arnoux P, Guigliarelli B, Magalon A. 2012.
675 Cardiolipin binding in bacterial respiratory complexes: structural and functional
676 implications. *Biochim Biophys Acta* 1817:1937-49.
- 677 60. Romantsov T, Gonzalez K, Sahtout N, Culham DE, Coumoundouros C, Garner
678 J, Kerr CH, Chang L, Turner RJ, Wood JM. 2018. Cardiolipin synthase A
679 colocalizes with cardiolipin and osmosensing transporter ProP at the poles of
680 *Escherichia coli* cells. *Mol Microbiol* 107:623-638.
- 681 61. van Tilburg AY, Warmer P, van Heel AJ, Sauer U, Kuipers OP. 2022.
682 Membrane composition and organization of *Bacillus subtilis* 168 and its
683 genome-reduced derivative mini*Bacillus* PG10. *Microb Biotechnol* 15:1633-
684 1651.
- 685 62. Akiyama Y. 2009. Quality control of cytoplasmic membrane proteins in
686 *Escherichia coli*. *J Biochem* 146:449-54.
- 687 63. Hinz A, Lee S, Jacoby K, Manoil C. 2011. Membrane proteases and
688 aminoglycoside antibiotic resistance. *J Bacteriol* 193:4790-7.
- 689 64. Venter H, Mowla R, Ohene-Agyei T, Ma S. 2015. RND-type drug efflux pumps
690 from Gram-negative bacteria: molecular mechanism and inhibition. *Front
691 Microbiol* 6:377.
- 692 65. Nikaido E, Shirozaka I, Yamaguchi A, Nishino K. 2011. Regulation of the
693 AcrAB multidrug efflux pump in *Salmonella enterica* serovar *Typhimurium* in
694 response to indole and paraquat. *Microbiology* 157:648-655.

- 695 66. Garneau-Tsodikova S, Labby KJ. 2016. Mechanisms of Resistance to
696 Aminoglycoside Antibiotics: Overview and Perspectives. *Medchemcomm* 7:11-
697 27.
- 698 67. Baba T, Ara T, Hasegawa M, Takai Y, Okumura Y, Baba M, Datsenko KA,
699 Tomita M, Wanner BL, Mori H. 2006. Construction of *Escherichia coli* K-12 in-
700 frame, single-gene knockout mutants: the Keio collection. *Mol Syst Biol*
701 2:2006.0008.
- 702 68. Chaveroche MK, Ghigo JM, d'Enfert C. 2000. A rapid method for efficient gene
703 replacement in the filamentous fungus *Aspergillus nidulans*. *Nucleic Acids Res*
704 28:E97.
- 705 69. Cherepanov PP, Wackernagel W. 1995. Gene disruption in *Escherichia coli*:
706 TcR and KmR cassettes with the option of Flp-catalyzed excision of the
707 antibiotic-resistance determinant. *Gene* 158:9-14.
- 708 70. Boudjemaa R, Cabriel C, Dubois-Brissonnet F, Bourg N, Dupuis G, Gruss A,
709 Leveque-Fort S, Briandet R, Fontaine-Aupart MP, Steenkeste K. 2018. Impact
710 of Bacterial Membrane Fatty Acid Composition on the Failure of Daptomycin
711 To Kill *Staphylococcus aureus*. *Antimicrob Agents Chemother* 62.
- 712 71. Cabriel C, Bourg N, Dupuis G, Leveque-Fort S. 2018. Aberration-accounting
713 calibration for 3D single-molecule localization microscopy. *Opt Lett* 43:174-
714 177.
- 715

716 **FIGURE LEGENDS**

717
 718 **Figure 1. Cell localization patterns of HflC and QmcA.** Epifluorescence microscopy
 719 of cells expressing QmcA-GFP (A) and HflC-mCherry (B). Representative images are
 720 shown. Percentages indicate the frequencies of cells showing localization foci.
 721 Arrowheads indicate polar or punctate localization foci. Scales are indicated as white bars.
 722

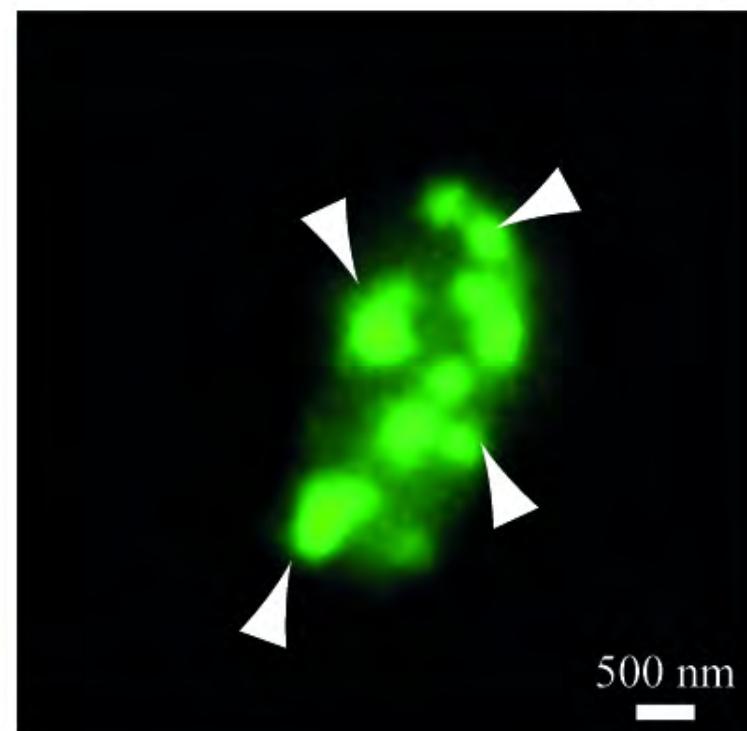
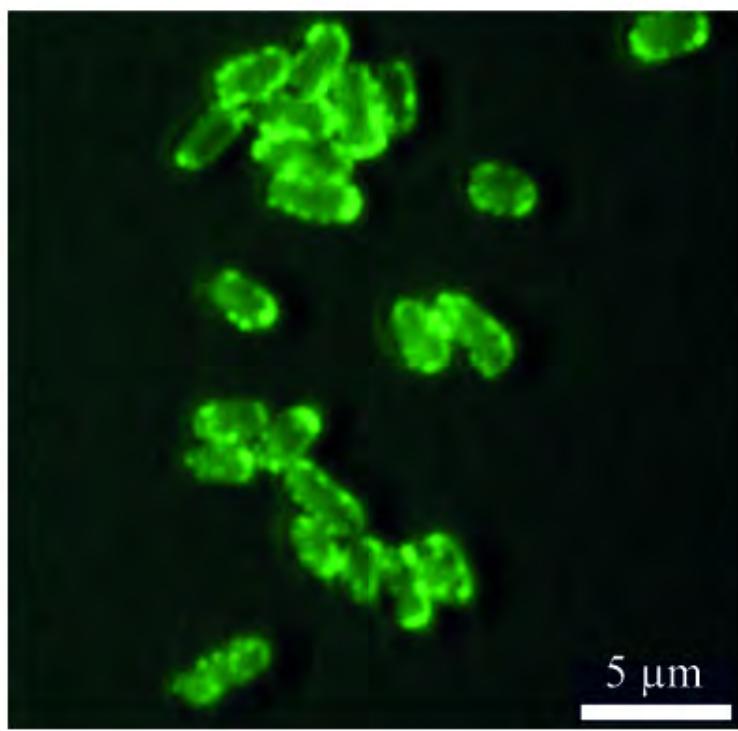
723 **Figure 2. QmcA and HflC localize to the inner membrane.** SDS-PAGE and
 724 immunodetection analyses of whole-cell extracts, cytosolic fractions, and inner (IM) or
 725 outer membrane (OM) fractions prepared from cells expressing QmcA-GFP (A) and
 726 HflC-mCherry (B). Anti-GFP and anti-mCherry antibodies were used to detect the
 727 presence of QmcA-GFP and HflC-mCherry, respectively. An anti-ExbB antibody were
 728 used to detect the inner membrane- (IM) marker ExbB and anti-TolC antibodies to detect
 729 the outer membrane- (OM) marker TolC.
 730

731 **Figure 3. The localization pattern and membrane topology of full-length, domain**
 732 **swapped or truncated versions of QmcA and HflC.** (A) GFP fusion derivatives of
 733 QmcA and (B) mCherry fusion derivatives of HflC. The representative images are shown
 734 in each strain with the frequencies of cells showing punctate (A) or polar localization (B).
 735 In figure 3A, first panel, the control WT QmcA-GFP is re-named TM^{QmcA}-SPFH^{QmcA}-
 736 GFP and the fluorescence microscopy image corresponding to its localization is therefore
 737 a duplicate of the one presented in Figure 1A. Similarly, In figure 3B, first panel, the
 738 control WT HflC-mCherry is re-named TM^{HflC}-SPFH^{HflC}-mCherry and the fluorescence
 739 microscopy image corresponding to its localization is therefore a duplicate of the one
 740 presented in Figure 1B. In membrane topology, helical structures represent
 741 transmembrane (TM) domains; silver, native TM domain of QmcA; pink, Pf3 domain;
 742 green, native TM domain of HflC; black, Cmi domain. Scale bars are 2 μ m.
 743

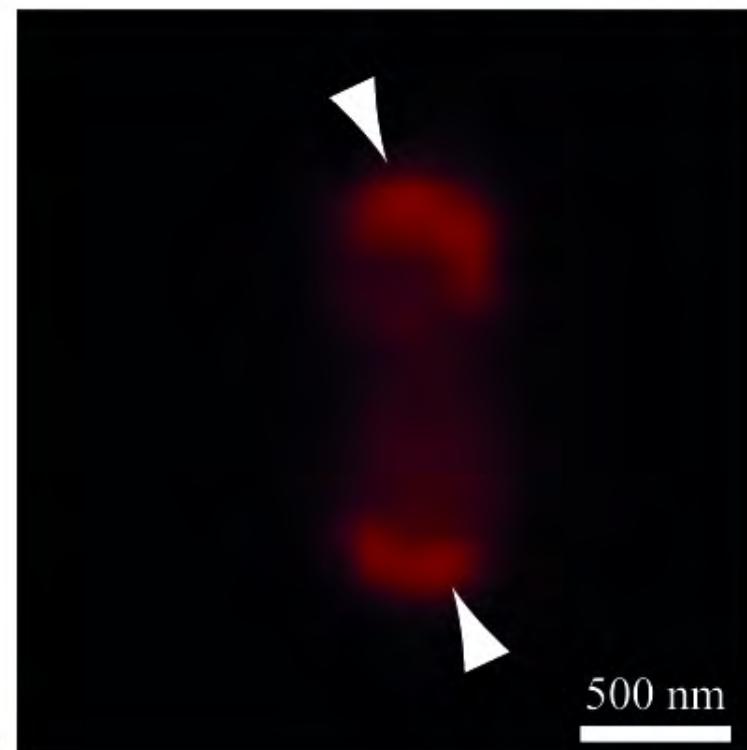
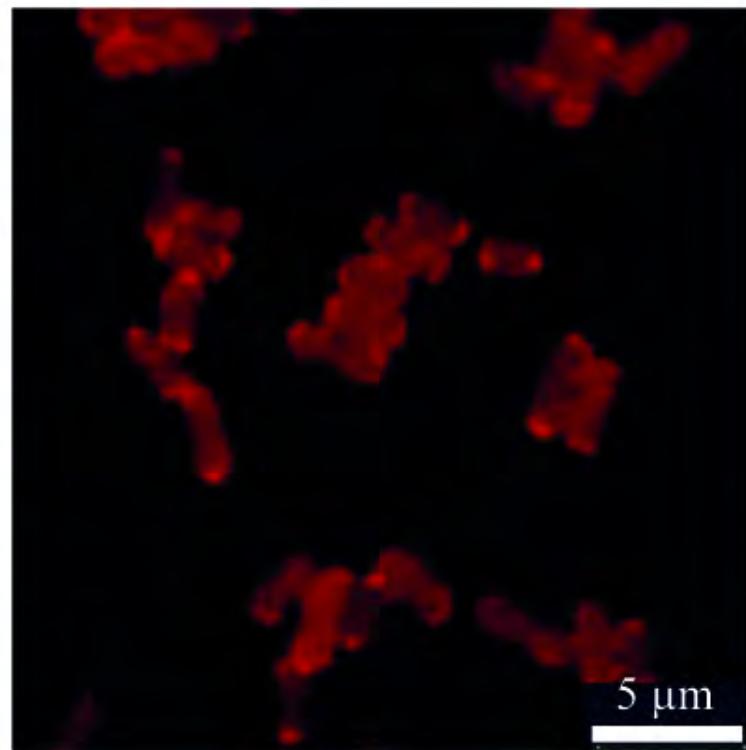
744 **Figure 4. Alteration of QmcA and HflC cell localization in *E. coli* cardiolipin and**
 745 **isoprenoid pathway mutants.** Two-dimensional super-resolution microscopy images of
 746 WT, Δ clsABC, and Δ idi strains expressing QmcA-GFP (A) and HflC-mCherry (B) in
 747 stationary phase. Number or nature of detected cluster is indicated. Scales are indicated
 748 as white bars.
 749

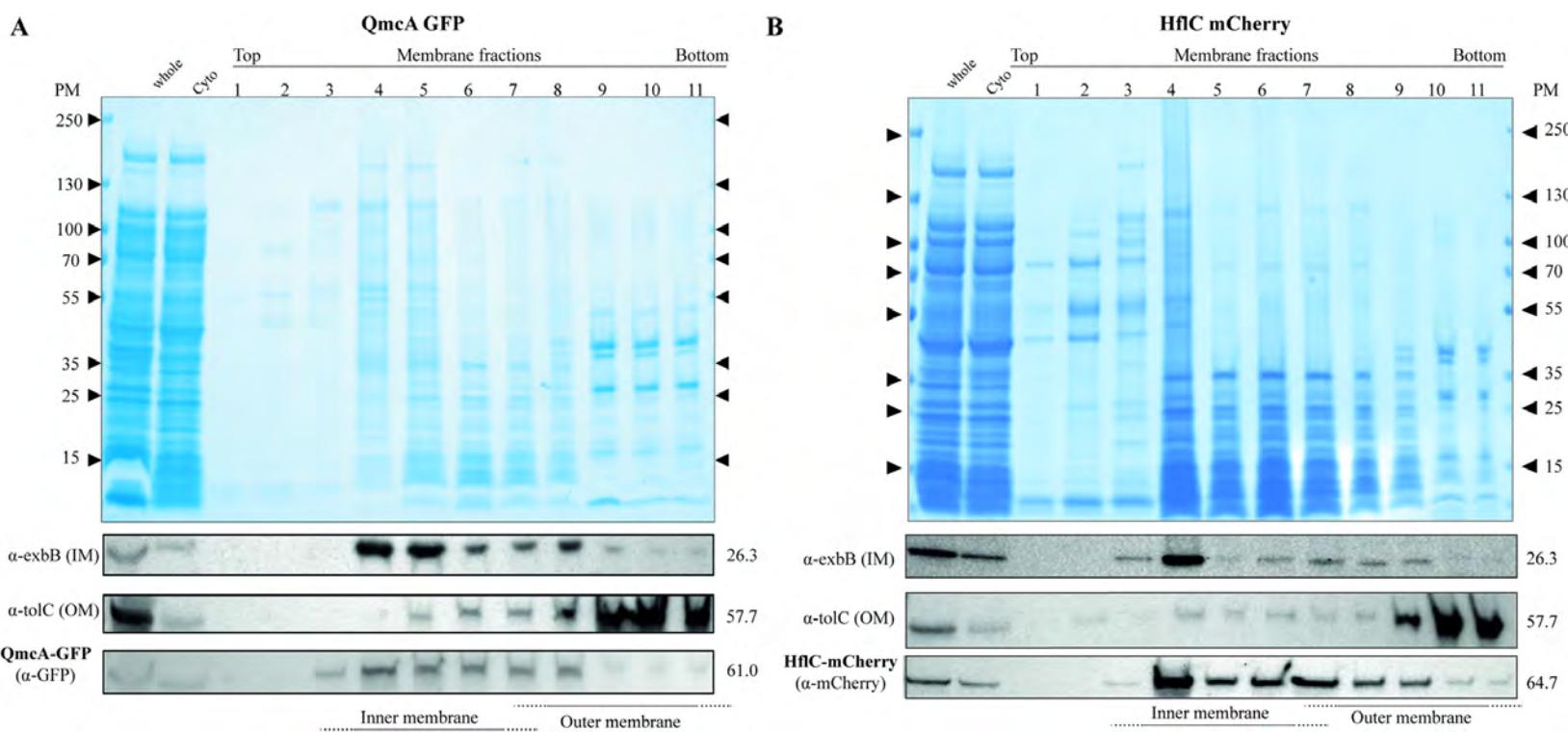
750 **Figure 5. Phenotypic analysis of *E. coli* SPFH mutants.** A: Bacterial growth curve of
 751 WT and SPFH gene deletion mutants in LB medium. B: Biolog bacterial growth curve of
 752 WT and Δ SPFH in the presence of tobramycin and paraquat. C: Minimum inhibitory
 753 concentration (MIC) for tobramycin of *E. coli* WT and indicated mutants. D: Minimum
 754 inhibitory concentration (MIC) for paraquat of *E. coli* WT and indicated mutants. * $p <$
 755 0.05, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$ compared with WT.
 756
 757

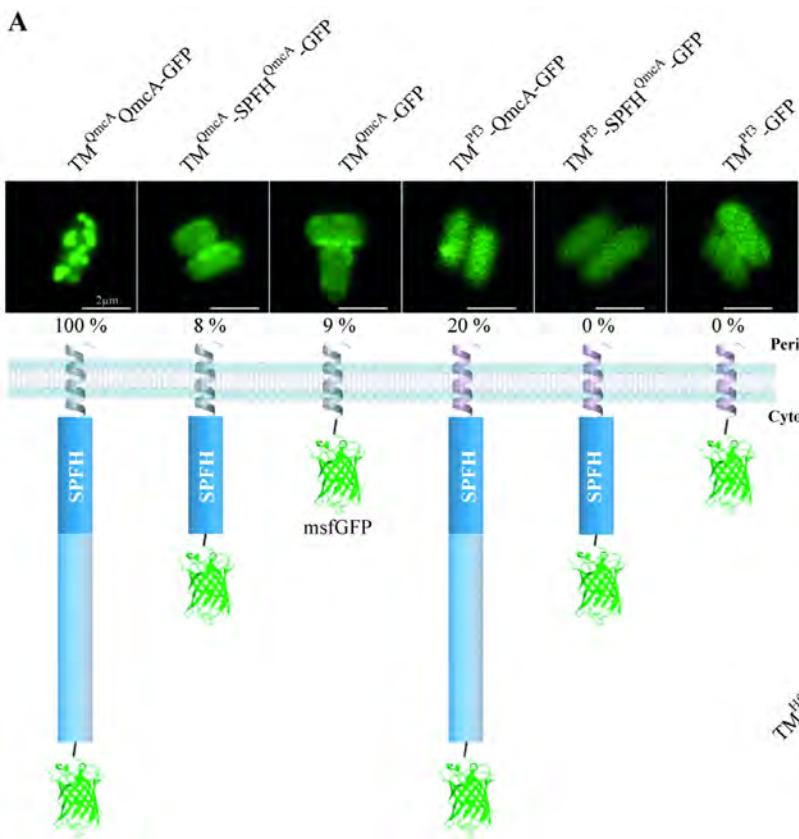
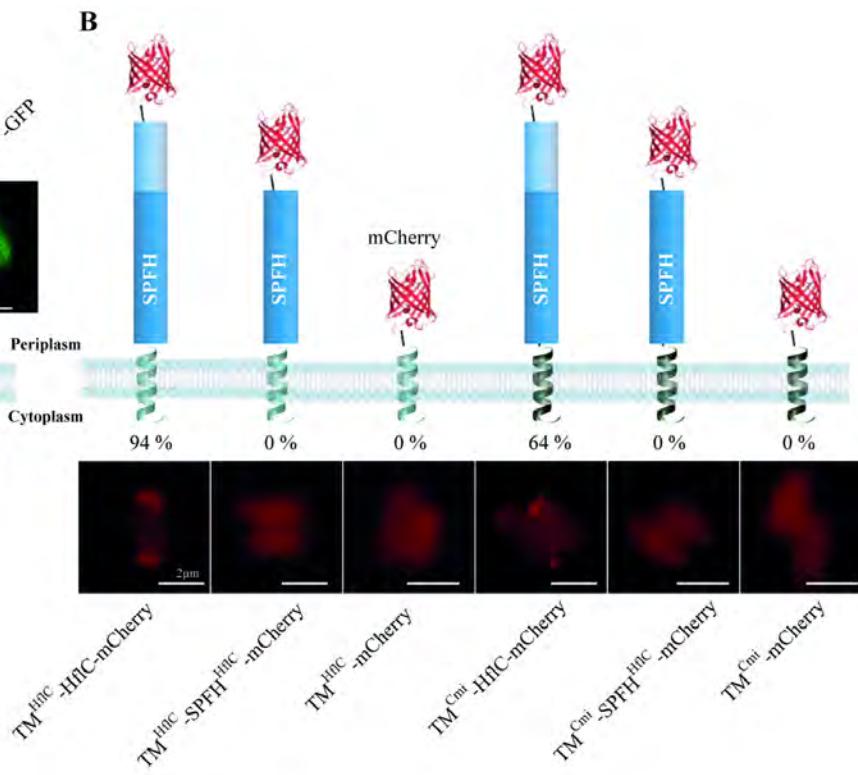
A
E. coli qmCA-gfp

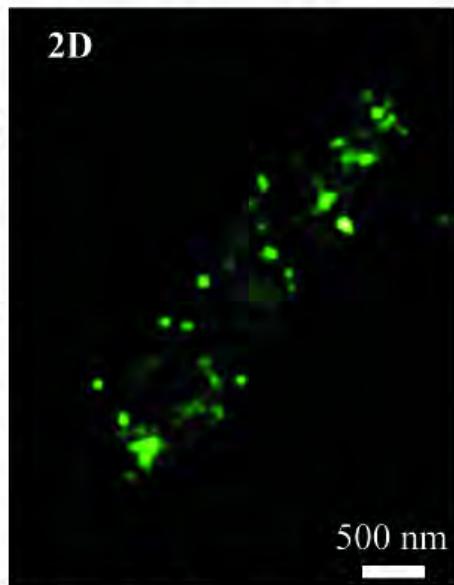
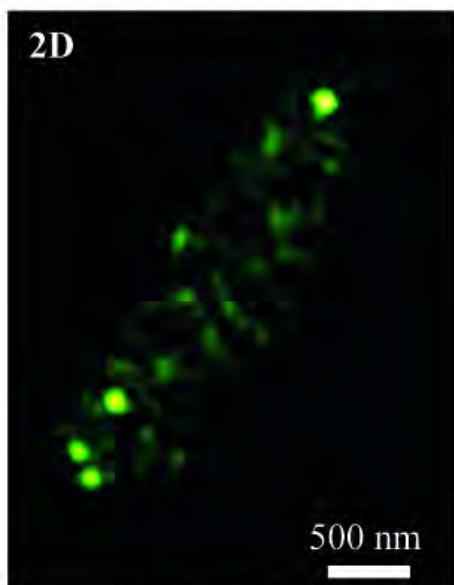
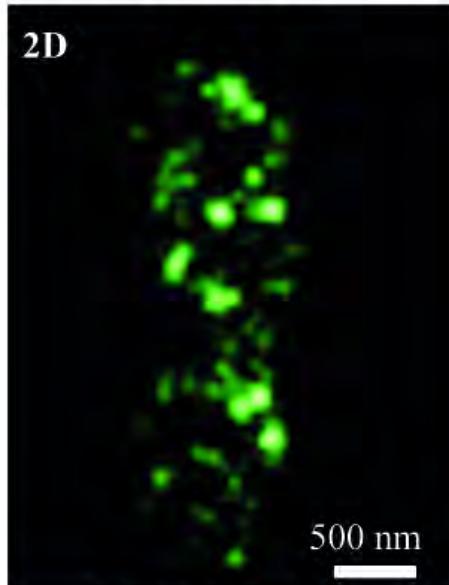
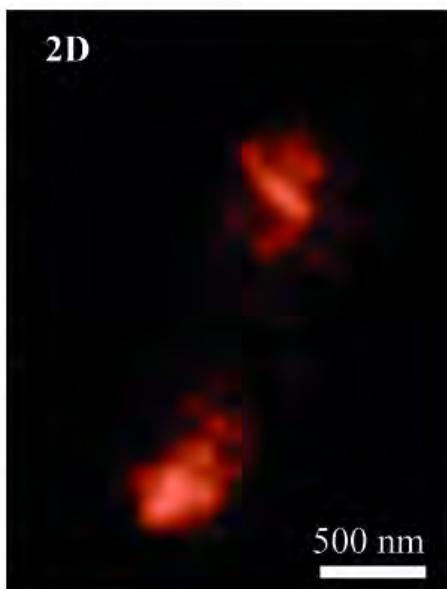


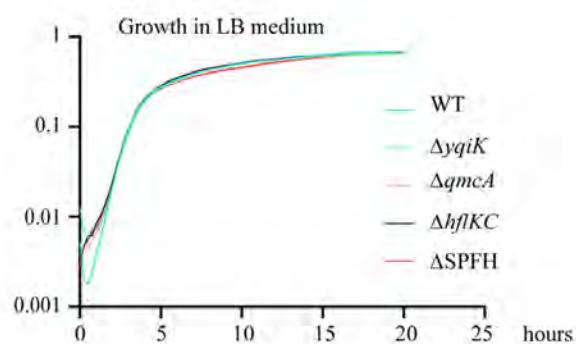
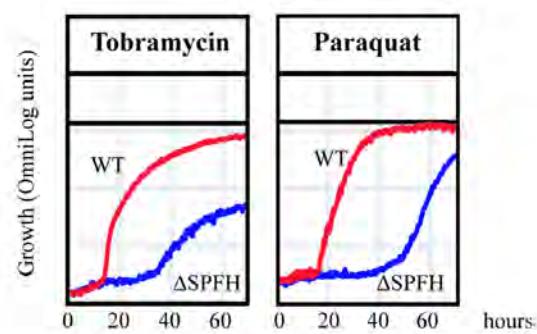
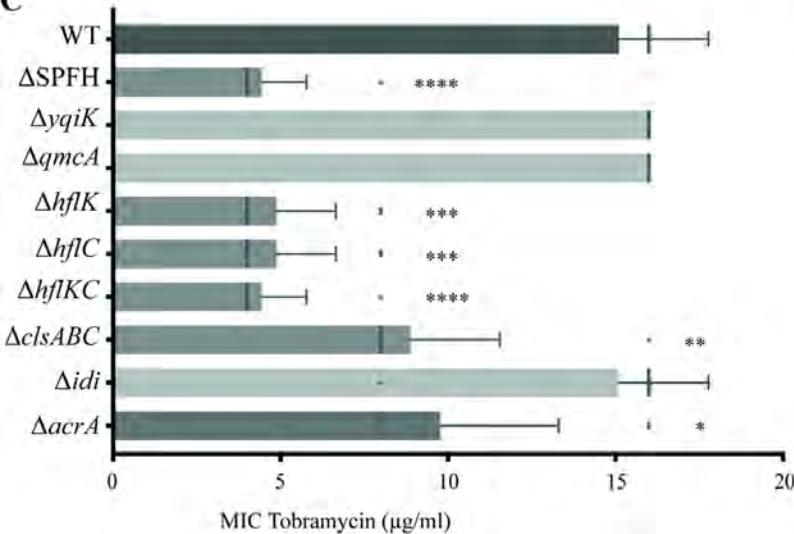
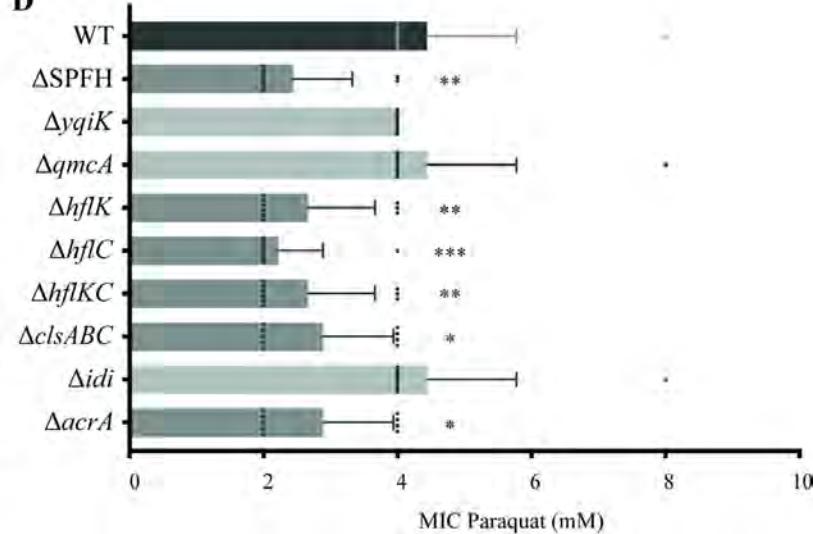
B
E. coli hflC-mCherry





A**B**

A*E. coli* WT*E. coli qmcA-gfp*10-15 clusters
per bacterium*E. coli* Δ clsABC1-5 clusters
per bacterium*E. coli* Δ idi4-10 clusters
per bacterium**B***E. coli hflC-mCherry*2 polar clusters
per bacteriumPolar and intracellular
clustersIntracellular
clusters

A**B****C****D**

SUPPLEMENTARY MATERIALS

Escherichia coli SPFH membrane microdomain proteins HflKC contributes to aminoglycoside and oxidative stress tolerance

Wessel AK, Yoshii Y *et al.*

This pdf file includes supplementary methods, supplementary figures S1 to S9 and supplementaryTables S2 and S3. Supplementary Table S1 is provided separately as a dataset.

SUPPLEMENTARY METHODS

Construction of YqiK tagged with GFP and HflK tagged with mCherry

YqiK-GFP chromosomal construct

The *yqiK* (except for the stop codon), *msfGfp*, and *aphAIII* genes encoding YqiK, msfGFP, and KmFRT cassette were amplified from MG1655 *strep*, MG1655mreB-GFP (1), and MG1655 Δ *cpxP*::KmFRT (2) chromosomes, respectively. Then, the intermediate plasmid pUC18 *yqiK-gfp-aphAIII* was constructed by combining these three DNA fragments with the linearized backbone vector pUC18, using Gibson assembly (New England Biolabs, Ipswich, MA, USA) and primers described in Table S3. Next, the DNA fragment encoding YqiK-GFP-KmFRT was amplified from the plasmid pUC18*yqiK-gfp-aphAIII* using the long recombining primers described in Table S3. The resulting PCR product was introduced on its native location under the *yqiK* promoter in strain MG1655 *strep* using pKOBEG plasmid by λ -red recombination to produce YqiK-GFP.

HflK-mCherry chromosomal construct

The DNA gene block corresponding to the entire *hflK* gene except for the stop codon, mCherry, and KmFRT with 40 bp-long homology regions of upstream of the *hflK* start codon and downstream of the *aphAIII* last codon was designed from the DNA sequence of MG1655 *strep*, MG1655mreB-mCherry (3), and MG1655 Δ *cpxP*::KmFRT (2) chromosomes, respectively, and purchased from Eurofins Genomics (France). Then, the DNA oligonucleotide was introduced on its native location under the *hflK* promoter in MG1655 *strep* using pKOBEG plasmid by λ -red recombination to produce HflK-mCherry.

Construction of QmcA-GFP and QmcA-derivatives tagged with GFP

The *qmcA* and *ybbJ*, *msfGfp*, and *aphAIII* genes encoding QmcA and YbbJ, msfGFP and KmFRT cassette, respectively, were amplified from MG1655 *strep*, MG1655mreB-GFP, and MG1655Δ*cpxP*::KmFRT (2) chromosomes. The sequence of information on the *pf3* gene was obtained from (4).

- ***TM^{QmcA}-QmcA-GFP chromosomal construct***

The intermediate plasmid pUC18*qmcA-gfp-aphAIII* was constructed by combining DNA fragments of the entire *qmcA* gene except for the stop codon, msfGFP, the entire *ybbJ* gene followed by 20 bp upstream regions of the start codon, and KmFRT, with the linearized backbone vector pUC18 using Gibson assembly (New England Biolabs). The DNA fragment encoding QmcA-GFP-KmFRT was amplified from the plasmid pUC18*qmcA-gfp-aphAIII* using the long recombining primers described in Table S3, and introduced on its native location under the *qmcA* promoter in strain MG1655 *strep* using pKOBEG plasmid by λ-red recombination to produce TM^{qmcA}-QmcA-GFP.

- ***TM^{QmcA}-SPFH^{QmcA}-GFP chromosomal construct***

The DNA fragment encoding msfGFP-KmFRT with 40 bp-long upstream and downstream homology regions was amplified from the TM^{pf3}-SPFH^{QmcA}-GFP chromosomal construct using the long recombining primers described in Table S3. Then, the resulting PCR product was introduced on the chromosome at the downstream position of the *qmcA* SPFH domain region in strain MG1655 *strep* by λ-red recombination to produce TM^{QmcA}-SPFH^{QmcA}-GFP.

- ***TM^{QmcA}-GFP chromosomal construct***

The DNA fragment encoding to msfGFP-KmFRT with 40 bp-long upstream and downstream homology regions was amplified from the TM^{QmcA}-QmcA-GFP chromosomal construct using long recombining primers described in Table S3. Then, the resulting PCR product was introduced on the chromosome at the downstream position of the *qmcA* TM domain region in strain MG1655 *strep* by λ-red recombination to produce TM^{QmcA}-GFP.

- ***ΔqmcA::zeo chromosomal construct***

The *zeo* gene with 40 bp-long upstream and downstream homology regions was amplified from

the MG1655 λ ATT:*amp_GFPmut3* Δ *fimAICDFGH::zeo
 Δ *yadyadN**ecpD**htrE**yadMLKC::cat (5) using long recombining primers described in Table S3. Then, the resulting PCR product was introduced on the native location under the *qmca* promoter in strain MG1655 strep by λ -red recombination to generate Δ *qmca*::*zeo*.**

• ***TM^{pf3}-QmcA-GFP chromosomal construct***

The plasmid pZS*12*TM^{pf3}-gfp-aphAIII* was constructed via pZS*12*TM^{pf3}-gfp*, by combining DNA fragments of *pf3*, msfGFP, and KmFRT, with the linearized backbone vector pZS*12 using Gibson assembly (New England Biolabs) and primers described in Table S3. Then, the intermediate plasmid pZS*12*TM^{pf3}-qmca-gfp-aphAIII* was constructed by combining the DNA fragment of *qmca* gene except for the native TM domain region with the linearized vector pZS*12*TM^{pf3}-gfp* using Gibson assembly (New England Biolabs). Next, the DNA fragment encoding *TM^{pf3}*-QmcA-GFP-KmFRT with 40 bp-long upstream and downstream homology regions was amplified from the intermediate plasmid using the long recombining primers described in Table S3. The resulting PCR product was introduced on its native location under *qmca* promoter by λ -red recombination into strain Δ *qmca*::*zeo* using pKOBEG plasmid to produce *TM^{pf3}-QmcA-GFP*.

• ***TM^{pf3}-SPFH^{QmcA}-GFP chromosomal construct***

The intermediate plasmid pZS*12*TM^{pf3}-SPFH^{QmcA}-gfp-aphAIII* was constructed by combining the SPFH domain region of *qmca* gene with the linearized vector PZ*12 *TM^{pf3}-gfp-aphAIII* using Gibson assembly (New England Biolabs). Then, the DNA fragment encoding *TM^{pf3}-SPFH^{QmcA}-GFP-KmFRT* with 40 bp-long upstream and downstream homology regions was amplified from the plasmid pZS*12 *TM^{pf3}-SPFH^{QmcA}-GFP-aphAIII* using the long recombining primers described in Table S3. The resulting PCR product was introduced on its native location under *qmca* promoter by λ -red recombination into Δ *qmca*::*zeo* strain using pKOBEG plasmid to produce *TM^{pf3}-SPFH^{QmcA}-GFP*.

• ***TM^{pf3}-GFP chromosomal construct***

The DNA fragment encoding *TM^{pf3}-GFP-KmFRT* with 40 bp-long upstream and downstream homology regions was amplified from pZS*12*TM^{pf3}-gfp-aphAIII* using the long recombining primers described in Table S3. The resulting PCR product was introduced on its native location under *qmca* promoter by λ -red recombination into Δ *qmca*::*zeo* strain using pKOBEG plasmid to produce *TM^{pf3}-GFP*.

*Construction of *HflC* derivatives tagged with mCherry*

The *hflC*, *mCherry*, and *cat* genes encoding HflC, mCherry, and CmFRT cassette, respectively, were amplified from MG1655 *strep*, MG1655mreB-mCherry, and MG1655 Δ yfcV-P::CmFRT (6) chromosomes. The sequence of information on *cmi* gene was obtained from (4).

• ***TM^{HflC}-HflC-mCherry chromosomal construct***

The intermediate plasmid pUC18*TM^{hflC}-HflC-mCherry-aphAIII* was constructed by combining DNA fragments of the *hflC* gene except for the stop codon, mCherry, and KmFRT, with the linearized backbone vector pUC18 using Gibson assembly (New England Biolabs) and primers described in Table S3. The DNA fragment encoding HflC-mCherry-KmFRT with 40 bp-long upstream and downstream homology regions was amplified from the plasmid pUC18*TM^{hflC}-HflC-mCherry-aphAIII* using the long recombining primers described in Table S3 and introduced on its native location under the *hflC* promoter in strain *MG1655 strep* using pKOBEG plasmid by λ -red recombination to *TM^{hflC}-HflC-mCherry*.

• ***TM^{HflC}-SPFH^{HflC} -mCherry chromosomal construct***

The DNA fragment encoding mCherry-CmFRT with 40 bp-long upstream and downstream homology regions was amplified from the *TM^{cmi}-SPFH^{HflC}-mCherry* chromosomal construct, using the long recombining primers described in Table S3. The resulting PCR product was introduced on the chromosome at the downstream position of the *hflC* SPFH domain region by λ -red recombination into *MG1655 strep* strain using pKOBEGA plasmid to produce *TM^{hflC}-SPFH^{HflC}-mCherry*.

• ***TM^{HflC}-mCherry chromosomal construct***

The DNA fragment encoding mCherry-KmFRT with 40 bp-long upstream and downstream homology regions was amplified form the plasmid pUC18*TM^{hflC}-HflC-mCherry-aphAIII* using the long recombining primers described in Table S3. The resulting PCR product was introduced on the chromosome at the downstream position of the *hflC* TM domain region by λ -red recombination into *MG1655 strep* strain using pKOBEGA plasmid to produce *TM^{hflC}-mCherry*.

• ***TM^{cmi}-HflC-mCherry chromosomal construct***

The plasmid pZS*12*TM^{cmi}-mCherry-cat* was constructed, via pZS*12*TM^{cmi}-mCherry*, by combining DNA fragments encoding *TM^{cmi}*, mCherry, and CmFRT, with the linearized backbone vector pZS*12 using Gibson assembly (New England Biolabs) and the primers described in Table S3. Then, the intermediate plasmid pZS*12*TM^{cmi}-hflC-mCherry-cat* was constructed by combining the DNA fragment of *hflC* gene except for the native TM domain region with the linearized vector pZS*12*TM^{cmi}-mCherry-cat* using Gibson assembly (New England Biolabs). Then, the DNA fragment encoding *TM^{cmi}-HflC-mCherry-CmFRT* with 40 bp-long upstream and downstream homology regions was amplified from the intermediated plasmid using the long recombining primers described in Table S3. The resulting PCR product was introduced on its native location under *hflC* promoter by λ-red recombination into $\Delta hflC::\text{KmFRT}$ strain using pKOBEGA plasmid to produce *TM^{cmi}-HflC-mCherry*.

- ***TM^{cmi}-SPFH^{HflC}-mCherry chromosomal construct***

The intermediated plasmid pZS*12*TM^{cmi}-SPFH^{HflC}-mCherry-cat* was constructed by combining the *hflC* SPFH domain region with the linearized initial plasmid pZS*12*TM^{cmi}-mCherry-cat*, which was used for generating *TM^{cmi}-HflC-mCherry* chromosomal construct, using Gibson assembly (New England Biolabs). Then, the DNA fragment encoding *TM^{cmi}-SPFH^{HflC}-mCherry-CmFRT* with 40 bp-long upstream and downstream homology regions was amplified from the intermediated plasmid using the long recombining primers described in Table S3. The resulting PCR product was introduced on its native location under *hflC* promoter by λ-red recombination into $\Delta hflC::\text{KmFRT}$ strain using pKOBEGA plasmid to produce *TM^{cmi}-SPFH^{HflC}-mCherry*.

- ***TM^{cmi}-mCherry chromosomal construct***

The DNA fragment encoding *TM^{cmi}-GFP-CmFRT* with 40 bp-long upstream and downstream homology regions was amplified from the plasmid pZS*12*TM^{cmi}-mCherry-cat* using the long recombining primers described in Table S3. The resulting PCR product was introduced on its native location under *hflC* promoter by λ-red recombination into $\Delta hflC::\text{KmFRT}$ strain using pKOBEGA plasmid to produce *TM^{cmi}-mCherry*.

Construction of QmcA-GFP and HflC-mCherry in the ΔclsABC and Δidi mutants

- ***QmcA-GFP chromosomal construct in the ΔclsABC strain***

TM^{QmcA}-QmcA-GFP-KmFRT mutation from *TM^{QmcA}-QmcA-GFP* chromosomal construct

was introduced into strain Δ *clsABC* by P1vir phage transduction (Δ *clsABC* QmcA-GFP).

- ***TM^{QmcA}-QmcA-GFP chromosomal construct in the Δ idi strain***

TM^{QmcA} -QmcA-GFP-KmFRT mutation from TM^{QmcA} -QmcA-GFP chromosomal construct was introduced into strain Δ *idi* by P1vir phage transduction (Δ *idi* QmcA-GFP).

- ***TM^{HflC}-HflC-mCherry chromosomal construct in the Δ clsABC strain***

TM^{HflC} -HflC-mCherry-KmFRT mutation from TM^{HflC} -HflC-mCherry chromosomal construct was introduced into strain Δ *clsABC* by P1vir phage transduction (Δ *clsABC* HflC-mCherry).

- ***TM^{HflC}-HflC-mCherry chromosomal construct in the Δ idi strain***

TM^{HflC} -HflC-mCherry-KmFRT mutation from TM^{HflC} -HflC-mCherry chromosomal construct was introduced into strain Δ *idi* by P1vir phage transduction (Δ *idi* HflC-mCherry).

- ***AcrA-GFP***

The DNA fragment encoding GFP-KmFRT region with 40 bp-long upstream and downstream homology regions was amplified from the TM^{Pf3} -SPFH $^{\text{QmcA}}$ -GFP chromosomal construct using the long recombining primers described in Table S3. The resulting PCR product was introduced on chromosome at the downstream position of the *acrA* gene (without stop codons) in *MG1655 strep* by λ -red recombination, to produce a GFP fusion. The mutation harboring KmFRT was introduced into a *MG1655 strep* strain having clean background by P1vir phage transduction (AcrA-GFP).

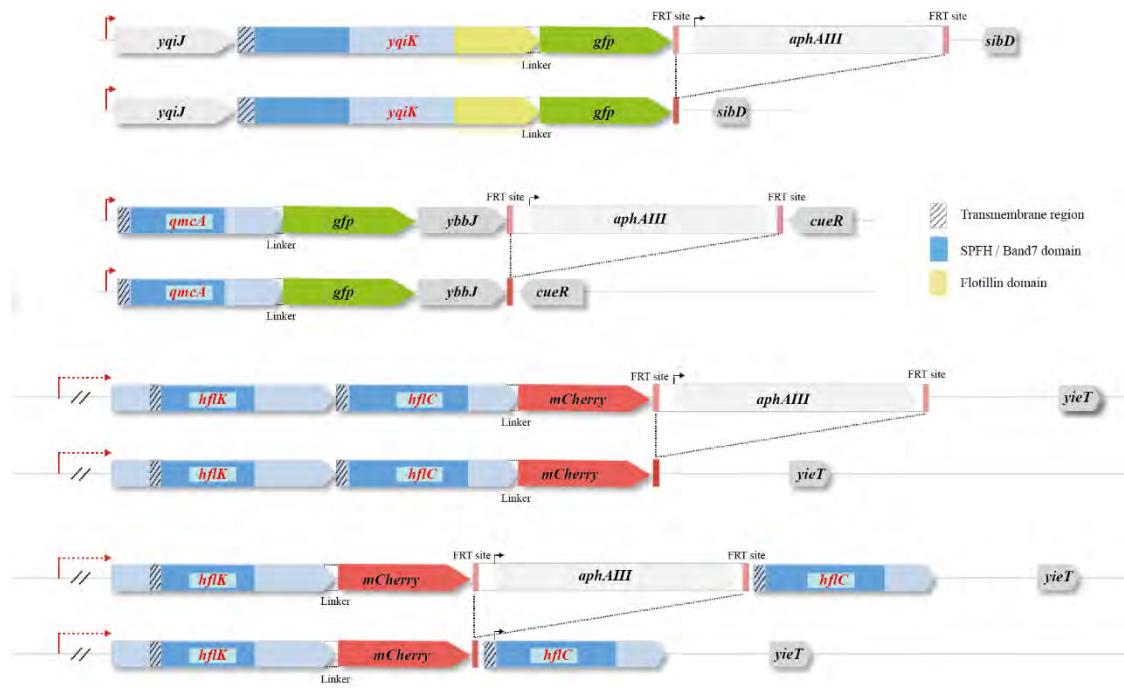
REFERENCES

1. Pédelacq JD, Cabantous S, Tran T, Terwilliger TC, Waldo GS. 2006. Engineering and characterization of a superfolder green fluorescent protein. *Nat Biotechnol* **24**:79-88.10.1038/nbt1172: 10.1038/nbt1172
2. Beloin C, Valle J, Latour-Lambert P, Faure P, Kzreminski M, Balestrino D, Haagensen JA, Molin S, Prensier G, Arbeille B, Ghigo JM. 2004. Global impact of mature biofilm lifestyle on *Escherichia coli* K-12 gene expression. *Mol Microbiol* **51**:659-674.10.1046/j.1365-2958.2003.03865.x: 10.1046/j.1365-2958.2003.03865.x
3. Bendezú FO, Hale CA, Bernhardt TG, de Boer PA. 2009. RodZ (YfgA) is required for proper assembly of the MreB actin cytoskeleton and cell shape in *E. coli*. *Embo j* **28**:193-204.10.1038/emboj.2008.264: 10.1038/emboj.2008.264
4. Luiten RG, Putterman DG, Schoenmakers JG, Konings RN, Day LA. 1985. Nucleotide sequence of the genome of Pf3, an IncP-1 plasmid-specific filamentous bacteriophage of *Pseudomonas aeruginosa*. *J Virol* **56**:268-276

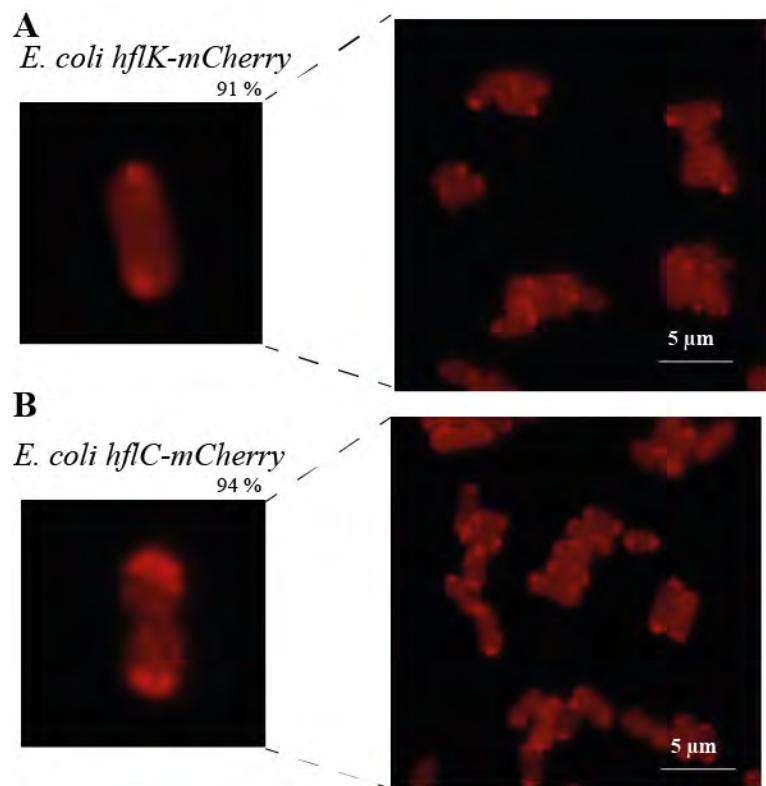
5. **Larsonneur F, Martin FA, Mallet A, Martinez-Gil M, Semetey V, Ghigo JM, Beloin C.** 2016. Functional analysis of *Escherichia coli* Yad fimbriae reveals their potential role in environmental persistence. *Environmental microbiology* 18:5228-5248.

6. **Korea CG, Badouraly R, Prevost MC, Ghigo JM, Beloin C.** 2010. *Escherichia coli* K-12 possesses multiple cryptic but functional chaperone-usher fimbriae with distinct surface specificities. *Environ Microbiol* 12: 1957–1977. <https://doi.org/10.1111/j.1462-2920.2010.02202.x>

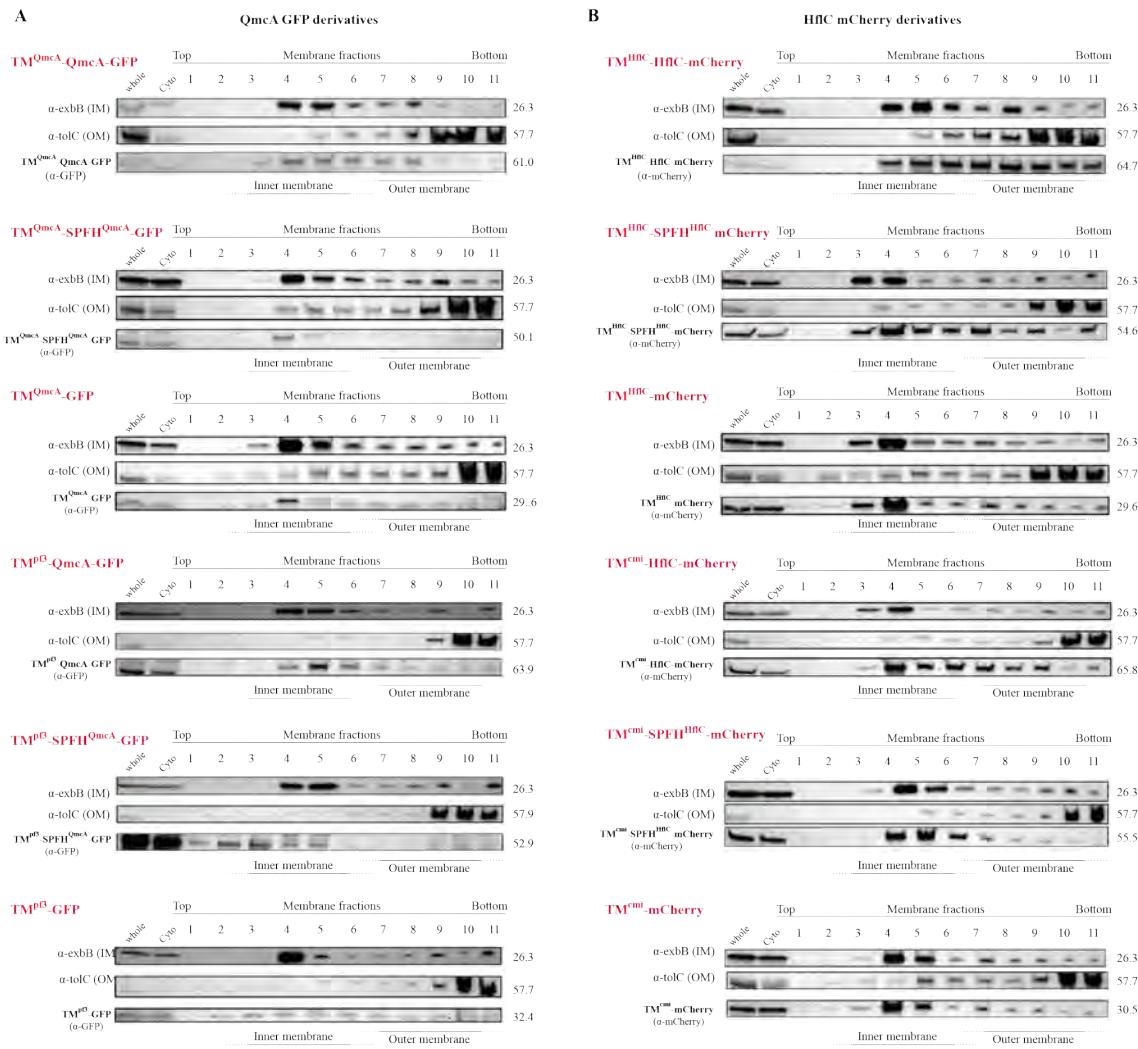
SUPPLEMENTARY FIGURES



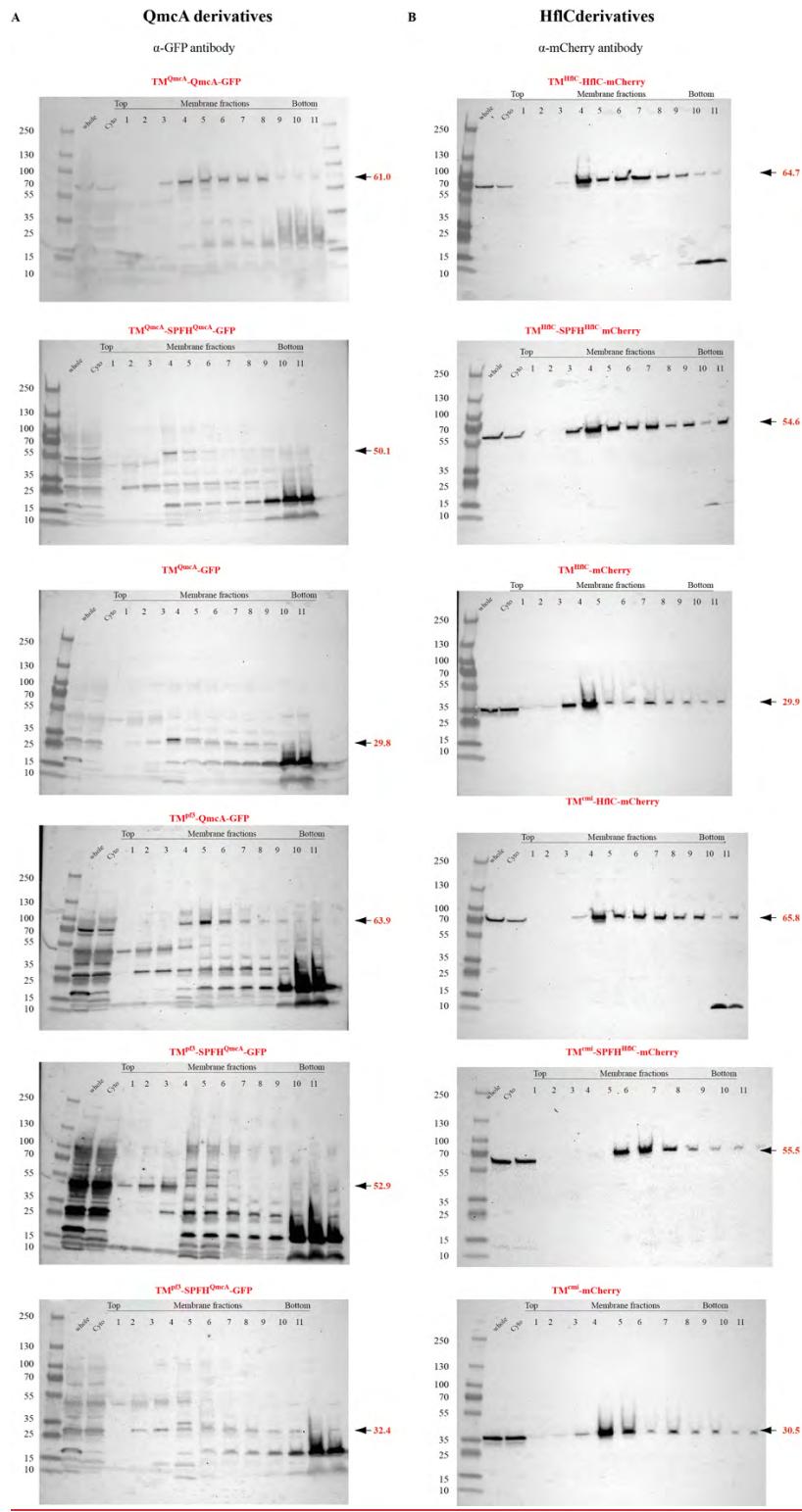
Supplementary Figure S1. Schematic representation of chromosomal GFP or mCherry fusions to genes encoding *E. coli* SPFH proteins. SPFH protein-encoding genes, *yqiK*, *qmcA*, *hflK*, and *hflC* are fused with monomeric super folder green fluorescent protein GFP (msfGFP) and *hflK*, and *hflC* to monomeric red fluorescent protein mCherry, respectively. Fusions were constructed as described in the Materials and Method section and the associated kanamycin antibiotic resistance marker (*aphAIII*) was inserted downstream of the fusion genes and removed using pCP20 plasmid, encoding the *flp* flippase.



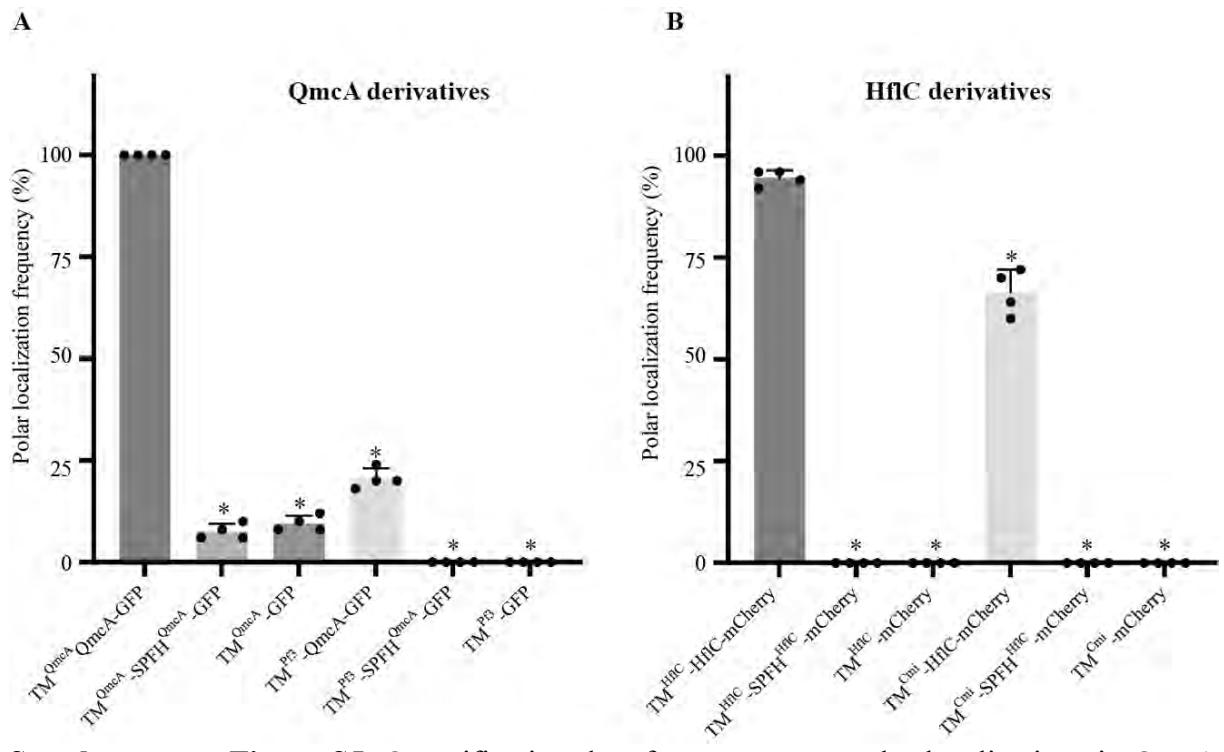
Supplementary Figure S2. Localization pattern of HflK and HflC. Epifluorescence microscopic images of cells expressing HflK-mCherry (A) and HflC-mCherry (B) in exponential phase with high and low magnifications.



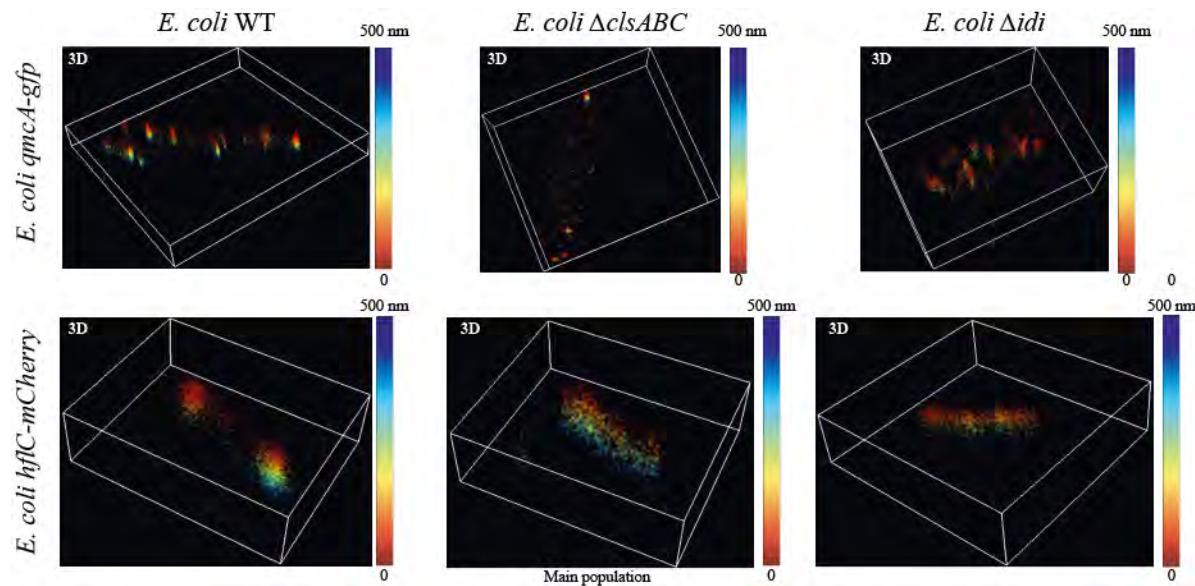
Supplementary Figure S3. Inner membrane localization of QmcA and HflC in domain swap constructs. SDS-PAGE and immunodetection analyses using proteins of whole-cell extract, cytosolic fraction, and membrane fractions prepared from cells expressing GFP fusion derivatives of QmcA (A) or mCherry fusion derivatives of HflC (B). In immunodetection analysis, anti-ExbB antibodies were used to detect the inner membrane- (IM) marker ExbB and anti-TolC antibodies to detect the outer membrane- (OM) marker TolC. Anti-GFP and anti-mCherry antibodies were used to detect the expressions of GFP and mCherry fused proteins, respectively.



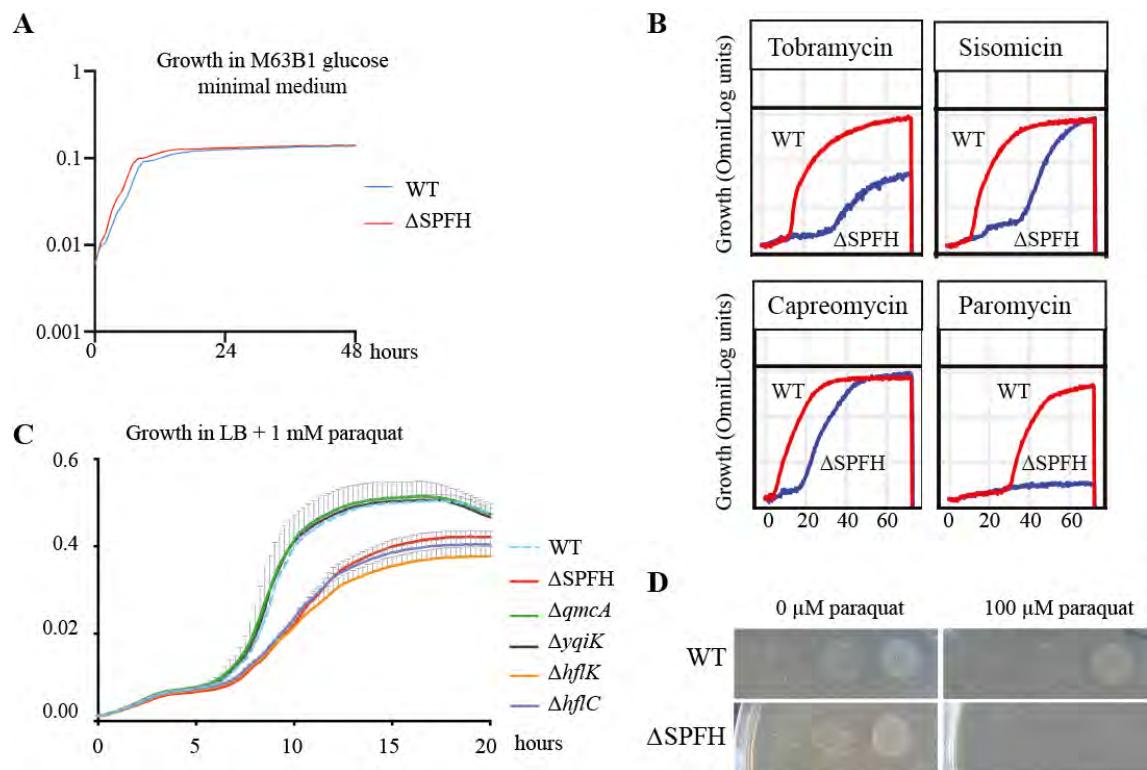
Supplementary Figure S4. Detection of QmcA and HflC fusion derivatives in domain swap constructs. **A:** immunodetection of GFP fusion derivatives of QmcA using anti-GFP antibody. **B:** immunodetection of mCherry fusion derivatives of HflC using anti-mCherry antibody.



Supplementary Figure S5. Quantification data for punctate or polar localizations in QmcA and HflC derivatives., **A:** QmcA derivatives. **B:** HflC derivatives. * $p < 0.05$ compared with $\text{TM}^{\text{QmcA}}\text{-QmcA-GFP}$ or $\text{TM}^{\text{HflC}}\text{-HflC-mCherry}$.

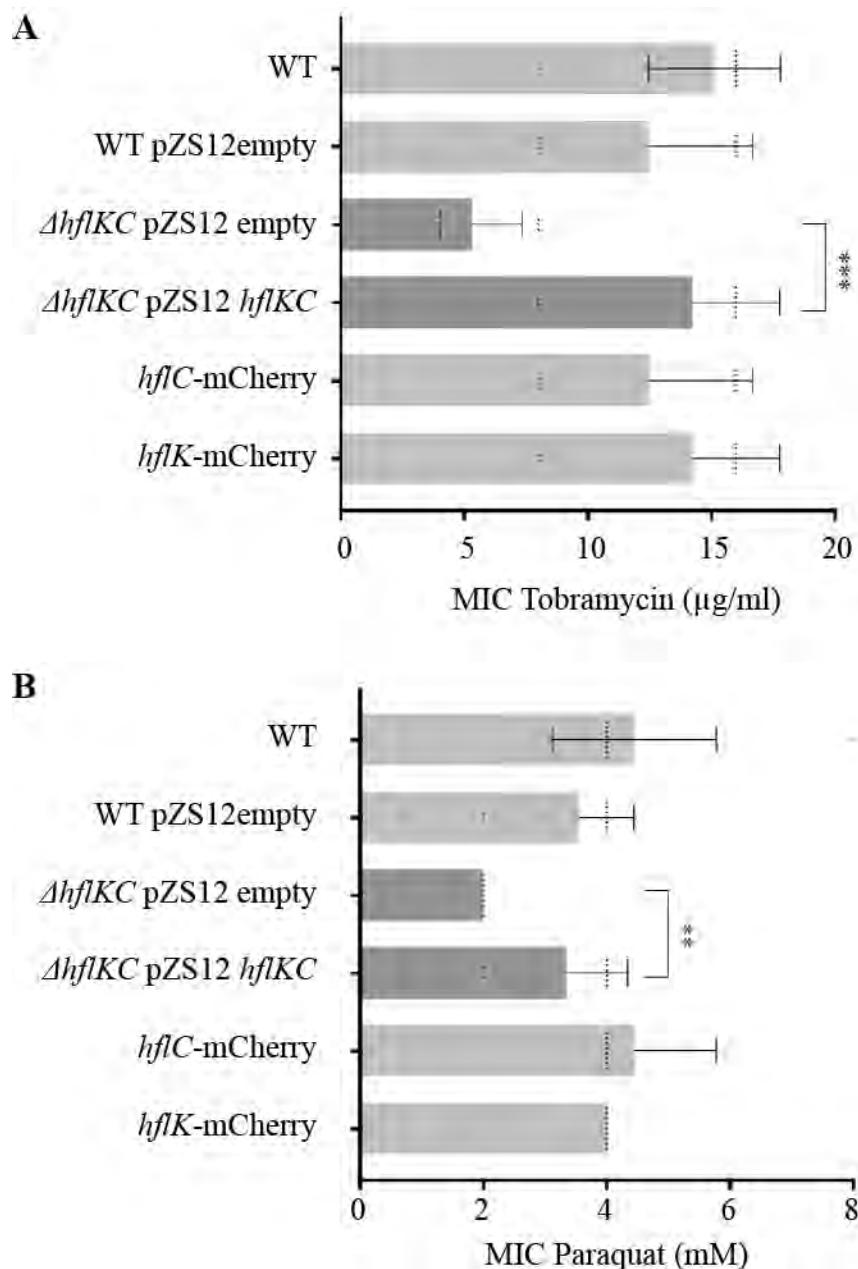


Supplementary Figure S6. The subcellular localization of QmcA and HflC in mutants with the alteration of cardiolipin or isoprenoid synthetic pathway. Three-dimensional super-resolution microscopy images of WT, Δ *clsABC*, and Δ *idi* strains expressing QmcA-GFP and HflC-mCherry in stationary phase, with colors corresponding to depth location along the Z axis, 0-500 nm, with 0 nm expressed in red, and 500 nm expressed in deep blue.

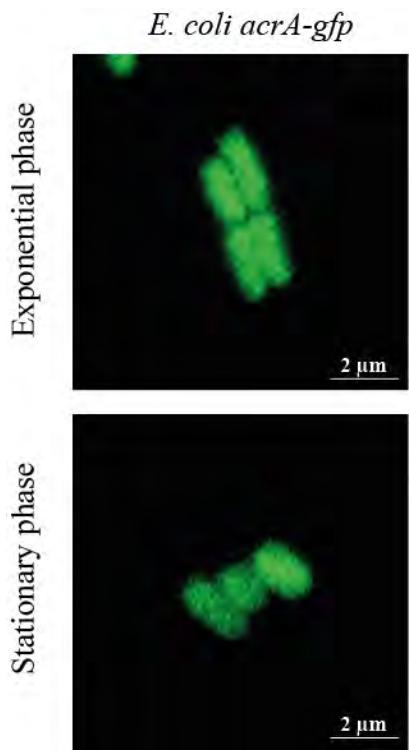


Supplementary Figure S7. Phenotypic analysis of *E. coli* SPFH mutant

(A) Growth curve of *E. coli* WT and Δ SPFH mutant in M63B1 glucose minimal medium. (B) Biolog metabolic activity curve of WT and Δ SPFH in presence of tobramycin, capreomycin, sisomicin, and paromycin. (C) Bacterial growth curve of WT and Δ SPFH in the presence of 0.8 mM paraquat. (D) Paraquat susceptibility assay of WT and Δ SPFH spotted on M63B1 glucose agar containing 100 μ M paraquat. (E) Growth curve of WT and indicated SPFH gene mutants in the presence of 0.8 mM paraquat.



Supplementary Figure S8. Susceptibility to tobramycin and paraquat of complemented mutants.
 Minimum inhibitory concentrations (MICs) for tobramycin (A) and paraquat (B) of *E. coli* Wt, $\Delta hflKC$ strains harboring empty vector and $hflKC$ - complemented strains or strain expressing $hflC$ or $hflK$ -*mCherry* constructs from their native chromosomal context. ** $p < 0.01$, *** $p < 0.001$.



Supplementary Figure S9. Localization of AcrA-GFP fusion protein does not show polar localization pattern when expressed from native chromosomal context. Epifluorescence microscopic images of cells expressing AcrA-GFP in exponential and stationary phases.

Supplementary Table S2. Bacterial strains and plasmids used in this study

<i>E. coli</i> strains and plasmids	Genotype or description	Antibiotic resistance(s)	Reference
Strains			
BW25113 Δ qiK::Kmfrt	Keio collection	Km ^R	(1)
BW25113 Δ qmcA::Kmfrt	Keio collection	Km ^R	(1)
BW25113 Δ hflK::Kmfrt	Keio collection	Km ^R	(1)
BW25113 Δ hflC::Kmfrt	Keio collection	Km ^R	(1)
BW25113 Δ clsA::Kmfrt	Keio collection	Km ^R	(1)
BW25113 Δ clsB::Kmfrt	Keio collection	Km ^R	(1)
BW25113 Δ clsC::Kmfrt	Keio collection	Km ^R	(1)
BW25113 Δ idi::Kmfrt	Keio collection	Km ^R	(1)
BW25113 Δ acrA::Kmfrt	Keio collection	Km ^R	(1)
MG1655 strep	Spontaneous streptomycin-resistant mutant of K-12 wild-type strain	Strep ^R	(2)
MG1655mreB-GFP	Source of msf _{GFP} gene	No resistance	Gift from Dr. Sven van Teeffelen
MG1655mreB-mCherry	Source of mCherry gene	No resistance	Gift from Dr. Sven van Teeffelen
MG1655 Δ cpxP::KmFRT	Source of kanamycin resistance cassette	Km ^R	(3)
MG1655 Δ yfcV-P::CmFRT	Source of chloramphenicol resistance cassette	Cm ^R	(4)
DH5alpir pSW25 ptetAccdB	Source of spectinomycin resistance cassette	Spec ^R	(5)

MG1655 λ ATT:amp_GFPmut3 $\Delta fimAICDFGH::zeo$ $\Delta yadyadNecpDhtrEyadMLKC::cat$	Source of zeocin resistance cassette	Zeo ^R	(6)
$\Delta yqiK$	P1 vir transduction from BW25113 $\Delta yqiK::Kmfrt$ into MG1655 <i>strep</i>	Strep ^R	This study
$\Delta qmcA$	P1 vir transduction from BW25113 $\Delta qmcA::Kmfrt$ into MG1655 <i>strep</i>	Strep ^R	This study
$\Delta hflK$	P1 vir transduction from BW25113 $\Delta hflK::Kmfrt$ into MG1655 <i>strep</i>	Strep ^R	This study
$\Delta hflC$	P1 vir transduction from BW25113 $\Delta hflC::Kmfrt$ into MG1655 <i>strep</i>	Strep ^R	This study
$\Delta hflKC$	Double mutant of $\Delta hflK$ and $\Delta hflC$. MG1655 <i>strepR</i> , $\Delta hflKC::Cmfrt$	Strep ^R	This study
$\Delta yqiJK$	Double mutant of $\Delta yqiJ$ and $\Delta yqiK$. MG1655 <i>strepR</i> , $\Delta yqiJK::Spec$	Strep ^R , Spec ^R	This study
$\Delta qmcA, \Delta yqiJK$	Triple mutant of $\Delta qmcA$ and $\Delta yqiJK$. MG1655 <i>strepR</i> , $\Delta qmcA$, $\Delta yqiJK::Spec$	Strep ^R , Spec ^R	This study
$\Delta SPFH$	Quintuple mutant of $\Delta yqiK$, $\Delta qmcA$, $\Delta hflK$, and $\Delta hflC$. MG1655 <i>strepR</i> , $\Delta qmcA$, $\Delta yqiJK::Spec$, $\Delta hflKC::Cmfrt$	Strep ^R , Spec ^R	This study
$\Delta clsA$	P1 vir transduction from BW25113 $\Delta clsA::Kmfrt$ into MG1655 <i>strep</i>	Strep ^R	This study
$\Delta clsB$	P1 vir transduction from BW25113 $\Delta clsB::Kmfrt$ into MG1655 <i>strep</i>	Strep ^R	This study
$\Delta clsC$	P1 vir transduction from BW25113 $\Delta clsC::Kmfrt$ into MG1655 <i>strep</i>	Strep ^R	This study

$\Delta clsAB$	Double mutant of $\Delta clsA$ and $\Delta clsB$. P1 vir transduction from BW25113 $\Delta clsA$::Kmfrt into $\Delta clsB$	Strep ^R	This study
$\Delta clsABC$	Triple mutant of $\Delta clsA$, $\Delta clsB$, and $\Delta clsC$. P1 vir transduction from BW25113 $\Delta clsC$::Kmfrt into $\Delta clsAB$	Strep ^R	This study
Δidi	P1 vir transduction from BW25113 Δidi ::Kmfrt into MG1655 <i>strep</i>	Strep ^R	This study
$\Delta acrA$	P1 vir transduction from BW25113 $\Delta acrA$::Kmfrt into MG1655 <i>strep</i>	Strep ^R	This study
$\Delta qmcA::zeo$	MG1655 <i>strep</i> , $\Delta qmcA::zeo$	Strep ^R , Zeo ^R	This study
$yqiK-gfp$	MG1655 <i>strep</i> , $yqiK::gfp$ Kmfrt	Strep ^R , Km ^R	This study
$qmcA-gfp$	MG1655 <i>strep</i> , $qmcA::gfp$ Kmfrt	Strep ^R , Km ^R	This study
$hflK-mCherry$	MG1655 <i>strep</i> , $hflK::mCherry$ Kmfrt	Strep ^R , Km ^R	This study
$hflC-mCherry$	MG1655 <i>strep</i> , $hflC::mCherry$ Kmfrt	Strep ^R , Km ^R	This study
$TM^{qmcA}-SPFH^{qmcA}-gfp$	MG1655 <i>strep</i> , $\Delta qmcA::TM^{qmcA}-SPFH^{qmcA}-gfp$ Kmfrt	Strep ^R , Km ^R	This study
$TM^{qmcA}-gfp$	MG1655 <i>strep</i> , $\Delta qmcA::TM^{qmcA}-gfp$ Kmfrt	Strep ^R , Km ^R	This study
$TM^{P\beta}-qmcA-gfp$	MG1655 <i>strep</i> , $\Delta qmcA::TM^{P\beta}-qmcA-gfp$ Kmfrt	Strep ^R , Km ^R	This study
$TM^{P\beta}-SPFH^{qmcA}-gfp$	MG1655 <i>strep</i> , $\Delta qmcA::TM^{P\beta}-SPFH^{qmcA}-gfp$ Kmfrt	Strep ^R , Km ^R	This study
$TM^{P\beta}-gfp$	MG1655 <i>strep</i> , $\Delta qmcA::TM^{P\beta}-gfp$ Kmfrt	Strep ^R , Km ^R	This study
$TM^{hflC}-SPFH^{hflC}-mCherry$	MG1655 <i>strep</i> , $\Delta hflC::TM^{hflC}-SPFH^{hflC}-mCherry$ Cmfrt	Strep ^R , Cm ^R	This study
$TM^{hflC}-mCherry$	MG1655 <i>strep</i> , $\Delta hflC::TM^{hflC}-mCherry$ Kmfrt	Strep ^R , Km ^R	This study
$TM^{cmi}-hflC-mCherry$	MG1655 <i>strep</i> , $\Delta hflC::TM^{cmi}-hflC-mCherry$ Cmfret	Strep ^R , Cm ^R	This study
$TM^{cmi}-SPFH^{hflC}-mCherry$	MG1655 <i>strep</i> , $\Delta hflC::TM^{cmi}-SPFH^{hflC}-mCherry$ Cmfret	Strep ^R , Cm ^R	This study
$TM^{cmi}-mCherry$	MG1655 <i>strep</i> , $\Delta hflC::TM^{cmi}-mCherry$ Cmfret	Strep ^R , Cm ^R	This study

$\Delta clsABC\ qmcA-gfp$	P1 vir transduction from <i>qmcA-gfp</i> into $\Delta clsABC$	Strep ^R , Km ^R	This study
$\Delta idi\ qmcA-gfp$	P1 vir transduction from <i>qmcA-gfp</i> into Δidi	Strep ^R , Km ^R	This study
$\Delta clsABC\ hflC-mCherry$	P1 vir transduction from <i>hflC-mCherry</i> into $\Delta clsABC$	Strep ^R , Km ^R	This study
$\Delta idi\ hflC-mCherry$	P1 vir transduction from <i>hflC-mCherry</i> into Δidi	Strep ^R , Km ^R	This study
<i>acrA-gfp</i>	MG1655 <i>strep</i> , <i>acrA::gfp</i> Kmfrt	Strep ^R , Km ^R	This study
Plasmids			
pKOBEG	<i>oriR101ts araC</i> arabinose-inducible λ red $\gamma\beta\alpha$ operon	Cm ^R	(7)
pKOBEGA	pKOBEG derivative	Amp ^R	(7)
pCP20	Rep(Ts) Flp ⁺	Cm ^R , Amp ^R	(8)
pUC18	High-copy-number, lac promoter cloning vector, ampicillin resistant (AmpR)	Amp ^R	(9)
pZS*12	Tightly regulated PLtetO-1 Low copy-number vector ampicillin resistant (AmpR)	Amp ^R	(10)
pUC18 <i>yqiK-gfp-aphAIII</i>	Assembly of <i>YqiK-mCherry-aphAIII</i> into pUC18	Amp ^R , Km ^R	This study
pUC18TM ^{QmcA} - <i>QmcA-gfp-aphAIII</i>	Assembly of TM ^{QmcA} - <i>QmcA-gfp-aphAIII</i> into pUC18	Amp ^R , Km ^R	This study
pZS*12TM ^{pβ} - <i>gfp</i>	Assembly of TM ^{pβ} - <i>gfp</i> into pZS*12	Amp ^R	This study
pZS*12TM ^{pβ} - <i>gfp-aphAIII</i>	Assembly of <i>aphAIII</i> into PZ*12TM ^{pβ} - <i>gfp</i>	Amp ^R , Km ^R	This study
pZS*12TM ^{pβ} - <i>QmcA-gfp-aphAIII</i>	Assembly of <i>qmcA</i> into PZ*12TM ^{pβ} - <i>gfp-aphAIII</i>	Amp ^R , Km ^R	This study
pZS*12 TM ^{pβ} -SPFH ^{QmcA} - <i>gfp-aphAIII</i>	Assembly of SPFH ^{QmcA} into PZ*12TM ^{pβ} - <i>gfp-aphAIII</i>	Amp ^R , Km ^R	This study
pUC18TM ^{HflC} - <i>HflC-mCherry-aphAIII</i>	Assembly of TM ^{HflC} - <i>HflC-mCherry-aphAIII</i> into pUC18	Amp ^R , Km ^R	This study
pZS*12TM ^{cmi} - <i>mCherry</i>	Assembly of <i>cmi-mCherry</i> into pZS*12	Amp ^R	This study
pZS*12TM ^{cmi} - <i>mCherry-cat</i>	Assembly of <i>Cmfrt</i> into PZ*12 <i>cmi-mCherry</i>	Amp ^R , Cm ^R	This study

pZS*12TM ^{cmi} - <i>hflC</i> -mCherry-cat	Assembly of <i>hflC</i> into PZ*12 <i>cmi-mCherry-Cmfrt</i>	Amp ^R , Cm ^R	This study
pZS*12TM ^{cmi} -SPFH ^{HflC} -mCherry-cat	Assembly of SPFH ^{HflC} into PZ*12 <i>cmi-mCherry-Cmfrt</i>	Amp ^R , Cm ^R	This study
pZS*12-H <i>flKC</i>	Assembly of <i>hflKC</i> into pZS*12	Amp ^R	This study

REFERENCES

1. Baba T, Ara T, Hasegawa M, Takai Y, Okumura Y, Baba M, Datsenko KA, Tomita M, Wanner BL, Mori H. 2006. Construction of Escherichia coli K-12 in-frame, single-gene knockout mutants: the Keio collection. *Molecular systems biology* 2:2006.0008. <https://doi.org/10.1038/msb4100050>
2. Ferrières L, Hémery G, Nham T, Guérout AM, Mazel D, Beloin C, Ghigo JM. 2010. Silent mischief: bacteriophage Mu insertions contaminate products of Escherichia coli random mutagenesis performed using suicidal transposon delivery plasmids mobilized by broad-host-range RP4 conjugative machinery. *Journal of bacteriology* 192: 6418–6427. <https://doi.org/10.1128/JB.00621-10>
3. Beloin C, Valle J, Latour-Lambert P, Faure P, Kzreminski M, Balestrino D, Haagensen JA, Molin S, Prensier G, Arbeille B, Ghigo JM. 2004. Global impact of mature biofilm lifestyle on Escherichia coli K-12 gene expression. *Molecular microbiology* 51:659–674. <https://doi.org/10.1046/j.1365-2958.2003.03865.x>
4. Korea CG, Badouraly R, Prevost MC, Ghigo JM, Beloin C. 2010. *Escherichia coli* K-12 possesses multiple cryptic but functional chaperone-usher fimbriae with distinct surface specificities. *Environmental microbiology* 12:1957–1977. <https://doi.org/10.1111/j.1462-2920.2010.02202.x>
5. Létoffé S, Audrain B, Bernier SP, Delepine M, Ghigo JM. 2014. Aerial exposure to the bacterial volatile compound trimethylamine modifies antibiotic resistance of physically separated bacteria by raising culture medium pH. *mBio* 5:e00944-00913.10.1128/mBio.00944-13: 10.1128/mBio.00944-13
6. Larsonneur F, Martin FA, Mallet A, Martinez-Gil M, Semetey V, Ghigo JM, Beloin C. 2016. Functional analysis of *Escherichia coli* Yad fimbriae reveals their potential role in environmental persistence. *Environmental microbiology* 18:5228-5248. doi: 10.1111/1462-2920.13559. Epub 2016 Oct 24. PMID: 27696649.
7. Chaveroche MK, Ghigo JM, d'Enfert C. 2000. A rapid method for efficient gene replacement in the filamentous fungus Aspergillus nidulans. *Nucleic acids research* 28: E97. <https://doi.org/10.1093/nar/28.22.e97>
8. Cherepanov PP, Wackernagel W. 1995. Gene disruption in Escherichia coli: TcR and KmR cassettes with the option of Flp-catalyzed excision of the antibiotic-resistance determinant. *Gene* 158:9–14. [https://doi.org/10.1016/0378-1119\(95\)00193-a](https://doi.org/10.1016/0378-1119(95)00193-a)
9. Norrander J, Kempe T, Messing J. 1983. Construction of improved M13 vectors using oligodeoxynucleotide-directed mutagenesis. *Gene*. 26:101-6. doi: 10.1016/0378-1119(83)90040-9.

10. **Lutz R, Bujard H.** 1997. Independent and tight regulation of transcriptional units in *Escherichia coli* via the LacR/O, the TetR/O and AraC/I1-I2 regulatory elements. Nucleic Acids Res **25**:1203-1210.10.1093/nar/25.6.1203: 10.1093/nar/25.6.1203

Supplementary Table S3. Primers used for generating chromosomal mutants or assembling plasmids in this study

Purpose	Name	Sequence (5'-3')
For amplifying the DNA fragment to generate $\Delta hflKC$ strain	Up. $\Delta hflKC$ -CmFRT-5	gacaacaggataccgcataacaatatggagcacaacgttaggctggagctcgaa g
	Down. $\Delta hflKC$ -CmFRT-3	ggatcggtggcttattgaccgtaccgcagtcgtatacatatgaatatcccttagttc
For amplifying the DNA fragment to generate $\Delta yqiJK$ strain	Up. $\Delta yqiJK$ -Spec-5	caaagtaaatattgcgtactaaatggacattggagtatgcgtcaattgcgccgaaataac
	Down. $\Delta yqiJK$ -Spec-3	ccccggctttggccaggatttcctgaaagagggtcattggctggcaccagcgttt
For amplifying the DNA fragment to generate $\Delta qmcA::zeo$ strain	Up. $\Delta qmcA$ -Zeo-5	caatttgctgattatggacggtaacaggaggtttccgtctggatccgagcacgtgtgac
	Down. $\Delta qmcA$ -Zeo-3	gactgagccagaaaatgtggatgaacgaccattaactccatctcagtcctgcctcgccac g
For assembling the pUC18yqiK-gfp- <i>aphAIII</i> plasmid	Up.GFP_pUC18yqiK-gfp-5	caccctaacctcaacaactccgtcgaagaaaaagcagaggcggcggcggcagcatgag taaagtgaagaaac
	Down.GFP_pUC18yqiK-gfp-3	caaaatcttcgtcgatttttagatccatccatg
	Up.KmFRT_pUC18yqiK-gfp-5	cgacagaaagatttggagcaaattgtgttaggc
	Down.KmFRT_pUC18yqiK-gfp-3	ccccggctttggccaggatttcctgaaagagggtcagggttactcatatgaatatc
	Up.linearized pUC18_pUC18yqiK-gfp-5	gcccaaaaagccggggaaattcgtaatcatggcatag
	Down.linearized pUC18_pUC18yqiK-gfp-5	gtttaggttaagggtggatcccttagactcgacctg
For amplifying the DNA fragment to generate YqiK-GFP strain	Up.yqiK_YqiK-GFP-KmFRT-5	Same as Up.GFP_pUC18yqiK-gfp-5
	Down.KmFRT_YqiK-GFP-KmFRT-3	Same as Down.KmFRT_pUC18yqiK-gfp-3
For assembling the pUC18TM ^{QmcA} - <i>QmcA-gfp-aphAIII</i> plasmid	Up.qmcA-gfp_pUC18qmcA-gfp-5	ccgagctggtaaagacgcgccaacaacggactcagccaggcggcggcggcagcatga gtaaaggtaagaactgttc
	Down.qmcA-gfp_pUC18qmcA-gfp-3	ggctgagtccgttgtggcttattgttagatccatgcgtgatccatgt
	Up.ybbJ_pUC18qmcA-gfp-5	cagcaggtatcacgcacggcatggatgaactctacaataagccaacaacggactcagcc
	Down.ybbJ_pUC18qmcA-gfp-3	caaaatcttcgtcgtaagacgagacggctggatatg
	Up.KmFRT_pUC18qmcA-gfp-5	cgacagaaagatttggagcaaattgtgttaggc

	Down.KmFRT_pUC18qmcA-gfp-3	gaaaatctccggctgtcatcatggcagggtgatcagggttactcataatatc
	Up.linearized pUC18_pUC18qmcA-gfp-5	cagccggagagatttcgaattcgatatggtcatag
	Down.linearized pUC18_pUC18qmcA-gfp-5	cttcaccagctccccatcttagatcgacactg
For amplifying the DNA fragment to generate TM ^{qmcA} -QmcA-GFP strain	Up.qmcA_QmcA-GFP-KmFRT-5	Same as Up.qmcA-gfp_pUC18qmcA-gfp-5
	Down.KmFRT_QmcA-GFP-KmFRT-3	Down.KmFRT_pUC18qmcA-gfp-3
For amplifying the DNA fragment to generate TM ^{qmcA} -SPFH ^{qmcA} -GFP strain	UP.SPFHqmcA_SPFHqmcA-GFP-KmFRT-5	gcggaaggatccgtcaggcggaaatctcaagccgaaggtaattacaacaacatgataaagg
	Down.KmFRT_SPFHqmcA-GFP-KmFRT-3	gaaaatctccggctgtcatcatggcagggtgatcagggttactcatatgaatatc
For amplifying the DNA fragment to generate TM ^{qmcA} -GFP strain	Up.TMqmcA_TMqmcA-GFP-KmFRT-5	ctcttttgtcgccgtggcattgtcgccgggtcaaaatctagaattacaacaacatgatgaaagg
	Down.KmFRT_TMqmcA-GFP-KmFRT-3	Same sequence as Down.KmFRT_SPFHqmcA-GFP-KmFRT-3
For assembling the pZS*12TM ^{pβ} -gfp plasmid	Up.pf3-GFP_pZS*12pf3-gfp-5	gtgagcggataacaagatacatcaatccgtattactg
	Down.pf3-GFP_pZS*12pf3-gfp-3	ctttaactcatgttgtttaattcaaagaatttg
	Up.GFP_pZS*12pf3-gfp-5	taacaacaacatgagtaaaggtaagaac
	Down.GFP_pZS*12pf3-gfp-3	tctagactcagctaattaagtcatgttagttcatcc
	Up.linearized pZS*12 pZS*12pf3-gfp-5	ctacaatgacttaattagctgagcttagag
	Down.linearized pZS*12pZS*12pf3-gfp-3	cggattgcatttatgttatccgctc
For assembling the pZS*12TM ^{pβ} -gfp-aphAIII plasmid	Up.KmFRT_pZS*12pf3-gfp-KmFRT-5	cgaaaggctcagtcgaacgacagaaagatttggag
	Down.KmFRT_pZS*12pf3-gfp-KmFRT-3	cgaaaggcccagtcattcagggttactcatatgaatatcc
	Up. linearized pZS*12_pZS*12pf3-gfp-KmFRT-5	ggatattcatatgagtaaaccctgaagactggcccttcg
	Down. linearized pZS*12_pZS*12pf3-gfp-KmFRT-3	ctttctgtcgactgagcccttcgtttatgttgc
For assembling the pZS*12TM ^{pβ} -qmcA-gfp-aphAIII plasmid	Up. qmcA_pZS*12pf3-qmcA-gfp-KmFRT-5	tggatcaaaggcgaattttatcgatccgcaggctatc
	Down. qmcA_pZS*12pf3-qmcA-gfp-KmFRT-3	actcatgtgtgttaattctggctgatcgatccgtttggc

	Up. linearized pZS*12_pZS*12pf3-gfp-Kmfrt-5	ggatattcatatgagtaaacccctgaagactggcccttcg
	Down. linearized pZS*12_pZS*12pf3-gfp-Kmfrt-3	ggtagataagaattgcgcgttgatcc
For assembling the pZS*12TM ^{Pf3} -SPFH ^{QmcA} -gfp-aphAIII plasmid	Up. SPFHqmcA_pZS*12pf3-SPFHqmcA-gfp-KmFRT-5	Same as Up. qmcA_pZS*12pf3-qmcA-gfp-KmFRT-5
	Down. SPFHqmcA_pZS*12pf3-SPFHqmcA-gfp-KmFRT-3	actcatgttgtttaattcacccggcttgaggattcc
	Up. Linearised pZS*12_pZS*12pf3-SPFHqmcA-gfp-KmFRT-5	caaagecgaaggtaattacaacaacatgagtaaagg
	Down. Linearised pZS*12_pZS*12pf3-SPFHqmcA-gfp-KmFRT-3	Same as Down. linearized pZS*12_pZS*12pf3-gfp-Kmfrt-3
For amplifying the DNA fragments to generate TM ^{Pf3} -QmcA-GFP, TM ^{Pf3} -SPFH ^{QmcA} -GFP, and TM ^{Pf3} -GFP strains	Up.Pf3_pf3-(QmcA)-GFP-KmFRT-5	caattttgctgattatggacggtacaacaggaggtttccgatgcaatccgttattactgatg
	Down.KmFRT_pf3-(QmcA)-GFP-KmFRT-3	Same sequence as Down.KmFRT_SPFHqmcA-GFP-KmFRT-3
For assembling the pUC18TM ^{HflC} -HflC-mCherry-aphAIII plasmid	Up.hflC-mCherry_pUC18hflC-mCherry-KmFRT-5	gattttccgcgtacatgaagacggactccgcaacgcgtggccggccggcagcatggtt ccaaggcgaggag
	Down. hflC-mCherry_pUC18hflC-mCherry-KmFRT-3	caaaatcttctgtgttattgtacagtcattccatg
	Up.KmFRT_pUC18hflC-mCherry-KmFRT-5	cgacagaaagattttggagcaaatgtgtgttaggc
	Down.KmFRT_pUC18hflC-mCherry-KmFRT-3	gaggatcggtggcttattgacctgtaccgcagtcgttatcagggttactcatatgaatatc
	Up.linearized pUC18_pUC18hflC-mCherry-KmFRT-5	caataaagccaccgcattctgaattcgtaatcatggcatag
	Down.linearized pUC18_pUC18hflC-mCherry-KmFRT-3	catgtcgaaagaaatcggtacccttagactcgacactg
For amplifying the DNA fragment to generate TM ^{HflC} -HflC-mCherry strain	Up.hflC_HflC-mCherry-KmFRT-5	Same as Up.hflC-mCherry_pUC18hflC-mCherry-5
	Down.KmFRT_HflC-mCherry-KmFRT-3	gaggatcggtggcttattgacctgtaccgcagtcgttatcagggttactcatatgaatatc
For amplifying the DNA fragment to generate TM ^{HflC} -SPFH ^{HflC} -mCherry strain	Up.SPFHhflC_SPFHhflC-mCherry-CmFRT-5	gagcgtgaaggcgtagcgcgtcgtaccgtcacaaggcaggaattacaacaacatggtt ccaagg
	Down.CmFRT_SPFHhflC-mCherry-CmFRT-3	ggatcggtggcttattgacctgtaccgcagtcgttatcataatcctccttagttccatttc
For amplifying the DNA fragment to generate TM ^{HflC} -mCherry strain	Up.TMhflC_TMhflC-mCherry-KmFRT-5	catcgctggtagtgcattacatgtctgttgcgtccggccggccggcagcatg
	Down.KmFRT_TMhflC-mCherry-KmFRT-3	gaggatcggtggcttattgacctgtaccgcagtcgttatcagggttactcatatgaatatc
	Up.cmi-pZS*12cmi-mcherry-5	gaaaggattccatgaaagtgatttagcatgaaattttttatc

For assembling the pZS*12 <i>TM^{cmi}-mCherry</i> plasmid	Down.cmi-pZS*12cmi-mCherry-3	tggaaaccatgttgtttaattcgcc
	Up.mCherry_pZS*12cmi-mCherry-5	taacaacaacatggttccaaggcgag
	Down.mCherry_pZS*12cmi-mCherry-3	ctaattaagcttattgtacagctcatccatgc
	Up.linearized pZS*12_pZS12cmi-mCherry-5	gtacaataagcttaatttagtcgacttagagg
	Down.linearized pZS*12_pZS12cmi-mCherry-3	tcactttcatggtaccttctccctttaatg
For assembling the pZS*12 <i>TM^{cmi}-mCherry-cat</i> plasmid	Up.CmFRT_pZS*12cmi-mCherry-CmFRT-5	gctcagtcgagtctaggctggagctgcctc
	Down. CmFRT _pZS*12cmi-mCherry-CmFRT-5	gcccaagtcgttcatatgaatatcctcttagtcctattcc
	Up.linearized pZS*12_ pZS*12cmi-mCherry-CmFRT-5	tattcatatgaagactggcccttcgtttatc
	Down.linearized pZS*12_ pZS*12cmi-mCherry-CmFRT-3	cagcctacactcgactgagcttcgtttatcg
For assembling the pZS*12 <i>TM^{cmi}-hflC-mCherry-cat</i> plasmid	Up.hflC_ pZS*12cmi-mCherry-CmFRT-5	agataaaggcgctgtcaaagaagggtgagcgc
	Down.hflC_ pZS*12cmi-mCherry-CmFRT-3	tgttaattcacgcgttgccggaaagtgg
	Up.linearized pZS*12_ pZS*12cmi-hflC-mCherry-CmFRT-5	cgcaacgcgtgaatttaacaacaacatggttcc
	Down.linearized pZS*12_ pZS*12cmi-hflC-mCherry-CmFRT-3	cttgacgacgccttatctcgctccaaaaaac
For assembling the pZS*12 <i>TM^{cmi}-SPFH^{HflC}-mCherry-cat</i> plasmid	Up. SPFHhflC_ pZS*12cmi-SPFHhflC-mCherry-CmFRT-5	Same as Up.hflC_ pZS*12cmi-mCherry-CmFRT-5
	Down. SPFHhflC_ pZS*12cmi-SPFHhflC-mCherry-CmFRT-3	tgttaattcctgaccctgtgaacgggt
	Up.linearized pZS*12_ pZS*12cmi-SPFHhflC-mCherry-CmFRT-5	acaaggctcggaaatttaacaacaacatggttcc
	Down.linearized pZS*12_ pZS*12cmi-SPFHhflC-mCherry-CmFRT-5	Same as Down.linearized pZS*12_ pZS*12cmi-hflC-mCherry-CmFRT-3
For amplifying the DNA fragments to generate <i>TM^{cmi}-HflC-mCherry</i> , <i>TM^{cmi}-SPFH^{HflC}-mCherry</i> , <i>TM^{cmi}-mCherry</i>	Up.cmi_cmi-(HflC)-mCherry-CmFRT-5	ccaacgcgcagcgtaacgactaccagcgctaggggataacgatgaaagtgattagcatga a
	Down.CmFRT_cmi-(HflC)-mCherry-CmFRT-3	ggatgcggtggtttattgacctgtaccgcagtcgttatacatatgaatatcctcttag
For amplifying the DNA fragment to generate AcrA-GFP strain	Up.acrA_AcrA-GFP-KmFRT-5	ccagcaagccgcaagcggtgctcagctgaacagtctgaatttaacaacaacatgag taaagggtgaaagac
	Down.KmFRT_AcrA-GFP-KmFRT-3	cgggcgatcgataaagaattaggcatgtttaacggctctgttaagtcaagggttactcatat gaatatcctcc

For assembling the pZS12* <i>hflKC</i> plasmid	Up.hflKC_pZS*12-HflKC-5	cattaaagaggagaaggtaccatggcgtggaatcagcccgtaataacgg
	Down.hflKC_pZS*12-HflKC -3	gatgcctctagactcagctaattaagctttaacgcgttgccaagtccgcg
	Up.linearized pZS*12_pZS*12 -5	aagcttaatttagctgagtctag
	Down.linearized pZS*12_pZS*12-3	ggtaccttctccctttaatgaattcgg

PM1 MicroPlate™ Carbon Sources

A1 Negative Control	A2 L-Arabinose	A3 N-Acetyl-D-Glucosamine	A4 D-Saccharic Acid	A5 Succinic Acid	A6 D-Galactose	A7 L-Aspartic Acid	A8 L-Proline	A9 D-Alanine	A10 D-Trehalose	A11 D-Mannose	A12 Dulcitol
B1 D-Serine	B2 D-Sorbitol	B3 Glycerol	B4 L-Fucose	B5 D-Glucuronic Acid	B6 D-Gluconic Acid	B7 D,L- α -Glycerol-Phosphate	B8 D-Xylose	B9 L-Lactic Acid	B10 Formic Acid	B11 D-Mannitol	B12 L-Glutamic Acid
C1 D-Glucose-6-Phosphate	C2 D-Galactonic Acid- γ -Lactone	C3 D,L-Malic Acid	C4 D-Ribose	C5 Tween 20	C6 L-Rhamnose	C7 D-Fructose	C8 Acetic Acid	C9 α -D-Glucose	C10 Maltose	C11 D-Melibiose	C12 Thymidine
D-1 L-Asparagine	D2 D-Aspartic Acid	D3 D-Glucosaminic Acid	D4 1,2-Propanediol	D5 Tween 40	D6 α -Keto-Glutamic Acid	D7 α -Keto-Butyric Acid	D8 α -Methyl-D-Galactoside	D9 α -D-Lactose	D10 Lactulose	D11 Sucrose	D12 Uridine
E1 L-Glutamine	E2 M-Tartaric Acid	E3 D-Glucose-1-Phosphate	E4 D-Fructose-6-Phosphate	E5 Tween 80	E6 α -Hydroxy Glutaric Acid- γ -Lactone	E7 α -Hydroxy Butyric Acid	E8 β -Methyl-D-Glucoside	E9 Adonitol	E10 Maltotriose	E11 2-Deoxy Adenosine	E12 Adenosine
F1 Glycyl-L-Aspartic Acid	F2 Cltric Acid	F3 M-Inositol	F4 D-Threonine	F5 Fumaric Acid	F6 Bromo Succinic Acid	F7 Propionic Acid	F8 Mucic Acid	F9 Glycolic Acid	F10 Glyoxylic Acid	F11 D-Cellobiose	F12 Inosine
G1 Glycyl-L-Glutamic Acid	G2 Tricarballylic Acid	G3 L-Serine	G4 L-Threonine	G5 L-Alanine	G6 L-Alanyl-Glycine	G7 Acetoacetic Acid	G8 N-Acetyl- β -D-Mannosamine	G9 Mono Methyl Succinate	G10 Methyl Pyruvate	G11 D-Malic Acid	G12 L-Malic Acid
H1 Glycyl-L-Proline	H2 p-Hydroxy Phenyl Acetic Acid	H3 m-Hydroxy Phenyl Acetic Acid	H4 Tyramine	H5 D-Psicose	H6 L-Lyxose	H7 Glucuronamide	H8 Pyruvic Acid	H9 L-Galactonic Acid- γ -Lactone	H10 D-Galacturonic Acid	H11 Phenylethylamine	H12 2-Aminoethanol

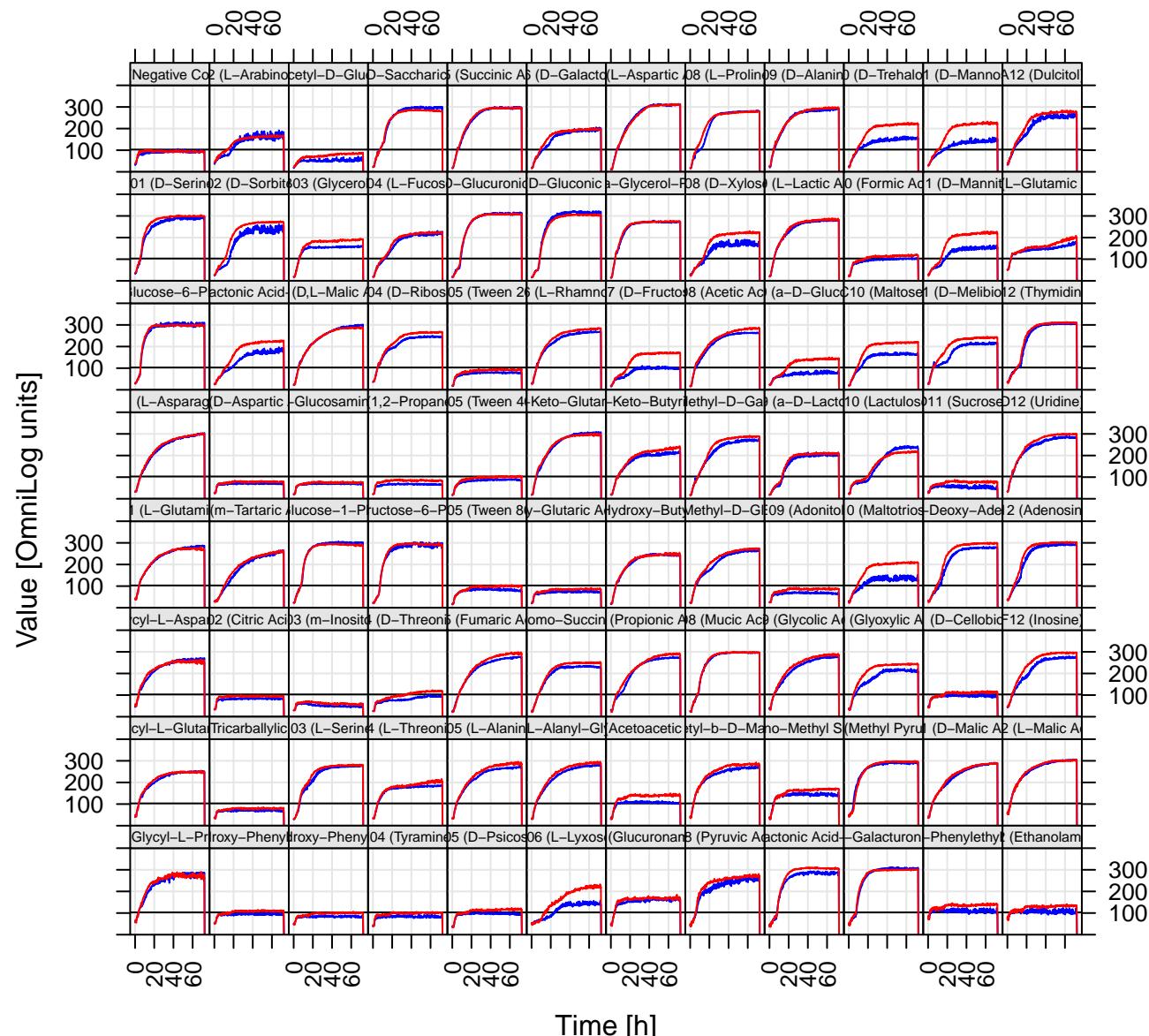
PM2A MicroPlate™ Carbon Sources

A1 Negative Control	A2 Chondroitin Sulfate C	A3 α -Cyclodextrin	A4 β -Cyclodextrin	A5 γ -Cyclodextrin	A6 Dextrin	A7 Gelatin	A8 Glycogen	A9 Inulin	A10 Laminarin	A11 Mannan	A12 Pectin
B1 N-Acetyl-D-Galactosamine	B2 N-Acetyl-Neuraminic Acid	B3 β -D-Allose	B4 Amygdalin	B5 D-Arabinose	B6 D-Arabinol	B7 L-Arabinol	B8 Arbutin	B9 2-Deoxy-D-Ribose	B10 L-Erythritol	B11 D-Fucose	B12 3-O- β -D-Galactopyranosyl-D-Arabinose
C1 Gentibiose	C2 L-Glucose	C3 Lactitol	C4 D-Melezitose	C5 Maltitol	C6 α -Methyl-D-Glucoside	C7 β -Methyl-D-Galactoside	C8 3-Methyl Glucose	C9 β -Methyl-D-Glucuronic Acid	C10 α -Methyl-D-Mannoside	C11 β -Methyl-D-Xyloside	C12 Palatinose
D1 D-Raffinose	D2 Salicin	D3 Sedoheptulosa n	D4 L-Sorbose	D5 Stachyose	D6 D-Tagatose	D7 Turanose	D8 Xylitol	D9 N-Acetyl-D-Glucosaminitol	D10 γ -Amino Butyric Acid	D11 δ -Amino Valeric Acid	D12 Butyric Acid
E1 Capric Acid	E2 Caproic Acid	E3 Citraconic Acid	E4 Citramalic Acid	E5 D-Glucosamine	E6 2-Hydroxy Benzolic Acid	E7 4-Hydroxy Benzolic Acid	E8 β -Hydroxy Butyric Acid	E9 γ -Hydroxy Butyric Acid	E10 α -Keto Valeric Acid	E11 Itaconic Acid	E12 5-Keto-D-Gluconic Acid
F1 D-Lactic Acid Methyl Ester	F2 Malonic Acid	F3 Mellibionic Acid	F4 Oxalic Acid	F5 Oxalomalic Acid	F6 Quinic Acid	F7 D-Ribono-1,4-Lactone	F8 Sebacic Acid	F9 Sorbic Acid	F10 Succinamic Acid	F11 D-Tartaric Acid	F12 L-Tartaric Acid
G1 Acetamide	G2 L-Alaninamide	G3 N-Acetyl-L-Glutamic Acid	G4 L-Arginine	G5 Glycine	G6 L-Histidine	G7 L-Homoserine	G8 Hydroxy-L-Proline	G9 L-Isoleucine	G10 L-Leucine	G11 L-Lysine	G12 L-Methionine
H1 L-Ornithine	H2 L-Phenylalanine	H3 L-Pyroglutamic Acid	H4 L-Valline	H5 D,L-Carnitine	H6 Sec-Butylamine	H7 D,L-Octopamine	H8 Putrescine	H9 Dihydroxy Acetone	H10 2,3-Butanediol	H11 2,3-Butanone	H12 3-Hydroxy 2-Butanone

PM01 (Carbon Sources)

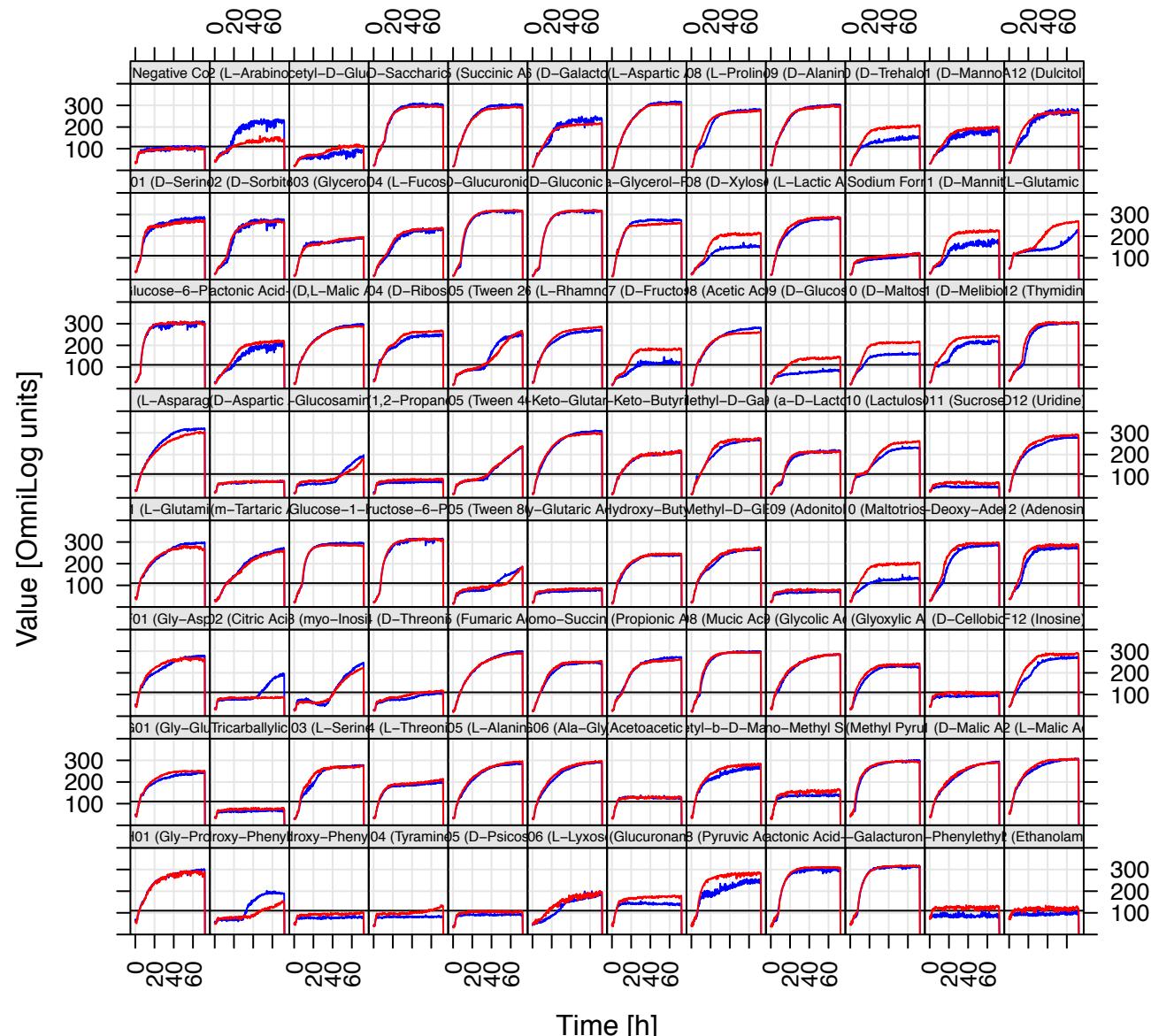
Δ SPFH-1

WT-1



PM01 (Carbon Sources)

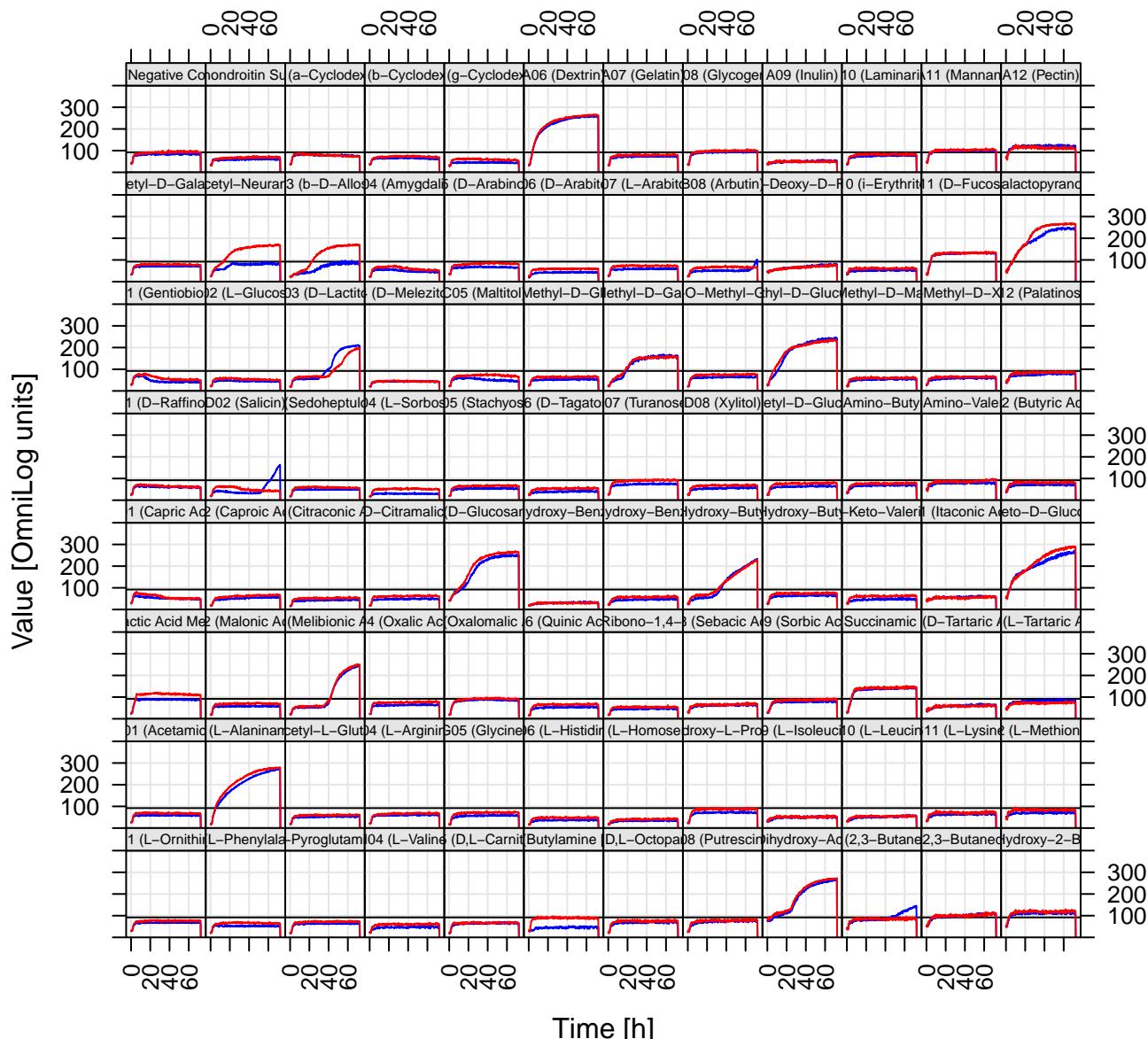
Δ SPFH-2
WT-2



PM02 (Carbon Sources)

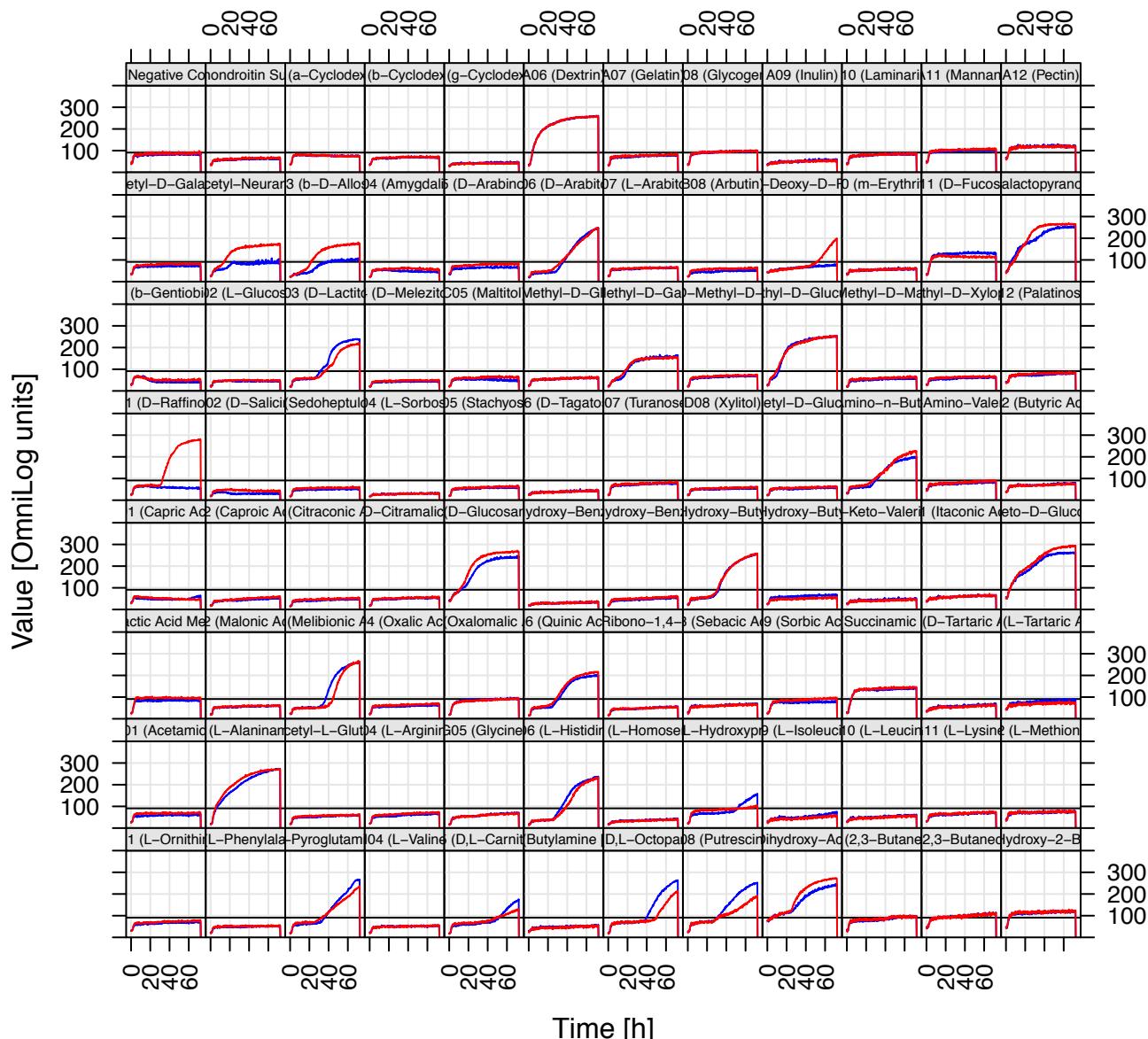
ΔSPFH-1

WT-1



PM02 (Carbon Sources)

Δ SPFH-2
WT-2



PM3B MicroPlate™ Nitrogen Sources

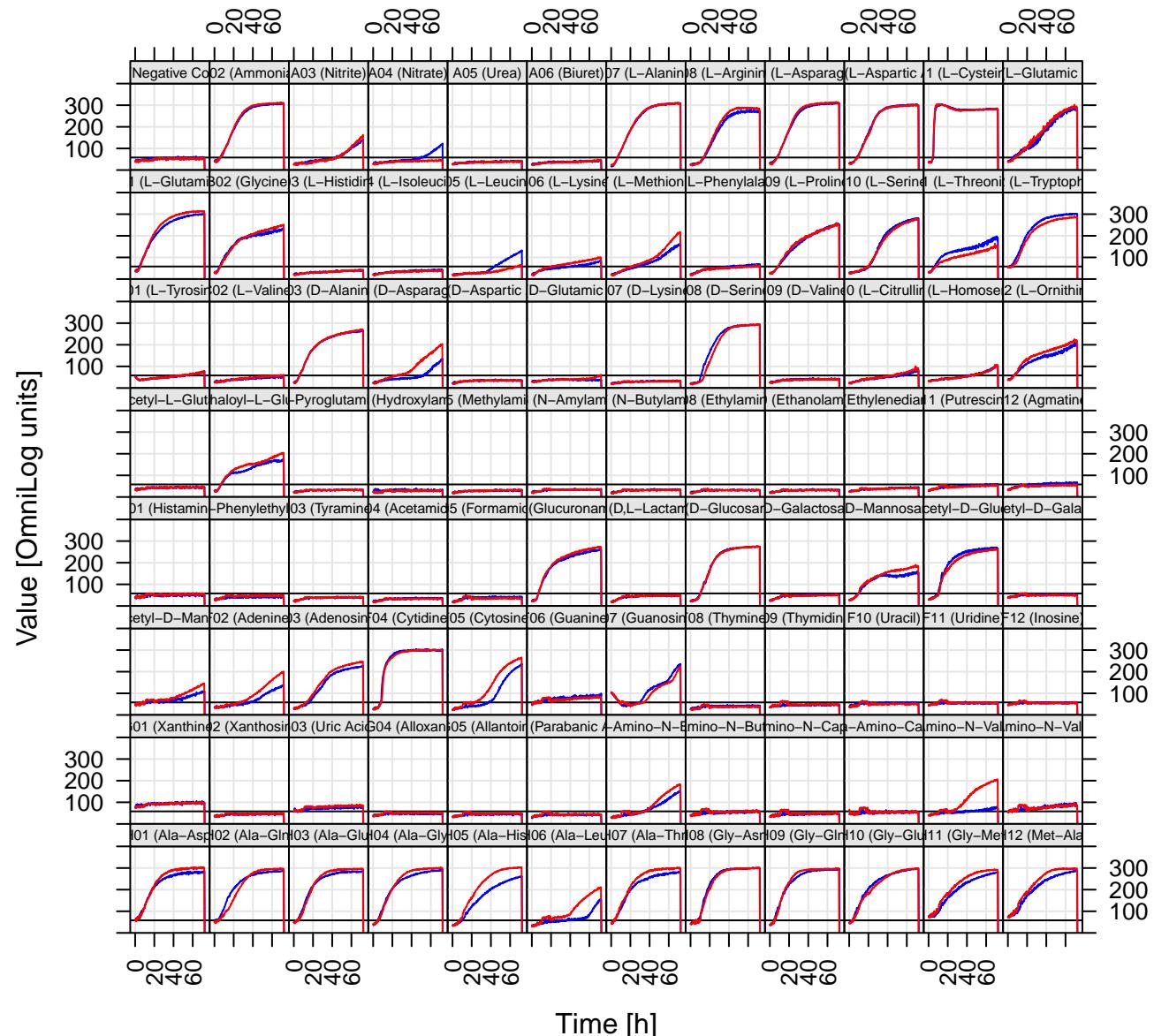
A1 Negative Control	A2 Ammonia	A3 Nitrite	A4 Nitrate	A5 Urea	A6 Bluret	A7 L-Alanine	A8 L-Arginine	A9 L-Asparagine	A10 L-Aspartic Acid	A11 L-Cysteine	A12 L-Glutamic Acid
B1 L-Glutamine	B2 Glycine	B3 L-Histidine	B4 L-Isoleucine	B5 L-Leucine	B6 L-Lysine	B7 L-Methionine	B8 L-Phenylalanine	B9 L-Proline	B10 L-Serine	B11 L-Threonine	B12 L-Tryptophan
C1 L-Tyrosine	C2 L-Valine	C3 D-Alanine	C4 D-Asparagine	C5 D-Aspartic Acid	C6 D-Glutamic Acid	C7 D-Lysine	C8 D-Serine	C9 D-Valine	C10 L-Citrulline	C11 L-Homoserine	C12 L-Ornithine
D-1 N-Acetyl-D,L- Glutamic Acid	D2 N-Pthaloyl-L- Glutamic Acid	D3 L-Pyroglutamic Acid	D4 Hydroxylamine	D5 Methylamine	D6 N-Amylamine	D7 N-Butylamine	D8 Ethylamine	D9 Ethanolamine	D10 Ethylenediamine	D11 Putrescine	D12 Agmatine
E1 Histamine	E2 β-Phenylethyl- amine	E3 Tyramine	E4 Acetamide	E5 Formamide	E6 Glucuronamide	E7 D,L-Lactamide	E8 D-Glucosamine	E9 D-Galactosamine	E10 D-Mannosamine	E11 N-Acetyl-D- Glucosamine	E12 N-Acetyl-D- Galactosamine
F1 N-Acetyl-D- Mannosamine	F2 Adenine	F3 Adenosine	F4 Cytidine	F5 Cytosine	F6 Guanine	F7 Guanosine	F8 Thymine	F9 Thymidine	F10 Uracil	F11 Uridine	F12 Inosine
G1 Xanthine	G2 Xanthosine	G3 Uric Acid	G4 Alloxan	G5 Allantoin	G6 Parabanic Acid	G7 D,L-α-Amino-N- Butyric Acid	G8 γ-Amino-N- Butyric Acid	G9 ε-Amino-N- Caprylic Acid	G10 D,L-α-Amino- Caprylic Acid	G11 δ-Amino-N- Valeric Acid	G12 α-Amino-N- Valeric Acid
H1 Ala-Asp	H2 Ala-Gln	H3 Ala-Glu	H4 Ala-Gly	H5 Ala-His	H6 Ala-Leu	H7 Ala-Thr	H8 Gly-Asn	H9 Gly-Gln	H10 Gly-Glu	H11 Gly-Met	H12 Met-Ala

PM4A MicroPlate™ Phosphorus and Sulfur Sources

A1 Negative Control	A2 Phosphate	A3 Pyrophosphate	A4 Trimeta- phosphate	A5 Tripoly- phosphate	A6 Triethyl Phosphate	A7 Hypophosphite	A8 Adenosine- 2'- monophosphate	A9 Adenosine- 3'- monophosphate	A10 Adenosine- 5'- monophosphate	A11 Adenosine- 2',3'-cyclic monophosphate	A12 Adenosine- 3',5'-cyclic monophosphate
B1 Thiophosphate	B2 Dithiophosphate	B3 D,L-α-Glycerol Phosphate	B4 β-Glycerol Phosphate	B5 Carbamyl Phosphate	B6 D-2-Phospho- Glyceric Acid	B7 D-3-Phospho- Glyceric Acid	B8 Guanosine- 2'- monophosphate	B9 Guanosine- 3'- monophosphate	B10 Guanosine- 5'- monophosphate	B11 Guanosine- 2',3'-cyclic monophosphate	B12 Guanosine- 3',5'-cyclic monophosphate
C1 Phosphoenol Pyruvate	C2 Phospho- Glycolic Acid	C3 D-Glucose-1- Phosphate	C4 D-Glucose-6- Phosphate	C5 2-Deoxy-D- Glucose 6- Phosphate	C6 D- Glucosamine-6- Phosphate	C7 6-Phospho- Gluconic Acid	C8 Cytidine- 2'- monophosphate	C9 Cytidine- 3'- monophosphate	C10 Cytidine- 5'- monophosphate	C11 Cytidine- 2',3'- cyclic monophosphate	C12 Cytidine- 3',5'- cyclic monophosphate
D1 D-Mannose-1- Phosphate	D2 D-Mannose-6- Phosphate	D3 Cysteamine-S- Phosphate	D4 Phospho-L- Arginine	D5 O-Phospho-D- Serine	D6 O-Phospho-L- Serine	D7 O-Phospho-L- Threonine	D8 Uridine- 2'- monophosphate	D9 Uridine- 3'- monophosphate	D10 Uridine- 5'- monophosphate	D11 Uridine- 2',3'- cyclic monophosphate	D12 Uridine- 3',5'- cyclic monophosphate
E1 O-Phospho-D- Tyrosine	E2 O-Phospho-L- Tyrosine	E3 Phosphocreatin e	E4 Phosphoryl Choline	E5 O-Phosphoryl- Ethanolamine	E6 Phosphono Acetic Acid	E7 2-Aminoethyl Phosphonic Acid	E8 Methylene Diphosphonic Acid	E9 Thymidine- 3'- monophosphate	E10 Thymidine- 5'- monophosphate	E11 Inositol Hexaphosphate	E12 Thymidine 3',5'-cyclic monophosphate
F1 Negative Control	F2 Sulfate	F3 Thiosulfate	F4 Tetrathionate	F5 Thiophosphate	F6 Dithiophosphate	F7 L-Cysteine	F8 D-Cysteine	F9 L-Cysteinyl- Glycine	F10 L-Cysteic Acid	F11 Cysteamine	F12 L-Cysteine Sulfenic Acid
G1 N-Acetyl-L- Cysteine	G2 S-Methyl-L- Cysteine	G3 Cystathione	G4 Lanthionine	G5 Glutathione	G6 D,L-Ethionine	G7 L-Methionine	G8 D-Methionine	G9 Glycyl-L- Methionine	G10 N-Acetyl-D,L- Methionine	G11 L- Methionine Sulfoxide	G12 L-Methionine Sulfone
H1 L-Djenkolic Acid	H2 Thiourea	H3 1-Thio-β-D- Glucose	H4 D,L-Lipoamide	H5 Taurocholic Acid	H6 Taurine	H7 Hypotaurine	H8 p-Amino Benzene Sulfonic Acid	H9 Butane Sulfonic Acid	H10 2-Hydroxyethane Sulfonic Acid	H11 Methane Sulfonic Acid	H12 Tetramethylene Sulfone

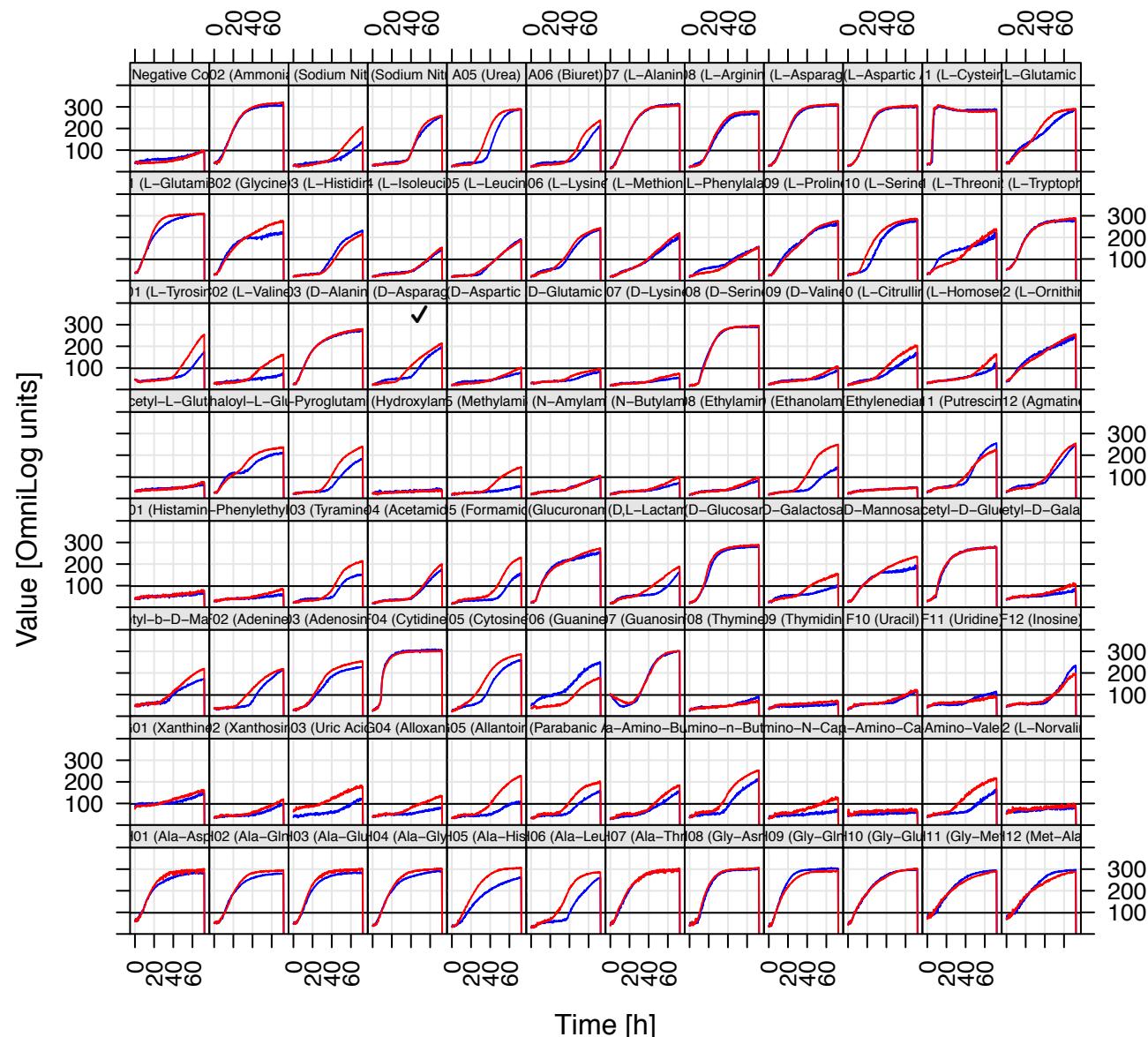
PM03 (Nitrogen Sources)

**ΔSPFH-1
WT-1**



PM03 (Nitrogen Sources)

Δ SPFH-2
WT-2





Phenotype MicroArrays™

PM9 MicroPlate™ Osmolytes

A1 NaCl 1%	A2 NaCl 2%	A3 NaCl 3%	A4 NaCl 4%	A5 NaCl 5%	A6 NaCl 5.5%	A7 NaCl 6%	A8 NaCl 6.5%	A9 NaCl 7%	A10 NaCl 8%	A11 NaCl 9%	A12 NaCl 10%
B1 NaCl 6%	B2 NaCl 6% + Betaine	B3 NaCl 6% + N-N Dimethyl glycine	B4 NaCl 6% + Sarcosine	B5 NaCl 6% + Dimethyl sulphonyl propionate	B6 NaCl 6% + MOPS	B7 NaCl 6% + Ectoine	B8 NaCl 6% + Choline	B9 NaCl 6% + Phosphoryl choline	B10 NaCl 6% + Creatine	B11 NaCl 6% + Creatinine	B12 NaCl 6% + L- Carnitine
C1 NaCl 6% + KCl	C2 NaCl 6% + L-proline	C3 NaCl 6% + N-Acetyl L-glutamine	C4 NaCl 6% + β-Glutamic acid	C5 NaCl 6% + γ-Amino -n- butyric acid	C6 NaCl 6% + Glutathione	C7 NaCl 6% + Glycerol	C8 NaCl 6% + Trehalose	C9 NaCl 6% + Trimethylamine -N-oxide	C10 NaCl 6% + Trimethylamine	C11 NaCl 6% + Octopine	C12 NaCl 6% + Trigonelline
D-1 Potassium chloride 3%	D2 Potassium chloride 4%	D3 Potassium chloride 5%	D4 Potassium chloride 6%	D5 Sodium sulfate 2%	D6 Sodium sulfate 3%	D7 Sodium sulfate 4%	D8 Sodium sulfate 5%	D9 Ethylene glycol 5%	D10 Ethylene glycol 10%	D11 Ethylene glycol 15%	D12 Ethylene glycol 20%
E1 Sodium formate 1%	E2 Sodium formate 2%	E3 Sodium formate 3%	E4 Sodium formate 4%	E5 Sodium formate 5%	E6 Sodium formate 6%	E7 Urea 2%	E8 Urea 3%	E9 Urea 4%	E10 Urea 5%	E11 Urea 6%	E12 Urea 7%
F1 Sodium Lactate 1%	F2 Sodium Lactate 2%	F3 Sodium Lactate 3%	F4 Sodium Lactate 4%	F5 Sodium Lactate 5%	F6 Sodium Lactate 6%	F7 Sodium Lactate 7%	F8 Sodium Lactate 8%	F9 Sodium Lactate 9%	F10 Sodium Lactate 10%	F11 Sodium Lactate 11%	F12 Sodium Lactate 12%
G1 Sodium Phosphate pH 7 20mM	G2 Sodium Phosphate pH 7 50mM	G3 Sodium Phosphate pH 7 100mM	G4 Sodium Phosphate pH 7 200mM	G5 Sodium Benzoate pH 5.2 20mM	G6 Sodium Benzoate pH 5.2 50mM	G7 Sodium Benzoate pH 5.2 100mM	G8 Sodium Benzoate pH 5.2 200mM	G9 Ammonium sulfate pH 8 10mM	G10 Ammonium sulfate pH 8 20mM	G11 Ammonium sulfate pH 8 50mM	G12 Ammonium sulfate pH 8 100mM
H1 Sodium Nitrate 10mM	H2 Sodium Nitrate 20mM	H3 Sodium Nitrate 40mM	H4 Sodium Nitrate 60mM	H5 Sodium Nitrate 80mM	H6 Sodium Nitrate 100mM	H7 Sodium Nitrite 10mM	H8 Sodium Nitrite 20mM	H9 Sodium Nitrite 40mM	H10 Sodium Nitrite 60mM	H11 Sodium Nitrite 80mM	H12 Sodium Nitrite 100mM

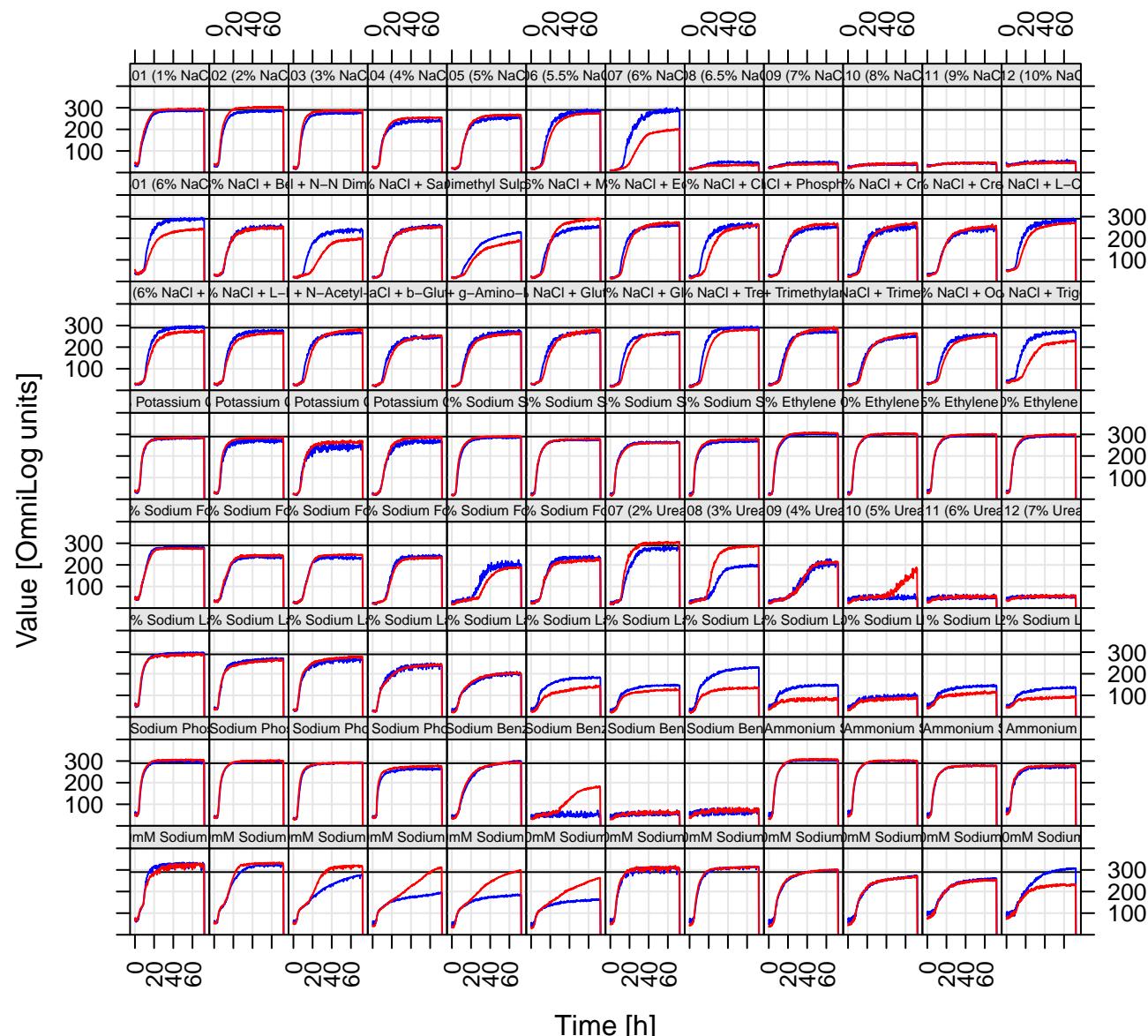
PM10 MicroPlate™ pH

A1 pH 3.5	A2 pH 4	A3 pH 4.5	A4 pH 5	A5 pH 5.5	A6 pH 6	A7 pH 7	A8 pH 8	A9 pH 8.5	A10 pH 9	A11 pH 9.5	A12 pH 10
B1 pH 4.5	B2 pH 4.5 + L-Alanine	B3 pH 4.5 + L-Arginine	B4 pH 4.5 + L-Asparagine	B5 pH 4.5 + L-Aspartic Acid	B6 pH 4.5 + L-Glutamic Acid	B7 pH 4.5 + L-Glutamine	B8 pH 4.5 + Glycine	B9 pH 4.5 + L-Histidine	B10 pH 4.5 + L-Isoleucine	B11 pH 4.5 + L-Leucine	B12 pH 4.5 + L-Lysine
C1 pH 4.5 + L-Methionine	C2 pH 4.5 + L- Phenylalanine	C3 pH 4.5 + L-Proline	C4 pH 4.5 + L-Serine	C5 pH 4.5 + L-Threonine	C6 pH 4.5 + L-Tryptophan	C7 pH 4.5 + L-Tyrosine	C8 pH 4.5 + L-Valline	C9 pH 4.5 + Hydroxy- L-Proline	C10 pH 4.5 + L-Ornithine	C11 pH 4.5 + L-Homoarginine	C12 pH 4.5 + L-Homoserine
D-1 pH 4.5 + Anthranilic acid	D2 pH 4.5 + L-Norleucine	D3 pH 4.5 + L-Norvaline	D4 pH 4.5 + α- Amino-N- butyric acid	D5 pH 4.5 + p- Aminobenzoate	D6 pH 4.5 + L-Cysteic acid	D7 pH 4.5 + D-Lysine	D8 pH 4.5 + 5-Hydroxy Lysine	D9 pH 4.5 + 5-Hydroxy Tryptophan	D10 pH 4.5 + D,L-Diamino pimelic acid	D11 pH 4.5 + Trimethyl amine-N-oxide	D12 pH 4.5 + Urea
E1 pH 9.5	E2 pH 9.5 + L-Alanine	E3 pH 9.5 + L-Arginine	E4 pH 9.5 + L-Asparagine	E5 pH 9.5 + L-Aspartic Acid	E6 pH 9.5 + L-Glutamic Acid	E7 pH 9.5 + L-Glutamine	E8 pH 9.5 + Glycine	E9 pH 9.5 + L-Histidine	E10 pH 9.5 + L-Isoleucine	E11 pH 9.5 + L-Leucine	E12 pH 9.5 + L-Lysine
F1 pH 9.5 + L-Methionine	F2 pH 9.5 + L- Phenylalanine	F3 pH 9.5 + L-Proline	F4 pH 9.5 + L-Serine	F5 pH 9.5 + L-Threonine	F6 pH 9.5 + L-Tryptophan	F7 pH 9.5 + L-Tyrosine	F8 pH 9.5 + L-Valline	F9 pH 9.5 + Hydroxy- L-Proline	F10 pH 9.5 + L-Ornithine	F11 pH 9.5 + L-Homoarginine	F12 pH 9.5 + L-Homoserine
G1 pH 9.5 + Anthranilic acid	G2 pH 9.5 + L-Norleucine	G3 pH 9.5 + L-Norvaline	G4 pH 9.5 + Agmatine	G5 pH 9.5 + Cadaverine	G6 pH 9.5 + Putrescine	G7 pH 9.5 + Histamine	G8 pH 9.5 + Phenylethylamine	G9 pH 9.5 + Tyramine	G10 pH 9.5 + Creatine	G11 pH 9.5 + Trimethyl amine-N-oxide	G12 pH 9.5 + Urea
H1 X-Caprylate	H2 X-α-D- Glucoside	H3 X-β-D- Glucoside	H4 X-α-D- Galactoside	H5 X-β-D- Galactoside	H6 X-α-D- Glucuronide	H7 X-β-D- Glucuronide	H8 X-β-D- Glucosaminide	H9 X-β-D- Galactosaminid e	H10 X-α-D- Mannoside	H11 X-PO4	H12 X-SO4

PM09 (Osmolytes)

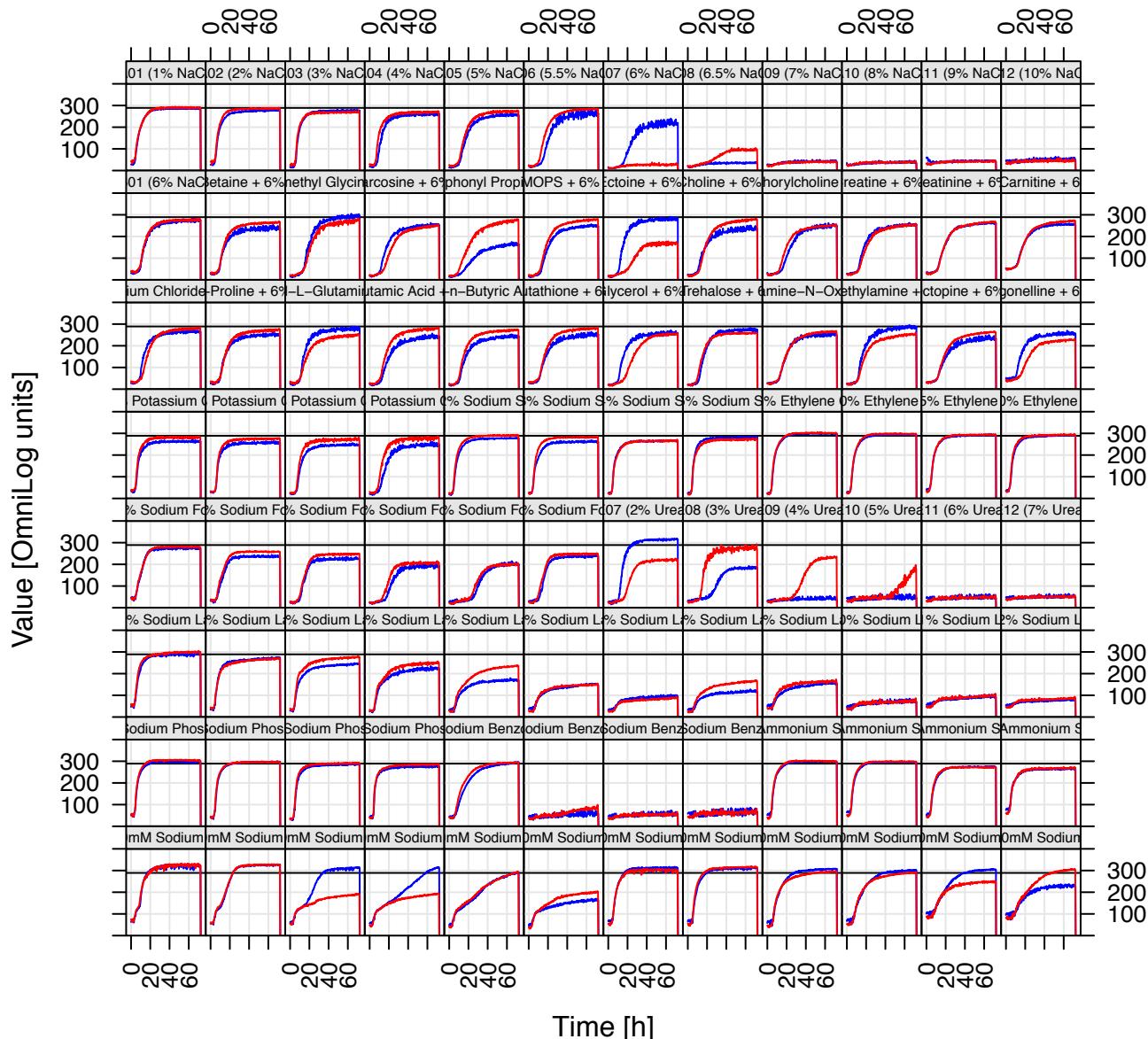
Δ SPFH-1

WT-1



PM09 (Osmolytes)

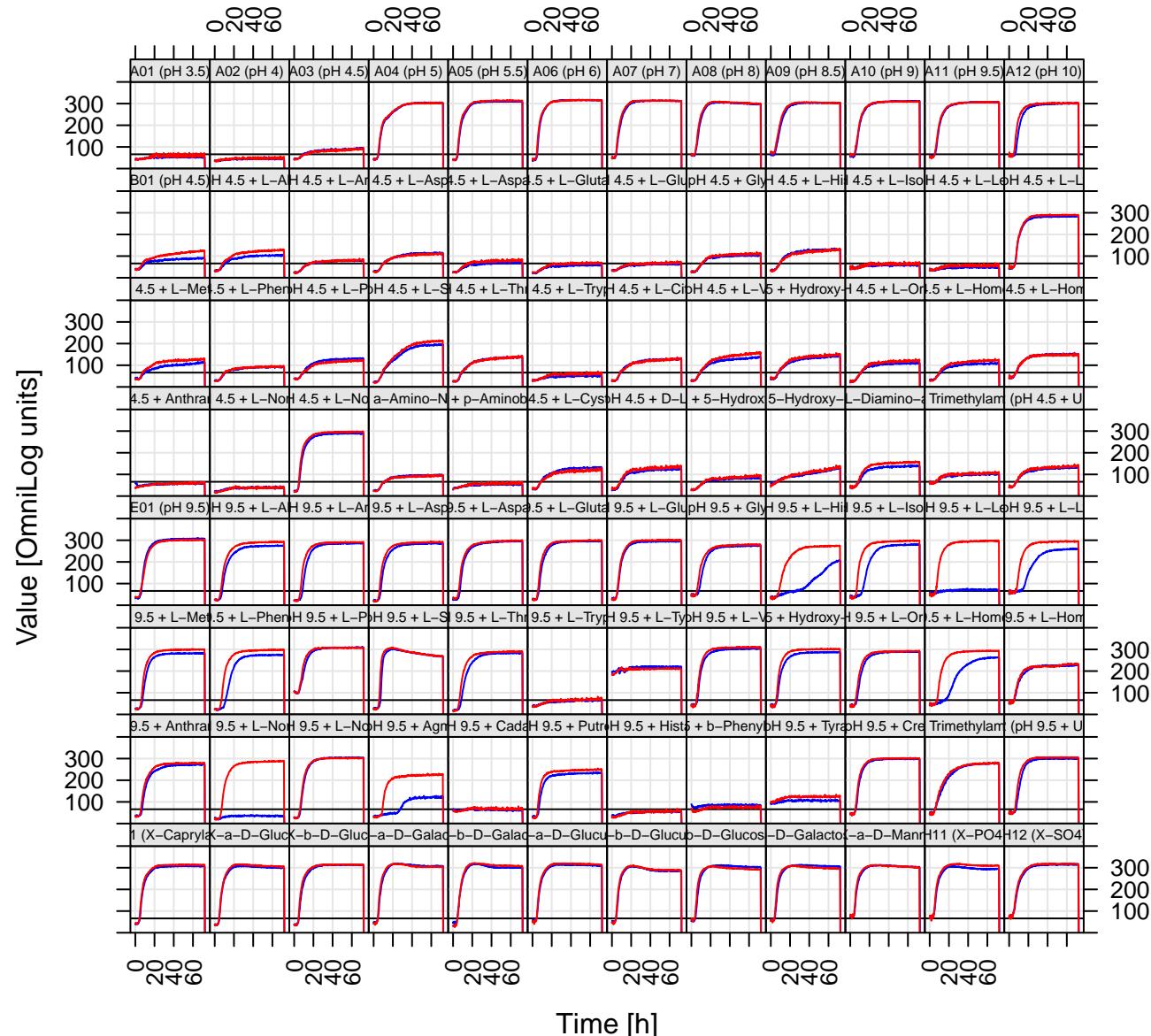
ΔSPFH-2
WT-2

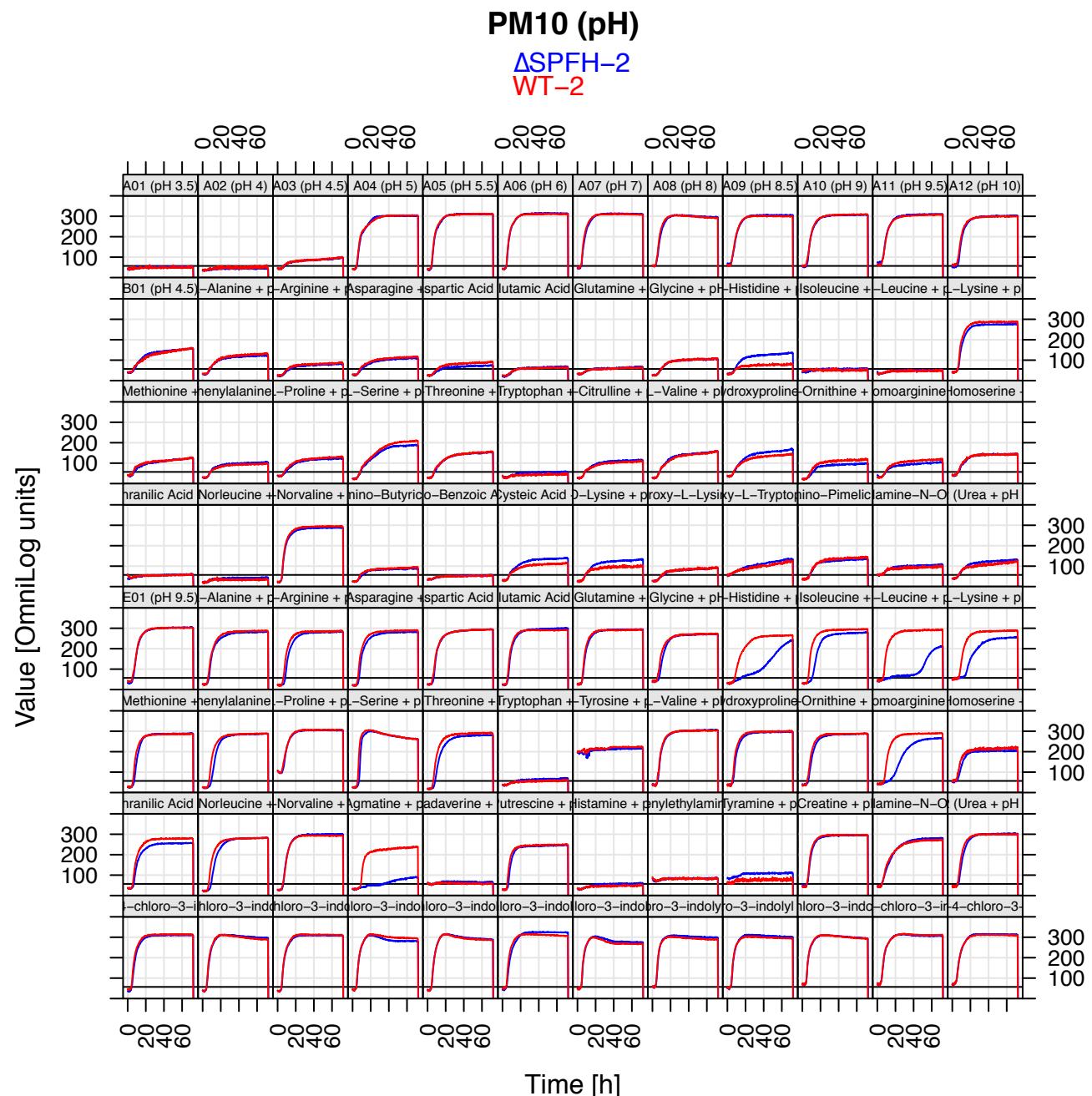


PM10 (pH)

Δ SPFH-1

WT-1





PM11C MicroPlate™

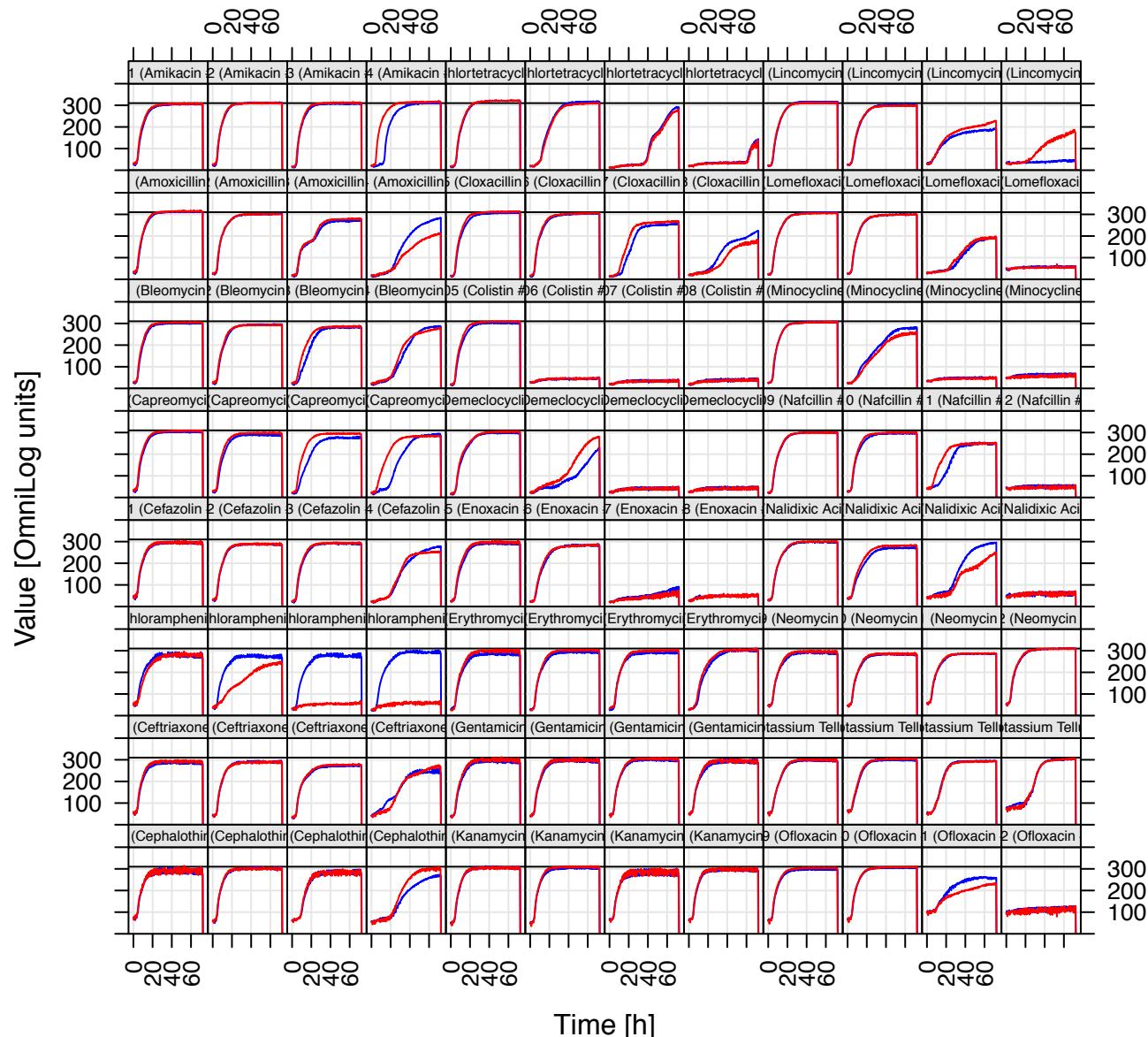
A1 Amikacin	A2 Amikacin	A3 Amikacin	A4 Amikacin	A5 Chlortetracycline	A6 Chlortetracycline	A7 Chlortetracycline	A8 Chlortetracycline	A9 Lincomycin	A10 Lincomycin	A11 Lincomycin	A12 Lincomycin
1	2	3	4	1	2	3	4	1	2	3	4
B1 Amoxicillin	B2 Amoxicillin	B3 Amoxicillin	B4 Amoxicillin	B5 Cloxacillin	B6 Cloxacillin	B7 Cloxacillin	B8 Cloxacillin	B9 Lomefloxacin	B10 Lomefloxacin	B11 Lomefloxacin	B12 Lomefloxacin
1	2	3	4	1	2	3	4	1	2	3	4
C1 Bleomycin	C2 Bleomycin	C3 Bleomycin	C4 Bleomycin	C5 Colistin	C6 Colistin	C7 Colistin	C8 Colistin	C9 Minocycline	C10 Minocycline	C11 Minocycline	C12 Minocycline
1	2	3	4	1	2	3	4	1	2	3	4
D1 Capreomycin	D2 Capreomycin	D3 Capreomycin	D4 Capreomycin	D5 Demeclocycline	D6 Demeclocycline	D7 Demeclocycline	D8 Demeclocycline	D9 Nafcillin	D10 Nafcillin	D11 Nafcillin	D12 Nafcillin
1	2	3	4	1	2	3	4	1	2	3	4
E1 Cefazolin	E2 Cefazolin	E3 Cefazolin	E4 Cefazolin	E5 Enoxacin	E6 Enoxacin	E7 Enoxacin	E8 Enoxacin	E9 Nalidixic acid	E10 Nalidixic acid	E11 Nalidixic acid	E12 Nalidixic acid
1	2	3	4	1	2	3	4	1	2	3	4
F1 Chloramphenicol	F2 Chloramphenicol	F3 Chloramphenicol	F4 Chloramphenicol	F5 Erythromycin	F6 Erythromycin	F7 Erythromycin	F8 Erythromycin	F9 Neomycin	F10 Neomycin	F11 Neomycin	F12 Neomycin
1	2	3	4	1	2	3	4	1	2	3	4
G1 Ceftriaxone	G2 Ceftriaxone	G3 Ceftriaxone	G4 Ceftriaxone	G5 Gentamicin	G6 Gentamicin	G7 Gentamicin	G8 Gentamicin	G9 Potassium tellurite	G10 Potassium tellurite	G11 Potassium tellurite	G12 Potassium tellurite
1	2	3	4	1	2	3	4	1	2	3	4
H1 Cephalothin	H2 Cephalothin	H3 Cephalothin	H4 Cephalothin	H5 Kanamycin	H6 Kanamycin	H7 Kanamycin	H8 Kanamycin	H9 Ofloxacin	H10 Ofloxacin	H11 Ofloxacin	H12 Ofloxacin
1	2	3	4	1	2	3	4	1	2	3	4

PM12B MicroPlate™

A1 Penicillin G	A2 Penicillin G	A3 Penicillin G	A4 Penicillin G	A5 Tetracycline	A6 Tetracycline	A7 Tetracycline	A8 Tetracycline	A9 Carbenicillin	A10 Carbenicillin	A11 Carbenicillin	A12 Carbenicillin
1	2	3	4	1	2	3	4	1	2	3	4
B1 Oxacillin	B2 Oxacillin	B3 Oxacillin	B4 Oxacillin	B5 Penimepiclycline	B6 Penimepiclycline	B7 Penimepiclycline	B8 Penimepiclycline	B9 Polymyxin B	B10 Polymyxin B	B11 Polymyxin B	B12 Polymyxin B
1	2	3	4	1	2	3	4	1	2	3	4
C1 Paromomycin	C2 Paromomycin	C3 Paromomycin	C4 Paromomycin	C5 Vancomycin	C6 Vancomycin	C7 Vancomycin	C8 Vancomycin	C9 D,L-Serine hydroxamate	C10 D,L-Serine hydroxamate	C11 D,L-Serine hydroxamate	C12 D,L-Serine hydroxamate
1	2	3	4	1	2	3	4	1	2	3	4
D1 Sisomicin	D2 Sisomicin	D3 Sisomicin	D4 Sisomicin	D5 Sulfamethazine	D6 Sulfamethazine	D7 Sulfamethazine	D8 Sulfamethazine	D9 Novobiocin	D10 Novobiocin	D11 Novobiocin	D12 Novobiocin
1	2	3	4	1	2	3	4	1	2	3	4
E1 2,4-Diamino-6,7-diisopropyl-pteridine	E2 2,4-Diamino-6,7-diisopropyl-pteridine	E3 2,4-Diamino-6,7-diisopropyl-pteridine	E4 2,4-Diamino-6,7-diisopropyl-pteridine	E5 Sulfadiazine	E6 Sulfadiazine	E7 Sulfadiazine	E8 Sulfadiazine	E9 Benzethonium chloride	E10 Benzethonium chloride	E11 Benzethonium chloride	E12 Benzethonium chloride
1	2	3	4	1	2	3	4	1	2	3	4
F1 Tobramycin	F2 Tobramycin	F3 Tobramycin	F4 Tobramycin	F5 Sulfathiazole	F6 Sulfathiazole	F7 Sulfathiazole	F8 Sulfathiazole	F9 5-Fluoroorotic acid	F10 5-Fluoroorotic acid	F11 5-Fluoroorotic acid	F12 5-Fluoroorotic acid
1	2	3	4	1	2	3	4	1	2	3	4
G1 Spectinomycin	G2 Spectinomycin	G3 Spectinomycin	G4 Spectinomycin	G5 Sulfa-methoxazole	G6 Sulfa-methoxazole	G7 Sulfa-methoxazole	G8 Sulfa-methoxazole	G9 L-Aspartic-β-hydroxamate	G10 L-Aspartic-β-hydroxamate	G11 L-Aspartic-β-hydroxamate	G12 L-Aspartic-β-hydroxamate
1	2	3	4	1	2	3	4	1	2	3	4
H1 Spiramycin	H2 Spiramycin	H3 Spiramycin	H4 Spiramycin	H5 Rifampicin	H6 Rifampicin	H7 Rifampicin	H8 Rifampicin	H9 Dodecytrimethyl ammonium bromide	H10 Dodecytrimethyl ammonium bromide	H11 Dodecytrimethyl ammonium bromide	H12 Dodecytrimethyl ammonium bromide
1	2	3	4	1	2	3	4	1	2	3	4

PM11 (Chemical Sensitivity Bacteria)

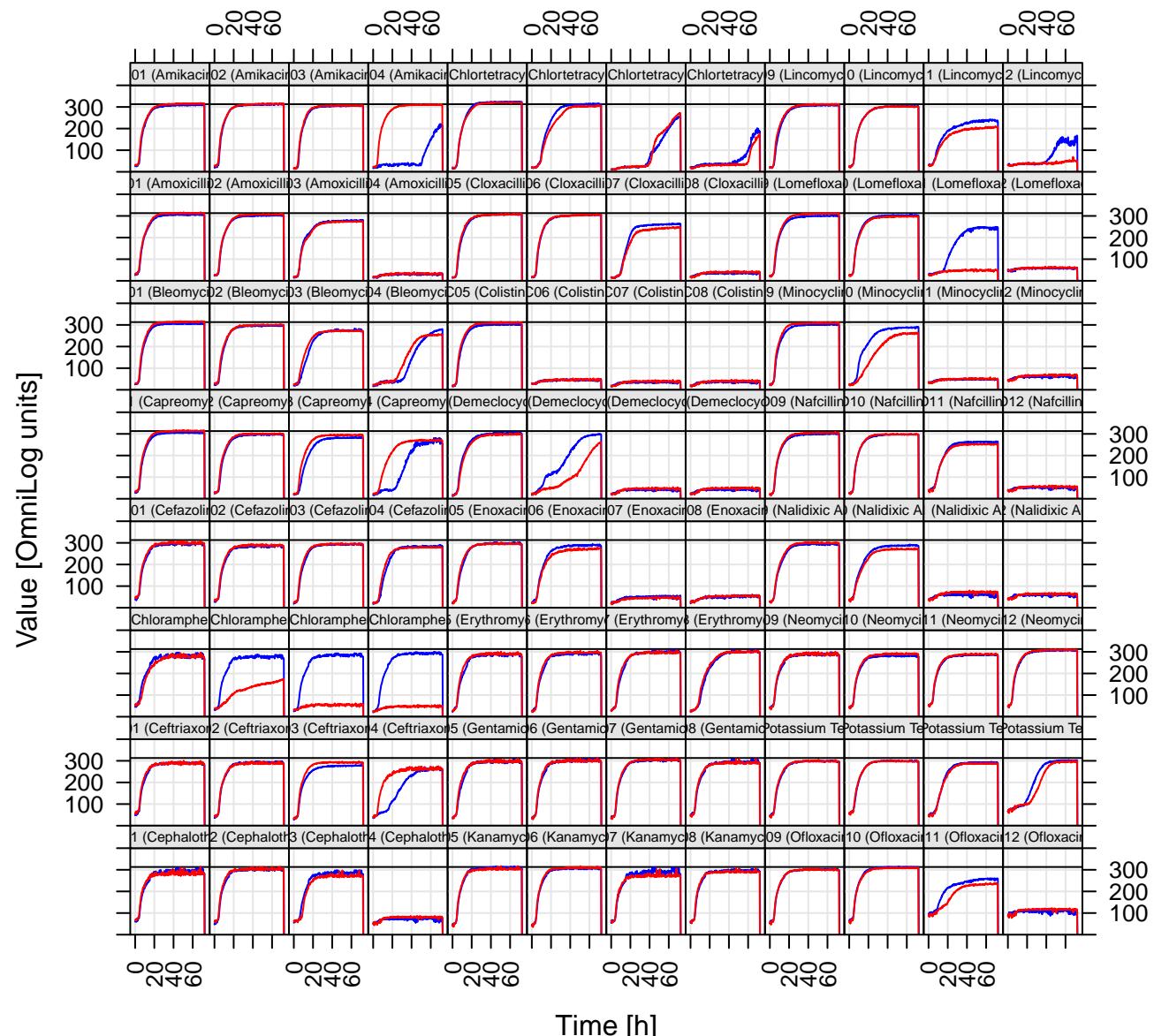
Δ SPFH-2
WT-2



PM11 (Chemicals)

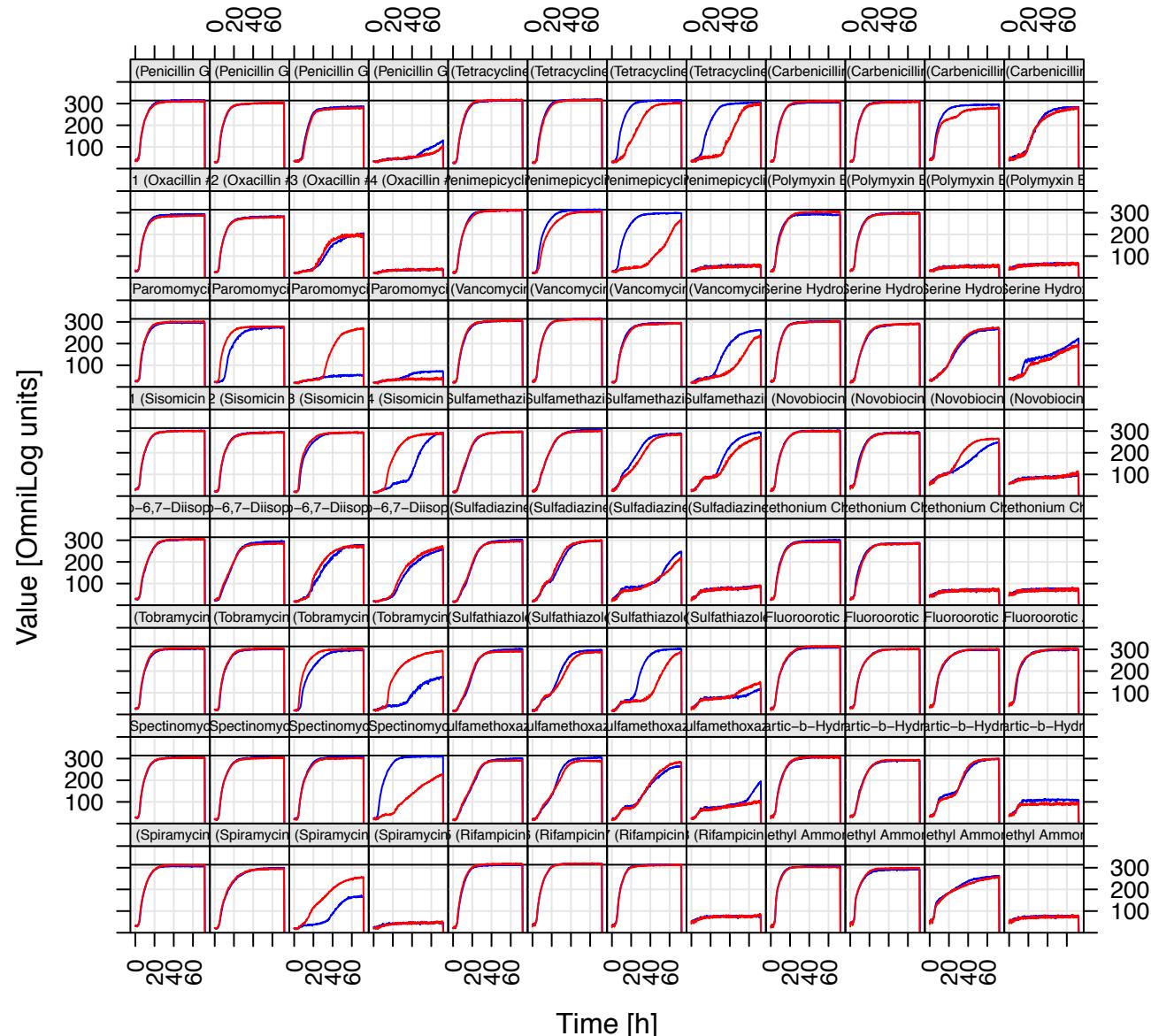
Δ SPFH-1

WT-1



PM12 (Chemical Sensitivity Bacteria)

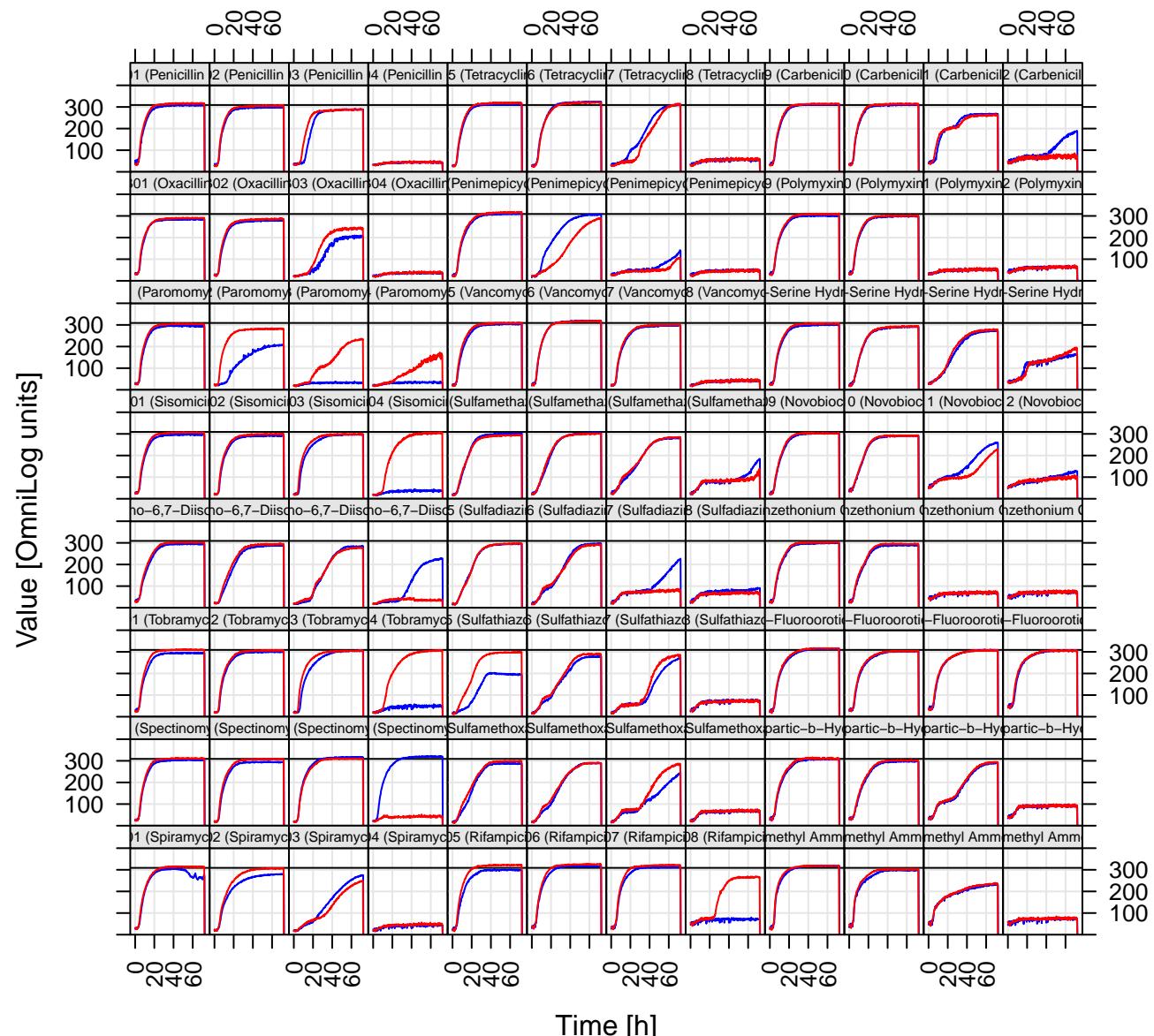
Δ SPFH-2
WT-2



PM12 (Chemicals)

Δ SPFH-1

WT-1



PM13B MicroPlate™

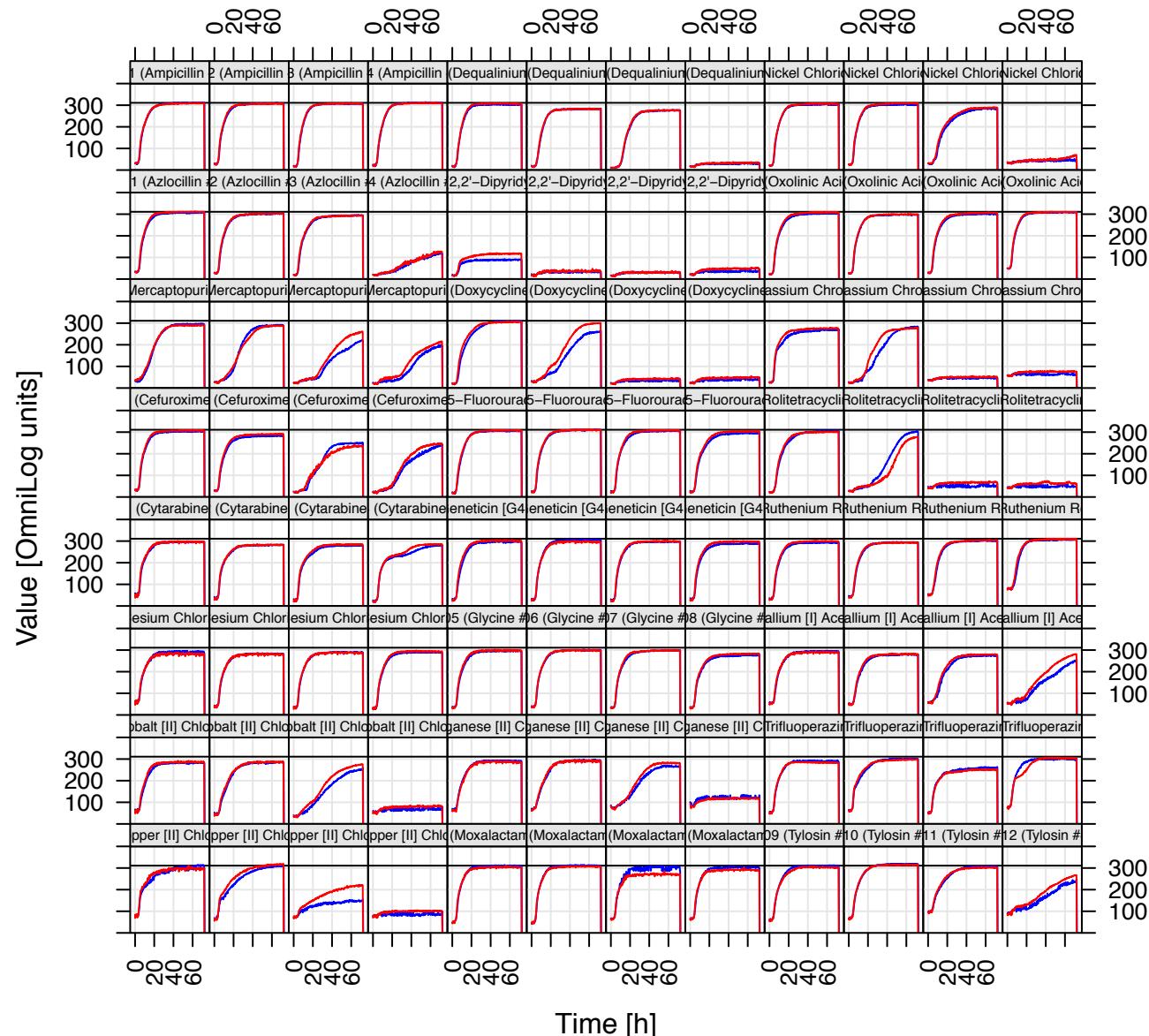
A1 Ampicillin	A2 Ampicillin	A3 Ampicillin	A4 Ampicillin	A5 Dequalinium chloride	A6 Dequalinium chloride	A7 Dequalinium chloride	A8 Dequalinium chloride	A9 Nickel chloride	A10 Nickel chloride	A11 Nickel chloride	A12 Nickel chloride
1	2	3	4	1	2	3	4	1	2	3	4
B1 Azlocillin	B2 Azlocillin	B3 Azlocillin	B4 Azlocillin	B5 2, 2'-Dipyridyl	B6 2, 2'-Dipyridyl	B7 2, 2'-Dipyridyl	B8 2, 2'-Dipyridyl	B9 Oxolinic acid	B10 Oxolinic acid	B11 Oxolinic acid	B12 Oxolinic acid
1	2	3	4	1	2	3	4	1	2	3	4
C1 6-Mercapto-purine	C2 6-Mercapto-purine	C3 6-Mercapto-purine	C4 6-Mercapto-purine	C5 Doxycycline	C6 Doxycycline	C7 Doxycycline	C8 Doxycycline	C9 Potassium chromate	C10 Potassium chromate	C11 Potassium chromate	C12 Potassium chromate
1	2	3	4	1	2	3	4	1	2	3	4
D1 Cefuroxime	D2 Cefuroxime	D3 Cefuroxime	D4 Cefuroxime	D5 5-Fluorouracil	D6 5-Fluorouracil	D7 5-Fluorouracil	D8 5-Fluorouracil	D9 Rolutetracycline	D10 Rolutetracycline	D11 Rolutetracycline	D12 Rolutetracycline
1	2	3	4	1	2	3	4	1	2	3	4
E1 Cytosine-1-beta-D-arabinofuranoside	E2 Cytosine-1-beta-D-arabinofuranoside	E3 Cytosine-1-beta-D-arabinofuranoside	E4 Cytosine-1-beta-D-arabinofuranoside	E5 Geneticin (G418)	E6 Geneticin (G418)	E7 Geneticin (G418)	E8 Geneticin (G418)	E9 Ruthenium red	E10 Ruthenium red	E11 Ruthenium red	E12 Ruthenium red
1	2	3	4	1	2	3	4	1	2	3	4
F1 Cesium chloride	F2 Cesium chloride	F3 Cesium chloride	F4 Cesium chloride	F5 Glycine	F6 Glycine	F7 Glycine	F8 Glycine	F9 Thallium (I) acetate	F10 Thallium (I) acetate	F11 Thallium (I) acetate	F12 Thallium (I) acetate
1	2	3	4	1	2	3	4	1	2	3	4
G1 Cobalt chloride	G2 Cobalt chloride	G3 Cobalt chloride	G4 Cobalt chloride	G5 Manganese chloride	G6 Manganese chloride	G7 Manganese chloride	G8 Trifluoperazine	G9 Trifluoperazine	G10 Trifluoperazine	G11 Trifluoperazine	G12 Trifluoperazine
1	2	3	4	1	2	3	4	1	2	3	4
H1 Cupric chloride	H2 Cupric chloride	H3 Cupric chloride	H4 Cupric chloride	H5 Moxalactam	H6 Moxalactam	H7 Moxalactam	H8 Moxalactam	H9 Tylosin	H10 Tylosin	H11 Tylosin	H12 Tylosin
1	2	3	4	1	2	3	4	1	2	3	4

PM14A MicroPlate™

A1 Acriflavine	A2 Acriflavine	A3 Acriflavine	A4 Acriflavine	A5 Furaladone	A6 Furaladone	A7 Furaladone	A8 Furaladone	A9 Sanguinarine	A10 Sanguinarine	A11 Sanguinarine	A12 Sanguinarine
1	2	3	4	1	2	3	4	1	2	3	4
B1 9-Aminoacridine	B2 9-Aminoacridine	B3 9-Aminoacridine	B4 9-Aminoacridine	B5 Fusaric acid	B6 Fusaric acid	B7 Fusaric acid	B8 Fusaric acid	B9 Sodium arsenate	B10 Sodium arsenate	B11 Sodium arsenate	B12 Sodium arsenate
1	2	3	4	1	2	3	4	1	2	3	4
C1 Boric Acid	C2 Boric Acid	C3 Boric Acid	C4 Boric Acid	C5 1-Hydroxy-pyridine-2-thione	C6 1-Hydroxy-pyridine-2-thione	C7 1-Hydroxy-pyridine-2-thione	C8 1-Hydroxy-pyridine-2-thione	C9 Sodium cyanate	C10 Sodium cyanate	C11 Sodium cyanate	C12 Sodium cyanate
1	2	3	4	1	2	3	4	1	2	3	4
D1 Cadmium chloride	D2 Cadmium chloride	D3 Cadmium chloride	D4 Cadmium chloride	D5 Iodoacetate	D6 Iodoacetate	D7 Iodoacetate	D8 Iodoacetate	D9 Sodium dichromate	D10 Sodium dichromate	D11 Sodium dichromate	D12 Sodium dichromate
1	2	3	4	1	2	3	4	1	2	3	4
E1 Cefoxitin	E2 Cefoxitin	E3 Cefoxitin	E4 Cefoxitin	E5 Nitrofurantoin	E6 Nitrofurantoin	E7 Nitrofurantoin	E8 Nitrofurantoin	E9 Sodium metaborate	E10 Sodium metaborate	E11 Sodium metaborate	E12 Sodium metaborate
1	2	3	4	1	2	3	4	1	2	3	4
F1 Chloramphenicol	F2 Chloramphenicol	F3 Chloramphenicol	F4 Chloramphenicol	F5 Piperacillin	F6 Piperacillin	F7 Piperacillin	F8 Piperacillin	F9 Sodium metavanadate	F10 Sodium metavanadate	F11 Sodium metavanadate	F12 Sodium metavanadate
1	2	3	4	1	2	3	4	1	2	3	4
G1 Chelerythrine	G2 Chelerythrine	G3 Chelerythrine	G4 Chelerythrine	G5 Carbenicillin	G6 Carbenicillin	G7 Carbenicillin	G8 Carbenicillin	G9 Sodium nitrite	G10 Sodium nitrite	G11 Sodium nitrite	G12 Sodium nitrite
1	2	3	4	1	2	3	4	1	2	3	4
H1 EGTA	H2 EGTA	H3 EGTA	H4 EGTA	H5 Promethazine	H6 Promethazine	H7 Promethazine	H8 Promethazine	H9 Sodium orthovanadate	H10 Sodium orthovanadate	H11 Sodium orthovanadate	H12 Sodium orthovanadate
1	2	3	4	1	2	3	4	1	2	3	4

PM13 (Chemical Sensitivity Bacteria)

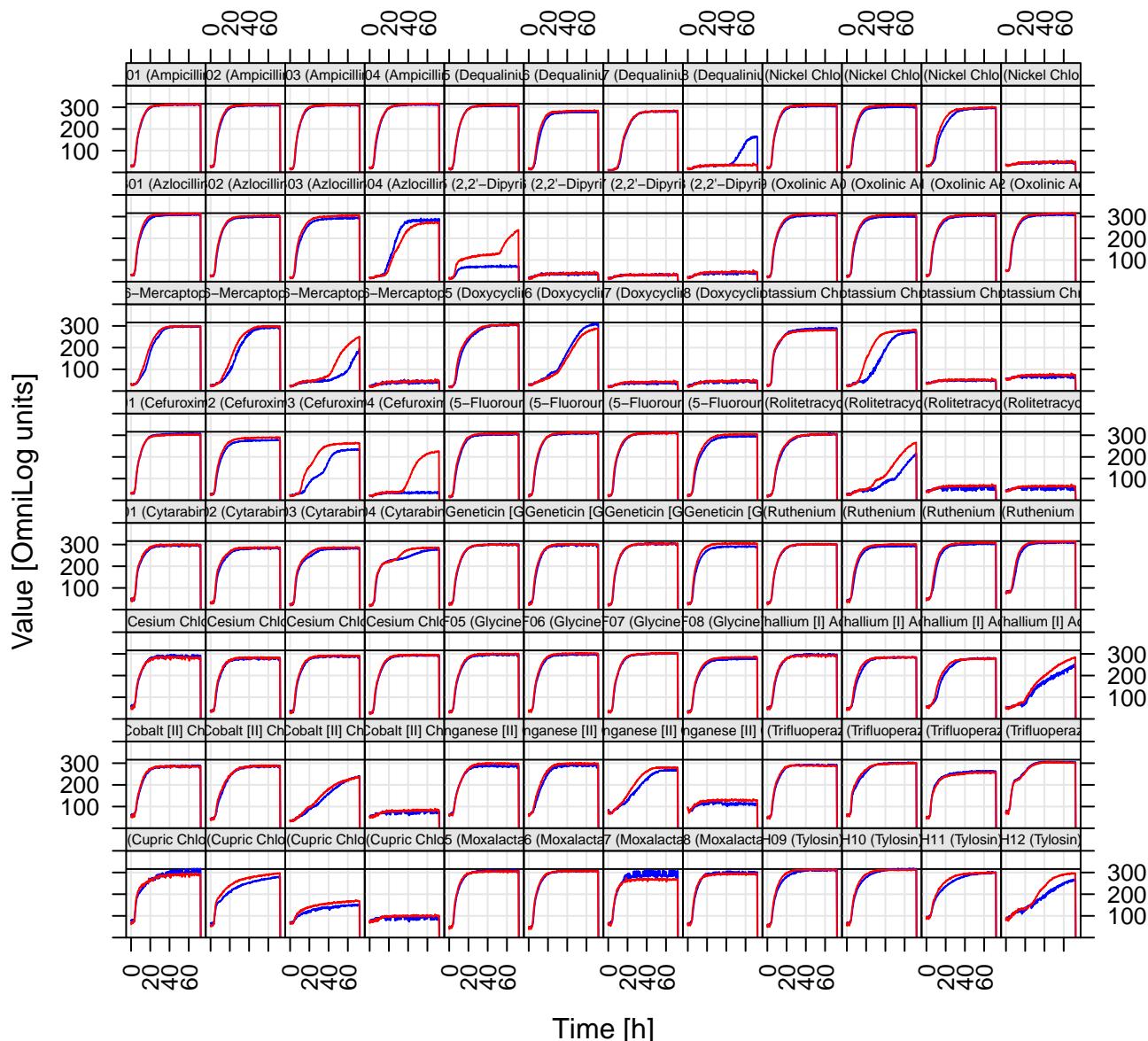
Δ SPFH-2
WT-2



PM13 (Chemicals)

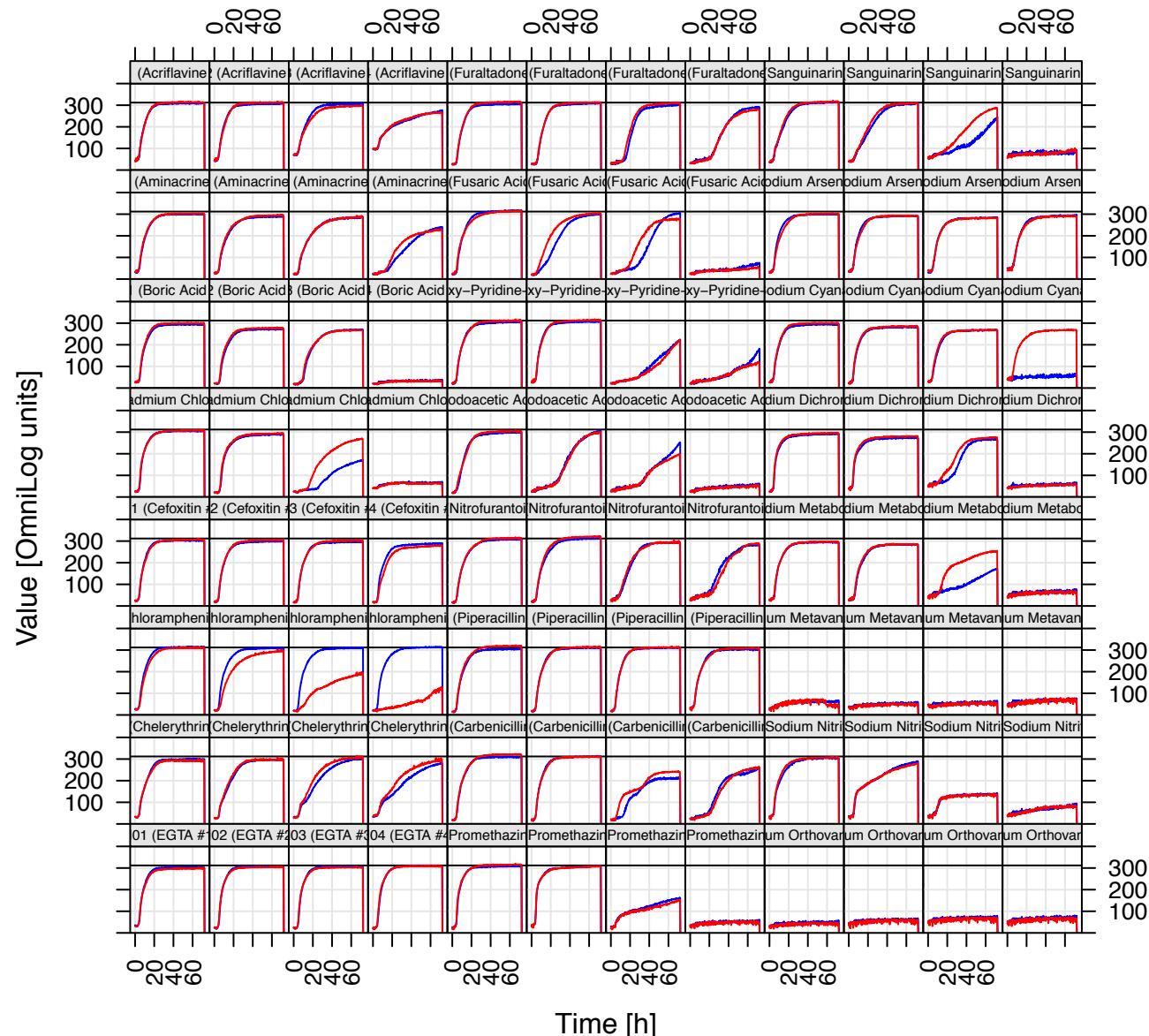
ASP FH-1

WT-1



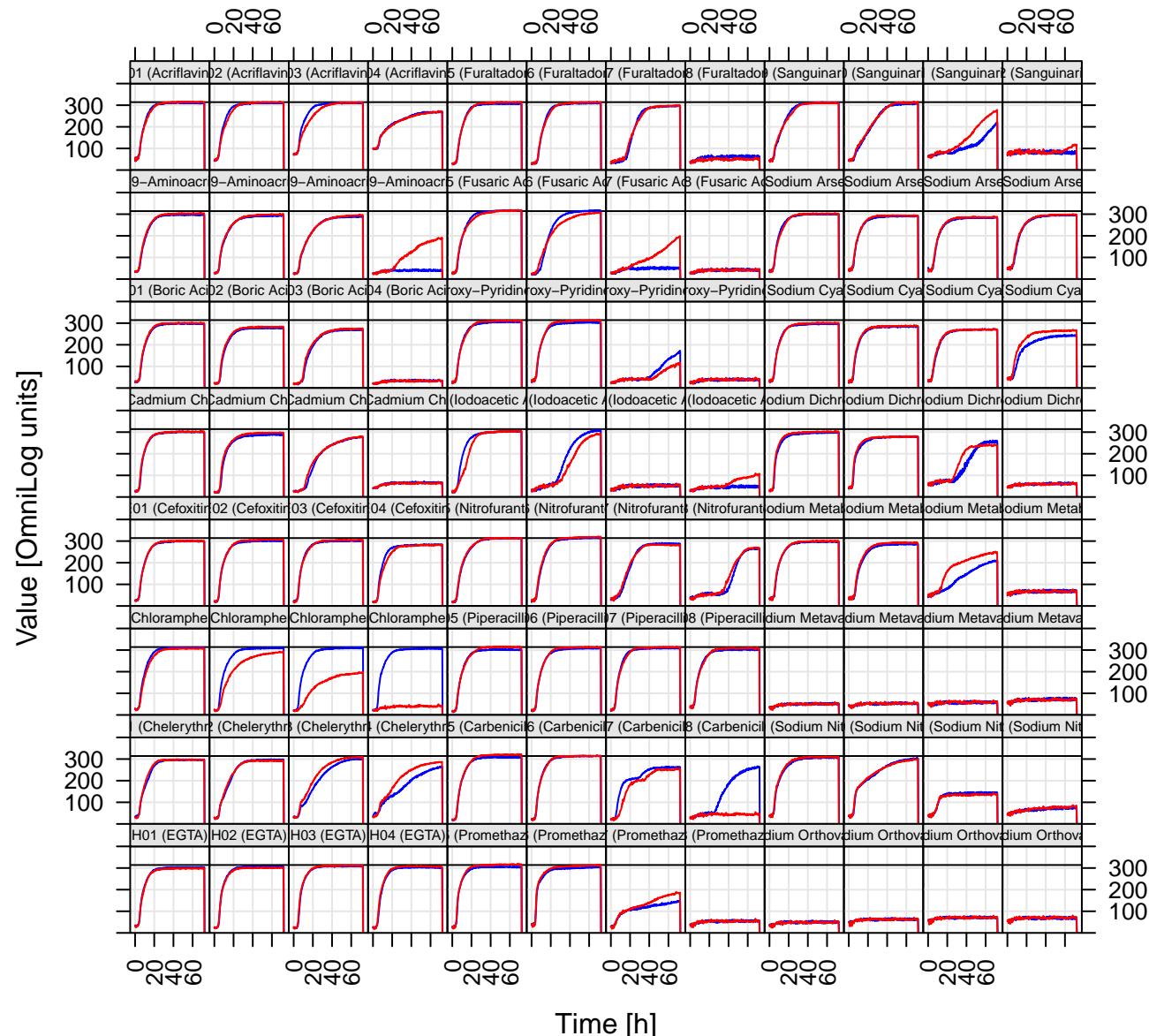
PM14 (Chemical Sensitivity Bacteria)

Δ SPFH-2
WT-2



PM14 (Chemicals)

ΔSPFH-1
WT-1



PM15B MicroPlate™

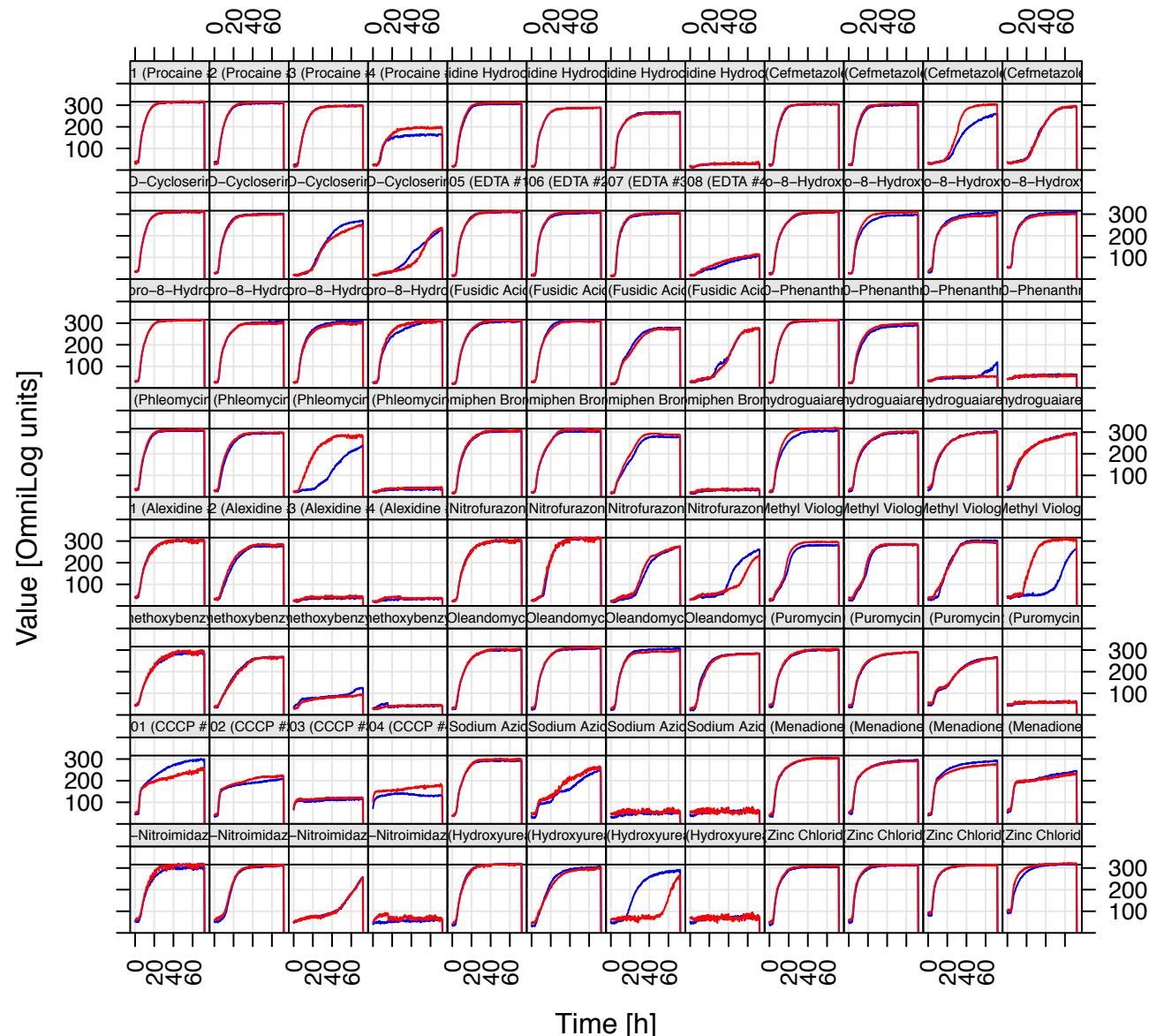
A1 Procaine	A2 Procaine	A3 Procaine	A4 Procaine	A5 Guanidine hydrochloride	A6 Guanidine hydrochloride	A7 Guanidine hydrochloride	A8 Guanidine hydrochloride	A9 Cefmetazole	A10 Cefmetazole	A11 Cefmetazole	A12 Cefmetazole
1	2	3	4	1	2	3	4	1	2	3	4
B1 D-Cycloserine	B2 D-Cycloserine	B3 D-Cycloserine	B4 D-Cycloserine	B5 EDTA	B6 EDTA	B7 EDTA	B8 EDTA	B9 5,7-Dichloro-8-hydroxy-quinaldine	B10 5,7-Dichloro-8-hydroxy-quinaldine	B11 5,7-Dichloro-8-hydroxy-quinaldine	B12 5,7-Dichloro-8-hydroxy-quinaldine
1	2	3	4	1	2	3	4	1	2	3	4
C1 5,7-Dichloro-8-hydroxyquinoline	C2 5,7-Dichloro-8-hydroxyquinoline	C3 5,7-Dichloro-8-hydroxyquinoline	C4 5,7-Dichloro-8-hydroxyquinoline	C5 Fusidic acid	C6 Fusidic acid	C7 Fusidic acid	C8 Fusidic acid	C9 1,10-Phenanthroline	C10 1,10-Phenanthroline	C11 1,10-Phenanthroline	C12 1,10-Phenanthroline
1	2	3	4	1	2	3	4	1	2	3	4
D1 Phleomycin	D2 Phleomycin	D3 Phleomycin	D4 Phleomycin	D5 Domiphen bromide	D6 Domiphen bromide	D7 Domiphen bromide	D8 Domiphen bromide	D9 Nordihydroguaiaretic acid	D10 Nordihydroguaiaretic acid	D11 Nordihydroguaiaretic acid	D12 Nordihydroguaiaretic acid
1	2	3	4	1	2	3	4	1	2	3	4
E1 Alexidine	E2 Alexidine	E3 Alexidine	E4 Alexidine	E5 5-Nitro-2-furaldehyde semicarbazone	E6 5-Nitro-2-furaldehyde semicarbazone	E7 5-Nitro-2-furaldehyde semicarbazone	E8 5-Nitro-2-furaldehyde semicarbazone	E9 Methyl viologen	E10 Methyl viologen	E11 Methyl viologen	E12 Methyl viologen
1	2	3	4	1	2	3	4	1	2	3	4
F1 3,4-Dimethoxybenzyl alcohol	F2 3,4-Dimethoxybenzyl alcohol	F3 3,4-Dimethoxybenzyl alcohol	F4 3,4-Dimethoxybenzyl alcohol	F5 Oleandomycin	F6 Oleandomycin	F7 Oleandomycin	F8 Oleandomycin	F9 Puromycin	F10 Puromycin	F11 Puromycin	F12 Puromycin
1	2	3	4	1	2	3	4	1	2	3	4
G1 CCCP	G2 CCCP	G3 CCCP	G4 CCCP	G5 Sodium azide	G6 Sodium azide	G7 Sodium azide	G8 Sodium azide	G9 Menadione	G10 Menadione	G11 Menadione	G12 Menadione
1	2	3	4	1	2	3	4	1	2	3	4
H1 2-Nitroimidazole	H2 2-Nitroimidazole	H3 2-Nitroimidazole	H4 2-Nitroimidazole	H5 Hydroxyurea	H6 Hydroxyurea	H7 Hydroxyurea	H8 Hydroxyurea	H9 Zinc chloride	H10 Zinc chloride	H11 Zinc chloride	H12 Zinc chloride
1	2	3	4	1	2	3	4	1	2	3	4

PM16A MicroPlate™

A1 Cefotaxime	A2 Cefotaxime	A3 Cefotaxime	A4 Cefotaxime	A5 Phosphomycin	A6 Phosphomycin	A7 Phosphomycin	A8 Phosphomycin	A9 5-Chloro-7-iodo-8-hydroxy-quinoline	A10 5-Chloro-7-iodo-8-hydroxy-quinoline	A11 5-Chloro-7-iodo-8-hydroxy-quinoline	A12 5-Chloro-7-iodo-8-hydroxy-quinoline
1	2	3	4	1	2	3	4	1	2	3	4
B1 Norfloxacin	B2 Norfloxacin	B3 Norfloxacin	B4 Norfloxacin	B5 Sulfanilamide	B6 Sulfanilamide	B7 Sulfanilamide	B8 Sulfanilamide	B9 Trimethoprim	B10 Trimethoprim	B11 Trimethoprim	B12 Trimethoprim
1	2	3	4	1	2	3	4	1	2	3	4
C1 Dichlofluanid	C2 Dichlofluanid	C3 Dichlofluanid	C4 Dichlofluanid	C5 Protamine sulfate	C6 Protamine sulfate	C7 Protamine sulfate	C8 Protamine sulfate	C9 Cetylpyridinium chloride	C10 Cetylpyridinium chloride	C11 Cetylpyridinium chloride	C12 Cetylpyridinium chloride
1	2	3	4	1	2	3	4	1	2	3	4
D1 1-Chloro-2,4-dinitrobenzene	D2 1-Chloro-2,4-dinitrobenzene	D3 1-Chloro-2,4-dinitrobenzene	D4 1-Chloro-2,4-dinitrobenzene	D5 Diamide	D6 Diamide	D7 Diamide	D8 Diamide	D9 Cinoxacin	D10 Cinoxacin	D11 Cinoxacin	D12 Cinoxacin
1	2	3	4	1	2	3	4	1	2	3	4
E1 Streptomycin	E2 Streptomycin	E3 Streptomycin	E4 Streptomycin	E5 5-Azacytidine	E6 5-Azacytidine	E7 5-Azacytidine	E8 5-Azacytidine	E9 Rifamycin SV	E10 Rifamycin SV	E11 Rifamycin SV	E12 Rifamycin SV
1	2	3	4	1	2	3	4	1	2	3	4
F1 Potassium tellurite	F2 Potassium tellurite	F3 Potassium tellurite	F4 Potassium tellurite	F5 Sodium selenite	F6 Sodium selenite	F7 Sodium selenite	F8 Sodium selenite	F9 Aluminum sulfate	F10 Aluminum sulfate	F11 Aluminum sulfate	F12 Aluminum sulfate
1	2	3	4	1	2	3	4	1	2	3	4
G1 Chromium chloride	G2 Chromium chloride	G3 Chromium chloride	G4 Chromium chloride	G5 Ferric chloride	G6 Ferric chloride	G7 Ferric chloride	G8 Ferric chloride	G9 L-Glutamic-g-hydroxamate	G10 L-Glutamic-g-hydroxamate	G11 L-Glutamic-g-hydroxamate	G12 L-Glutamic-g-hydroxamate
1	2	3	4	1	2	3	4	1	2	3	4
H1 Glycine hydroxamate	H2 Glycine hydroxamate	H3 Glycine hydroxamate	H4 Glycine hydroxamate	H5 Chloroxenol	H6 Chloroxenol	H7 Chloroxenol	H8 Chloroxenol	H9 Sorbic acid	H10 Sorbic acid	H11 Sorbic acid	H12 Sorbic acid
1	2	3	4	1	2	3	4	1	2	3	4

PM15 (Chemical Sensitivity Bacteria)

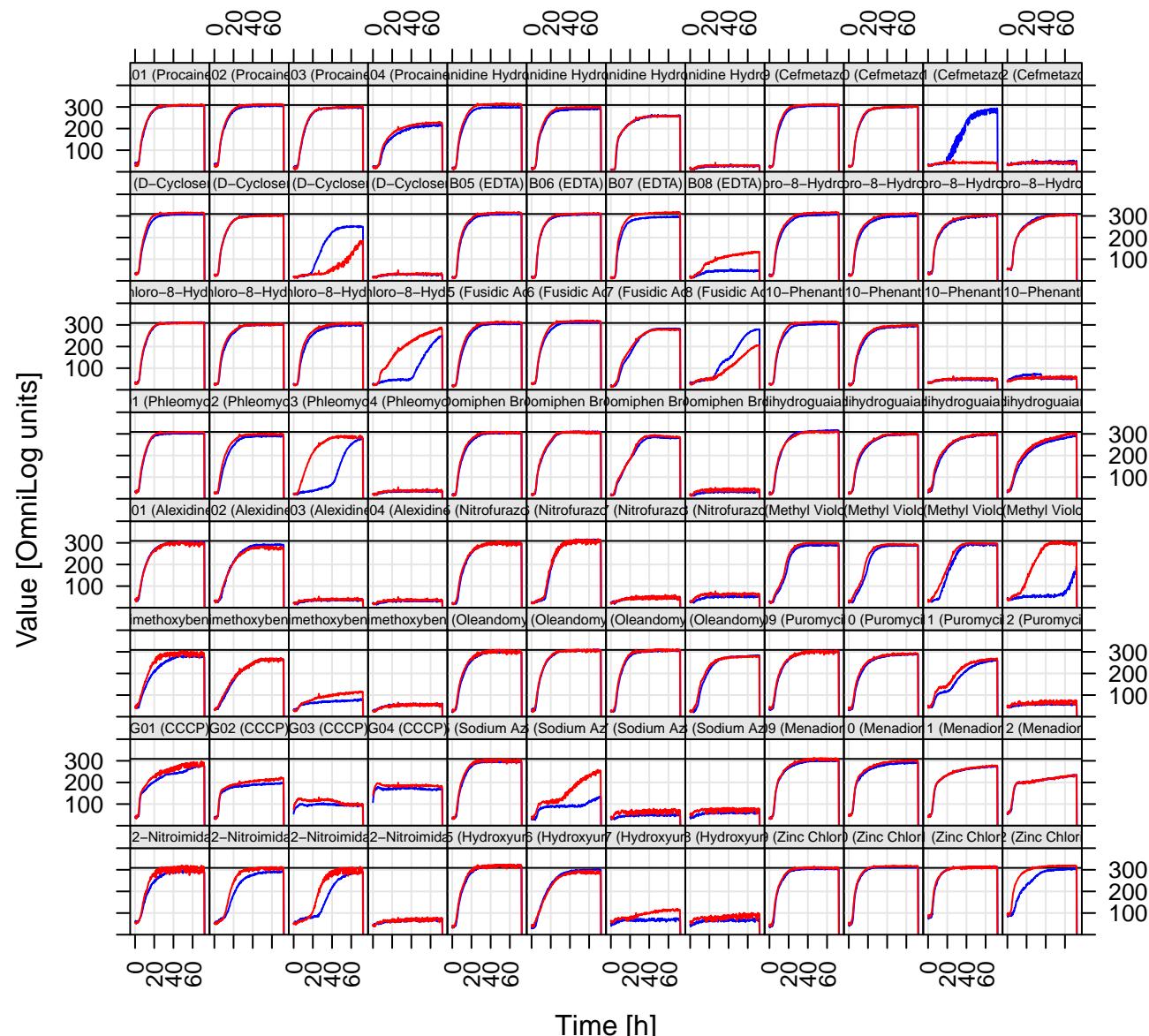
Δ SPFH-2
WT-2



PM15 (Chemicals)

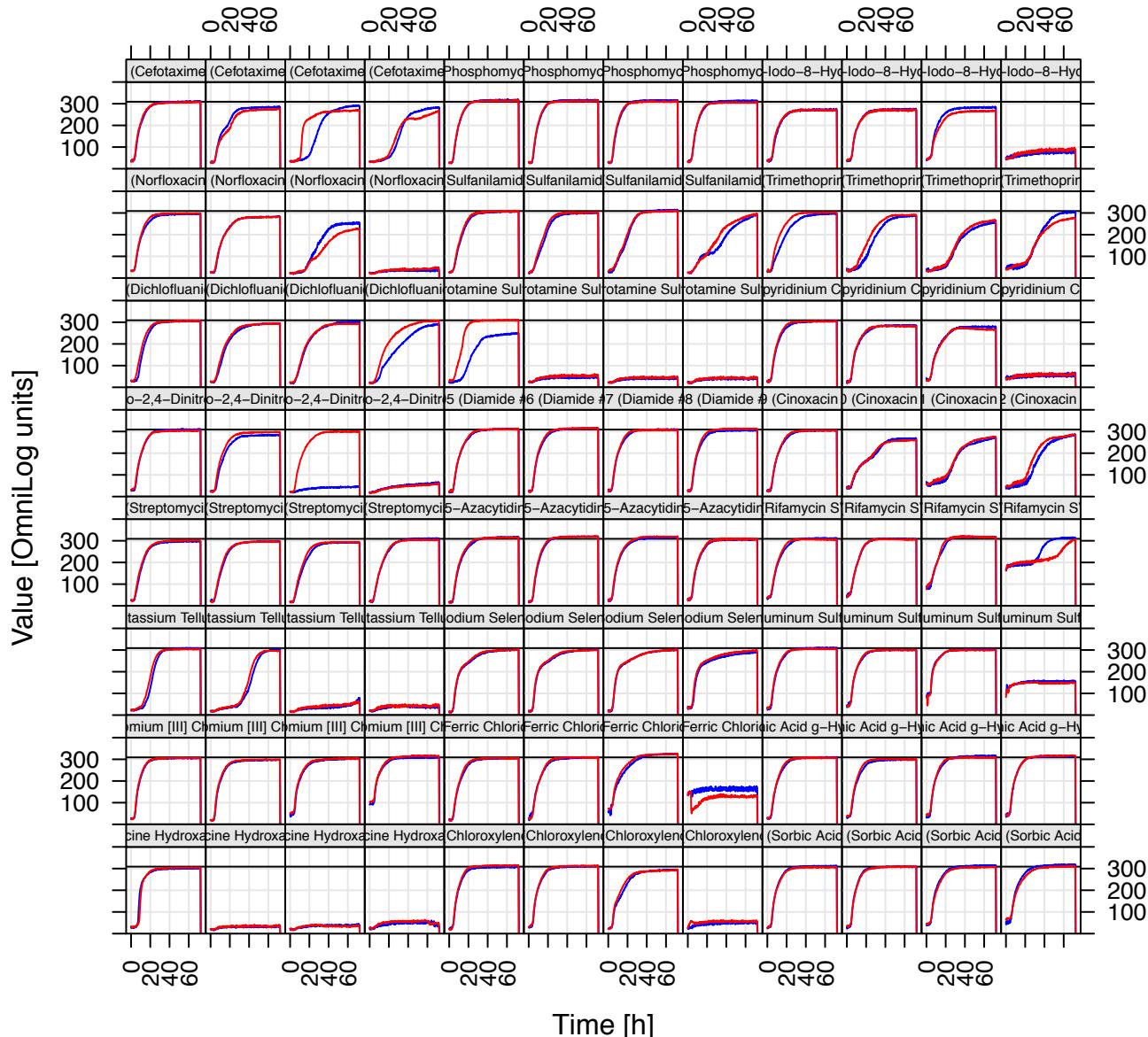
ΔSPFH-1

WT-1



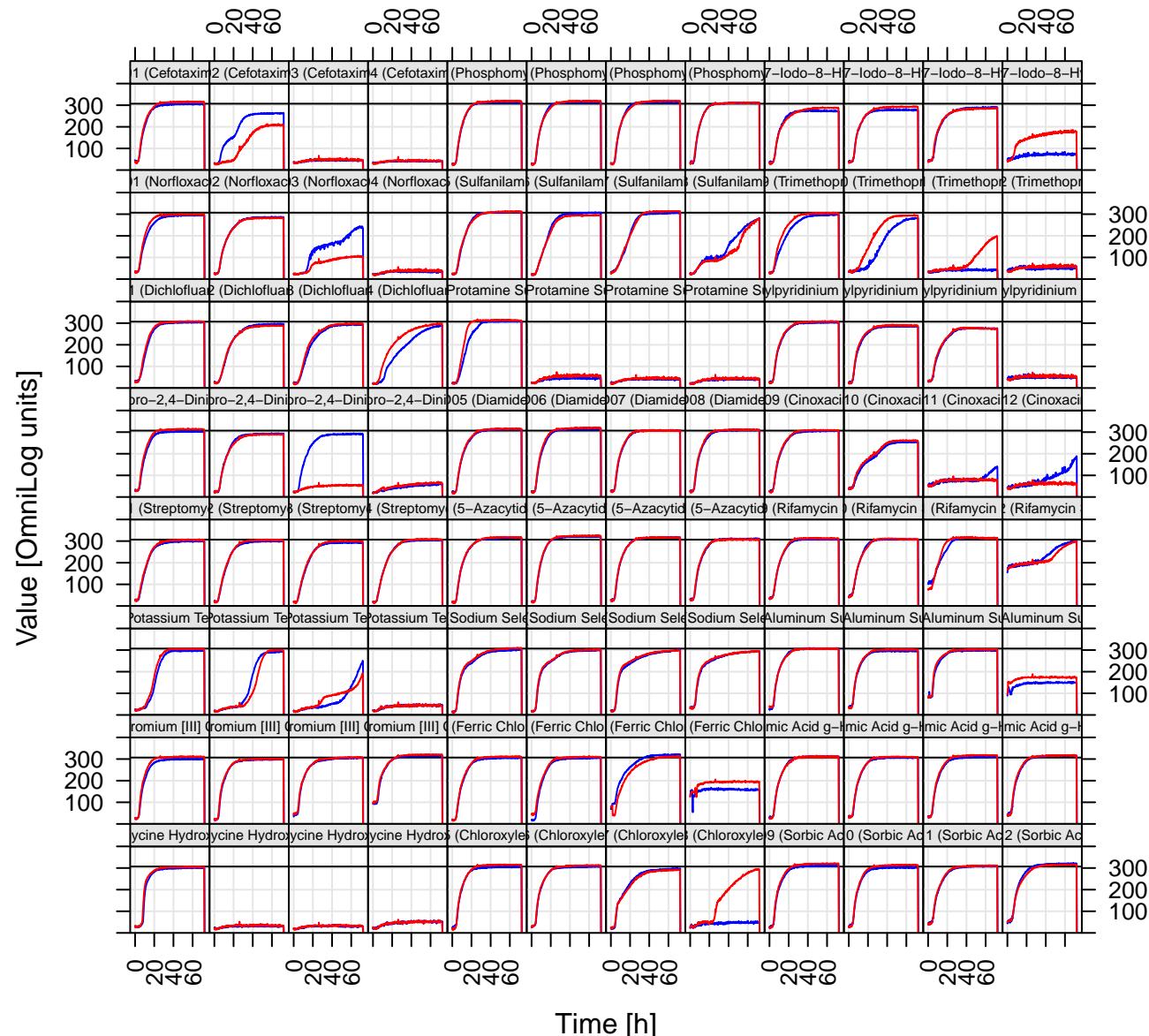
PM16 (Chemical Sensitivity Bacteria)

ΔSPFH-2
WT-2



PM16 (Chemicals)

Δ SPFH-1
WT-1



PM17A MicroPlate™

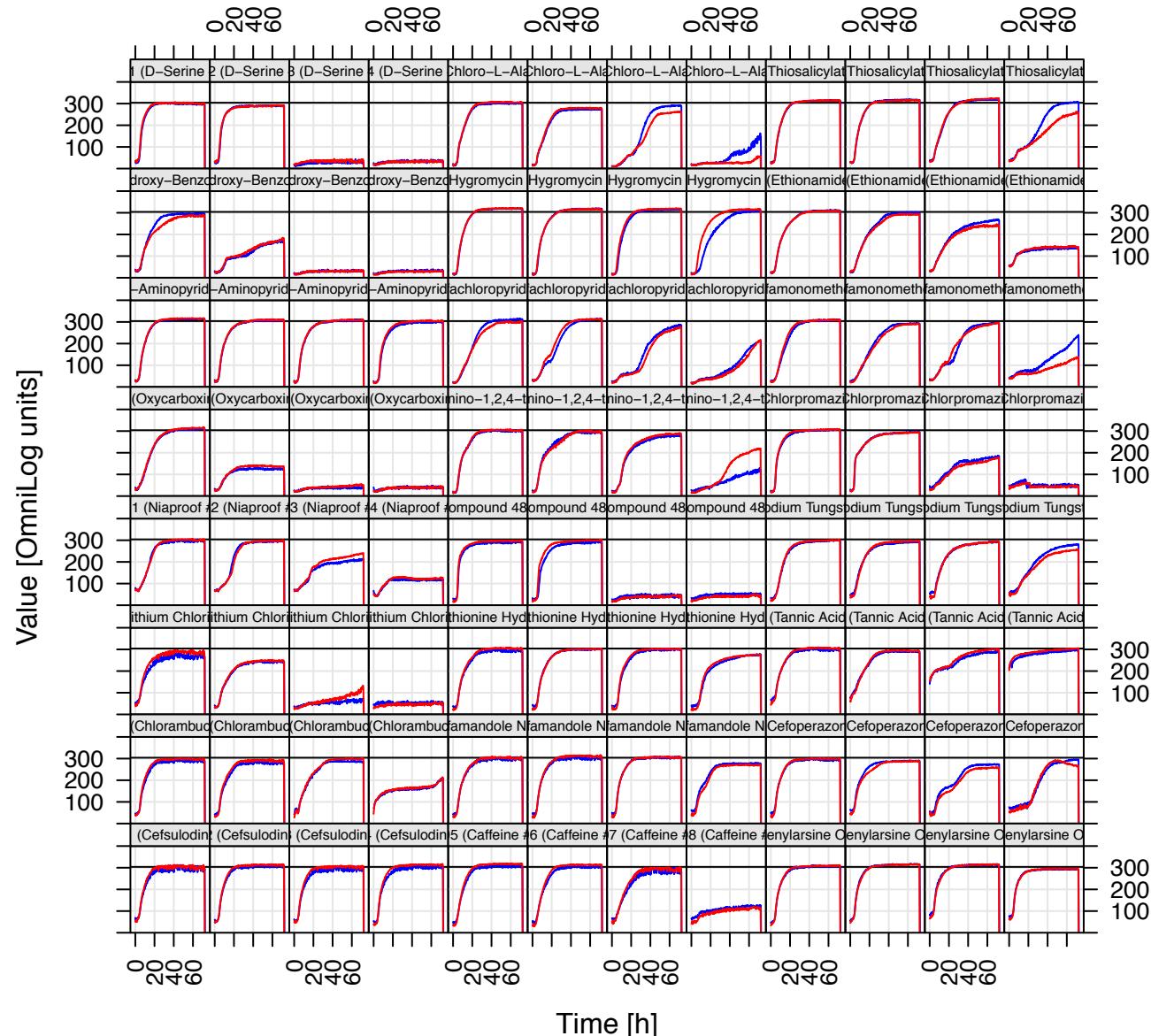
A1 D-Serine	A2 D-Serine	A3 D-Serine	A4 D-Serine	A5 β-Chloro- L-alanine hydrochloride	A6 β-Chloro- L-alanine hydrochloride	A7 β-Chloro- L-alanine hydrochloride	A8 β-Chloro- L-alanine hydrochloride	A9 Thiosalicylic acid	A10 Thiosalicylic acid	A11 Thiosalicylic acid	A12 Thiosalicylic acid
1	2	3	4	1	2	3	4	1	2	3	4
B1 Sodium salicylate	B2 Sodium salicylate	B3 Sodium salicylate	B4 Sodium salicylate	B5 Hygromycin B	B6 Hygromycin B	B7 Hygromycin B	B8 Hygromycin B	B9 Ethionamide	B10 Ethionamide	B11 Ethionamide	B12 Ethionamide
1	2	3	4	1	2	3	4	1	2	3	4
C1 4-Aminopyridine	C2 4-Aminopyridine	C3 4-Aminopyridine	C4 4-Aminopyridine	C5 Sulfachloro- pyridazine	C6 Sulfachloro- pyridazine	C7 Sulfachloro- pyridazine	C8 Sulfachloro- pyridazine	C9 Sulfamono- methoxine	C10 Sulfamono- methoxine	C11 Sulfamono- methoxine	C12 Sulfamono- methoxine
1	2	3	4	1	2	3	4	1	2	3	4
D1 Oxycarboxin	D2 Oxycarboxin	D3 Oxycarboxin	D4 Oxycarboxin	D5 3-Amino-1,2,4- triazole	D6 3-Amino-1,2,4- triazole	D7 3-Amino-1,2,4- triazole	D8 3-Amino-1,2,4- triazole	D9 Chlorpromazine	D10 Chlorpromazine	D11 Chlorpromazine	D12 Chlorpromazine
1	2	3	4	1	2	3	4	1	2	3	4
E1 Niaproof	E2 Niaproof	E3 Niaproof	E4 Niaproof	E5 Compound 48/80	E6 Compound 48/80	E7 Compound 48/80	E8 Compound 48/80	E9 Sodium tungstate	E10 Sodium tungstate	E11 Sodium tungstate	E12 Sodium tungstate
1	2	3	4	1	2	3	4	1	2	3	4
F1 Lithium chloride	F2 Lithium chloride	F3 Lithium chloride	F4 Lithium chloride	F5 DL-Methionine hydroxamate	F6 DL-Methionine hydroxamate	F7 DL-Methionine hydroxamate	F8 DL-Methionine hydroxamate	F9 Tannic acid	F10 Tannic acid	F11 Tannic acid	F12 Tannic acid
1	2	3	4	1	2	3	4	1	2	3	4
G1 Chlorambucil	G2 Chlorambucil	G3 Chlorambucil	G4 Chlorambucil	G5 Cefamandole nafate	G6 Cefamandole nafate	G7 Cefamandole nafate	G8 Cefoperazone	G9 Cefoperazone	G10 Cefoperazone	G11 Cefoperazone	G12 Cefoperazone
1	2	3	4	1	2	3	4	1	2	3	4
H1 Cefsulodin	H2 Cefsulodin	H3 Cefsulodin	H4 Cefsulodin	H5 Caffeine	H6 Caffeine	H7 Caffeine	H8 Caffeine	H9 Phenylarsine oxide	H10 Phenylarsine oxide	H11 Phenylarsine oxide	H12 Phenylarsine oxide
1	2	3	4	1	2	3	4	1	2	3	4

PM18C MicroPlate™

A1 Ketoprofen	A2 Ketoprofen	A3 Ketoprofen	A4 Ketoprofen	A5 Sodium pyrophosphate decahydrate	A6 Sodium pyrophosphate decahydrate	A7 Sodium pyrophosphate decahydrate	A8 Sodium pyrophosphate decahydrate	A9 Thiamphenicol	A10 Thiamphenicol	A11 Thiamphenicol	A12 Thiamphenicol
1	2	3	4	1	2	3	4	1	2	3	4
B1 Trifluorothymidine	B2 Trifluorothymidine	B3 Trifluorothymidine	B4 Trifluorothymidine	B5 Pipemicid Acid	B6 Pipemicid Acid	B7 Pipemicid Acid	B8 Pipemicid Acid	B9 Azathioprine	B10 Azathioprine	B11 Azathioprine	B12 Azathioprine
1	2	3	4	1	2	3	4	1	2	3	4
C1 Poly-L-lysine	C2 Poly-L-lysine	C3 Poly-L-lysine	C4 Poly-L-lysine	C5 Sulfisoxazole	C6 Sulfisoxazole	C7 Sulfisoxazole	C8 Sulfisoxazole	C9 Pentachloro- phenol	C10 Pentachloro- phenol	C11 Pentachloro- phenol	C12 Pentachloro- phenol
1	2	3	4	1	2	3	4	1	2	3	4
D1 Sodium m-arsenite	D2 Sodium m-arsenite	D3 Sodium m-arsenite	D4 Sodium m-arsenite	D5 Sodium bromate	D6 Sodium bromate	D7 Sodium bromate	D8 Sodium bromate	D9 Lidocane	D10 Lidocane	D11 Lidocane	D12 Lidocane
1	2	3	4	1	2	3	4	1	2	3	4
E1 Sodium metasilicate	E2 Sodium metasilicate	E3 Sodium metasilicate	E4 Sodium metasilicate	E5 Sodium m-periodate	E6 Sodium m-periodate	E7 Sodium m-periodate	E8 Sodium m-periodate	E9 Antimony (III) chloride	E10 Antimony (III) chloride	E11 Antimony (III) chloride	E12 Antimony (III) chloride
1	2	3	4	1	2	3	4	1	2	3	4
F1 Semicarbazide	F2 Semicarbazide	F3 Semicarbazide	F4 Semicarbazide	F5 Tinidazole	F6 Tinidazole	F7 Tinidazole	F8 Tinidazole	F9 Aztreonam	F10 Aztreonam	F11 Aztreonam	F12 Aztreonam
1	2	3	4	1	2	3	4	1	2	3	4
G1 Triclosan	G2 Triclosan	G3 Triclosan	G4 Triclosan	G5 3,5-Diamino- 1,2,4-triazole (Guanazole)	G6 3,5-Diamino- 1,2,4-triazole (Guanazole)	G7 3,5-Diamino- 1,2,4-triazole (Guanazole)	G8 3,5-Diamino- 1,2,4-triazole (Guanazole)	G9 Myricetin	G10 Myricetin	G11 Myricetin	G12 Myricetin
1	2	3	4	1	2	3	4	1	2	3	4
H1 5-fluoro-5'- deoxyuridine	H2 5-fluoro-5'- deoxyuridine	H3 5-fluoro-5'- deoxyuridine	H4 5-fluoro-5'- deoxyuridine	H5 2-Phenylphenol	H6 2-Phenylphenol	H7 2-Phenylphenol	H8 2-Phenylphenol	H9 Plumbagin	H10 Plumbagin	H11 Plumbagin	H12 Plumbagin
1	2	3	4	1	2	3	4	1	2	3	4

PM17 (Chemical Sensitivity Bacteria)

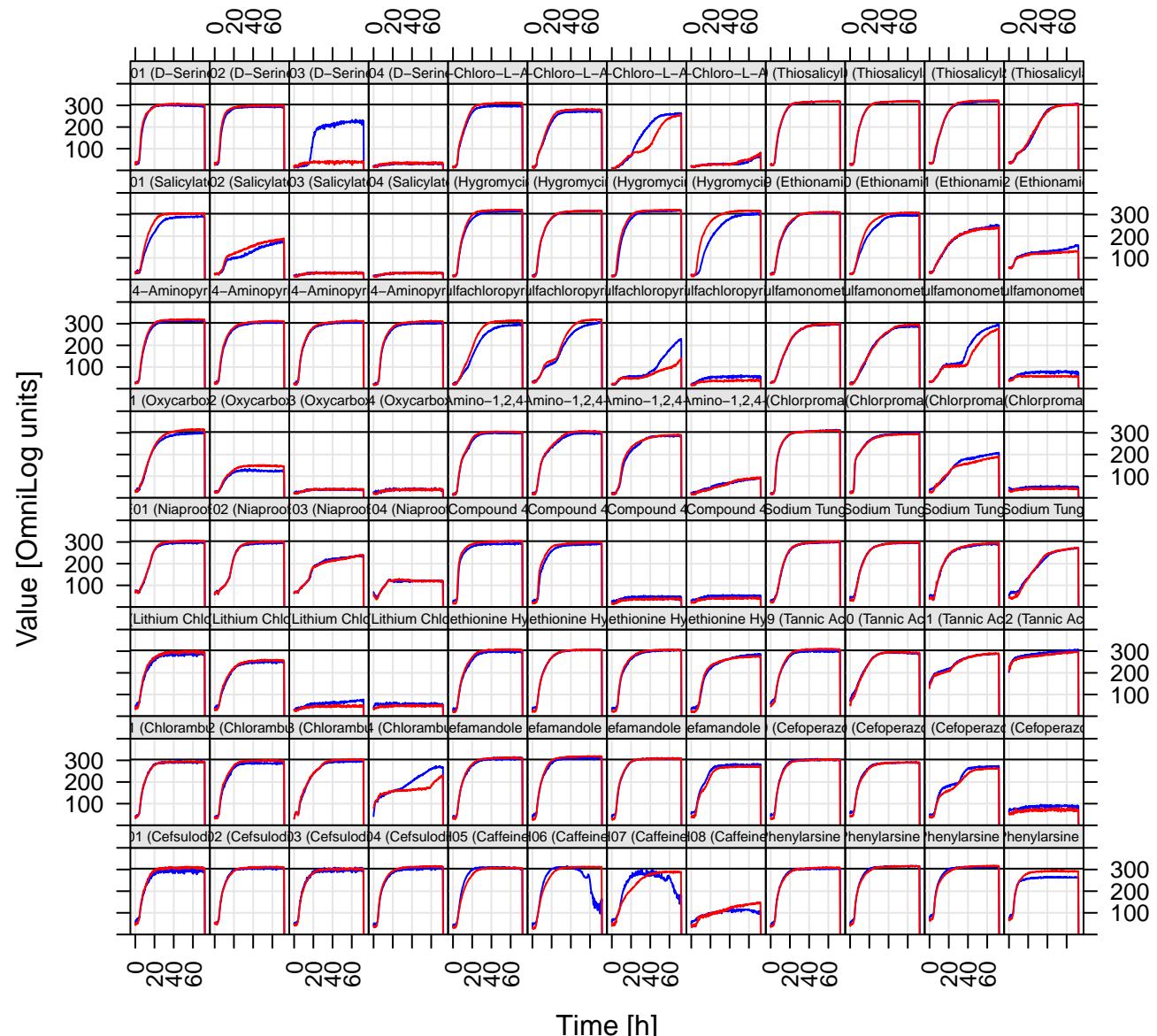
Δ SPFH-2
WT-2



PM17 (Chemicals)

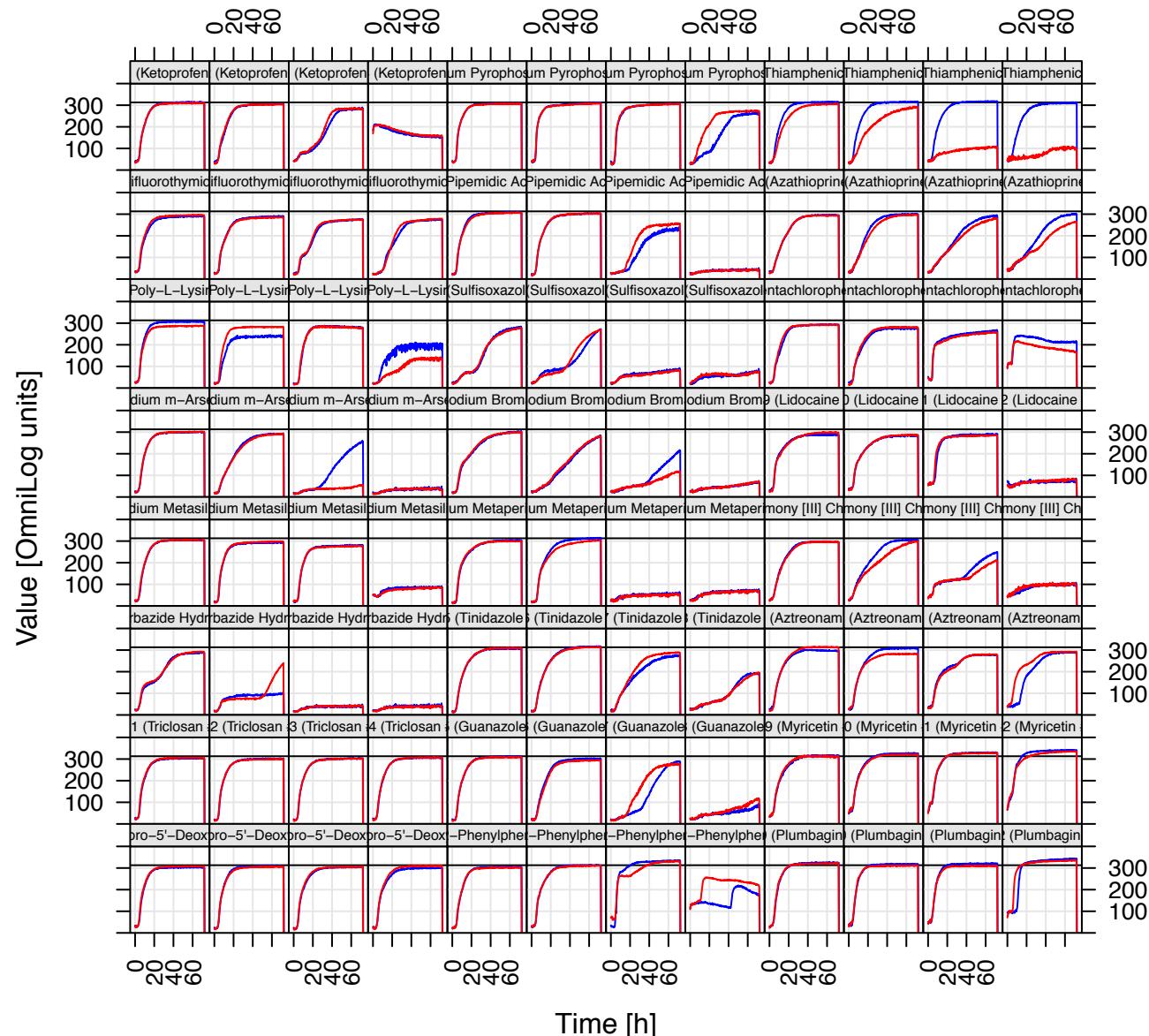
Δ SPFH-1

WT-1



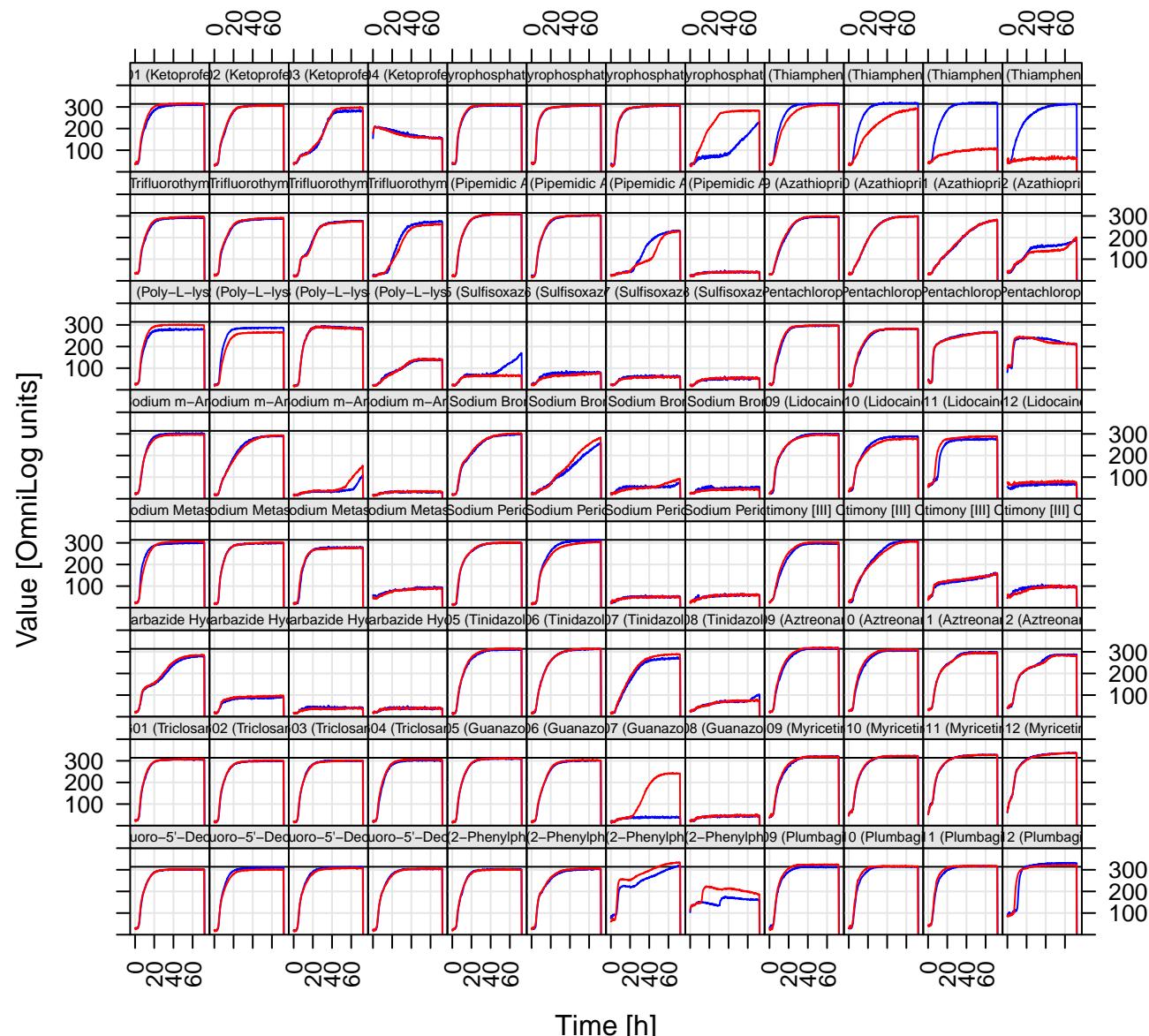
PM18 (Chemical Sensitivity Bacteria)

Δ SPFH-2
WT-2



PM18 (Chemicals)

ΔSPFH-1
WT-1



PM19 MicroPlate™

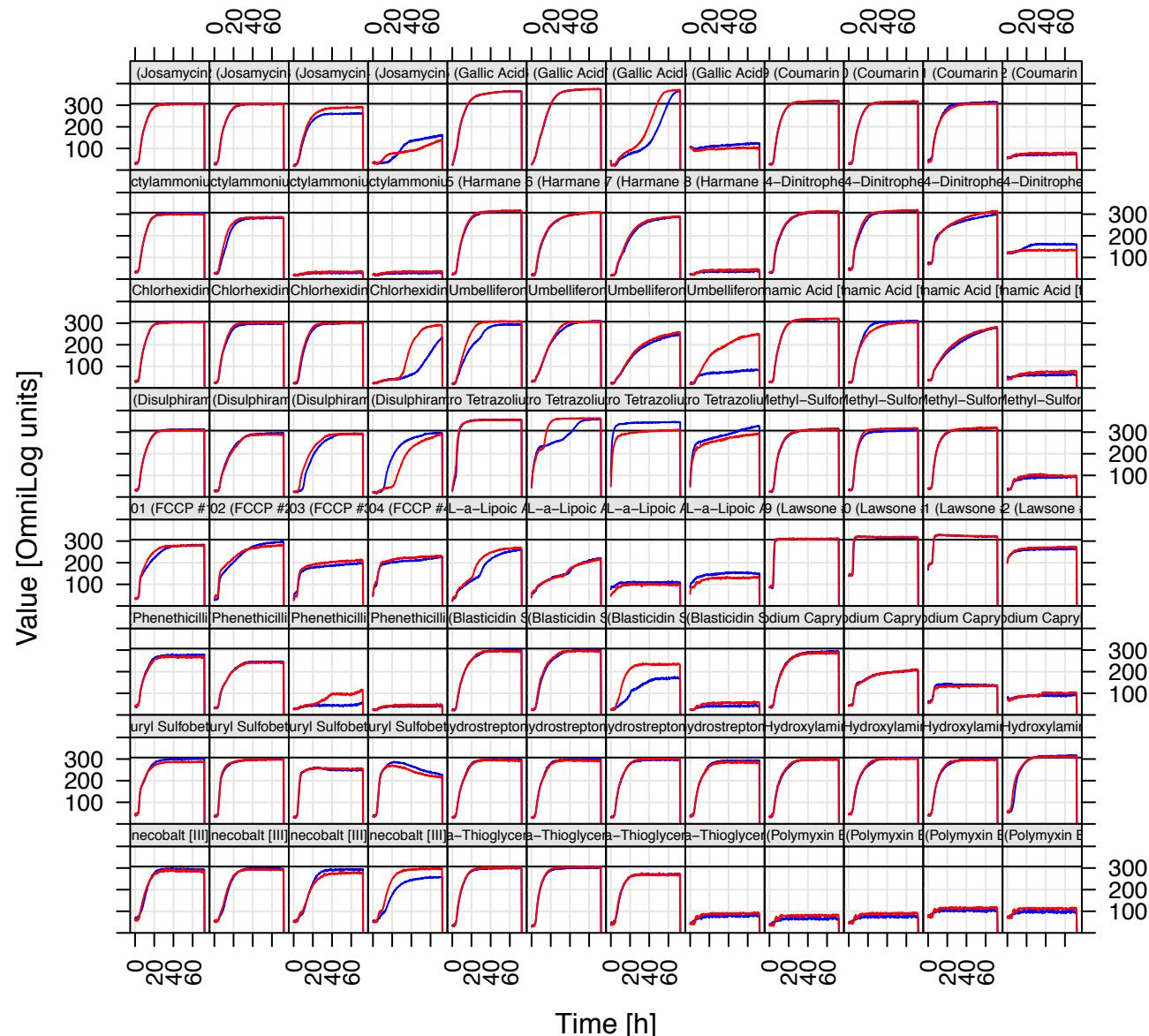
A1 Josamycin	A2 Josamycin	A3 Josamycin	A4 Josamycin	A5 Gallic acid	A6 Gallic acid	A7 Gallic acid	A8 Gallic acid	A9 Coumarin	A10 Coumarin	A11 Coumarin	A12 Coumarin
1	2	3	4	1	2	3	4	1	2	3	4
B1 Methyltriocetyl- ammonium chloride	B2 Methyltriocetyl- ammonium chloride	B3 Methyltriocetyl- ammonium chloride	B4 Methyltriocetyl- ammonium chloride	B5 Harmane	B6 Harmane	B7 Harmane	B8 Harmane	B9 2,4-Dintrophenol	B10 2,4-Dintrophenol	B11 2,4-Dintrophenol	B12 2,4-Dintrophenol
1	2	3	4	1	2	3	4	1	2	3	4
C1 Chlorhexidine	C2 Chlorhexidine	C3 Chlorhexidine	C4 Chlorhexidine	C5 Umbelliferone	C6 Umbelliferone	C7 Umbelliferone	C8 Umbelliferone	C9 Cinnamic acid	C10 Cinnamic acid	C11 Cinnamic acid	C12 Cinnamic acid
1	2	3	4	1	2	3	4	1	2	3	4
D1 Disulphiram	D2 Disulphiram	D3 Disulphiram	D4 Disulphiram	D5 Iodonitro Tetrazolium Violet	D6 Iodonitro Tetrazolium Violet	D7 Iodonitro Tetrazolium Violet	D8 Iodonitro Tetrazolium Violet	D9 Phenyl- methyl- sulfonyl- fluoride (PMSF)	D10 Phenyl- methyl- sulfonyl- fluoride (PMSF)	D11 Phenyl- methyl- sulfonyl- fluoride (PMSF)	D12 Phenyl- methyl- sulfonyl- fluoride (PMSF)
1	2	3	4	1	2	3	4	1	2	3	4
E1 FCCP	E2 FCCP	E3 FCCP	E4 FCCP	E5 D,L-Thioctic Acid	E6 D,L-Thioctic Acid	E7 D,L-Thioctic Acid	E8 D,L-Thioctic Acid	E9 Lawsone	E10 Lawsone	E11 Lawsone	E12 Lawsone
1	2	3	4	1	2	3	4	1	2	3	4
F1 Phenethicillin	F2 Phenethicillin	F3 Phenethicillin	F4 Phenethicillin	F5 Blasticidin S	F6 Blasticidin S	F7 Blasticidin S	F8 Blasticidin S	F9 Sodium caprylate	F10 Sodium caprylate	F11 Sodium caprylate	F12 Sodium caprylate
1	2	3	4	1	2	3	4	1	2	3	4
G1 Lauryl sulfobetaine	G2 Lauryl sulfobetaine	G3 Lauryl sulfobetaine	G4 Lauryl sulfobetaine	G5 Dihydro- streptomycin	G6 Dihydro- streptomycin	G7 Dihydro- streptomycin	G8 Dihydro- streptomycin	G9 Hydroxylamine	G10 Hydroxylamine	G11 Hydroxylamine	G12 Hydroxylamine
1	2	3	4	1	2	3	4	1	2	3	4
H1 Hexamine cobalt (III) chloride	H2 Hexamine cobalt (III) chloride	H3 Hexamine cobalt (III) chloride	H4 Hexamine cobalt (III) chloride	H5 Thioglycerol	H6 Thioglycerol	H7 Thioglycerol	H8 Thioglycerol	H9 Polymyxin B	H10 Polymyxin B	H11 Polymyxin B	H12 Polymyxin B
1	2	3	4	1	2	3	4	1	2	3	4

PM20B MicroPlate™

A1 Amitriptyline	A2 Amitriptyline	A3 Amitriptyline	A4 Amitriptyline	A5 Aramycin	A6 Aramycin	A7 Aramycin	A8 Aramycin	A9 Benserazide	A10 Benserazide	A11 Benserazide	A12 Benserazide
1	2	3	4	1	2	3	4	1	2	3	4
B1 Orphenadrine	B2 Orphenadrine	B3 Orphenadrine	B4 Orphenadrine	B5 D,L-Propranolol	B6 D,L-Propranolol	B7 D,L-Propranolol	B8 D,L-Propranolol	B9 Tetrazolium violet	B10 Tetrazolium violet	B11 Tetrazolium violet	B12 Tetrazolium violet
1	2	3	4	1	2	3	4	1	2	3	4
C1 Thioridazine	C2 Thioridazine	C3 Thioridazine	C4 Thioridazine	C5 Atropine	C6 Atropine	C7 Atropine	C8 Atropine	C9 Ornidazole	C10 Ornidazole	C11 Ornidazole	C12 Ornidazole
1	2	3	4	1	2	3	4	1	2	3	4
D1 Proflavine	D2 Proflavine	D3 Proflavine	D4 Proflavine	D5 Ciprofloxacin	D6 Ciprofloxacin	D7 Ciprofloxacin	D8 Ciprofloxacin	D9 18-Crown-6 ether	D10 18-Crown-6 ether	D11 18-Crown-6 ether	D12 18-Crown-6 ether
1	2	3	4	1	2	3	4	1	2	3	4
E1 Crystal violet	E2 Crystal violet	E3 Crystal violet	E4 Crystal violet	E5 Dodine	E6 Dodine	E7 Dodine	E8 Dodine	E9 Hexa- chlorophene	E10 Hexa- chlorophene	E11 Hexa- chlorophene	E12 Hexa- chlorophene
1	2	3	4	1	2	3	4	1	2	3	4
F1 4-Hydroxy- coumarin	F2 4-Hydroxy- coumarin	F3 4-Hydroxy- coumarin	F4 4-Hydroxy- coumarin	F5 Oxytetracycline	F6 Oxytetracycline	F7 Oxytetracycline	F8 Oxytetracycline	F9 Pridinol	F10 Pridinol	F11 Pridinol	F12 Pridinol
1	2	3	4	1	2	3	4	1	2	3	4
G1 Captan	G2 Captan	G3 Captan	G4 Captan	G5 3,5-Dinitro- benzene	G6 3,5-Dinitro- benzene	G7 3,5-Dinitro- benzene	G8 3,5-Dinitro- benzene	G9 8-Hydroxy- quinoline	G10 8-Hydroxy- quinoline	G11 8-Hydroxy- quinoline	G12 8-Hydroxy- quinoline
1	2	3	4	1	2	3	4	1	2	3	4
H1 Patulin	H2 Patulin	H3 Patulin	H4 Patulin	H5 Tolyfluanid	H6 Tolyfluanid	H7 Tolyfluanid	H8 Tolyfluanid	H9 Troleandomycin	H10 Troleandomycin	H11 Troleandomycin	H12 Troleandomycin
1	2	3	4	1	2	3	4	1	2	3	4

PM19 (Chemical Sensitivity Bacteria)

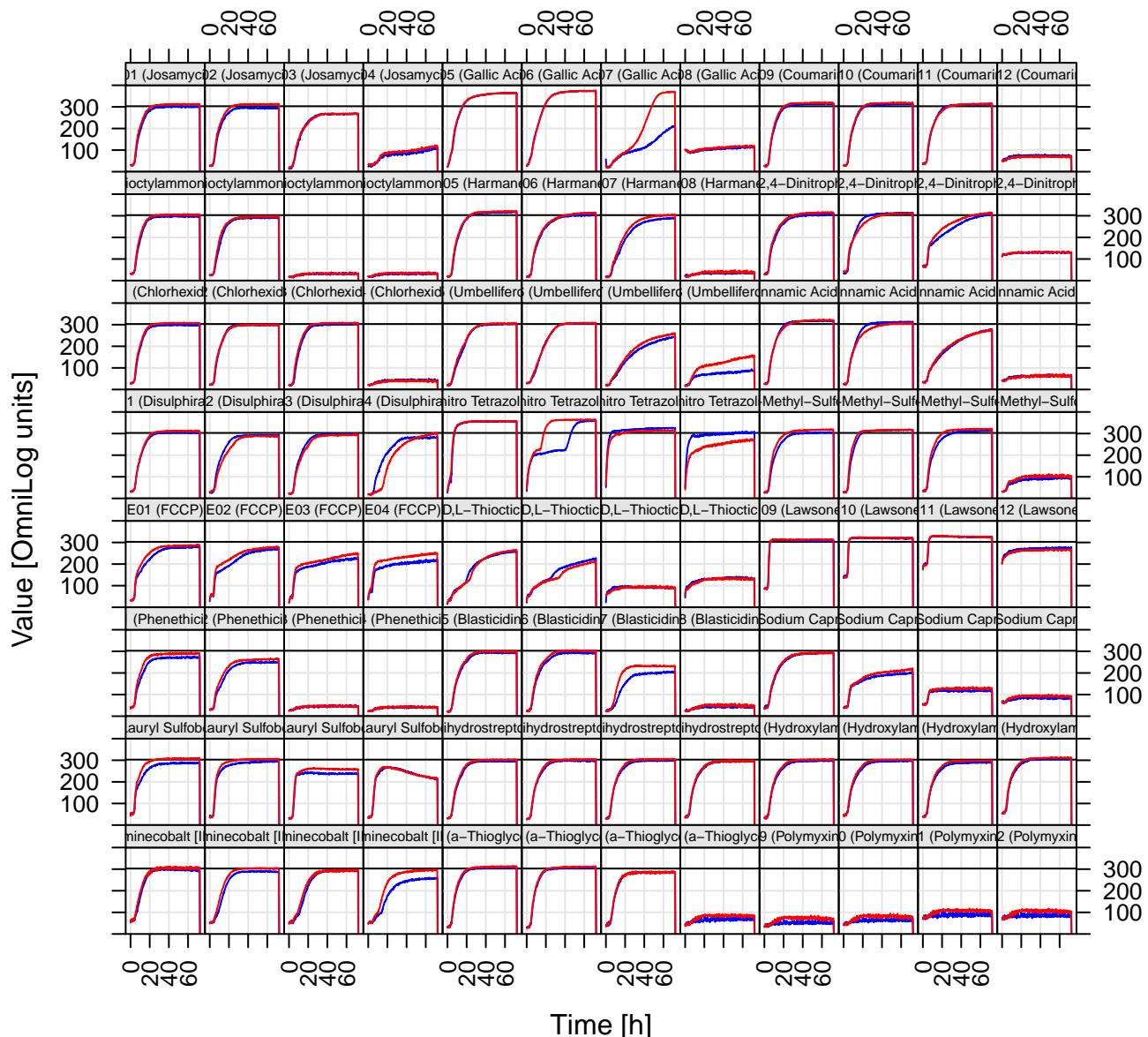
Δ SPFH-2
WT-2



PM19 (Chemicals)

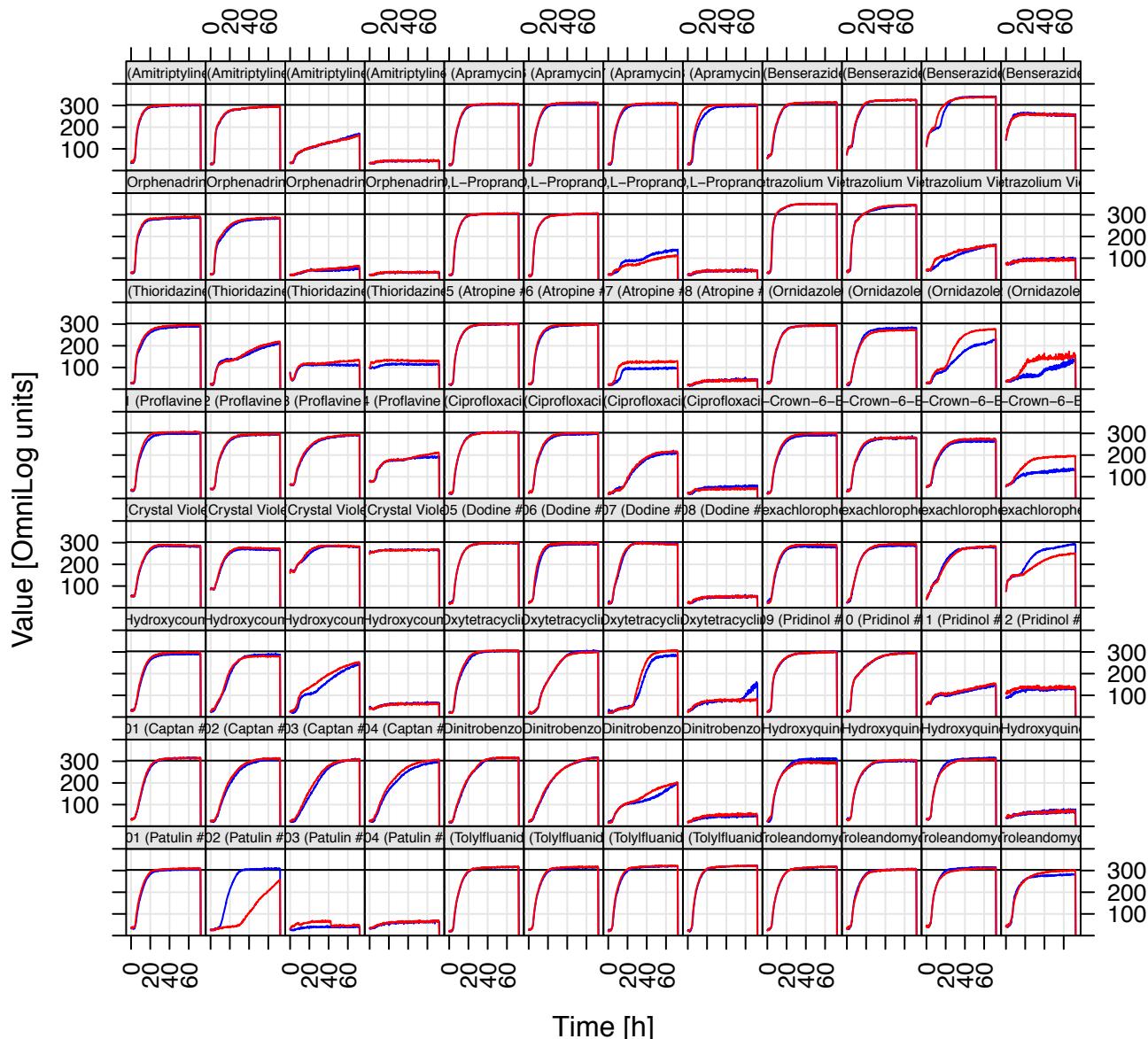
ASPFH-1

WT-1



PM20 (Chemical Sensitivity Bacteria)

Δ SPFH-2
WT-2



PM20 (Chemicals)

ASPFH-1

WT-1

