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### ► To cite this version:

Jean-Philippe Barnier, Julie Meyer, Subramania Kolappan, Haniaa Bouzinba-Ségard, Gaël Gesbert, et al.. The minor pilin PilV provides a conserved adhesion site throughout the antigenically variable meningococcal type IV pilus. *Proceedings of the National Academy of Sciences of the United States of America*, 2021, 118 (45), pp.e2109364118. 10.1073/pnas.2109364118 . hal-03552815

**HAL Id: hal-03552815**

**<https://hal.science/hal-03552815>**

Submitted on 15 Feb 2022

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1 **THE MINOR PILIN PILV PROVIDES A CONSERVED ADHESION SITE**  
2 **THROUGHOUT THE ANTIGENICALLY VARIABLE MENINGOCOCCAL TYPE IV**  
3 **PILUS**

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23 **ABSTRACT**

24 *Neisseria meningitidis* utilizes type IV pili to adhere to and colonize host endothelial cells, a  
25 process at the heart of meningococcal invasive diseases leading to meningitis and sepsis. Type  
26 IV pili are polymers of an antigenically variable major pilin building block, PilE, plus several  
27 core minor pilins that initiate pilus assembly and are thought to be located at the pilus tip.  
28 Adhesion of *N. meningitidis* to human endothelial cells requires both PilE and a conserved non-  
29 core minor pilin PilV but the localization of PilV and its precise role in this process remains to  
30 be clarified. Here we show that both PilE and PilV promote adhesion to endothelial vessels *in*  
31 *vivo*. The substantial adhesion defect observed for *pilV* mutants suggests it is the main adhesin.  
32 Consistent with this observation, super-resolution microscopy showed its abundant distribution  
33 throughout the pilus. We determined the crystal structure of PilV and modeled in within the  
34 pilus filament. The small size of PilV causes it to be recessed relative to adjacent PilE subunits,  
35 which are dominated by a prominent hypervariable loop. Nonetheless, we identified a  
36 conserved surface-exposed adhesive loop on PilV by alanine scanning mutagenesis. Critically,  
37 antibodies directed against PilV inhibit *N. meningitidis* colonization of human skin grafts. These  
38 findings explain how *N. meningitidis* T4P undergo antigenic variation to evade the humoral  
39 immune response while maintaining their adhesive function, and establish the potential of this  
40 highly conserved minor pilin as a vaccine and therapeutic target for the prevention and  
41 treatment of *N. meningitidis* infections.

42 **SIGNIFICANCE STATEMENT**

43 Type IV pili (T4P) are among the most widespread adhesive factors in prokaryotes. In  
44 pathogenic *Neisseria* the major pilin, which provides the structural framework for the  
45 filamentous T4P, undergoes antigenic variation allowing the bacteria to evade the humoral  
46 immune response without impacting host cell adhesion. Here we show that a minor pilin, PilV,  
47 is distributed throughout the pilus and contributes to *Neisseria meningitidis* adhesion, and that  
48 antibodies to PilV block meningococcal adhesion *in vivo*. Our results provide a mechanism  
49 whereby *N. meningitidis* varies its immunodominant major pilin to escape antibody recognition  
50 while maintaining conserved sites throughout the pilus for host receptor binding. They further  
51 suggest a strategy to prevent or block deadly *N. meningitidis* infections by targeting this minor  
52 pilin.

## 53 INTRODUCTION

54 The human-restricted bacterial pathogen *Neisseria meningitidis* is a leading cause of meningitis  
55 and sepsis worldwide and represents a significant global public health threat (Chang et al., 2012;  
56 Muttalif et al., 2019). *N. meningitidis* is carried asymptotically in the protective mucus layer  
57 of the throat for 5% to 25% of the population (Christensen et al., 2010; Coureuil et al., 2019;  
58 Audry et al., 2019). In some cases, *N. meningitidis* disseminates into the bloodstream, an  
59 environment to which this bacterium is remarkably well-adapted. Meningococci possess a  
60 polysaccharide capsule that protects them against complement deposition, plus several  
61 membrane associated factors that are important for survival, including factor H binding protein  
62 and iron uptake systems (Siena et al., 2018). Critical to *N. meningitidis* survival in the  
63 bloodstream are the type IV pili (T4P), which mediate vascular colonization; non-piliated  
64 meningococci are rapidly cleared from the blood (Barnier et al., 2021; Capel et al., 2017; Denis  
65 et al., 2019). T4P are long filamentous appendages displayed peritrichously on the bacterium.  
66 The major pilin protein, Pile, is the primary building block of the pilus. This and other surface-  
67 displayed *N. meningitidis* proteins undergo antigenic variation, allowing this pathogen to evade  
68 a protective immune response (Cahoon and Seifert, 2009; Vink et al., 2012; Wörmann et al.,  
69 2014).

70 T4P are responsible for acute colonization of human blood vessels and are thus essential  
71 in establishing invasive meningococcal diseases (Barnier et al., 2021; Bernard et al., 2014;  
72 Denis et al., 2019; Join-Lambert et al., 2013). T4P are helical polymers of the major pilin  
73 assembled by the T4P machinery (Craig et al., 2019; McCallum et al., 2019). The conserved  
74 N-terminus of the major pilin is a hydrophobic  $\alpha$ -helix that tethers the C-terminal globular  
75 domain in the inner membrane prior to pilus assembly, and forms a helical array in the core of  
76 the intact pilus, displaying the globular domain on the filament surface. Pilus assembly is  
77 initiated by a cluster of pilin-like proteins called minor pilins (Nguyen et al., 2015; Kolappan

78 et al., 2015; Ng et al., 2016; Treuner-Lange et al., 2020). These “core” minor pilins are thought  
79 to localize to the pilus tip. The major pilin, PilE, is highly conserved in amino acid sequence  
80 and structure between *N. meningitidis* and the urogenital pathogen *Neisseria gonorrhoeae* with  
81 the exception of a hypervariable  $\beta$ -hairpin near the C-terminus that is prominent on the pilus  
82 surface (Parge et al., 1995; Craig et al., 2006; Kolappan et al., 2016; Wang et al., 2017). In *N.*  
83 *meningitidis*, PilE has been shown to bind to sialylated N-glycans on the human endothelial cell  
84 receptor CD147 (also called EMMPRIN or Basigin) (Le Guennec et al., 2020) and the  $\beta$ 2-  
85 adrenergic receptor (Virion et al., 2019), two membrane proteins that form a heterotrimeric  
86 complex with cytoplasmic  $\alpha$ -actinin 4 (Maïssa et al., 2017).

87 The pathogenic *Neisseria* possess a set of core minor pilins, PilH (FimT), PilI (PilV), PilJ  
88 (PilW) PilK and PilX, that are encoded within a single gene cluster and prime pilus assembly  
89 (Winther-Larsen et al., 2005) plus “non-core” minor pilins PilV and ComP, which are encoded  
90 elsewhere on the genome. ComP shares the canonical T4P-pilin structure of the major pilin,  
91 PilE, with the N-terminal  $\alpha$ -helix and C-terminal globular domain (Berry et al., 2016). ComP  
92 is involved in natural transformation of exogenous DNA (Cehovin et al., 2013). PilV, which is  
93 highly conserved in *N. meningitidis* isolates (Cehovin et al., 2010), participates in adhesion and  
94 signaling in host cells (Winther-Larsen et al., 2001; Mikaty et al., 2009; Takahashi et al., 2012;  
95 Bernard et al., 2014; Virion et al., 2019). In *N. meningitidis*, PilV, like PilE, directly interacts  
96 with CD147 and the  $\beta$ 2-adrenergic receptor, suggesting that PilV colocalizes with PilE within  
97 the T4P filament (Bernard et al., 2014; Virion et al., 2019). However, another report concluded  
98 that PilV functions exclusively from within the periplasm, fine-tuning pilus surface display to  
99 regulate its interactions with host cells (Imhaus and Dumenil, 2014).

100 The T4P-receptor interaction represents a key step in *N. meningitidis* adhesion and  
101 colonization of endothelial cells in peripheral and brain vasculature and is thus an attractive  
102 target for preventive and therapeutic approaches to tackle meningococcal infection. Interfering

103 with piliation prevents *N. meningitidis* colonization of human endothelial cells and vasculature  
104 (Aubey et al., 2019) and improves sepsis outcome in a mouse model grafted with human skin  
105 (Denis et al., 2019). Although both PilE and PilV are involved in adhesion, PilE exhibits  
106 considerable amino acid sequence variability in its exposed hypervariable region. This  
107 variability contributes to Neisseria immune escape. In contrast PilV is highly conserved and  
108 has been shown to be immunogenic in humans (Cehovin et al., 2011). Thus, PilV may prove to  
109 be a more promising target than PilE for blocking endothelial cell adhesion. A molecular  
110 understanding of this minor pilin with respect to its structure, localization within the pilus and  
111 interactions with host receptors will be valuable in assessing its potential as a therapeutic target.  
112 Here we report the atomic structure of PilV and super-resolution microscopy images showing  
113 that it is incorporated throughout the *N. meningitidis* T4P. We identify residues involved in  
114 adhesion to host cells and map these onto the PilV structure, modeled within the cryo-electron  
115 microscopy-derived pilus filament structure. Finally, we show that anti-PilV antibodies inhibit  
116 meningococcal adhesion *in vivo*. These data provide insights into PilV-mediated adhesion and  
117 suggest that blocking its adherence functions may inhibit *N. meningitidis* vascular colonization  
118 and pathogenesis.  
119

## 120 RESULTS

### 121 **PilE and PilV make distinct contributions to T4P-dependent meningococcal adhesion**

122 Both PilE and PilV have been shown to directly interact with host cell receptors (Bernard et al.,  
123 2014; Virion et al., 2019). To investigate their specific roles in meningococcal adhesion to  
124 human cells we compared adhesion for wild-type (WT) *N. meningitidis* strain 2C4.3 with that  
125 of derivative strains lacking either PilE or PilV on three endothelial cell types (Fig. 1A): primary  
126 human dermal microvascular endothelial cells (HDMEC) that are thought to have conserved  
127 their *in vivo* phenotype (Aird, 2012); the human cerebral microvascular endothelial cell line D3  
128 (hCMEC/D3) that possesses characteristics of brain endothelial cells; and EA.Hy926 cells,  
129 obtained by fusion of human umbilical vein endothelial cells (HUVECs) with the human  
130 epithelial carcinoma cell line A549. While both  $\Delta pilE$  ( $\Delta E$ ) and  $\Delta pilV$  ( $\Delta V$ ) mutants showed  
131 substantial adhesion defects compared to WT bacteria, the defect of the  $\Delta E$  mutant is more  
132 pronounced on primary human dermal microvascular endothelial cells (HDMECs) compared  
133 to the  $\Delta V$  mutant (2.4 fold decrease between means of  $\Delta V$  vs.  $\Delta E$ ). PilV complementation of  
134 the  $\Delta pilV$  strain ( $\Delta V+V$ ) partially restored adhesion to endothelial cells.

135 To assess the adhesive role of PilE *in vivo* we used a SCID mouse model grafted with  
136 human skin (Join-Lambert et al., 2013) to quantify bacterial adhesion on human vessels *in vivo*.  
137 Grafted mice were infected intravenously with the WT,  $\Delta E$  or  $\Delta V$  mutant strains and bacterial  
138 loads in the graft and in the blood were quantified by counting colony forming units (CFUs) at  
139 different time points (Fig. 1B and supplemental Fig. 1A). Blood bacterial loads were identical  
140 between the three strains at 1 hour post-infection, indicating that equivalent inocula were  
141 administered for each bacterial strain (Supplemental Fig. 1A). Whereas more than  $10^8$  CFUs  
142 were recovered 4 hours after infection from the graft infected with WT *N. meningitidis*, only  $6$   
143  $\times 10^3$  CFUs were recovered from the grafts infected with PilE-defective meningococci,  
144 representing  $\sim 0.0005\%$  of the WT strain. The small number of  $\Delta E$  bacteria are likely non-

145 adherent cells present in the bloodstream of the graft microvasculature, as shown previously  
146 (Join-Lambert et al., 2013). The colonization efficiency of the PilV-defective strain was also  
147 impaired substantially at ~0.08% of the WT strain, yet it was 170-fold greater than that of the  
148 PilE-defective strain, suggesting an important role for PilV in human endothelial cell adhesion.

149 We next assessed pilus levels in the  $\Delta V$  strain to determine whether loss of piliation  
150 might explain its adhesion defect. T4P were mechanically sheared from WT,  $\Delta V$  and  $\Delta V + V$   
151 strains by vortexing, separated from the cells by centrifugation, and concentrated using  
152 ammonium sulfate precipitation, producing a crudely purified pilus fraction that contains both  
153 major and minor pilins (Helaine et al., 2005; Winther-Larsen et al., 2001; Wolfgang et al.,  
154 1998). Pilus levels were reported as a piliation index, determined by quantifying the PilE  
155 content in sheared pili fraction normalized to the PilE in the bacteria fraction. As shown in Fig.  
156 1C and Supplemental Fig. 1B, all three strains express equivalent amounts of PilE in the whole  
157 cell lysates, but PilE is reduced in the sheared fraction of the  $\Delta V$  strain relative to WT,  
158 corresponding to a piliation index of 50%. Thus, while deletion of PilV reduces pilus levels in  
159 the  $\Delta V$  this reduction does not account for the pronounced adhesion defects observed for the  
160 PilV-defective strain in cell culture and in the mouse graft model. These results suggest that  
161 PilV is in fact the major adhesin on the *N. meningitidis* T4P.

162

### 163 **PilV-mediated adhesion is a conserved feature of *N. meningitidis***

164 In contrast to PilE, which contains a surface exposed hypervariable loop providing extensive  
165 antigenic variation, PilV is conserved among clinical isolates (Cehovin et al., 2010). We  
166 examined 17,732 *N. meningitidis* genomes available in the PubMLST database, we identified  
167 699 distinct PilV sequences having a mean sequence identity greater than 80% ( $86.6\% \pm 5.9\%$   
168 SD) between every possible sequence pair, indicating high conservation (Supplemental Table  
169 S1).

170

171 ***N. meningitidis* PilV is distributed throughout the T4P filament**

172 Both PilV and PilE were shown previously to bind to CD147 and the  $\beta$ 2-adrenergic (Bernard  
173 et al., 2014; Virion et al., 2019), suggesting that PilV colocalizes with PilE in the pilus filament.  
174 To investigate PilV localization and understand how it might serve as the main adhesin *in vivo*,  
175 we tested for the presence of PilV in *N. meningitidis* T4P. Immunoblotting of ammonium  
176 sulfate-precipitated pili with anti-PilV antibody showed that PilV is present along with PilE  
177 (Supplemental Fig. 2A). This finding does not appear to be due to contamination of cell-  
178 associated proteins as the sheared fractions lacked both the cytosolic marker NADP-glutamate-  
179 deshydrogenase and the membrane marker, Rmp4 (Supplemental Fig. 2A). To further  
180 demonstrate that PilV is incorporated into the meningococcal T4P filament, we  
181 immunoprecipitated pili from a crude preparation using anti PilE and anti-PilV antibodies. PilV  
182 is present in the pilus fraction immunoprecipitated with anti-PilE antibody and, conversely, PilE  
183 is present in the pilus fraction immunoprecipitated with anti-PilV antibody, consistent with  
184 these proteins colocalizing within the pilus (Supplemental Fig. 2B, C).

185 To directly visualize PilV in the T4P filaments, we analyzed the spatial organization of  
186 both PilV and PilE at the molecular level (~ 20 nm) using super-resolution microscopy  
187 technique based on single-molecule localization (dSTORM) (Maïssa et al., 2017; Denis et al.,  
188 2019). Anti-PilE antibody 20D9 binds in a continuous pattern to pili on WT cells grown in  
189 broth, whereas the pattern is punctate for adherent diplococci grown on endothelial cells, in  
190 which the pili are under stress (Biais et al., 2010; Brissac et al., 2012) (Fig. 2A, B). Surprisingly,  
191 PilV also shows a punctate and abundant distribution along the same filaments. As control, PilE  
192 but not PilV was detected on type IV filaments in the  $\Delta pilV$  mutant, confirming the specificity  
193 of the antibodies. Together, these data demonstrate that the minor pilin PilV is incorporated  
194 throughout the pilus filament consistent with its role as an adhesin.

195

## 196 **Structure of *N. meningitidis* PilV**

197 To better understand the role of PilV in host cell adhesion, we solved the x-ray crystal structure  
198 of rPilV (residues 29-122, Fig. 3A, B) in two space groups, C2 (monoclinic) and P2<sub>1</sub>2<sub>1</sub>2<sub>1</sub>  
199 (orthorhombic) at 1.41 Å and 1.96 Å, respectively (Table 1). The structures are very similar,  
200 superimposing with a root mean square deviation (RMSD) of 0.5 Å for main chain atoms. The  
201 higher resolution monoclinic structure is described here. The rPilV structure represents the pilin  
202 globular domain; the missing residues 1-28 correspond to the N-terminal half of an extended  
203  $\alpha$ -helix,  $\alpha$ 1. rPilV possesses the canonical type IV pilin fold, with the C-terminal half of  $\alpha$ 1,  
204  $\alpha$ 1C, packed against a 4-stranded antiparallel  $\beta$ -sheet (Fig. 3B). The  $\alpha\beta$ -loop that connects the  
205 top of  $\alpha$ 1C to the bottom of strand  $\beta$ 1 is extended and has a central  $3_{10}$  helix. On the other side  
206 of the  $\beta$ -sheet, a C-terminal loop curves under  $\beta$ 4 and links back to the  $\beta$ -sheet via a disulfide  
207 bond to the  $\beta$ 2- $\beta$ 3 loop just before  $\beta$ 3 (Cys99 and Cys118). The disulfide bond delineates the  
208 D-region of the pilin. Short loops of 6 and 5 residues at the top of the globular domain connect  
209 strands  $\beta$ 1- $\beta$ 2 and  $\beta$ 3- $\beta$ 4, respectively, whereas the  $\beta$ 2- $\beta$ 3 loop at the bottom of this domain is  
210 longer, with 12 amino acids.

211         Though, PilV has only limited sequence homology beyond  $\alpha$ 1N to the *N. meningitidis*  
212 major pilin PilE, and is substantially smaller, with 122 amino acids compared to PilE's 161  
213 amino acids (Fig. 3A), PilV is similar in structure to PilE from both *N. meningitidis* and *N.*  
214 *gonorrhoeae* (Fig. 3D). The most significant differences are (i) the  $\beta$ -strands, which decrease  
215 in length from  $\beta$ 1- $\beta$ 4 for PilV but become increasingly longer for PilE; the absence on PilV of  
216 the hypervariable  $\beta$ -hairpin loop insertion comprising much of the D-region of PilE; (ii) and  
217 the  $\alpha$ 1C structure, which is curved in PilE due to the presence of the helix-breaking Gly42, but  
218 straight in PilV, which has a histidine at this position (Fig. 3E). This straight  $\alpha$ 1C is seen in  
219 other *N. meningitidis* minor pilins of known structure, the core minor pilin PilX and the

220 competence-associated minor pilin ComP, despite PilX having a glycine at position 42 (Fig.  
221 3E-G). However, all these pilins possess the conserved curvature-inducing Gly14 and Pro22.  
222 These conserved residues delineate a segment of  $\alpha$ 1N that is helical in the full-length pilin  
223 subunit but melted in the pilus filament, presumably to allow packing of  $\alpha$ 1N into the  
224 hydrophobic core of the filament (Kolappan et al., 2016; Wang et al., 2017). PilV is the smallest  
225 and simplest of the *Neisseria* pilins; each of the others have unique  $\alpha\beta$ -loop and/or D-region  
226 structural features that contribute to pilus functions and are predicted to be surface-exposed.  
227 The hypervariable  $\beta$ -hairpin contributes to immune escape for the *Neisseria* major pilins. The  
228 PilX D-region has a short “pigtail”  $\alpha$ -helix that is involved in pilus-mediated bacterial  
229 aggregation and adhesion (Helaine et al., 2007), and ComP has an extended loop that lies across  
230 the  $\beta$ -sheet and is implicated in DNA recognition (Berry et al., 2016).

231

### 232 **Model of minor pilin within pilus filament**

233 To understand how PilV might integrate into the pilus filament to influence its functions, the  
234 PilV structure was fit into the *N. meningitidis* pilus filament model, derived by cryoEM  
235 reconstruction (Kolappan et al., 2016), in place of one of the major pilins, PilE (Fig. 3H,  
236 Supplemental Fig. 3). The two  $\alpha$ 1Cs were aligned at their N- and C-terminal ends, resulting in  
237 good superposition of the  $\alpha\beta$ -loop and  $\beta$ -sheet, including its loops, with no steric clashes.  
238 However, the PilV globular domain is smaller than that of PilE, with a shorter  $\beta$ 3- $\beta$ 4 strand-  
239 loop-strand and a more compact C-terminus, which leaves a gap between PilV and the adjacent  
240 PilE that exposes the melted region of  $\alpha$ 1 of a higher subunit (Fig. 3H, I). The structure of the  
241 exposed face of PilV, which lacks the hypervariable loop, and its chemistry (Fig. 3J) differs  
242 substantially from that of PilE (Fig. 3K). Thus, inserting PilV in place of PilE would change  
243 both the packing of the pilin subunits and the surface stereochemistry, which may impact the  
244 flexibility of the pilus and its interactions with host receptors. Importantly, the *N. meningitidis*

245 T4P structure used in this model was built using only PilE as the building block (Kolappan et  
246 al., 2016). Our findings here show that PilV is distributed randomly throughout the pilus, which  
247 will have averaged out the electron density and likely limited the resolution of the  
248 reconstruction.

249

### 250 **Mutational scanning of *pilV***

251 To identify the residues/regions of PilV responsible for interactions with host cell receptors, we  
252 used a two-step scanning mutagenesis. Mutations were introduced into the *pilV* gene inserted  
253 in the pKH37 plasmid (Ramsey et al., 2012), which was used to transform the PilV-deficient  
254 *N. meningitidis* 2C4.3 strain. Step 1: consecutive amino acid triplets throughout the globular  
255 domain were substituted with alanine triplets (or valine when the WT amino acid was alanine).  
256 Mutants expressing PilV variants within the pilus were screened for adhesion to hCMEC/D3  
257 cells (Fig. 4A). Mutants that express PilV and incorporate this minor pilin into surface pili but  
258 showed poor adhesion indicate PilV defects related to adhesion rather than to protein stability,  
259 pilus biogenesis or integration into the pilus. Such mutants were selected for Step two (Fig. 4A  
260 and Supplemental Methods). Step 2: A panel of single amino-acid alanine substitutions were  
261 generated at sites associated with adhesion defects. These *pilV* mutants were expressed in the  
262  $\Delta V$  strain, as for the triplet mutants. The single amino acid mutants were tested for PilV  
263 localization within pili and then for adhesion to hCMEC/D3 cells (Fig. 4B). Of particular  
264 interest were the  $\Delta V$  mutants that have WT levels of PilV in their sheared pilus fractions yet  
265 showed little or no adhesion (Fig. 4B and see Supplemental Methods): residues corresponding  
266 to these substitutions, 60-64 as well as L75, P91, G106, G107, A110 and G113 may be directly  
267 involved in host cell adhesion (see Supplemental Methods). To further confirm the roles of  
268 these amino acids in adhesion to endothelial cells, we introduced the corresponding  
269 alanine/valine changes into the *pilV* plasmid used to produce recombinant His-tagged PilV

270 (rPilV-His, residues 29-122), and generated rPilV-His variants. As demonstrated previously  
271 (Bernard et al., 2014), addition of wild type rPilV-His reduces adhesion of meningococci to  
272 endothelial cells (hCMEC/D3) by ~ 70%, whereas a similar dose of recombinant minor pilin  
273 ComP (rComP-His) has no effect on binding (Supplemental Fig. 4A, B). The ability of these  
274 rPilV-His variant to inhibit *N. meningitidis* adhesion to hCMEC/D3 endothelial cells is shown  
275 in Fig. 4C and summarized in Supplemental Table S2. Among the rPilV-His variants that were  
276 produced at levels comparable to that of WT PilV-His, the rPilV-His-G113A variant inhibited  
277 adhesion at a level comparable to that of WT rPilV-His, ruling out this residue as a receptor  
278 binding candidate. rPilV-His-K62A showed a 2-fold inhibition of adhesion which was not  
279 statistically significant compared to buffer. rPilV-His-N63A, -K64A and -A110V showed only  
280 partial inhibition of adhesion and rPilV-His-Y60A, -D61A, -L75A and -G106A showed little  
281 to no inhibition. These results are consistent with the adhesion defects observed for the *N.*  
282 *meningitidis* PilV point mutants and implicate residues Y60-D61, N63-K64, L75, G106 and  
283 A110 in adhesion to endothelial cells.

284         These amino acids are highlighted on PilV in Fig. 4D-F. Residues Y60-K64 are centered  
285 on the  $3_{10}$  helix within the  $\alpha\beta$ -loop of PilV. The aromatic side chain of Tyr60 is buried within  
286 the globular domain and may be required to orient this loop and properly present the  
287 polar/charged side chains of Asp61, Asn63 and K64 on the PilV surface for binding to host cell  
288 receptors. Leu75 lies on strand  $\beta 1$  and appears to stabilize the Y60-K64 loop, contacting the  
289 side chains of Tyr60, Leu65 and the aliphatic portion of the Lys62 side chain. The Y60-K64  
290 loop protrudes from the globular domain and lies on the pilus surface and is adjacent to the PilE  
291 subunit in our filament model (Fig. 4E, F). Thus, this loop may influence the conformation of  
292 PilE and comprise part of a larger binding site that involves one or more PilE subunits. A  
293 graphical representation of the amino acid multiple sequence alignment shows Y60, D61 and  
294 K64 as conserved among the 699 distinct PilV sequences identified above, and K62 and N63

295 are present in about 50% of these sequences (Supplemental Table S1, Supplemental Fig. 4D),  
296 consistent with the importance of these residues in adhesion (Fig 4C). The three *N. meningitidis*  
297 genomes, 2C4.3, FAM18 and Z2491, which are commonly used in laboratory, have several  
298 amino acid differences but share the residues implicated in adhesion, Y60-K64, L75 and G106,  
299 while A110 is replaced by a serine in Z2491 PilV sequence (Fig. 4G). Consistent with these  
300 residues being involved in T4P-mediated adhesion, complementation of the 2C4.3  $\Delta V$  with *pilV*  
301 of FAM18 or Z2491 had no significant impact on adhesion to endothelial cells (Supplemental  
302 Fig. 4C).

303 Interestingly, no *pilV* mutants were identified that produced wild type levels of PilV that  
304 were not incorporated into the pilus. Such mutants might have indicated residues involved in  
305 PilV:PilE interactions within the pilus. However, these results are consistent with our  
306 knowledge of Type IV pilus structure, in which subunits are held together primarily by  
307 interactions among  $\alpha 1N$  residues: hydrophobic interactions as well as a salt bridge between  
308 Glu5 and the N-terminal amino group (Li et al., 2012; Kolappan et al., 2016; Wang et al., 2017).  
309 To test the role of key residues in  $\alpha 1N$  we substituted the conserved Phe1 and Glu5 with alanine.  
310 As predicted these changes do not impact PilV expression but PilV is poorly incorporated into  
311 the pilus (Supplementary Fig. 5). Pilus levels, as assessed by PilE in the crude pilus  
312 preparations, are not affected in these mutants.

313

#### 314 **Anti-PilV antibodies inhibit *N. meningitidis* adhesion**

315 We next investigated the potential for PilV targeted antibodies to inhibit bacterial adhesion *in*  
316 *vivo* using the human skin-grafted mouse model (Join-Lambert et al., 2013). Anti-PilV  
317 polyclonal antibodies were produced in rabbits immunized with rPilV and monoclonal  
318 antibodies were produced in mice immunized with PilV peptides spanning the residues  
319 implicated in adhesion (peptide 58-66, 98-119) and the  $\beta$ -strand 2 (peptide 80-97). No

320 antibodies were obtained in mice with the peptide spanning neither the Y60-K64 adhesive loop  
321 nor the 98-119 D-region. Only immunizations with peptide 80-97 (residues  
322 PDHFTLQADPNPTTNDGE of mature PilV) were successful, resulting in four monoclonal  
323 antibodies. Antibodies were injected in the tail vein of grafted animals two hours prior to  
324 intravenous infection with WT *N. meningitidis*. Bacterial colonization of human skin grafts was  
325 determined 4 hours after infection by counting CFUs (Fig. 4H). Two different batches of rabbit  
326 polyclonal antibodies raised against rPilV reduced vascular colonization by 9.8-fold and 3.4-  
327 fold respectively, relative to the unimmunized controls. Two different mixtures of monoclonal  
328 antibodies raised against peptide 80-97 also significantly inhibited vascular colonization  
329 (6E9+17C7 by 2.4-fold; 16C1+12D4 by 2.8-fold), while rabbit and mouse isotype control  
330 antibodies had no effect. The reduced colonization in the presence of these antibodies is not due  
331 to a bactericidal effect of the antibodies since counts of CFU in the blood of the grafted mice  
332 were not statistically different between the control and antibody groups 4 hours after infection  
333 (Supplemental Fig. 6). These results demonstrate that anti-PilV antibodies can efficiently block  
334 *N. meningitidis* T4P-dependant adhesion to human host-cell receptors.

335

336 **DISCUSSION**

337 Here we show that the conserved non-core minor pilin PilV is involved in adhesion to host  
338 endothelial cells by virtue of its incorporation throughout the pilus filament. PilV has a  
339 canonical type IV pilin fold but lacks the surface adornments seen in PilE (the hypervariable  $\beta$ -  
340 hairpin), PilX (the  $\alpha$ -helix “pigtail”) and ComP (the DNA-binding strand). When modeled into  
341 the pilus filament in place of PilE a gap is created that may expose additional binding sites and  
342 influence filament flexibility.

343 To our knowledge this is the first demonstration of a minor pilin being abundantly  
344 distributed throughout the pilus, and indeed calls into question its designation as a minor pilin.  
345 Core minor pilins are encoded within a single gene cluster and have been shown to interact with  
346 each other and with the major pilin (Nguyen et al., 2015). These low abundance pilins share the  
347 canonical type IV pilin fold and are thought to form a cluster that initiates pilus assembly and  
348 caps the filament. In contrast to the core minor pilins, both PilV and ComP are encoded in  
349 separate sites on the *N. meningitidis* genome. They share the pilin fold but have specific roles  
350 in the bacterial life cycle, in adhesion and DNA uptake, respectively. The reduction in pili in  
351 the  $\Delta pilV$  mutant suggests that PilV may have an additional non-essential role in pilus assembly  
352 or stability. The localization of PilV, and presumably ComP, further distinguish them from the  
353 putative tip-associated core minor pilins. These non-core minor pilins are unique to the  
354 pathogenic *Neisseria*, perhaps because their major pilin undergoes antigenic variability.

355 PilV maintains a low profile on the pilus surface due to the small size of its globular  
356 domain relative to that of the major pilin PilE. The critical Y60-K64 adhesion loop identified  
357 by iterative alanine scanning mutagenesis appears to be located in close apposition to PilE, in  
358 a shallow well beneath the protruding, hypervariable  $\beta$ -hairpin of PilE. The Y60-K64 loop is  
359 conserved among *N. meningitidis* strains, and thus provides a recessed receptor binding site,  
360 distributed abundantly along the length of the pilus. We show here that PilV mediates adhesion

361 to host cells *in vitro* and *in vivo*. Yet rather than simply providing a filamentous scaffold for  
362 the primary adhesin PilV, PilE is itself adhesive, as the piliated  $\Delta V$  mutant retains some  
363 adhesion capability, whereas a non-piliated  $\Delta E$  mutant is non-adherent. Our data are consistent  
364 with previous observations that both PilE and PilV interact with host cell receptors and are  
365 required for efficient adhesion (Bernard et al., 2014; Virion et al., 2019; Le Guennec et al.,  
366 2020). Our findings help to explain how *N. meningitidis* can alter the amino acid sequence of  
367 its major pilin from one generation to the next to evade the host immune response while  
368 maintaining its ability to adhere to host endothelial cells. The hypervariable PilE  $\beta$ -hairpin is  
369 prominently displayed on the pilus surface and may elicit neutralizing antibodies, but these  
370 would be rendered ineffective due to antigenic variation, whereas the recessed and conserved  
371 PilV maintains adhesion capability for the pilus.

372         The recessed nature of the Y60-64 loop in the context of the intact pilus makes it an even  
373 less likely epitope for recognition by human antibodies. Nonetheless, monoclonal antibodies  
374 targeting peptide 80-97 and rabbit sera raised against rPilV inhibit vascular colonization *in vivo*,  
375 demonstrating the viability of PilV in eliciting a protective immune response. Consistent with  
376 these findings, convalescent sera from patients with meningococcal disease recognized PilV in  
377 an ELISA assay (Cehovin et al., 2011), although their impact on bacterial adhesion was not  
378 tested. The ability of anti-PilV antibodies to inhibit vascular colonization by *N. meningitidis* in  
379 a human skin graft is a key finding of this study. PilV may be the Achilles heel of the *N.*  
380 *meningitidis* T4P, providing a conserved and critical target to block adhesion and treat  
381 meningococcal infections, and a protective antigen for meningococcal subunit vaccines. A  
382 finding that may also be relevant for *N. gonorrhoeae*, which also possesses PilV.

383 **METHODS**

384 **Bacterial strains and endothelial cells**

385 *Neisseria meningitidis* 2C4.3 strain, (formerly clone 12) that is a piliated encapsulated Opa-  
386 Opc- variant of the serogroup C meningococcal clinical isolate NEM8013 and its isogenic non-  
387 piliated Pile-defective mutant ( $\Delta E$ ), the PilV-defective mutant ( $\Delta V$ ) and the PilV-  
388 complemented strain ( $\Delta V+V_{2C4.3}$ ) were described before (Bernard et al., 2014). The *pilV*  
389 sequence of strains FAM18 (Dyer et al., 1987) or Z2491 (Achtman et al., 1988) were extracted  
390 from genomic DNA by PCR and *pilV* genes were inserted by Gibson assembly in plasmid  
391 pKH37 between the *N. meningitidis* genes *lctP* and *aspC* and downstream of the *lacP* promoter  
392 (Ramsey et al., 2012). Bacterial strains were stored frozen at -80 °C and routinely grown at 37°  
393 C in a moist atmosphere with 5% CO<sub>2</sub> on gonococcal base (GC) agar plates (Difco) containing  
394 Kellogg's supplements. Antibiotics were added as indicated. Strains, plasmids and primers are  
395 listed in Supplemental table S3.

396 Human Cerebral Microvascular Endothelial Cells (hCMEC/D3) are a fully  
397 differentiated brain endothelial cell line derived from human brain capillaries that recapitulate  
398 the major phenotypic features of the blood-brain barrier (Weksler et al., 2005). hCMEC/D3  
399 were grown onto Cultrex rat collagen type I-coated dishes (R&D) in Endothelial Cell Basal  
400 Medium-2 (Lonza) supplemented with 5% of fetal calf serum (FCS), 1.4  $\mu$ M hydrocortisone  
401 (Lonza), 5  $\mu$ g/mL ascorbic acid (Lonza), 1 ng/mL b-FGF (Lonza), at 37 °C in 5% CO<sub>2</sub>. Human  
402 Dermal Microvascular Endothelial Cells (HDMEC) were purchased from Promocell and grown  
403 onto Cultrex rat collagen type I-coated dishes (R&D) in Endothelial Cell Growth Medium MV  
404 (Promocell) supplemented with Endothelial Cell Growth Medium Supplement Mix  
405 (Promocell), at 37 °C under 5% CO<sub>2</sub>. EA.Hy926 (ATCC CRL-2922) are endothelial cells  
406 established by fusing primary human umbilical vein cells with a thioguanine-resistant clone of  
407 A549. Cells are grown in Dulbecco's Modified Eagle's Medium (DMEM) supplemented with

408 10% FCS, at 37 °C under 5% CO<sub>2</sub>.

409

#### 410 **Endothelial cell infection and adhesion assays**

411 On the day of infection, a suspension of bacteria from an overnight culture on GCB agar plate  
412 was adjusted to OD<sub>600</sub> 0.05 and incubated for 2 hours at 37 °C in pre-warmed cell culture  
413 medium (according to cell type). Cells were infected with bacteria at a multiplicity of infection  
414 (MOI) of 100 bacteria per cell for 30 min, washed six times to remove unbound bacteria and  
415 colony forming units (CFU) were counted by plating serial dilutions on GCB agar plates. When  
416 required, cells were treated with recombinant His--PilV at indicated concentrations for 30 min  
417 before infection.

418

#### 419 **Infection of human skin grafted mice**

420 Six to 8-week old CB17/Icr-*Prkdc<sup>scid</sup>* (Severe Combined Immunodeficiency: SCID) female  
421 mice were obtained from Janvier Labs (Saint-Berthevin, France). Mice were grafted with  
422 normal human skin as previously described (Join-Lambert et al., 2013). Briefly, full thickness  
423 human skin was grafted onto the back of SCID mice by surgical stitching. Grafted mice were  
424 randomized into control and treated groups. When required, anti-PilV antibodies or buffer  
425 (physiological saline) were administered intravenously 2 hours prior infection at a total dose of  
426 100 µg for polyclonal anti-PilV or 50 µg each of two monoclonal anti-PilV preparations. *N.*  
427 *meningitidis* strains were grown overnight on GCB agar plates without iron (Kellogg  
428 supplement II) and supplemented with deferoxamine (Desferal, Novartis) at 37 °C. On the day  
429 of infection, bacteria were harvested and grown under agitation in RPMI medium with 1%  
430 bovine serum albumin (BSA) and 0.06 µM deferoxamine to exponential phase. Bacteria were  
431 then resuspended in physiological saline and mice were infected intravenously with *N.*  
432 *meningitidis* 2C4.3 WT strain or the mutant strains defective for PilE or PilV ( $\Delta E$  and  $\Delta V$ ) (5 x

433  $10^5$  or  $5 \times 10^6$  bacteria). Bacteremia was assessed at 1 hour and 4 hours by collecting a blood  
434 sample by tail vein puncture. Mice were sacrificed 4 hours after infection and human skin grafts  
435 were removed sterilely. The grafts were crushed and homogenized with Lysing Matrix M tubes  
436 using FastPrep (MP Biomedicals) with 2 cycles of 15 s at speed 6 m/s. Bacterial counts were  
437 determined by plating serial dilution of the samples onto GC agar plates.

438

### 439 **Crude pilus purification**

440 *Ammonium sulfate precipitation.* *N. meningitidis* strains were grown overnight on GCB agar  
441 plates, scraped off of the plates and resuspended in 2 mL of 20 mM ethanolamine, pH 10.5  
442 supplemented with 1 mM dithiothreitol (DTT) at 4 °C. To shear pili off, the bacteria were  
443 vortexed vigorously 3 times for 1 min bursts, returning them to ice for 1 min between each  
444 burst. Bacterial cells were removed from the pilus suspension by two successive centrifugations  
445 at 10 000 x g for 20 min at 4 °C. Cell pellets were resuspended in lysis buffer (50 mM Tris pH  
446 7.5, 25 mM HEPES, 2 mM EDTA, 1% (w/v) SDS - bacterial fraction). The supernatant  
447 containing the pili was collected and supplemented with saturated ammonium sulfate in 20 mM  
448 ethanolamine, pH 10.5 at a final concentration of 0.15 M, before overnight agitation at 4 °C.  
449 Aggregated pili were pelleted by centrifugation at 17 000 x g for 20 min at 4 °C and resuspended  
450 overnight at 4 °C, in 400 µl of 20 mM ethanolamine, pH 10.5. The pili solution was  
451 centrifugated at 10 000 x g for 20 min at 4 °C to remove residual cell debris and the supernatant  
452 was concentrated 10-fold using an Amicon 10 kDa MWCO membrane (Merck Millipore).

453

### 454 **Colocalization of PilV and PilE by immunoprecipitation**

455 Bacteria grown on GC agar plates were adjusted to  $OD_{600}=0.2$  in prewarmed liquid GCB  
456 medium then incubated at 37 °C under 5%  $CO_2$  during 1 h. Bacterial suspension was then  
457 vortexed, passed through a 26 G needle and centrifugated at 1500 g for 15 min. The cleared

458 supernatants were used for immunoprecipitation with specific antibodies against PilE (5C5  
459 mAb) or PilV (rabbit serum Acfp) coated on protein G magnetic beads (Pierce Thermo  
460 Scientific). Precipitated proteins were separated on SDS-PAGE gels and transferred to  
461 nitrocellulose (GE Healthcare). After blocking for 1 h in PBS - 1% BSA - 0.05% Tween-20,  
462 filters were probed overnight with specific antibodies against PilE (rabbit polyclonal antibodies  
463 #9410), PilV (Acfp), anti-NADP-glutamate-dehydrogenase (NADPGH, cytosolic marker) and  
464 anti-Rmp4 (membrane marker) and revealed in ECL (Thermo Scientific), after probing with  
465 peroxidase-coupled secondary antibodies (GE Healthcare).

466

#### 467 **Immunoblotting and piliation index calculations**

468 Bacteria grown overnight were scraped from GC plates and resuspended in PBS and Laemmli  
469 buffer for whole bacterial lysate samples. Laemmli buffer was added to pilus preparations and  
470 bacterial fractions (see Crude pilus purification). Samples were analyzed for the presence of  
471 PilV, PilE, NADP-glutamate-dehydrogenase or Rmp4 by SDS-PAGE and immunoblotting.  
472 The piliation index was determined by quantifying PilE in sheared pilus fraction based on  
473 densitometry of immunoblots bands and normalizing this value to the PilE content in the  
474 corresponding bacterial fraction (ImageJ Software).

475

#### 476 **PilV sequence comparison**

477 All sequences correspond to the query *pilV* (NEIS0487) in the MRF Meningococcus Genome  
478 Library (PubMLST) database (864 non-redundant nucleotide sequences on the 14<sup>th</sup> January  
479 2019). DNA sequences were translated into protein sequences using EMBOSS Transeq,  
480 [https://www.ebi.ac.uk/Tools/st/emboss\\_transeq/](https://www.ebi.ac.uk/Tools/st/emboss_transeq/). The redundancy of the corresponding protein  
481 sequence dataset was reduced using CD-HIT v4.7 (Fu et al., 2012) with a 100% identity  
482 threshold yielding 699 clusters. The longest representative sequence of each cluster was aligned

483 with Clustal Omega v1.2.4 (Sievers and Higgins, 2014) using the default parameters. We then  
484 used the SIAS (Sequence Identity And Similarity) server  
485 (<http://imed.med.ucm.es/Tools/sias.html>) to calculate pairwise sequence identity and similarity  
486 from the multiple sequence alignment with default parameters for similarity, amino acid  
487 grouping and length of multiple sequence alignment for the denominator (Supplemental Table  
488 S1). A graphical representation of the amino acid multiple sequence alignment is shown as a  
489 sequence logo (Crooks et al., 2004) generated by using Weblogo 3.7.4.

490

### 491 **Stochastic optical reconstruction microscopy (dSTORM)**

492 Bacteria were grown in Endothelial Cell Growth medium MV (Promocell), spread in 22 mm  
493 high-precision cover glasses with thickness of 170  $\mu\text{m}$ , (No. 1.5H, Marienfield) with cytospin  
494 and fixed in 4% paraformaldehyde for 10 min before immunolabelling. HDMEC cells were  
495 seeded on the high-precision cover glasses (No. 1.5H, Marienfield), infected with meningococci  
496 for 90 min, and fixed in 4% paraformaldehyde for 10 min. Bacteria or endothelial cells were  
497 blocked with 3% BSA-PBS for 10 min, labelled with the monoclonal anti-PilE antibody 20D9  
498 and the polyclonal anti-PilV antibody 6488 (1:100 in 2% BSA-PBS) 4 °C overnight, then  
499 incubated with goat anti-mouse Alexa Fluor 647F(ab')<sub>2</sub> secondary antibody fragments and goat  
500 anti-rabbit Alexa Fluor 555 F(ab')<sub>2</sub> secondary antibody fragments (Life Technologies; A-  
501 21237) (1:500). Marienfield cavity slides were poured with blinking reagent (Smart Kit buffer  
502 optimized for dSTORM, Abbelight) and the cover glasses were sealed with a Twinsil 22 silicon-  
503 glue (Rotec) as described previously (Maïssa et al., 2017). Images were acquired on a Leica SR  
504 GSD system, with a x 160 oil (NA 1.43) objective. Fluorescence images were collected using  
505 an EMCCD camera (iXon Andor technology), providing an effective pixel size of 100 nm and  
506 processed with the LAS X Software (Leica). Approximately 50,000 frames were recorded for  
507 each acquisition with 10 ms exposure time, EM gain of 300 and the number of photons per

508 pixels set to 75. 2D reconstructions were obtained from stacks (16 planes) with 50 nm axial  
509 step size, using the LAS X Software (Leica) or ImageJ.

510

### 511 **PilV expression, crystallization and structure determination**

512 Methods for PilV expression for crystallization and that of His-tagged PilV and His-tagged  
513 ComP for competition assay are described in supplemental methods.

514 *Crystallization and structure determination.* Initial crystallization conditions for PilV were  
515 identified using the High-Throughput Crystallization Screening Center at the Hauptman-  
516 Woodward Medical Research Institute (Luft). Conditions were optimized in house using the  
517 hanging drop vapour diffusion method. Crystals were grown in 100 mM sodium acetate pH 5,  
518 100 mM ammonium chloride, 28 % (w/v) PEG 8000. The crystals were cryo-cooled in mother  
519 liquor containing 30 % v/v glycerol as cryoprotectant. Crystals were screened at the Stanford  
520 Synchrotron Radiation Lightsource (SSRL) Beamline 7-1 and x-ray diffraction data were  
521 collected at Beamlines 7-1 and 12-1 using Blu-Ice (Gonzalez) (Table 1). PilV datasets were  
522 processed, integrated, and scaled using XDS and the CCP4 programs iMosflm, POINTLESS,  
523 AIMLESS, & TRUNCATE. PilV crystals belonging to 2 different space groups, monoclinic  
524 C2 and orthorhombic P2<sub>1</sub>2<sub>1</sub>2<sub>1</sub>, were obtained in similar crystallization conditions. Data were  
525 collected for the orthorhombic crystal form at wavelengths corresponding to inflection point  
526 and high energy remote and the PilV structure was solved by the 2-wavelength anomalous  
527 diffraction method (Table 1). The automated structure solution program SOLVE located two  
528 selenium sites and initial phases were calculated. Density modification was performed using  
529 RESOLVE resulting in an interpretable electron density map. A Matthews coefficient of 2.1  
530 was calculated for the orthorhombic crystal, indicating a single molecule in the asymmetric unit  
531 with 42.4% solvent content. An initial model for PilV was built in COOT. The model was  
532 refined and water oxygens were located using the PHENIX suite. R-values for the refined model

533 are  $R_{\text{work}} = 0.185$  and  $R_{\text{free}} = 0.255$  with a resolution of 1.96 Å. Data were collected to 1.4 Å for  
534 one of the monoclinic PilV crystals. The Matthews coefficient is 1.9 for this crystal, giving 1  
535 molecule per asymmetric unit and a solvent content of 33.8%. The monoclinic PilV structure  
536 was solved by molecular replacement method using the lower resolution orthorhombic PilV  
537 structure as a model. PHASER gave a solution with high Z-scores (RFZ = 7.6 & and TFZ =  
538 24.3). This model was further improved using the crystallographic macromolecular model  
539 building program ARP/wARP. Several cycles of fitting and refinement were performed in  
540 COOT and PHENIX, respectively. Water oxygens were located and final PilV model was  
541 anisotropically refined with hydrogen atoms. Both monoclinic and orthorhombic crystal  
542 structures were validated using MOLPROBITY. The resolution of the monoclinic PilV  
543 structure is 1.41 Å, with an  $R_{\text{work}}$  of 0.172 and an  $R_{\text{free}}$  of 0.206. Data collection and model  
544 statistics are given in Table 1.

545

#### 546 **Scanning mutagenesis**

547 The mutations were introduced by PCR mutagenesis (primers are listed in Supplemental Table  
548 S3) into the *pilV* gene inserted in pKH37 plasmid. Plasmids were used to transform the PilV-  
549 deficient *N. meningitidis* 2C4.3 strain ( $\Delta V$ ). To examine the impact of the alanine substitutions,  
550 complemented  $\Delta V$  mutants were first tested for their ability to assemble T4P and to incorporate  
551 PilV into the pili by shearing the pili of the bacterial surface, concentrating them using  
552 ammonium sulfate and assessing PilE and PilV levels by SDS-PAGE and immunoblotting.  
553 Next, the piliated alanine substituted mutants were tested for their ability to adhere to  
554 hCMEC/D3 endothelial cells. Mutations in PilV sequence affecting PilV incorporation into  
555 pilus filament or T4P stability were excluded of our study.

556

#### 557 **Generation of anti-PilV antibodies**

558 Anti-PilV polyclonal antibodies were produced in two rabbits immunized with rPilV  
559 (Proteogenix, France). Anti-PilV monoclonal antibodies were produced in mice against three  
560 different PilV peptides (peptide 58-66, 80-97 and 98-119). Hybridomas were selected for their  
561 production of antibodies that inhibited bacterial adhesion to human endothelial cells. Selected  
562 hybridomas were amplified and antibodies were purified. No antibodies for peptides 58-66 and  
563 98-119 were obtained, either because they are not immunogenic or hybridomas were unstable.  
564 Two different antibody-producing companies were involved (Proteogenix, France; Biotem,  
565 France). Peptide 80-97 allowed for hybridoma selection and purification of antibodies (Biotem,  
566 France). Isotype control antibodies were produced and purified by Biotem, France.

567

#### 568 **Statistical analysis**

569 Statistical analyses were performed with GraphPad Prism. Multiple comparison analyses were  
570 assessed with a one-way ANOVA or a one-way Brown-Forsythe and Welch ANOVA test  
571 depending on the variance analysis and data were expressed as mean  $\pm$  95% CI (relevant *p*  
572 values were reported in the figures). In case of failed normality test or positive Bartlett's test  
573 and important differences in mean and SD, a Kruskal-Wallis test was used and data were  
574 expressed as median  $\pm$  interquartile range (corrected *p* values were reported in the figures). The  
575 H0 hypothesis was rejected for a significance level of  $p \leq 0.05$ . Multiple comparison reports and  
576 descriptive statistics are available in Supplemental Statistics.

577

#### 578 **Ethics Statements**

579 The animal experimental procedures described in this work conform to the European ethical  
580 regulations (Directive 2010/63/EU). The project was approved by Comité d'Ethique en matière  
581 d'Expérimentation Animale Paris Descartes and the Ministère de l'Éducation Nationale de  
582 l'Enseignement Supérieur et de la Recherche (Project Number APAFIS#16345-

583 2018012515596498 v5). Human skin tissues were obtained from surgical wastes from patients  
584 undergoing plastic surgery (Groupe Hospitalier Paris Saint-Joseph). In accordance with the  
585 French legislation, the study was declared to the Comité d’Ethique de la Recherche Paris  
586 Descartes and patients were informed of the research purpose and oral consent was recorded.

587

#### 588 **ACKNOWLEDGEMENTS**

589 This work was supported by research grants ANR-15-CE15-0002-01 (to MC), Fondation pour  
590 la Recherche Médicale (XN and EC), ANR-14-IFEC-0006-01 (to SB and XN), INSERM and  
591 Université de Paris (to MC, SB, XN) and by a Natural Sciences and Engineering Research  
592 Council of Canada grant (to LC).

593

594 **FIGURE LEGEND**

595 **Figure 1. Differential adhesion of PilE and PilV defective strains of *N. meningitidis*. (A)**

596 HDMECs, hCMEC/D3 and EA.Hy926 human endothelial cells were incubated 30 min with  
597 meningococci (wild type: WT;  $\Delta pilE$ :  $\Delta E$ ;  $\Delta pilV$ :  $\Delta V$ ;  $\Delta pilV$  complemented strain: Cp).

598 Following infection, unbound bacteria were removed and adherent bacteria were quantified by  
599 plating serial dilution on GCB agar plates and counting CFUs after overnight growth. Adhesion  
600 is expressed as the mean  $\pm$  95% CI (Confidence Interval) of CFUs normalized to the control  
601 infection (WT). Data were analyzed using Brown-Forsythe and Welch ANOVA. **(B)** Human-

602 skin grafted SCID mice were infected intravenously with  $5 \times 10^6$  *N. meningitidis* (WT;  $\Delta E$ ;  $\Delta V$ ).  
603 Graft bacterial loads were quantified at 4 hours after infection by serial dilutions on GCB agar  
604 plates. Two independent experiments performed with a skin batch from a different donor. Each  
605 dot represents a single mouse; data are expressed as log<sub>10</sub> of the mean  $\pm$  95% CI of CFU/g (B).

606 Data were analyzed using Bonferroni's multiple comparisons. **(C)** Piliation index. Pili of WT,  
607  $\Delta V$  and  $\Delta pilV$  complemented strain ( $\Delta V+V$ ) were sheared from the bacterial cells by vortexing  
608 and then precipitated with ammonium sulfate (AS). To determine the piliation index, the  
609 sheared pilus fraction and the bacteria fraction were analyzed by SDS-PAGE and  
610 immunoblotting with anti-PilE antibodies. Piliation indices were normalized to that of the WT.  
611 Data are expressed as the mean  $\pm$  95% CI and were analyzed using Brown-Forsythe and Welch  
612 ANOVA.

613

614 **Figure 2. PilV is distributed throughout the *N. meningitidis* type IV pilus. (A, B, C)**

615 dSTORM images of *N. meningitidis* grown in liquid broth (wild-type or  $\Delta pilV$ ) or attached to  
616 endothelial cells (wild-type). Images were acquired on a Leica SR GSD 3D system. Fifty  
617 thousand frames were recorded and reconstructed using LAS X Software (scale bar, 2  $\mu$ m).

618

619 **Figure 3. X-ray crystal structure of *N. meningitidis* PilV and model of PilV within *N.***  
620 ***meningitidis* type IV pilus. (A)** Sequence alignment of the *N. meningitidis* (*Nm*) minor pilin  
621 PilV (NCBI WP\_002244869) and the major pilin PilE (WP\_014573675). Identical residues are  
622 highlighted orange and conserved residues in yellow. Helix-breaking Gly and Pro in  $\alpha 1$  are  
623 highlighted in cyan and are boxed in black, as are Cys. Residues implicated in host-cell  
624 adhesion are boxed in blue. Secondary structures are indicated. The hypervariable region of  
625 PilE is underlined. **(B)** Crystal structure of *N. meningitidis* recombinant PilV, residues 29-122.  
626 The  $\alpha\beta$ -loop between  $\alpha 1$  and the  $\beta$ -sheet is colored green and the D-region, delineated by the  
627 disulfide-bonded cysteines is magenta. Cysteines are shown as yellow sticks. The histidine at  
628 position 42 is colored cyan. **(C)** *N. meningitidis* major pilin PilE (residues 29-161, PDB 5JW8).  
629 **(D)** *N. gonorrhoeae* (*Ng*) major pilin PilE (full-length, residues 1-158, 2HI2). **(E)** Sequence  
630 alignment of  $\alpha 1$  for *N. meningitidis* pilins and *N. gonorrhoeae* PilE, colored as in A (*Nm* PilX,  
631 CWT82783; *Nm* ComP, WP\_002218144; *Ng* PilE, P02974). **(F)** *N. meningitidis* minor pilin  
632 PilX (residues 28-147, 2OPE). **(G)** *N. meningitidis* minor pilin ComP (residues 29-118, 5HZ7).  
633 Residues at positions 14 and 22 (*N. gonorrhoeae* PilE) and 42 (all pilins) are colored cyan. **(H)**  
634 The globular domain of a PilE subunit in the *N. meningitidis* T4P reconstruction (5KUA) was  
635 replaced with the rPilV structure (blue) by superimposing the N- and C-terminal ends of  $\alpha 1C$ ,  
636 leaving only  $\alpha 1N$  of PilE (red). All other PilE subunits are colored grey, with  $\alpha 1$  (residues 1-  
637 55) shown in yellow and  $\alpha 1N$  residues Gly14 and Pro22 in cyan. The model is shown in cartoon  
638 (left) and space filling representations (middle and right). The filament has been rotated about  
639 its long axis in the right panel to show how the narrower PilV globular domain exposes  $\alpha 1N$  of  
640 a higher PilE subunit (dashed oval). **(I)** For comparison, the *N. meningitidis* T4P reconstruction  
641 is shown with a single PilE subunit colored red. **(J, K)** Electrostatic surface representation of  
642 PilV (J) and PilE (K), shown in approximately the same orientation as in (H) and (I).  
643

644 **Figure 4. PilV residues involved in host cell adhesion. (A, B)** Identification of PilV mutant  
645 defective for adhesion. Volcano plots, adhesion of *N. meningitidis*  $\Delta pilV$  strain expressing PilV  
646 variants. Data are shown for mutants in which pili are produced at approximately WT levels  
647 and PilV is detected in the pilus preparation. Adhesion is expressed as  $\log_2$  of Fold Change  
648 between mutated and wild type PilV ( $\log_2(\text{FC})$ ) and statistical significance is expressed as -  
649  $\log_2(q \text{ value})$  ( $-\log_2(q)$ ). Red dot represents mutant defective for adhesion. **(A)** Mutants selected  
650 during the first step of mutagenesis with triplet Ala/Val substitutions; **(B)** mutants selected  
651 during the second step of mutagenesis looking at single Ala/Val substitutions at sites of  
652 adhesion defects (see Supplemental Methods). **(C)** The ability of WT rPilV and rPilV variants  
653 to competitively inhibit *N. meningitidis* adhesion to hCMEC/D3 cells was assessed. Endothelial  
654 cells were treated with 50  $\mu\text{g/mL}$  of recombinant proteins for 30 min prior to infection with *N.*  
655 *meningitidis* WT strain for 30 minutes. The number of adherent cell-associated bacteria was  
656 determined by counting CFUs. Data shown are averaged values for two independent  
657 experiments. Adhesion is expressed as  $\log_2(\text{mean}) \pm 95\% \text{ CI}$  of fold inhibition, normalized on  
658 bacterial adhesion of cells treated with buffer only. Statistical analyses were performed against  
659 buffer using the Kruskal-Wallis test. **(D-F)** *N. meningitidis* T4P structure with one Pile subunit  
660 replaces with PilV as for Fig. 3. **(D)** Cartoon representation of the pilus with PilV shown in  
661 blue, Pile in grey with  $\alpha 1$  colored yellow. Residues implicated in host cell binding are shown  
662 in stick representation with carbon atoms in green, nitrogens blue and oxygens in red. The  
663 YDKNK loop is the Y60-K64 loop. **(E, F)** Cartoon and space-filling representations of the pilus  
664 model rotated about its axis to show how the Y60-K64 loop contacts the neighboring Pile and  
665 may form part of a larger receptor binding site. The hypervariable loop, which is part of the  
666 protruding  $\beta$ -hairpin of Pile is colored magenta in **(F)**. **(G)** Alignment of PilV protein sequences  
667 from *N. meningitidis* 2C4.3, FAM18, Z2491 strains and that of the PubMLST consensus  
668 sequence (see Supplemental Fig. 4). Conserved residues are highlighted in red and non-

669 conserved residues are highlighted in blue. Residues implicated in host-cell adhesion are boxed  
670 in red. **(H)** Graft bacterial loads of human-skin grafted SCID mice injected intravenously with  
671 buffer (control), 100 µg of anti-PilV rabbit polyclonal IgG antibodies (#1, #2), 100 µg of anti-  
672 PilV peptide mouse monoclonal IgG antibodies (raised against the  
673 P<sub>80</sub>DHFTLQADPNPTTNDGE<sub>97</sub> peptide: 6E9+17C7, 16C1+12D4) or their respective isotype  
674 control antibodies, followed by infection with 5 x 10<sup>5</sup> CFU of WT meningococci. Graft bacterial  
675 loads were determined 4 hours after infection and normalized to that of the control (buffer only).  
676 Values shown are the averages of two independent experiments  
677 performed with a skin patch from different donors. Each dot represents a single mouse; data  
678 are expressed as the mean ± 95% CI of CFU/g. Statistical analyses were performed against the  
679 control with Brown-Forsythe and Welch ANOVA.

680

681 **Table 1. X-ray data collection and refinement statistics**

| <b>Data collection</b>                 | <b>PilV (orthorhombic)</b>                    |   | <b>PilV (monoclinic)</b> |
|--|---|---|--------------------------|
| SSRL beamline                          | SSRL 7-1                                      | SSRL 7-1                                      | SSRL 12-2                |
| Wavelength (Å)                         | 0.976   | 0.979   | 0.969                    |
| Space group                            | P2 <sub>1</sub> 2 <sub>1</sub> 2 <sub>1</sub> | P2 <sub>1</sub> 2 <sub>1</sub> 2 <sub>1</sub> | C2                       |
| Unit-cell parameters                   |   |   |                          |
| a, b, c (Å)                            | 21.8, 39.3, 109.6                             | 21.8, 39.3, 109.6                             | 46.3, 21.8, 83.8         |
| α, β, γ (°)                            | 90, 90, 90                                    | 90, 90, 90                                    | 90 104, 90               |
| Resolution (Å)                         | 1.96  | 1.96 (2.07 – 1.96)                            | 1.41 (1.43 -1.41)        |
| Solvent content (%)                    | 42.4  | 42.4  | 33.8                     |
| Molecules/AU <sup>1</sup>              | 1   | 1   | 1                        |
| Total no. of reflections <sup>2</sup>  | 53268 (2538)                                  | 52638 (6230)                                  | 91105 (4625)             |
| Unique reflections                     | 7263 (442)                                    | 7182 (947)                                    | 15424 (772)              |
| Multiplicity                           | 7.3 (5.7)                                     | 7.3 (6.6)                                     | 5.9 (6.0)                |
| Completeness (%)                       | 98.7 (89.2)                                   | 98.8 (94.6)                                   | 95.9 (97.0)              |
| $\langle I/\sigma(I) \rangle$          | 23.9 (5.5)                                    | 24.3 (6.9)                                    | 12.2 (4.0)               |
| R <sub>merge</sub> <sup>3</sup> (%)    | 6.6 (28.8)                                    | 5.4 (23.7)                                    | 10.8 (90.0)              |
| R <sub>pim</sub> <sup>4</sup> (%)      | 2.6 (12.9)                                    | 2.5 (10.8)                                    | 4.3 (0.359)              |
| CC <sub>1/2</sub> <sup>5</sup>         | 0.999 (0.981)                                 | 0.999 (0.986)                                 | 0.997 (0.843)            |
| Wilson B factor (Å <sup>2</sup> )      | 17.1  |   | 8.8                      |
| <b>Refinement and model statistics</b> |   |   |                          |
| No. of reflections used                | 7217  |   | 15402                    |
| R <sub>work</sub> <sup>6</sup>         | 0.185   |   | 0.172                    |
| R <sub>free</sub> <sup>7</sup>         | 0.255   |   | 0.206                    |
| RMSD                                   |   |   |                          |
| Bond lengths (Å)                       | 0.007   |   | 0.009                    |
| Bond angles (°)                        | 0.932   |   | 1.024                    |
| No. of non-H atoms:                    |   |   |                          |
| Protein                                | 792   |   | 835                      |
| Ligand                                 | 18  |   | 14                       |
| Water oxygens                          | 73  |   | 106                      |
| Average B factor (Å <sup>2</sup> ):    |   |   |                          |
| Protein atoms                          | 27.1  |   | 13.3                     |
| Ligands                                | 46.8  |   | 33.5                     |
| Water oxygens                          | 35  |   | 22.6                     |
| Ramachandran plot:                     |   |   |                          |
| Favoured (%)                           | 100   |   | 99                       |
| Allowed (%)                            | 100   |   | 0                        |
| Outlier (%)                            | 0   |   | 1                        |
| PDB code                               | 5V23  |   | 5V0M                     |

682

683 <sup>1</sup>Values in parentheses indicate the highest resolution shell

684 <sup>2</sup>AU, asymmetric unit

685  $R_{\text{merge}} = \frac{\sum_h \sum_i |I_i(\mathbf{h}) - \langle I(\mathbf{h}) \rangle|}{\sum_h \sum_i I_i(\mathbf{h})}$

686  $R_{\text{pim}} = \frac{\sum_{\text{hkl}} \{1/(N_{\text{hkl}} - 1)\}^{1/2} \sum_i |I_i(\text{hkl}) - \langle I(\text{hkl}) \rangle|}{\sum_{\text{hkl}} \sum_i I_i(\text{hkl})}$

687 <sup>5</sup>CC<sub>1/2</sub>

688  $R_{\text{work}} = \frac{\sum_{\text{hkl}} |F_{\text{obs}}| - |F_{\text{calc}}|}{\sum_{\text{hkl}} |F_{\text{obs}}|}$

689 <sup>7</sup>R<sub>free</sub> is the cross-validation R factor for 5% of the reflections against which the model was not refined.

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864

FIGURE 1

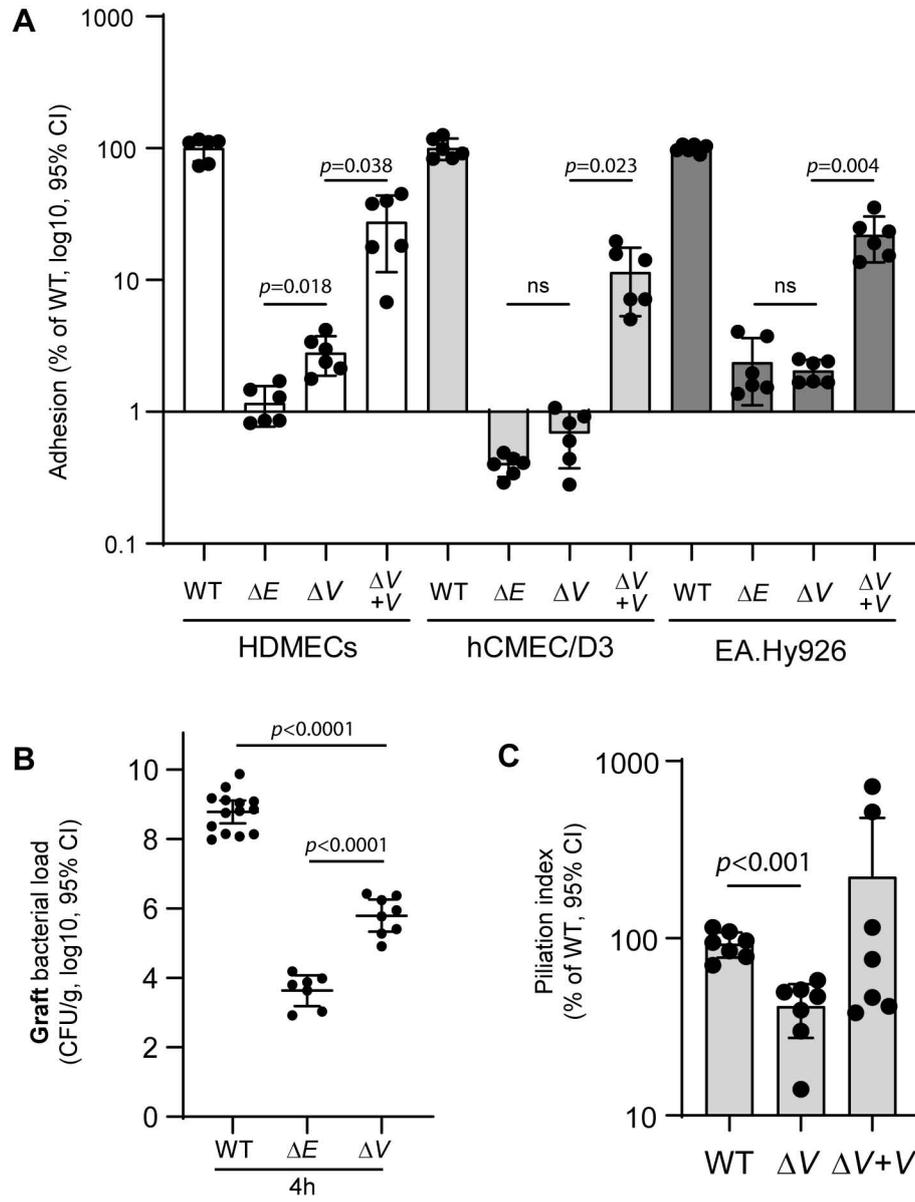


FIGURE 2

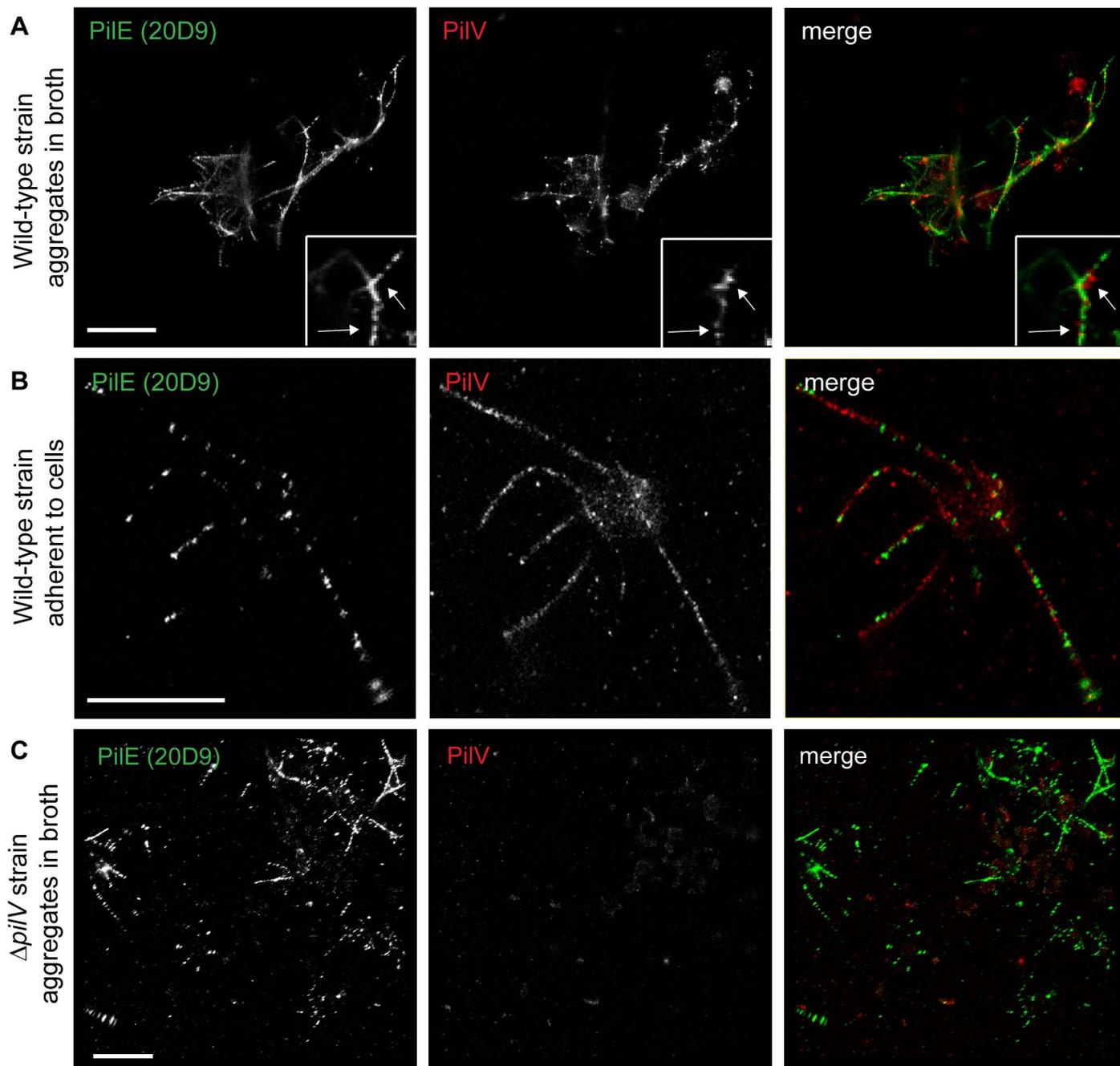


FIGURE 3

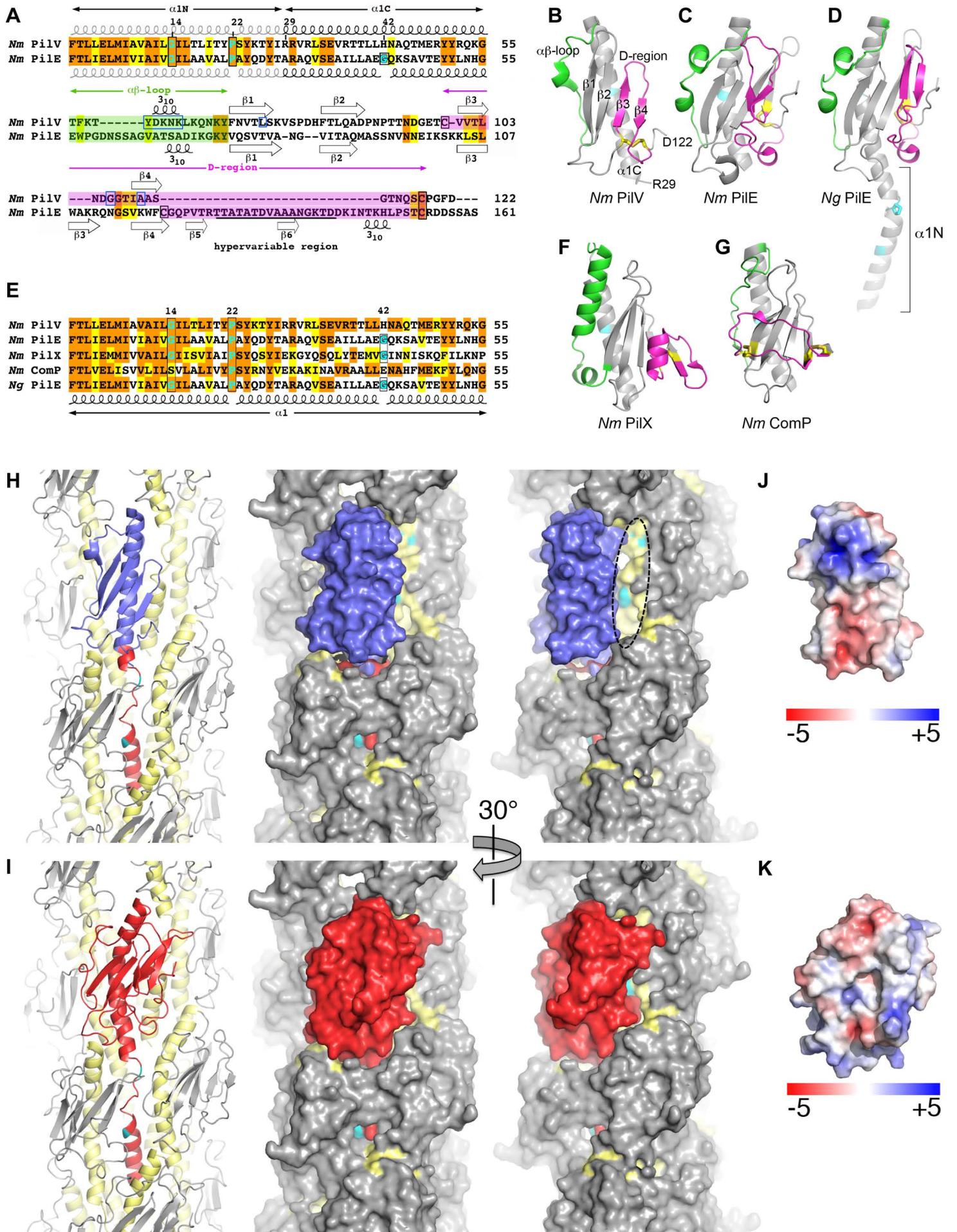
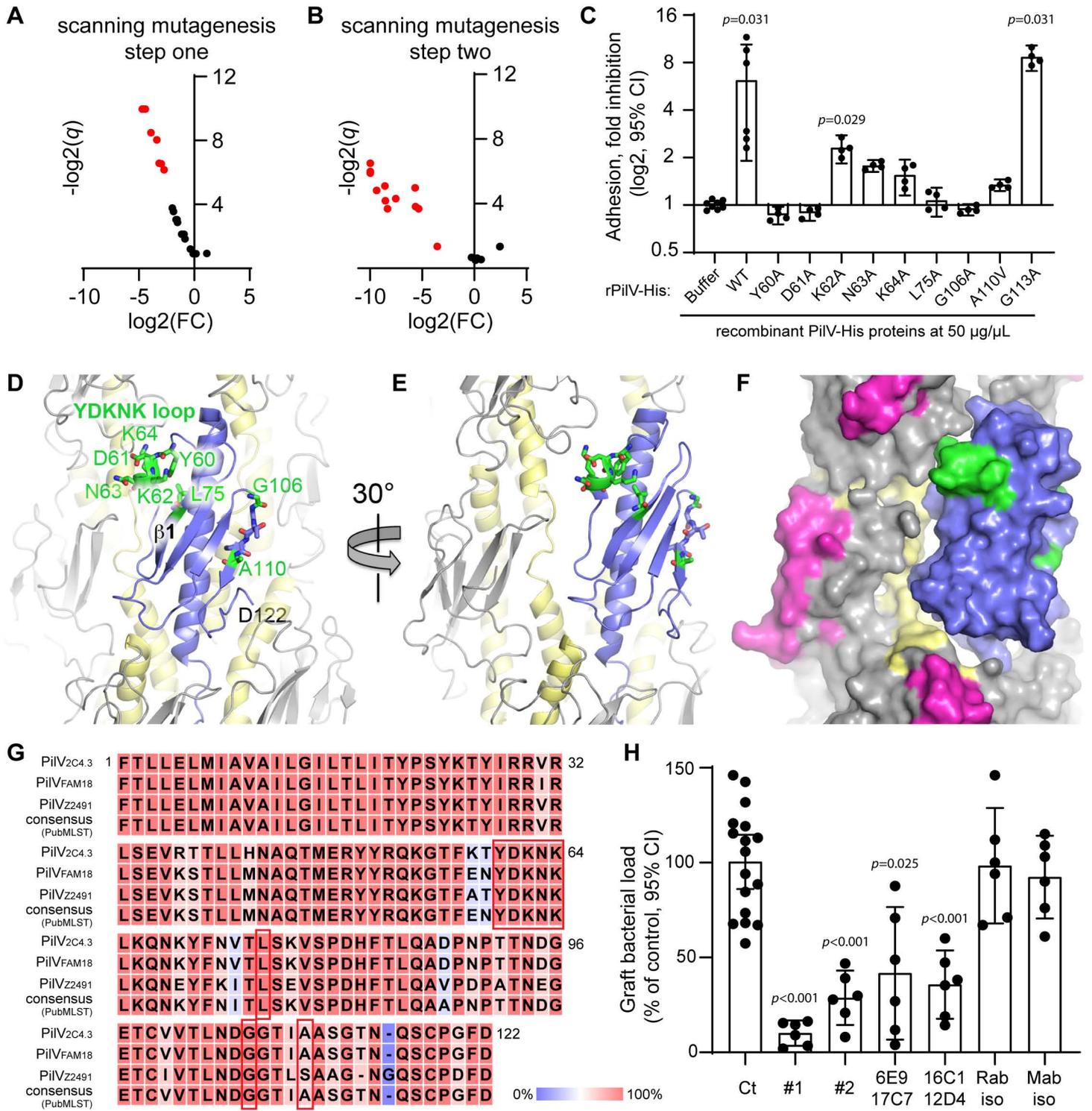


FIGURE 4



## SI APPENDIX

**The minor pilin PilV provides a conserved adhesion site throughout the antigenically variable meningococcal Type IV pilus.**

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## SUPPLEMENTAL FIGURES LEGENDS

**Supplemental Figure 1. Effect of *pilV* and *pilE* mutations on bacteremia, PilV expression and piliation.** (A) Bacteremia in bloodstream of human skin grafted SCID mice infected intravenously with  $5 \times 10^6$  *N. meningitidis* (WT;  $\Delta pilE$ ,  $\Delta E$ ;  $\Delta pilV$ ,  $\Delta V$ ). Bacteremia, quantified by serial dilution on GCB agar plates, was determined at 1 hour and 4 hours after infection. Two independent experiments were performed using a skin batch from a different donor. Each dot represents a single mouse; data are expressed as log<sub>10</sub> of the mean  $\pm$  95% CI of CFU/mL. Data were analyzed using Bonferroni's multiple comparisons. ns: no statistical difference. (B) Pili of WT,  $\Delta V$  and  $\Delta pilV$  complemented strain ( $\Delta V+V$ ) were sheared from the bacterial cells by vortexing and then precipitated with ammonium sulfate (AS). The sheared pilus fraction, the bacteria fraction and whole bacterial lysate were analyzed by SDS-PAGE and immunoblotting with anti-PilE or anti-PilV antibodies. Total proteins were detected in the gel by Stain-Free technology. Images are representative of three experiments made in duplicates or triplicates.

**Supplemental Figure 2. PilV and PilE expression and co-localization.** (A) Anti-PilE, anti-PilV, anti-NADP-glutamate-deshydrogenase (NADPGH, cytosolic marker) and anti-Rmp4 (membrane marker) immunoblots of sheared ammonium sulfate-precipitated (AS) pili from WT and  $\Delta pilV$  strains and immunoblots of whole bacterial lysate from WT. Representative results are shown. (B, C) Co-immunoprecipitation of PilV and PilE in the sheared pili fraction. Sheared pili from *N. meningitidis* wild-type (WT) and  $\Delta pilV$  were immunoprecipitated with anti-PilE or anti-PilV antibodies and analyzed by SDS-PAGE and immunoblotting with anti-PilE or anti-PilV antibodies.

**Supplemental Figure 3. Superposition of rPilV on a PilE subunit in the *N. meningitidis***

**T4P reconstruction.** rPilV (blue) was superimposed onto PilE (red) by aligning residues at the N- and C-terminal ends of  $\alpha$ C1. Residues at positions 14, 22 and 42 are colored cyan. With the exception of PilV His42, these residues are Gly/Pro.

**Supplemental Figure 4. Adhesion, sequence conservation and expression of recombinant**

**PilV. (A)** Human endothelial cells (hCMEC/D3) were incubated with varying amounts of His-tagged recombinant PilV (rPilV-His) prior to infection with WT *N. meningitidis*. Following infection, unbound bacteria were removed by washes and adherent bacteria were quantified by plating on GCB agar plates and counting CFUs after overnight growth. Adhesion is expressed as the mean  $\pm$  95% CI of CFUs normalized to the control infection in which no rPilV-His was added (0). Data are shown from two independent experiments. Statistical analysis was performed comparing the various amounts of rPilV with the buffer-only controls (rPilV-His, 0). Data were analysed using one-way ANOVA. **(B)** The ability of rPilV-His to inhibit bacterial adhesion was examined in comparison with recombinant His-tagged ComP (rComP-His). Gray dots and triangles represent the data obtained using two different batches of rPilV-His. WT and rPilV-His, five independent experiments; rComP-His, two independent experiments. Adhesion is expressed as the mean  $\pm$  95% CI of CFUs normalized to the control infection in which no recombinant protein was added. Data were analyzed using Brown-Forsythe and Welch ANOVA. **(C)** Adhesion of *N. meningitidis*  $\Delta V$  and  $\Delta V$  complemented with *pilV* alleles from strain 2C4.3, FAM18 or Z2491. Human endothelial cells (hCMEC/D3) were infected for 30 min and the number of cell-associated bacteria was determined by counting CFUs. Experiments were performed three times in duplicate. Adhesion is expressed as mean  $\pm$  95% CI of CFUs normalized to PilV<sub>2C4.3</sub> adhesion. Statistical analyses were performed against PilV<sub>2C4.3</sub> with Brown-Forsythe and Welch ANOVA. **(D)** The sequence of *N. meningitidis* PilV is conserved. Gene sequences corresponding to the query *N. meningitidis pilV* (accession number NEIS0487;

query was made in March 2020) in the MRF Meningococcus Genome Library (PubMLST) database were retrieved and translated. Redundancy of the corresponding protein sequence dataset was reduced with a 100% identity threshold yielding 699 clusters. Sequences representative of each cluster were aligned with Clustal Omega v1.2.4 (Sievers and Higgins, 2014) with default parameters (Percent Identity Matrix created by Clustal 2.1 is available in Supplemental Table S2). A graphical representation of the amino acid multiple sequence alignment is shown as a sequence logo generated using Weblogo 3.7.4. Blue: hydrophilic residues; green: neutral residues; black: hydrophobic residues. Residues implicated in host cell adhesion are boxed in green. **(E)** Recombinant His-tagged rPilV (residues 29-122) and alanine/valine-substituted mutants were produced in *E. coli*. Proteins were analyzed by SDS-PAGE and Coomassie Blue staining.

**Supplemental Figure 5. Expression and incorporation of PilV F1A and E5A mutants.** **(A)** Anti-PilE, anti-PilV, anti-NADP-glutamate-dehydrogenase (NADPGH, cytosolic marker) immunoblots of whole cell lysates and sheared ammonium sulfate-precipitated (AS) pili from WT and  $\Delta pilV$  strains expressing PilV wild type (WT) or PilV mutants.

**Supplemental Figure 6. Bacterial loads in bloodstream of human-skin grafted SCID mice injected intravenously with buffer or anti-PilV antibodies.** Mice were injected with buffer (control), 100  $\mu$ g of anti-PilV rabbit polyclonal IgG antibodies (#1, #2), 100  $\mu$ g of anti-PilV peptide mouse monoclonal IgG antibodies (raised against the P<sub>80</sub>DHFTLQADPNPTTNDGE<sub>97</sub> peptide: 6E9+17C7, 16C1+12D4) or their respective isotype control antibodies, followed by infection with  $5 \times 10^5$  CFU of WT meningococci. Blood bacterial loads were determined 4 hours after infection and expressed as CFU per ml. Each dot represents a single mouse; data are expressed as the mean  $\pm$  95% CI of CFU/ml. Statistical analysis were performed against the

control with ANOVA. No statistical significance.

**Supplemental Table S1:** PilV identity matrix (separate file)

**Supplemental Table S2:** Effect of PilV single amino acid substitutions on bacterial adhesion, recombinant pilin expression and inhibition of adhesion.

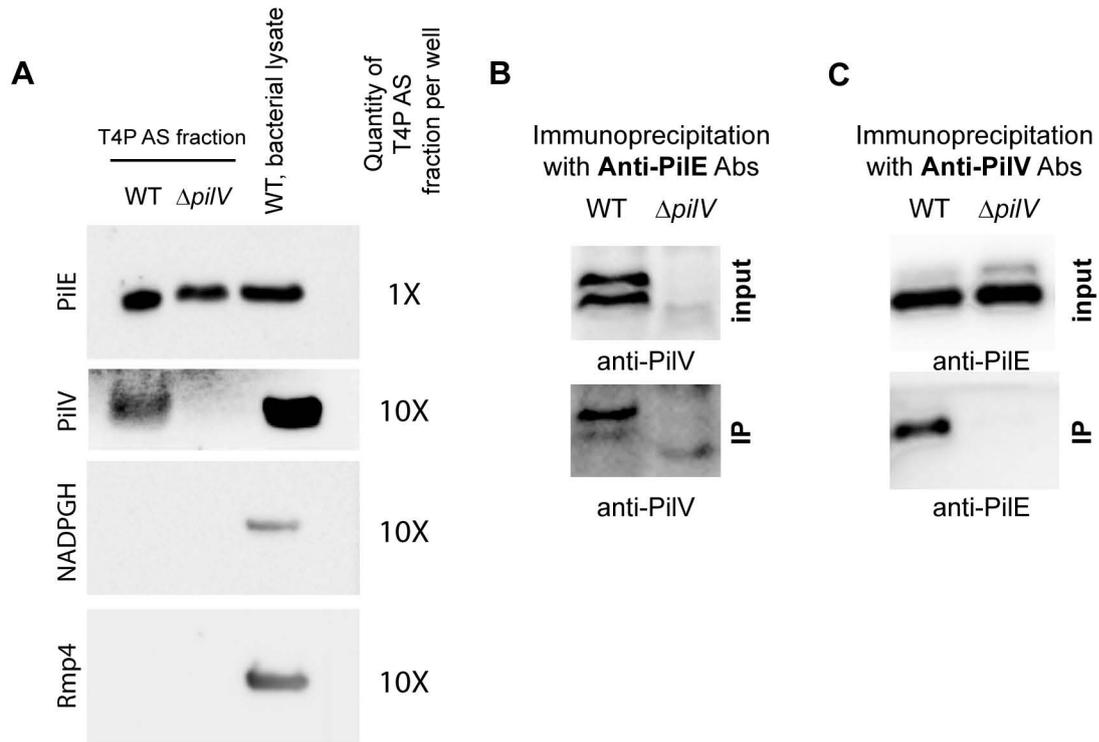
**Supplemental Table S3:** Bacterial strains, plasmids and primers.

**Supplemental statistics:** Statistical analysis and descriptive statistics (separate file)

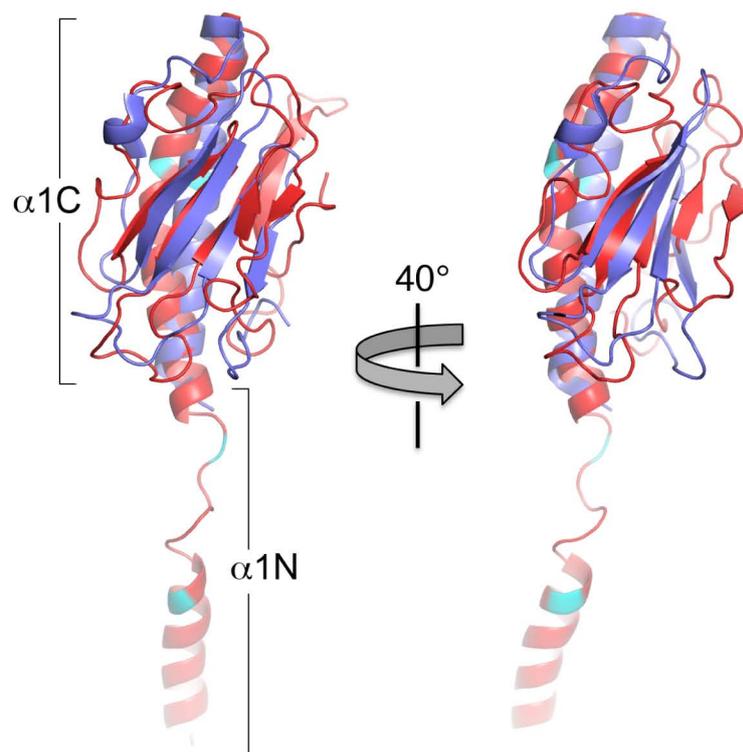
**Supplemental methods**



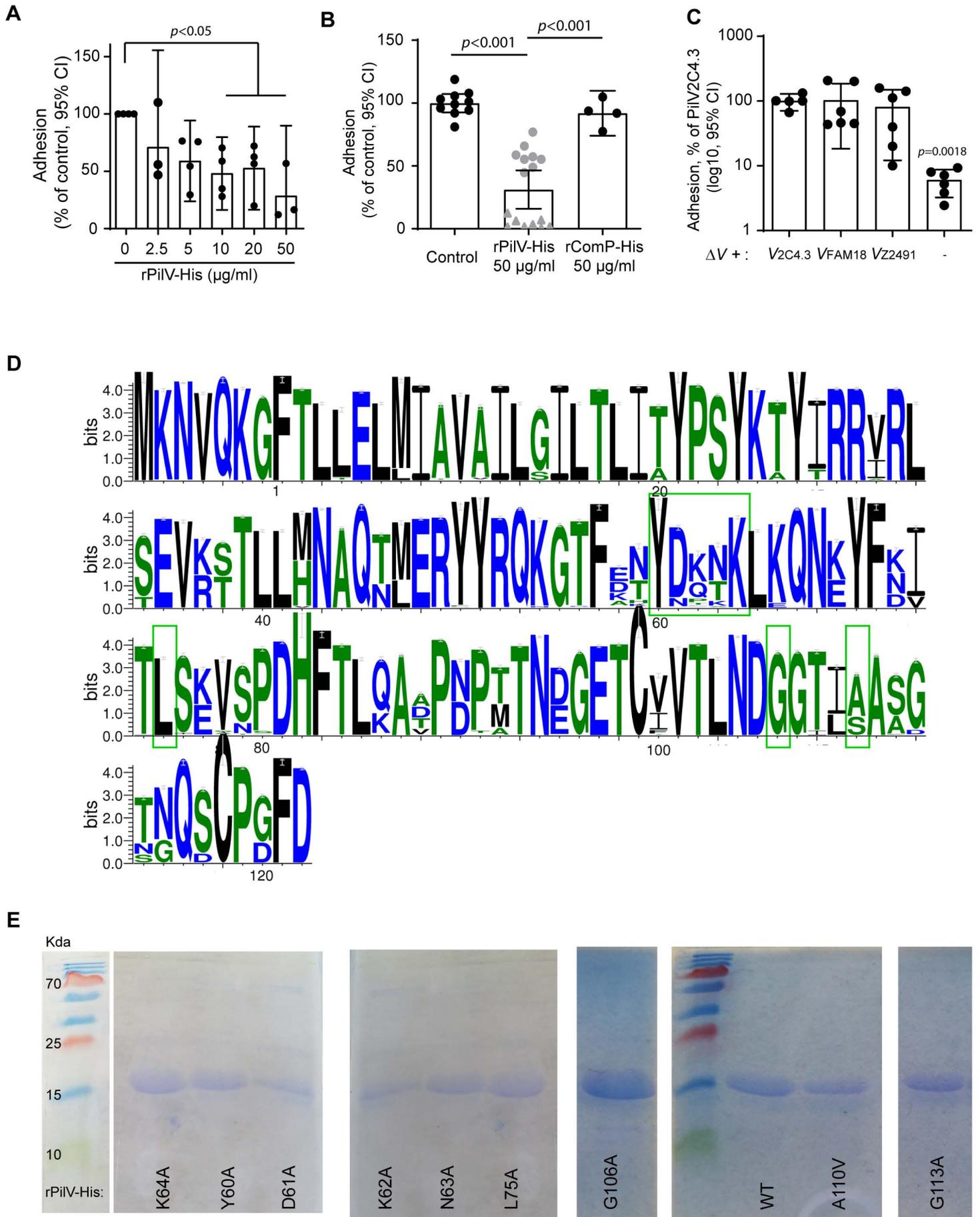
Supplemental figure 2



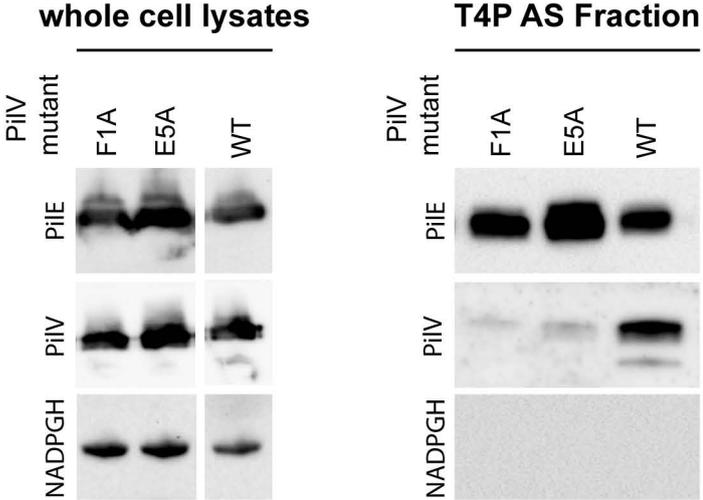
Supplemental figure 3



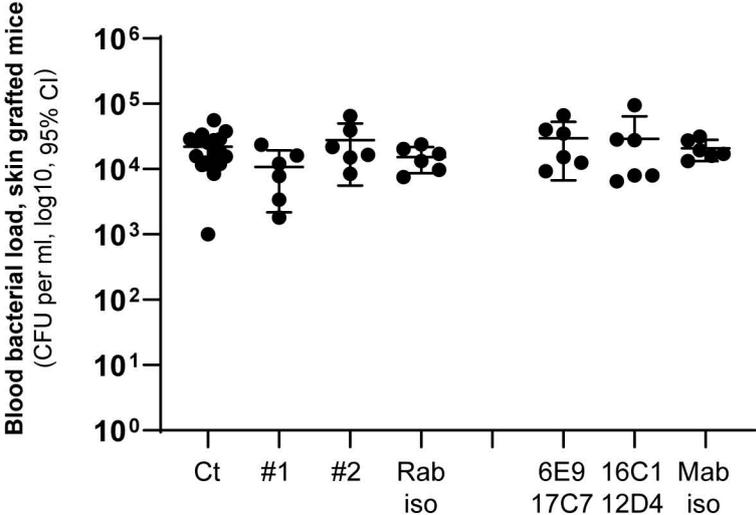
Supplemental figure 4



Supplemental figure 5



Supplemental figure 6



**Table S2. Effect of PilV single amino acid substitutions on bacteria adhesion, recombinant pilin expression and inhibition of adhesion.**

| Mutant        | Adhesion of bacteria <sup>1</sup> | rPilV variant expression | Inhibition of adhesion <sup>2</sup> |
|---------------|-----------------------------------|--------------------------|-------------------------------------|
| WT            | ++ <sup>3</sup>                   | +                        | +++                                 |
| $\Delta pilV$ | +/-                               | NA                       | NA                                  |
| Y60A          | -                                 | +                        | -                                   |
| D61A          | -                                 | +                        | -                                   |
| K62A          | -                                 | +                        | ++                                  |
| N63A          | -                                 | +                        | +                                   |
| K64A          | +/-                               | +                        | +/-                                 |
| L65A          | -                                 | NO                       | NO                                  |
| L75A          | +/-                               | +                        | -                                   |
| P91A          | -                                 | NO                       | NO                                  |
| D95A          | -                                 | NO                       | NO                                  |
| G106A         | +/-                               | +                        | -                                   |
| G107A         | -                                 | NO                       | NO                                  |
| A110V         | +/-                               | +                        | +/-                                 |
| G113A         | -                                 | +                        | +++                                 |

<sup>1</sup> Adhesion: % of of *pilV*<sub>WT</sub> complemented strain

<sup>2</sup> Inhibition of *N. meningitidis* binding to hCMEC/D3 cells

<sup>3</sup> ++ = 100% ; +/- < 20% ; - < 1%

NA = not applicable

NO = not obtained

**Table S3. Bacterial strains, plasmids and primers**

| Reagent   | Description   | Source/reference         |
|---|---|--------------------------|
| <b>Strains</b>  |   |                          |
| <i>E. coli</i> SHuffle® T7<br>Express <i>lysY</i> Competent<br><i>E. coli</i> cells | <i>MiniF lysY (Cam<sup>R</sup>) / fhuA2 lacZ::T7 gene1 [lon] ompT ahpC gal λatt::pNEB3-r1-cDsbC (Spec<sup>R</sup>, lacI<sup>q</sup>) ΔtrxB sulA11 R(mcr-73::miniTn10--Tet<sup>S</sup>)2 [dcm] R(zgb-210::Tn10--Tet<sup>S</sup>) endA1 Δgor Δ(mcrC-mrr)114::IS10</i> | New England Biolabs      |
| <i>E. coli</i> BL21 (DE3)   | <i>F- ompT hsdSB (rBmB-) gal dcm (DE3)</i>  | Thermo Fisher Scientific |
| <i>N. meningitidis</i> strain 8013<br>Wild type, Δ <i>pilE</i> & Δ <i>pilV</i>      | piliated capsulated Opa- Opc- variant of the serogroup C meningococcal clinical isolate NEM8013   | (Bernard et al., 2014)   |
| <b>Plasmids</b>   |   |                          |
| pET15b  | Encodes an N-terminal His•Tag® sequence followed by a thrombin site, Ap <sup>R</sup> , T7 <i>lac</i>  | Novagen                  |
| pET15b- <i>pilV</i>   | Encodes PilV (residues 29-122) with an N-terminal His-tag and a thrombin cleavage site  | This study               |
| pET22b  | Carries an N-terminal pelB signal sequence for potential periplasmic localization, plus optional C-terminal His•Tag sequence  | Novagen                  |
| pET22b- <i>pilV</i>   | Encodes PilV (residues 29-122) with an C-terminal His-tag   | (Virion et al., 2019)    |
| pET22b- <i>comP</i>   | Encodes ComP (residues 29-149) with an C-terminal His-tag   | (Virion et al., 2019)    |

**Primers used in this work****Complemented strain: pkh37-*pilV*FAM18 and pkh37-*pilV*Z2491**

|              |  |
|--------------|--|
| PilVFAM18_fw | CAATTGGAGCTCGGAGTAATTTTATGAAAAACGTTCAAAAA<br>GGCTTTACGC          |
| PilVFAM18_rv | GGGGATCCACTAGTTCTAGACATGCATAGTACTTAATTAATT<br>AGTCGAAGCCGGGGCA   |
| PilVZ2491_fw | CAATTGGAGCTCGGAGTAATTTTATGAAAAACGTTCAAAAA<br>GGCTTTACGC          |
| PilVZ2491_rv | GGGGATCCACTAGTTCTAGACATGCATAGTACTTAATTAATC<br>AGTCGAAGTCCGGGCAGG |

**Primers for structure study: pET15b-*pilV***

|                  |                                 |
|------------------|---------------------------------|
| <i>pilV</i> -for | GCAATTCCATATGCGGCGCGTCCGCCTG TC |
| <i>pilV</i> -rev | CCGCGGATCCTTAGTCGAAGCCGGGGCAG   |

**Triple mutant: XXX->AAA**

Mutants were obtained by PCR mutagenesis. Mutations are carried by the forward primer (FW)

|                        |  |
|------------------------|--|
| Vmut_SCPGFD_117-122_rv | TAATTAATTAAGTACTATGCATGTCTAGA                  |
| Vmut_GFD_fw            | TGCGGCAGCGGGGCAGGATTGGTTTGTACC                 |
| Vmut_SCP_fw            | GTCGAAGCCTGCGGCAGCTTGGTTTGTACC                 |
| Vmut_ASGTNQ_111-116_rv | TCCTGCCCCGGCTTCGAC                             |
| Vmut_TNQ_fw            | TGCGGCAGCACCGGAAGCGGCAATGGTAC                  |
| Vmut_ASG_fw            | TTGGTTTGTTCGCGGCAGCGGCAATGGTAC                 |
| Vmut_DGGTIA_105-110_rv | GCTTCCGGTACAAACCAATCC                          |
| Vmut_TIA_fw            | TGCGGCAGCACCGCCGTCGTTGAGCGTAAC                 |
| Vmut_DGG_fw            | GGCAATGGTTGCGGCAGCGTTGAGCGTAAC                 |
| Vmut_CVVTLN_99-104_rv  | GACGGCGGTACCATTGCCGCTTCCGG                     |
| Vmut_TLN_fw            | TGCGGCAGCAAACGACGCAGGTTTCGCCGTCGTTGG           |
| Vmut_CVV_fw            | GTTGAGCGTTGCGGCAGCGGTTTCGCCGTCGTTGG            |
| Vmut_TNDGET_93-98_rv   | TGCGTTCGTTACGCTCAACG                           |
| Vmut_GET_fw            | TGCGGCAGCGTCGTTGGTGGTGGGATTG                   |
| Vmut_TND_fw            | GGTTTCGCCTGCGGCAGCGGTGGGATTGGGGTC              |
| Vmut_ADPNPT_87-92_rv   | ACCAACGACGGCGAAACC                             |
| Vmut_NPT_fw            | TGCGGCAGCGGGGTCGGCCTGAAGG                      |
| Vmut_ADP_fw            | GGTGGGATTTGCGGCAGCCTGAAGGGTAAAGTGGTTCG         |
| Vmut_DHFTLQ_81-86_rv   | GCCGACCCCAATCCAC                               |
| Vmut_TLQ_fw            | TGCGGCAGCAAAGTGGTCGGGGCTGAC                    |
| Vmut_DHF_fw            | CTGAAGGGTTGCGGCAGCGGGGCTGACTTTGCTTAAG          |
| Vmut_LSKVSP_75-80_rv   | GACCACTTTACCCTTCAGGCC                          |
| Vmut_VSP_fw            | TGCGGCAGCTTTGCTTAAGGTAACGTTGAAATATTTGTTTTG     |
| Vmut_LSK_fw            | GGGGCTGACTGCGGCAGCGGTAACGTTGAAATATTTGTTTTG     |
| Vmut_KYFNVT_69-74_rv   | TTAAGCAAAGTCAGCCCCGAC                          |
| Vmut_NVT_fw            | TGCGGCAGCGAAATATTTGTTTTGTTTCAGTTTGTTTTTGTTCG   |
| Vmut_KYF_fw            | GGTAACGTTTTCGCGGCAGCGTTTTGTTTCAGTTTGTTTTTGTTCG |
| Vmut_NKLKQN_63-68_rv   | AAATATTTCAACGTTACCTTAAGCAAAGTCAGC              |
| Vmut_KQN_fw            | TGCGGCAGCCAGTTTGTTTTTGTTCGTTAGGTTTTAAACGTC     |
| Vmut_NKL_fw            | GTTTTGTTTTGCGGCAGCTTTGTTCGTTAGTTTTAAACG        |
| Vmut_FKTYDK_57-62_rv   | AACAAACTGAAACAAAACAAATATTTTC                   |
| Vmut_YDK_fw            | TGCGGCAGCGGTTTTAAACGTCCCTTTTTTG                |
| Vmut_FKT_fw            | TTTGTTCGTATGCGGCAGCCGTCCCTTTTTTG               |
| Vmut_YRQGT_51-56_rv    | TTTAAAACCTACGACAAAACAAACTG                     |
| Vmut_KGT_fw            | TGCGGCAGCTTGGCGGTAGTAACGTTCC                   |
| Vmut_YRQ_fw            | CGTCCCTTTTTGCGGCAGCGTAACGTTCCATGGTCTGC         |
| Vmut_ERY_48-50_rv      | TACCGCCAAAAGGGACG                              |
| Vmut_ERY_fw            | TGCGGCAGCCATGGTCTGCGCGTTG                      |
| Vmut_TLLHNA_39-44_rv   | CAGACCATGGAACGTTACTACC                         |
| Vmut_HNA_fw            | TGCGGCAGCCAGCAGGGTCGTCCTG                      |
| Vmut_TLL_fw            | CGCGTTGTGTGCGGCAGCCGTCCTGACTTCCGAC             |
| Vmut_TSEVRT_33-38_rv   | ACCCTGCTGCACAACCG                              |
| Vmut_VRT_fw            | TGCGGCAGCTTCCGACAGGCGGACG                      |
| Vmut_TSE_fw            | CGTCTGACTGCGGCAGCGCGGACGCGCC                   |

**Single mutant : X->A (or A->V)**

Mutants were obtained by PCR mutagenesis. Mutations are carried by the forward primer (FW)

|                      |  |
|----------------------|--|
| SgMut_ASG_111-113_rv | TCCTGCCCCGGCTTCGAC                       |
| SgMut_G_113_fw       | TTGGTTTGTtgcGGAAGCGGCAATGGT              |
| SgMut_S_112_fw       | TTGGTTTGTACtgcAGCGGCAATGGT               |
| SgMut_A_111_fw       | TTGGTTTGTACCGGAtgcGGCAATGGT              |
| SgMut_TIA_108-110_rv | GCTTCCGGTACAAACCAATCC                    |
| SgMut_A_110_fw       | tgcAATGGTACCGCCGTCGTTGAGCGT              |
| SgMut_I_109_fw       | GGCtgcGGTACCGCCGTCGTTGAGCGT              |
| SgMut_T_108_fw       | GGCAATtgcACCGCCGTCGTTGAGCGT              |
| SgMut_DGG_105-107_rv | GCTTCCGGTACAAACCAATCC                    |
| SgMut_G_107_fw       | GGCAATGGTtgcGCCGTCGTTGAGCGTA             |
| SgMut_G_106_fw       | GGCAATGGTACCtgcGTCGTTGAGCGTA             |
| SgMut_D_105_fw       | GGCAATGGTACCGCtgcGTTGAGCGTA              |
| SgMut_CVV_99-101_rv  | GACGGCGGTACCATTGCCGC                     |
| SgMut_V_101_fw       | GTTGAGCGTtgcGACGCAGGTTTCGCCGT            |
| SgMut_V_100_fw       | GTTGAGCGTAAcgcGCAGGTTTCGCCGT             |
| SgMut_C_99_fw        | GTTGAGCGTAAcgcGAGTTCGCCGT                |
| SgMut_TND_93-95_rv   | TGCGTCGTTACGCTCAACG                      |
| SgMut_D_95_fw        | GGTTTCGCCtgcGTTGGTGGTGGGATTGG            |
| SgMut_N_94_fw        | GGTTTCGCCGTCtgcGGTGGTGGGATTGG            |
| SgMut_T_93_fw        | GGTTTCGCCGTCGTTtgcGGTGGGATTGG            |
| SgMut_NPT_90-92_rv   | ACCAACGACGGCGAAACC                       |
| SgMut_T_92_fw        | tgcGGGATTGGGGTCGGCCTGAAGGGTAA            |
| SgMut_P_91_fw        | GGTtgcATTGGGGTCGGCCTGAAGGGTAA            |
| SgMut_N_90_fw        | GGTGGGtgcGGGGTCGGCCTGAAGGGTAA            |
| SgMut_TLQ_84-86_rv   | GCCGACCCCAATCCAC                         |
| SgMut_Q_86_fw        | tgcAAGGGTAAAGTGGTCGGGGCTGACTT            |
| SgMut_L_85_fw        | CTGtgcGGTAAAGTGGTCGGGGCTGACTT            |
| SgMut_T_84_fw        | CTGAAGtgcAAAGTGGTCGGGGCTGACTT            |
| SgMut_LSK_75-77_rv   | GACCACTTTACCCTTCAGGCC                    |
| SgMut_K_77_fw        | GGGGCTGACTtgcGCTTAAGGTAACGTTGAA          |
| SgMut_S_76_fw        | GGGGCTGACTTTtgcTAAGGTAACGTTGAA           |
| SgMut_L_75_fw        | GGGGCTGACTTTGCTtgcGGTAACGTTGAA           |
| SgMut_NKL_63-65_rv   | AAATATTTCAACGTTACCTTAAGCAAAGTCAGC        |
| SgMut_L_65_fw        | GTTTTGTTTTtgcTTTTTTTTGTCGTAGGTTTTAAACG   |
| SgMut_K_64_fw        | GTTTTGTTTCAGtgcGTTTTTGTGTCGTAGGTTTTAAACG |
| SgMut_N_63_fw        | GTTTTGTTTCAGTTTtgcTTTTGTCGTAGGTTTTAAACG  |
| SgMut_YDK_60-62_rv   | AACAACTGAAACAAAACAAATATTTTC              |
| SgMut_K_62_fw        | tgcGTCGTAGGTTTTAAACGTCCCTTTTTGG          |
| SgMut_D_61_fw        | TTTtgcGTAGGTTTTAAACGTCCCTTTTTGG          |
| SgMut_Y_60_fw        | TTTGTcgcGGTTTTAAACGTCCCTTTTTGG           |
| SgMut_E_1_fw         | GCCACGCTGCTCGAGCTGATGATTG                |
| SgMut_E_1_rv         | GCCTTTTTGAACGTTTTTCATAAAAT               |

|               |                                |
|---------------|--------------------------------|
| SgMut_F_5_fw  | GCCCTGATGATTGCCGTCGCCATC       |
| SgMut_F_5_rv  | GAGCAGCGTAAAGCCTTTTTGAAC       |
| SgMut_L_65_fw | GCCAAACAAAACAAATATTTCAACGTTACC |
| SgMut_L_65_rv | TTTGTTTTTGTCGTAGGTTTTAAACG     |
| SgMut_K_66_fw | GCCCAAACAAATATTTCAACGTTACCTTA  |
| SgMut_K_66_rv | CAGTTTGTTTTGTCGTAGGTTTTA       |
| SgMut_K69_fw  | GCCTATTTCAACGTTACCTTAAGCAAAGTC |
| SgMut_K69_rv  | GTTTTGTTTCAGTTTGTTTTGTCGT      |
| SgMut_Y_70_fw | GCCTTCAACGTTACCTTAAGCAAAGTCAG  |
| SgMut_Y_70_rv | TTTGTTTTGTTTCAGTTTGTTTTG       |

## Supplemental Methods

### *PilV expression for crystallization.*

The *pilV* gene encoding residues 29-122 of PilV (rPilV) was cloned from *N. meningitidis* 8013 strain genomic DNA using primers *pilV*-for and *pilV*-rev (Table 1). PCR products were digested with *NdeI* and *BamHI* and ligated into pET15b (Novagen) digested with the same enzymes. The new plasmid, pET15b-*pilV* encoding PilV with an N-terminal hexahistidine tag (His-tag), was transformed into SHuffle® T7 Express *lysS* Competent *E. coli* cells (New England Biolabs). L-selenomethionine-substituted PilV was expressed by growing the bacterial cells in M9 minimal medium (3.4 mM Na<sub>2</sub>HPO<sub>4</sub>, 2.2 mM KH<sub>2</sub>PO<sub>4</sub>, 0.94 mM NH<sub>4</sub>Cl, 0.86 mM NaCl) supplemented with 0.2% glucose (w/v), 2 mM MgSO<sub>4</sub>, 0.1 mM CaCl<sub>2</sub>, 0.00005% thiamine (w/v) and 40 mg/L of all naturally occurring amino acids except Gly, Ala, Pro, Asn, Cys and Met shaking at 37 °C to an OD<sub>600</sub> of 0.5 (Van Duyne et al., 1993). At this point, additional amino acids were added: Lys, Thr and Phe, 100 mg/L; Leu, Ile and Val, 50 mg/L; and L-SeMet, 60 mg/L. PilV expression was induced with 0.4 mM isopropyl β-D-1-thiogalactopyranoside (final concentration) and the culture was incubated for 5 hours at 37 °C. Bacterial cells were pelleted by centrifugation at 5000g for 30 min at 4 °C. The cell pellet was washed and resuspended in Buffer 1 (20 mM, Tris-HCl, pH 8.0, 100 mM NaCl) containing 1 mg/mL lysozyme and EDTA-free protease inhibitor cocktail (Roche, 1 tablet/L original culture). The cells were incubated at room temperature for 2 hours then cooled on ice and lysed by sonication. The cell lysate was centrifuged at 7,000 x g for 20 min at 4 °C and the supernatant was discarded. The cell pellet containing insoluble PilV was resuspended in ice cold Buffer 2 (20 mM Tris-HCl, pH 8.0, 0.5 M NaCl, 2% Triton X-100) containing 2 M urea and the sonication and centrifugation steps were repeated. The resulting pellet was suspended in ice cold Buffer 2 and centrifuged at 7,000 x g for 20 min at 4 °C. The pellet was resuspended in Buffer 3 (20 mM

Tris-HCl pH 8.0, 0.5 M NaCl, 5 mM imidazole) containing 6 M guanidine hydrochloride and stirred for an hour at room temperature. The solution was centrifuged at 7,000 x g for 15 min at 4 °C and the supernatant was passed through 0.4 µm filter to remove thin particles and insoluble aggregates. The filtered supernatant was loaded onto a Ni-NTA column (GE Healthcare Life Sciences) and the column with bound denatured His-PilV was washed with 5 column volumes of Buffer 3 containing 6 M guanidine hydrochloride. Next, the column was washed with 5 column volumes of Buffer 4 (20 mM Tris-HCl, pH 8.0, 0.5 M NaCl, 20 mM imidazole, 1 mM 2-mercaptoethanol) containing 6 M urea followed by 5 column volumes of Buffer 4 containing 3 M urea and 5 column volumes of Buffer 4 alone. The denatured and refolded His-PilV was eluted with Buffer 5 (20 mM Tris-HCl pH 8.0, 0.5 M NaCl, 250 mM imidazole). Where appropriate, thrombin was added to the protein (1 U/mg), to cleave off the N-terminal His tag and the solution was dialyzed against Buffer 1. PilV was concentrated to 8 mg/mL using an Amicon stirred cell concentrator (Millipore) and benzamidine was added to a final concentration of 2 mM. The protein was cryocooled in liquid nitrogen and stored at -80 °C.

#### *Recombinant expression of His-tagged PilV and His-tagged ComP*

Recombinants PilV (residues 29-122) and ComP (residues 29-149), both with a C-terminal hexahistidine tag (rPilV-His, rComP-His) were produced as periplasm-directed proteins using the pET22b plasmid (pET22β-*pilV* and pET22β-*comP*) as described previously (Virion et al., 2019). Plasmids were used to transform *E. coli* BL21 (DE3) (Thermo Fisher Scientific) and bacteria were grown for 3 hours at 30 °C in lysogeny broth (LB) followed by 16 hours at 16 °C in LB supplemented with 1 mM isopropyl β-D-1-thiogalactopyranoside. rPilV-His and rComP-His were extracted from the periplasm and loaded onto a Ni-NTA column (Thermo Scientific). The His-tagged pilin was eluted using elution buffer (50 mM NaH<sub>2</sub>PO<sub>4</sub>, pH 8, 300 mM NaCl,

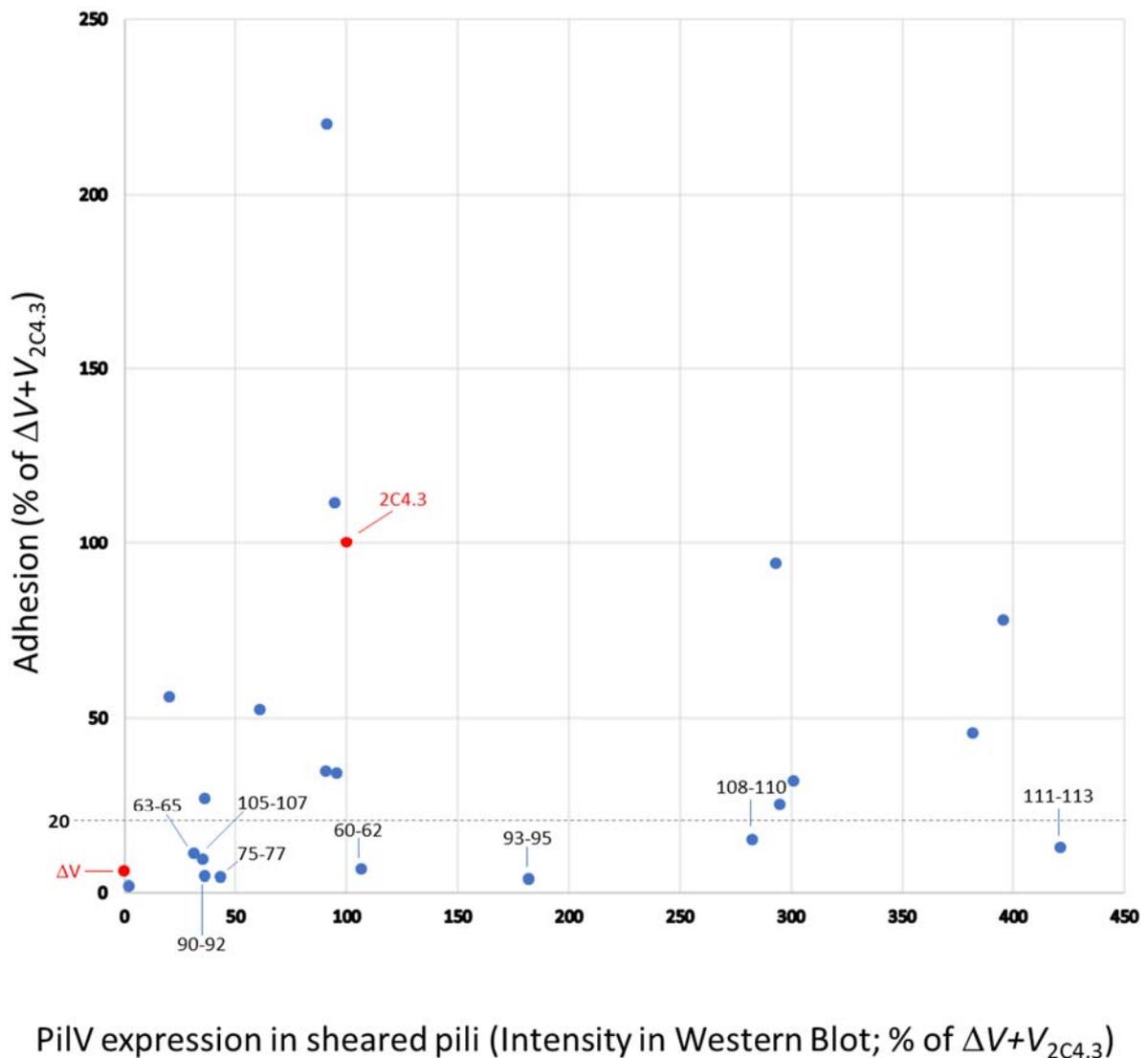
250 mM imidazole) and the buffer was exchanged with phosphate-buffered saline (PBS) using an Amicon 10 kDa molecular weight cut-off (MWCO) membrane (Merck Millipore) to a concentration of 1 mg/mL. The purity of His-tagged pilins was assessed by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and Coomassie blue staining (Supplemental Fig. 4E). rPilV variants were generated by PCR mutagenesis of *pilV* on pET22b-*pilV* with the mutagenesis primers used for *pilV* mutants expressed in the  $\Delta$ *pilV* strain (Supplemental table S3).

#### *Scanning mutagenesis of N. meningitidis pilV*

Mutations were introduced into the *pilV* gene inserted in plasmid pKH37 between the *N. meningitidis* genes *lctP* and *aspC* and downstream of the *lacP* promoter (Ramsey et al., 2012). These mutations substituted amino acid triplets with alanine triplets (or valine when the WT amino acid is alanine) throughout the globular domain, from residue 33 to 122. The plasmids were used to transform the PilV deficient *N. meningitidis* strain 2C4.3 ( $\Delta$ V), whereby recombination occurs between the plasmid-borne *pilV* mutant allele and the genome between *lctP* and *aspC* and *pilV* is expressed under control of the *lacP* promoter (Ramsey et al., 2012). To examine the impact of the alanine substitutions, complemented  $\Delta$ V mutants were first tested for their ability to incorporate PilV into the pili by shearing the pili from the bacterial surface, concentrating them using ammonium sulfate precipitation and assessing PilV levels by SDS-PAGE and immunoblotting (Fig. SM1). Mutants expressing PilV in surface pili were tested for their ability to adhere to hCMEC/D3 endothelial cells (Fig. SM1). Of these mutants, several show profound adhesion defects comparable to that of the uncomplemented  $\Delta$ V mutant: 60-62, 63-65, 75-77, 90-92, 93-95, 99-101, 105-107, 108-110, 111-113.

To identify individual residues involved in adhesion, we generated a panel of single amino-acid

alanine substitutions and expressed these *pilV* mutants ectopically in *N. meningitidis*  $\Delta V$ . PilV levels in sheared pili and adherence to endothelial cells were tested as for the triple mutants (Fig. SM2). Of particular interest are the complemented strains that expressed mutant PilV in their sheared pilus fractions yet show little or no adhesion: mutants spanning residues 60-64 as well as L75A, G106A, G107A, A110V and G113A. These residues may be directly involved in host cell adhesion.



**Figure SM1. Analysis of pilus-mediated adhesion to endothelial cells for *pilV* triple mutants.**

Adhesion of  $\Delta V$  strain and  $\Delta V$  strains complemented with wild-type *N. meningitidis* *pilV* or *pilV* triple mutants. Human endothelial cells (hCMEC/D3) were infected with *pilV*-complemented strains for 30 minutes and the number of cell-associated bacteria was determined by counting CFUs. Adhesion is expressed as mean of CFUs normalized on mean of CFUs for the strain expressing wild type *pilV* from two independent experiments. *PilV* expression in sheared pili was assessed by immunoblots of sheared ammonium sulfate-precipitated pili from *N. meningitidis*  $\Delta V$  complemented with *pilV* mutants and expressed as a percentage of the density of the *PilV* band for the strain expressing wild type sequence of *pilV* ( $\Delta V+V_{2C4.3}$ ).

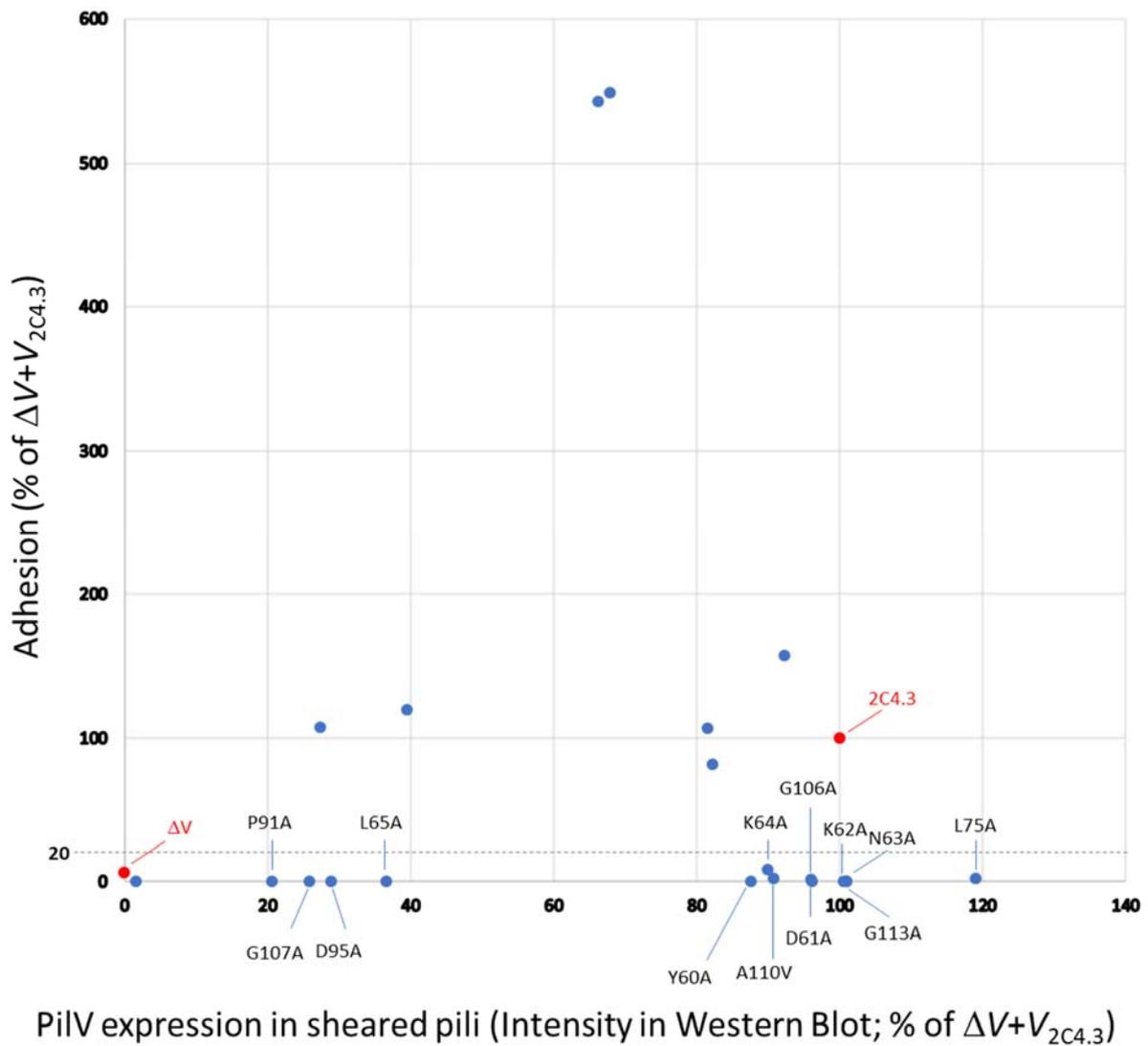


Figure SM2. Analysis of pilus-mediated adhesion to endothelial cells for *pilV* single mutants.

*Adhesion of  $\Delta V$  strain and  $\Delta V$  strains complemented with wild-type *N. meningitidis* pilV or pilV single mutants. Human endothelial cells (hCMEC/D3) were infected with pilV-complemented strains for 30 minutes and the number of cell-associated bacteria was determined by counting CFUs. Adhesion is expressed as mean of CFUs normalized on mean of CFUs for the strain expressing wild type sequence of pilV for two independent experiments. PilV expression in sheared pili was assessed by immunoblots of sheared ammonium sulfate-precipitated pili from pilV-complemented strains, and expressed as percentage of PilV band intensity for the strain expressing wild type sequence of pilV ( $\Delta V+V_{2C4.3}$ ).*

**Reference:**

Ramsey, M.E., Hackett, K.T., Kotha, C., Dillard, J.P., 2012. New Complementation Constructs for Inducible and Constitutive Gene Expression in *Neisseria gonorrhoeae* and *Neisseria meningitidis*. *Appl. Environ. Microbiol.* 78, 3068–3078. <https://doi.org/10.1128/AEM.07871-11>