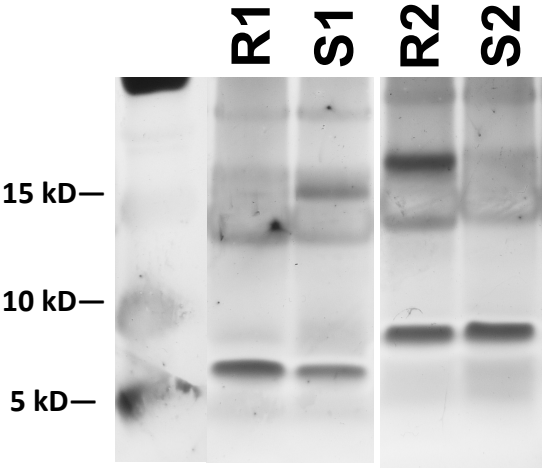


**Supplementary Figure S1. Bactericidal activity of anti-FHbp antibodies to variant group 1 (sub-family B) antigenic variants mismatched to isolates.**  
**Panel A.** Anti-FHbp ID 1 titers (sequence variant in Novartis 4CMenB vaccine).  
**Panel B.** Anti-FHbp ID 55 titers (Sub-family B sequence variant in Pfizer vaccine). The isolates had sub-family B FHbp sequence variants ID 4 or 13. Data represent geometric means and ranges represent from duplicate measurements. Representative results shown from three experiments.

**Supplemental Figure S2. Silver stain SDS PAGE of Proteinase K treated LOS preparations.** LOS from each strain (R-S) pair was normalized by DNA content ( $\mu\text{g}/\text{mL}$ ). See Methods for detection details.



|                                    |      |      |       |       |
|------------------------------------|------|------|-------|-------|
| LOS immunotype                     | 8-1  | 8-1  | 3-7-9 | 3-7-9 |
| DNA loaded $\mu\text{g}/\text{ml}$ | 7.04 | 4.03 | 4.53  | 5.2   |

**Supplemental Figure S3.** Alignment of amino acid sequences of NspA from isolates R1, R2, S1 and S2. In red, amino acid differences. All mutations were located outside of the exposed loops.

```

R1      MKKALATLIALAIPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
R2      MKKALATLIALAIPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
S1      MKKALATLIALAIPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
S2      MKKALAALLIALALLPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
        *****:*****:*****

```

```

R1      FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF
R2      FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF
S1      FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF
S2      FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF
        *****

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R1      SQTSTGLGVLAVSYAVTPNVLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF
R2      SQTSTGLGVLAVSYAVTPNVLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF
S1      SQTSTGLGVLAVSYAVTPNVLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF
S2      SQTSTGLGVLAVSYAVTPNVLDAGYRYNYIGKVNTVKNVRSGELSAGMRVKF
        *****:*****

```

## Supplemental Figure S3. Alignment of amino acid sequences of PorB3. Panel A isolates R1 and S1. Panel B, isolates R2 and S2. Amino acids shown in bold are predicted to be located on surface exposed loops. \*, conserved residues.

**A**

```

R1 MKKSLIALTLAALPVAAMADVTLYGTIKAGVETSRSVEHNRGQVVSVETGTGIVDLGSKI 60
S1 MKKSLIALTLAALPVAAMADVTLYGTIKAGVETSRSVVAHNGAQAASVETGTGIVDLGSKI 60
***** ** .*.*****

R1 GFKGQEDLGNLKAIWQVEQKASIAGTDSGWGNRQSFIGLKGGFGKLRVGRLNSVLKDTG 120
S1 GFKGQEDLGNLKAIWQVEQKASIAGTDSGWGNRQSFIGLKGGFGKLRVGRLNSVLKDTG 120
*****

R1 DINPWDSKSDYLGVNKIAEPEARLISVRYDSPEFAGLSGSVQYALNDNAGRHNSESYHAG 180
S1 DINPWDSKSDYLGVNKIAEPEARLISVRYDSPEFAGLSGSVQYALNDNAGRHNSESYHAG 180
*****

R1 FNYKNGGFFVQYGGAYKRHQDV-DDVKIEKYQIHRLVSGYDNDALHASVAVQQDAKLVE 239
S1 FNYKNGGFFVQYGGAYKRHQVQEDLNIEKYQIHRLVSGYDNDALYASVAVQQDAKLAL 240
*****:;* :*:*****:*****.

R1 DN-YSHNSQTEVAAATLAYRFGNVTPRVSYAHGFKGSFDDADLSNDYDQVVVGAEYDFSKR 298
S1 PNDNSHNSQTEVAAATLAYRFGNVTPRVSYAHGFKGSFDDADLSNDYDQVVVGAEYDFSKR 300
* *****

R1 TSALVSAGWLQEGKGENKFVSTAGGVGLRHKF 330
S1 TSALVSAGWLQEGKGENKFVSTAGGVGLRHKF 332
*****

```

**B**

```

R2 MKKSLIALTLAALPVAAMADVTLYGTIKAGVETSRSVEHNGGQVVSVETGTGIVDLGSKI 60
S2 MKKSLIALTLAALPVAAMADVTLYGTIKAGVETSRSVVAHNGAQAASVETGTGIVDLGSKI 60
***** ** .*.*****

R2 GFKGQEDLGNLKAIWQVEQKASIAGTDSGWGNRQSFIGLKGGFGKLRVGRLNSVLKDTG 120
S2 GFKGQEDLGNLKAIWQVEQKASIAGTDSGWGNRQSFIGLKGGFGKLRVGRLNSVLKDTG 120
*****

R2 DINPWDSKSDYLGVNKIAEPEARLISVRYDSPEFAGLSGSVQYALNDNAGKYNSESYHAG 180
S2 DINPWDSKSDYLGVNKIAEPEARLISVRYDSPEFAGLSGSVQYALNDNAGRHNSESYHAG 180
*****:*****

R2 FNYKNGGFFVQYGGAYKRHVRVDENVNIEKYQIHRLVSGYDNDALHASVAVQQDAKLVE 240
S2 FNYKNGGFFVQYGGAYKRHQVQENVNIEKYQIHRLVSGYDNDALYASVAVQQDAKLVE 240
***** :*:*****:*****

R2 DNYSHNSQTEVAAATLAYRFGNVTPRVSYAHGFKGSFDDADLSNDYDQVVVGAEYDFSKRT 300
S2 ENYSHNSQTEVAAATLAYRFGNVTPRVSYAHGFKGSFDATNYNNDYDQVVVGAEYDFSKRT 300
:***** :.*****

R2 SALVSAGWLQEGKGENKFVSTAGGVGLRHKF 331
S2 SALVSAGWLQEGKESKFVSTAGGVGLRHKF 331
*****.*****

```

**Supplemental Figure S4. Predicted locations of amino acid differences mapped to structural models of PorB3 (PDB ID 3WI4) shown as a homotrimer. Panel A, PorB3 from R1 and S1. Panel B, PorB3 from R2 and S2. From the published coordinates of a crystal structure (Kattner C, Toussi D, Zaucha J, Wetzler L, Ruppel N et al. Crystallographic analysis of *Neisseria meningitidis* porb extracellular loops potentially implicated in TLR2 recognition. J Struct Biol 2014;185:440-447)**

