

SUPPLEMENTAL FIGURE S1. Phylogenetic analysis of factor H binding protein (fHBP) sequences. Neighbor-joining tree is based on the Clustal W alignment of unique fHBP protein sequences.³² The tree was drawn using MEGA 4.0,³³ and the scale bar indicates genetic distance based on protein sequence. The end of each branch on the tree represents a protein variant. Dotted rectangles denote A and B subfamily designations. Dotted ovals denote the alternative variant 1,2,3 nomenclature by Masignani et al.¹⁹ The most prevalent sequence variants found in this study are indicated with solid circles (red or blue). *B09 and B64 differ by only 2 amino acids.

