described in the legend of Figure 3. The scale bar represents 2 amino acid changes per 100 residues.

Figure 6. Schematic representation of six fHbp modular groups deduced from phylogenic analysis. Forty of the 70 proteins contained only α type segments or β type segments, and were designated as modular groups I and II, respectively. The remaining 30 proteins were chimeras with different combinations of α (shown in gray) and β segments (shown in white) and could be assigned to one of four modular groups (III-VI). The relationship between the modular group and Masignani variant group designation, and the number of unique sequences observed within each fHbp modular group, are shown.

Figure 7. Space-filled structural models of factor H binding protein based on the coordinates of fHbp in a complex with a fragment of human factor H (Schneider *et al.*, 2009). The five variable segments V_A through V_E are depicted in different colors (V_A, blue; V_B, orange; V_C, green; V_D, aqua; V_E, violet) and the invariant blocks of residues separating each of the variable segments are shown in white. The model in the middle was generated by rotation of 180° around the Y-axis relative to the respective model on the far left. The model on the right was generated by a 90° rotation around the X-axis relative to the model in the middle. The factor H contact residues are depicted in black, and the residues affecting the epitopes of anti-fHbp mAbs are shown in yellow. The figure was constructed with PyMol (http://www.pymol.org).

Supplementary Figure S1. For each of the five modular variable segments, V_A to V_E, the mean number of peptides (Y-axis) and percent amino acid identity (X axis) are shown. The histograms on the left were generated by comparing each of the α types to the corresponding α and β types for the other 69 peptides and calculating the respective mean frequency at each

percent identity. The histograms on the right were generated by comparing each of the β types to the corresponding α and β types. Solid bars represent comparisons with sequences of α types and open bars represent comparisons with sequences of β types.