

Supplemental Figure 1. Alignment of PspC sequences. PspC sequences were aligned using COBALT Multiple sequence alignment tool (http://www.ncbi.nlm.nih.gov/tools/cobalt/cobalt.cgi?link_loc=BlastHomeAd). Aminoacids identical to the motif ALNIKLSAIKTK of D39 for FH binding are shown in blue and the conserved aminoacids at positions 2 (leucine), 6 (leucine), 9 (isoleucine) and 10 (lysine) are highlighted in blue. The sIgA hexpeptide motif R(Y or H or F or L) RNYPT is shown in red and the YPT critical aminoacids for binding are highlighted in yellow.

Supplemental Figure 2. Densitometric analysis of Western Blot bands in Figure 3. Density of bands of the indicated strains in blots incubated with anti-PspC3 or anti-PspC5 IgG in Figure 3 were determined using ImageJ (<http://rsb.info.nih.gov/ij>) and are indicated as percentage of the same bands in blots incubated with the control anti-Intimin IgG before detection of FH (A) or sIgA (B).