Supplementary Figure 1

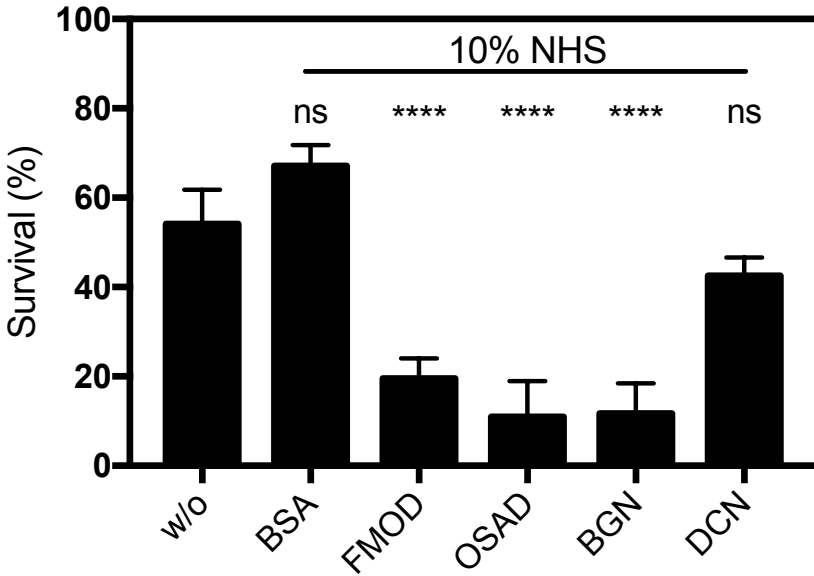

Figure S1. Removal of excess SLRPs does not impede serum killing

Serum killing of strain RH4 following washing of bacterial-SLRP solution after 30 min incubation, removing unbound SLRPs. Survival is calculated as the percentage of colony-forming units (CFU) at 30 min to time 0. Error bars represent SD of three independent experiments. 50 µg/ml BSA was used as a negative protein control. Statistical differences were calculated using a one-way ANOVA with Dunnett's posttest versus bacteria without SLRPs. **** $p < 0.0001$.

Supplementary Figure 2

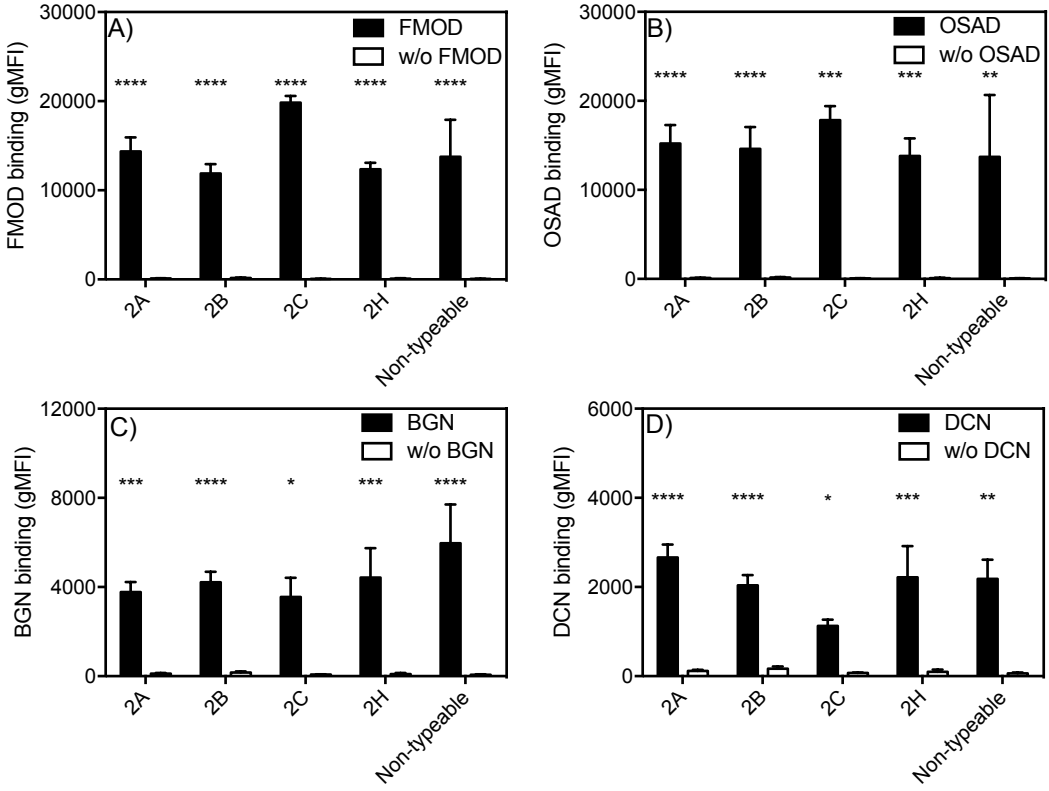

Figure S2. *M. catarrhalis* isolates of different N-terminal repeats (NTER) of head domains bind SLRPs in similar fashion

The SLRP binding capacities of *M. catarrhalis* clinical isolates expressing UspA2/2H were grouped according to their N-terminal repeat (NTER) domain; 2A, 2B, 2C, and 2H, and non-typeable. No significant difference in binding to SLRPs was observed between NTER groups and all NTER groups bound SLRPs in a statistically significant manner. Statistical differences were calculated using a one-way ANOVA with Dunnett's posttest. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.

Supplementary Figure 3

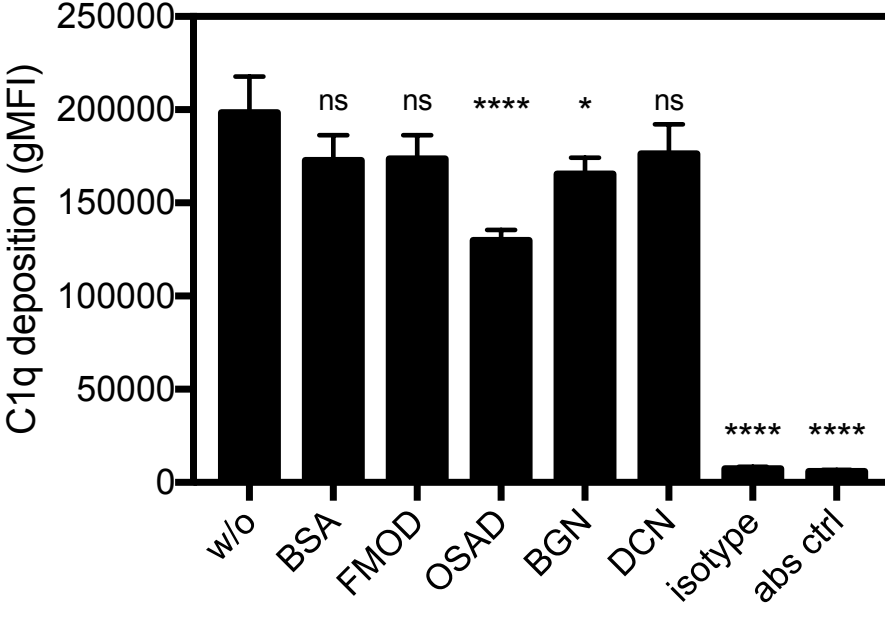

Figure S3. OSAD and BGN significantly reduce C1q binding on *M. catarrhalis*

Deposition of C1q on the surface of *M. catarrhalis* was analysed by flow cytometry using 1% OmCI-treated serum. Data illustrates the mean and SD of three independent experiments. Statistical differences were calculated using a one-way ANOVA with Dunnett's posttest. * $p < 0.05$, **** $p < 0.0001$.

Supplementary Figure 4

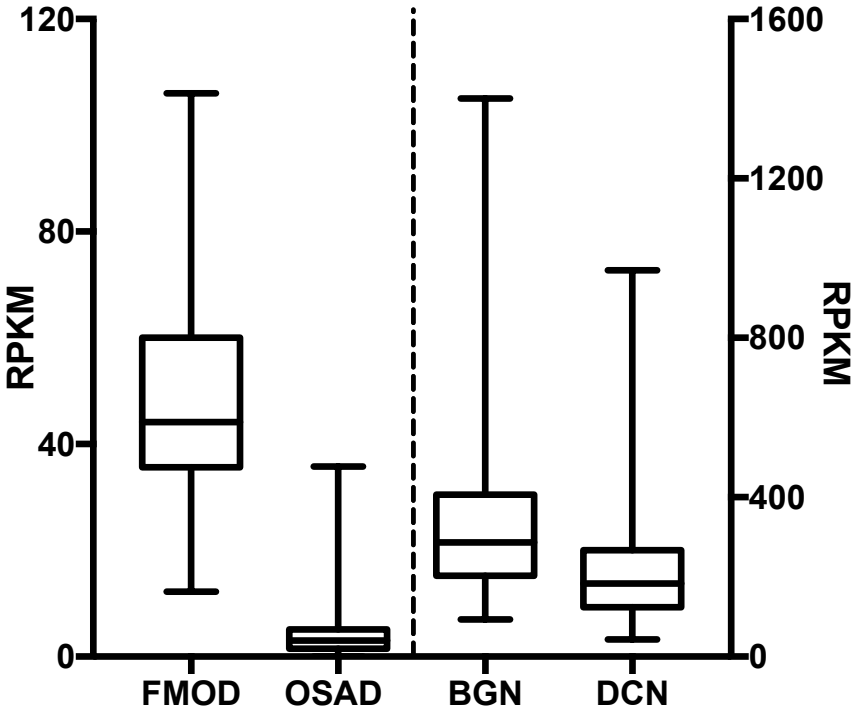

Figure S4. SLRP RNA expression from lung tissue

RNA expression of SLRPs from lung tissue samples (n=320) adapted from the Human Protein Atlas program (www.proteinatlas.org) (32). RNA sequencing data is reported in reads per kilobase per million mapped reads (RPKM).