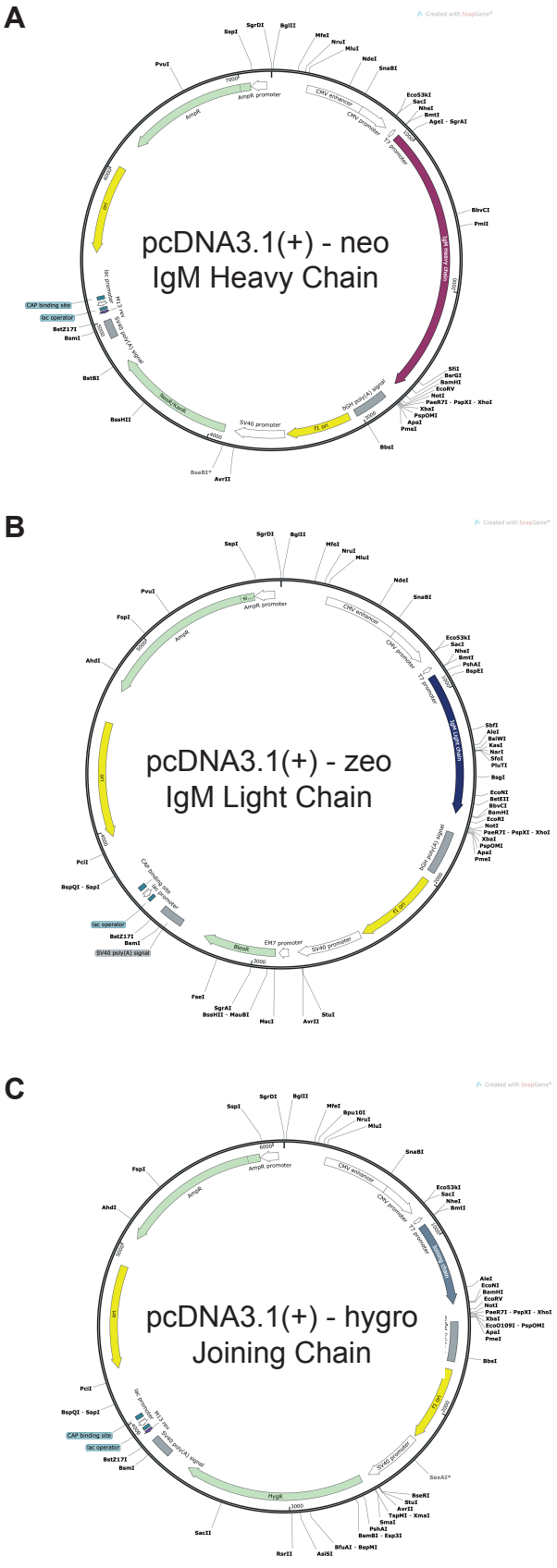
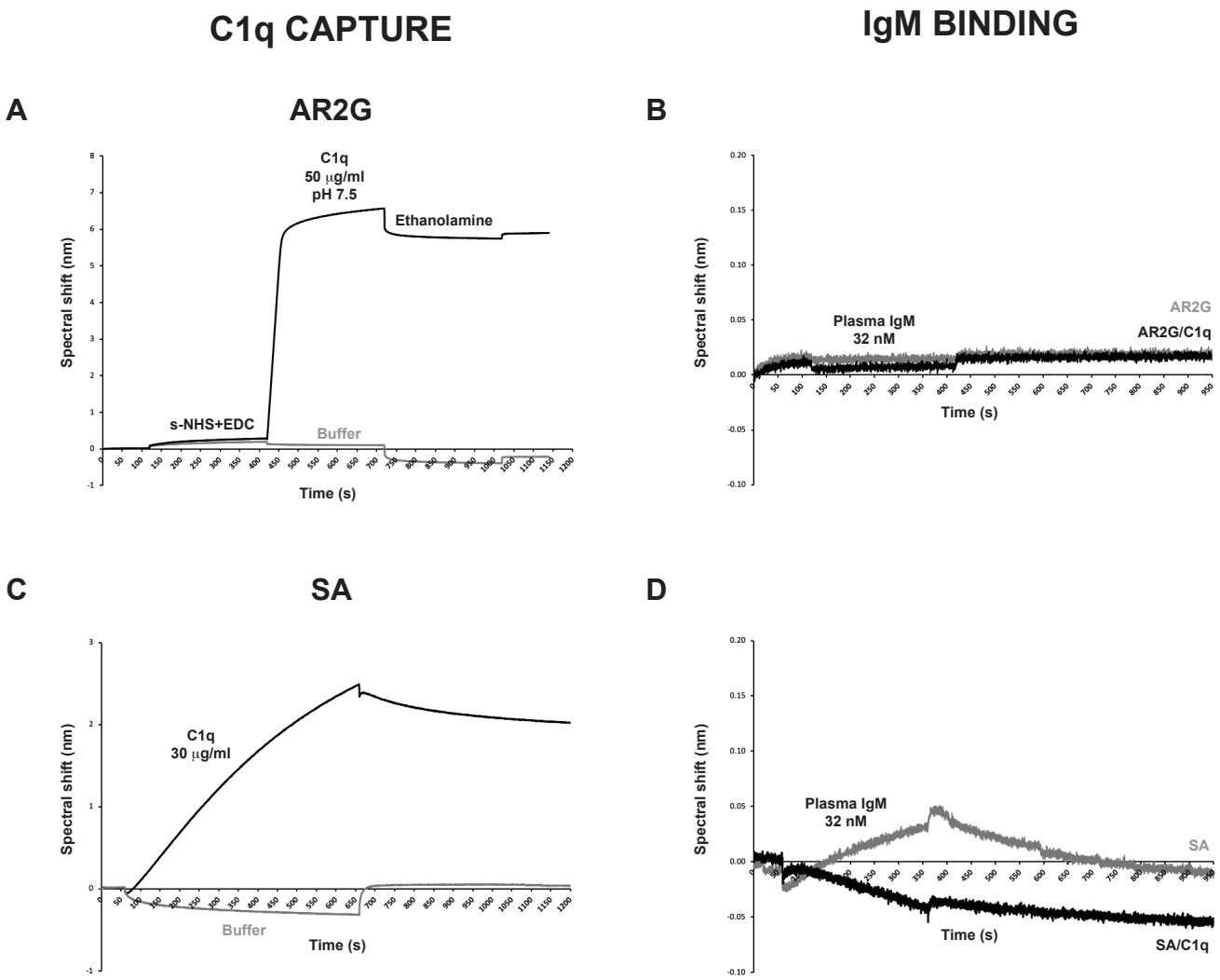
# Supplementary Figure S1



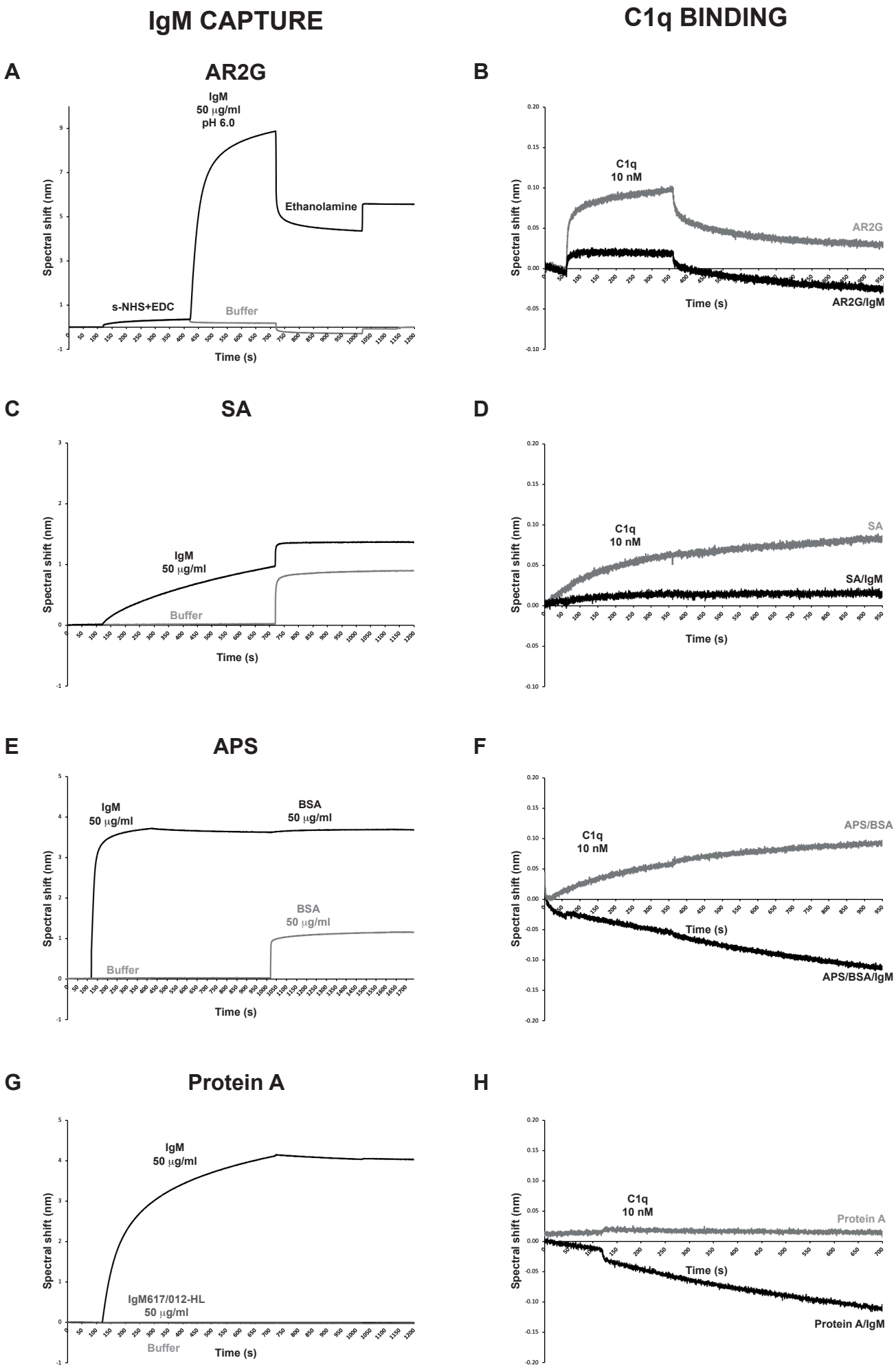

**Supplementary Figure S1.** Plasmid maps of pcDNA3.1(+) constructs used to obtain stable HEK293F cell lines expressing IgM617-HL, IgM617-HLJ, IgM012-HL and IgM012-HLJ.

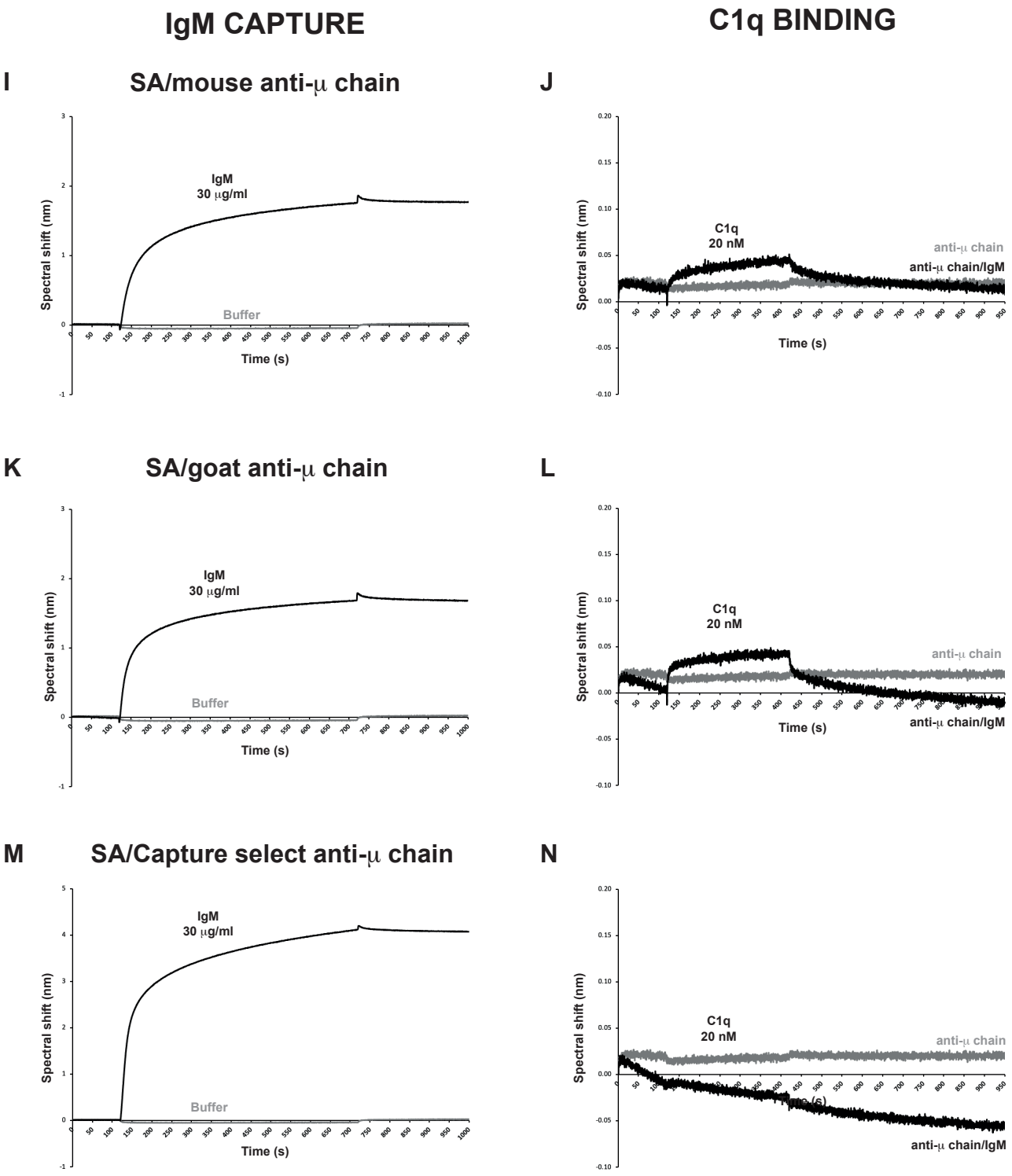
# Supplementary Figure S2




**Supplementary Figure S2.** Examples of C1q captures on (**A**) AR2G or (**C**) SA biosensors. (**B and D**) and examples of plasma IgM bindings at 32 nM to functionalyzed biosensors (in black) or reference biosensors (in grey).

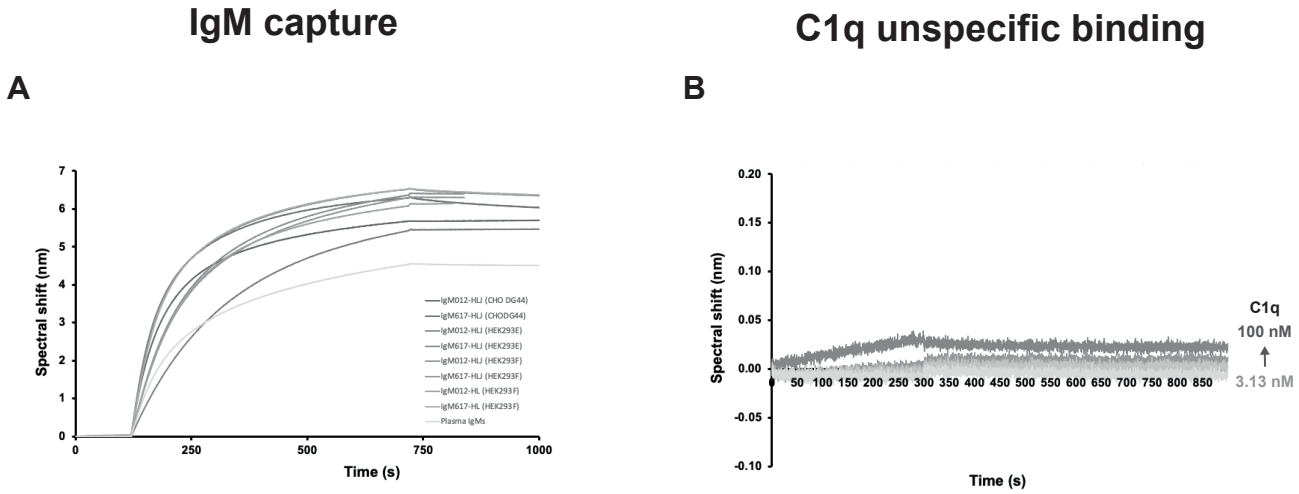
# Supplementary Figure S3





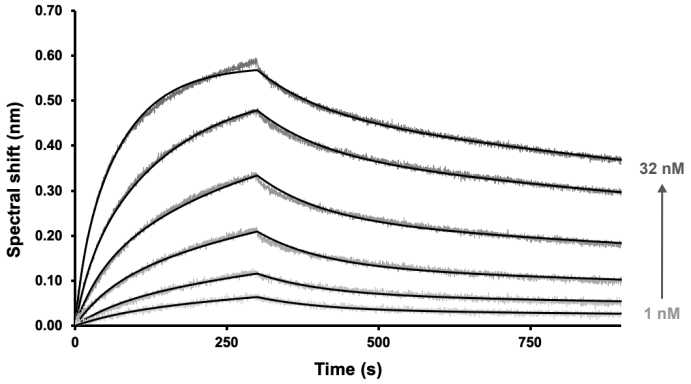

**Supplementary Figure S3.** Examples of plasma IgM captures on (**A**) AR2G, (**C**) SA, (**E**) APS, (**G**) Protein A, (**I, K, M**) anti-μ chain biosensors and (**B, D, F, H, J, L, N**) of plasma C1q binding at 10 or 20 nM to functionalized (in black) and reference (in grey) biosensors.

# Supplementary Figure S4




**Supplementary Figure S4**. (**A**) Capture of IgM samples onto Protein L biosensors (IgM concentration = 30 μg/ml). (**B**) C1q unspecific binding on Protein L biosensor at different concentrations from 3.13 nM to 100 nM.

# Supplementary Figure S5




| $k_{a1}$ | $k_{d1}$ | **$K_{D1}$** | $k_{a2}$ | $k_{d2}$ | **$K_{D2}$** |
|---|---|---|---|---|---|
| $10^5$/Ms | $10^{-4}$/s | **$10^{-9}$ M** | $10^6$/Ms | $10^{-3}$/s | **$10^{-9}$ M** |
| 4.06 ± 0.01 | 4.02 ± 0.03 | **10.00 ± 0.07** | 2.14 ± 0.02 | 9.28 ± 0.01 | **4.33 ± 0.01** |

**Supplementary Figure S5.** Kinetics analysis of the interaction between C1q from plasma and recombinant $C1r_2C1s_2$. C1q was immobilized on AR2G biosensor (supplementary Figure S1). The tetramer was expressed in mammalian cells (Bally et al., 2019). The functionalized biosensors were dipped in wells containing $C1r_2C1s_2$ at different concentrations (1, 2, 4, 8, 16, 32 nM). The binding signals (grey-scaled sensorgrams) were obtained by subtracting the signals from empty AR2G biosensor and from zero-concentration samples. Fitted curved are depicted as black lines and were obtained by global fitting using a 2:1 heterogenous ligand model. Kinetics parameters and affinities are reported in the table.