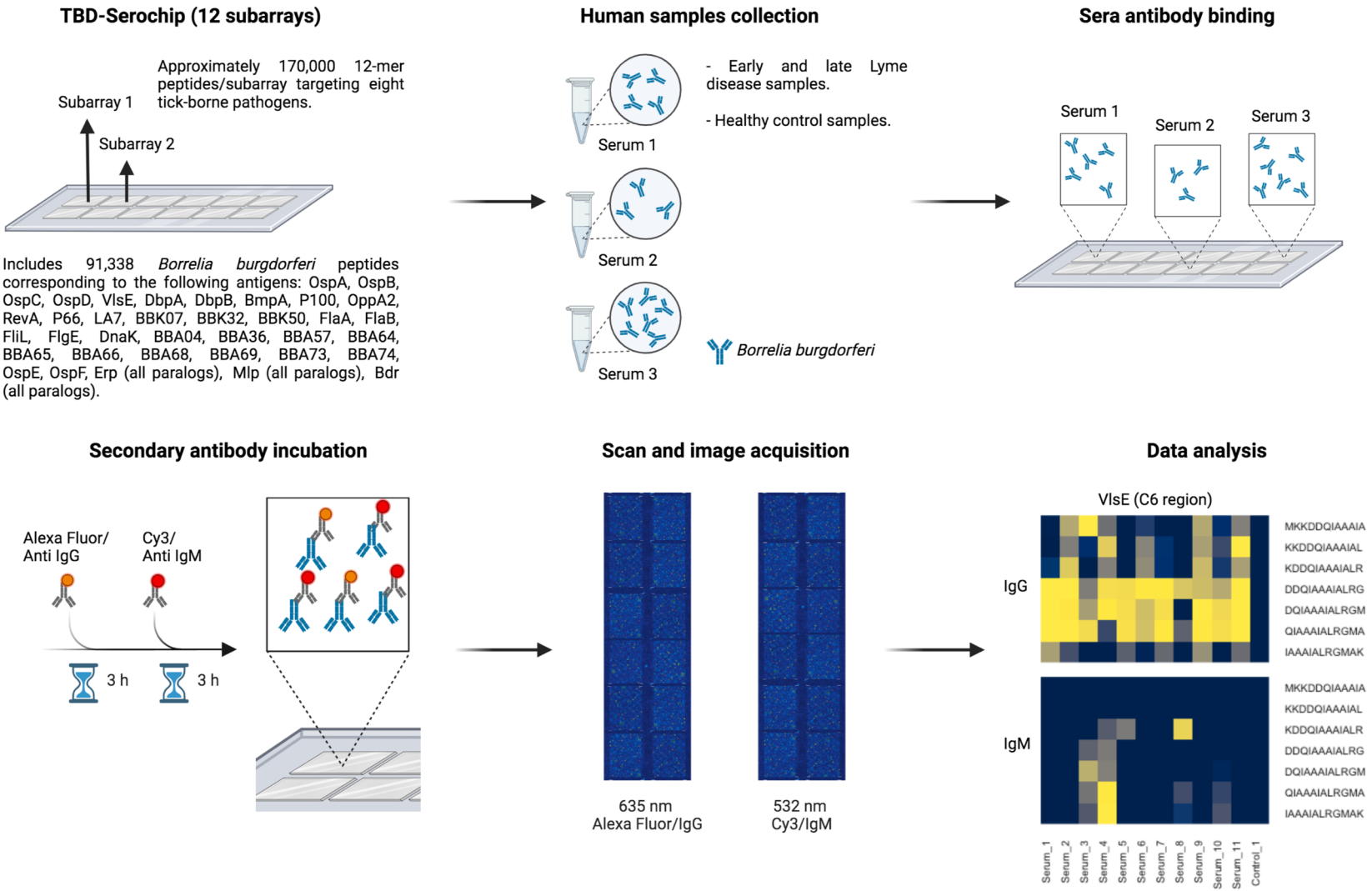

Fig. S1. Schematic for sera testing on the TBD-Serochip.

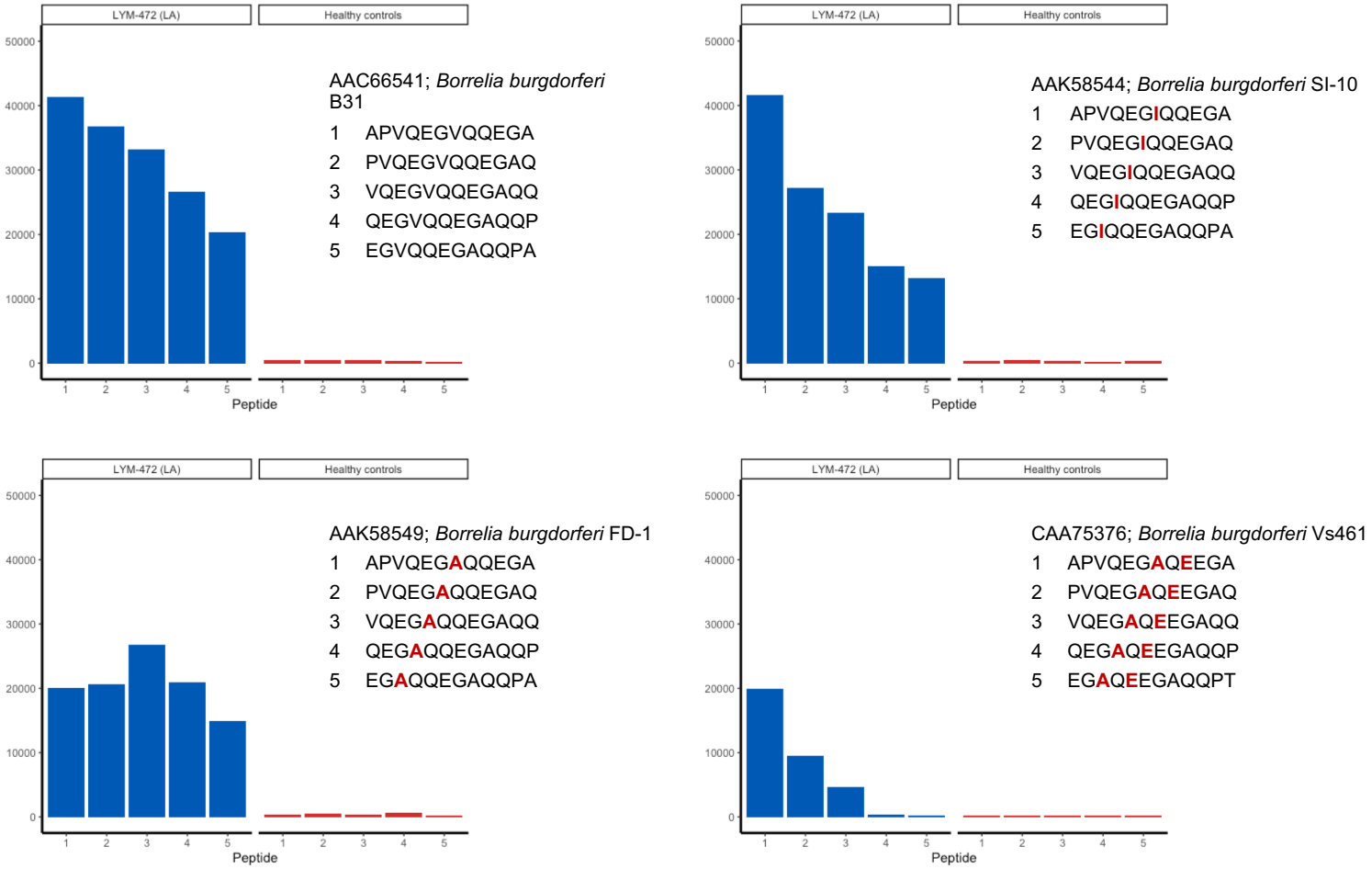

Fig. S2. Demonstration of amino acid heterogeneity of antibody binding on the TBD-Serochip. Shown is the reactivity to five FlaB peptides from the B31 strain and their variants from other *B. burgdorferi* strains. The blue bars represent the reactivity of a single Lyme disease positive serum from a patient with Lyme arthritis (LYM-472). The bars represent an average of 47 healthy control sera from the National Institutes of Health. The Y-axis indicates reactivity and the numbers 1-5 on the X-axis correspond to the peptide sequences. Substantial cross-reactivity can still be detected despite amino acid substitution at multiple positions (shown in red) within the 12-mer peptide.

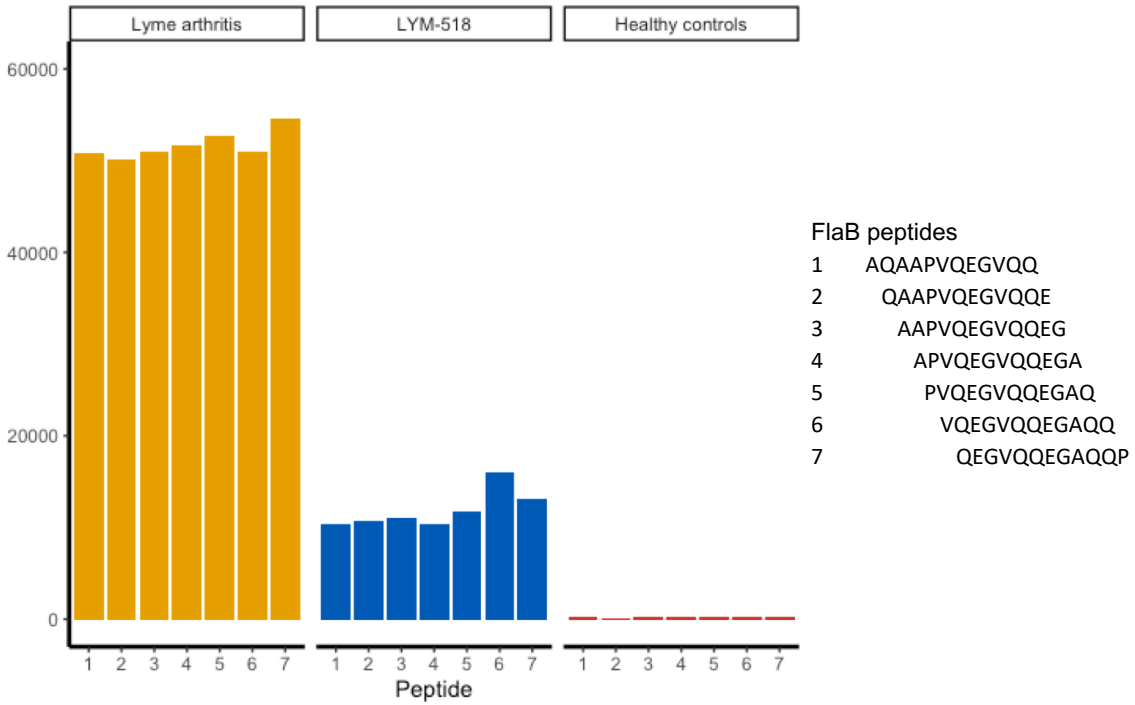

Fig. S3. Elevated reactivity of a control sample LYM-518 to seven consecutive peptides within the 207-229 FlaB region. LYM-518 was classified as Lyme disease by the diagnostic model. Numbers 1-7 on the X axis represent the seven FlaB peptides. Reactivity is indicated on the Y axis. Yellow bars indicate average reactivity of 27 Lyme arthritis samples, blue bars indicate reactivity from LYM-518 and the red bars represent the average of 47 control samples. All samples were from the National Institutes of Health cohort.

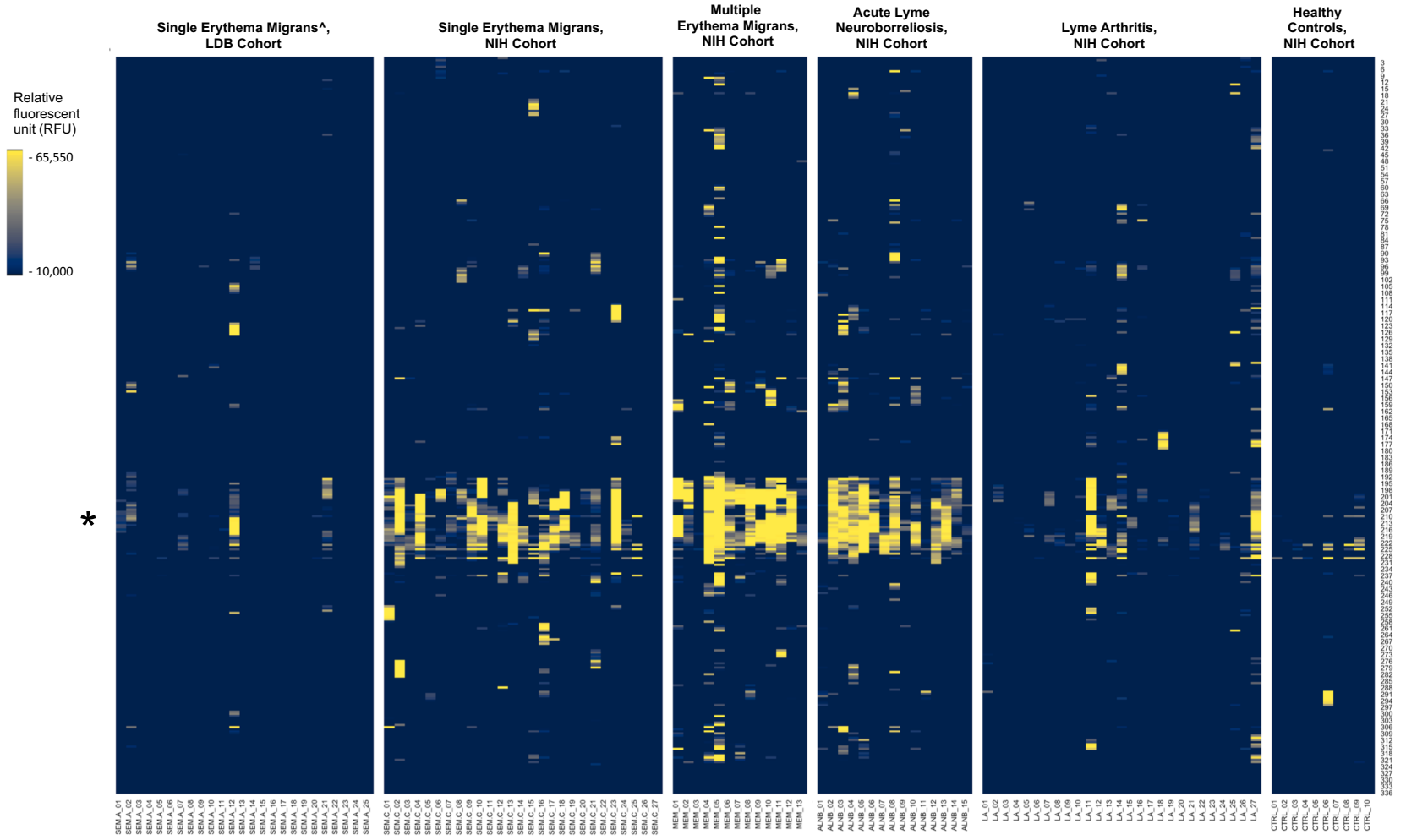

Fig. S4. IgM reactivity to FlaB peptides in the five sample types. The Y axis indicates the relative amino acid coordinates of the peptides within the full-length FlaB protein. Reactivity is shown in yellow. For clarity, only peptides with reactivity above 10,000 RFU are shown. Samples are indicated on the X axis. To illustrate baseline reactivity ten random control samples were selected and shown on the right. * - indicates the highly immunoreactive region encompassing residues 191-231.
^ - includes only confirmed Lyme disease cases.