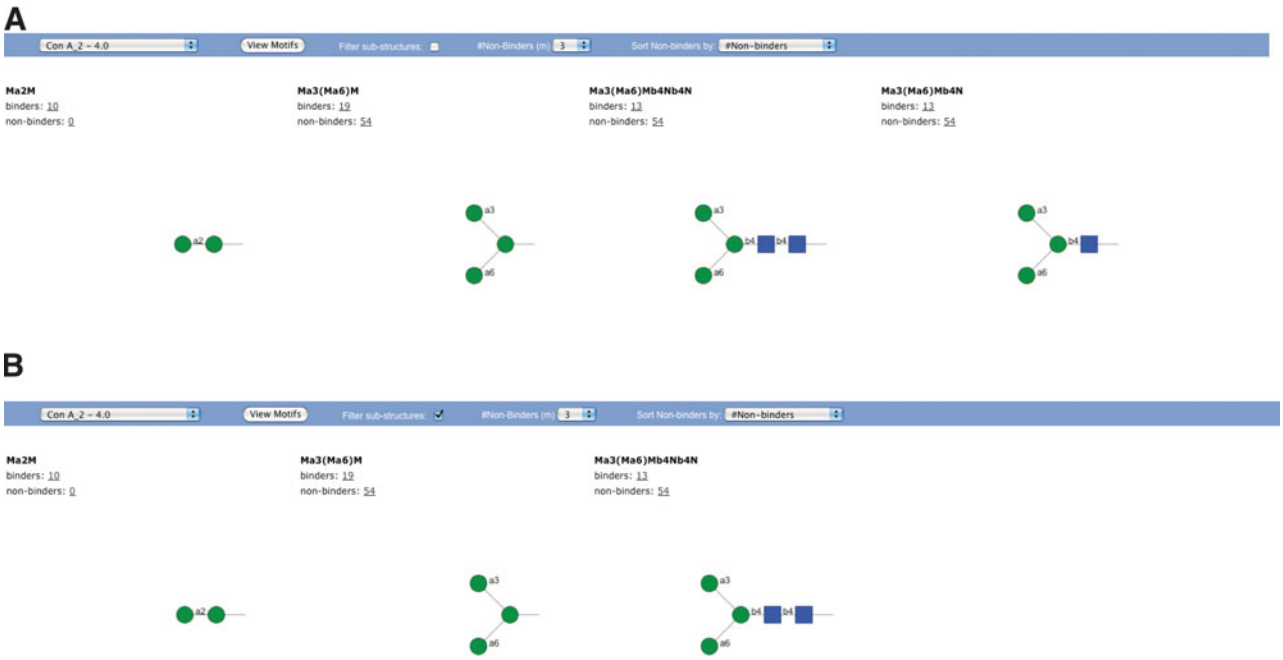

SUPPLEMENTARY FIG. S6. Graphical user interface generated by the algorithm in GLYMMR with parameters set to m = 3, normal sorting, according to Figure 2 for the motifs of Con A from data at two different Con A concentrations. (**A**) Not filtered to remove the subsets of identical structures. (**B**) Filtered to remove the subsets of identical structures. The designation Con A_3-4.0 is generated using the dropdown menu to select what data to display from v4.0 of the array. "View motifs" is a command field. Checking the box labeled "Filter sub-structures" filters the results (**B**). The m value [#Non-Binders (m)] can be 3–14, selected from the dropdown menu. The sorting method may also be modified, but is not demonstrated here. A single-letter code for the glycan structures is presented (S, Neu5Ac; L, Gal; N, GlcNAc; A, GalNAc; M, Man; F, Fuc, G, Glc). The numbers are the linkage position on the monosaccharide to the right of the number, and a = α and b = β. Below the single-letter designation of each oligosaccharide, the underlined numbers indicate the number of binding glycans on the array that possess the displayed motif (binders), and the number of non-binding glycans (non-binders) on the array that possess the displayed motif (binders).