Supporting Information Figures

Simultaneous immunoglobulin A and G glycopeptide profiling for high-throughput applications

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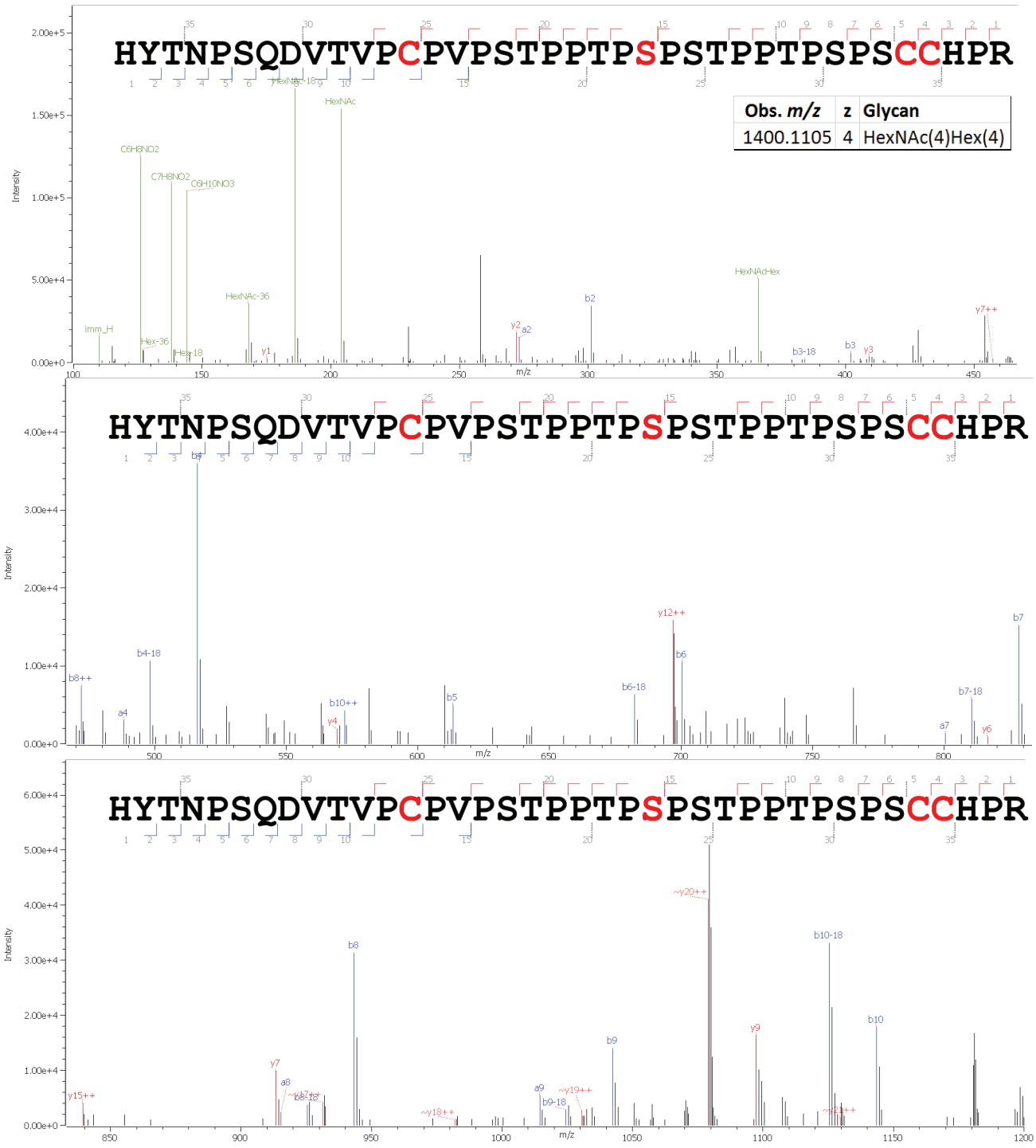

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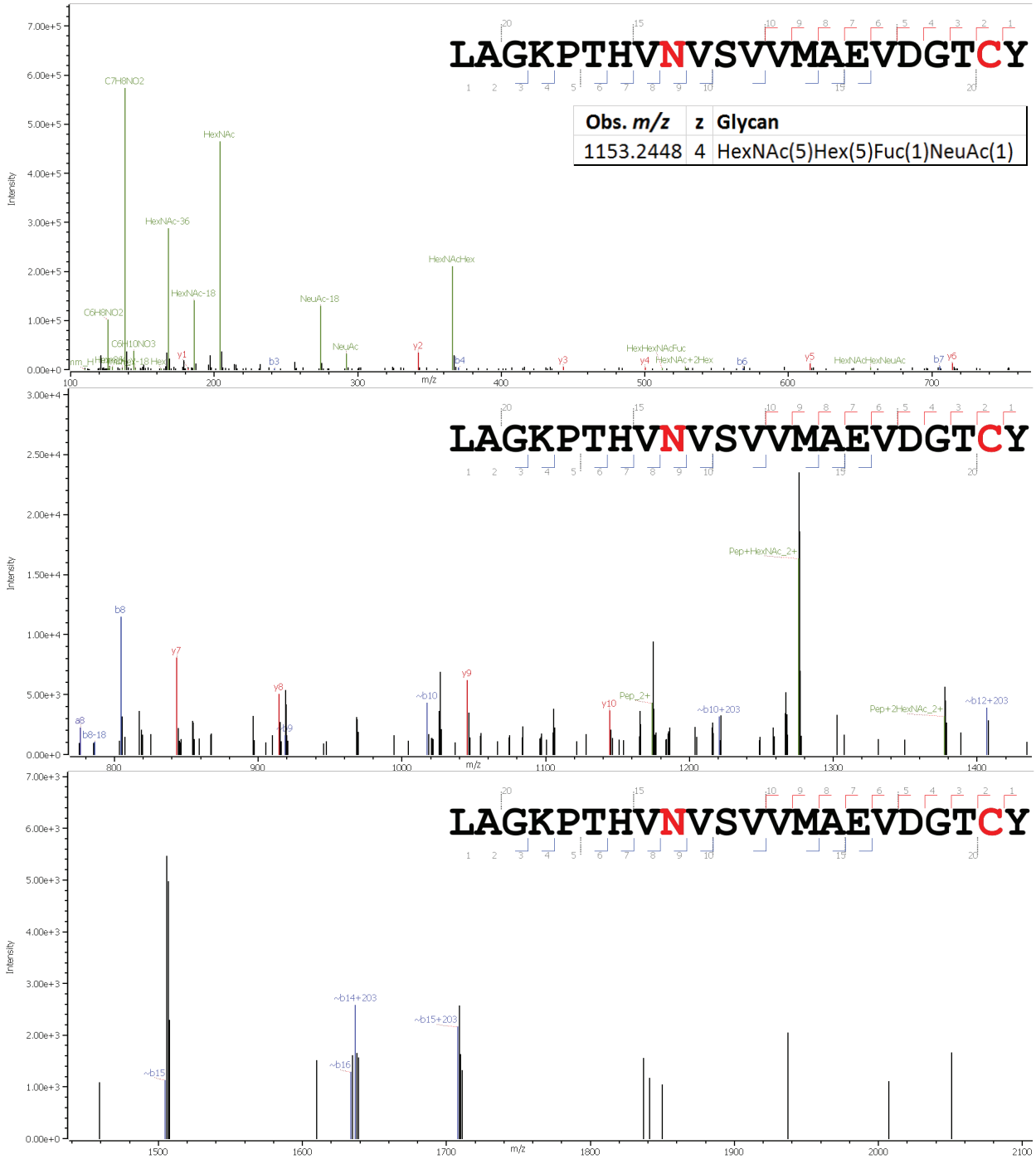

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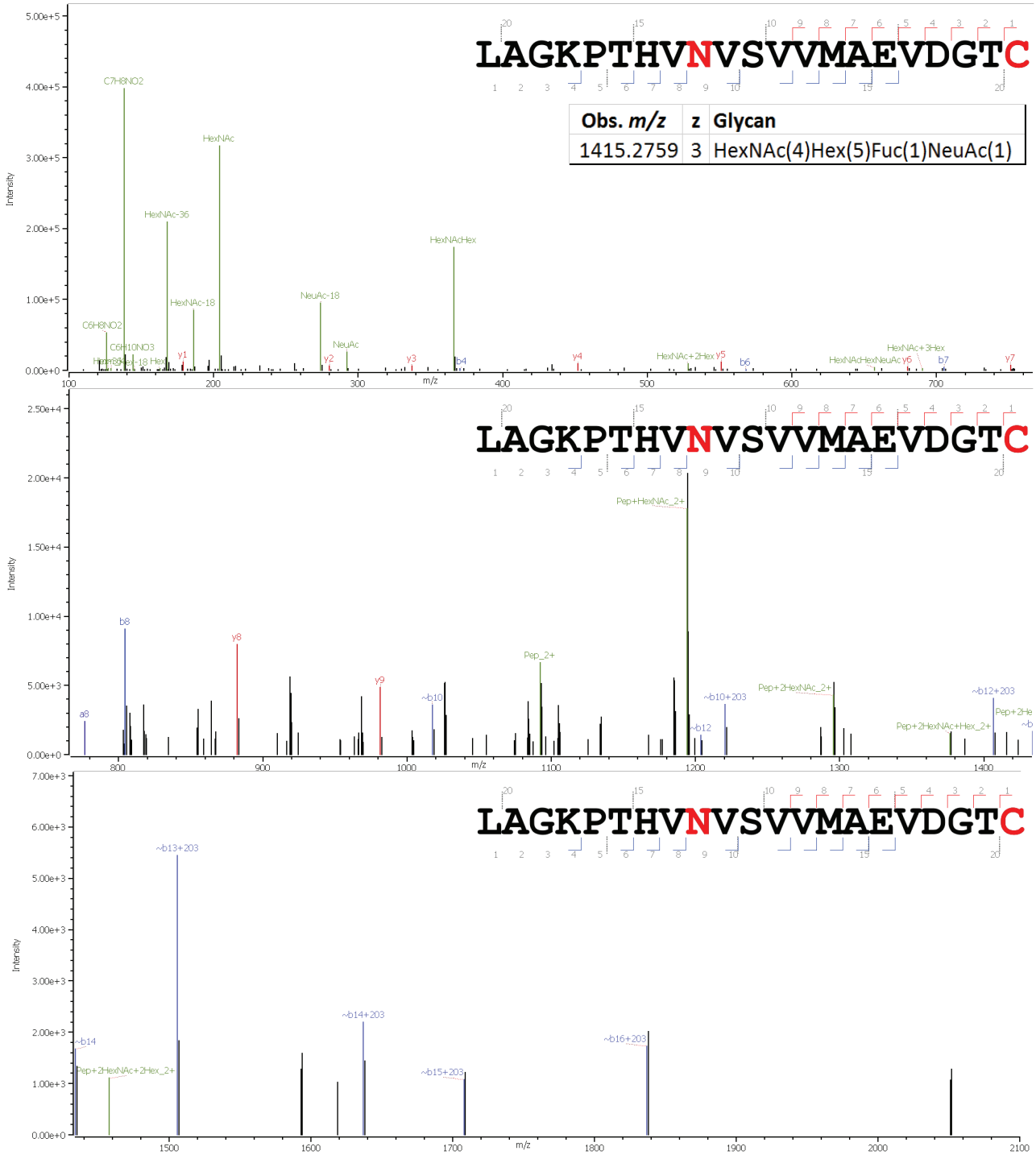

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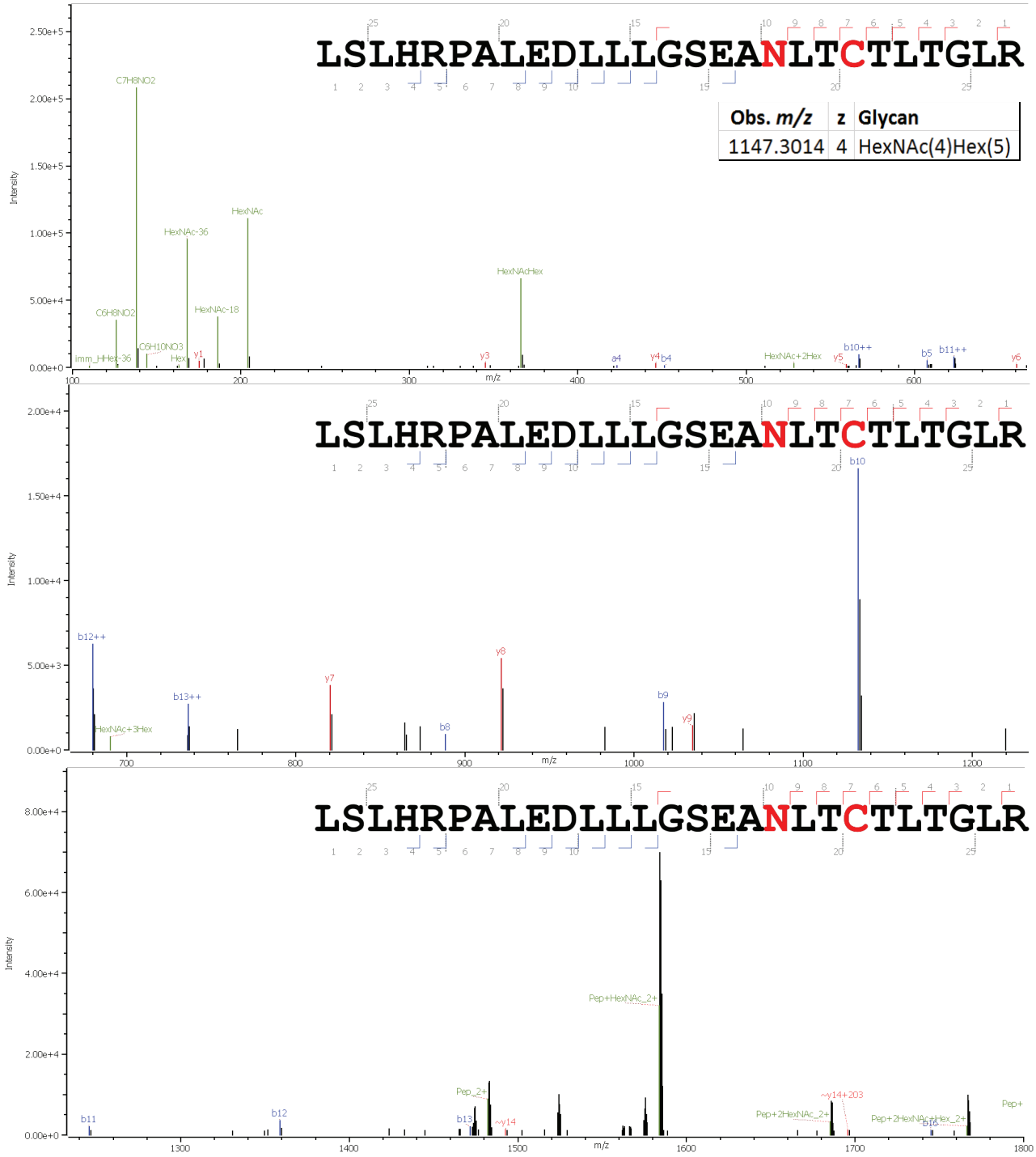

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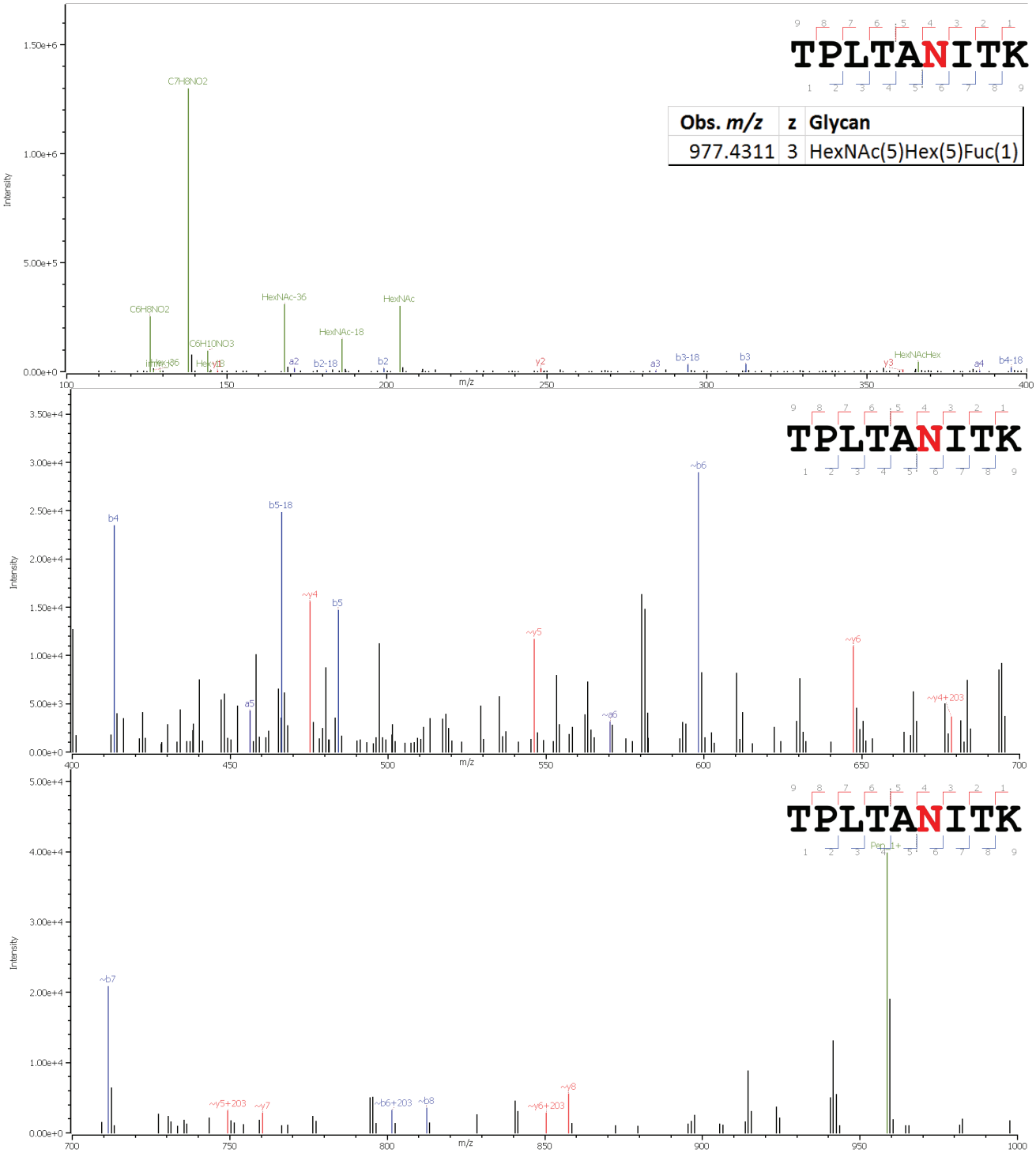

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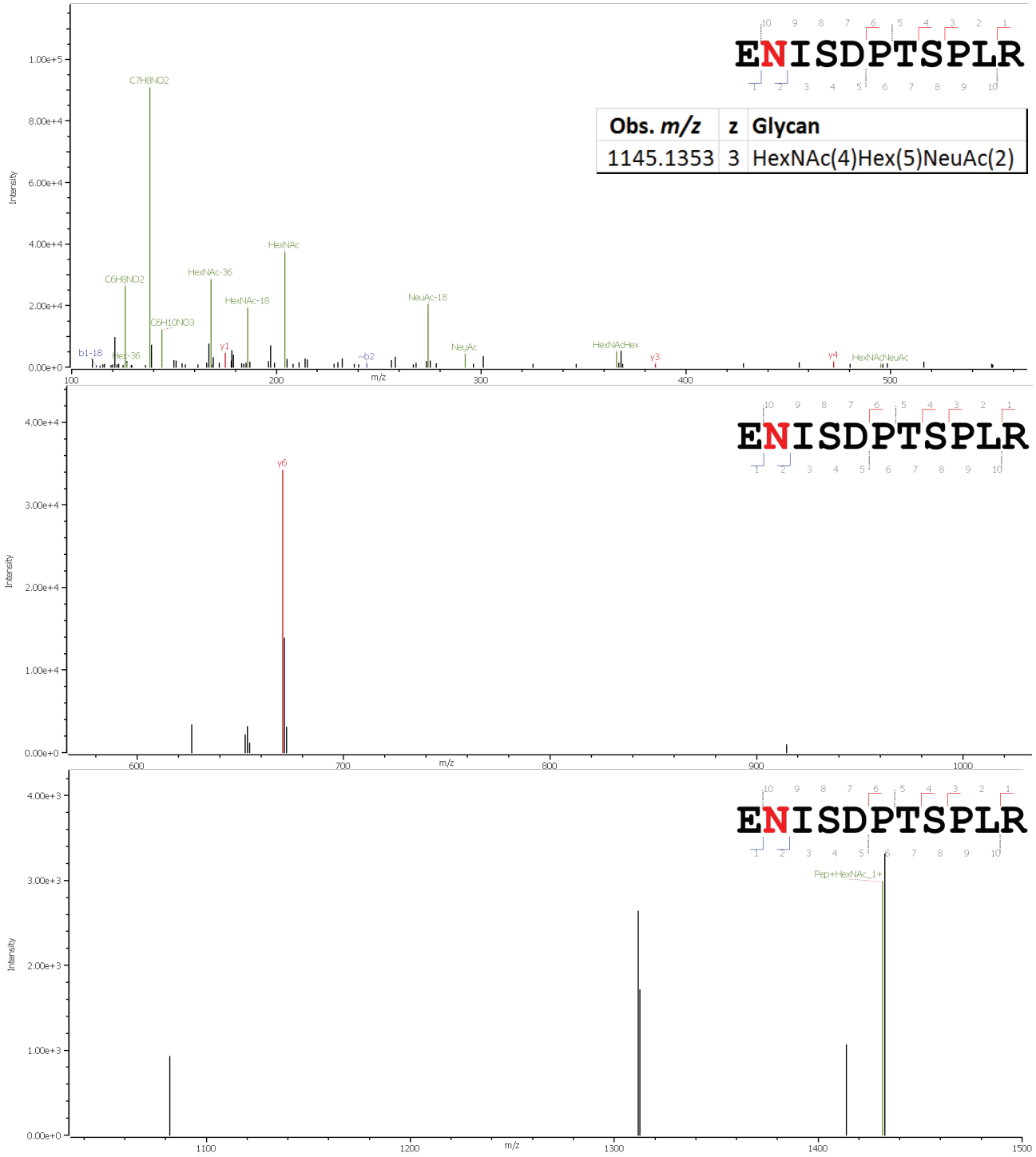

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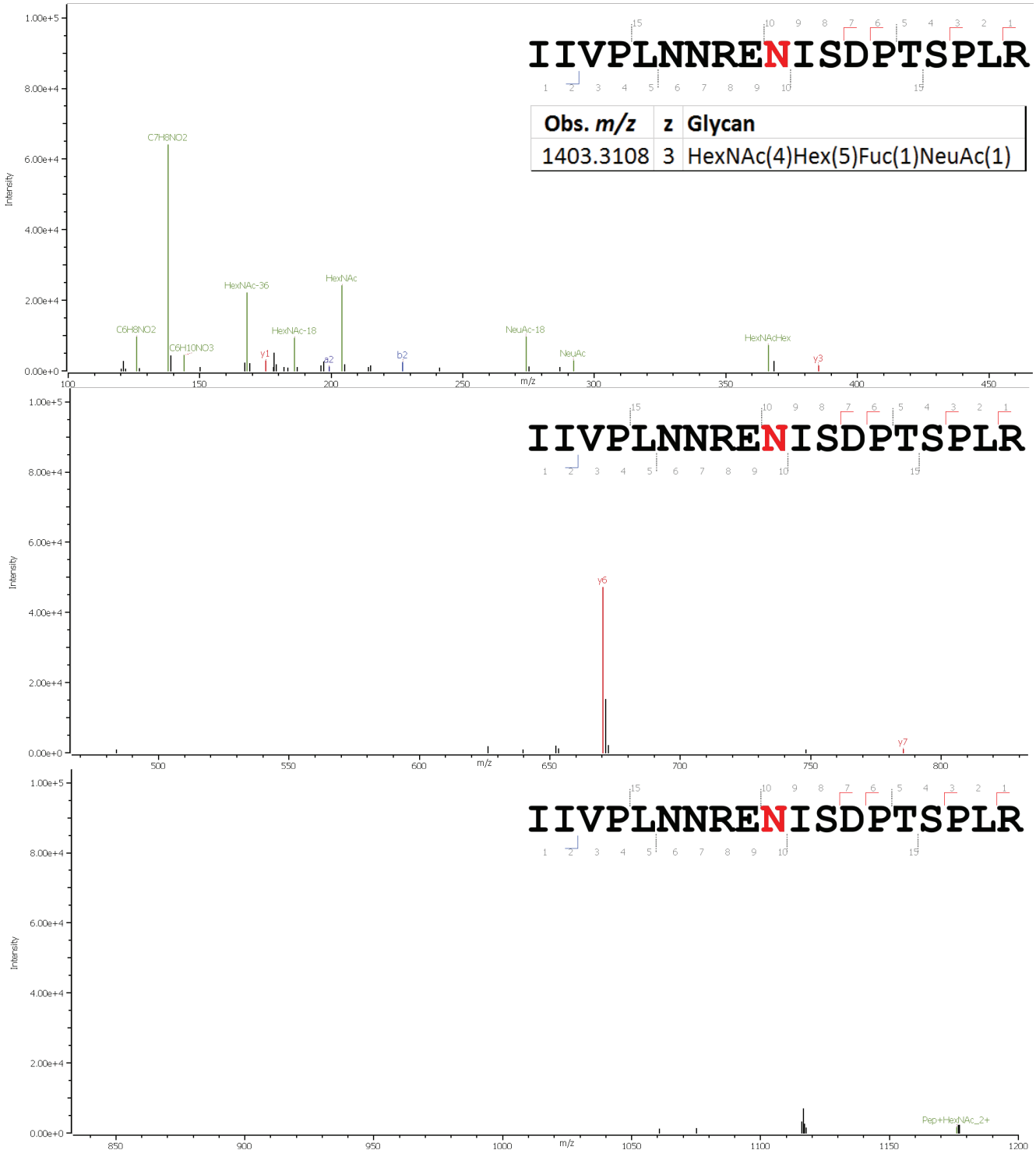

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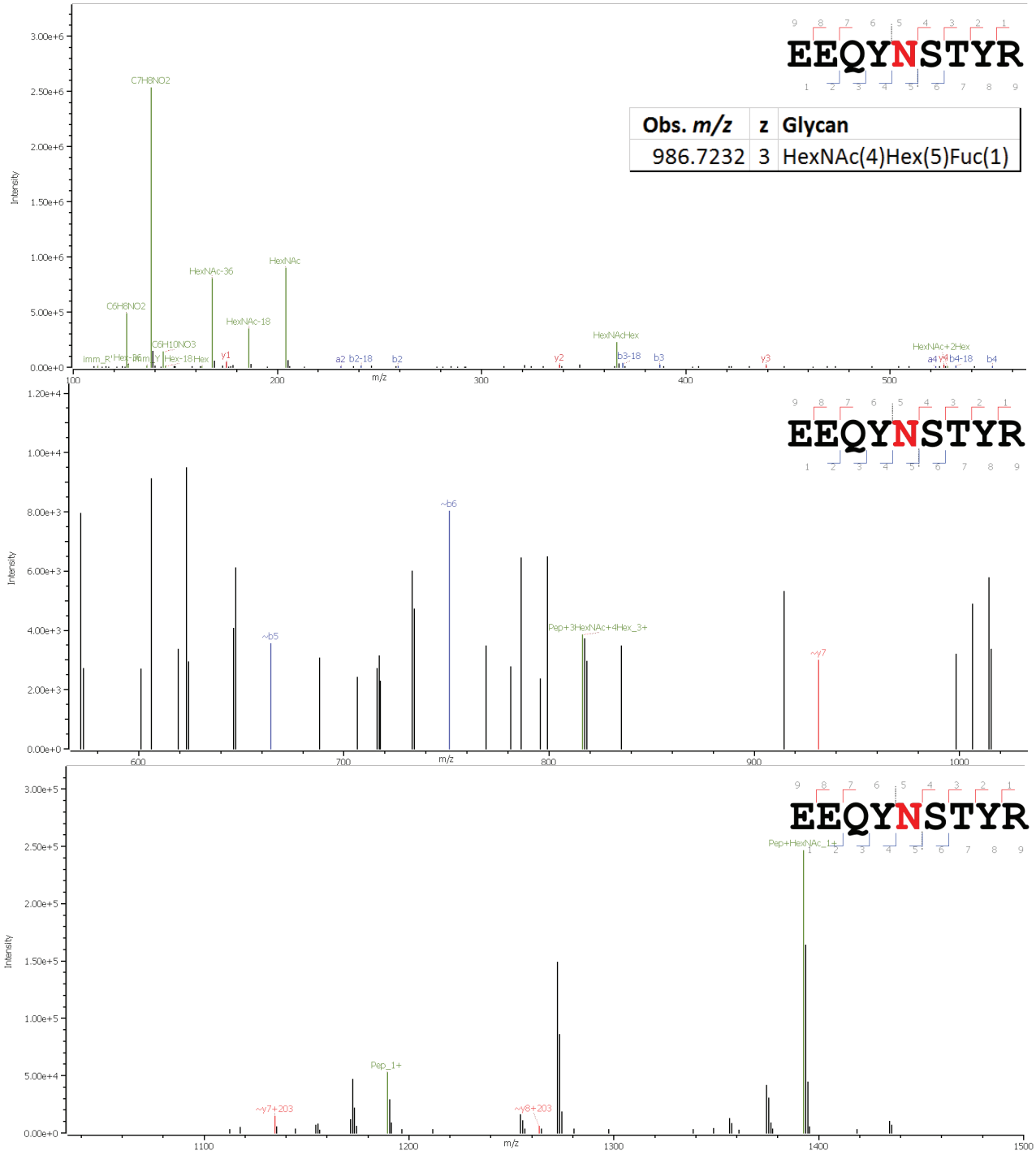

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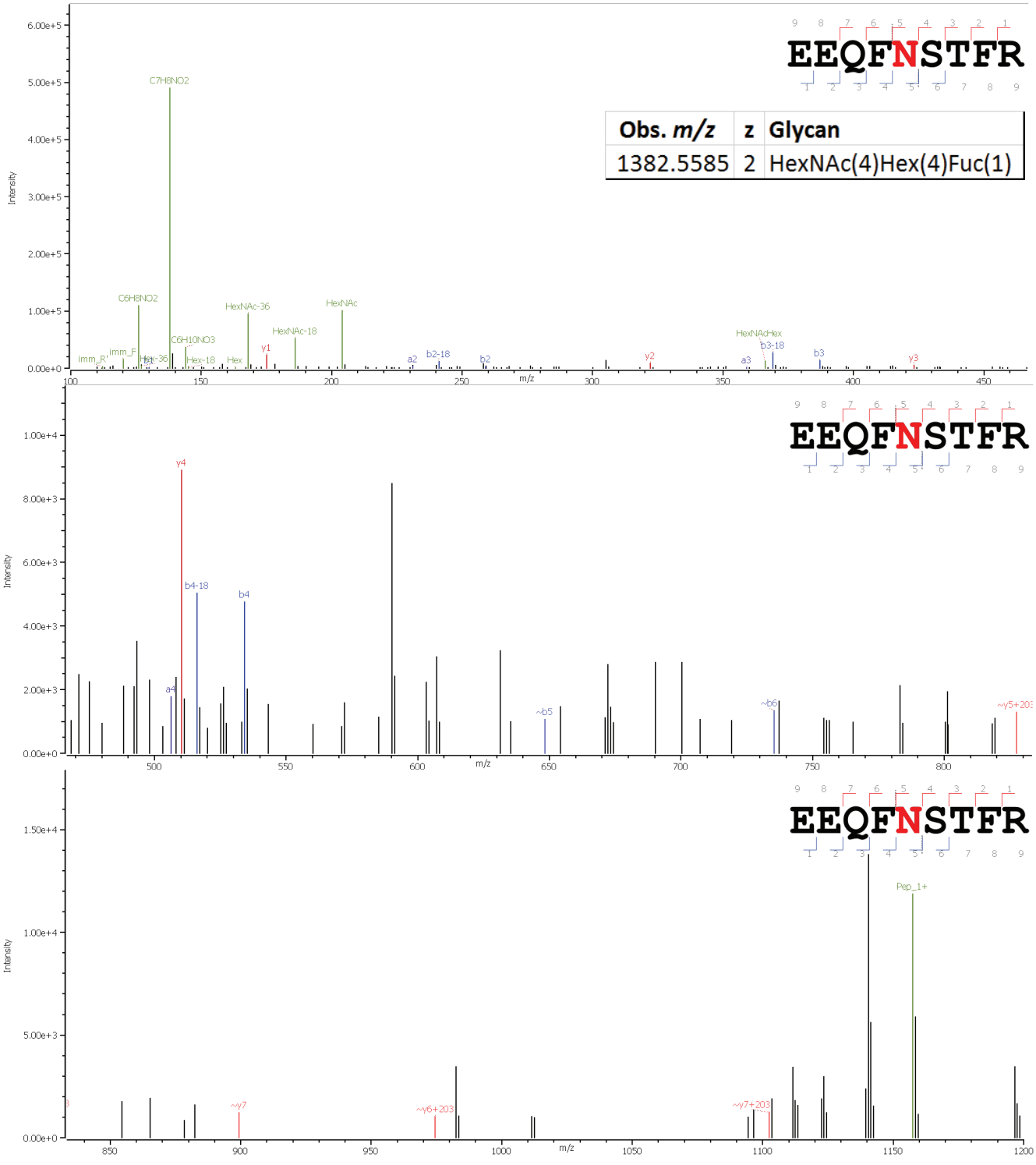

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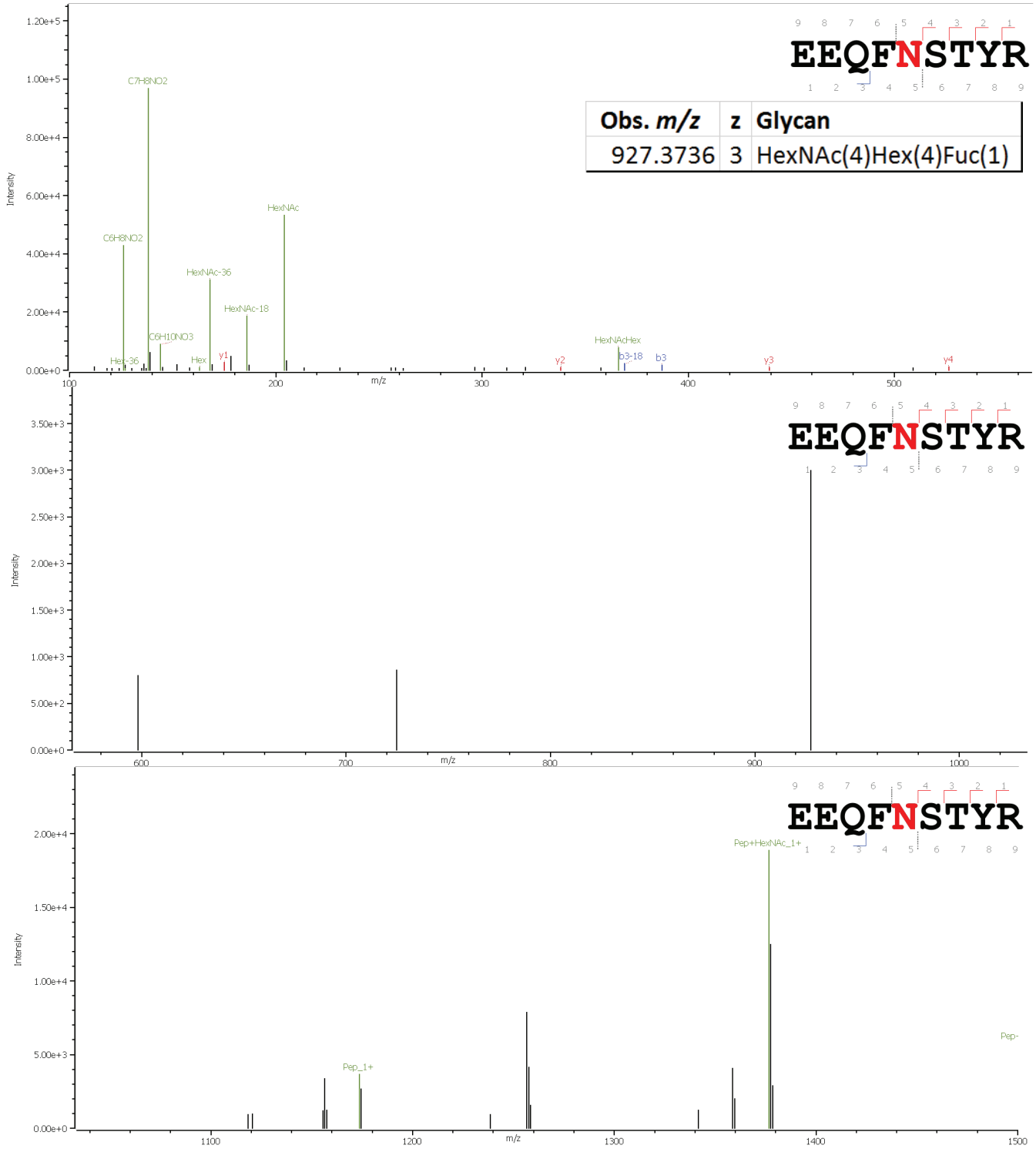

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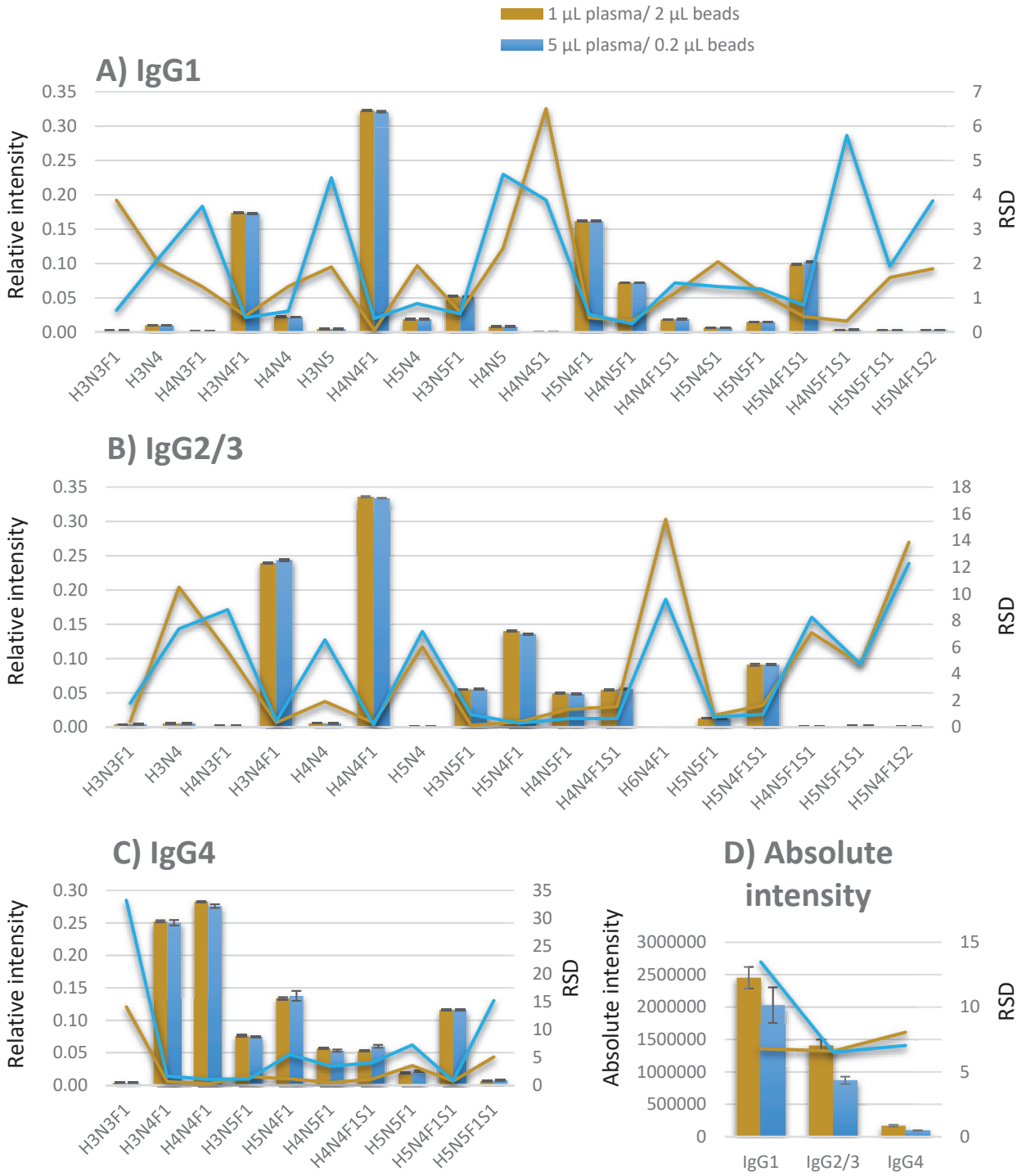

Figure S2 IgG glycosylation profiles and absolute intensities at different capturing conditions.
Total IgG was captured either with high (brown) or low (blue) recovery and plotted for the different subclasses IgG1 (A), IgG2/3 (B), and IgG4 (C). Absolute intensities of IgG glycopeptides are reduced due to undercapturing (D). Error bars (standard deviation) and respective relative standard deviations (RSD) are calculated from triplicate samples that went through the entire workflow as described in the Methods section, with the exception of the amount of plasma and beads used for the high-recovery capturing, i.e. 1 µL plasma with 2 µL beads.
Non-fucosylated glycopeptide species in IgG4 were not included here due to their overlapping *m/z* values with respective fucosylated IgG1 species. H = hexose, N = *N*-acetylhexosamine, F = fucose, S = *N*-acetylneuraminic acid.

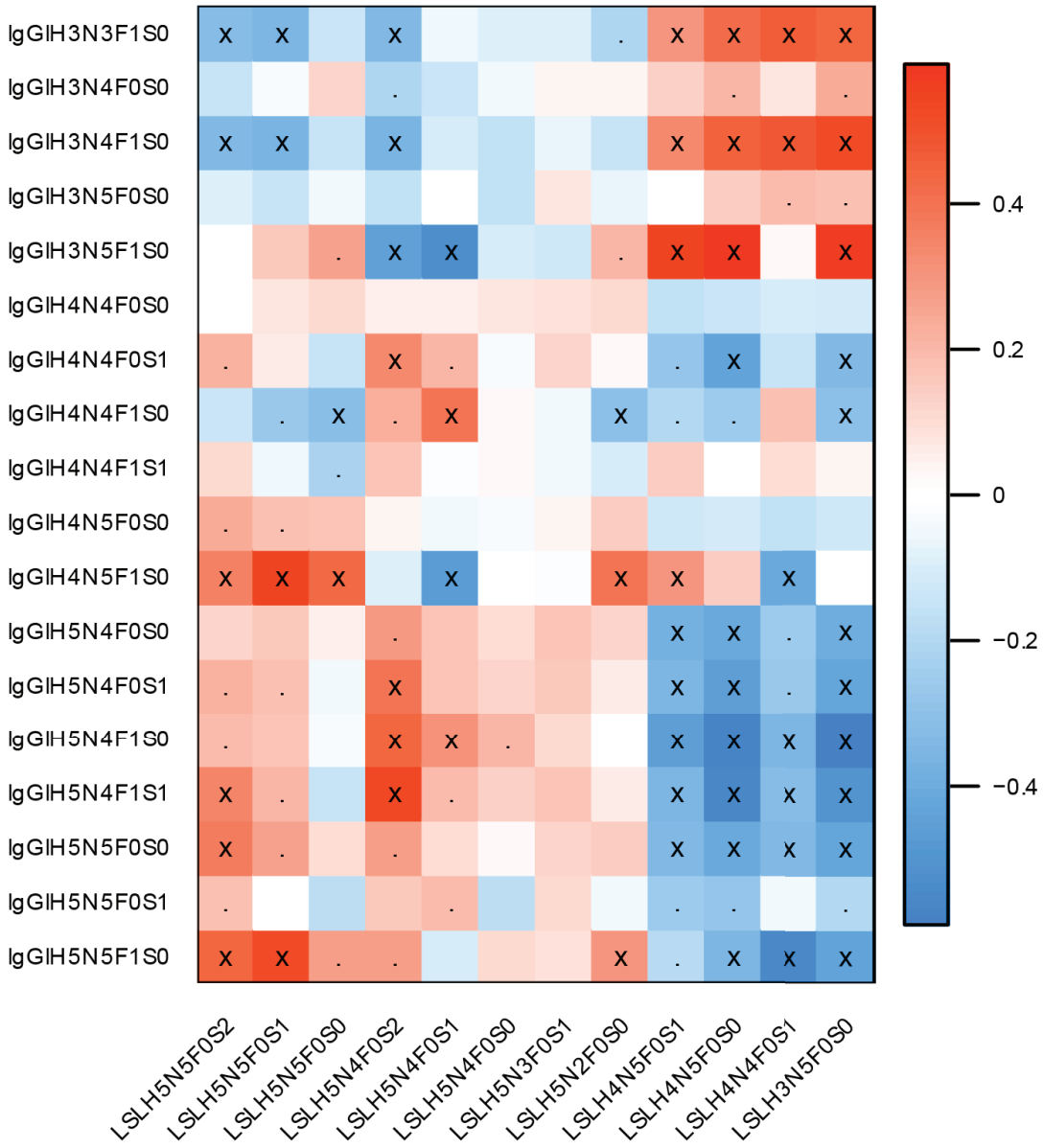

Figure S3 Correlation heatmap of IgG1 and IgA1/2 LSL glycopeptides

Spearman correlation coefficients are depicted as indicated in the color legend. Dots (.) indicate a statistical significance of $p \leq 0.05$ while crosses (X) mark significance of $p \leq 1.6 \times 10^{-3}$ which is the Bonferroni corrected threshold.