

A comprehensive landscape of human organ N-glycoproteome

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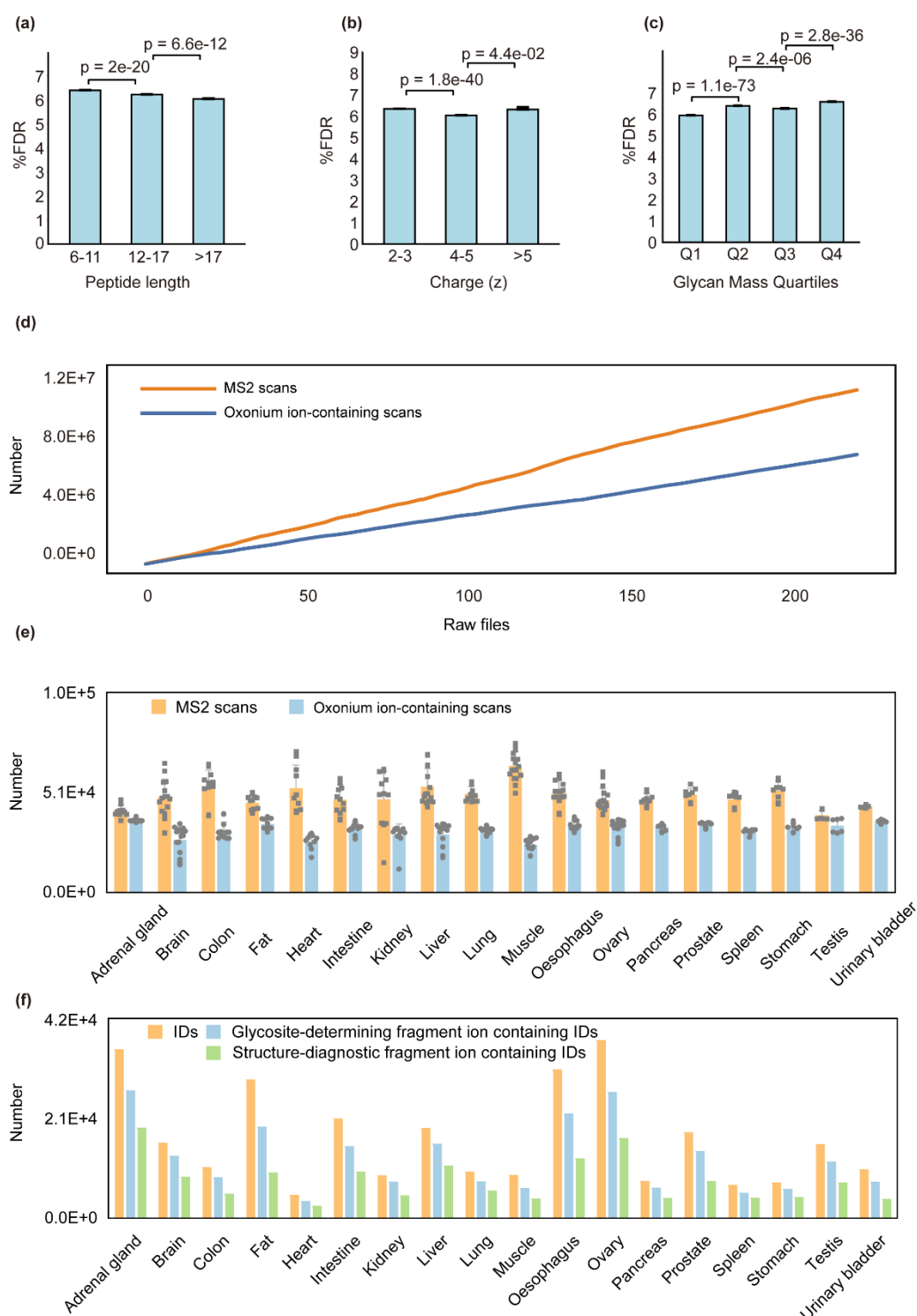
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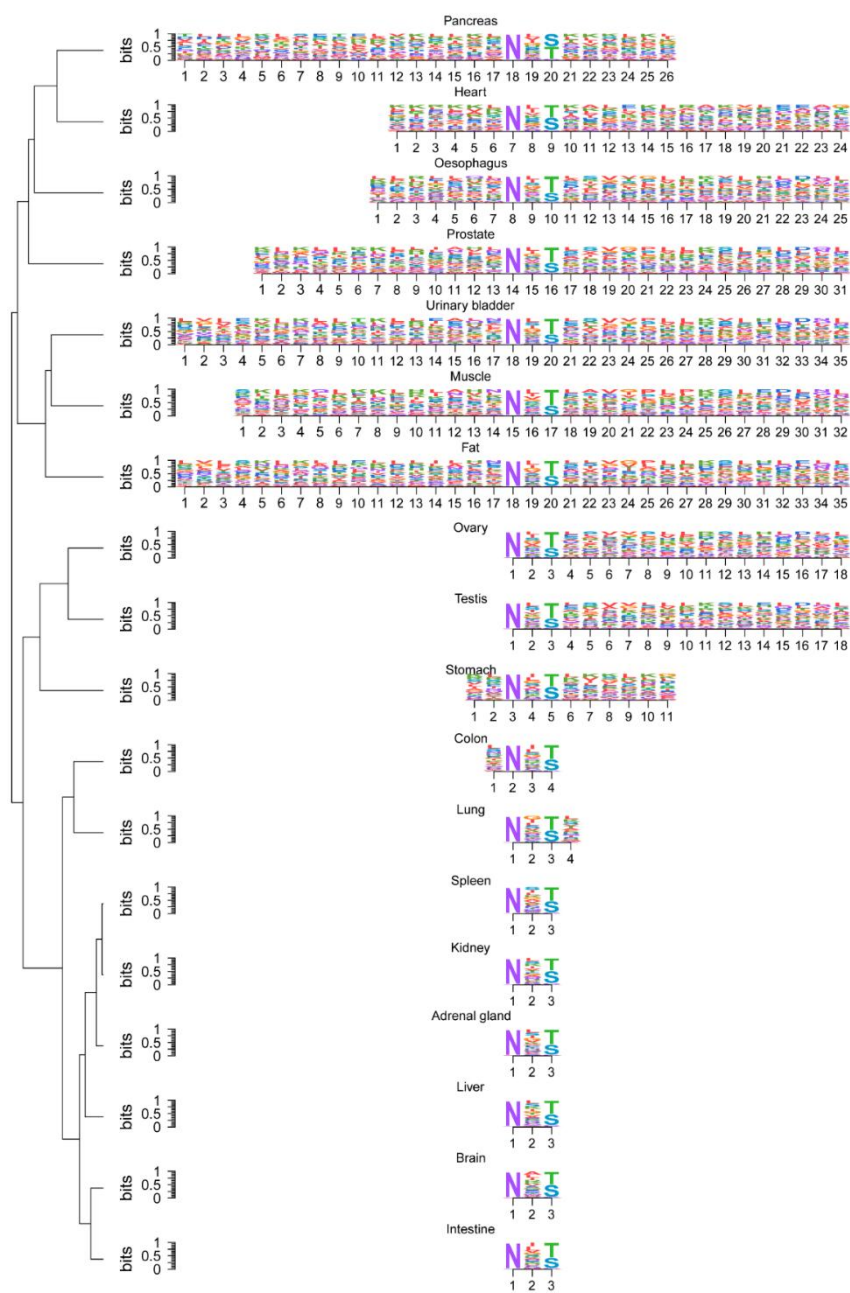
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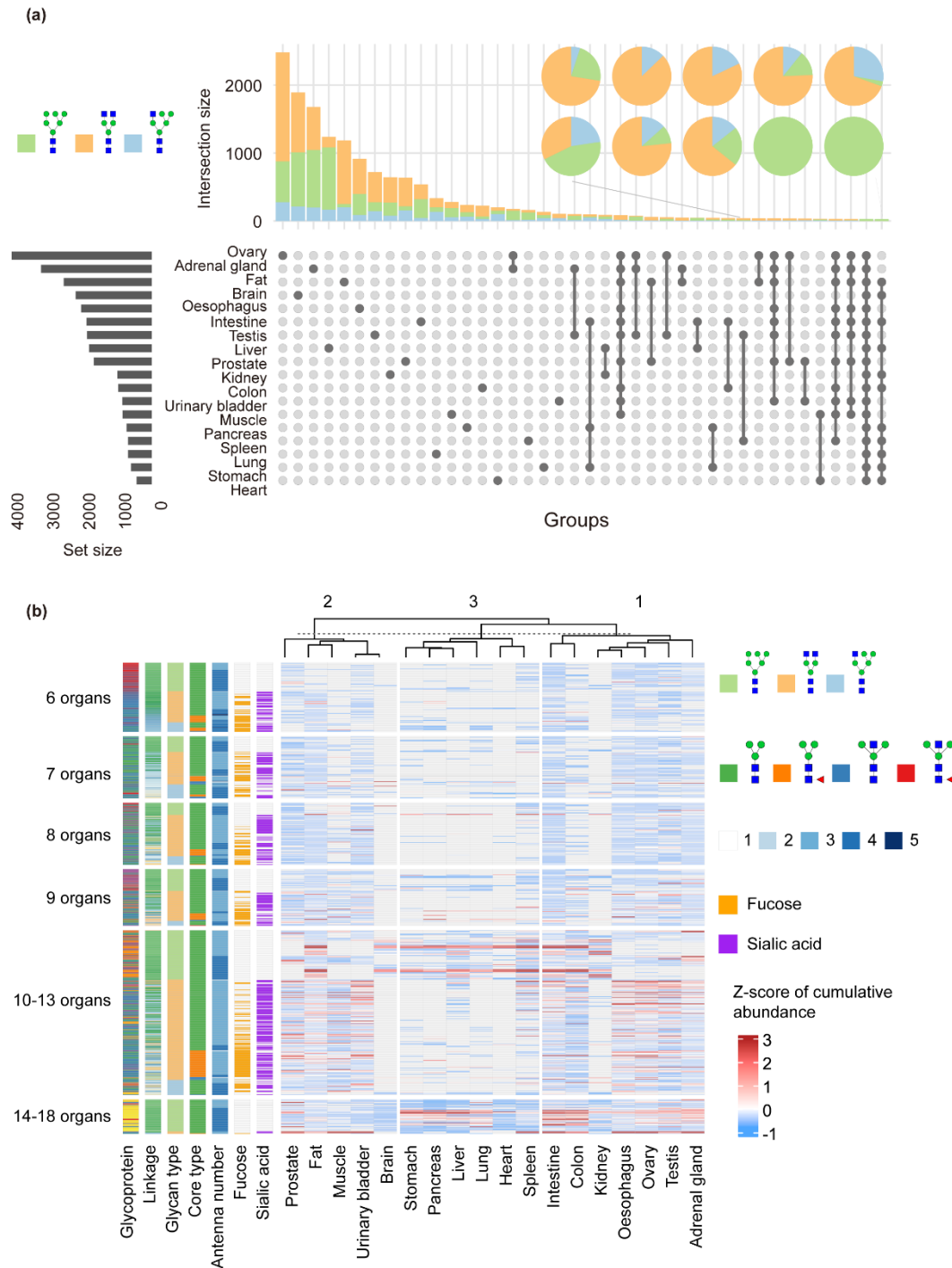


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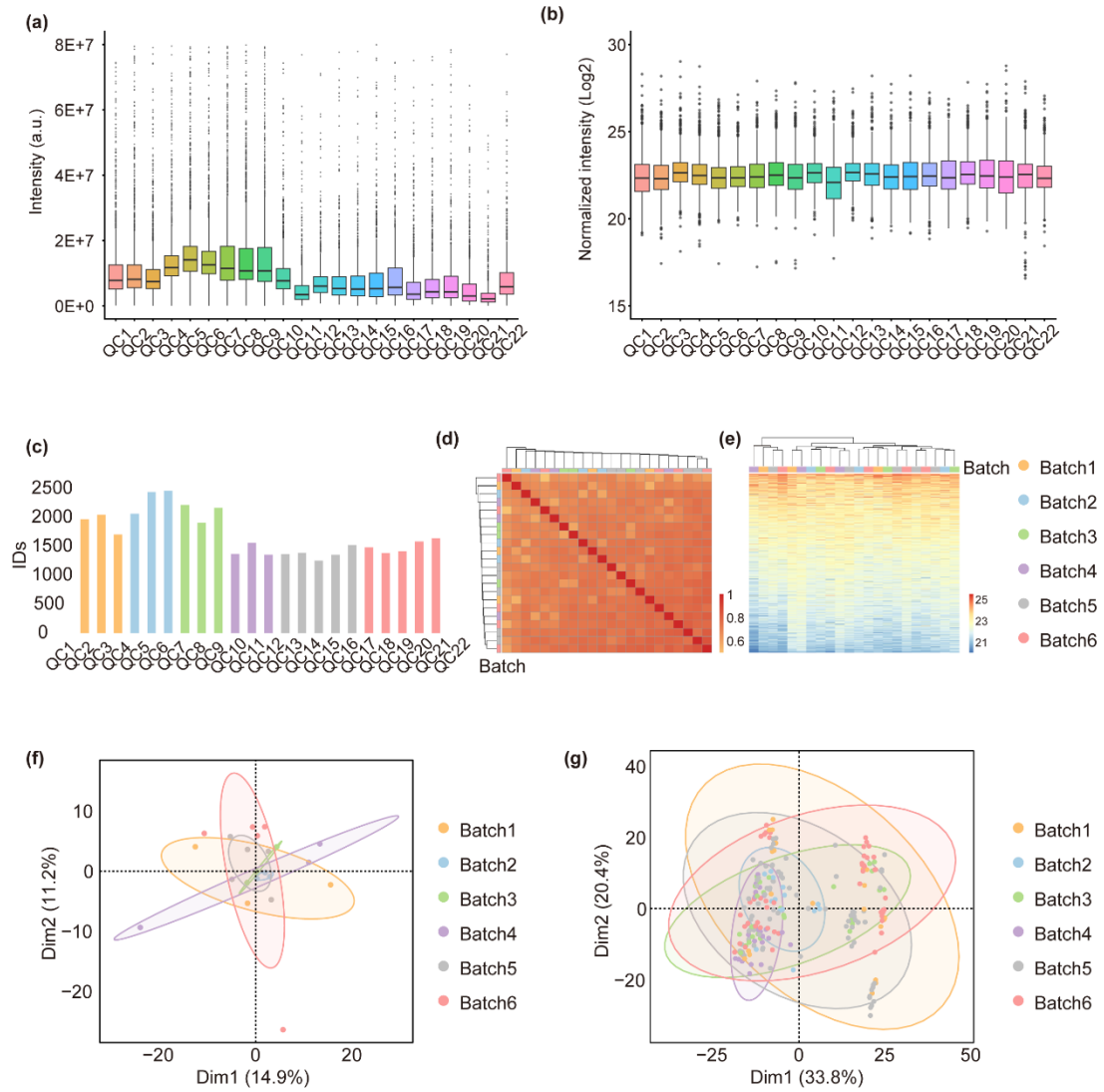
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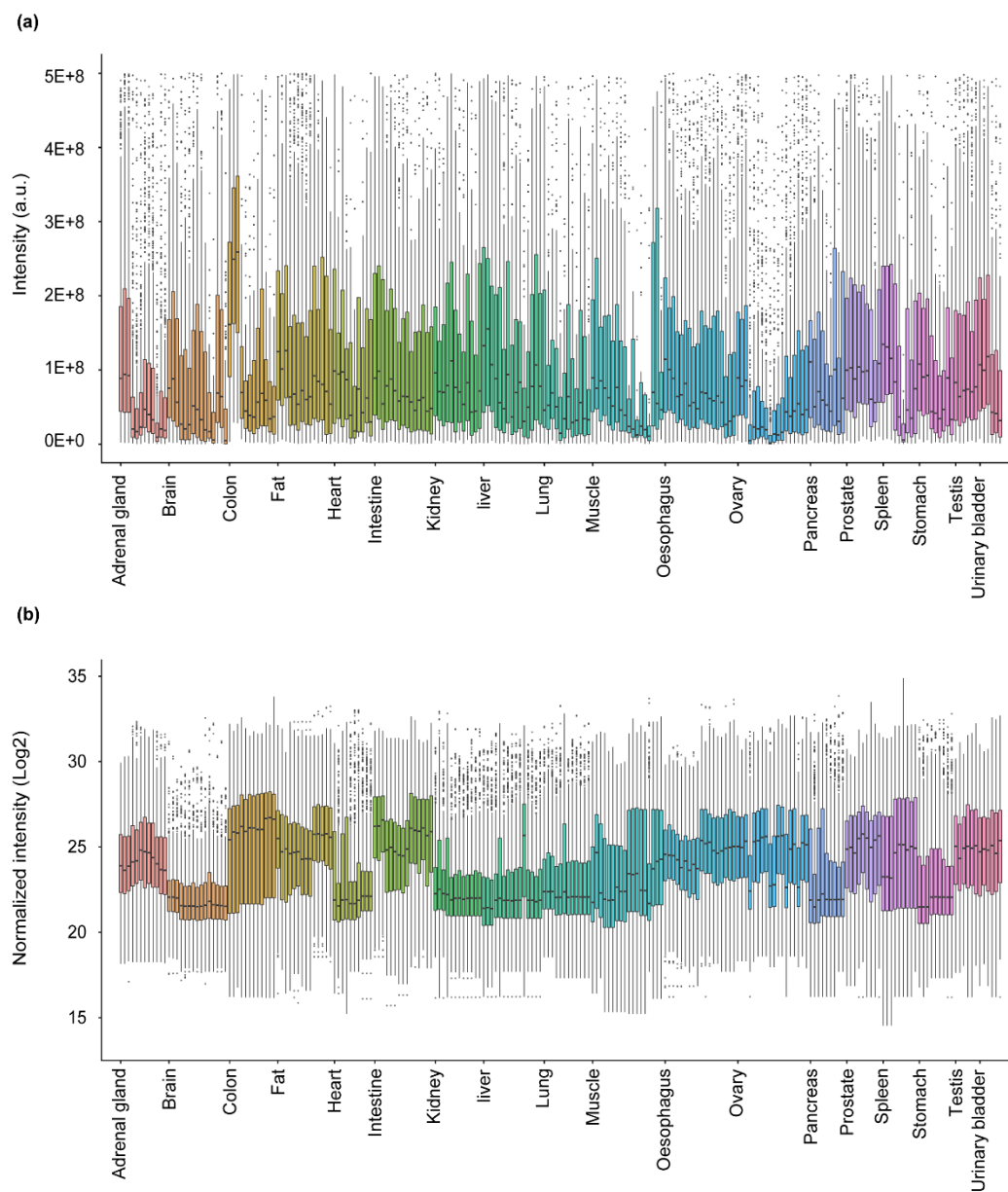
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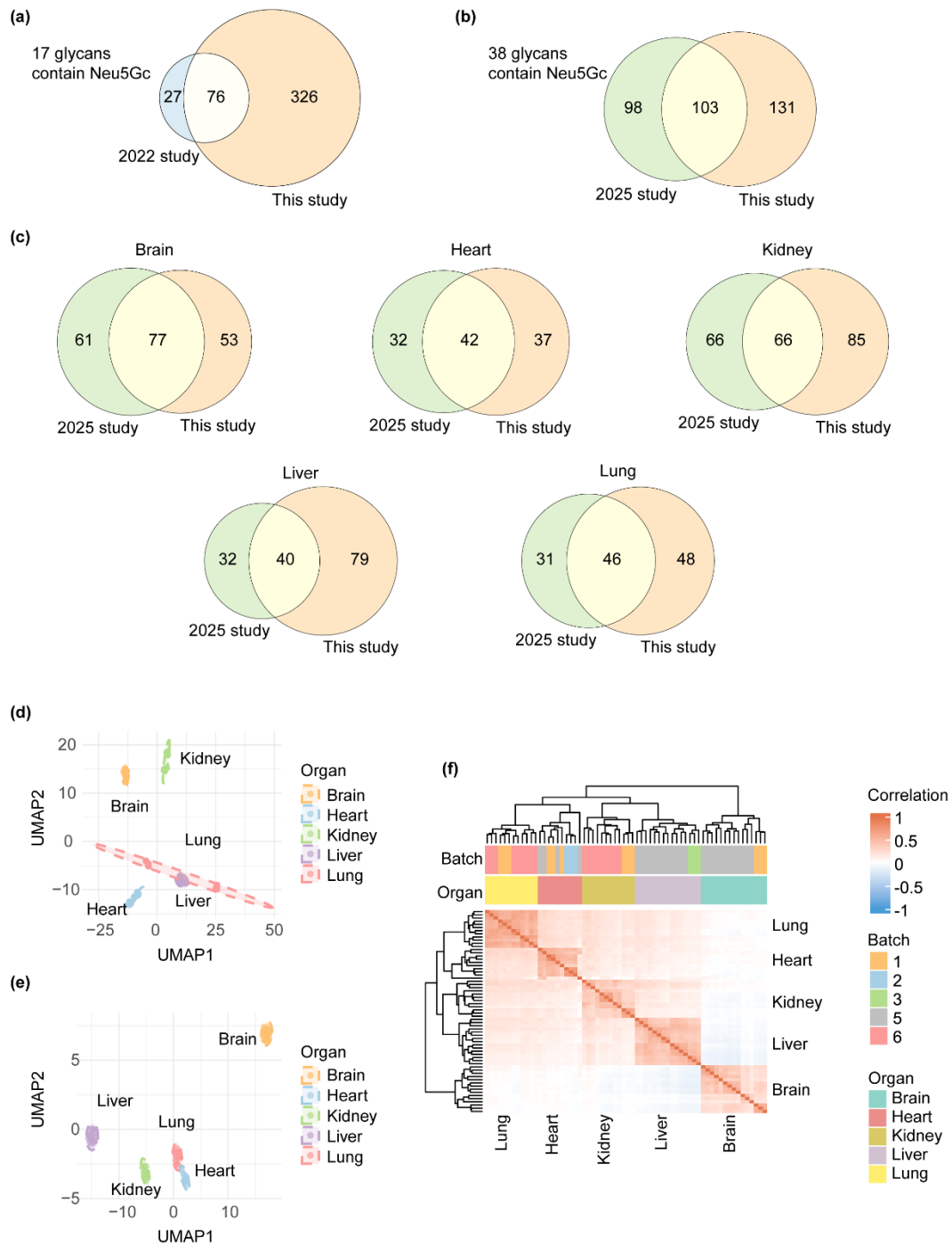
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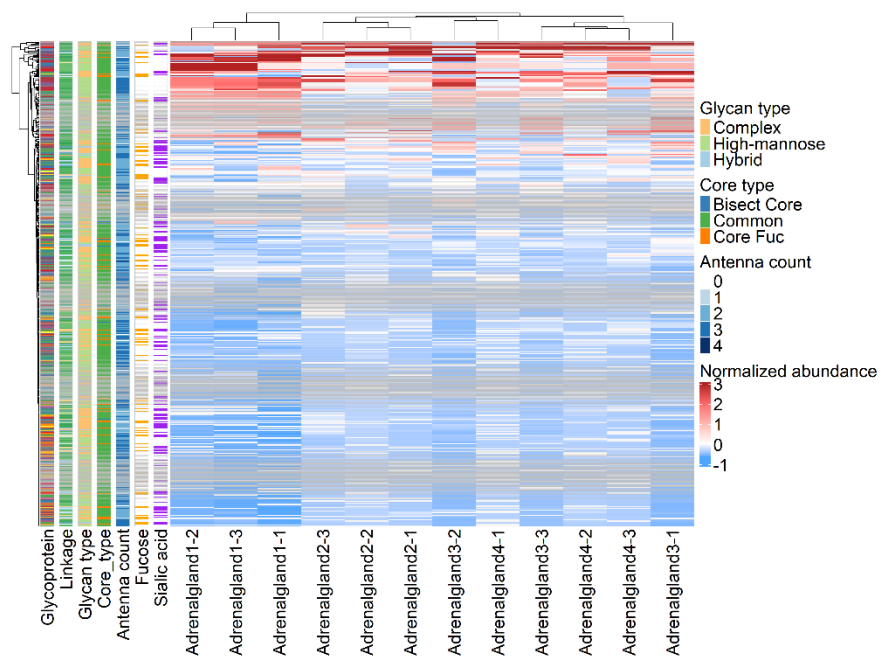
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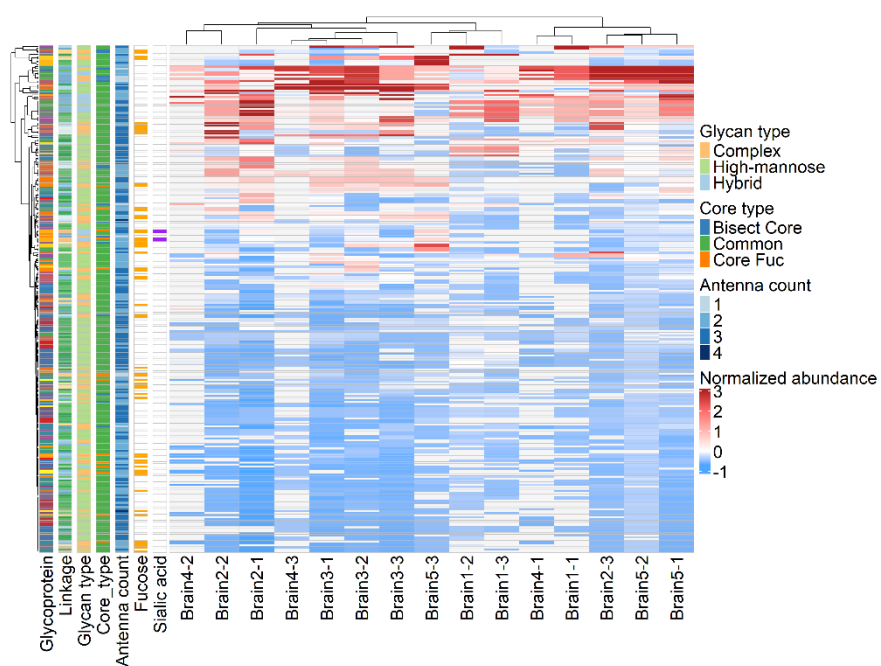
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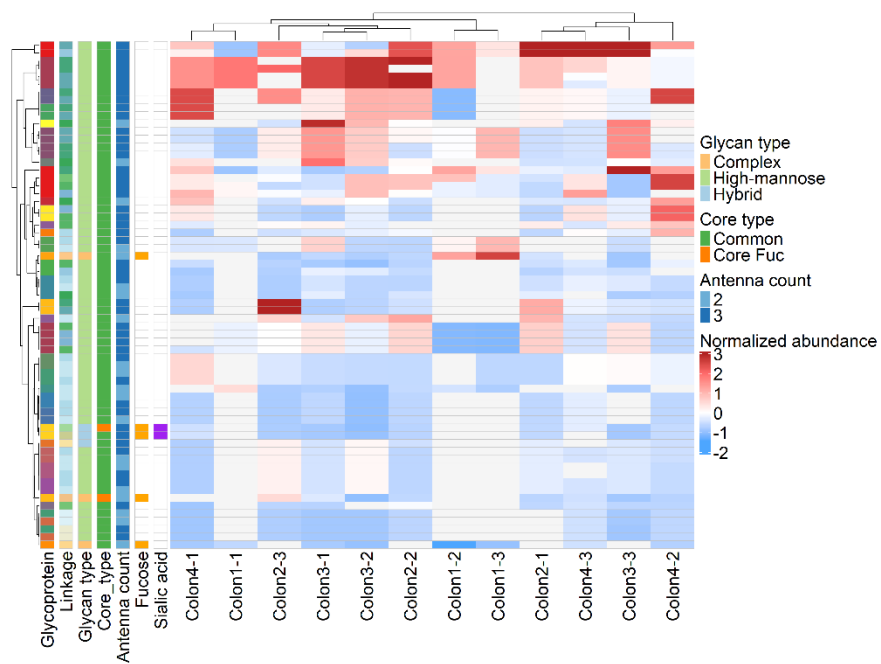
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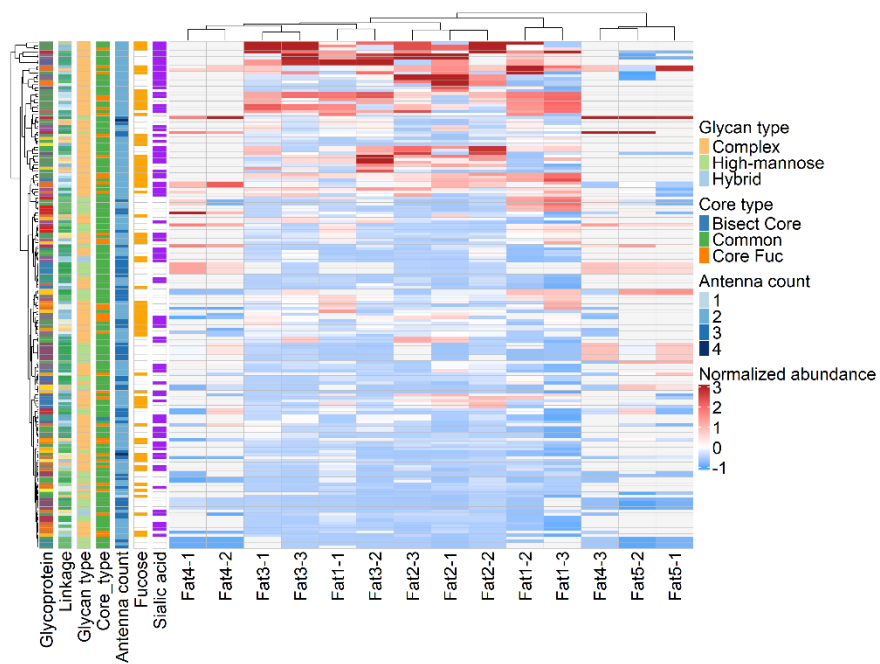
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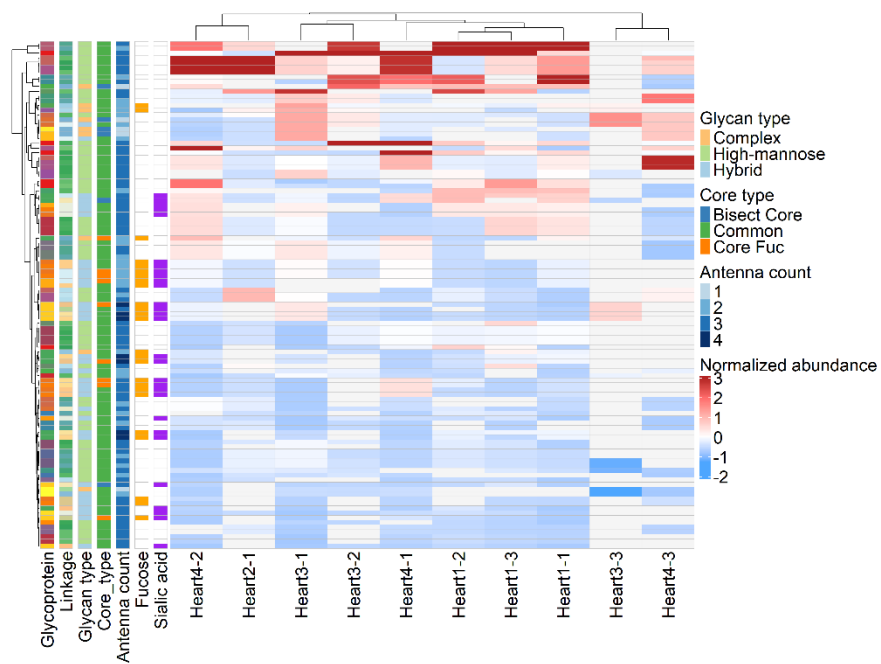
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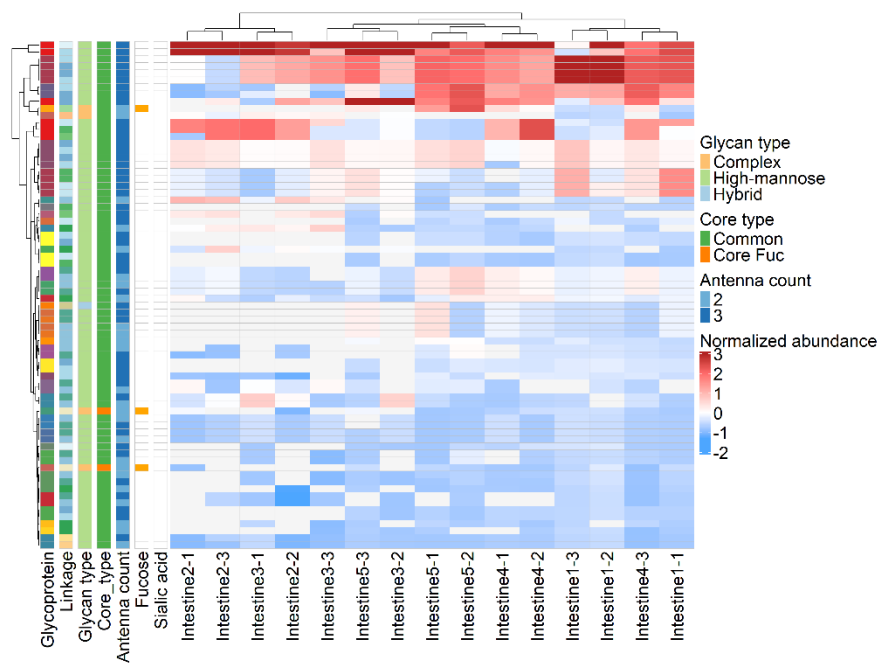
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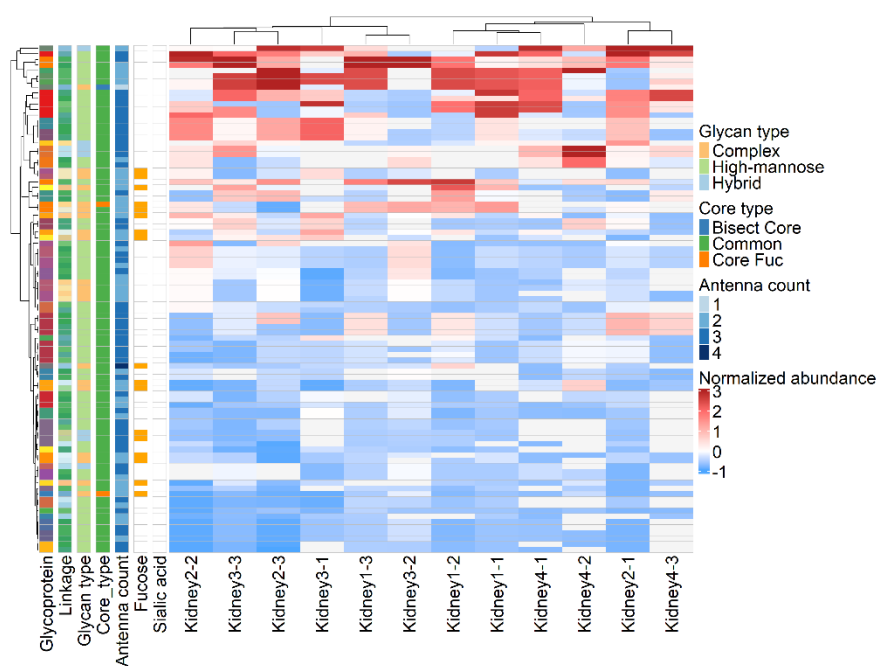
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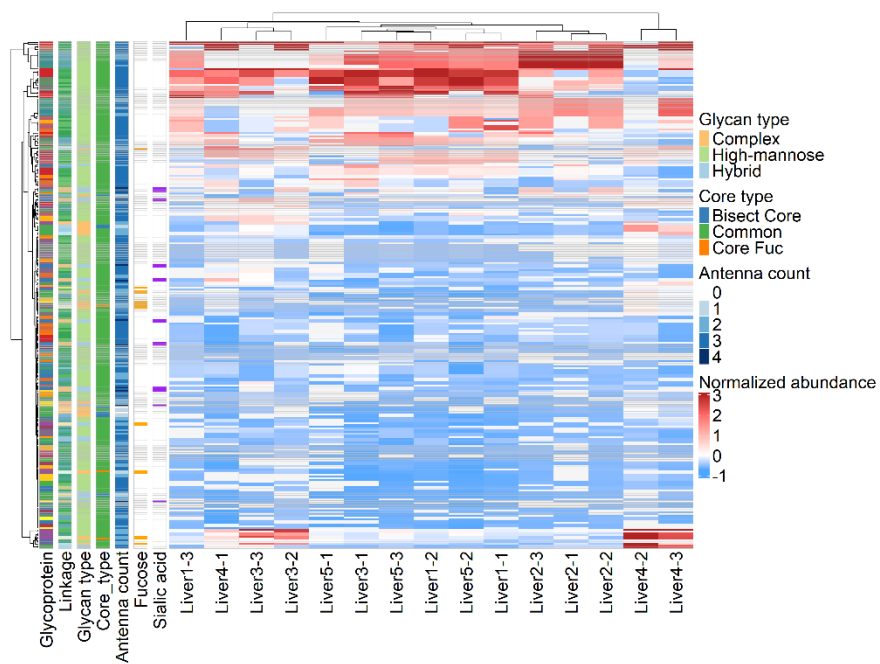
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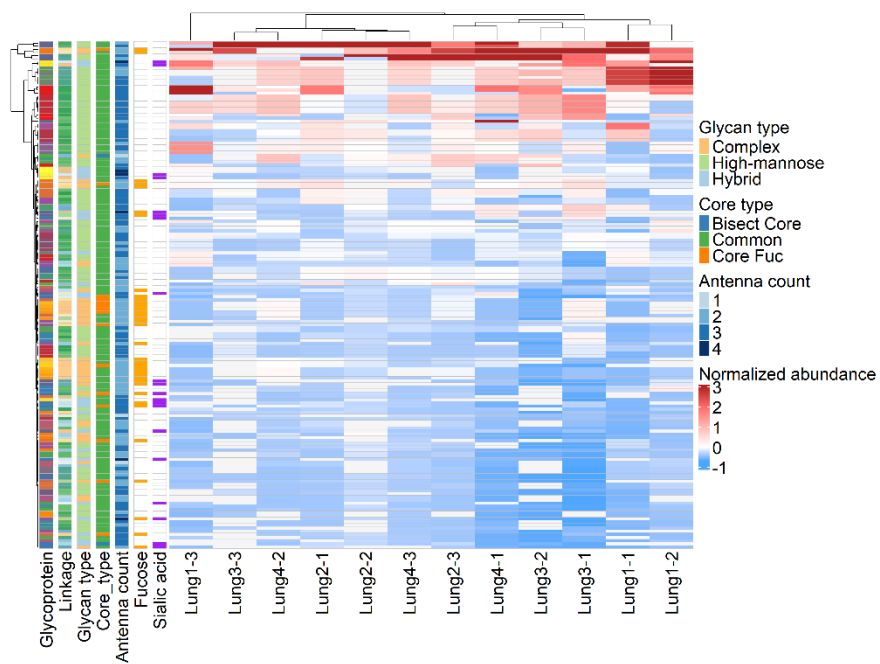
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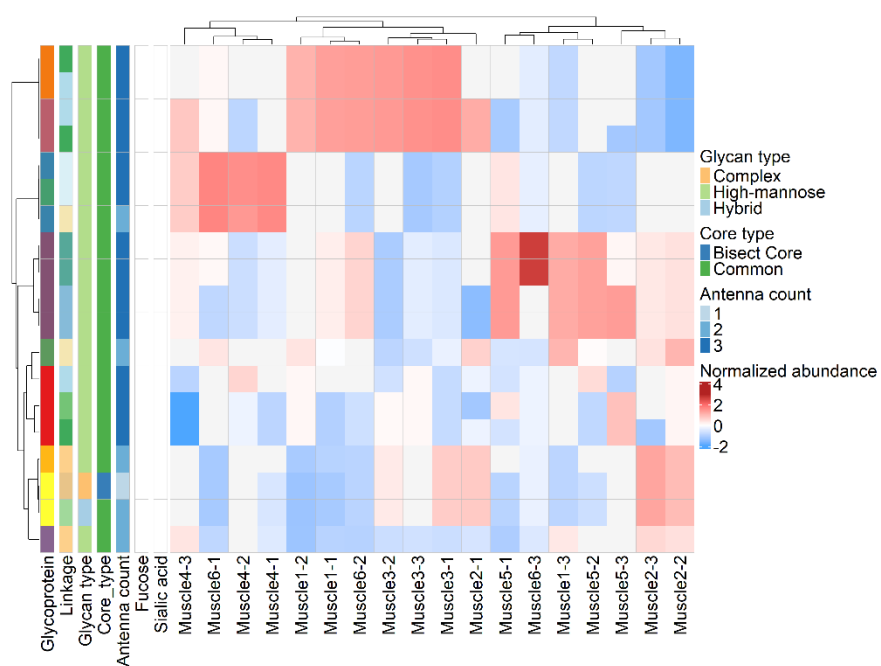
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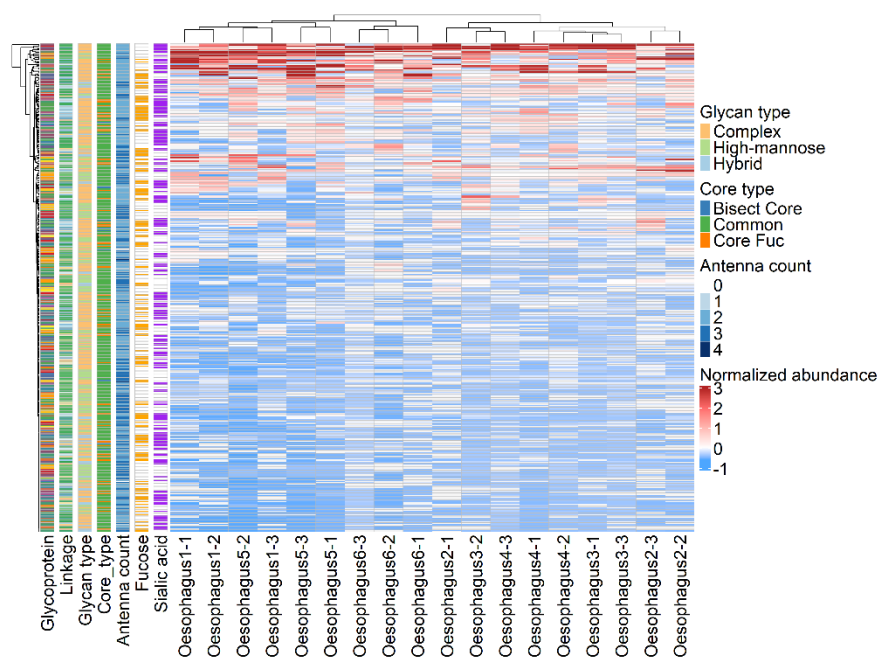
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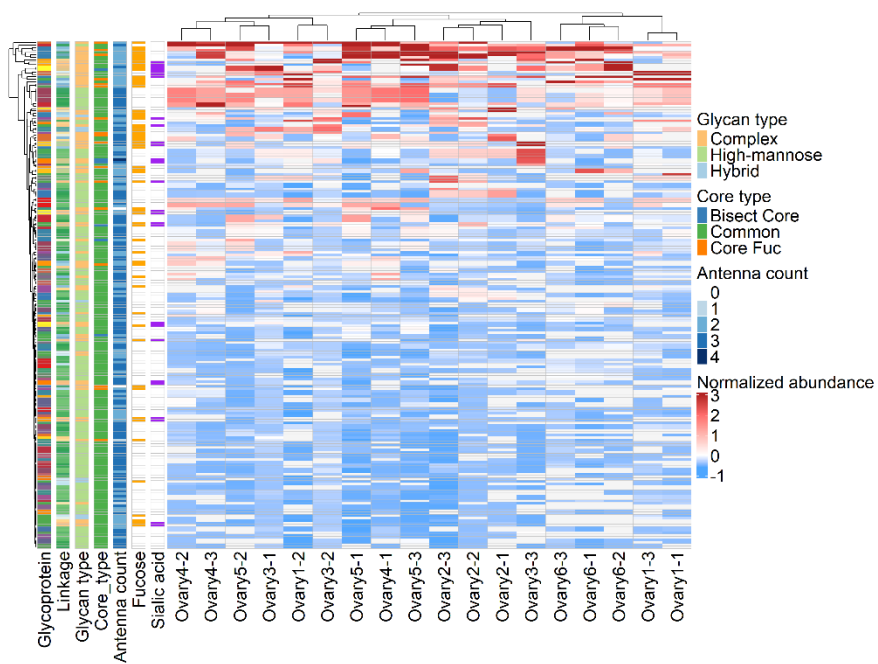
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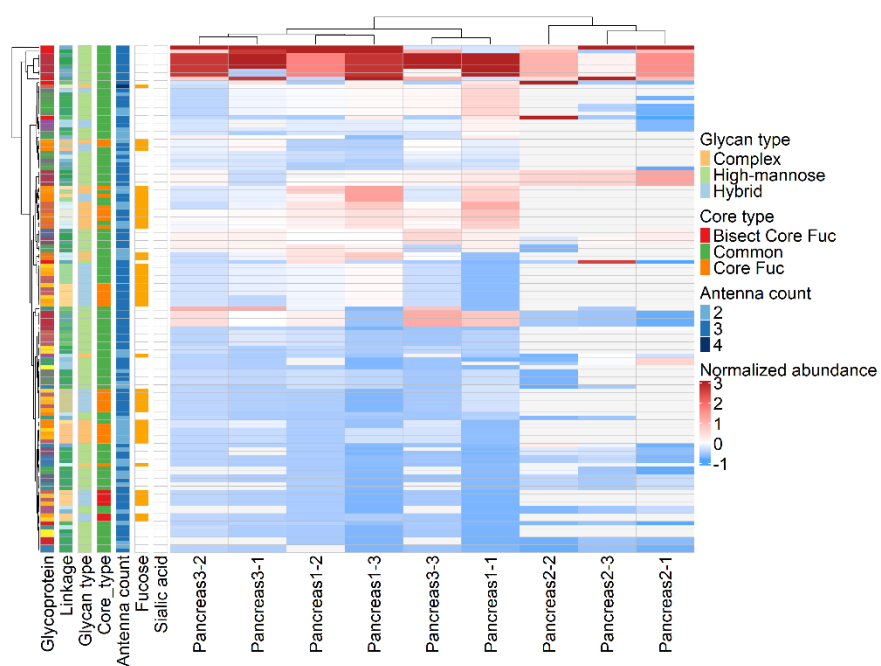
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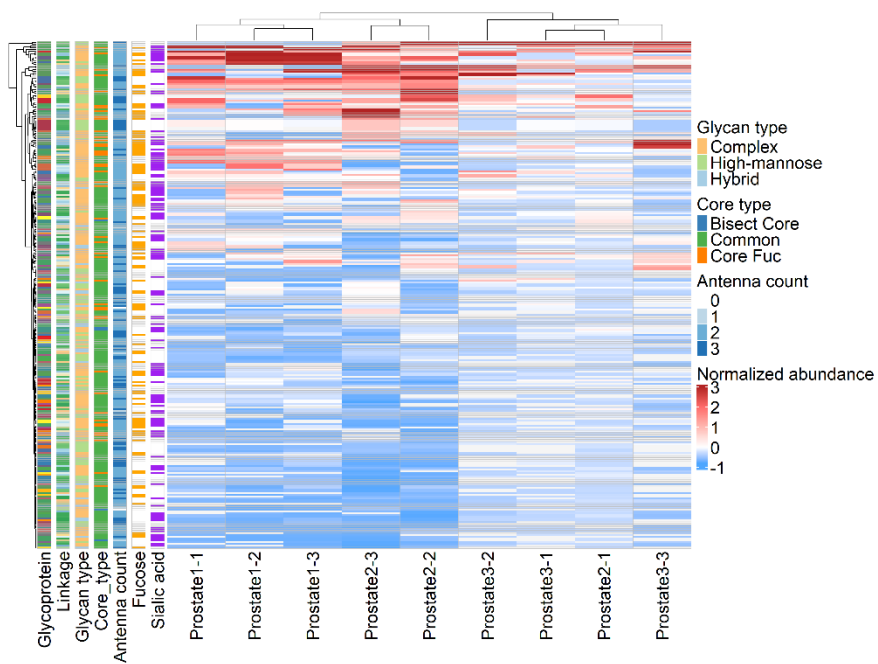
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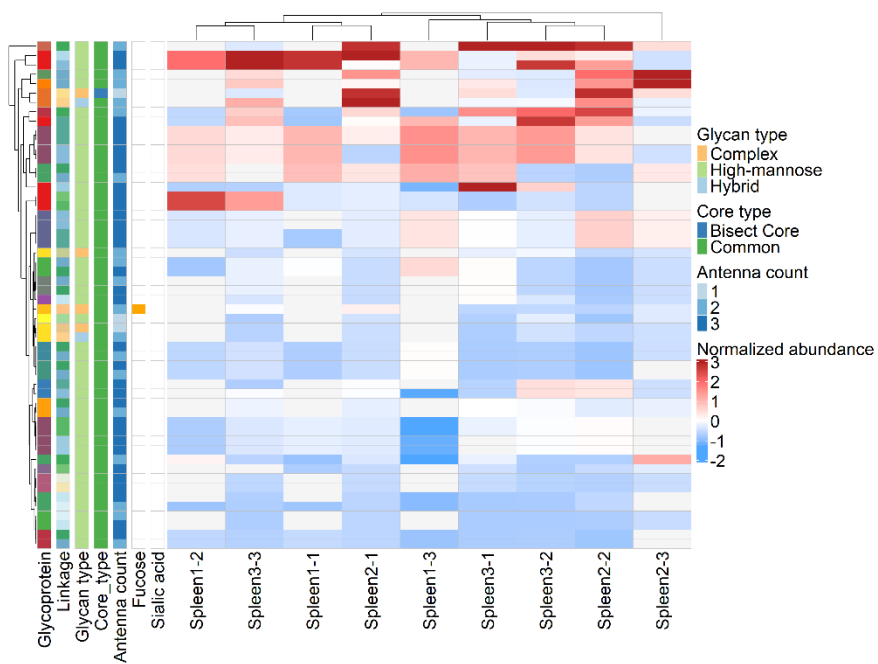
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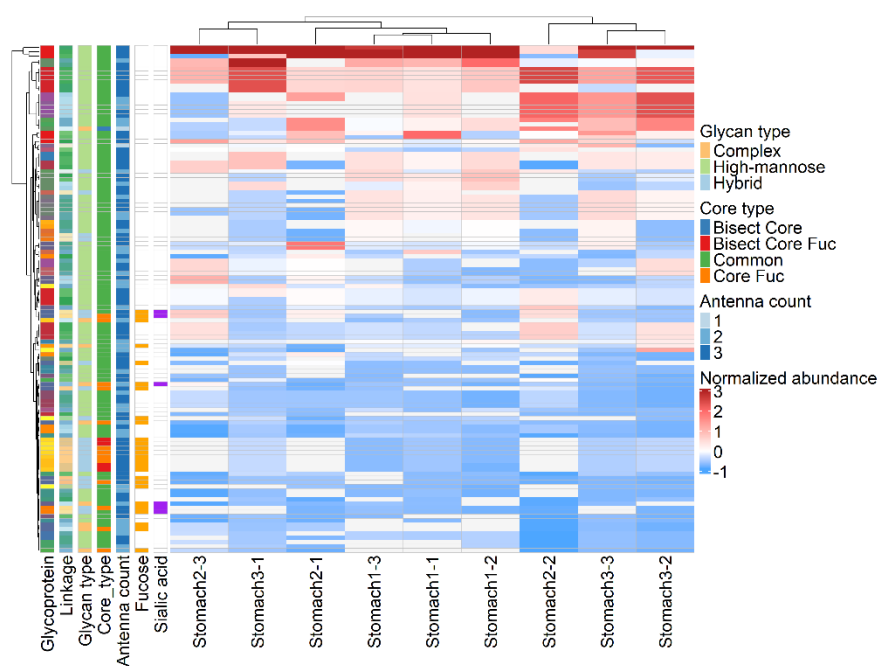
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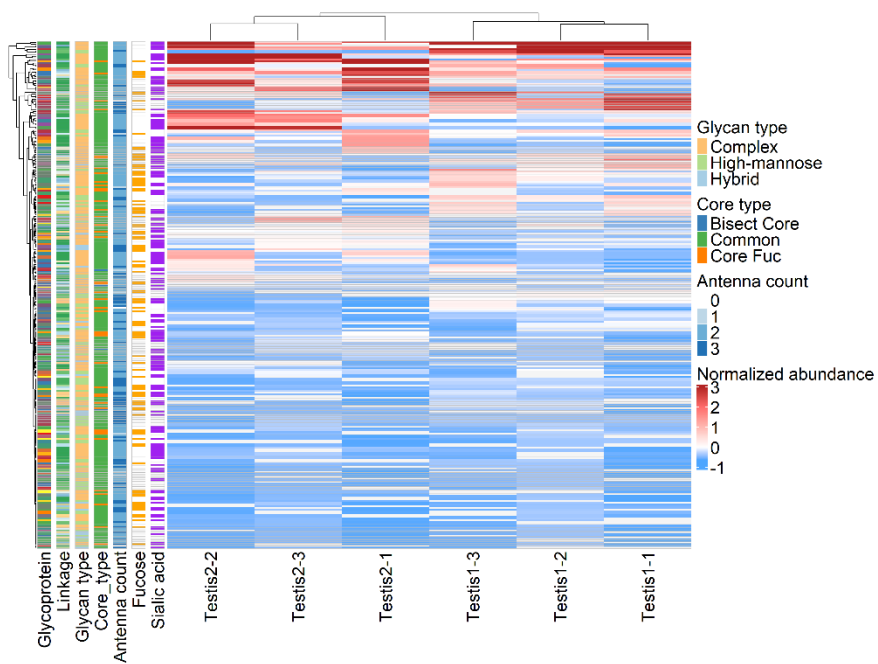
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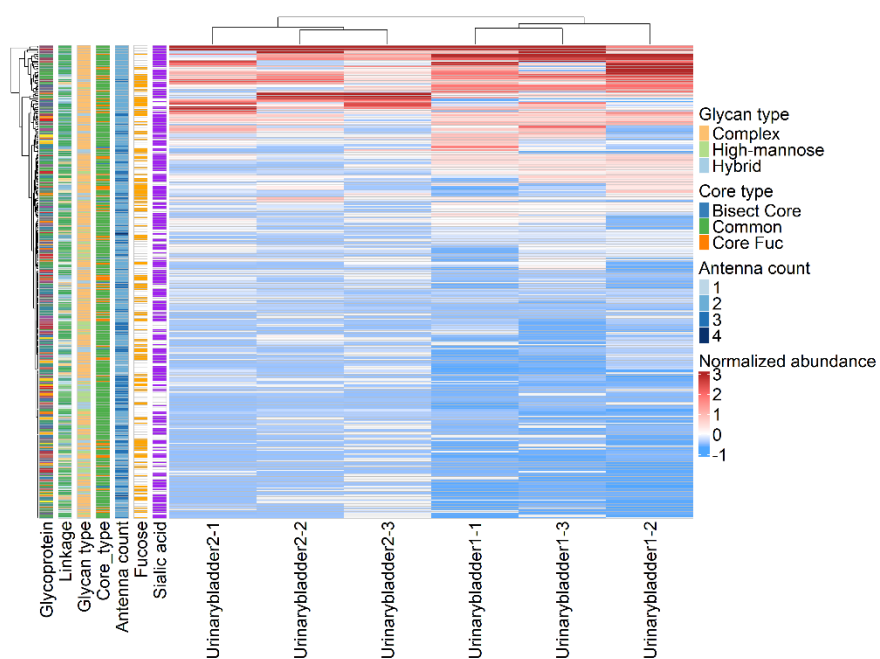
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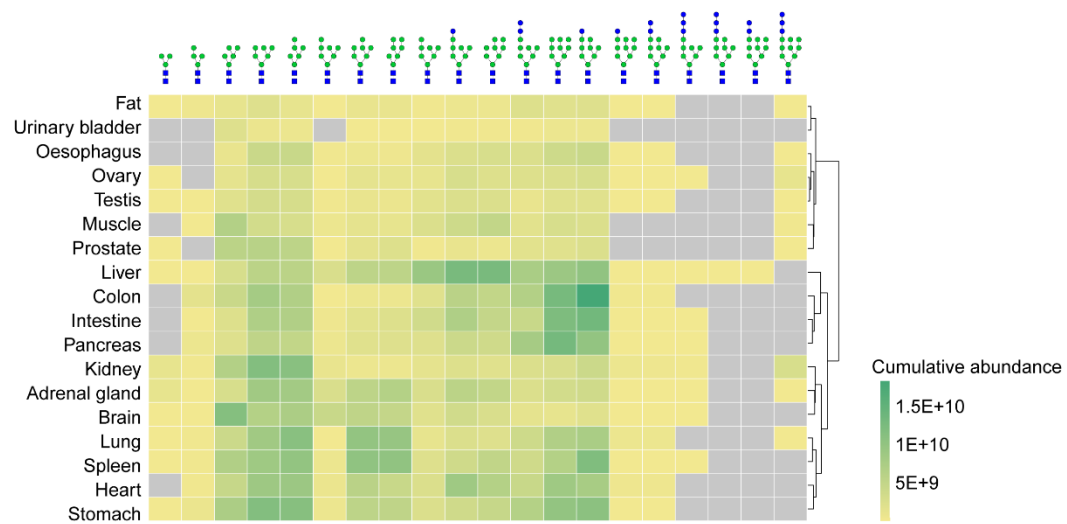
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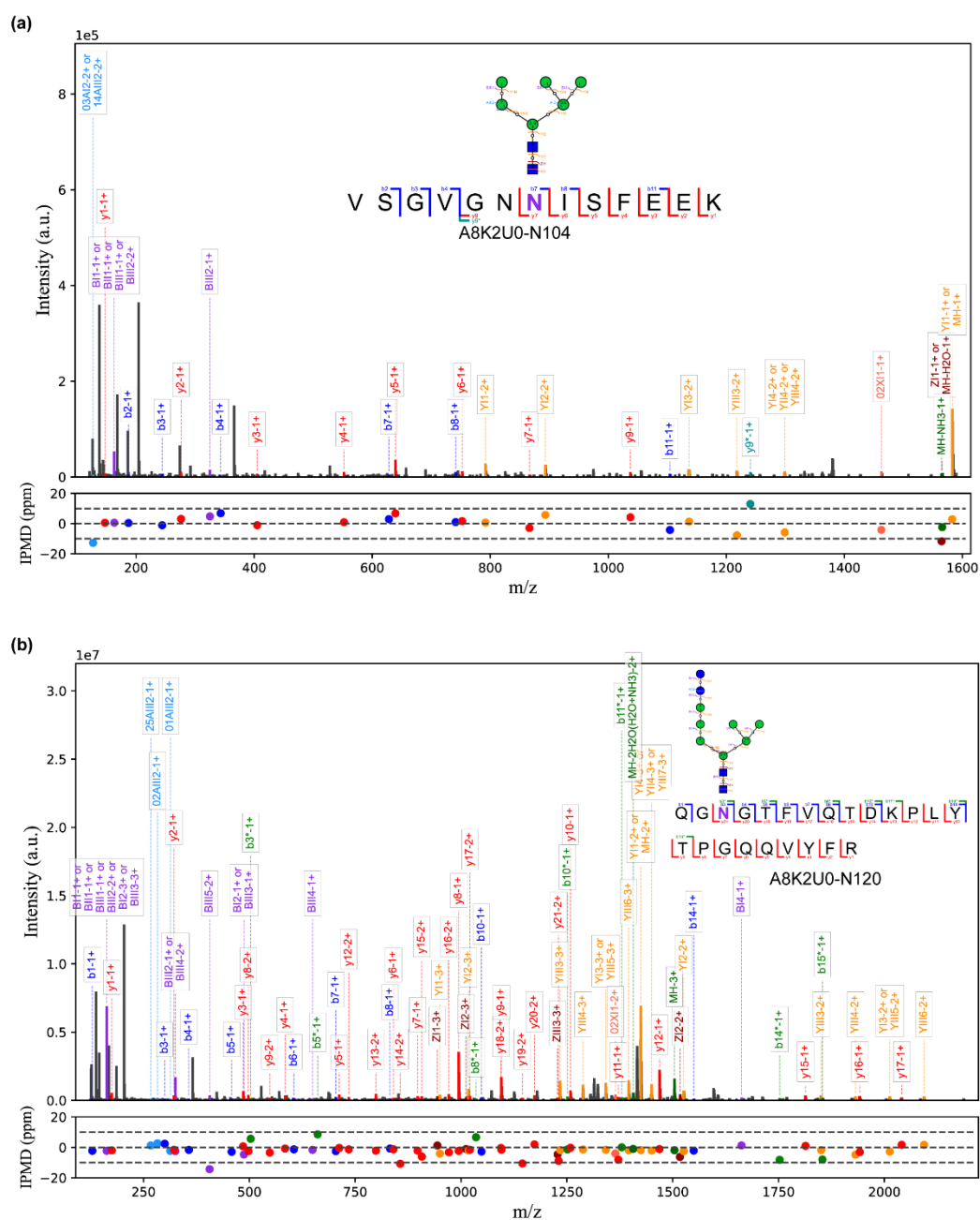
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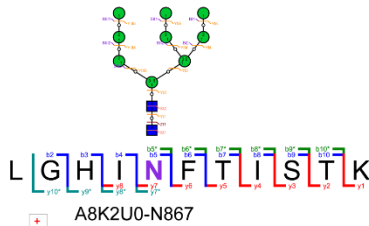
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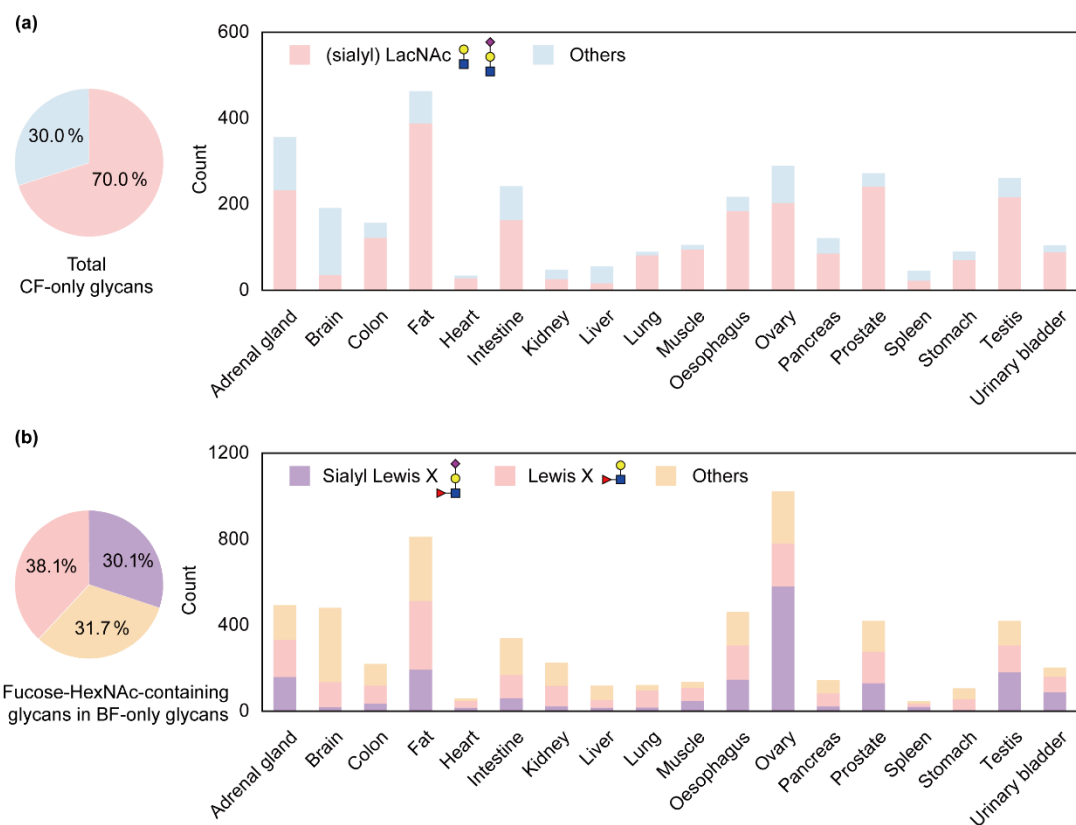
Supplementary Figure 25. Heatmap of the raw cumulative abundance of the 20 distinct sequence structures



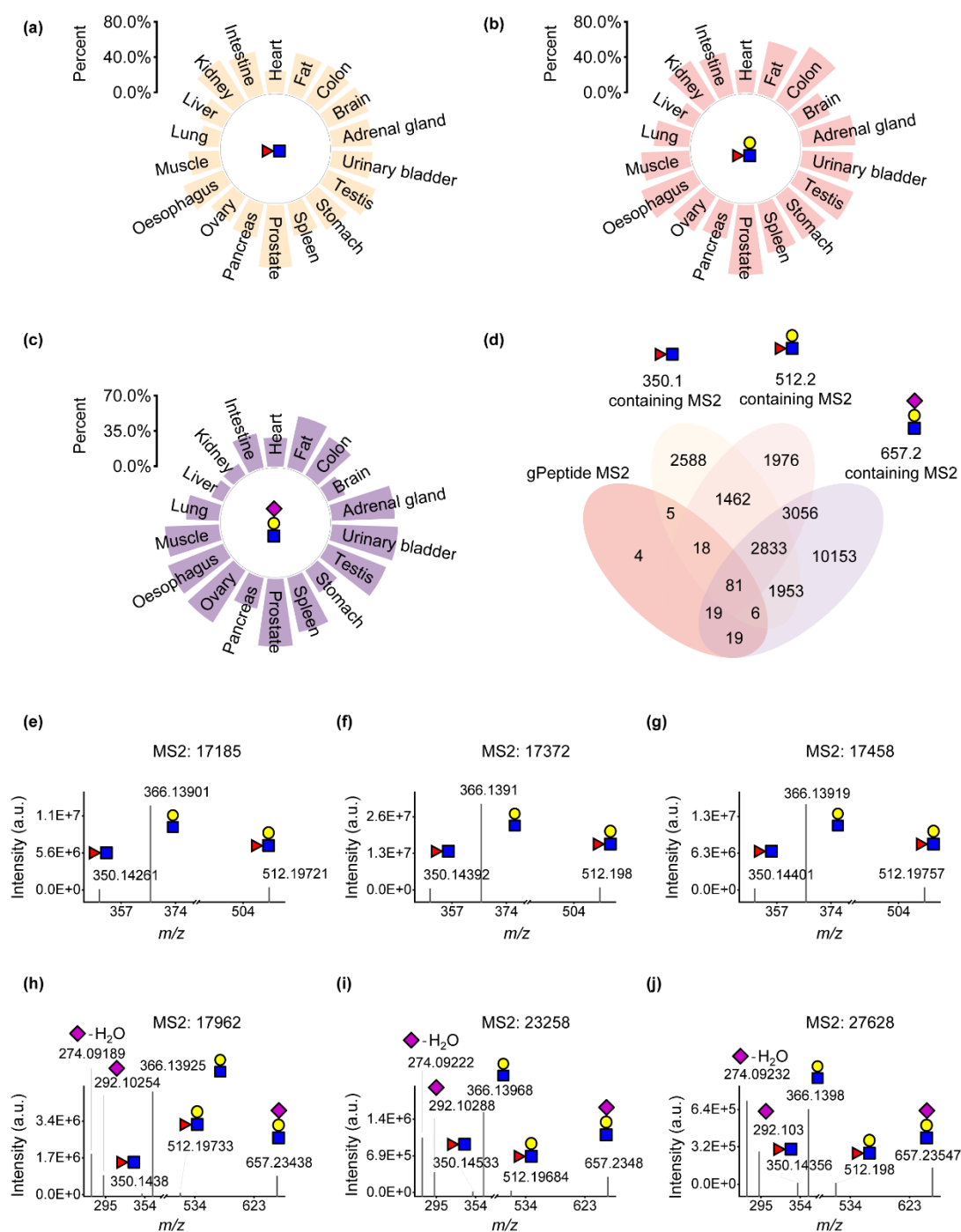
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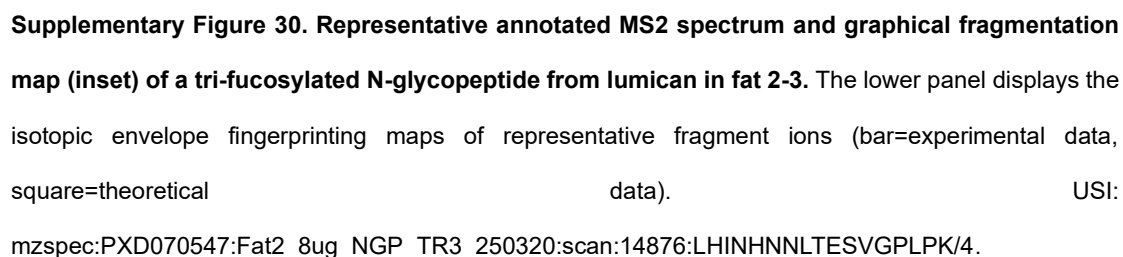
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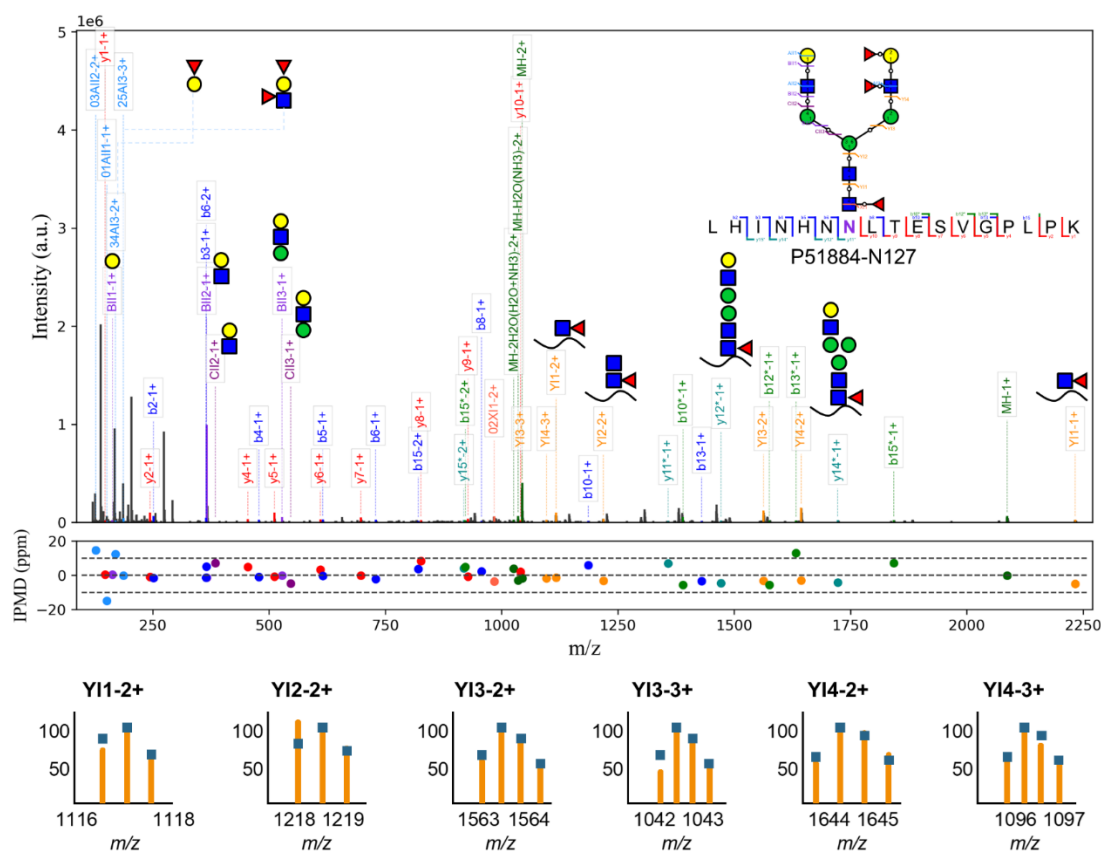
Supplementary Figure 28. Branch distribution. (a) CF-only group, (b) HexNAc-Fucose-containing glycans in BF-only group.



Supplementary Figure 29. Spectral overlap. (a-c) Overlap between the fragment ions of 350.1, 512.2, 657.2 amu and HexNAc-Fucose-containing glycans in BF-only glycans across 18 organs; (d) spectral overlap in adrenal gland1-1; (e-g) three representative MS/MS spectra with fragment ions of Lewis X structures of adrenal gland1-1; (h-j) three representative MS/MS spectra with fragment ions of sialyl Lewis X structures of adrenal gland1-1.



Supplementary Figure 30. Representative annotated MS2 spectrum and graphical fragmentation map (inset) of a tri-fucosylated N-glycopeptide from lumican in fat 2-3. The lower panel displays the isotopic envelope fingerprinting maps of representative fragment ions (bar=experimental data, square=theoretical data). USI: [mzspec:PXD070547:Fat2_8ug_NGP_TR3_250320:scan:14876:LHINHNLTESVGPLPK/4.](#)



Supplementary Figure 31. Representative annotated MS2 spectrum and graphical fragmentation

map (inset) of a tri-fucosylated N-glycopeptide from lumican in ovary3-2. The lower panel displays

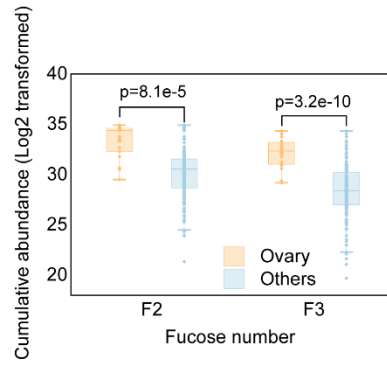
the isotopic envelope fingerprinting maps of representative fragment ions (bar=experimental data,

square=theoretical

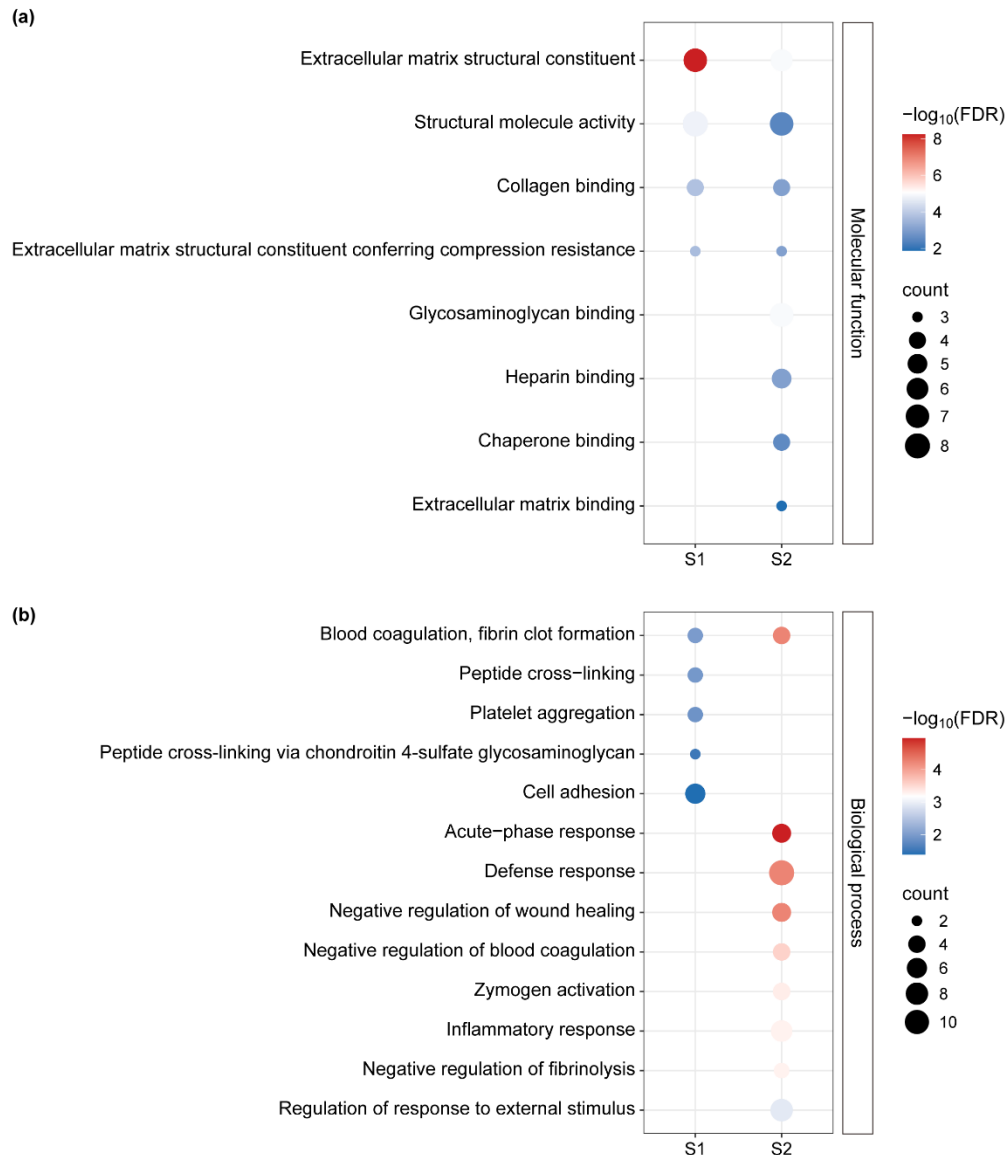
data).

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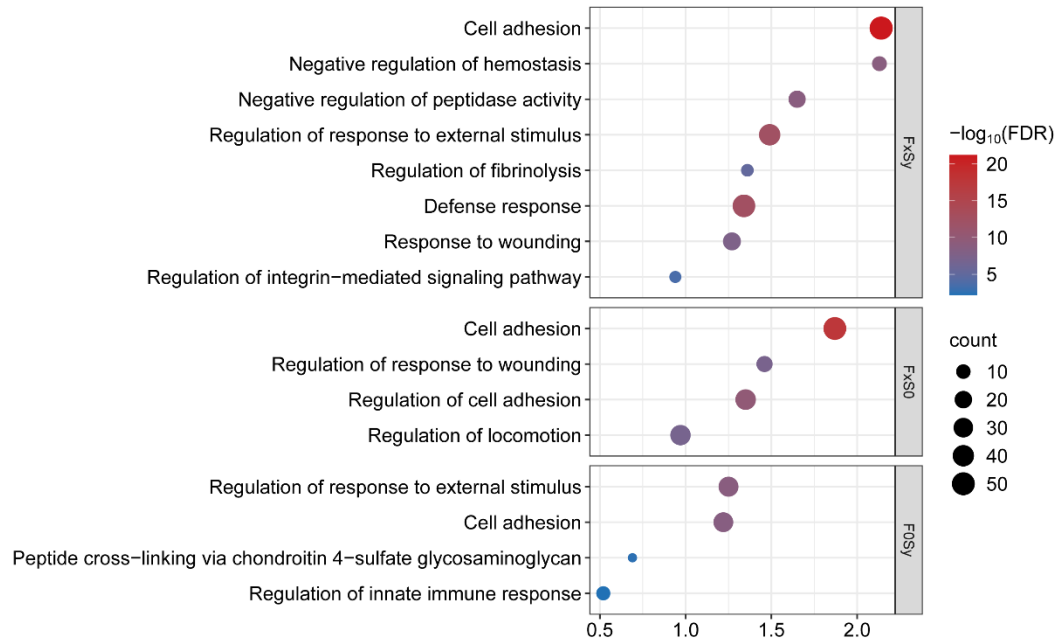
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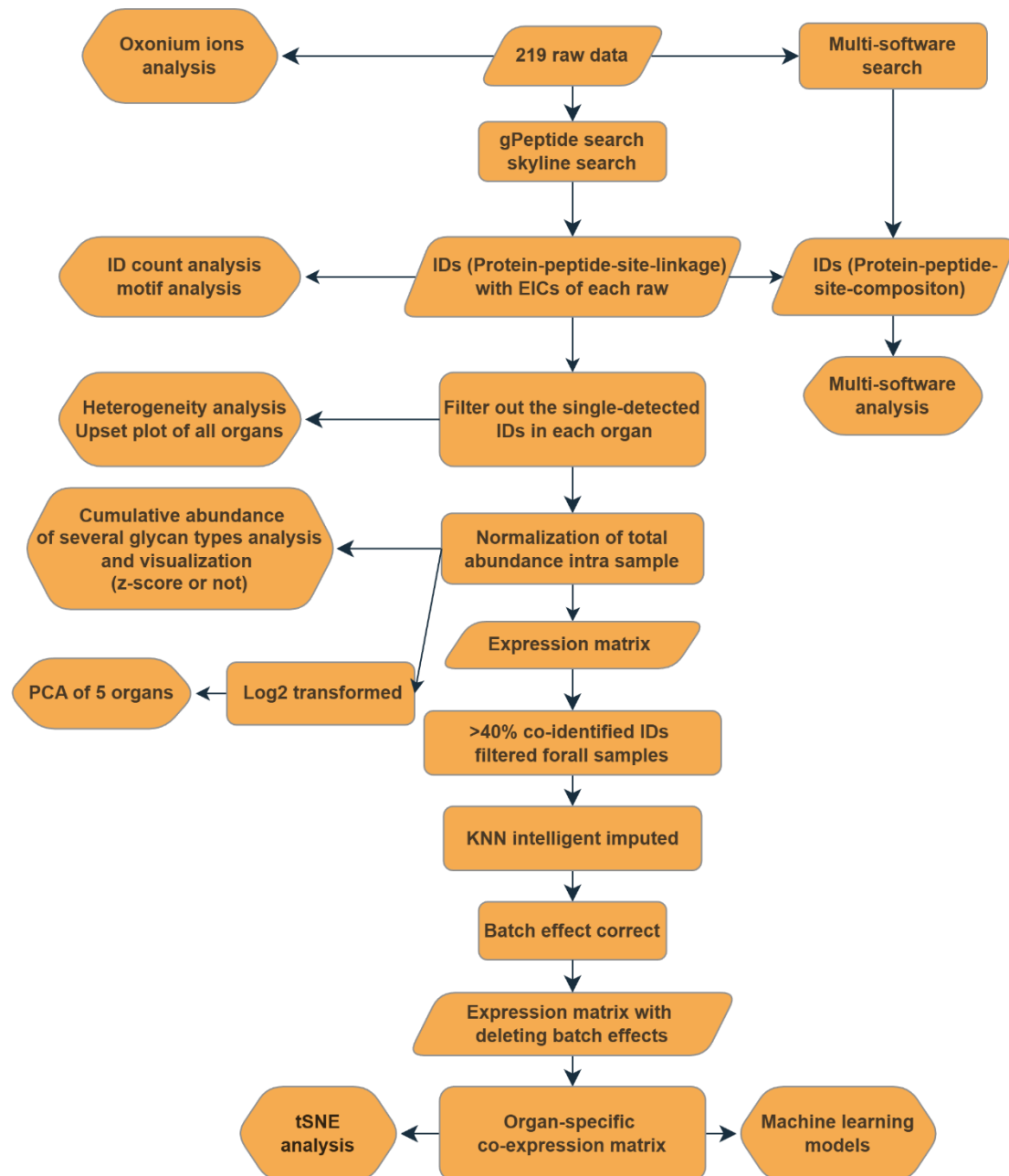
Supplementary Figure 32. Comparison of the cumulative expression level of fucose number in the ovary with those in other tissues. In the box plots, the centre line represents the mean, the bounds of the box represent the 25th and 75th percentiles (interquartile range, IQR), the whiskers extend to the minima and maxima values within $1.5 \times \text{IQR}$ from the box bounds, and individual data points are overlaid. Statistical significance was assessed using two-tailed Welch's t-tests, which do not assume equal variances between groups.



Supplementary Figure 33. Bioinformatics comparison between S1 and S2 N-glycoproteins. (a-b) Enriched molecular function and biological processes. Statistical significance was calculated using a one-sided hypergeometric test via the STRING database, p values were adjusted for multiple comparisons using the Benjamini-Hochberg method to generate the False Discovery Rate (FDR).



Supplementary Figure 34. Biological processes of the N-glycoproteins with different FS compositions (FxSy, FxS0, and F0Sy). Statistical significance was calculated using a one-sided hypergeometric test via the STRING database, p values were adjusted for multiple comparisons using the Benjamini-Hochberg method to generate the False Discovery Rate (FDR).



Supplementary Figure 36. The data processing flow of this study.