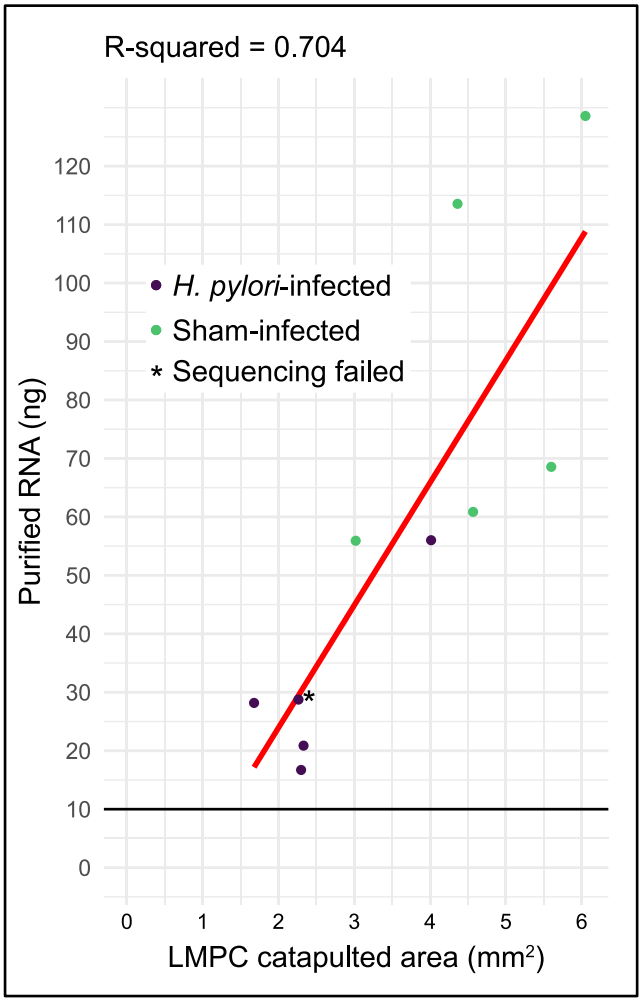
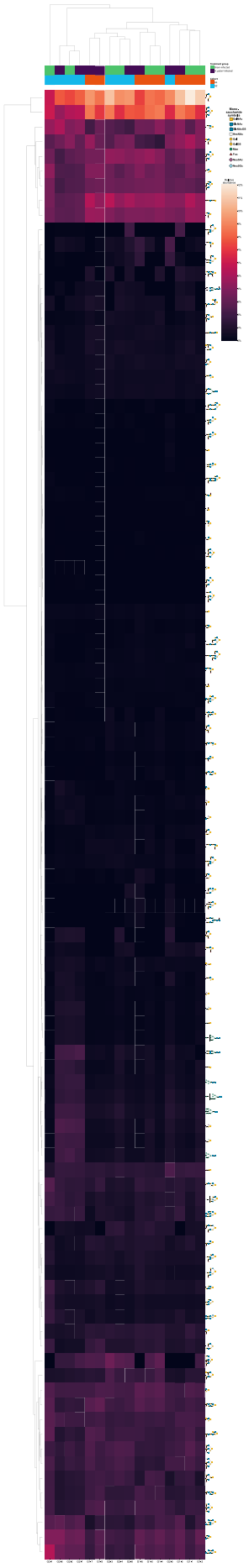
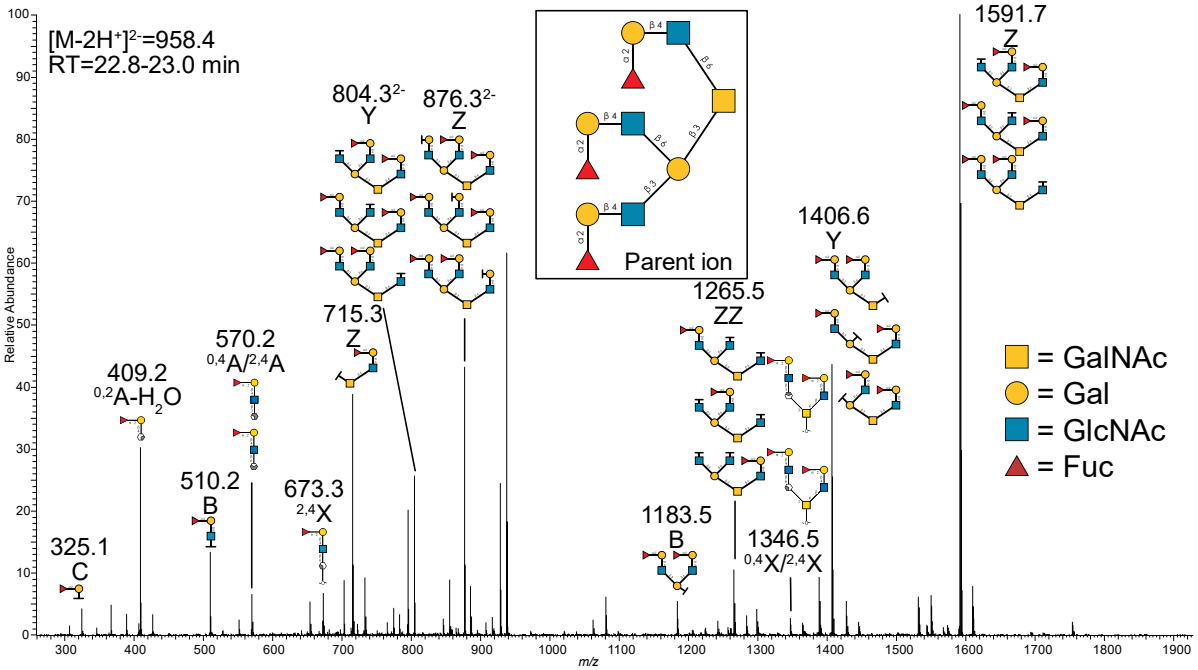


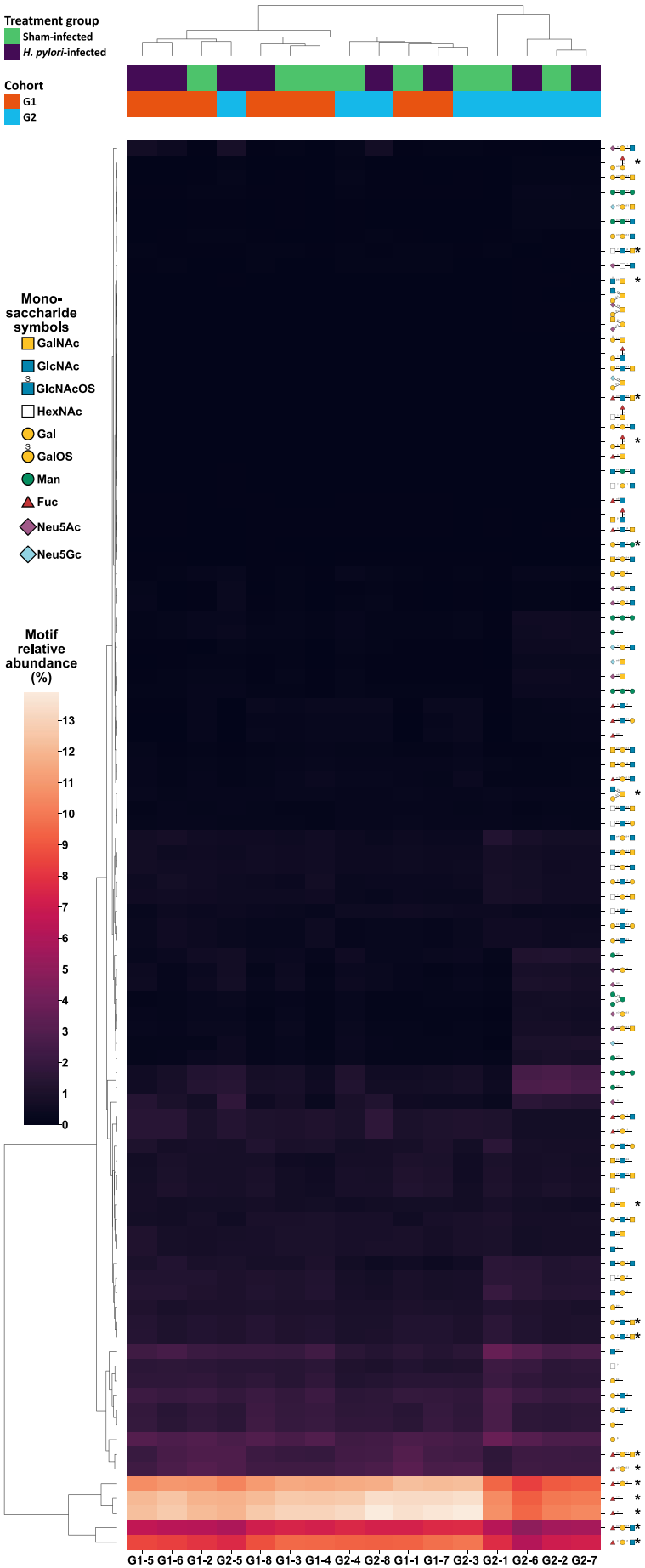
Supplemental Figure S1. Dotplot of the correlation between collected area with LCM (x-axis) and amount of purified RNA (y-axis). The recommended input amount of 10 ng for library prep is demarcated with the black horizontal line. A linear model (red line) with R square 0.704 was fit to the data. There was a strong correlation between the collected area and the amount of RNA that was purified from the sample. *Sequencing failed for this mouse.



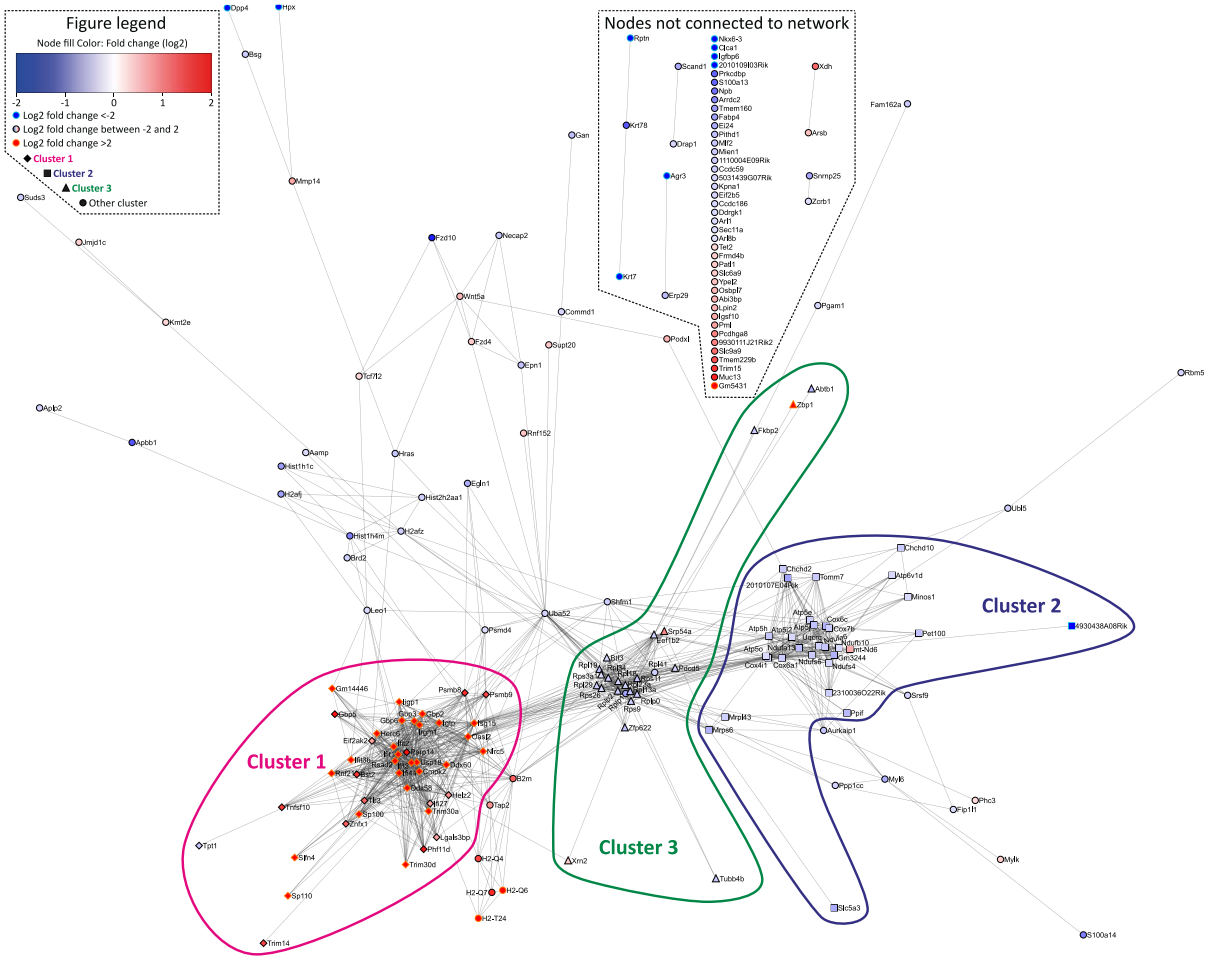
Supplemental Figure S2. Heatmap showing relative abundances of glycans characterized with mass spectrometry. The dendrogram at the top of the heatmap shows the hierarchical agglomerative clustering (HAC) which was used to cluster the mice. Likewise, the dendrogram on the left side shows the HAC for the glycans, in other words which glycans have similar relative abundances. Cohort and treatment denoted by color. Glycans were visualized using symbols according to the Symbol Nomenclature for Glycans (SNFG) guidelines. GalNAc = N-Acetylgalactosamine. GlcNAc = N-Acetylglucosamine. GlcNAcOS = Sulfated N-Acetylglucosamine. HexNAc = Either GalNAc or GlcNAc, but couldn't be determined which. Gal = Galactose. GalOS = Sulfated Galactose. Man = Mannose. Fuc = Fucose. Neu5Ac = N-Acetylneuraminic acid. Neu5Gc = N-Glycolylneuraminic acid.



Supplemental Figure S3. Spectra annotation of diagnostic ions for the glycan with identifier 085 proposed to have the sequence (Fuc(α1-2)Gal(β1-4)GlcNAc(β1-3)[Fuc(α1-2)Gal(β1-4)GlcNAc(β1-6)]Gal(β1-3)[Fuc(α1-2)Gal(β1-4)GlcNAc(β1-6)]GalNAcol). Fragment ions were visualized using symbols according to the SNFG guidelines (1). Not all possible combinations of diagnostic ions are shown in the mass spectra, but rather a selection of the most probable. Of note: there may be other less abundant isomers with overlapping retention time and mass with some β1-3 linkages between the terminal galactose and GlcNAc. Cross ring fragments denoted according to Domon and Costello (2).


Treatment group
Sham-infected
H. pylori-infected
Cohort
G1
G2
Mono-saccharide symbols
GalNAc
GlcNAc
GlcNAcOS
HexNAc
Gal
GalOS
Man
Fuc
Neu5Ac
Neu5Gc
Motif relative abundance (%)
13
12
11
10
9
8
7
6
5
4
3
2
1
0
G1-5 G1-6 G1-2 G2-5 G1-8 G1-3 G1-4 G2-4 G2-8 G1-1 G1-7 G2-3 G2-1 G2-6 G2-2 G2-7

Supplemental Figure S4. Heatmap of relative abundances of glycan terminal motifs. Terminal motifs of one, two, or three monosaccharides in size were identified using the python package glycowork. The dendrogram at the top of the heatmap shows the hierarchical agglomerative clustering (HAC) which was used to cluster the mice. Likewise, the dendrogram on the left side shows the HAC for the glycan motifs, in other words which motifs have similar relative abundances. Cohort and treatment are denoted by color. * = significant difference in relative abundance between cohorts for this glycan motif. Glycans are visualized using symbols according to the SNFG guidelines. GalNAc = N-Acetylgalactosamine. GlcNAc = N-Acetylglucosamine. GlcNAcOS = Sulfated N-Acetylglucosamine. HexNAc = Either GalNAc or GlcNAc, but couldn't be determined which. Gal = Galactose. GalOS = Sulfated Galactose. Man = Mannose. Fuc = Fucose. Neu5Ac = N-Acetylneuraminic acid. Neu5Gc = N-Glycolylneuraminic acid.



Supplemental Figure S5. Cytoscape STRING network of significantly differentially expressed genes. R packages were used to create a cytoscape network based on full STRING interactions with default confidence score of 400. Significant genes without a STRING interaction to another significant gene were not included in the network. Node fill was colored by log2 fold changes on a continuous scale from blue (down-regulated) to red (up-regulated) with H. pylori infection. Minimum and maximum values in the color scale was set to -2 and 2 respectively to facilitate visualization, where the more extreme fold-changes would otherwise distort the scale. There were 3 visually obvious clusters, and they were picked out with a systematic approach using MCL clustering with the default inflation parameter of 2.5 and selecting the top 3 clusters. To highlight these 3 clusters, the opacity of all nodes which did not belong to them was reduced. The colored loops indicate which cluster the full opacity nodes within belonged to.

Supplementary references

1. Neelamegham S, Aoki-Kinoshita K, Bolton E, Frank M, Lisacek F, Lütteke T, et al. Updates to the Symbol Nomenclature for Glycans guidelines. Glycobiology. 2019;29(9):620-4.
2. Domon B, Costello CE. A systematic nomenclature for carbohydrate fragmentations in FAB-MS/MS spectra of glycoconjugates. Glycoconjugate Journal. 1988;5(4):397-409.