SUPPORTING INFORMATION for

A novel LC-MS^2 product dependent parallel data acquisition function and data analysis workflow for sequencing and identification of intact glycopeptides

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Table S2 Glycopeptides Correctly Identified by Direct Database Search Using Byonic

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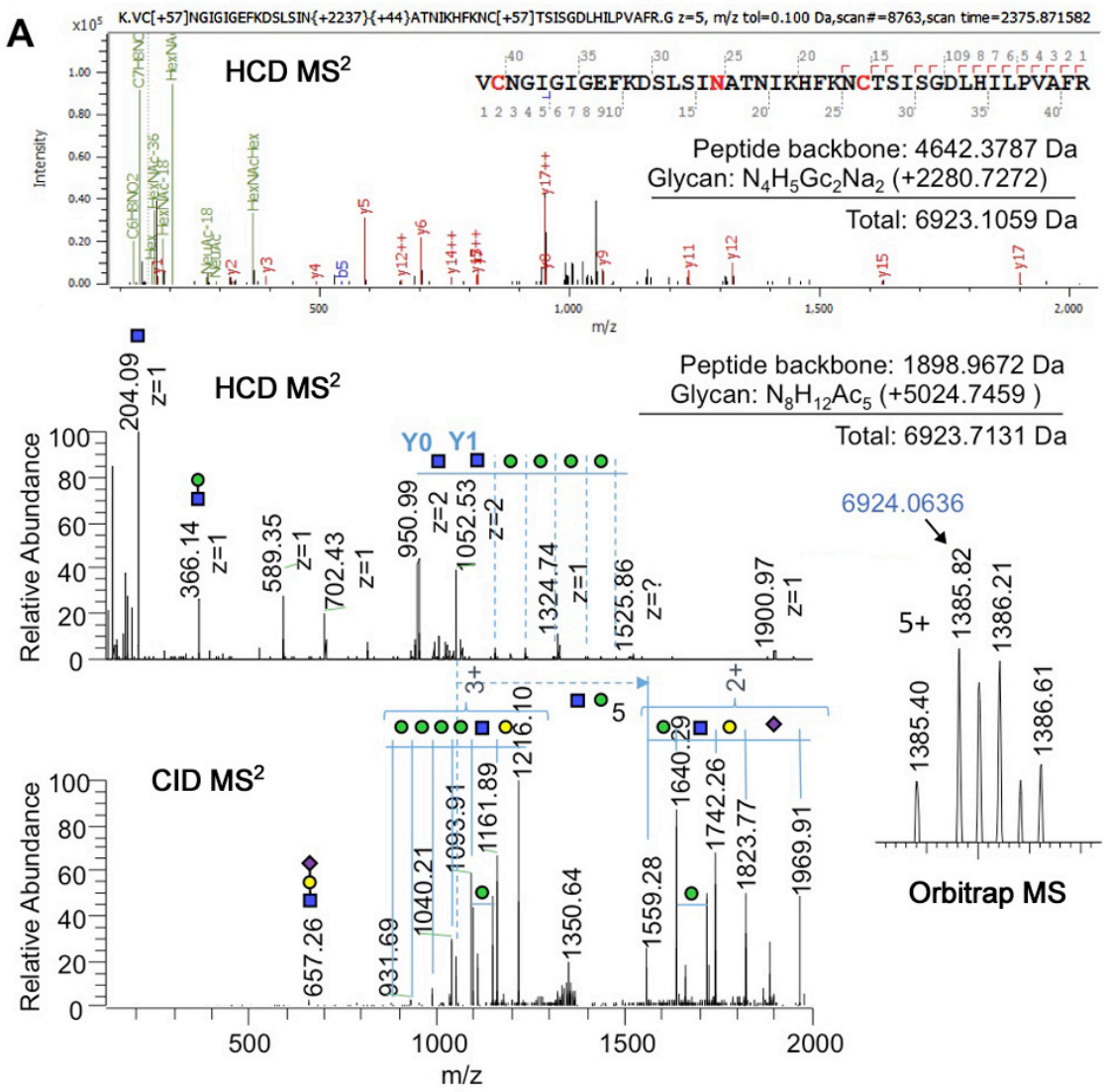


Figure S1. More examples of false positives due to incorrect peptide backbone identification and glycan assignment. In each of the 3 cases shown here (**A**-**C**), the extra masses assigned by Byonic to a stretch of amino acids extending from tryptic mis-cleavage sites can be alternatively attributed to larger glycan moiety, consistent with the Y1 ion (m/z 1052.53) most readily identified in the HCD MS^2 data (upper panel), and the sequential glycosyl losses evident in manually assigned CID MS^2 spectra (lower panel). The zoomed in mass region of the precursors shows that the most likely monoisotopic precursor within the isotopic cluster cannot always be determined unambiguously, particularly for signals of low intensity corresponding to high molecular weight glycopeptides.

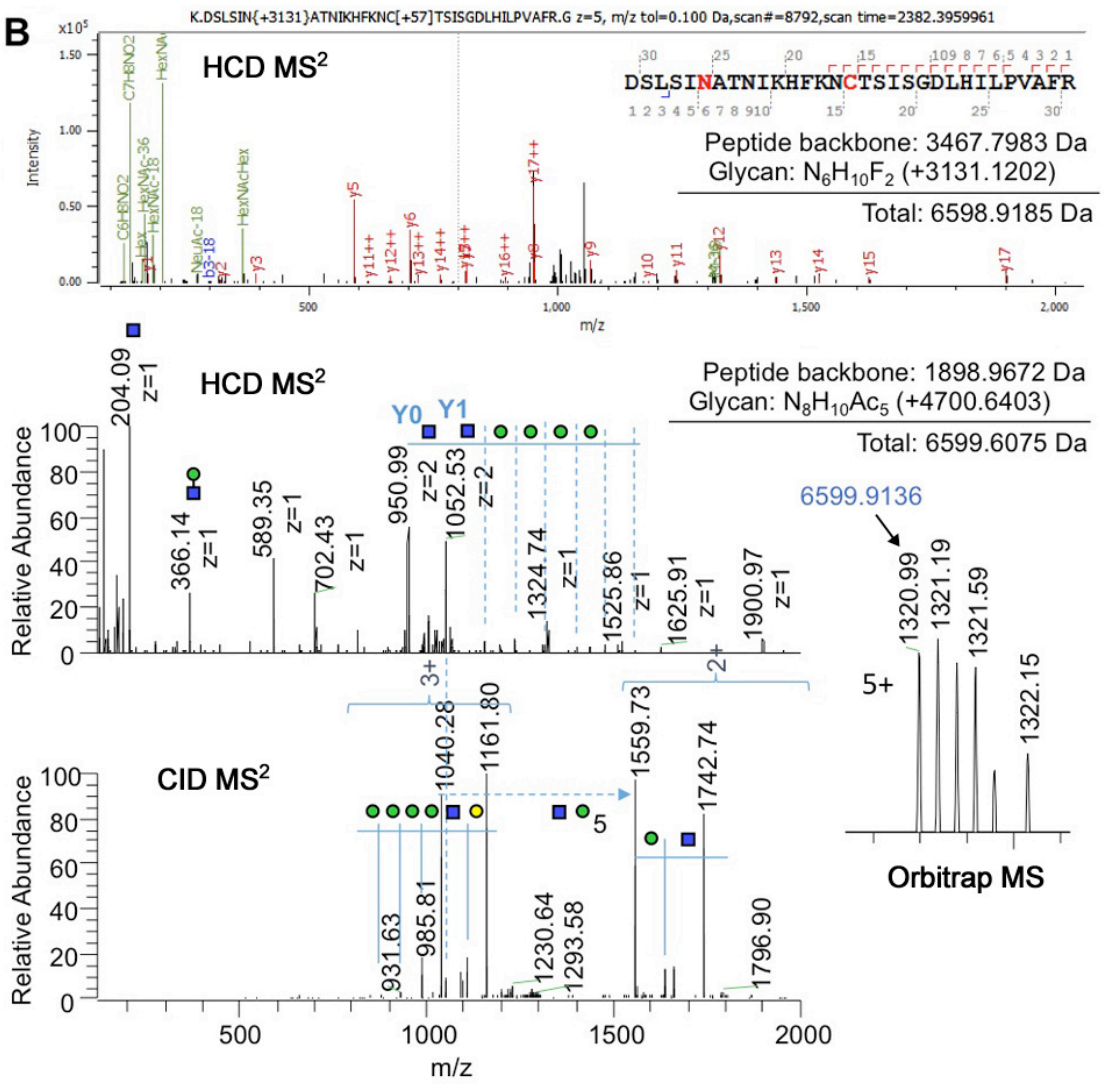


Figure S1B. More examples of false positives due to incorrect peptide backbone identification and glycan assignment (continued from previous page).

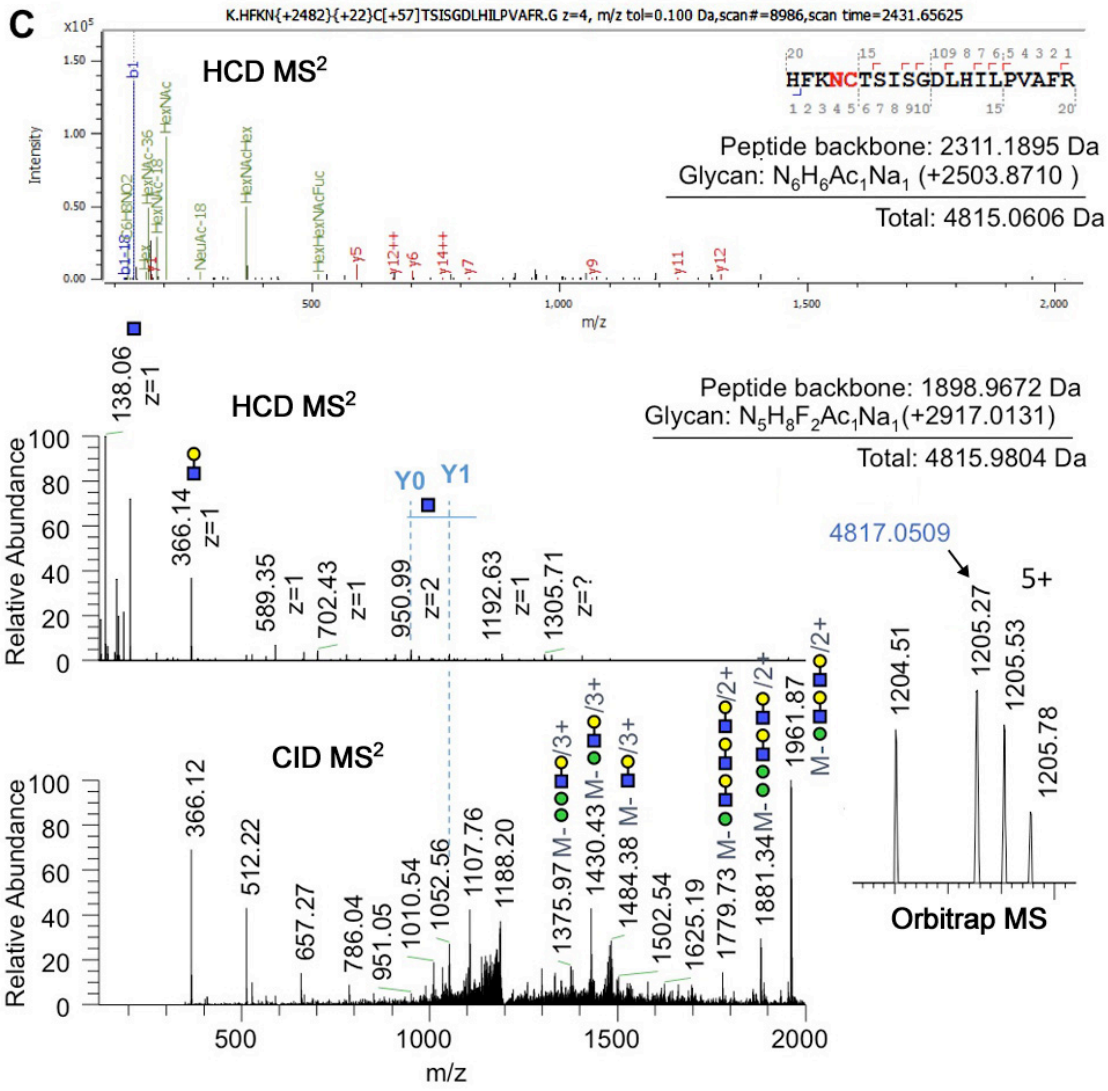


Figure S1C. More examples of false positives due to incorrect peptide backbone identification and glycan assignment (continued from previous page).

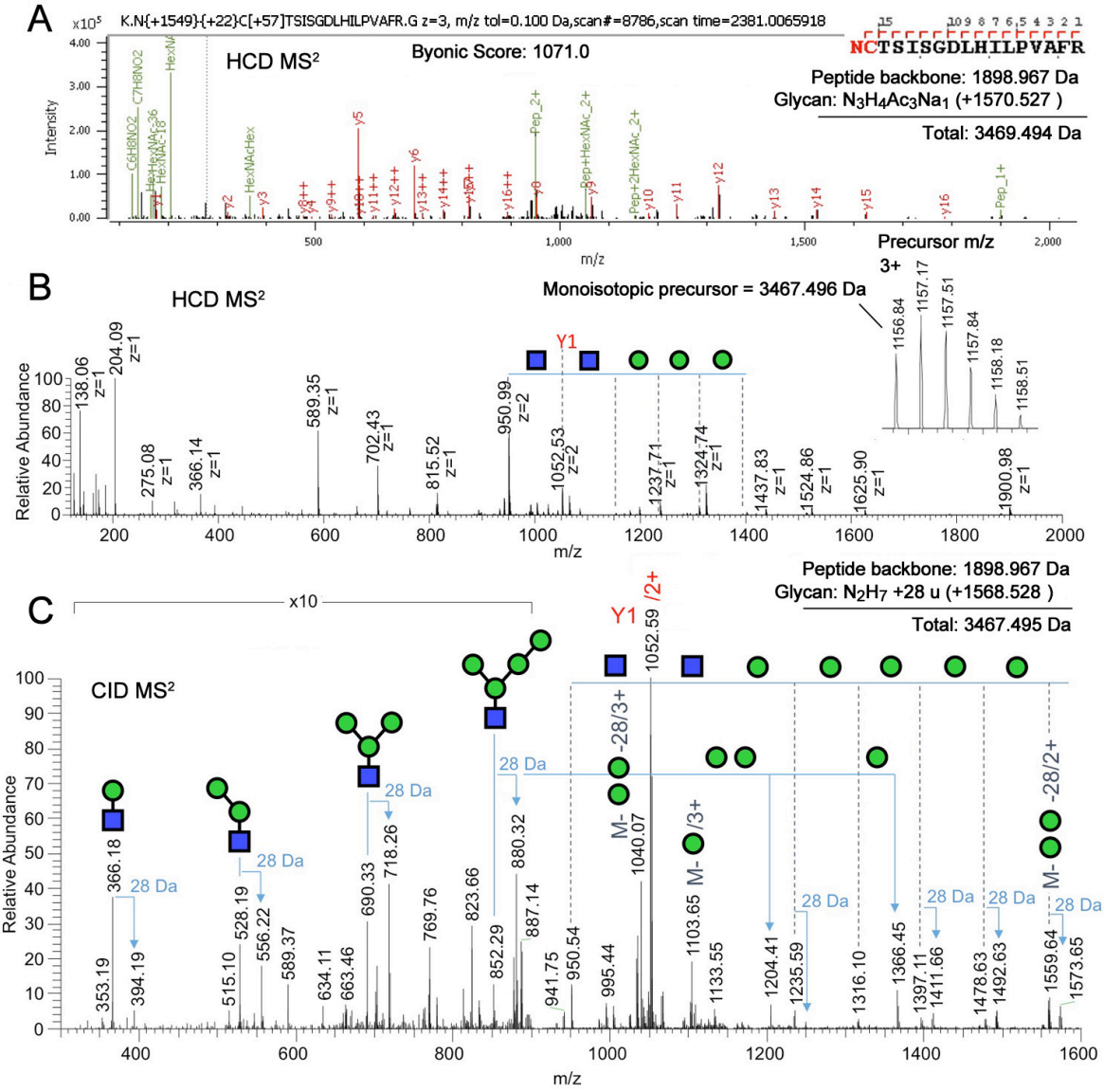


Figure S2. Exemplary false positive due to incorrect glycan assignment despite correct peptide backbone identification. The glycan composition assigned by Byonic (**A**) is inconsistent with the sequential glycosyl losses evident in both manually assigned HCD (**B**) and CID (**C**) MS^2 spectra. The peptide backbone of the 3+ glycopeptide precursor at m/z 1157.51 (M = 3469.5) was identified by both glycopeptide and Y1-based search as ^{337}NCTSISGDLHILPVAFR, and clearly detected as doubly charged Y0 and Y1 ions at m/z 950.99 and 1052.53, respectively (B). In the absence of other glycan-related fragment ions, the glycan moiety was best fitted to a reasonable $NeuAc_1Hex_4HexNAc_3Na_1$ composition by Byonic (A), to give a total glycopeptide mass of 3469.5 Da. However, no evidence could be found to corroborate the presence of a NeuAc-Hex-HexNAc antenna in the corresponding CID MS^2 spectrum (C). Instead, it clearly exhibited a fragmentation ladder that would support a HexNAc and up to 5 Hex extending from the Y1 ion, as well as a $Hex_nHexNAc^+$ oxonium ion series that extended up to $Hex_7HexNAc^+$. Interestingly, both series were accompanied by ions at 28 u higher, indicating that an unknown modification of 28 u, possibly a formyl or ethyl substituent, was present on an inner Man residue of a $Man_7GlcNAc_2$ to give a total glycopeptide mass of 3467.5 Da. This is apparently 2 u off from the registered m/z value of the precursor ion selected for MS^2 but a manual examination of the isotopic cluster (B, inset) revealed that the most likely triply charged monoisotopic precursor was the one at m/z 1156.84 (M=3467.5) and not 1157.51 (M=3469.5).

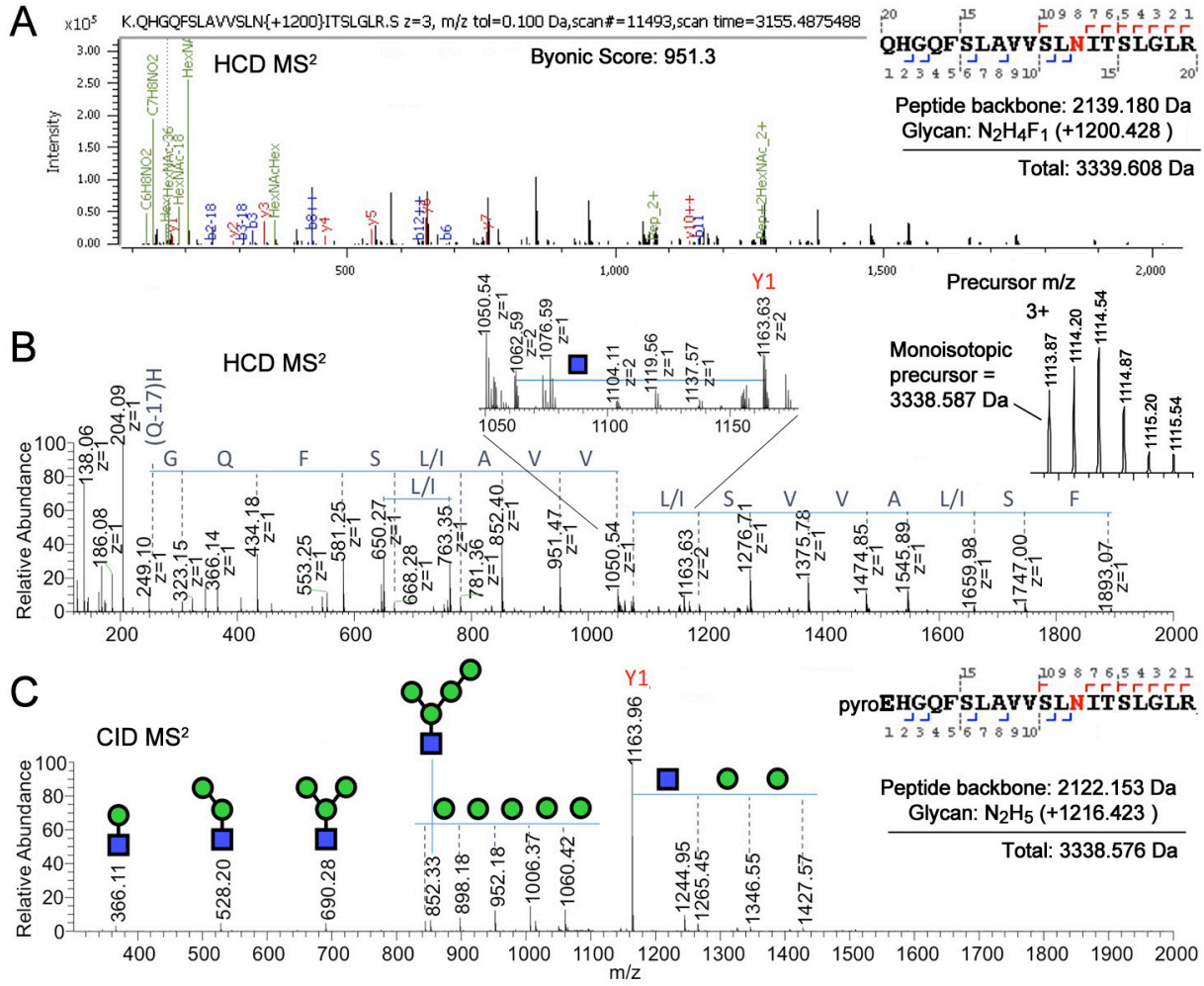


Figure S3. Exemplary false positive due to unanticipated modification on correctly identified peptide backbone leading to incorrect glycan assignment. The peptide backbone identified by Byonic (**A**) is inconsistent with the Y1 ion evident in both manually assigned HCD (**B**) and CID (**C**) MS^2 spectra, which is 17 u less than that anticipated and attributable to conversion of N-terminal Gln to pyroglutamate (pyroE). This is supported by the presence of a series of b ions in the HCD MS^2 spectrum, most notably the b_2 (m/z 249) and b_3 (m/z 323) ions, which carried the -17 u modification but erroneously assigned as b_2-18 and b_3-18, respectively. Working backwards, the correct glycan moiety should be $Man_5GlcNAc_2$, which added up to 3338.576 Da for the intact glycopeptide with an N-terminal pyro-glutamate and matched precisely the registered 3+ monoisotopic precursor at m/z 1113.87 selected for CID MS^2, corresponding to a glycopeptide of 3338.587 Da (**B**, inset). The Byonic assignment based on HCD MS^2 data would give instead 3339.608 Da for the intact glycopeptide, with a very unlikely glycan composition of $Hex_4HexNAc_2Fuc_1$.

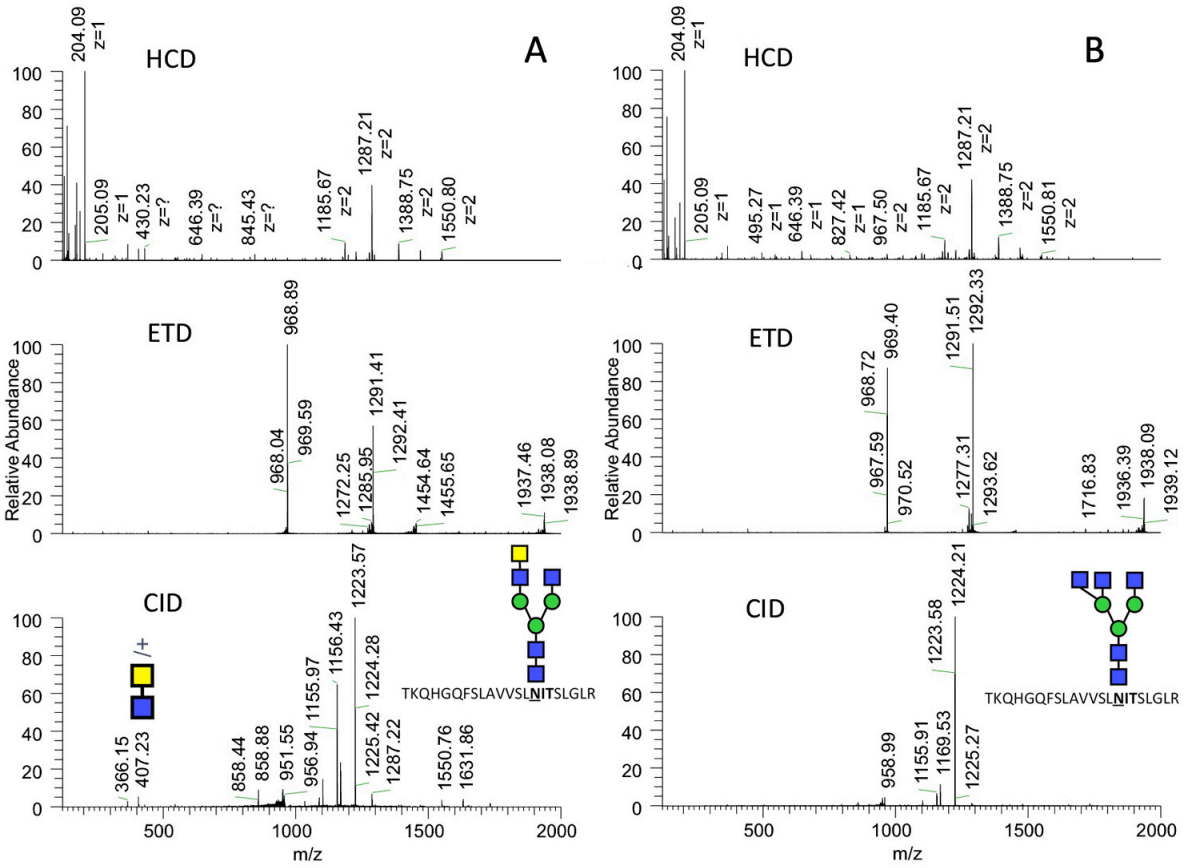


Figure S4. Additional information on glycan sequence or structural motifs provided by CID MS^2 data. As shown in Fig. 6, HexNAc-HexNAc terminal epitope could be identified on an earlier eluting glycoform (**A**), whereas the later eluting peak (**B**) carried mostly 3 single terminal HexNAc. This structural difference in glycan moiety could only be resolved by CID MS^2 (bottom panel, same as Fig 6B). Both HCD (top panel) and ETD (middle panel) MS^2 spectra were almost identical for the 2 glycoforms.

Table S1-1. Subset of Incorrect Glycopeptide Identification by Direct Database Search Despite Giving Positive ID by Y1-based Search

Byonic search results							Y1-based Mascot search		Y1-based Byonic search		Byonic-assigned glycan composition (-H3N2)*							Correct Y1		Glycan Composition (-H3N2)*						
Sequence	PSMs	n	Modification Type(s)	m/z	z	Score	Score	Identified peptide	Score	Identified peptide	F	H	N	Ac	Gc	Na	Total mass (Da)#	Y1 (m/z)	Z	F	H	N	Ac	Gc	+ Extra Mod	Total mass (Da)#
DIVSSDFLSNMSMDFQNHLGSCQK	6	2	C[+57], M[+16]*2	1214.49	4	569.88	34.45	same	518.98	same	3	2	2	0	0	0	2060.76	1498.41	2	1	2	2	1	0		2059.73
		1	C[+57], M[+16]*2	1227.47	4	434.29	27.26	same	315.71	same	0	3	2	0	1	1	2114.71	1498.7	2	1	2	3	1	0		2116.76
		2	C[+57], M[+16]*2	1251.01	4	497.35	29.65	same	450.78	same	4	2	2	0	0	0	2206.81	1498.39	2	2	2	2	1	0		2205.79
		1	C[+57], M[+16]	1141.47	4	350.06			301.9	same	0	3	2	0	0	0	1784.63	1490.61	2	1	2	2	0	0	17	1785.64
DSLSINATNIKHFKNCTSISGDLHILPVAFR	4	2	C[+57]	1321.19	5	905.72	34.85	NCTSISGDLHILPVAFR	464.9	NCTSISGDLHILPVAFR	2	7	4	0	0	0	3131.12	1052.62	2	0	3	0	0	0	3322.47	4700.95
		2	C[+57]	1345	5	948.61	43.5	NCTSISGDLHILPVAFR	480.24	NCTSISGDLHILPVAFR	1	2	5	3	0	0	3251.16	1052.72	2	0	4	0	0	0	3277.90	4819.00
EITGFLLIQAWPENR	2	2		1137.86	3	260.38			508.24	same	0	2	2	0	0	0	1622.58	996.15	2	1	1	2	0	0	17.00	1623.59
HFKNCTSISGDLHILPVAFR	7	2	C[+57]	893.67	4	1448.27	40	same	658.47	same	0	1	1	0	0	0	1257.45	839.29	3	0	2	0	0	0	42	1258.42
		2	C[+57]	804.37	5	1262.09	22.45	same	523.67	same	0	0	4	0	0	0	1704.63	839.49	3	0	5	0	0	0		1702.58
		2	C[+57]	777.55	5	1376.8	28.12	same	564.39	same	0	1	1	1	0	1	1571.53	629.82	4	0	4	0	0	0	28	1568.53
		1	C[+57]	1205.27	4	417.92			212.72	NCTSISGDLHILPVAFR	0	3	4	1	0	1	2504.88	1052.56	2	2	5	3	1	0	Na	2917.01
NCTSISGDLHILPVAFR	8	2	C[+57]	1161.84	3	864.42	74.2	same	607.01	same	0	3	1	0	0	0	1581.56	1052.64	2	0	4	0	0	0	42	1582.53
		2	C[+57]	1202.2	3	1094.91	67.53	same	616.81	same	0	0	4	0	0	0	1704.63	1052.42	2	0	5	0	0	0		1702.58
		2	C[+57]	1202.53	3	1077.61	66.63	same	619.22	same	0	0	4	0	0	0	1704.63	1052.65	2	0	5	0	0	0		1702.58
		2	C[+57]	1157.51	3	1082.28	68.58	same	629.01	same	0	1	1	1	0	1	1571.53	1052.59	2	0	4	0	0	0	28	1568.53
TKQHGQFSLAVVSLNITSLGLR	2	2		1082.52	4	663.12	19.79	same			2	1	3	0	0	0	1955.72	858.88	3	0	1	3	1	0		1954.70
VCNGIGIGEFKDSLSINATNIKHFKNCTSISGDLHILPVAFR	2	2	C[+57]*2	1385.82	5	654.03	27.74	NCTSISGDLHILPVAFR	369.68	NCTSISGDLHILPVAFR	0	2	2	0	2	2	2282.74	1052.63	2	0	4	0	0	0	3483.02	5023.10

n = number of redundancies

same : the peptide identified by Y1-based search is the same as the peptide bakbone identified by direct Byonic search

*Glycan composition in terms of Fuc (F), Hex (H), HexNAc (N), NeuAc (Ac), NeuGc (Gc), and Na is given without counting the trimannosyl core (H3N2)

#Total mass refers to the entire glycan moiety plus any extra modification (Mod)

Table S1-2. Subset of Incorrect Glycopeptide Identification by Direct Database Search Without Supporting Positive ID by Y1-based Search

Byonic search results							Assigned glycan composition (-H3N2)*							Correct Y1		Glycan Composition (-H3N2)*						
Sequence	PSMs	n	Modification(s)	m/z	z	Score	F	H	N	Ac	Gc	Na	Total mass (Da)#	Y1 (m/z)	Z	F	H	N	Ac	Gc	Extra Mod	Total mass(Da)#
DIVSSDFLSNMSMDFQNHLGSCQK	11	4	C[+57], M[+16]	1111.21	4	581.76	0	1	3	0	0	0	1663.61	1466.62	2	2	2	1	0	0		1711.62
		1	C[+57]	1147.73	4	353.77	0	2	3	0	0	0	1825.66	1458.7	2	2	3	1	0	0		1873.67
		2	C[+57], M[+16]	1151.72	4	481.49	0	2	3	0	0	0	1825.66	1466.65	2	2	3	1	0	0		1873.67
		2	C[+57], M[+16]*2	1161.98	4	505.07	1	0	4	0	0	0	1850.69	978.25	3	2	2	2	0	0		1914.70
		2	C[+57]	1188.24	4	438.07	0	3	3	0	0	0	1987.71	978.27	3	3	3	1	0	0		2019.73
DSLSINATNIKHFKNCTSISGDLHILPVAFR	7	2	C[+57]	1294.1	4	428.93	0	5	0	0	0	0	1702.58	1052.03	2	0	5	0	0	0	1569.8328	3272.41
		2	C[+57]	1383.81	5	670.11	0	4	5	2	1	0	3445.21	1060.03	2	0	5	0	0	0	3294.9784	4996.92
		2	C[+57]	1448.42	5	659.16	0	5	4	4	0	4	3771.24	1060.03	2	0	6	0	0	0	3456.0684	5320.07
		1	C[+57]	1469.91	4	373.59	0	2	3	2	0	0	2407.85	1052.03	2	0	2	0	0	0	2759.0256	3974.65
EFVENSECIQCHPECLPQAMNITCTGR	2	2	C[+57]*4, M[+16]	1135.47	4	468.36	1	0	1	0	0	0	1257.45	1168.15	3	0	2	0	0	0	+Na	1239.42
HFKNCTSISGDLHILPVAFR	16	2	C[+57]	893.41	4	412.69	0	1	1	0	0	0	1257.45	848.47	3	0	2	0	0	0	42	1258.42
		2	C[+57]	971.44	4	649.56	0	1	1	1	0	1	1571.53	848.47	3	0	4	0	0	0		1540.53
		2	C[+57]	974.69	4	1177.81	0	3	1	0	0	0	1581.56	847.76	3	0	4	0	0	0	17	1557.53
		2	C[+57]	981.94	4	494.34	0	0	2	1	0	1	1612.56	849.03	3	0	4	0	0	0	42	1582.53
		2	C[+57]	1011.95	4	673.25	0	2	1	1	0	1	1733.59	848.68	3	0	5	0	0	0		1702.58
		1	C[+57]	1021.21	4	502.91	1	2	2	0	0	0	1768.64	860.96	3	0	5	0	0	0		1702.58
		2	C[+57]	1022.46	4	741.13	0	1	2	1	0	1	1774.61	849.04	3	0	5	0	0	0	42	1744.58
		2	C[+57]	1112.5	4	539.59	1	3	3	0	0	0	2133.77	894.5	3	1	2	3	0	0		1971.72
		1	C[+57]	1205.27	4	389.49	0	3	4	1	0	1	2504.88	1052.56	2	3	6	3	0	0		2912.05
NCTSISGDLHILPVAFR	32	2	C[+57]	1053.81	3	580.64	0	1	1	0	0	0	1257.45	1073.37	2	0	2	0	0	0		1216.42
		2	C[+57]	1088.15	3	480.63	1	2	0	0	0	0	1362.48	1043.59	2	0	3	0	0	0		1378.48
		2	C[+57]	1094.72	4	385.47	0	6	3	0	0	0	2473.87	1259.84	2	1	2	2	1	0		2059.73
		2	C[+57]	1107.83	3	845.88	0	2	1	0	0	0	1419.50	1073.57	2	0	3	0	0	0		1378.48
		2	C[+57]	1161.85	3	895.19	0	3	1	0	0	0	1581.56	1073.54	2	0	4	0	0	0		1540.53
		2	C[+57]	1171.51	3	652.79	0	0	2	1	0	1	1612.56	1079.06	2	0	4	0	0	0	17	1557.53
		2	C[+57]	1173.73	4	695.18	0	4	3	1	1	2	2793.93	1490.32	2	2	2	2	0	0		1914.70
		2	C[+57]	1173.98	4	540.55	0	4	3	1	1	2	2793.93	1490.67	2	2	2	2	0	0		1914.70
		2	C[+57]	1174.24	4	500.47	0	4	3	1	1	2	2793.93	1490.68	2	2	2	2	0	0		1914.70
		2	C[+57]	1183.2	3	657.36	1	0	3	0	0	0	1647.61	1104.56	2	0	4	0	0	0		1540.53
		2	C[+57]	1187.99	4	447.45	3	3	2	2	0	2	2850.98	1490.76	2	1	2	3	0	0		1971.72
		2	C[+57]	1196.19	3	547.85	1	4	0	0	0	0	1686.59	1043.56	2	0	5	0	0	0		1702.58
		2	C[+57]	1220.03	4	480.18	2	3	5	1	0	0	2977.08	1510.17	2	1	2	2	1	0		2059.73
		2	C[+57]	1224.75	4	590.25	0	4	4	1	1	2	2997.01	1490.37	2	2	2	3	0	0		2117.78
		1	C[+57]	1246.76	4	408.29	0	4	3	2	1	2	3085.03	1490.6	2	2	2	2	1	0		2205.79
		1	C[+57]	1250.21	3	306.39	1	5	0	0	0	0	1848.64	1104.57	2	0	5	0	0	0	42	1744.58
		2	C[+57]	1283.78	4	362.45	1	3	4	3	0	1	3233.13	1490.74	2	1	3	4	0	0	17	2353.85
QHGQFSLAVVSLNITSLGLR	69	2		952.21	4	571.81	0	1	3	0	0	0	1663.61	1164.1	2	0	1	3	0	0	17	1680.61
		1		1020.48	4	411.63	1	0	3	1	0	0	1938.71	1164.12	2	0	1	3	1	0		1954.70
		2		1024.98	4	469.58	0	1	3	1	0	0	1954.70	1172.65	2	0	1	3	1	0		1954.70
		2		1114.54	3	951.28	1	1	0	0	0	0	1200.43	1163.96	2	0	2	0	0	0		1216.42
		5		1119.88	3	945.98	0	2	0	0	0	0	1216.42	1164.17	2	0	2	0	0	0	17	1233.42
		2		1120.21	3	972.48	0	2	0	0	0	0	1216.42	1164.76	2	0	2	0	0	0	17	1233.42
		2		1133.88	3	872.33	0	1	1	0	0	0	1257.45	1164.14	2	0	1	1	0	0	17	1274.45
		4		1215.26	3	870.36	0	0	3	0	0	0	1501.56	1164.14	2	0	0	3	0	0	17	1518.56
		2		1228.25	3	805.35	0	4	0	0	0	0	1540.53	1164.18	2	0	4	0	0	0	17	1557.53
		2		1263.6	3	770.46	1	0	3	0	0	0	1647.61	1164.21	2	1	0	3	0	0	17	1664.61
		5		1269.27	3	755.23	0	1	3	0	0	0	1663.61	1164.29	2	0	1	3	0	0	17	1680.61
		2		1282.94	3	789.64	0	0	4	0	0	0	1704.63	1164.23	2	0	0	4	0	0	17	1721.63
		6		1282.95	3	782.1	0	0	4	0	0	0	1704.63	1164.12	2	0	0	4	0	0	17	1721.63
		1		1284.94	3	336.92	2	2	1	0	0	0	1711.62	1172.65	2	0	2	1	1	0		1710.60
		1		1298.28	3	597.83	2	1	2	0	0	0	1752.64	1172.67	2	0	1	2	1	0		1751.62
		2		1298.95	3	523.11	2	1	2	0	0	0	1752.64	1172.66	2	0	1	2	1	0		1751.62
		1		1303.28	3	416.94	0	1	2	0	1	0	1767.62	1172.71	2	1	2	2	0	0		1768.64
		2		1311.95	3	690.58	2	0	3	0	0	0	1793.67	1164.15	2	1	1	3	0	0		1809.67
		1		1312.28	3	475.62	2	0	3	0	0	0	1793.67	1164.15	2	1	1	3	0	0		1809.67
		4		1352.3	3	733.53	2	2	2	0	0	0	1914.70	1164.22	2	0	2	2	1	0	17	1930.68
		4		1360.63	3	754.08	1	0	3	1	0	0	1938.71	1164.15	2	0	1	3	1	0		1954.70
		6		1366.31	3	964.91	2	1	3	0	0	0	1955.72	1172.77	2	0	1	3	1	0		1954.70
		2		1366.64	3	557.67	2	1	3	0	0	0	1955.72	1164.14	2	2	1	3	0	0	17	1972.72
		4		1379.98	3	757.85	2	0	4	0	0	0	1996.75	1172.5	2	0	0	4	1	0		1995.73
		1		1380.31	3	596.6	2	0	4	0	0	0	1996.75	1164.01	2	0	0	4	1	0	17	2012.73
		3		1380.32	3	647.38	2	0	4	0	0	0	1996.75	1164.23	2	0	0	4	1	0	17	2012.73
TKQHGQFSLAVVSLNITSLGLR	5	1		1082.27	4	437.34	2	1	3	0	0	0	1955.72	858.84	3	0	1	3	1	0		1954.70
		2		1129.04	4	535.61	3	0	4	0	0	0	2142.81	858.36	3	1	0	4	1	0		2141.79
		2		1442.69	3	478.59	2	1	3	0	0	0	1955.72	1286.76	2	0	1	3	1	0		1954.70
YADAGHVCHLCHPNCTYGCTGPGLEGCPTNGPK	30	2	C[+57]*5	1144.86	5	1163.74	3	2	2	0	0	0	2060.76	1288.16	3	1	2	2	1	0		2059.73
		2	C[+57]*5	1203.28	5	924.5	0	4	4	0	0	0	2352.85	1287.75	3	1	2	2	2	0		2350.83
		2	C[+57]*5	1217.89	5	1035.63	3	3	3	0	0	0	2425.89	1288.17	3	1	3	3	1	0		2424.87
		2	C[+57]*5	1223.08	5	950.94	0	2	3	2	0	2	2453.83	1287.65	3	1	3	3	1	0	+Na	2447.87
		2	C[+57]*5	1229.09	5	754.77	2	3	4	0	0	0	2482.91	1287.73	3	0	3	4	1	0		2481.89
		2	C[+57]*5	1229.29	5	753.25	2	3	4	0	0	0	2482.91	1288.78	3	0	3	4	1	0		2481.89
		2	C[+57]*5	1247.1	5	468.08	4	3	3	0	0	0	2571.95	1287.19	3	2	3	3	1	0		2570.93
		2	C[+57]*5	1276.31	5	1005.79	0	5	5	0	0	0	2717.98	1288.07	3	1	3	3	2	0		2715.96
		2	C[+57]*5	1287.7	5	627	0	4	3	2	0	2	2777.94	1287.54	3	0	3	4	2	0		2772.98
		2	C[+57]*5	1287.71	5	654.83	4	3	4	0	0	0	2775.02	1258.7	3	2	3	3	2	0		2862.02
		1	C[+57]*5	1291.31	5	502.18	0	3	4	2	0	1	2795.97	1932.47	2	1	4	4	1	0		2790.00
		2	C[+57]*5	1293.71	5	715.65	3	3	2	2	0	0	2805.00	1258.53	3	0	5	3	2	0		2894.01
		2	C[+57]*5	1302.51	5	699.48	3	3	2	2	0	2	2850.98	1288.37	3	1	3	5	1	0	14	2845.03
		2	C[+57]*5	1357.53	5	614.26	1	4	4	2	0	2	3127.07	1288.11	3	1	3	5	2	0		3122.12
		1	C[+57]*5	1357.73	5	315.06	1	4	4	2	0	2	3127.07	1287.83	3	1	3	5	2	0		3122.12
		2	C[+57]*5	1415.55	5	525.62	3	3	5	2	0	0	3414.24	1288.29	3	1	3	5	3	0		3413.22

n = number of redundancies

*Glycan composition in terms of Fuc (F), Hex (H), HexNAc (N), NeuAc (Ac), NeuGc (Gc), and Na is given without counting the trimannosyl core (H3N2)

#Total mass refers to the entire glycan moiety plus any extra modification (Mod)

Table S2. Glycopeptides Correctly Identified by Direct Database Search Using Byonic

Byonic search results							Assigned glycan composition (-H3N2)*							Y1-based Search**	
Sequence	PSMs	n	Modification(s)	m/z	z	Score	F	H	N	Ac	Gc	Na	Total mass (Da)#	Byonic	Mascot
DIVSSDFLSNMSMDFQNHLGSCQK	24	2	C[+57], M[+16]	1564.97	3	509.44	2	2	2	0	0	0	1914.70	613.28	23.36
		1	C[+57], M[+16]	1583.98	3	433.92	1	2	3	0	0	0	1971.72	261.73	
		4	C[+57], M[+16]*2	1141.47	4	704.28	1	2	2	0	0	0	1768.64	591.74	38.01
		2	C[+57], M[+16]*2	1177.98	4	623.96	2	2	2	0	0	0	1914.70	575.79	36.01
		1	C[+57], M[+16]*2	1181.99	4	356.12	1	3	2	0	0	0	1930.69	325.18	
		2	C[+57], M[+16]*2	1218.5	4	565.22	2	3	2	0	0	0	2076.75	475.98	43.59
		1	C[+57], M[+16]*2	1228.5	4	339.38	2	2	3	0	0	0	2117.78	270.84	
		1	C[+57], M[+16]*2	1261.01	4	350.8	2	1	3	1	0	0	2246.82	276.52	
		6	C[+57], M[+16]*2	1413.59	3	936.8	1	0	2	0	0	0	1444.53	777.14	47.15
		4	C[+57], M[+16]*2	1521.62	3	814.06	1	2	2	0	0	0	1768.64	766.61	42.82
DSLSINATNIK	50	3		798.36	3	488.16	0	2	0	0	0	0	1216.42	530.99	38.36
		2		812.03	3	412.72	0	1	1	0	0	0	1257.45	432.32	26.34
		2		852.37	3	331	0	3	0	0	0	0	1378.48	273.7	
		2		852.38	3	437.38	0	3	0	0	0	0	1378.48	524.39	40.69
		4		866.38	3	439.77	0	2	1	0	0	0	1419.50	429.2	34.28
		4		906.39	3	408.43	0	4	0	0	0	0	1540.53	456.4	39.12
		4		960.41	3	395.18	0	5	0	0	0	0	1702.58	419.16	43.16
		9		1197.03	2	432.68	0	2	0	0	0	0	1216.42	463.7	46.92
		16		1278.06	2	428.66	0	3	0	0	0	0	1378.48	474.71	48.71
		4		1359.08	2	451.98	0	4	0	0	0	0	1540.53	441.94	46.66
EFVENSECIQCHPECLPQAMNITCTGR	2	2	C[+57]*4, M[+16]	1129.21	4	322.55	0	2	0	0	0	0	1216.42		
EITGFLLIQAWPENR	3	1		1078.5	3	281.69	1	0	2	0	0	0	1444.53		
		2		1146.19	3	258.53	1	0	3	0	0	0	1647.61	275.06	
HFKNCTSISGDLHILPVAFR	24	4	C[+57]	771.75	5	1151.36	0	4	0	0	0	0	1540.53	604.25	56.33
		2	C[+57]	804.16	5	1399.52	0	5	0	0	0	0	1702.58	622.19	42.85
		2	C[+57]	817.38	5	1267.11	1	2	2	0	0	0	1768.64	480.33	
		4	C[+57]	883.16	4	1160.73	0	2	0	0	0	0	1216.42	721.92	43.38
		4	C[+57]	883.41	4	1130.34	0	2	0	0	0	0	1216.42	598.53	55.67
		2	C[+57]	923.93	4	1314.56	0	3	0	0	0	0	1378.48	533.32	34.01
			C[+57]	964.44	4	1102.83	0	4	0	0	0	0	1540.53	485.6	32.69
		2	C[+57]	964.44	4	1076.27	0	4	0	0	0	0	1540.53	486.22	41.31
		2	C[+57]	1004.95	4	1197.66	0	5	0	0	0	0	1702.58	437.58	27.43
		2	C[+57]	1177.55	3	1244.57	0	2	0	0	0	0	1216.42	742.01	55.01
KVCNGIGIGEFKDSLSINATNIK	16	2	C[+57]	924.69	4	711.23	0	2	0	0	0	0	1216.42	707.52	
		4	C[+57]	924.94	4	738.03	0	2	0	0	0	0	1216.42	743.4	
		2	C[+57]	965.45	4	715.32	0	3	0	0	0	0	1378.48	568.44	
		2	C[+57]	1005.97	4	773.39	0	4	0	0	0	0	1540.53	427.61	
		2	C[+57]	1046.48	4	878.65	0	5	0	0	0	0	1702.58		
		4	C[+57]	1286.93	3	749.42	0	3	0	0	0	0	1378.48	585.49	
NCTSISGDLHILPVAFR	70	2	C[+57]	780.11	4	1018.94	0	2	0	0	0	0	1216.42	628.46	61.07
		2	C[+57]	820.62	4	1085.45	0	3	0	0	0	0	1378.48	626.75	64.42
		2	C[+57]	861.13	4	1032.01	0	4	0	0	0	0	1540.53	582.5	61.33
		2	C[+57]	861.38	4	1024.82	0	4	0	0	0	0	1540.53	558.07	49.16
		4	C[+57]	901.9	4	1087.35	0	5	0	0	0	0	1702.58	568.16	51.36
		8	C[+57]	1039.81	3	1065.54	0	2	0	0	0	0	1216.42	685.93	66.2
		4	C[+57]	1040.14	3	925.14	0	2	0	0	0	0	1216.42	686.73	65.88
		4	C[+57]	1053.81	3	1039.59	0	1	1	0	0	0	1257.45	695.4	77.99
		8	C[+57]	1093.82	3	982.15	0	3	0	0	0	0	1378.48	638.55	73.52
		12	C[+57]	1147.84	3	1127.19	0	4	0	0	0	0	1540.53	664.08	75.66
		4	C[+57]	1148.18	3	1127.2	0	4	0	0	0	0	1540.53	639.85	65.65
		2	C[+57]	1150.18	3	661.79	0	1	1	1	0	0	1548.54	333.73	31.29
		2	C[+57]	1201.86	3	1153.03	0	5	0	0	0	0	1702.58	672.35	66.76
		4	C[+57]	1202.19	3	1227.09	0	5	0	0	0	0	1702.58	657.53	72.37
		2	C[+57]	1255.87	3	1111.52	0	6	0	0	0	0	1864.63	593.63	69.84
		6	C[+57]	1256.21	3	1149.59	0	6	0	0	0	0	1864.63	602.75	63.98
		2	C[+57]	1559.21	2	714.19	0	2	0	0	0	0	1216.42	481.16	39.35
QHGQFSLAVVSLNITSLGLR	25	4		1120.21	3	1261.24	0	2	0	0	0	0	1216.42		
		2		1201.58	3	828.09	0	1	2	0	0	0	1460.53		
		2		1255.6	3	692.39	0	2	2	0	0	0	1622.58		
		2		1268.94	3	965.15	0	1	3	0	0	0	1663.61		
		2		1269.27	3	1049.4	0	1	3	0	0	0	1663.61		
		2		1282.95	3	1038.21	0	0	4	0	0	0	1704.63		
		1		1284.6	3	479.79	0	2	1	1	0	0	1710.60		
		2		1317.63	3	416.67	1	1	3	0	0	0	1809.67		
		1		1352.63	3	411.21	0	2	2	1	0	0	1913.68		
		4		1371.98	3	639.51	1	2	3	0	0	0	1971.72		
		3		1414.99	3	796.93	1	1	3	1	0	0	2100.76		
TKQHGQFSLAVVSLNITSLGLR	32	2		867.44	4	559.62	0	0	1	0	0	0	1095.40	208.28	
		4		897.45	4	966.11	0	2	0	0	0	0	1216.42	813.05	57.12
		2		907.95	4	856.91	0	1	1	0	0	0	1257.45	679.06	39.76
		2		918.21	4	775.66	0	0	2	0	0	0	1298.48	534.98	29.67
		2		958.72	4	438.3	0	1	2	0	0	0	1460.53	202.71	
		6		968.98	4	802.77	0	0	3	0	0	0	1501.56	570.6	42.69
		2		988.98	4	709.86	0	3	1	0	0	0	1581.56	474.01	21.51
		2		1009.49	4	720.02	0	1	3	0	0	0	1663.61	442.39	39.36
		2		1019.75	4	753.63	0	0	4	0	0	0	1704.63	526.74	45.15
		1		1035.5	4	431.2	1	2	2	0	0	0	1768.64		
		2		1046.01	4	607.34	1	1	3	0	0	0	1809.67	263.75	14.12
		1		1056.26	4	344.21	1	0	4	0	0	0	1850.69		

		2		1072.01	4	604.76	0	2	2	1	0	0	1913.68	335.79	19.03
		2		1394.34	3	632.92	1	1	3	0	0	0	1809.67	237.88	
VCNGIGIGEFKDSLSINATNIK	18	1	C[+57]	933.18	4	421	0	3	0	0	0	0	1378.48	552.37	29.68
		5	C[+57]	1190.22	3	645.07	0	2	0	0	0	0	1216.42	769.4	45.66
		2	C[+57]	1243.9	3	558.68	0	3	0	0	0	0	1378.48	554.12	28.74
		6	C[+57]	1244.24	3	635.7	0	3	0	0	0	0	1378.48	622.99	38.43
		2	C[+57]	1297.92	3	722.86	0	4	0	0	0	0	1540.53	721.16	51.18
		2	C[+57]	1351.61	3	673.59	0	5	0	0	0	0	1702.58	647.03	45.39
YADAGHVCHLCHPNCTYGCTGPGLEGCPTNGPK	18	4	C[+57]*5	1062.23	5	1230.1	1	0	3	0	0	0	1647.61		
		2	C[+57]*5	1102.85	5	886.72	1	0	4	0	0	0	1850.69		
		2	C[+57]*5	1127.06	5	719.14	1	2	3	0	0	0	1971.72		
		1	C[+57]*5	1211.48	5	371.69	1	2	2	2	0	2	2396.81		
		2	C[+57]*5	1240.7	5	609.13	1	3	5	0	0	0	2539.93		
		1	C[+57]*5	1246.5	5	535.08	2	3	3	1	0	0	2570.93		
		2	C[+57]*5	1261.7	5	1017.03	2	4	4	0	0	0	2644.96		
		2	C[+57]*5	1308.12	5	604.47	1	4	3	2	0	0	2878.02		
		2	C[+57]*5	1319.92	5	1082.58	2	4	4	1	0	0	2936.06		

n = number of redundancies

*Glycan composition in terms of Fuc (F), Hex (H), HexNAc (N), NeuAc (Ac), NeuGc (Gc), and Na is given without counting the trimannosyl core (H3N2)

#Total mass refers to the entire glycan moiety plus any extra modification (Mod)

**Scores for Y1-based search identifying the same peptide backbone using 2 different search engines; not all PSMs by direct glycopeptide search yielded positive Y1-based search