

Figure S1. Endoglycosidase F3 reveals core fucosylated N-glycans. A) Endo F3 cleaves N-glycans between GlcNAc residues on the chitobiose core only in the presence of a core fucose residue and is unable to cleave terminally fucosylated isomers. B) Terminally fucosylated isomers were detected minimally (Hex4dHex1HexNAc3 m/z 1444.5071, Hex4dHex1HexNAc4 m/z 1647.5865, Hex6dHex1HexNAc5 m/z 2174.7715) or not at all (Hex4dHex1HexNAc5SO₄1 m/z 1952.6125). C) Endo F3 cleavage products from core fucosylated isomers with a distinct -349.1373 mass shift were observed in much greater abundance for the four representative structures shown (Hex4HexNAc2 m/z 1095.3698, Hex4HexNAc3 m/z 1298.4492, Hex4HexNAc4SO₄1 m/z 1603.4752, Hex6HexNAc4 m/z 1825.6342) as well as for most structures with at least one fucose residue in this report.

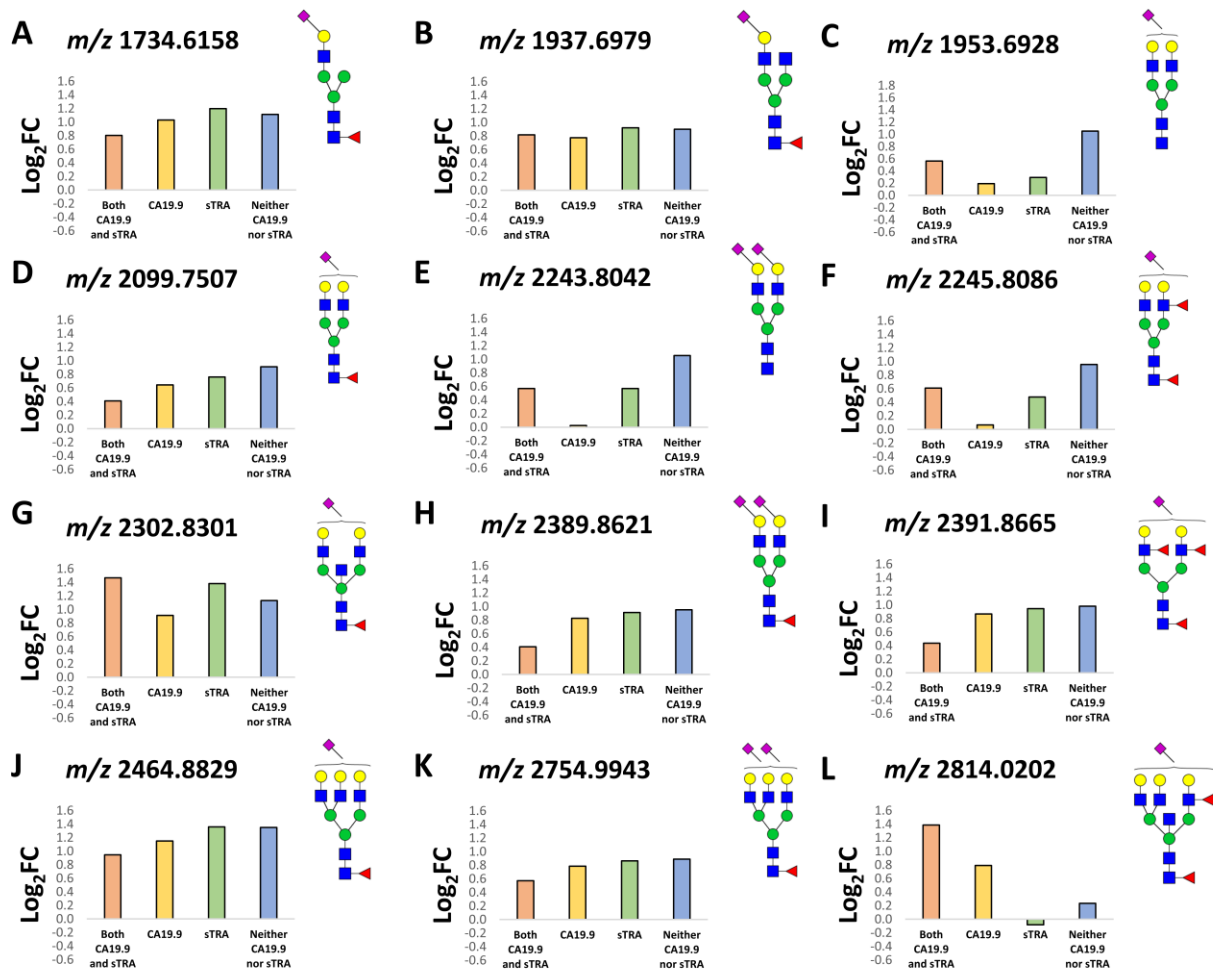


Figure S2. Sialic Acid Stabilization of TMA cores. A-L) Representative α 2,3-sialylated N-glycan structures enriched in tumor tissue cores as compared to patient matched normal tissue cores. Log₂ FC between patient matched tumor and normal cores, where positive values represent enrichment in tumor tissue.

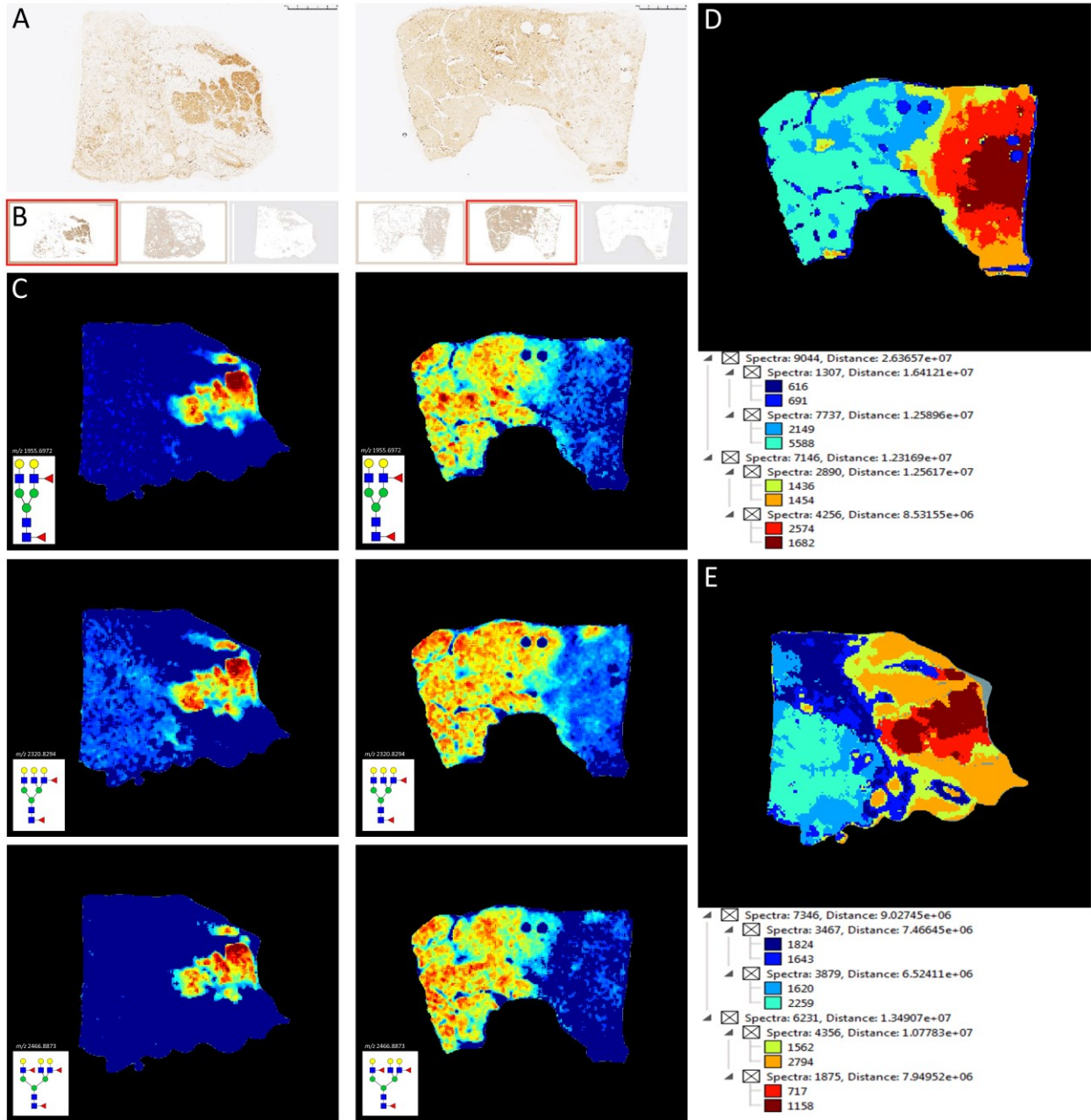


Figure S3. N-glycan colocalization with CA19-9. A) Representative whole tissue block sections from which TMA cores were derived were IHC stained for CA19-9 expression. B) A color-based k-means clustering algorithm was applied to high-resolution staining images to generate unbiased staining classifications, the most intense of which (outlined in red) were co-registered with original scans in Fleximaging and used to draw regions of interest around stained tissue. C) SCiLS lab software was used to identify and create images of N-glycans colocalized to areas of CA19-9 staining. Shown are

three representative N-glycans (Hex5dHex2HexNAc4 *m/z* 1955.6975, Hex6dHex2HexNAc5 *m/z* 2320.8294, Hex6dHex3HexNAc5 *m/z* 2466.8873). D, E) Segmentation analysis across eight nodes of 72 N-glycan structures showing differential associations of glycans between CA19-9-staining and non-CA19-9-staining tissue.

TB#	Race	Sex	Age	Vital Status	Recurrence	Type of Recurrence	Days between Surgery and Recurrence	Days between Surgery and Date of last contact/Death	Histological Type	Histological Grade	Staging
2204	WHITE	M	75	Unknown	Unknown	N/A	N/A	272	Adenocarcinoma	moderately differentiated	T3N0MX
2278	WHITE	M	76	Unknown	Unknown	N/A	N/A	211	cholangiocarcinoma	moderately differentiated	T3N1MX
2279	WHITE	F	61	Unknown	YES	distant recurrence - GAST	2233	2486	Adenocarcinoma	well differentiated	T3N0MX
2381	WHITE	M	73	Unknown	YES	Distant recurrence - CNS	2499	2587	Mucinous Adenocarcinoma	Not Reported	
2417	WHITE	M	80	Unknown	Unknown	N/A	N/A	23	Adenocarcinoma	poorly differentiated	T3N1MX
2454	WHITE	F	69	Unknown	Unknown	N/A	N/A	Unknown	Adenocarcinoma	moderately differentiated	T3N0MX
2487	BLACK	M	73	Unknown	Unknown	N/A	N/A	106	Adenocarcinoma	well differentiated	T3N1MX
2464	BLACK	F	61	Unknown	YES	metastacized to liver and omentum	N/A	Unknown	Adenocarcinoma	poorly differentiated	T4N1Mx
1751	WHITE	M	65	Unknown	Unknown	N/A	N/A	101	Adenocarcinoma	well differentiated	T3N1MX
1800	BLACK	F	67	Unknown	Unknown	N/A	N/A	204	Adenocarcinoma	poorly differentiated	T3N1MX
1691	WHITE	M	69	Unknown	Unknown	N/A	N/A	92	Adenocarcinoma	Not Reported	T3N1MX
1848	WHITE	M	71	Unknown	NO	Never disease free	N/A	314	Adenocarcinoma	poorly differentiated	T3N1MX
1911	WHITE	M	83	Unknown	NO	Disease free	N/A	118	Adenocarcinoma	moderately differentiated	T3N1MX
1747	WHITE	F	63	Unknown	NO	Possible recurrence	N/A	138	Adenocarcinoma	poorly differentiated	T3N1MX
1673	WHITE	M	78	Unknown	NO	Disease free	N/A	440	Adenocarcinoma	moderately differentiated	T3N1
1685	BLACK	M	66	Unknown	NO	Never disease free	N/A	173	Adenocarcinoma	poorly differentiated	T3N1MX
1987	WHITE	F	58	Unknown	NO	Disease free	N/A	404	Adenocarcinoma	moderately differentiated	T3N1MX
2055	WHITE	M	69	Unknown	Unknown	N/A	N/A	808	Adenocarcinoma	poorly differentiated	T3NXMX
1955	BLACK	F	51	Unknown	Unknown	N/A	N/A	392	Adenocarcinoma	moderately differentiated	T3N1MX
1958	WHITE	M	42	Unknown	Unknown	N/A	N/A	429	Adenocarcinoma	poorly differentiated	T3N1MX
1982	WHITE	F	66	Unknown	Unknown	N/A	N/A	336	Adenocarcinoma	moderately differentiated	T2N1MX
2572	WHITE	F	87	Unknown	NO	Disease free	N/A	1387	Adenocarcinoma	moderately differentiated	T1N0MX
2091	WHITE	F	54	Unknown	YES	Local Recurrence	406	547	Adenocarcinoma	Not Reported	T2N0MX
2495	WHITE	M	56	Dead	NO	Never disease free	N/A	76	Adenocarcinoma	Not Reported	T3N1MX
2807	BLACK	F	62	Unknown	NO	Never disease free	N/A	126	Adenocarcinoma	poorly differentiated	T3N0MX
2815	WHITE	F	76	Unknown	Unknown	N/A	N/A	Unknown	Ductal adenocarcinoma	moderately differentiated	T3N0MX
2893	BLACK	F	68	Unknown	YES	Local recurrence	613	613	Adenocarcinoma	moderately differentiated	T3N1MX
2916	WHITE	F	37	Unknown	YES	Distant recurrence	165	236	Adenocarcinoma	moderately differentiated	T3N1MX
2790	WHITE	M	78	Unknown	NO	Never disease free	N/A	32	Adenocarcinoma	moderately differentiated	T2N1bMX
2695	WHITE	M	70	Unknown	NO	Never disease free	N/A	185	Adenocarcinoma	Not Reported	T2N0MX
3721	WHITE	F	66	Unknown	NO	Never disease free	N/A	50	Ductal adenocarcinoma	poorly differentiated	T3N0MX
3627	BLACK	F	84	Unknown	Unknown	N/A	N/A	Unknown	Adenocarcinoma	moderately differentiated	T2N1MX
3508	WHITE	M	49	Unknown	NO	Never disease free	N/A	221	Adenocarcinoma	moderately differentiated	T3N1MX
3727	WHITE	M	74	Unknown	YES	Distant recurrence	140	140	Adenosquamous carcinoma	moderately differentiated	T3N0MX
3499	WHITE	F	66	Unknown	NO	Disease free	N/A	125	Ductal adenocarcinoma	Not Reported	T1N0MX
3463	WHITE	F	64	Unknown	NO	Disease free	N/A	215	Ductal adenocarcinoma	moderately differentiated	T3N1MX
3832	WHITE	M	68	Unknown	YES	Distant recurrence - LUNG	332	353	Adenocarcinoma	moderately differentiated	T3N1MX
3978	WHITE	M	63	Unknown	NO	Disease free	N/A	25	Adenocarcinoma	Not Reported	T2N1bMX
3922	BLACK	M	72	Unknown	NO	Disease free	N/A	94	Ductal adenocarcinoma	moderately differentiated	T1N0MX
3986	WHITE	F	70	Unknown	NO	Disease free	N/A	27	Adenocarcinoma	poorly differentiated	T3N1MX
3406	WHITE	F	74	Unknown	NO	Disease free	N/A	62	Ductal adenocarcinoma	moderately differentiated	T3N1MX
4038	WHITE	M	71	Unknown	YES	Distant recurrence - LUNG	525	318	Adenocarcinoma	moderately differentiated	T3N1MX
3859	WHITE	F	50	Dead	YES	Distant recurrence - HEPT	196	202	Ductal adenocarcinoma	moderately differentiated	T3N1MX
3915	WHITE	F	53	Dead	YES	Distant recurrence - LUNG	1182	1213	Ductal adenocarcinoma	moderately differentiated	T2N0MX
3891	WHITE	F	62	Unknown	Unknown	N/A	N/A	1148	Ductal adenocarcinoma	moderately differentiated	T3N1bM
3886	WHITE	M	62	Unknown	YES	Distant recurrence - HEPT	337	604	Adenocarcinoma	moderately differentiated	T3N1bMX
4072	WHITE	F	71	Unknown	NO	Disease Free	N/A	27	Ductal adenocarcinoma	moderately differentiated	T3N0MX
4524	WHITE	F	60	Unknown	NO	Disease Free	N/A	130	Ductal adenocarcinoma	moderately differentiated	T3N1MX
4071	BLACK	M	64	Unknown	NO	Disease Free	N/A	43	Ductal adenocarcinoma	moderately differentiated	T1N1bMX
4365	WHITE	F	78	Unknown	NO	Disease Free	N/A	90	Adenocarcinoma	moderately differentiated	T1N0MX
4180	WHITE	M	87	Unknown	NO	Disease Free	N/A	69	Adenocarcinoma	poorly differentiated	T3N1bMX
4374	BLACK	M	51	Unknown	YES	Distant recurrence - HEPT	735	736	Ductal adenocarcinoma	moderately differentiated	T3N1MX
4257	ASIAN	M	39	Dead	NO	Never disease free	N/A	9	Ductal adenocarcinoma	moderately differentiated	T3N1MX

Table S1. Clinical information for patient samples used for TMA cores and for whole tissue analysis.

Table with 12 columns: Composition, Theoretical Mass, Observed Mass, Mass Error, and then a repeating set of these four columns for 11 other compositions. The data lists various chemical structures (e.g., Hex3Hex1HexNAc2 + Na, Hex5HexNAc5(2,3)NeuAc1 + Na) and their corresponding mass values and errors.

Table S2. Composition and mass accuracy of 151 N-glycan structures obtained via MALDI-IMS analysis. All detected structures are monoisotopic, underivatized and singly-sodiated unless otherwise indicated. Sialic acid derivatization by amidation amidation (AA) reaction yields a mass difference of +290.1114 for 2,3 linked sialic acid residues and +318.1427 for 2,6 linked sialic acid residues. Mass error calculation: ((ABS(Theoretical m/z – Observed m/z)/Theoretical m/z)*1,000,000).

m/z	Structure	m/z	Structure	m/z	Structure	m/z	Structure	m/z	Structure	m/z	Structure
1079.3745*		1905.6338		2215.7980*		2539.9037*		2979.0808*		3485.2587	
1136.3964		1911.5859*		2232.7964		2581.9336		2986.1050		3487.2631	
1257.4226		1912.6662		2242.6469*		2592.9415		3017.0996		3544.2846	
1282.4543*		1937.6979		2243.8042		2594.9459		3036.1023*		3556.3210	
1298.4492		1952.6125*		2245.8086		2596.9252		3045.1309		3558.3002	
1419.4754		1953.6928		2271.8355		2608.9364		3047.1101		3560.2795	
1444.5071*		1955.6972*		2286.8352		2610.9408		3049.0894		3588.3108	
1460.5020		1993.6390*		2302.8301		2613.9486		3109.1187*		3633.3210	
1485.5337*		1994.7193		2304.8345*		2667.9623		3120.1265		3636.3037	
1501.5286		1996.7238*		2318.8250		2669.9667*		3122.1309		3674.3476	
1542.5552		2012.7187*		2320.8294*		2685.9616*		3124.1353*		3702.3789	
1581.5282		2022.7506		2330.8614		2742.9831*		3130.1585		3704.3330	
1588.5606		2028.7136		2346.8563		2754.9943		3132.1629		3709.3452	
1606.5599*		2057.6438		2377.8509*		2756.9987		3179.1524		3734.3687	
1647.5865*		2058.7242		2387.8828		2814.0202		3198.1551*		3779.3888	
1663.5814		2083.7558		2389.8621		2830.0151		3255.1766*		3836.4004	
1688.6131*		2095.5856*		2391.8665		2832.0195*		3264.1800		3850.3909	
1704.6080		2099.7507		2393.8458		2840.0471		3266.1844		3852.3953	
1734.6158		2101.7551*		2417.8934		2842.0515		3268.1888		3855.4031	
1743.5810		2127.7820		2419.8978		2858.0464		3270.1681*		3880.4266	
1750.6134		2139.6969*		2448.8880		2873.0461*		3323.2059		3982.4583	
1791.6489		2140.7773		2464.8829		2890.0444*		3325.2103			
1809.6393*		2156.7722		2466.8873*		2899.0729		3328.2181*			
1850.6659*		2158.7766*		2474.9149		2901.0522		3332.2790			
1866.6608		2174.7715*		2507.9139*		2903.0566		3410.2379			
1891.6925*		2184.8035		2523.9088*		2906.0393*		3469.2638			

Galactose (Hex)
 Mannose (Hex)
 N-acetylglucosamine (HexNAc)
 N-acetylgalactosamine (HexNAc)
 Fucose (dHex)
 2,3-Sialic Acid (2,3NeuAc)
 2,6-Sialic Acid (2,6NeuAc)

Table S3. Summary table of N-glycan structures cumulatively detected across all analyzed tissues. A key to the monosaccharide unit symbols is provided in the bottom right. N-glycan structures denoted with a * indicates that the presence of a core fucose residue has been confirmed via analysis

using Endo F3. It is important to note that the representative structures provided do not encompass all possible isomeric conformations for these N-glycans, but are the most likely based on previous reporting, orthogonal analyses and the available biosynthetic pathways.

Centroid [m/z]	Both CA19.9 and sTRA		CA19.9		sTRA		Neither CA19.9 nor sTRA	
	Fold Change	Intensity	Fold Change	Intensity	Fold Change	Intensity	Fold Change	Intensity
1079.3749	0.5580	1030.2615	0.5620	1013.5629	0.7529	799.8649	0.0691	681.6336
1136.3964	0.6459	676.5595	0.3493	637.1259	0.7473	578.7372	0.7534	556.2163
1257.4226	0.1402	2654.0624	-0.0147	2351.0033	0.3208	2490.4892	0.0796	2039.8801
1282.4543	0.3096	2313.2134	0.3698	2365.8460	0.6335	2372.4875	0.3087	1953.0532
1298.4492	0.2279	3618.3780	0.0596	3606.5293	0.4242	3475.8308	0.5033	3542.7250
1419.4754	-0.0708	4435.2276	0.0448	4359.8460	-0.0115	4282.9775	-0.0462	4038.3505
1444.5071	0.2024	6781.2728	0.2931	7440.2953	0.6529	7254.8175	0.4100	6397.8605
1460.5020	0.4495	1261.6067	0.2437	1421.0725	0.8493	1163.6526	0.5832	1078.5609
1485.5337	0.3397	4496.9126	0.1656	4925.8533	0.7496	4141.5008	0.5373	3847.4355
1501.5286	0.4488	3504.0746	0.1823	3252.7713	0.5833	3217.3858	0.6136	3322.8205
1542.5552	0.6699	631.8115	0.0037	479.5078	0.5234	704.8998	0.2051	472.3477
1581.5282	0.2772	3565.8188	0.2526	3591.4847	0.3927	2961.3900	0.1304	2688.9080
1606.5599	0.3671	940.9854	0.4849	1080.3293	0.9305	1025.6925	0.6006	931.9258
1647.5865	0.2576	10790.2408	0.2137	11085.4327	0.4937	11279.3008	0.3803	11031.1855
1663.5814	0.2230	47111.1360	0.0303	48719.1733	0.4207	45885.2833	0.5582	48841.2200
1688.6131	0.0528	2952.7942	-0.2663	2889.9897	0.5822	3677.0442	0.0743	2442.0707
1704.6080	0.9186	2452.2669	0.3307	2116.1872	1.1304	1949.8679	0.8319	1476.5198
1743.5810	-0.0583	8841.7870	0.0148	8836.4647	-0.0550	7861.5800	-0.1055	7811.1225
1791.6489	0.4449	3437.4208	0.5246	4130.0147	1.1472	2999.8529	0.5074	2359.7695
1809.6393	0.2343	126072.3760	0.3589	145564.3267	0.7564	141867.2083	0.5121	119715.5000
1850.6659	0.4498	13157.5664	0.1981	13928.0233	0.8493	14265.8200	0.5151	11948.0795
1866.6608	0.6915	5408.9500	0.3092	4009.2933	0.8292	4745.9275	0.6856	5016.9438
1891.6925	0.0593	771.5054	0.2295	1007.8143	-0.1452	546.2488	-0.7741	468.9750
1905.6338	-0.3614	4891.3512	-0.1989	5941.8553	-0.0484	4008.0575	-0.1055	4541.7310
1911.5859	0.0774	9652.6898	-0.2242	10247.3253	0.2193	9037.3833	0.6677	11668.2585
1955.6972	-0.2590	7289.5402	-0.0843	7869.6207	-0.0750	6896.1758	-0.3268	6893.2070
1996.7238	0.8381	4608.1824	0.6761	3736.5147	0.5950	3428.9295	-0.2268	2940.5792
2012.7187	0.4143	43498.1460	0.3009	45450.9400	0.9035	51220.2250	0.4612	38769.4650
2028.7136	0.4012	9839.5872	0.2221	10008.1940	0.7816	9078.7983	0.8338	9383.0765
2057.6438	0.0535	18426.9780	0.1073	21937.0833	0.4448	20046.7167	0.5167	21521.1305
2101.7551	-0.0692	7501.7748	0.0102	8503.1773	0.6562	7969.7775	0.2302	7388.0085
2158.7766	0.4011	11363.7478	0.3342	9282.0100	-0.0345	7989.2683	-0.5551	7531.1735
2174.7715	0.2815	53484.7100	0.4252	57246.1800	0.7232	64477.1917	0.5321	59652.0200
2215.7980	0.9590	4382.5464	0.5851	4778.4880	1.2673	3955.2642	0.4642	3491.0819
2232.7964	0.9598	4320.7963	0.8038	3384.2840	1.4892	2737.8392	0.8888	2981.5574
2304.8345	0.8943	6529.6180	0.9264	6704.9727	0.5532	3284.2436	-0.2947	3249.5261
2320.8294	-0.1965	6459.7967	-0.1060	6053.7300	0.1800	5034.5917	-0.4141	5075.9610
2377.8509	0.4545	16636.5238	0.2718	14331.7167	0.9078	18517.2333	0.2226	17797.5590
2393.8458	0.5722	4319.5450	0.4443	4369.4367	1.2084	3761.7533	1.2048	3747.1576
2466.8873	-0.2042	8261.3122	-0.1177	8194.9387	0.2008	8662.9767	-0.3248	8401.9900
2507.9139	0.6044	2482.9564	0.8787	2573.6232	-0.4874	1244.8233	-0.7505	1571.1613
2523.9088	0.6238	8240.1160	0.4511	6913.1740	0.5957	5074.2350	-0.5965	4028.8324
2539.9037	0.0839	34950.5440	0.2730	34169.4800	0.5440	47457.7000	0.3586	46961.3775
2581.9336	0.9281	3156.8733	0.4690	3384.8950	0.8477	2477.0816	0.2002	3008.1229
2613.9486	-0.5574	1040.7924	-0.1643	1097.4909	-1.0460	1052.5307	-1.6169	1427.1412
2669.9667	1.2122	3157.0727	0.8713	3087.5575	0.5335	865.8589	-0.6530	927.7440
2685.9616	-0.3670	6207.3348	-0.2400	5973.3425	-0.0170	5614.4558	-0.6943	5776.5140
2742.9831	0.9924	11120.2304	0.8345	10064.4913	1.9265	8673.5875	0.5077	5522.0960
2832.0195	-0.3598	7215.8054	-0.3907	6264.5160	-0.0894	7355.2933	-0.6649	7728.5317
2890.0444	1.1449	5095.1726	0.4796	4355.5224	1.0930	1939.7393	-0.6336	1792.3854
2906.0393	0.3592	13588.1608	0.5779	16725.3580	1.1644	16365.6783	1.0149	14296.7880
2979.0808	-0.7050	2110.1836	-0.8280	3538.4809	-0.7391	1756.5904	-1.4827	2281.3808
3036.1023	0.9367	12185.8834	0.6211	7251.7120	0.2973	6190.2181	-0.7168	5473.1566
3109.1187	0.7600	3619.1301	0.8687	3715.9760	0.6550	3580.1689	0.4216	3847.6254
3124.1102	-0.0703	1367.6939	-0.2554	1744.9258	-0.2194	1498.8243	-0.9417	1624.6381
3198.1551	-0.5800	4070.1716	-0.4382	4077.9780	-0.6499	5322.4083	-0.9959	4366.8126
3255.1766	0.4646	4019.1874	0.3279	3363.3185	0.2530	2510.7031	-0.5447	2158.0608
3270.1681	0.3299	2498.8385	0.7281	3600.9105	1.3078	3232.0292	0.7372	2983.1392
3328.2181	0.9078	6558.7212	1.1305	6332.3680	-0.0396	3531.0183	-0.1763	3367.1860
3636.3037	0.0741	7494.0596	0.4479	8220.9520	0.4143	10278.0333	0.2161	10434.0220
3709.3452	-0.6620	2239.3698	-0.7074	2430.1141	-0.7433	3195.2648	-1.0279	2632.6308
3855.4031	-0.4590	2145.1399	-0.5476	1865.9784	-0.7010	3220.6986	-0.9423	3064.2660

Table S4. Log₂FC and AUP intensity data for biomarker-classified TMA core groupings. Log₂FC of area under the peak (AUP) measurements for 62 N-glycan masses between individual patient normal and tumor cores were calculated then averaged for the 4 biomarker-designations. Positive values represent enrichment in tumor tissue. Shown too are the average tumor AUP intensities for each N-glycan in each category.

Table S5. Log₂FC and AUP intensity data for AA-stabilized TMA cores. Log₂FC of area under the peak (AUP) measurements for 84 AA-stabilized sialylated N-glycan masses between individual patient normal and tumor cores were calculated then averaged for the 4 biomarker-designations. Positive values represent enrichment in tumor tissue. Shown too are the average tumor AUP intensities for each sialylated N-glycan in each category.

Annotation of Reported N-glycan Structures by CID Fragmentation

timsTOF Flex MALDI-QTOF MS/MS Settings

Transfer

Funnel 1 RF: 425.0 Vpp
 Funnel 2: RF: 500.0 Vpp
 Multipole RF: 550.0 Vpp
 Deflection Δ : 70.0 V
 MALDI Plate Offset: 50.0 V

MS Settings

Scan Begin: 50 *m/z*
 Scan End: 2500 *m/z*
 Ion Polarity: Positive
 Scan Mode: MS/MS
 Laser Shots: 400
 Laser Power: 36%
 Frequency: 10000 Hz

Pre-TOF Focus

Transfer Time: 72.0 μ s
 Pre-Pulse Storage: 12.0 μ s

Collision Cell

Collision Energy: 25.0 eV
 Collision RF: 1500.0 Vpp

Quadrupole

Ion Energy: 4.0 eV
 Low Mass: 150 *m/z*

CID Settings

Isolation Width: 10.00 *m/z*
 Collision Energy: 150.00 eV

Notes on CID

CID fragmentation of 23 N-glycan base structures representing a mix of both core and terminally-fucosylated bi-, tri- and tetra-antennary configurations with and without bisecting GlcNAc residues. Where applicable EndoF3 was used to trim higher-mass core-fucosylated N-glycans to improve CID performance

CID Legend

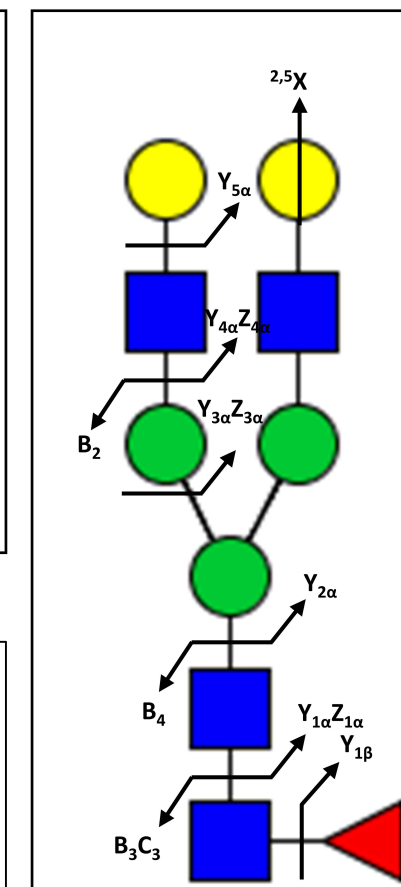
X,Y,Z ions

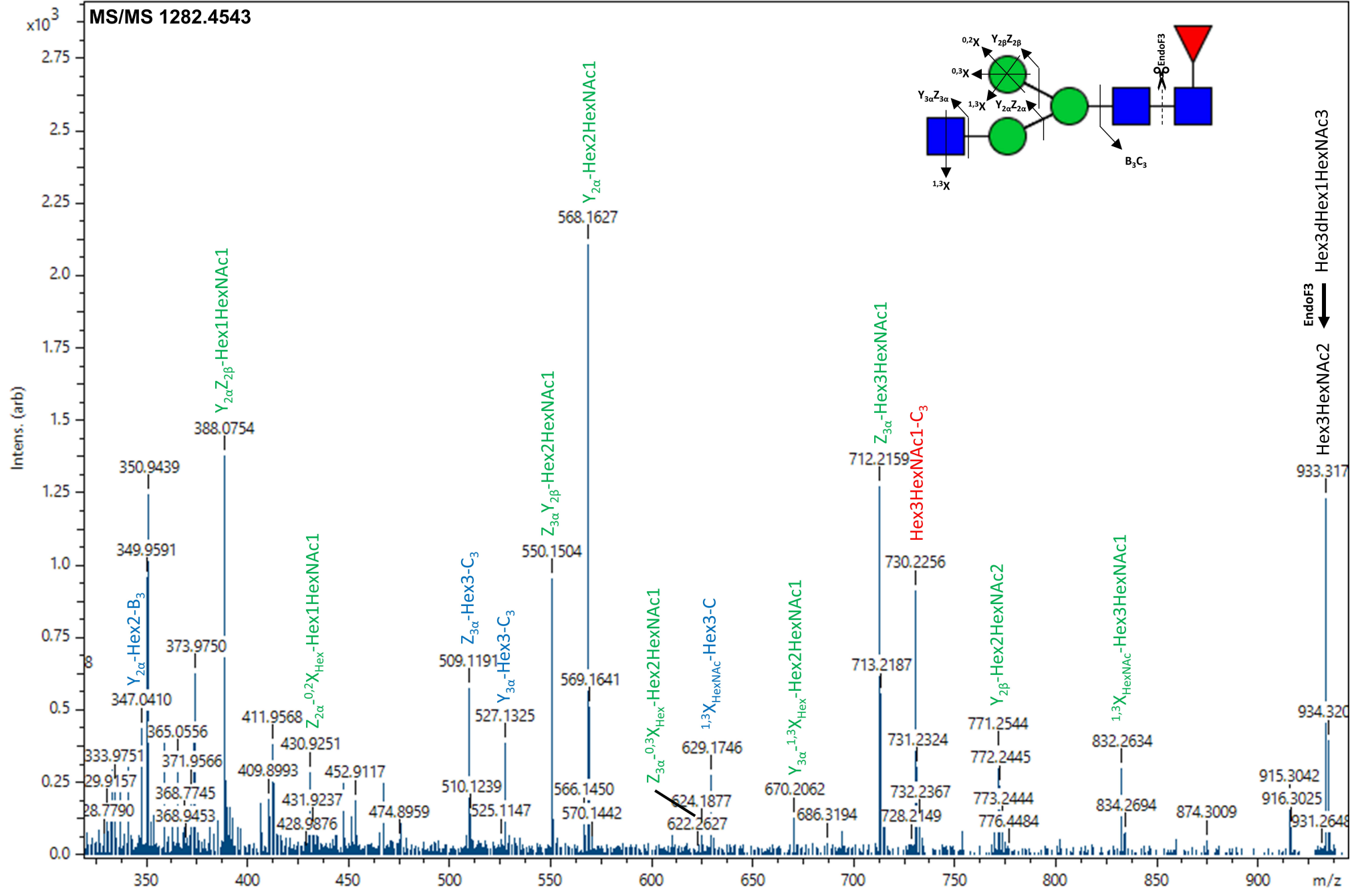
B,C ions

Intermixed X,Y,Z/B,C ions

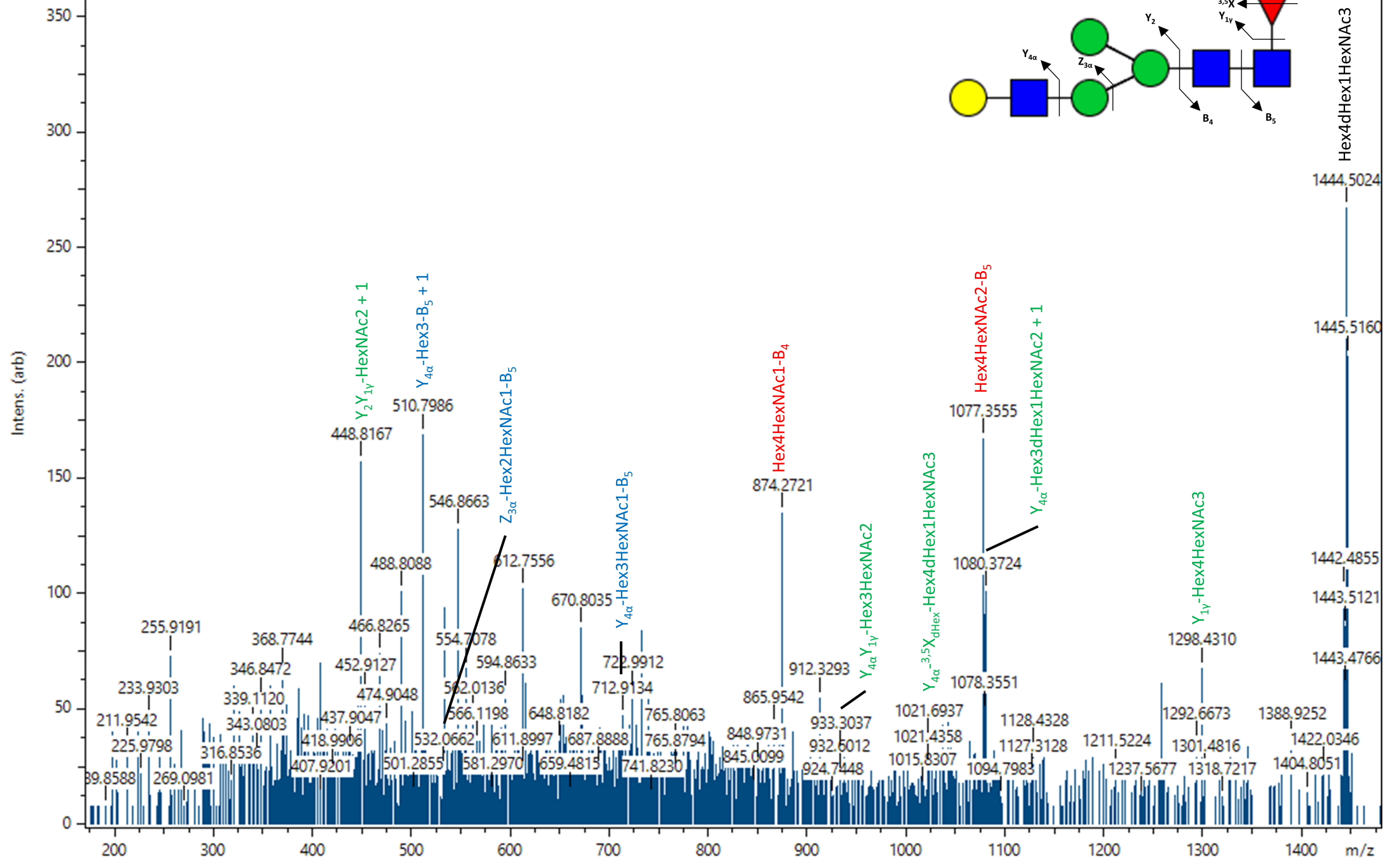
Precursor ions

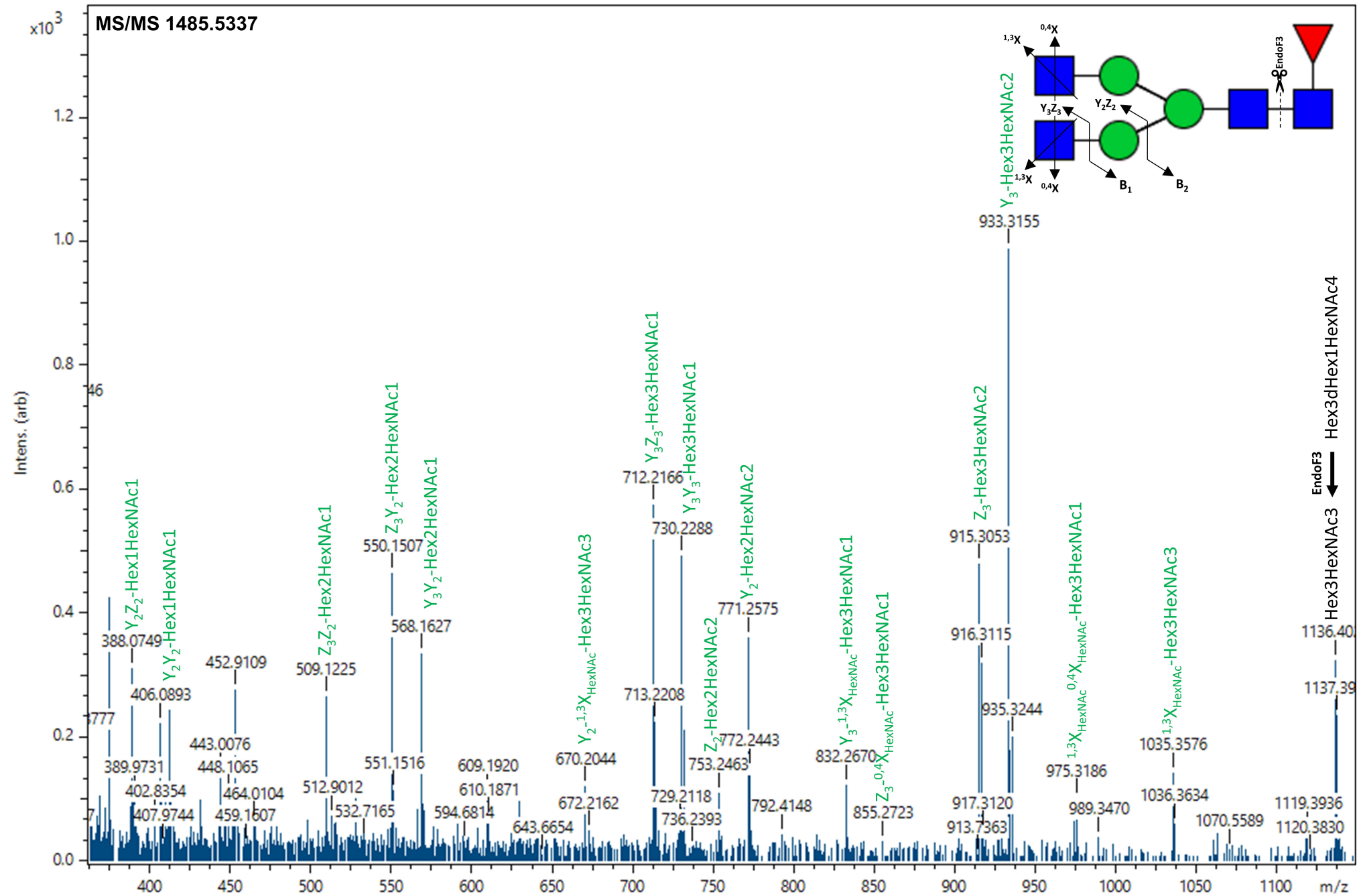
Example MS/MS

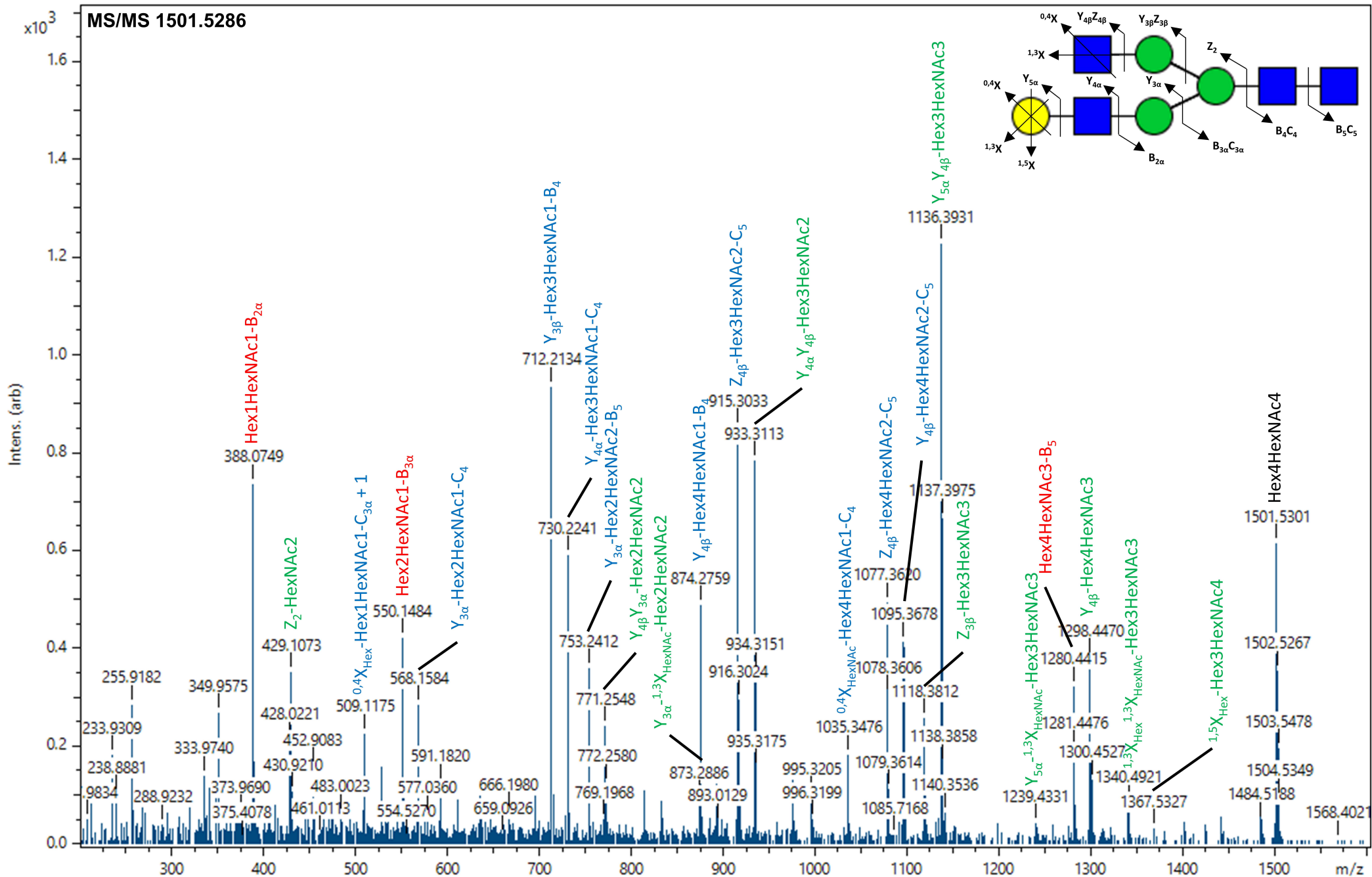




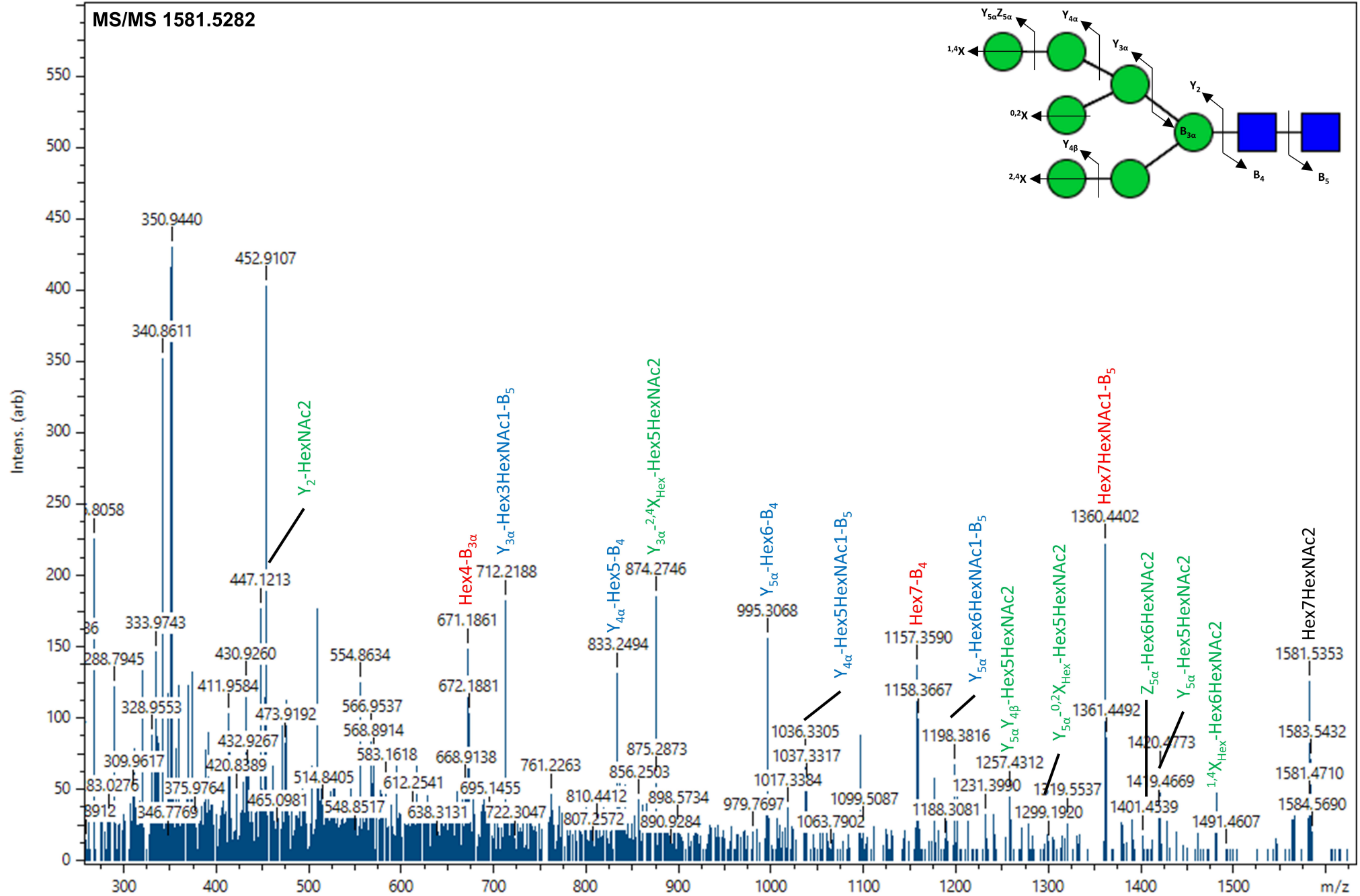
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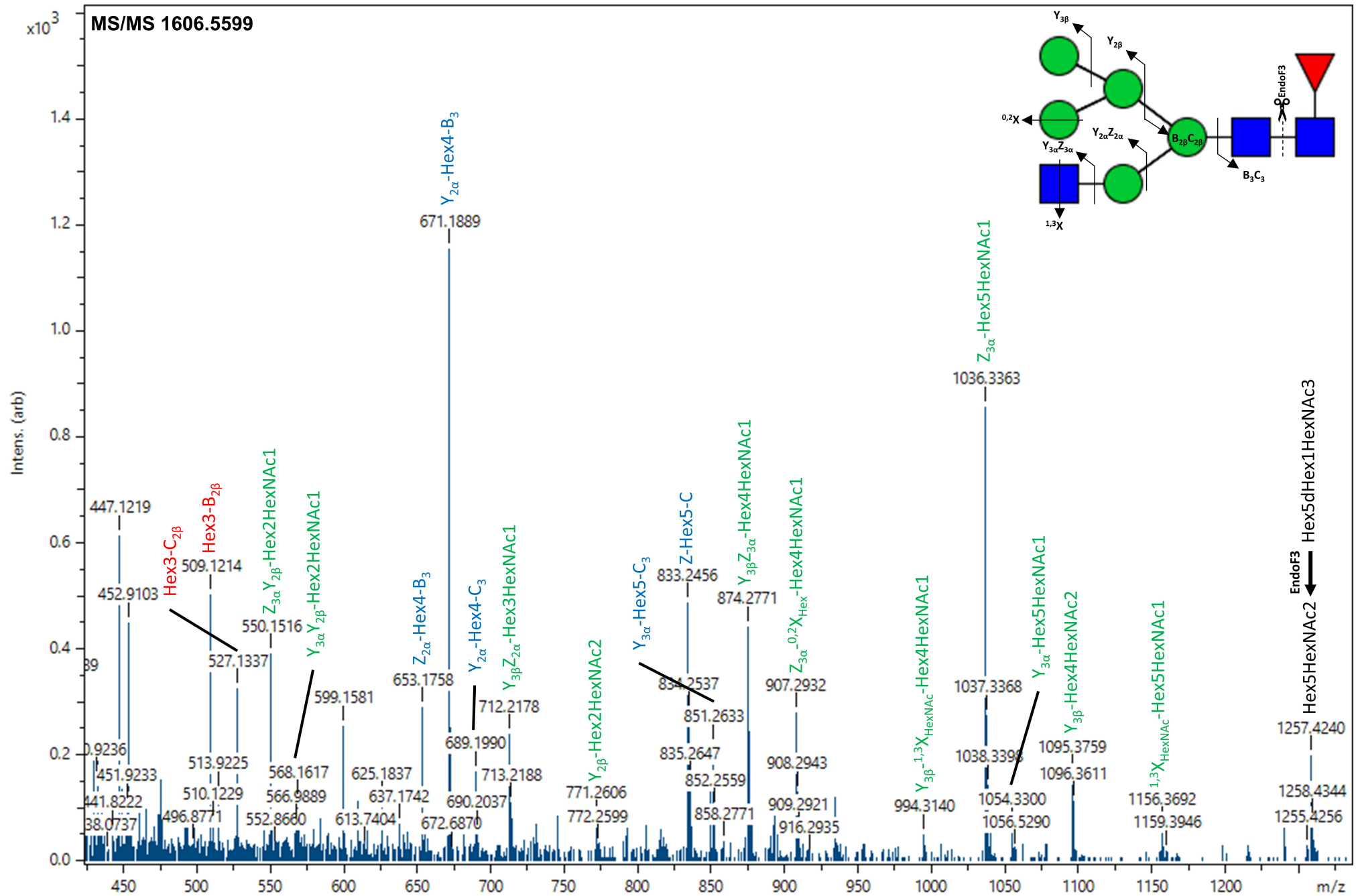


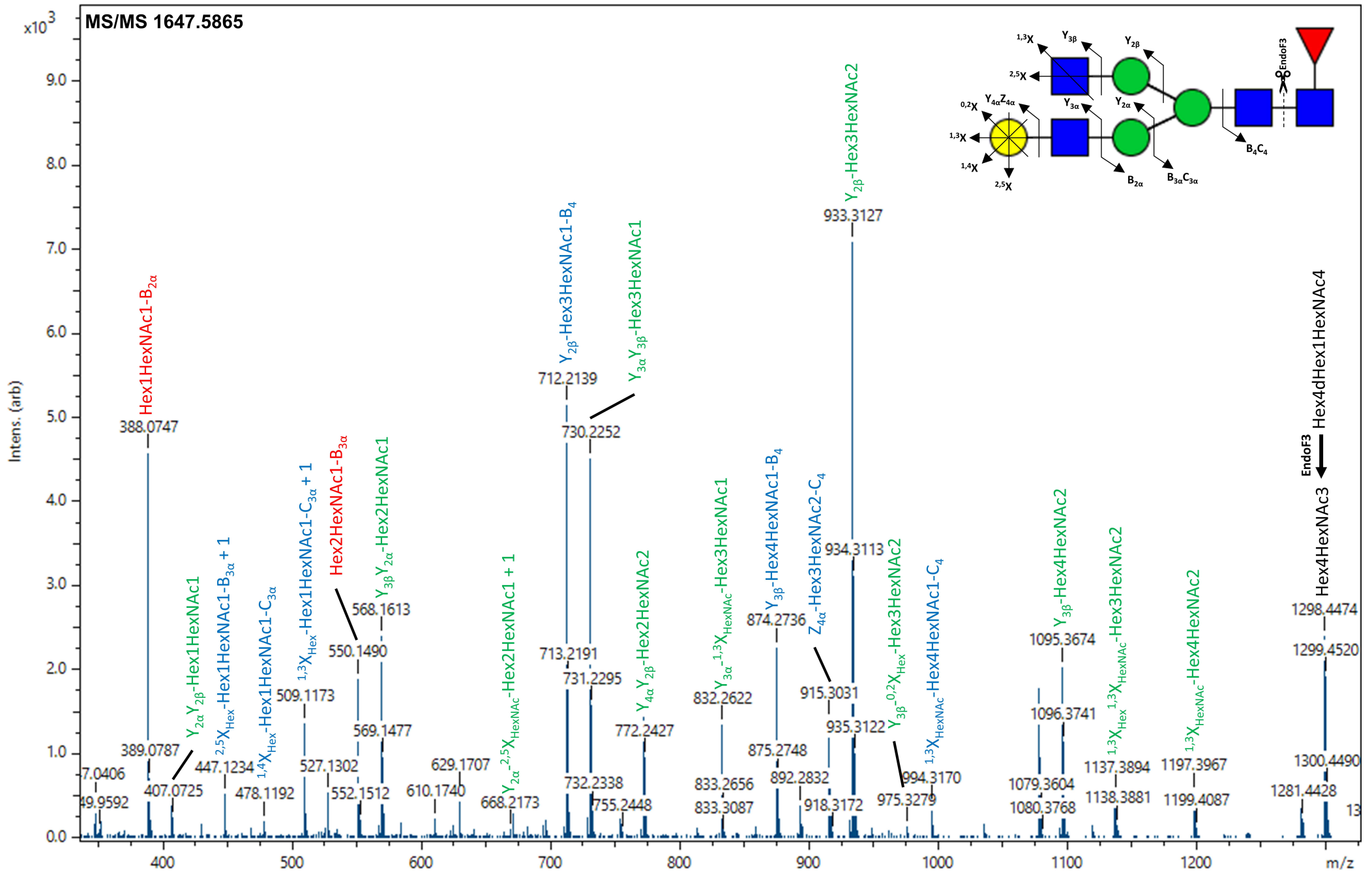




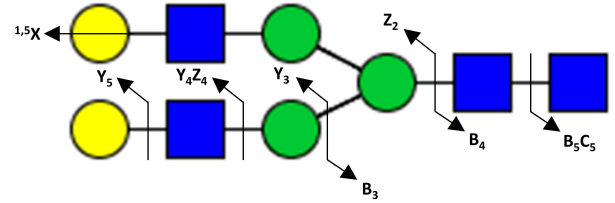
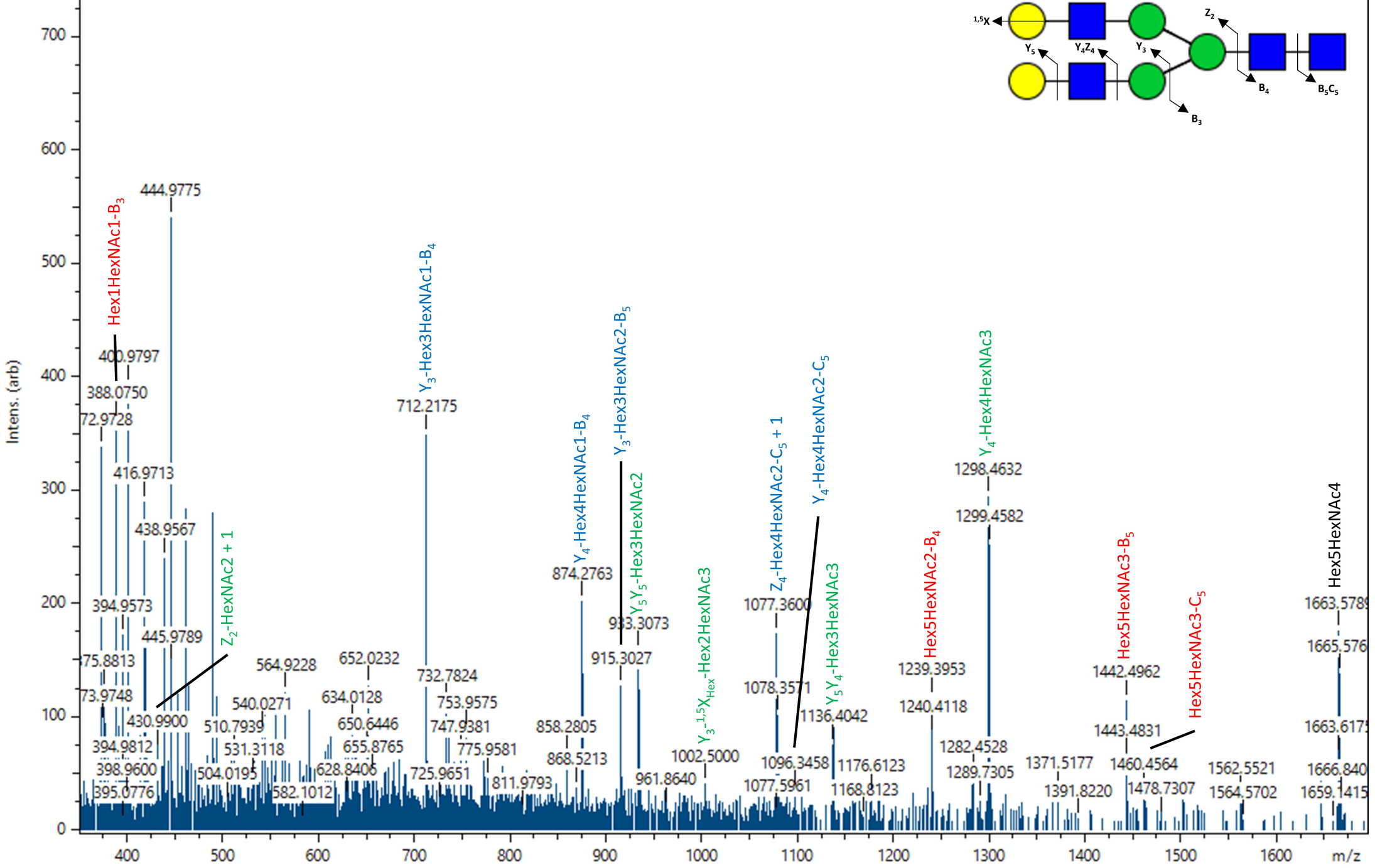
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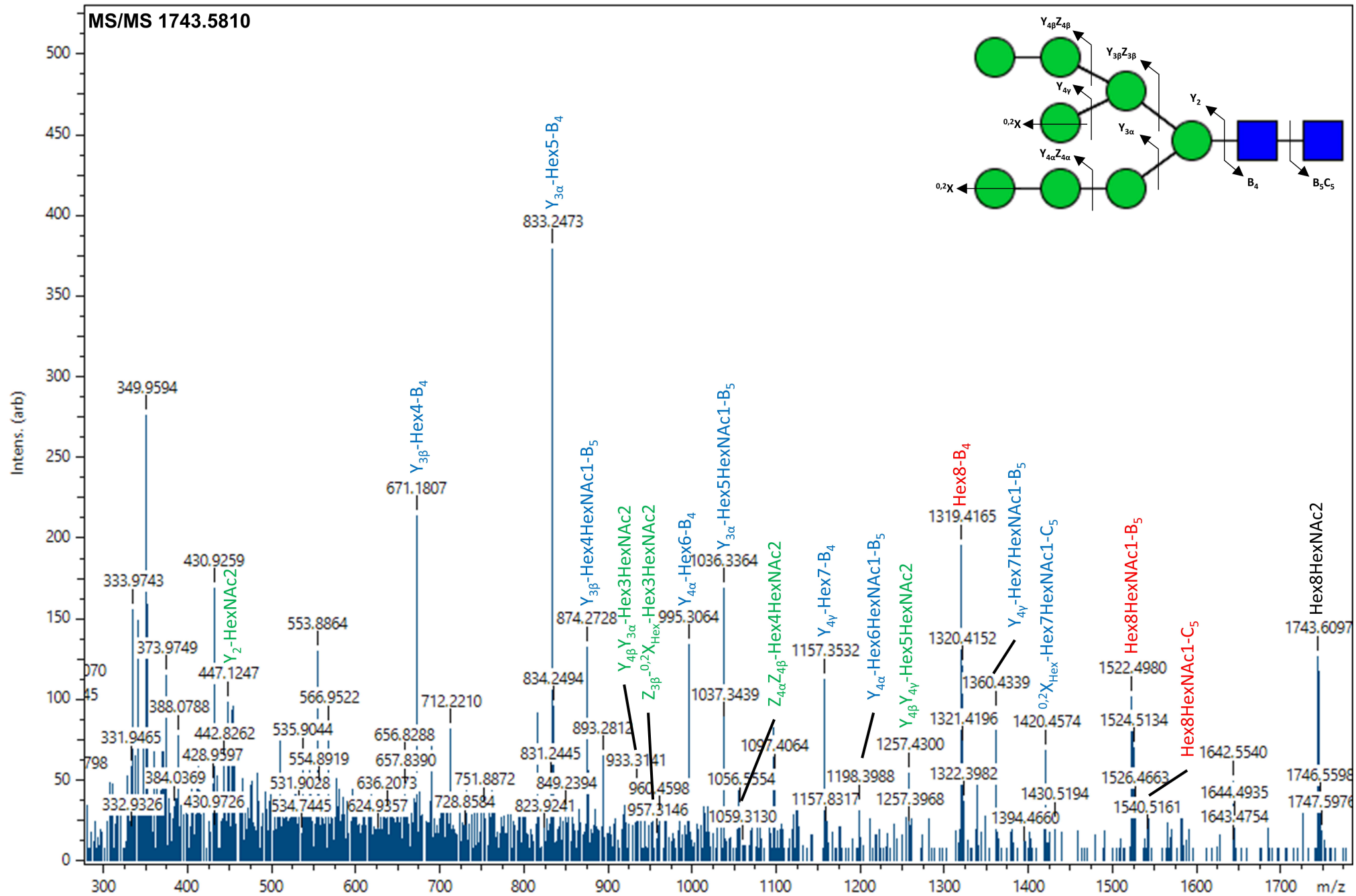


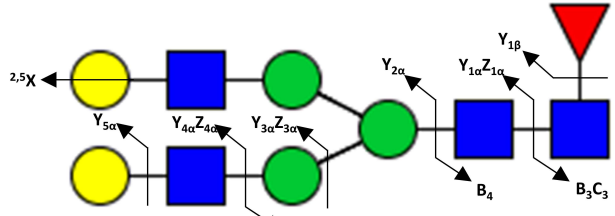
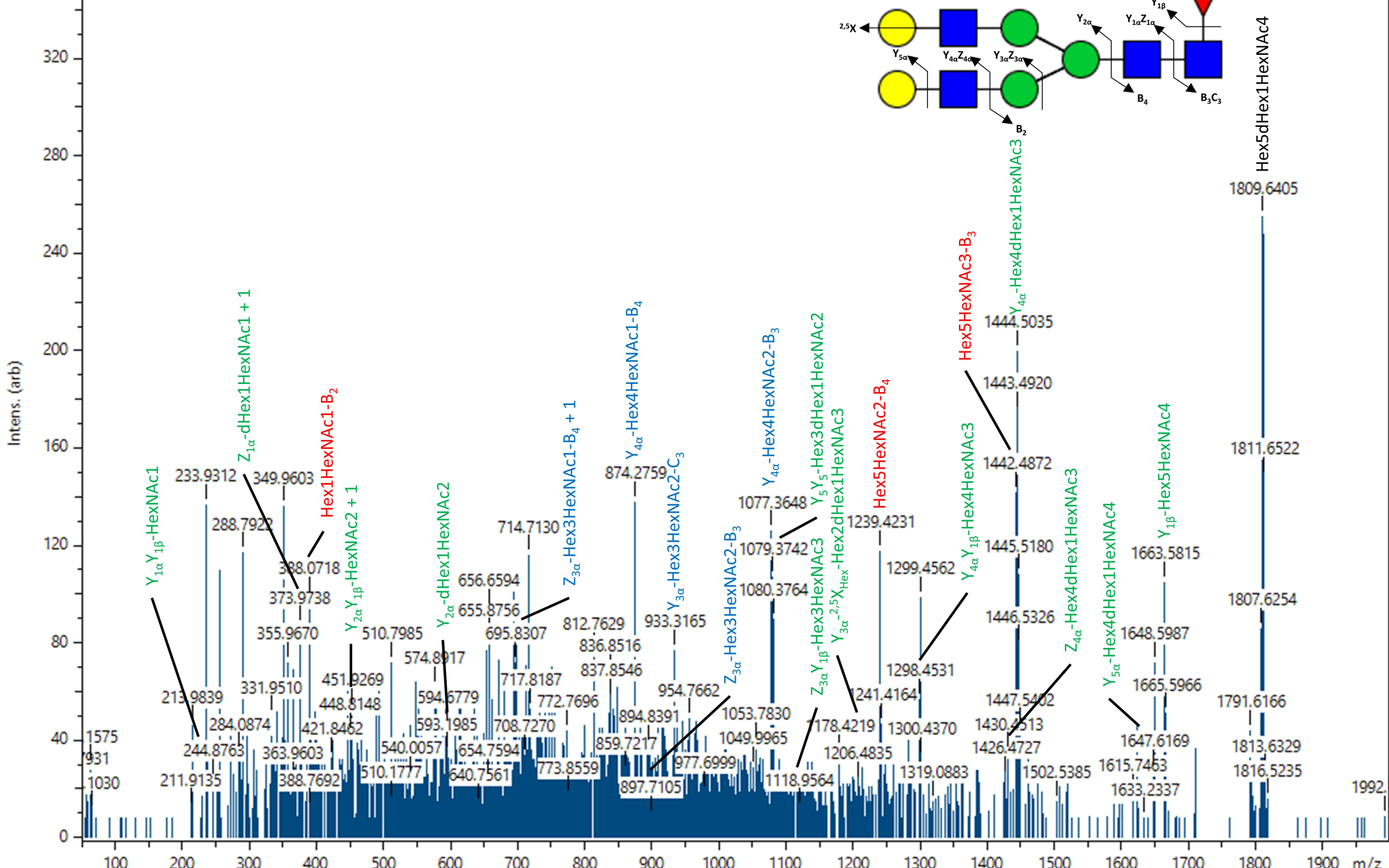


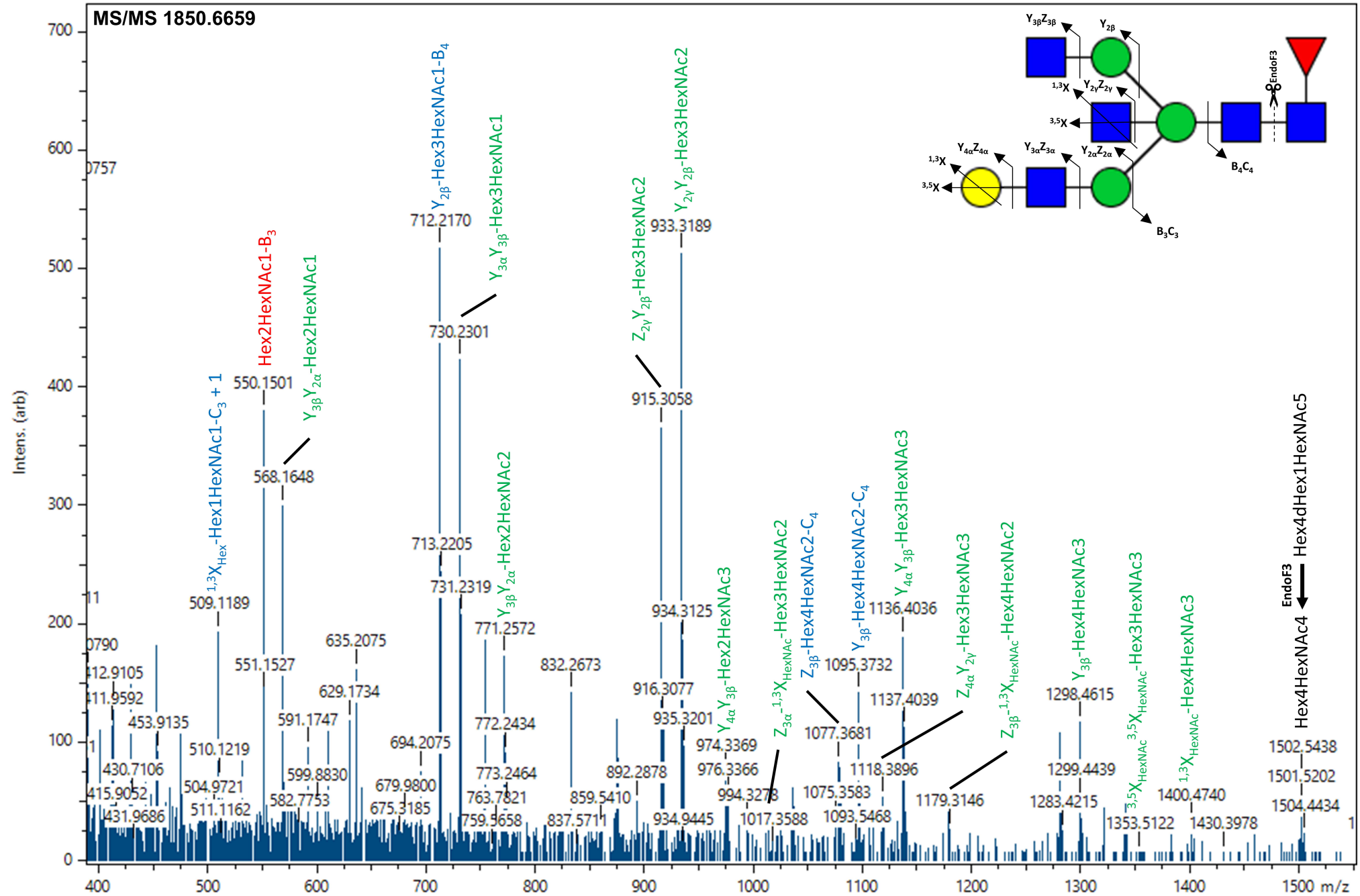
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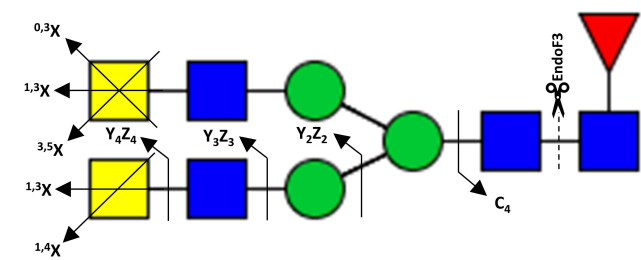
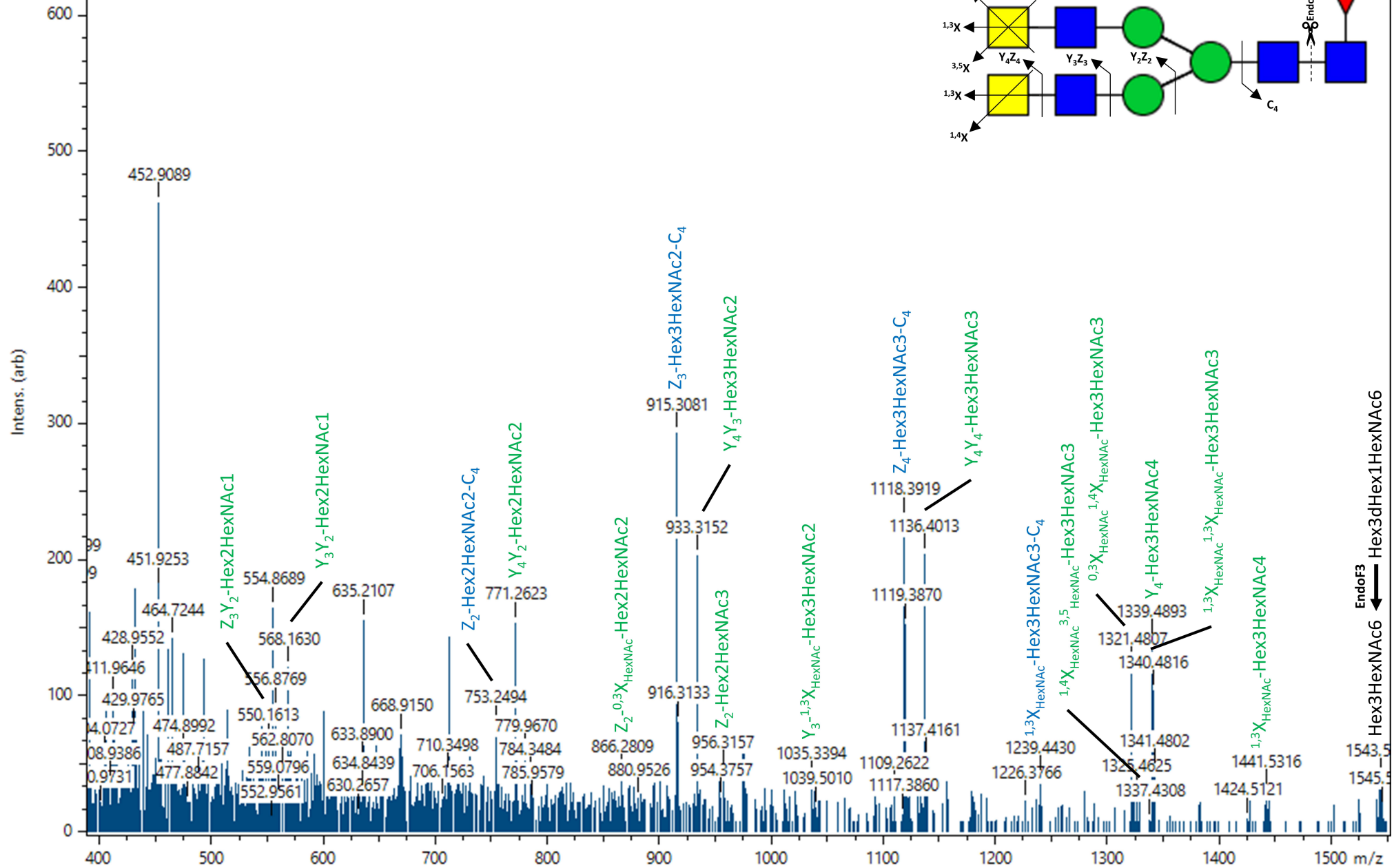
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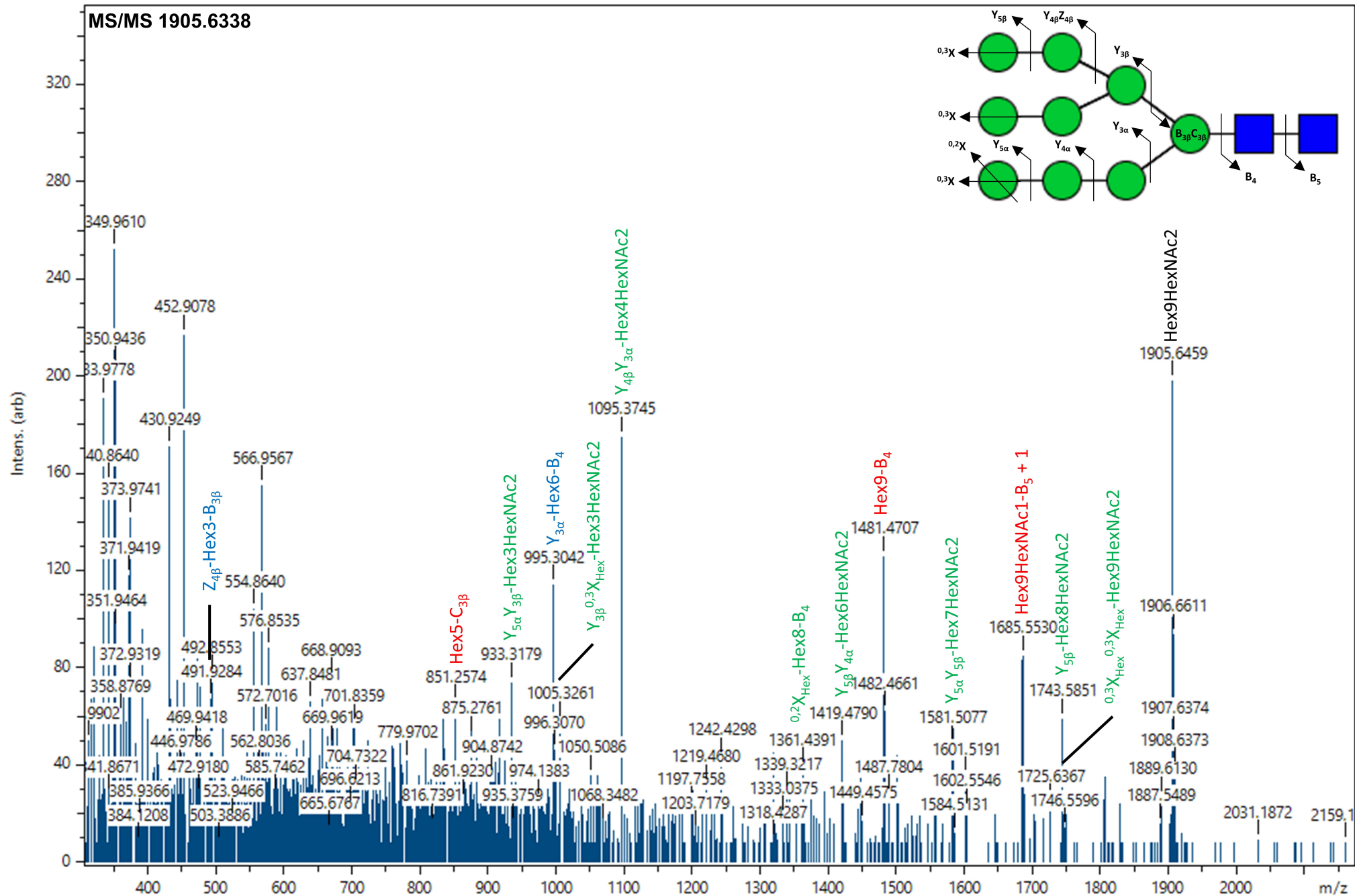




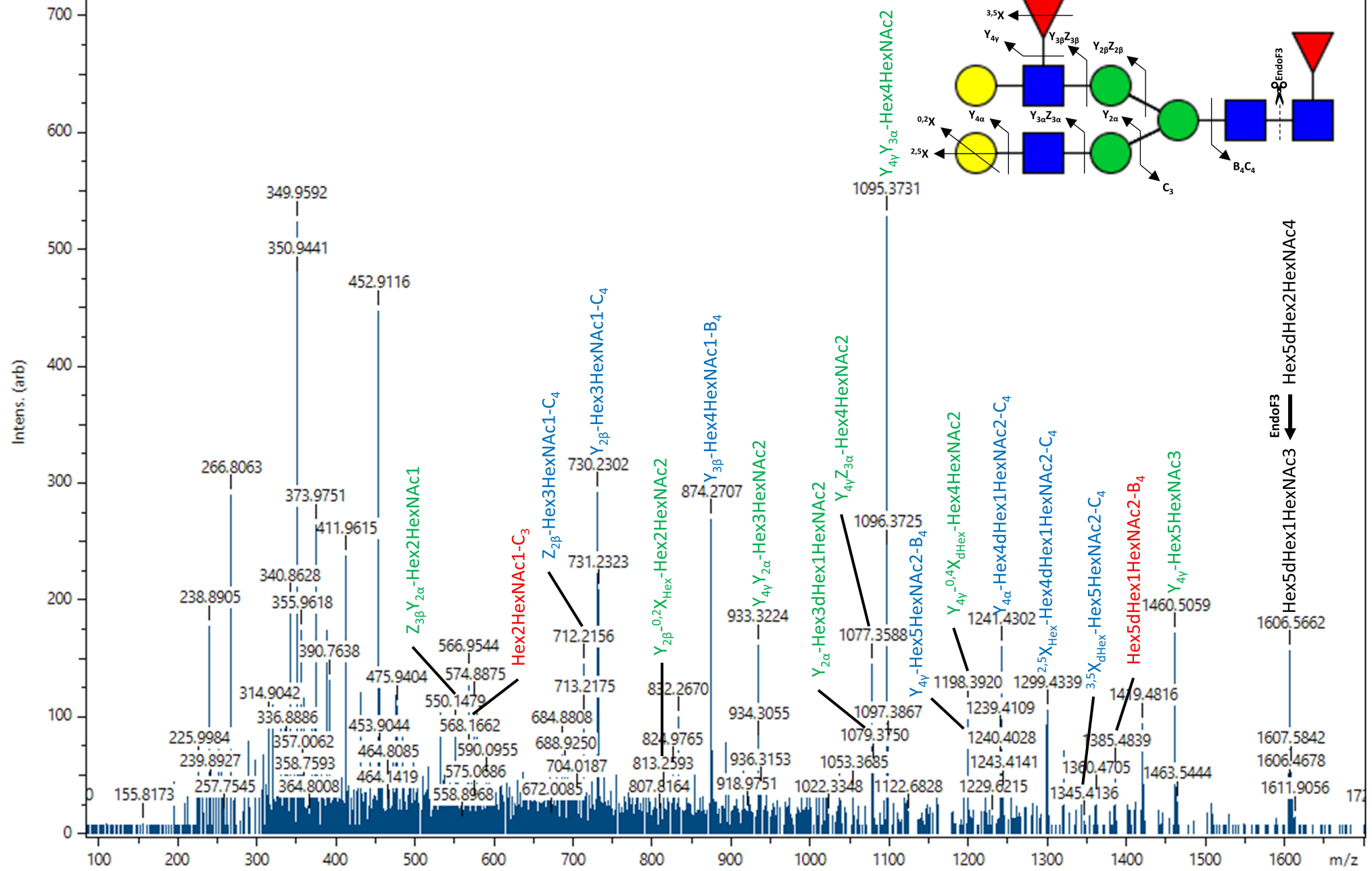
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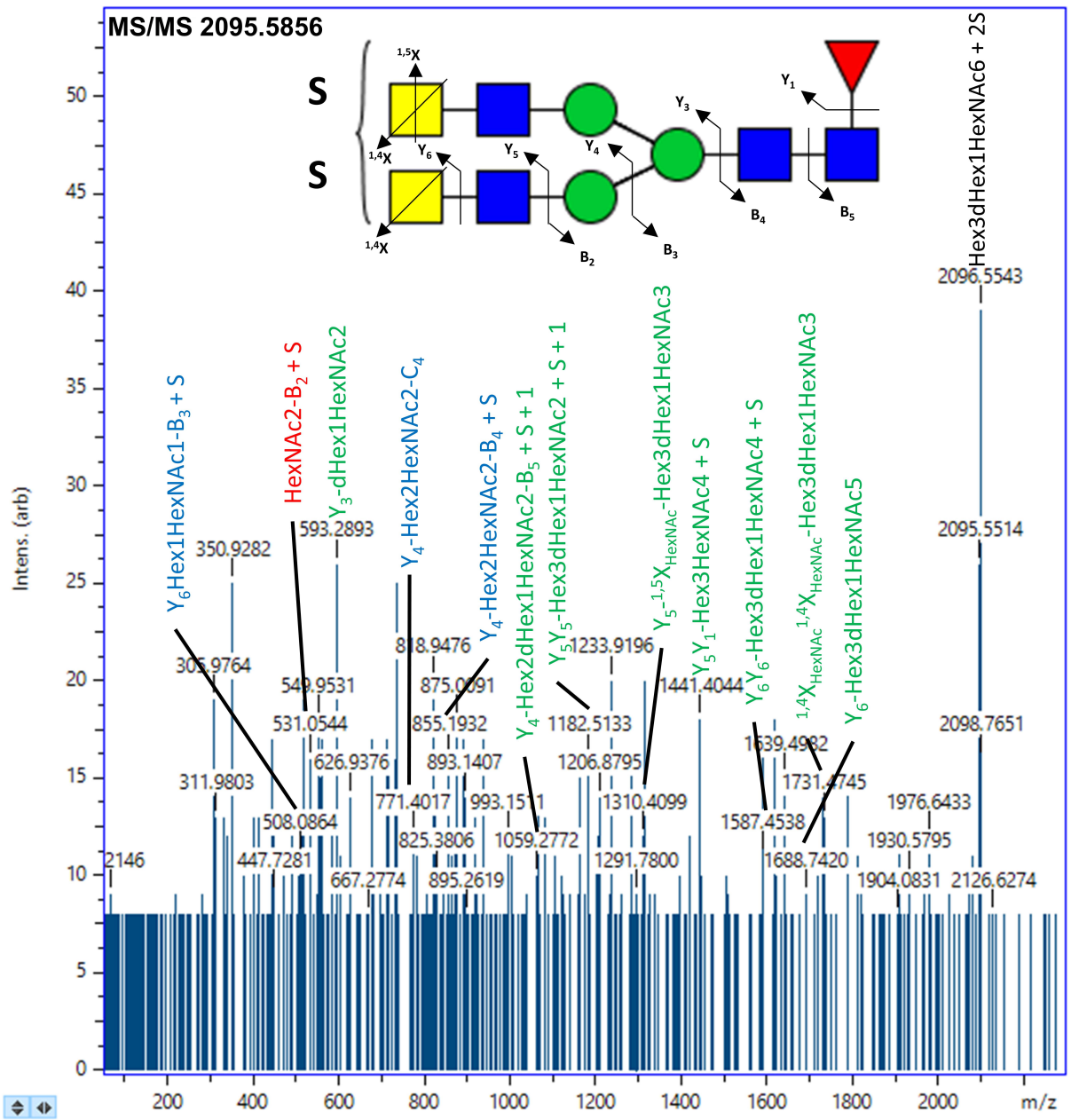
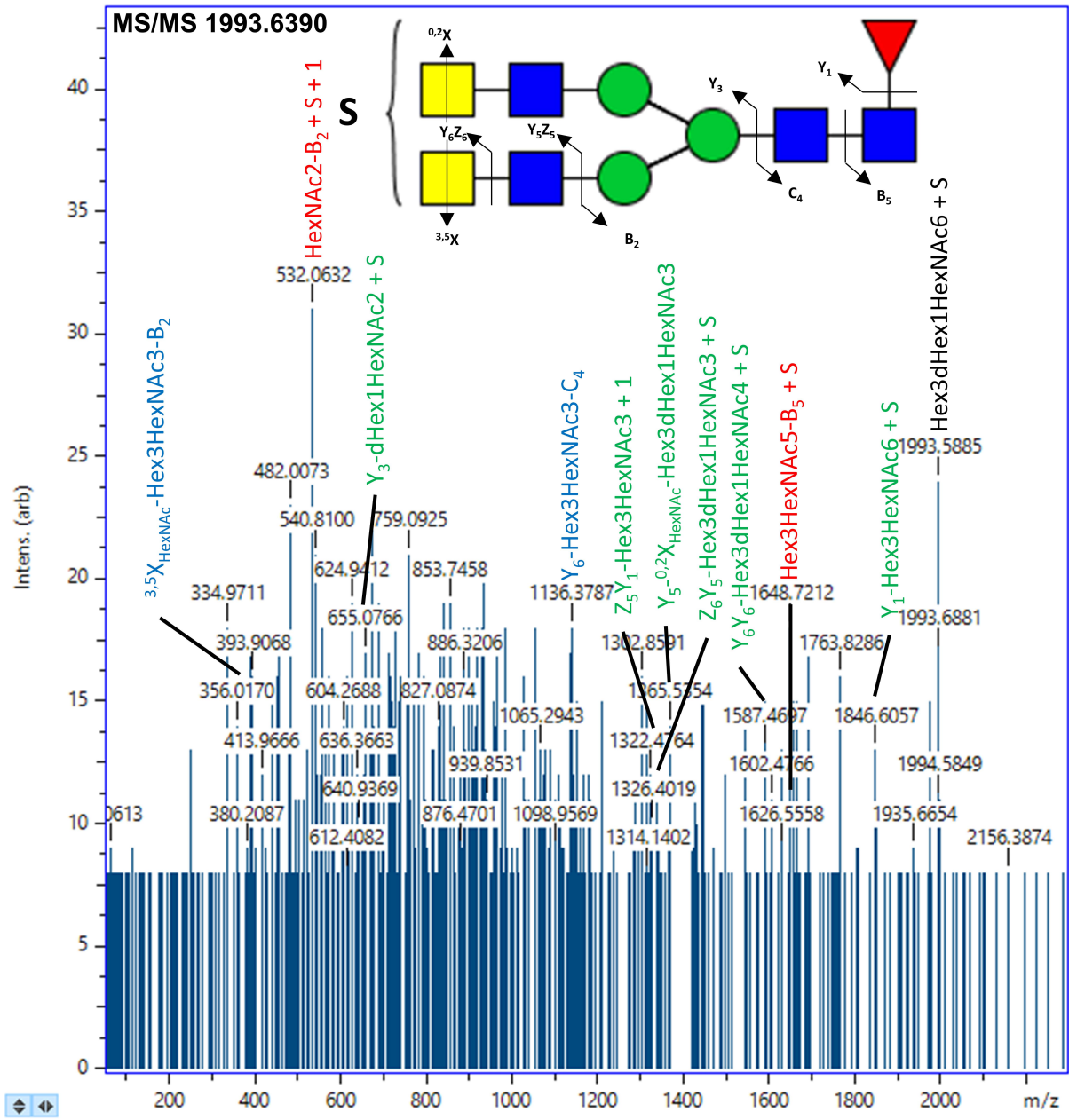


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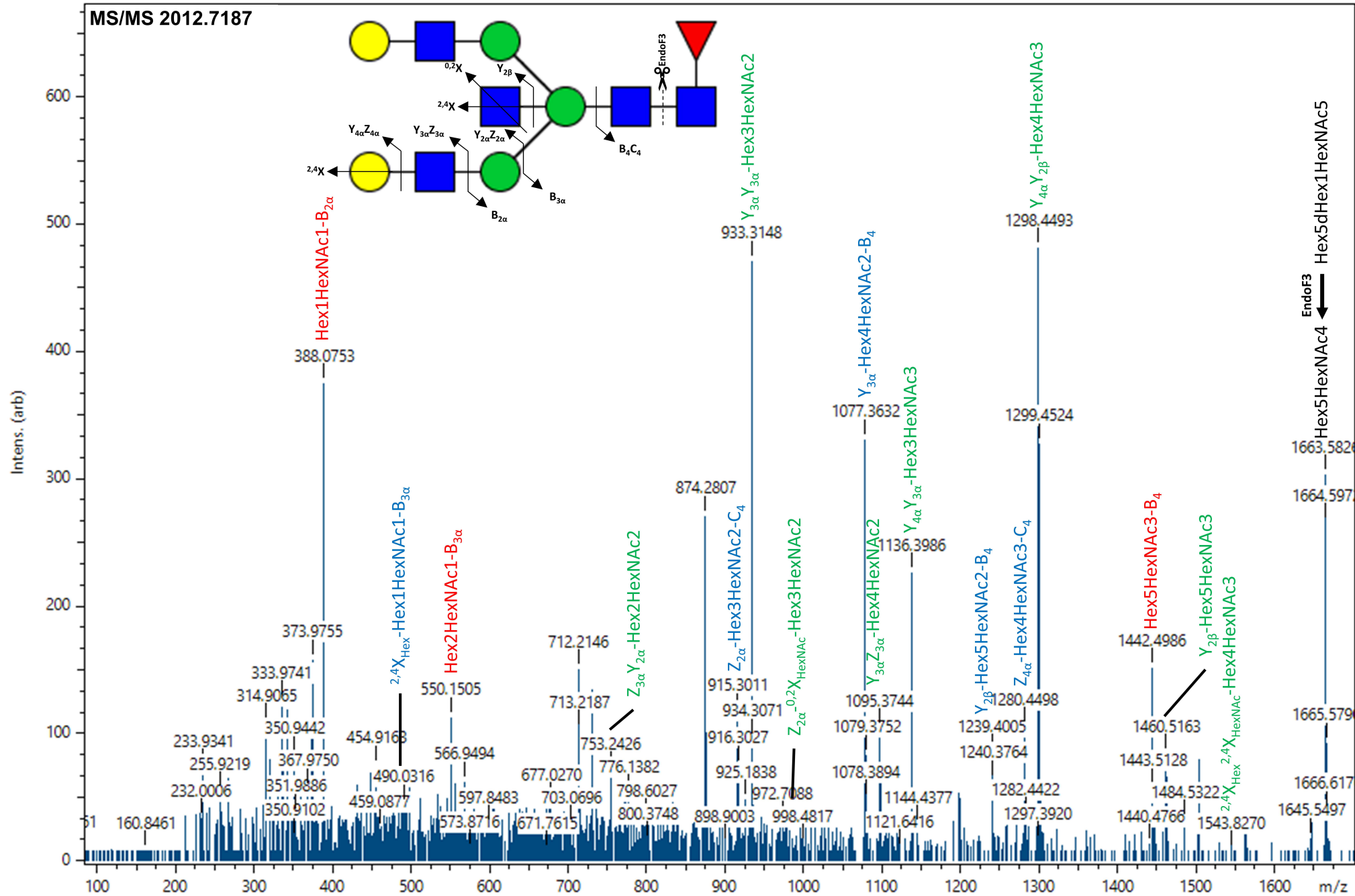


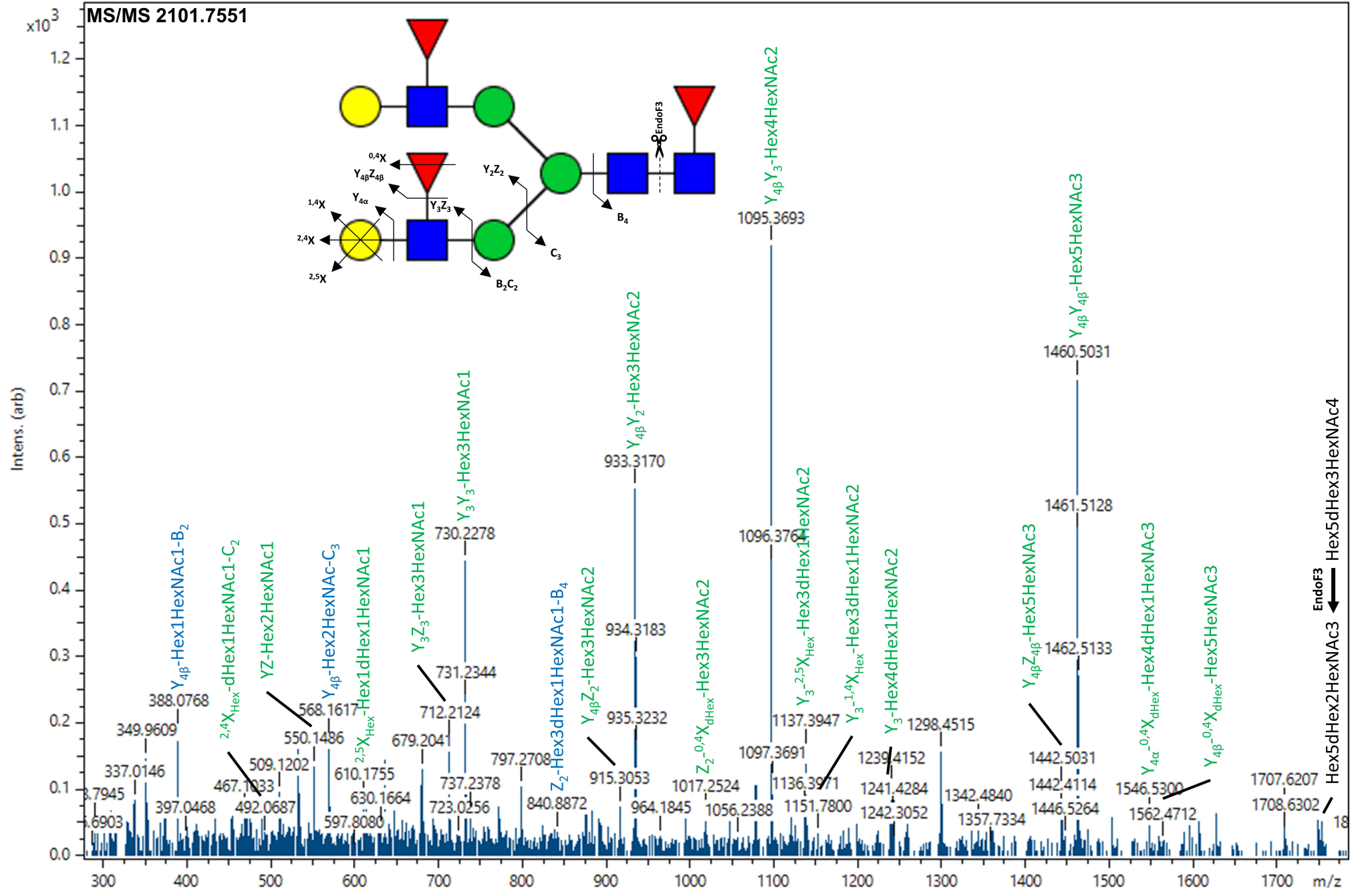
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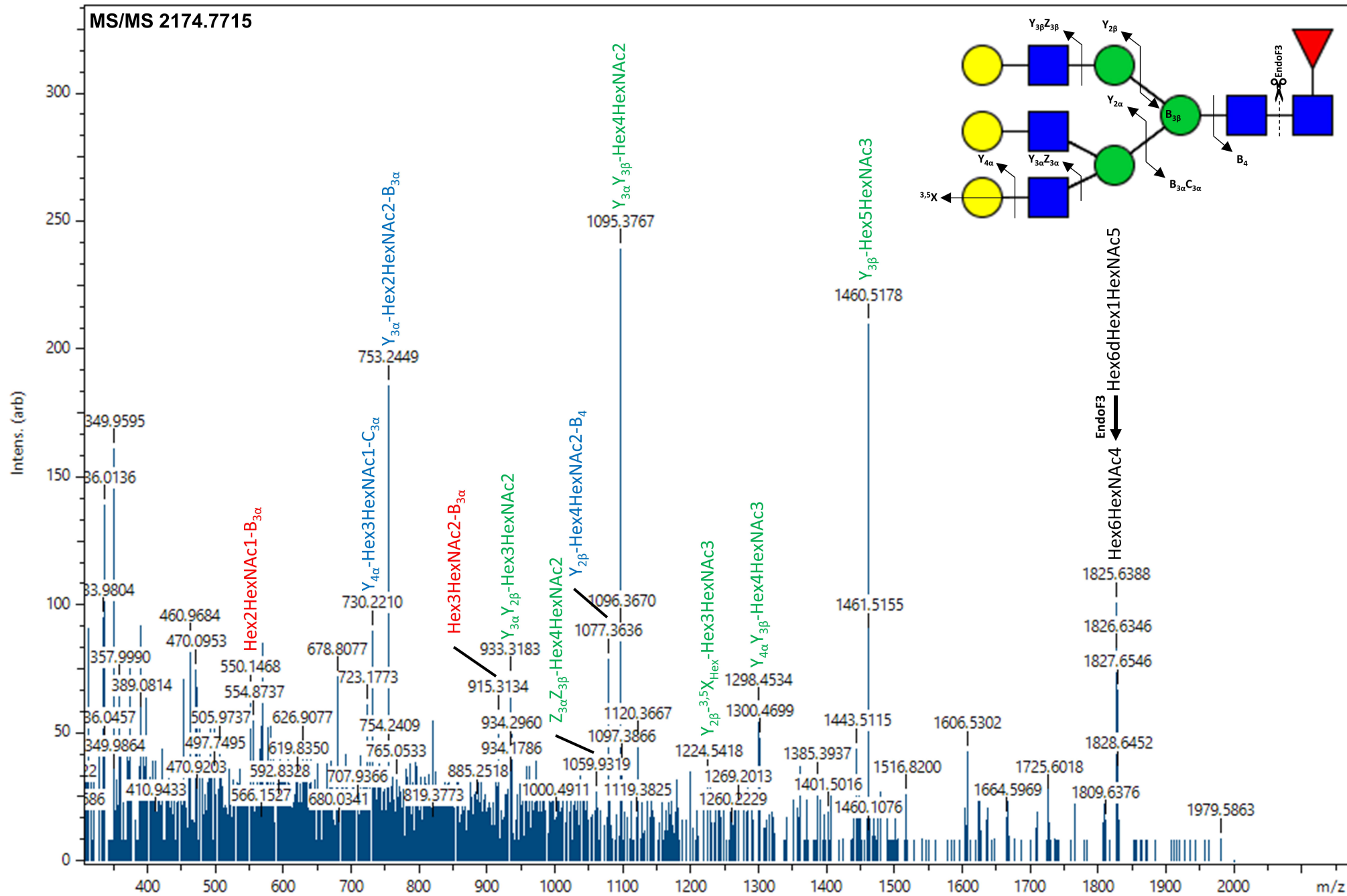


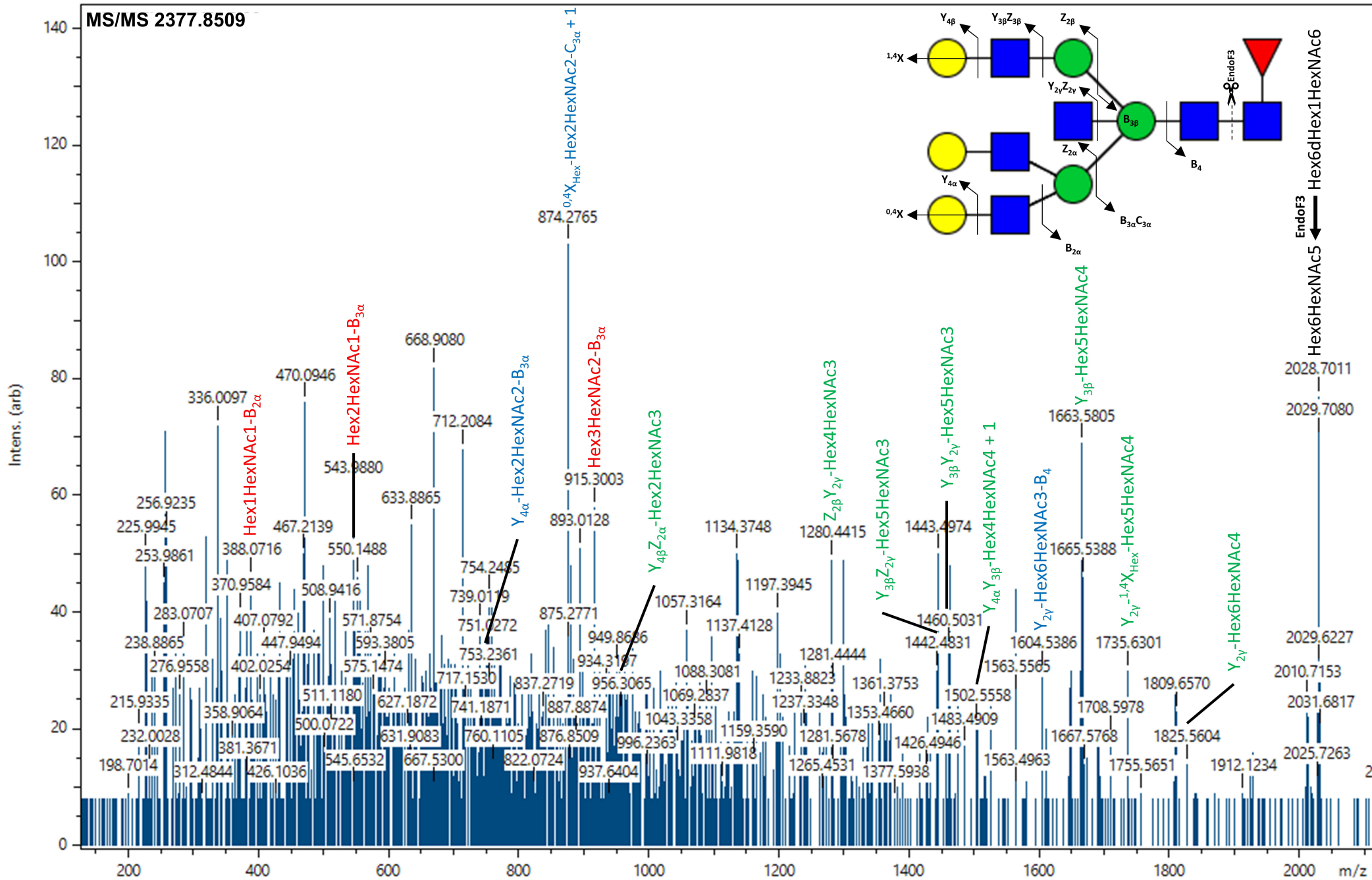
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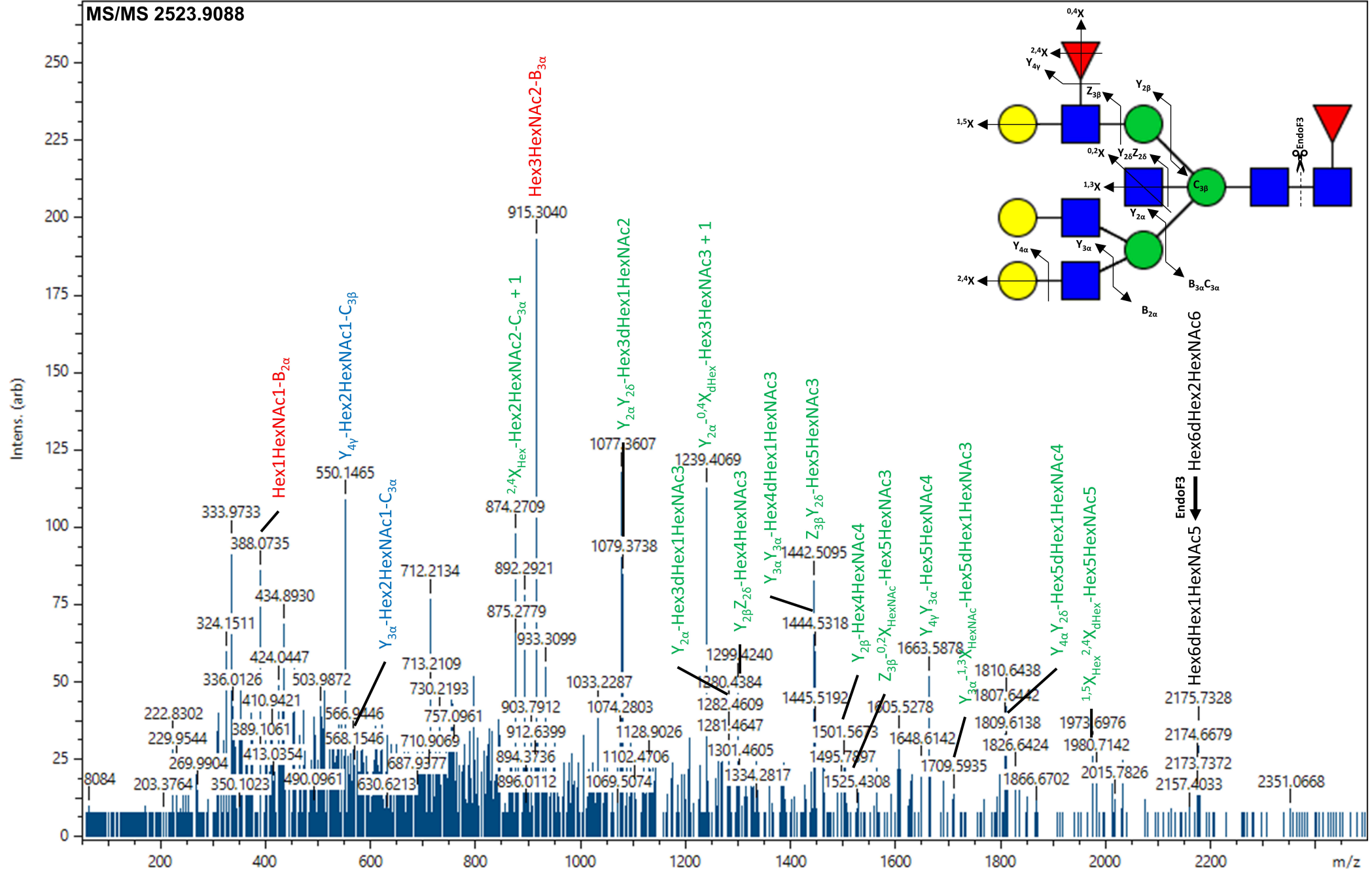


MS/MS 2174.7715

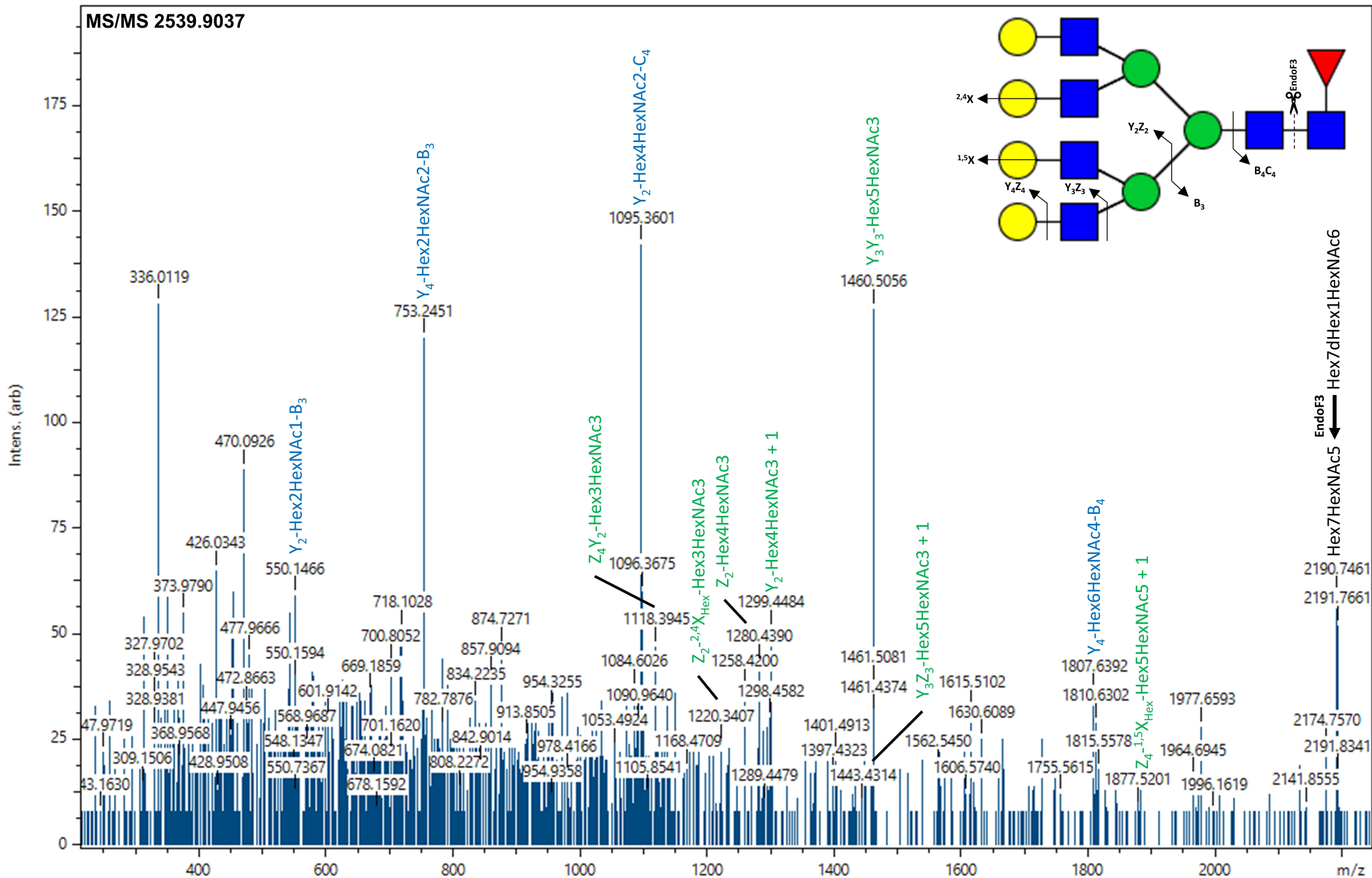




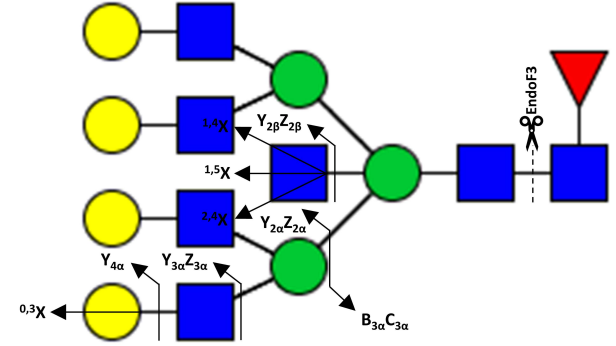
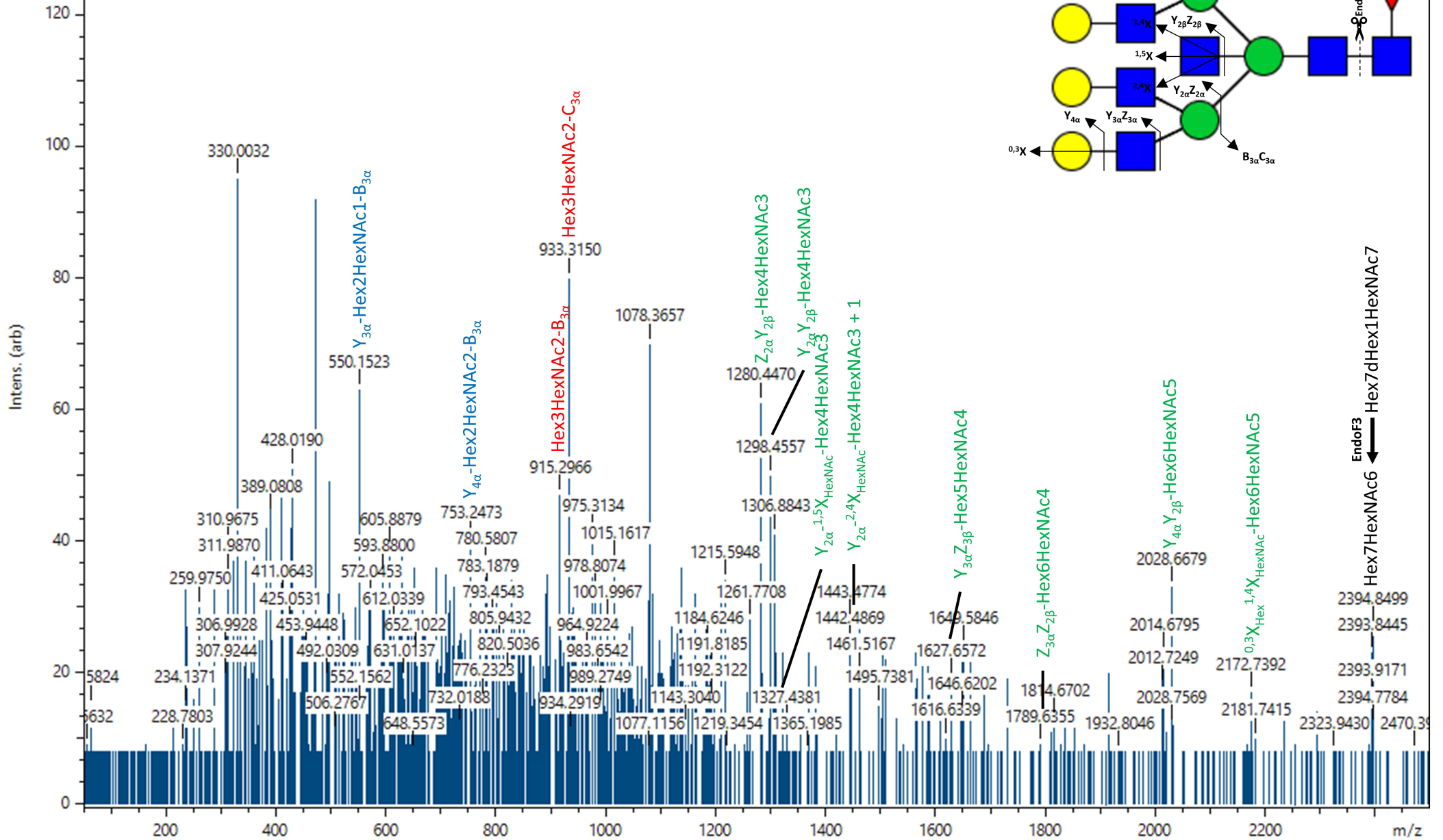
MS/MS 2523.9088



MS/MS 2539.9037



MS/MS 2742.9831



EndoF3 → Hex7HexNAc6 → Hex7dHex1HexNAc7