

Supplemental Figure and Table Legends

Supplemental Figure 1. Total ion current increases as a function of the number of multiple fills. A trace of total fragment ion current obtained upon fragmenting $[M+16H]^{16+}$ ions from recombinant H4 using a reaction time of 8 ms ETD, 20 ms IIPT as the number of multiple fragment ion fills is varied. Precursor m/z 703.4, 1 μ scan, r = 60,000, 1-20 multiple fills.

Supplemental Figure 2. Hand-annotated ETD/IIPT MS/MS spectra from Figure 1. Hand annotated MS/MS spectra of intact recombinant H4 (precursor charge state +16, m/z 703.40) following ETD (8 ms) and IIPT (20 ms) reactions with 1 and 20 fragment ion fills of the C-trap. Note, these are not exhaustive lists of fragments observed but rather those that are most abundant that are easily distinguishable. **(A)** Spectrum produced from a single iteration of ion/ion reactions (1 fill, 1 μ scan, r = 60,000 at 400 m/z, 0.56 sec elapsed scan time). **(B)** Spectrum produced from 20 iteration of ion/ion reactions (20 fills, 1 μ scan, r = 60,000 at 400 m/z, 6.24 sec elapsed scan time). **(C)** Spectrum produced by averaging 20 **(A)** spectra (1 fill, 1 μ scan, r = 60,000 at 400 m/z, 0.57 sec elapsed scan time/spectrum, 11.2 sec total acquisition time).

Supplemental Figure 3. ETD/IIPT MS/MS spectra recorded on intact H4. Precursor m/z 703.4, 1 μ scan, 15 multiple fills, r = 60,000, average of 5 spectra. **(A)** ETD spectrum recorded on $[M+16H]^{16+}$ ions from recombinant H4 using a reaction time of 6 ms. **(B)** Spectrum obtained by performing 20 ms IIPT reaction on the ETD-produced fragment ions in **A**. Precursor m/z 703.4, 1 μ scan, 15 multiple fills, r = 60,000, average of 5 spectra, elapsed scan time 3.62 sec (ETD only) or 4.73 sec (ETD/IIPT).

Supplemental Figure 4. Hand-annotated ETD/IIPT MS/MS spectrum from Figure 2.

ETD/IIPT spectrum recorded on $[M+19H]^{19+}$ ions from H2A type 1 (P0C0S8) using 4 ms ETD and 25 ms IIPT. Precursor m/z 738.0, 3 μ scans, 15 multiple-fills, r = 30,000, average of 6 spectra, 11.7 sec elapsed scan time/spectrum (~19.8 sec for single fill/transient equivalent spectrum). Note, these are not exhaustive lists of fragments observed but rather those that are most abundant that are easily distinguishable.

Supplemental Figure 5. Full MS spectrum indicated unique proteoforms of intact H2A identified by MS/MS. Averaged, high resolution full MS spectrum depicting sample heterogeneity. Proteoforms identified by MS/MS are indicated. All PTMs were site-localized (K5).

Supplemental Figure 6. Annotated ETD/IIPT MS/MS spectrum of intact H4 proteofrom. ETD/IIPT spectrum recorded on $[M+16H]^{16+}$ ions from H4 (P62805) containing 4 acetylated lysine residues (K4, K8, K12 and K16) along with K20 dimethylation using 4 ms ETD and 40 ms IIPT. Precursor m/z 718.0, 3 μ scans, 10 multiple-fills, r = 30,000, average of 8 spectra, 8.75 sec elapsed scan time/spectrum. The spectrum is renormalized to the largest peak in the subsection in increments of 250-750, depending on the density of the spectrum within each region. (A) m/z 220-750 & m/z 750-1250. (B) m/z 1250-1500 & 1500-1750. (C) m/z 1750-2000.

Supplemental Figure 7. ETD/IIPT MS/MS spectra recorded on intact H1 isoforms. (A) ETD/IIPT spectrum recorded on $[M+35H]^{35+}$ ions from H1.4 (P10412) using 2 ms ETD and 25

ms IIPT. Precursor m/z 623.1, 3 μ scans, 15 multiple fills, r = 30,000 average of 10 spectra, 11.6 sec elapsed scan time/spectrum. (B) Sequence coverage (~72%) obtained from MS/MS spectrum shown in A. (C) ETD/IIPT spectrum recorded on [M+36H]³⁶⁺ ions from H1.2 (P16403) using 2 ms ETD and 25 ms IIPT. Precursor m/z 609.0, 3 μ scans, 15 multiple fills, r = 30,000 average of 10 spectra, 11.6 sec elapsed scan time/spectrum. (D) Sequence coverage (~67%) obtained from MS/MS spectrum shown in C.

Supplemental Figure 8. Hand-annotated ETD/IIPT MS/MS spectrum from Figure 4. ETD/IIPT spectrum recorded on [M+23H]²³⁺ ions from H1.2 (P16403) with an undocumented single amino acid substitution (A141→T) using 4 ms ETD and 20 ms IIPT. Precursor m/z 927.5, 1 μ scan, 25 multiple-fills, r = 100,000 at 400 m/z, average of 11 spectra, 9.38 sec elapsed scan time/spectrum (27.6 sec for single fill/transient equivalent spectrum). Note, these are not exhaustive lists of fragments observed but rather those that are most abundant that are easily distinguishable.

Supplemental Figure 9. Expanded views of Figure 5 panel C. Expanded views of the m/z regions where +8 species A-E (Table 1) should be observed upon isolation. The distinct 0.125 m/z shift indicative of a +8 is only clearly observed in panels D and E (corresponding to species D and E, accordingly).

Supplemental Figure 10. Expanded view of m/z region containing intact histone H2B isoforms from Figure 5 panel D. Expanded view of m/z 2730-2800 region MS/MS spectrum

produced upon isolation of ions possessing m/z 790-830 and 140 ms IIPT with charge reduced precursor “parked” in the 2300-3900 m/z range.

Supplemental Figure 11. ETD/IIPT MS/MS spectrum recorded on truncated H2B proteoform. (A) ETD/IIPT spectrum recorded on $[M+15H]^{15+}$ ions from a truncated form of H2B (residues 26-125, possibly P62807) using 4 ms ETD and 40 ms IIPT. Precursor m/z 747.3, 3 μ scans, 10 multiple fills, r = 30,000 average of 5 spectra, 9.3 sec elapsed scan time/spectrum. (B) Sequence coverage (~90%) obtained from MS/MS spectrum shown in A.

Supplemental Figure 12. ETD/IIPT MS/MS spectra recorded on truncated H2A proteoforms. (A) ETD/IIPT spectrum recorded on $[M+11H]^{11+}$ ions from truncated H2A2A (residues 57-129, Q6FI13) using 8 ms ETD and 40 ms IIPT. Precursor m/z 733.7, 3 μ scans, 5 multiple fills, r = 30,000, average of 2 spectra, ~6.73 sec elapsed scan time/spectrum. Sequence coverage is also included. (B) ETD/IIPT spectrum recorded on $[M+6H]^{6+}$ ions from truncated H2A (residues 1-45, possibly Q6FI13) using 8 ms ETD and 40 ms IIPT. Precursor m/z 811.5, 3 μ scans, 5 multiple fills, r = 30,000, average of 2 spectra, ~6.41 sec elapsed scan time/spectrum. Sequence coverage is also included. (C) ETD/IIPT spectrum recorded on $[M+6H]^{6+}$ ions from truncated H2A (residues 1-44, possibly Q6FI13) using 8 ms ETD and 40 ms IIPT. Precursor m/z 799.5, 3 μ scans, 5 multiple fills, r = 30,000, average of 2 spectra, ~6.73 sec elapsed scan time/spectrum. Sequence coverage is also included. For all spectra, green circles indicate neutral losses from charge reduced precursor. Blue circles indicate other species that were co-isolated and charge reduced.

Supplemental Figure 13. LC-MS characterization of *in vitro* clipping of histone H2A type

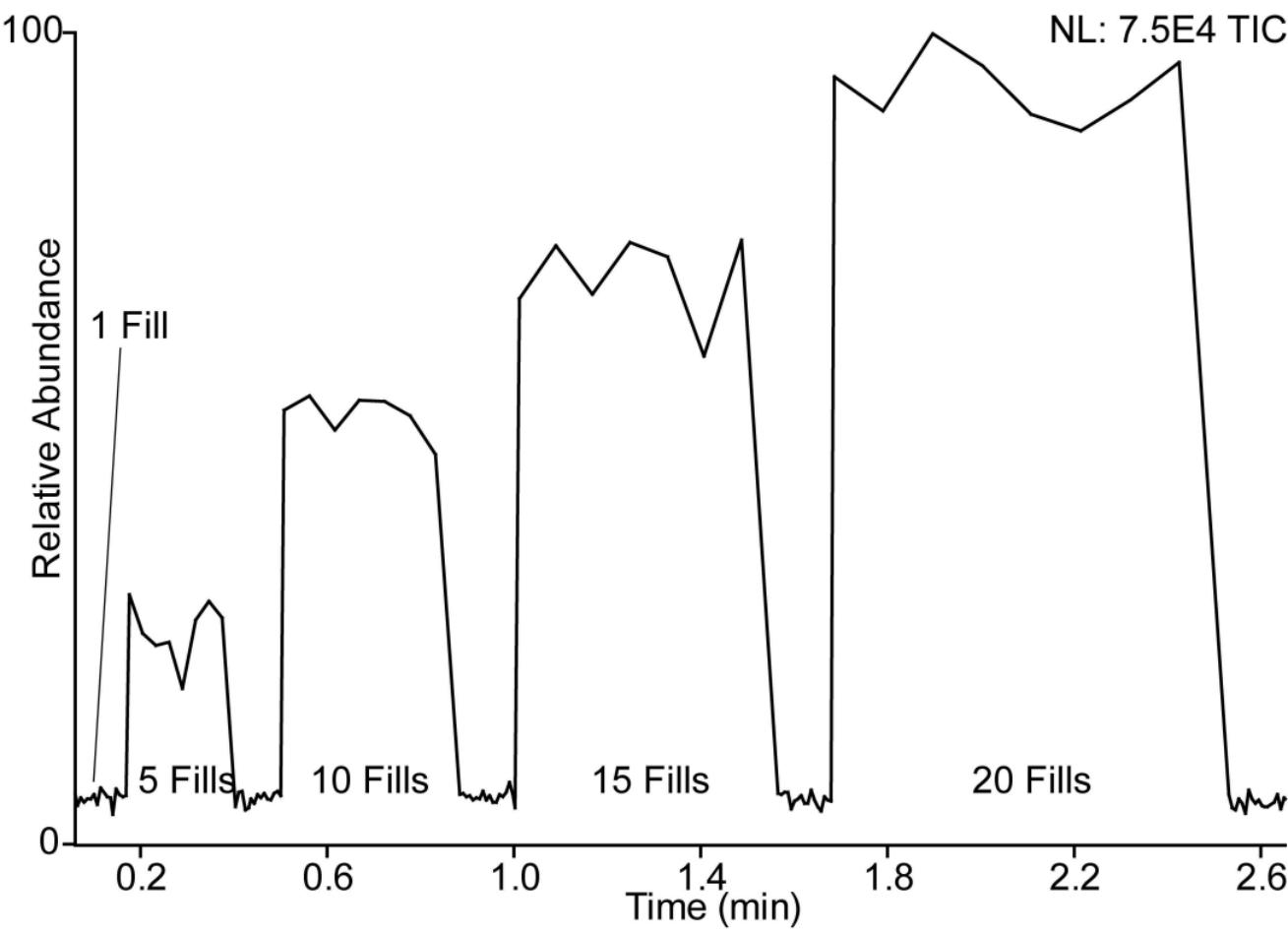
2A. (A) Extracted LC-MS chromatogram of (left) intact histone H2A and (right) clipped histone H2A after 15 min, 30 min and 1 hour of incubation with Cathepsin L. In italic above the peaks the area under the curve of the ion chromatogram. (B) Quantification of the C-terminal histone H2A peptides identified in the in-vitro experiment. The cleavage site is determined in the y-axis, including the intact protein form (full). The abundance is expressed in arbitrary units (AU), corresponding to the area under the curve of the extracted ion chromatogram. (C) Annotated MS/MS ETD spectrum of the G44 clipped histone H2A, deconvoluted using Xtract (Thermo). c and z fragments are marked with orange and yellow labels. On the right of the spectrum the signal of the intact peptide not fragmented. These data were acquired on an Orbitrap Fusion with FETD.

Supplemental Table 1. N-terminal truncated histones observed in H2A1 fraction from butyrate treated HeLa cells. Sequences of observed truncated H2A proteoforms are given along with their respective residue numbers and quantitation expressed in arbitrary units corresponding to the calculated area of the extracted ion chromatogram.

Supplemental Table 2. Identified peptides from the in-vitro histone H2A proteolytic digestion. Peptide sequences of the peptides identified using Mascot database searching (Matrix Science). The protein/peptide sequence is annotated with the respective mass (MH^+) and cleavage site. The cleavage site is annotated in the Motif column as “-“ with the surrounding ± 6 amino acid residues. Quantification is expressed in arbitrary units, corresponding to the

calculated area of the extracted ion chromatogram. Prior both database searching and LC peak area integration the raw files were deconvoluted using Xtract (Thermo).

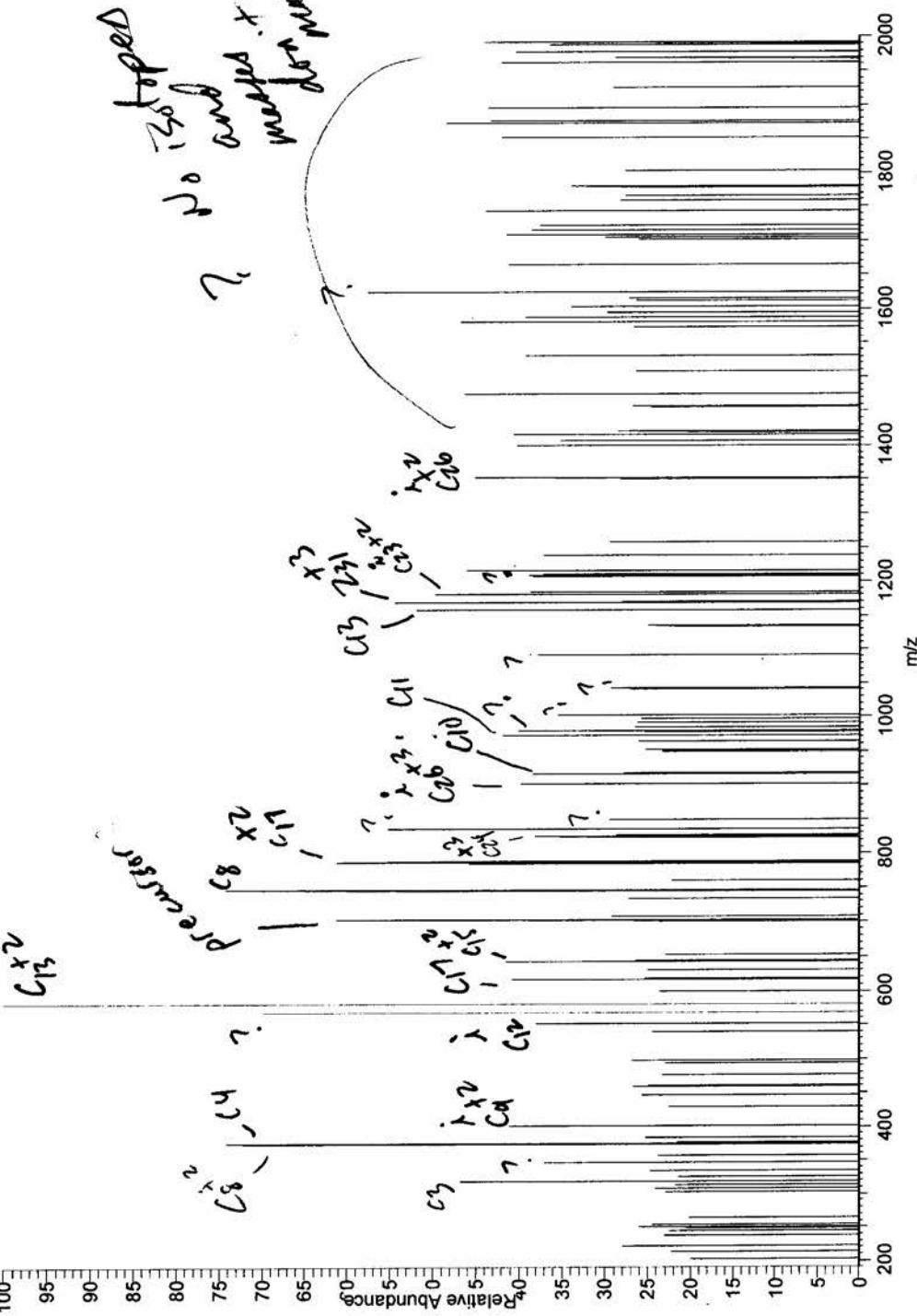
Supplemental Figure 1



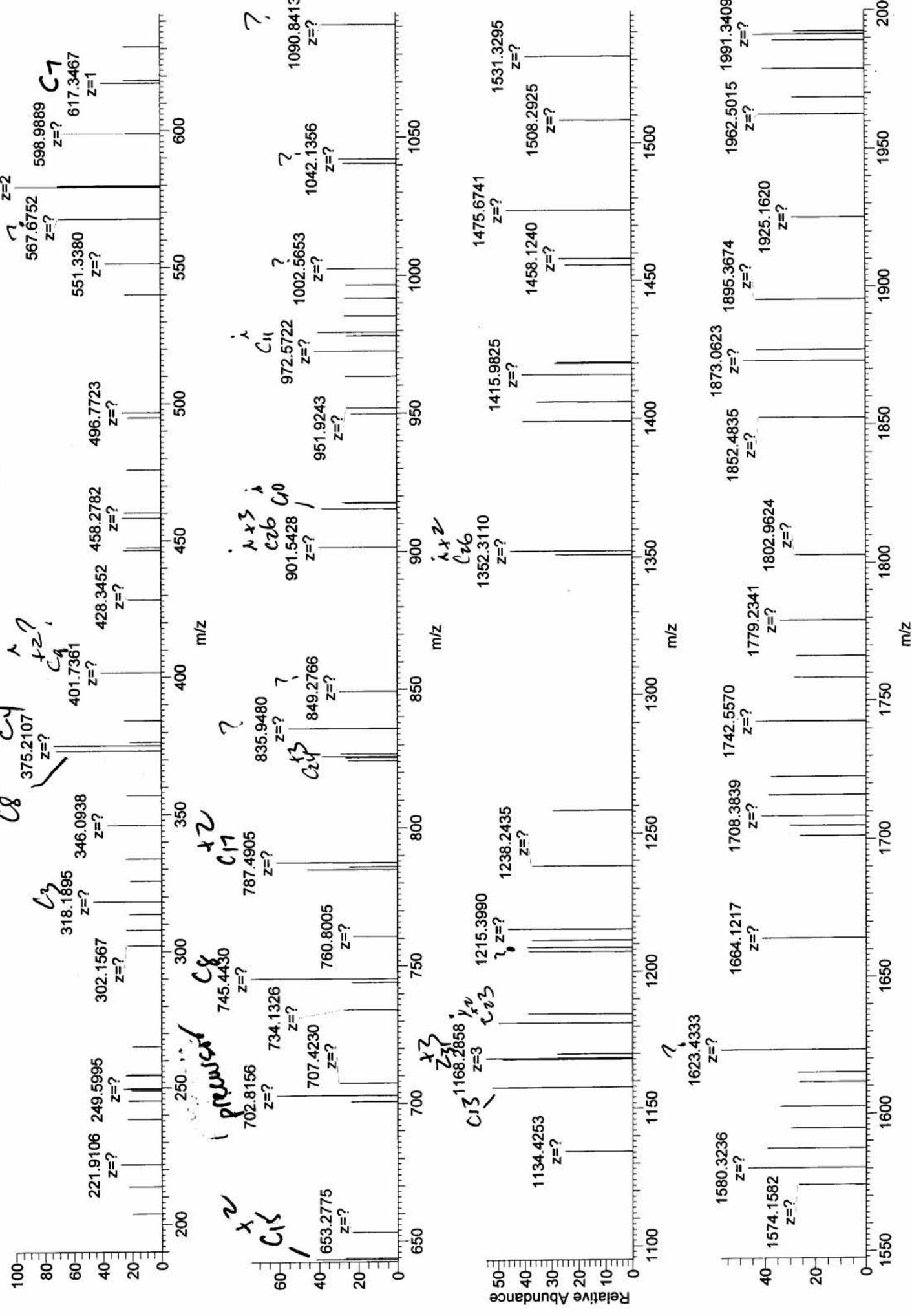
Supplemental Figure 2A

A

T: FTMS + p NSI Full ms2 703.40@etd8.00@etd8.00 [ptr20.00-2000.00]



062515_SAU_Recom_H4_Infusion_Var_Fills_ETD8 PTR20 Elite #11 RT: 0.07 AV: 1 NL: 3.93E4
T: FTMS + p NSI Full ms2-703.40@etd8.00@etd8.00 [190.00-2000.00]

A

A

Fragment Masses

+3 c ions	+2 c ions	+1 c ions		Sequence		+1 z ions	+2 z ions	+3 z ions
35.6935	53.0366	105.0659	1	S	102	11230.3485	5615.6779	3744.1210
54.7006	81.5473	162.0873	2	G	101	11127.2978	5564.1525	3709.7708
106.7343	159.5979	318.1884	3	R	100	11070.2763	5535.6418	3690.7636
125.7415	188.1086	375.2099	4	G	99	10914.1752	5457.5912	3638.7299
168.4398	252.1561	503.3049	5	K	98	10857.1538	5429.0805	3619.7228
187.4470	280.6668	560.3263	6	G	97	10729.0588	5365.0330	3577.0244
206.4541	309.1775	617.3478	7	G	96	10672.0373	5336.5223	3558.0173
249.1524	373.2250	745.4427	8	K	95	10615.0159	5308.0116	3539.0101
268.1596	401.7357	802.4642	9	G	94	10486.9209	5243.9641	3496.3118
305.8543	458.2778	915.5483	10	L	93	10429.8994	5215.4534	3477.3047
324.8614	486.7885	972.5697	11	G	92	10316.8154	5158.9113	3439.6100
367.5598	550.8360	1100.6647	12	K	91	10259.7939	5130.4006	3420.6028
386.5669	579.3467	1157.6862	13	G	90	10131.6989	5066.3531	3377.9045
405.5741	607.8575	1214.7076	14	G	89	10074.6775	5037.8424	3358.8973
429.2531	643.3760	1285.7447	15	A	88	10017.6560	5009.3316	3339.8902
471.9514	707.4235	1413.8397	16	K	87	9946.6189	4973.8131	3316.2112
523.9851	785.4740	1569.9408	17	R	86	9818.5239	4909.7656	3273.5128
569.6714	854.0035	1706.9997	18	H	85	9662.4228	4831.7151	3221.4791
621.7051	932.0541	1863.1008	19	R	84	9525.3639	4763.1856	3175.7928
664.4035	996.1015	1991.1958	20	K	83	9369.2628	4685.1350	3123.7591
697.4263	1045.6357	2090.2642	21	V	82	9241.1678	4621.0876	3081.0608
735.1209	1102.1778	2203.3483	22	L	81	9142.0994	4571.5534	3048.0380
787.1546	1180.2283	2359.4494	23	R	80	9029.0154	4515.0113	3010.3433
825.4970	1237.7418	2474.4763	24	D	79	8872.9143	4436.9608	2958.3096
863.5113	1294.7633	2588.5193	25	N	78	8757.8873	4379.4473	2919.9673
901.2060	1351.3053	2701.6033	26	I	77	8643.8444	4322.4258	2881.9530
943.8922	1415.3346	2829.6619	27	Q	76	8530.7603	4265.8838	2844.2583
962.8993	1443.8453	2886.6834	28	G	75	8402.7017	4201.8545	2801.5721
1000.5940	1500.3874	2999.7674	29	I	74	8345.6803	4173.3438	2782.5649
1034.2766	1550.9112	3100.8151	30	T	73	8232.5962	4116.8017	2744.8703
1076.9749	1614.9587	3228.9101	31	K	72	8131.5485	4066.2779	2711.1877
1109.3258	1663.4851	3325.9628	32	P	71	8003.4536	4002.2304	2668.4894
1133.0048	1699.0036	3397.0000	33	A	70	7906.4008	3953.7040	2636.1385
1170.6995	1755.5456	3510.0840	34	I	69	7835.3637	3918.1855	2612.4594
1222.7332	1833.5962	3666.1851	35	R	68	7722.2796	3861.6435	2574.7647
1274.7669	1911.6468	3822.2862	36	R	67	7566.1785	3783.5929	2522.7310
1312.4616	1968.1888	3935.3703	37	L	66	7410.0774	3705.5423	2470.6973
1336.1407	2003.7073	4006.4074	38	A	65	7296.9933	3649.0003	2433.0026
1388.1744	2081.7579	4162.5085	39	R	64	7225.9562	3613.4818	2409.3236
1440.2081	2159.8085	4318.6096	40	R	63	7069.8551	3535.4312	2357.2899
1459.2152	2188.3192	4375.6311	41	G	62	6913.7540	3457.3806	2305.2562
1478.2224	2216.8299	4432.6526	42	G	61	6856.7325	3428.8699	2286.2490
1511.2452	2266.3641	4531.7210	43	V	60	6799.7111	3400.3592	2267.2419
1553.9435	2330.4116	4659.8159	44	K	59	6700.6427	3350.8250	2234.2191
1605.9772	2408.4622	4815.9171	45	R	58	6572.5477	3286.7775	2191.5208
1643.6719	2465.0042	4929.0011	46	I	57	6416.4466	3208.7269	2139.4870
1672.6826	2508.5202	5016.0332	47	S	56	6303.3625	3152.1849	2101.7924
1691.6897	2537.0309	5073.0546	48	G	55	6216.3305	3108.6689	2072.7817
1729.3844	2593.5730	5186.1387	49	L	54	6159.3090	3080.1582	2053.7745
1767.0791	2650.1150	5299.2227	50	I	53	6046.2250	3023.6161	2016.0798
1821.4335	2731.6467	5462.2861	51	Y	52	5933.1409	2967.0741	1978.3852

Fragment Masses

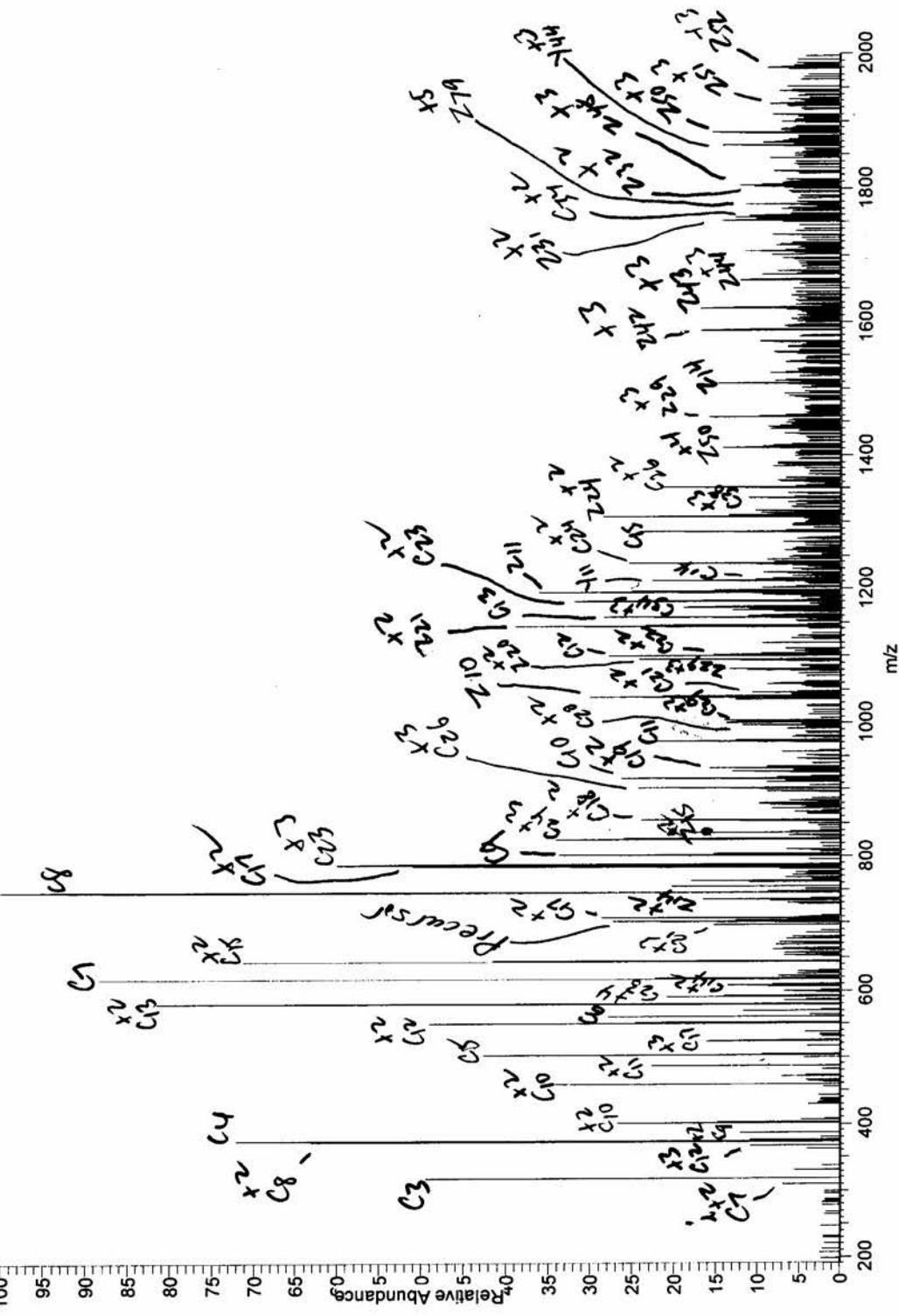
A

+3 c ions	+2 c ions	+1 c ions		Sequence		+1 z ions	+2 z ions	+3 z ions
1864.4477	2796.1680	5591.3287	52	E	51	5770.0776	2885.5424	1924.0307
1907.4619	2860.6893	5720.3713	53	E	50	5641.0350	2821.0211	1881.0165
1941.1445	2911.2131	5821.4189	54	T	49	5511.9924	2756.4998	1838.0023
1993.1782	2989.2637	5977.5200	55	R	48	5410.9447	2705.9760	1804.3198
2012.1854	3017.7744	6034.5415	56	G	47	5254.8436	2627.9254	1752.2860
2045.2082	3067.3086	6133.6099	57	V	46	5197.8221	2599.4147	1733.2789
2082.9028	3123.8506	6246.6940	58	L	45	5098.7537	2549.8805	1700.2561
2125.6012	3187.8981	6374.7890	59	K	44	4985.6697	2493.3385	1662.5614
2158.6240	3237.4323	6473.8574	60	V	43	4857.5747	2429.2910	1619.8631
2207.6468	3310.9665	6620.9258	61	F	42	4758.5063	2379.7568	1586.8403
2245.3415	3367.5086	6734.0098	62	L	41	4611.4379	2306.2226	1537.8175
2288.3557	3432.0299	6863.0524	63	E	40	4498.3538	2249.6805	1500.1228
2326.3700	3489.0513	6977.0954	64	N	39	4369.3112	2185.1592	1457.1086
2359.3928	3538.5855	7076.1638	65	V	38	4255.2683	2128.1378	1419.0943
2397.0875	3595.1276	7189.2478	66	I	37	4156.1999	2078.6036	1386.0715
2449.1212	3673.1781	7345.3490	67	R	36	4043.1158	2022.0615	1348.3768
2487.4635	3730.6916	7460.3759	68	D	35	3887.0147	1944.0110	1296.3431
2511.1425	3766.2101	7531.4130	69	A	34	3771.9877	1886.4975	1258.0008
2544.1653	3815.7444	7630.4814	70	V	33	3700.9506	1850.9790	1234.3217
2577.8479	3866.2682	7731.5291	71	T	32	3601.8822	1801.4447	1201.2989
2632.2023	3947.7999	7894.5924	72	Y	31	3500.8345	1750.9209	1167.6164 ✓
2665.8849	3998.3237	7995.6401	73	T	30	3337.7712	1669.3892	1113.2619
2708.8991	4062.8450	8124.6827	74	E	29	3236.7235	1618.8654	1079.5794
2754.5854	4131.3744	8261.7416	75	H	28	3107.6809	1554.3441	1036.5652
2778.2644	4166.8930	8332.7787	76	A	27	2970.6220	1485.8146	990.8789
2820.9628	4230.9405	8460.8737	77	K	26	2899.5849	1450.2961	967.1998
2872.9965	4308.9910	8616.9748	78	R	25	2771.4899	1386.2486	924.5015
2915.6948	4373.0385	8745.0698	79	K	24	2615.3888	1308.1981	872.4678
2949.3773	4423.5624	8846.1175	80	T	23	2487.2939	1244.1506	829.7695
2982.4001	4473.0966	8945.1859	81	V	22	2386.2462	1193.6267	796.0869
3016.0827	4523.6204	9046.2335	82	T	21	2287.1778	1144.0925	763.0641
3039.7617	4559.1390	9117.2707	83	A	20	2186.1301	1093.5687	729.3816
3083.4419	4624.6592	9248.3111	84	M	19	2115.0930	1058.0501	705.7025
3121.7842	4682.1727	9363.3381	85	D	18	1984.0525	992.5299	662.0224
3154.8070	4731.7069	9462.4065	86	V	17	1869.0256	935.0164	623.6800
3187.8298	4781.2411	9561.4749	87	V	16	1769.9571	885.4822	590.6572
3242.1843	4862.7728	9724.5382	88	Y	15	1670.8887	835.9480	557.6344
3265.8633	4898.2913	9795.5754	89	A	14	1507.8254	754.4163	503.2800
3303.5580	4954.8333	9908.6594	90	L	13	1436.7883	718.8978	479.6009
3346.2563	5018.8808	10036.7544	91	K	12	1323.7042	662.3557	441.9063
3398.2900	5096.9314	10192.8555	92	R	11	1195.6093	598.3083	399.2079
3440.9762	5160.9607	10320.9141	93	Q	10	1039.5081	520.2577	347.1742
3459.9834	5189.4714	10377.9355	94	G	9	911.4496	456.2284	304.4880
3512.0171	5267.5220	10534.0366	95	R	8	854.4281	427.7177	285.4809
3545.6996	5318.0458	10635.0843	96	T	7	698.3270	349.6671	233.4472
3583.3943	5374.5878	10748.1684	97	L	6	597.2793	299.1433	199.7646
3637.7488	5456.1195	10911.2317	98	Y	5	484.1953	242.6013	162.0699
3656.7559	5484.6302	10968.2532	99	G	4	321.1319	161.0696	107.7155
3705.7787	5558.1644	11115.3216	100	F	3	264.1105	132.5589	88.7083
3724.7859	5586.6752	11172.3431	101	G	2	117.0420	59.0247	39.6855
3744.1210	5615.6779	11230.3485	102	G	1	60.0206	30.5139	20.6784

Supplemental Figure 2B

B

T: FTMS + p NSI|Full ms2 703.40@etd8.00@ptr20.00 [190.00-2000.00]
062515 SAU Recom H4 Infusion Var Fills ETD8 PTR20 Elite #81 RT: 3.12 AV: 1 NL: 4.80E5

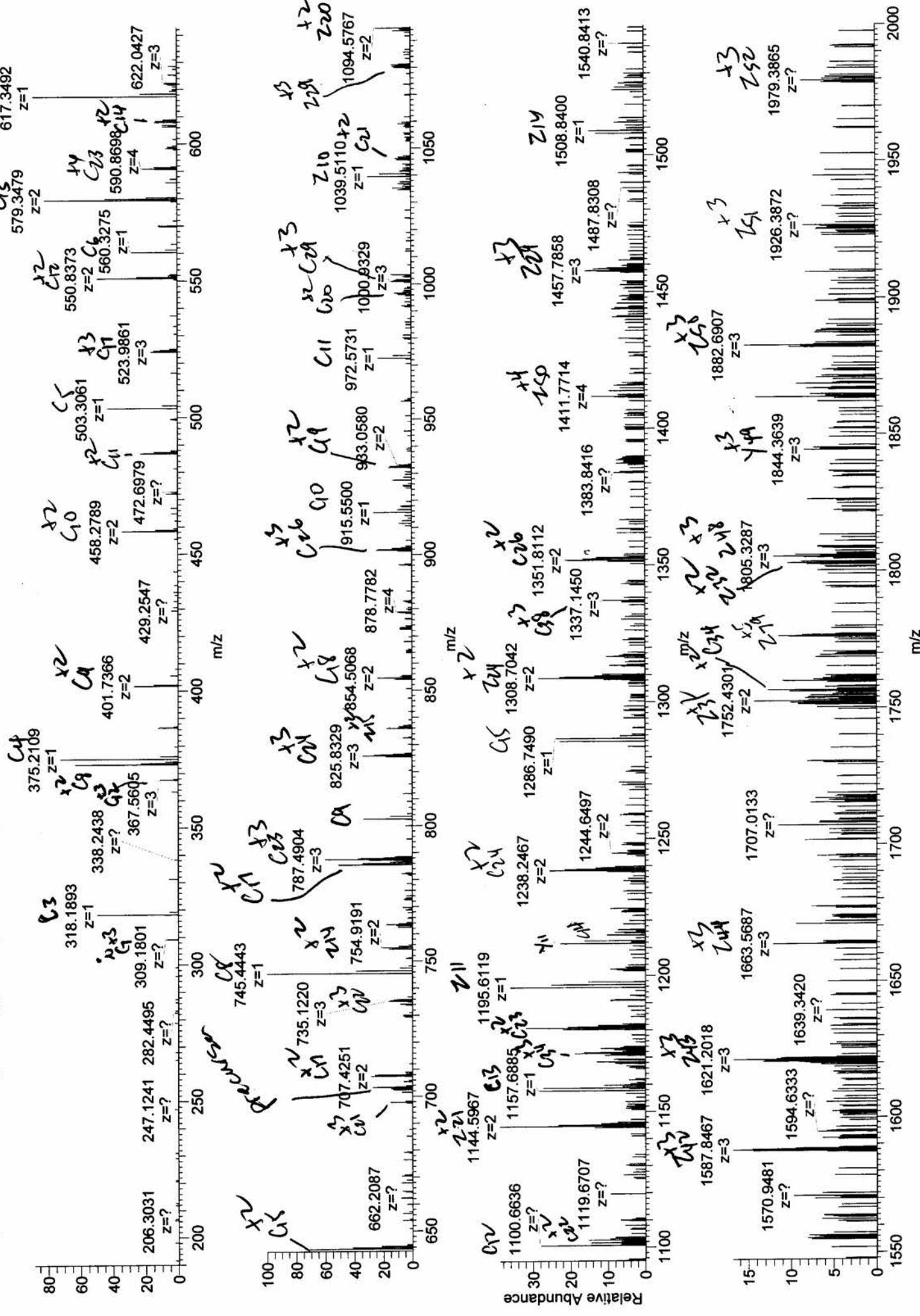


062515_SAU_Recom_H4_Infusion_Var_Fills_ETD8_PTR20 Elite #81 RT: 3.12 AV: 1 NL: 4.80E5

Supplemental Figure 2B (cont)

B

T: FTMS + p NSI Full ms2:703.40@etd8.00 [ptr20.00-2000.00]



Fragment Masses

B

+3 c ions	+2 c ions	+1 c ions		Sequence		+1 z ions	+2 z ions	+3 z ions
35.6935	53.0366	105.0659	1	S	102	11230.3485	5615.6779	3744.1210
54.7006	81.5473	162.0873	2	G	101	11127.2978	5564.1525	3709.7708
106.7343	159.5979	318.1884	3	R	100	11070.2763	5535.6418	3690.7636
125.7415	188.1086	375.2099	4	G	99	10914.1752	5457.5912	3638.7299
168.4398	252.1561	503.3049	5	K	98	10857.1538	5429.0805	3619.7228
187.4470	280.6668	560.3263	6	G	97	10729.0588	5365.0330	3577.0244
206.4541	309.1775	617.3478	7	G	96	10672.0373	5336.5223	3558.0173
249.1524	373.2250	745.4427	8	K	95	10615.0159	5308.0116	3539.0101
268.1596	401.7357	802.4642	9	G	94	10486.9209	5243.9641	3496.3118
305.8543	458.2778	915.5483	10	L	93	10429.8994	5215.4534	3477.3047
324.8614	486.7885	972.5697	11	G	92	10316.8154	5158.9113	3439.6100
367.5598	550.8360	1100.6647	12	K	91	10259.7939	5130.4006	3420.6028
388.5669	579.3467	1157.6862	13	G	90	10131.6989	5066.3531	3377.9045
405.5741	607.8575	1214.7076	14	G	89	10074.6775	5037.8424	3358.8973
429.2531	643.3760	1285.7447	15	A	88	10017.6560	5009.3316	3339.8902
471.9514	707.4235	1413.8397	16	K	87	9946.6189	4973.8131	3316.2112
523.9851	785.4740	1569.9408	17	R	86	9818.5239	4909.7656	3273.5128
569.6714	854.0035	1706.9997	18	H	85	9662.4228	4831.7151	3221.4791
621.7051	932.0541	1863.1008	19	R	84	9525.3639	4763.1856	3175.7928
664.4035	996.1015	1991.1958	20	K	83	9369.2628	4685.1350	3123.7591
697.4263	1045.6357	2090.2642	21	V	82	9241.1678	4621.0876	3081.0608
735.1209	1102.1778	2203.3483	22	L	81	9142.0994	4571.5534	3048.0380
787.1546	1180.2283	2359.4494	23	R	80	9029.0154	4515.0113	3010.3433
825.4970	1237.7418	2474.4763	24	D	79	8872.9143	4436.9608	2958.3096
863.5113	1294.7633	2588.5193	25	N	78	8757.8873	4379.4473	2919.9673
901.2060	1351.3053	2701.6033	26	I	77	8643.8444	4322.4258	2881.9530
943.8922	1415.3346	2829.6619	27	Q	76	8530.7603	4265.8838	2844.2583
962.8993	1443.8453	2886.6834	28	G	75	8402.7017	4201.8545	2801.5721
1000.5940	1500.3874	2999.7674	29	I	74	8345.6803	4173.3438	2782.5649
1034.2766	1550.9112	3100.8151	30	T	73	8232.5962	4116.8017	2744.8703
1076.9749	1614.9587	3228.9101	31	K	72	8131.5485	4066.2779	2711.1877
1109.3258	1663.4851	3325.9628	32	P	71	8003.4536	4002.2304	2668.4894
1133.0048	1699.0036	3397.0000	33	A	70	7906.4008	3953.7040	2636.1385
1170.6995	1755.5456	3510.0840	34	I	69	7835.3637	3918.1855	2612.4594
1222.7332	1833.5962	3666.1851	35	R	68	7722.2796	3861.6435	2574.7647
1274.7669	1911.6468	3822.2862	36	R	67	7566.1785	3783.5929	2522.7310
1312.4616	1968.1888	3935.3703	37	L	66	7410.0774	3705.5423	2470.6973
1336.1407	2003.7073	4006.4074	38	A	65	7296.9933	3649.0003	2433.0026
1388.1744	2081.7579	4162.5085	39	R	64	7225.9562	3613.4818	2409.3236
1440.2081	2159.8085	4318.6096	40	R	63	7069.8551	3535.4312	2357.2899
1459.2152	2188.3192	4375.6311	41	G	62	6913.7540	3457.3806	2305.2562
1478.2224	2216.8299	4432.6526	42	G	61	6856.7325	3428.8699	2286.2490
1511.2452	2266.3641	4531.7210	43	V	60	6799.7111	3400.3592	2267.2419
1553.9435	2330.4116	4659.8159	44	K	59	6700.6427	3350.8250	2234.2191
1605.9772	2408.4622	4815.9171	45	R	58	6572.5477	3286.7775	2191.5208
1643.6719	2465.0042	4929.0011	46	I	57	6416.4466	3208.7269	2139.4870
1672.6826	2508.5202	5016.0332	47	S	56	6303.3625	3152.1849	2101.7924
1691.6897	2537.0309	5073.0546	48	G	55	6216.3305	3108.6689	2072.7817
1729.3844	2593.5730	5186.1387	49	L	54	6159.3090	3080.1582	2053.7745
1767.0791	2650.1150	5299.2227	50	I	53	6046.2250	3023.6161	2016.0798
1821.4335	2731.6467	5462.2861	51	Y	52	5933.1409	2967.0741	1978.3852

B

Fragment Masses

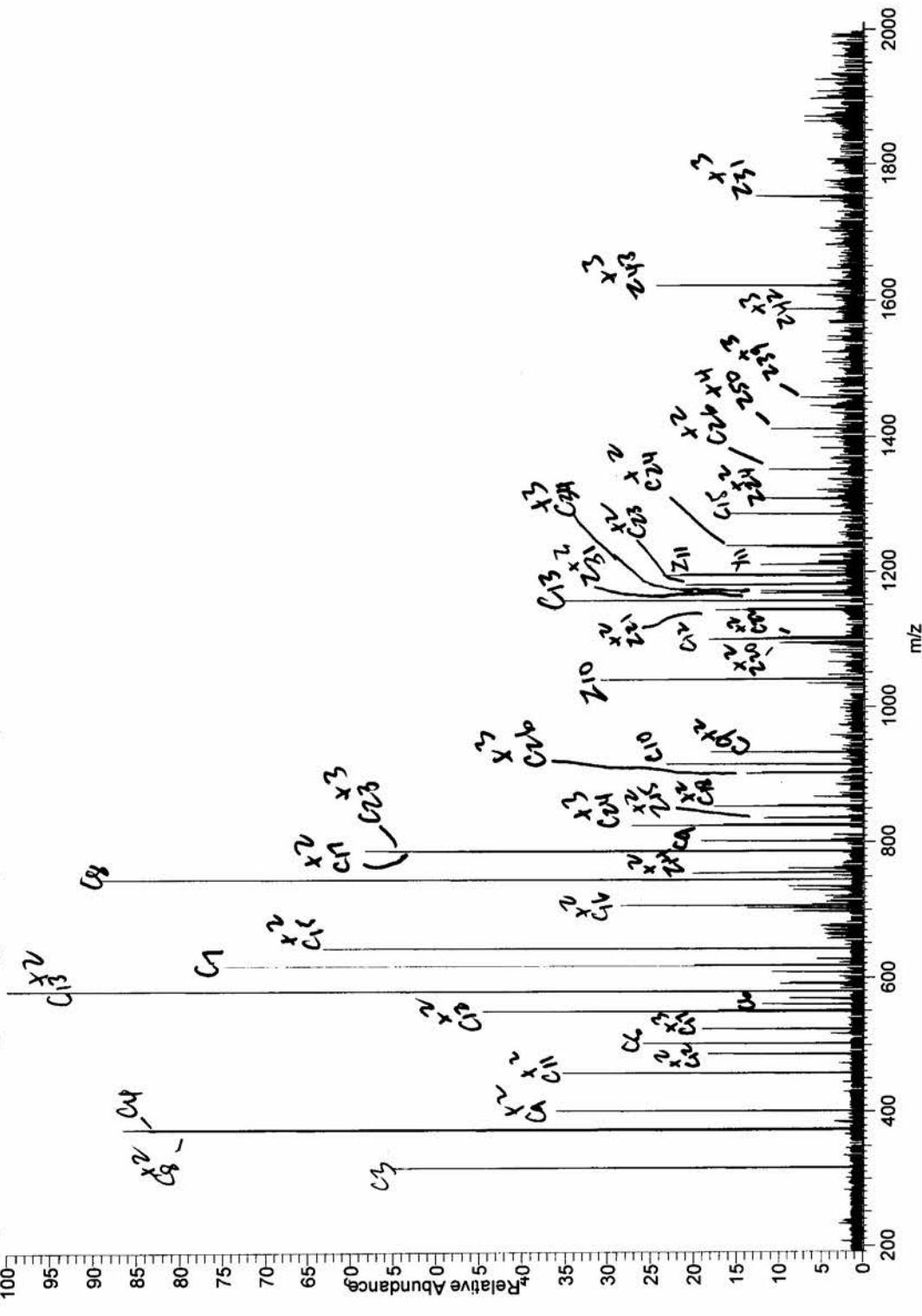
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1864.4477	2796.1680	5591.3287	52	E	51	5770.0776	2885.5424	1924.0307 ✓
1907.4619	2860.6893	5720.3713	53	E	50	5641.0350	2821.0211	1881.0165 ✓
1941.1445	2911.2131	5821.4189	54	T	49	5511.9924	2756.4998	1838.0023
1993.1782	2989.2637	5977.5200	55	R	48	5410.9447	2705.9760	1804.3198 ✓
2012.1854	3017.7744	6034.5415	56	G	47	5254.8436	2627.9254	1752.2860
2045.2082	3067.3086	6133.6099	57	V	46	5197.8221	2599.4147	1733.2789
2082.9028	3123.8506	6246.6940	58	L	45	5098.7537	2549.8805	1700.2561
2125.6012	3187.8981	6374.7890	59	K	44	4985.6697	2493.3385	1662.5614 ✓
2158.6240	3237.4323	6473.8574	60	V	43	4857.5747	2429.2910	1619.8631 ✓
2207.6468	3310.9665	6620.9258	61	F	42	4758.5063	2379.7568	1586.8403 ✓
2245.3415	3367.5086	6734.0098	62	L	41	4611.4379	2306.2226	1537.8175
2288.3557	3432.0299	6863.0524	63	E	40	4498.3538	2249.6805	1500.1228
2326.3700	3489.0513	6977.0954	64	N	39	4369.3112	2185.1592	1457.1086 ✓
2359.3928	3538.5855	7076.1638	65	V	38	4255.2683	2128.1378	1419.0943
2397.0875	3595.1276	7189.2478	66	I	37	4156.1999	2078.6036	1386.0715
2449.1212	3673.1781	7345.3490	67	R	36	4043.1158	2022.0615	1348.3768
2487.4635	3730.6916	7460.3759	68	D	35	3887.0147	1944.0110	1296.3431
2511.1425	3766.2101	7531.4130	69	A	34	3771.9877	1886.4975	1258.0008
2544.1653	3815.7444	7630.4814	70	V	33	3700.9506	1850.9790	1234.3217
2577.8479	3866.2682	7731.5291	71	T	32	3601.8822	1801.4447 ✓	1201.2989
2632.2023	3947.7999	7894.5924	72	Y	31	3500.8345	1750.9209 ✓	1167.6164
2665.8849	3998.3237	7995.6401	73	T	30	3337.7712	1669.3892	1113.2619
2708.8991	4062.8450	8124.6827	74	E	29	3236.7235	1618.8654	1079.5794 ✓
2754.5854	4131.3744	8261.7416	75	H	28	3107.6809	1554.3441	1036.5652
2778.2644	4166.8930	8332.7787	76	A	27	2970.6220	1485.8146	990.8789
2820.9628	4230.9405	8460.8737	77	K	26	2899.5849	1450.2961	967.1998
2872.9965	4308.9910	8616.9748	78	R	25	2771.4899	1386.2486	924.5015
2915.6948	4373.0385	8745.0698	79	K	24	2615.3888	1308.1981 ✓	872.4678
2949.3773	4423.5624	8846.1175	80	T	23	2487.2939	1244.1506	829.7695
2982.4001	4473.0966	8945.1859	81	V	22	2386.2462	1193.6267	796.0869
3016.0827	4523.6204	9046.2335	82	T	21	2287.1778	1144.0925 ✓	763.0641
3039.7617	4559.1390	9117.2707	83	A	20	2186.1301	1093.5687 ✓	729.3816
3083.4419	4624.6592	9248.3111	84	M	19	2115.0930	1058.0501	705.7025
3121.7842	4682.1727	9363.3381	85	D	18	1984.0525	992.5299	662.0224
3154.8070	4731.7069	9462.4065	86	V	17	1869.0256	935.0164	623.6800
3187.8298	4781.2411	9561.4749	87	V	16	1769.9571	885.4822	590.6572
3242.1843	4862.7728	9724.5382	88	Y	15	1670.8887	835.9480 ✓	557.6344
3265.8633	4898.2913	9795.5754	89	A	14	1507.8254 ✓	754.4163 ✓	503.2800
3303.5580	4954.8333	9908.6594	90	L	13	1436.7883	718.8978	479.6009
3346.2563	5018.8808	10036.7544	91	K	12	1323.7042	662.3557	441.9063
3398.2900	5096.9314	10192.8555	92	R	11	1195.6093 ✓	598.3083	399.2079
3440.9762	5160.9607	10320.9141	93	Q	10	1039.5081 ✓	520.2577	347.1742
3459.9834	5189.4714	10377.9355	94	G	9	911.4496	456.2284	304.4880
3512.0171	5267.5220	10534.0366	95	R	8	854.4281	427.7177	285.4809
3545.6996	5318.0458	10635.0843	96	T	7	698.3270	349.6671	233.4472
3583.3943	5374.5878	10748.1684	97	L	6	597.2793	299.1433	199.7646
3637.7488	5456.1195	10911.2317	98	Y	5	484.1953	242.6013	162.0699
3656.7559	5484.6302	10968.2532	99	G	4	321.1319	161.0696	107.7155
3705.7787	5558.1644	11115.3216	100	F	3	264.1105	132.5589	88.7083
3724.7859	5586.6752	11172.3431	101	G	2	117.0420	59.0247	39.6855
3744.1210	5615.6779	11230.3485	102	G	1	60.0206	30.5139	20.6784

Supplemental Figure 2B (cont)

Supplemental Figure 2C

C

062515 SAU Recom H4 Infusion Var Fills ETD8_PTR20 Elite #4-23 RT: 0.02-0.15 AV: 20 NL: 3.48E4
T: FTMS + p NSI Full ms2 703.40@elid8.00@ptr20.00 [190.00-2000.00]

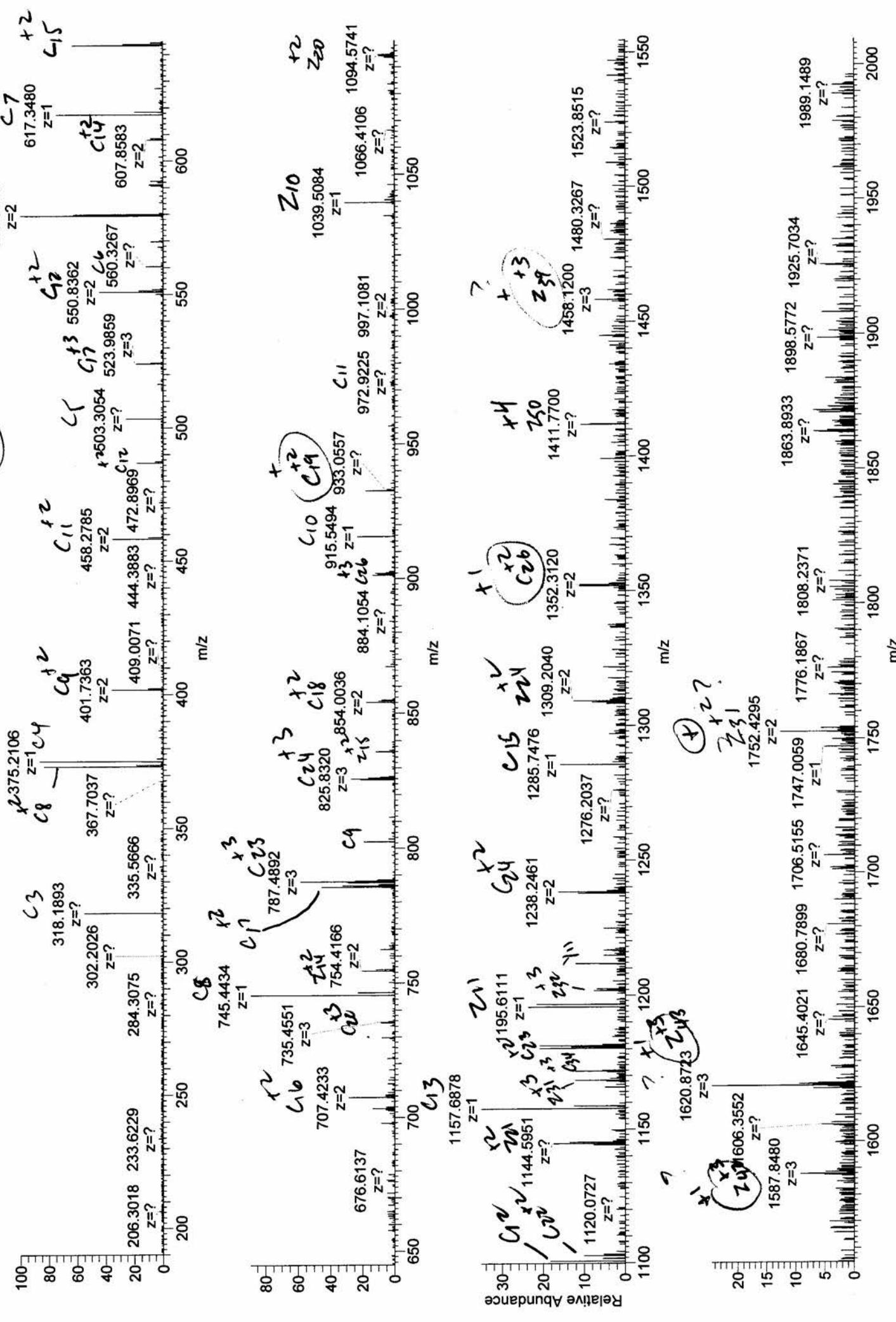


062515_SAU_Recom_H4_Infusion_Var_Fill... 06/25/15 14:23:31

Supplemental Figure 2C (cont)



062515_SAU_Recom_H4_Infusion_Var_Fills_ETD8_PTR20_Elite #4-23 RT: 0.02-0.15 AV: 20 NL: 3.48E4
T: FTMS + p NSI Full ms2_703.40@etd8_00@ptr20_00 [190.00-2000.00]



Fragment Masses

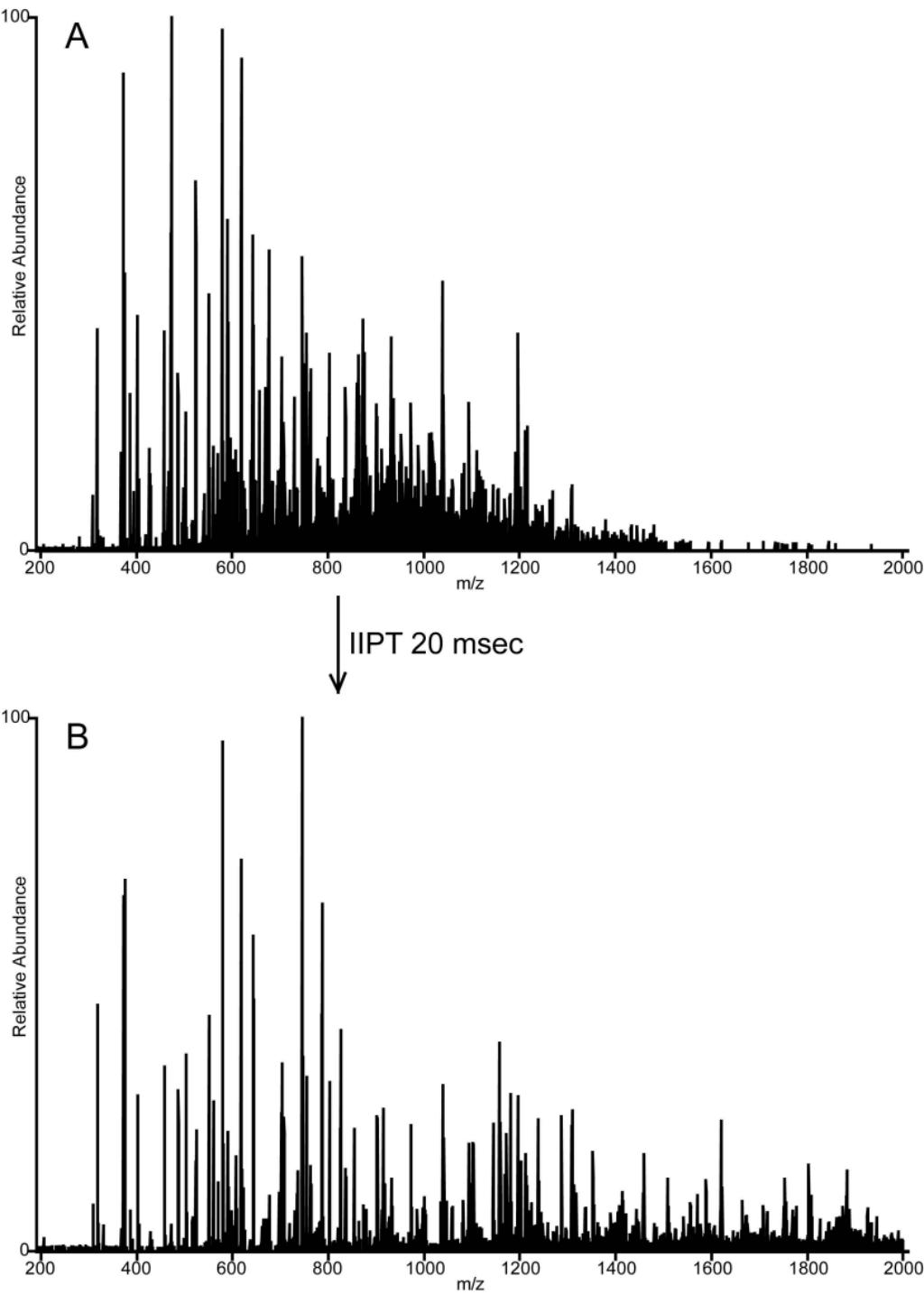
C

+3 c ions	+2 c ions	+1 c ions		Sequence		+1 z ions	+2 z ions	+3 z ions
35.6935	53.0366	105.0659	1	S	102	11230.3485	5615.6779	3744.1210
54.7006	81.5473	162.0873	2	G	101	11127.2978	5564.1525	3709.7708
106.7343	159.5979	318.1884 ✓	3	R	100	11070.2763	5535.6418	3690.7636
125.7415	188.1086	375.2099 ✓	4	G	99	10914.1752	5457.5912	3638.7299
168.4398	252.1561	503.3049 ✓	5	K	98	10857.1538	5429.0805	3619.7228
187.4470	280.6668	560.3263 ✓	6	G	97	10729.0588	5365.0330	3577.0244
206.4541	309.1775	617.3478 ✓	7	G	96	10672.0373	5336.5223	3558.0173
249.1524	373.2250 ✓	745.4427 ✓	8	K	95	10615.0159	5308.0116	3539.0101
268.1596	401.7357 ✓	802.4642 ✓	9	G	94	10486.9209	5243.9641	3496.3118
305.8543	458.2778 ✓	915.5483	10	L	93	10429.8994	5215.4534	3477.3047
324.8614	486.7885 ✓	972.5697 W	11	G	92	10316.8154	5158.9113	3439.6100
367.5598	550.8360 ✓	1100.6647 ✓	12	K	91	10259.7939	5130.4006	3420.6028
386.5669	579.3467 ✓	1157.6862 ✓	13	G	90	10131.6989	5066.3531	3377.9045
405.5741	607.8575 ✓	1214.7076	14	G	89	10074.6775	5037.8424	3358.8973
429.2531	643.3760 ✓	1285.7447 ✓	15	A	88	10017.6560	5009.3316	3339.8902
471.9514	707.4235 ✓	1413.8397	16	K	87	9946.6189	4973.8131	3316.2112
523.9851 ✓	785.4740 ✓	1569.9408	17	R	86	9818.5239	4909.7656	3273.5128
569.6714	854.0035 ✓	1706.9997	18	H	85	9662.4228	4831.7151	3221.4791
621.7051	932.0541 X1	1863.1008	19	R	84	9525.3639	4763.1856	3175.7928
664.4035	996.1015	1991.1958	20	K	83	9369.2628	4685.1350	3123.7591
697.4263	1045.6357 ✓	2090.2642	21	V	82	9241.1678	4621.0876	3081.0608
735.1209 ✓	1102.1778 ✓	2203.3483	22	L	81	9142.0994	4571.5534	3048.0380
787.1546 ✓	1180.2283 ✓	2359.4494	23	R	80	9029.0154	4515.0113	3010.3433
825.4970 ✓	1237.7418 ✓	2474.4763	24	D	79	8872.9143	4436.9608	2958.3096
863.5113	1294.7633	2588.5193	25	N	78	8757.8873	4379.4473	2919.9673
901.2060 ✓	1351.3053 X1	2701.6033	26	I	77	8643.8444	4322.4258	2881.9530
943.8922	1415.3346	2829.6619	27	Q	76	8530.7603	4265.8838	2844.2583
962.8993	1443.8453	2886.6834	28	G	75	8402.7017	4201.8545	2801.5721
1000.5940	1500.3874	2999.7674	29	I	74	8345.6803	4173.3438	2782.5649
1034.2766	1550.9112	3100.8151	30	T	73	8232.5962	4116.8017	2744.8703
1076.9749	1614.9587	3228.9101	31	K	72	8131.5485	4066.2779	2711.1877
1109.3258	1663.4851	3325.9628	32	P	71	8003.4536	4002.2304	2668.4894
1133.0048	1699.0036	3397.0000	33	A	70	7906.4008	3953.7040	2636.1385
1170.6995 ✓	1755.5456	3510.0840	34	I	69	7835.3637	3918.1855	2612.4594
1222.7332	1833.5962	3666.1851	35	R	68	7722.2796	3861.6435	2574.7647
1274.7669	1911.6468	3822.2862	36	R	67	7566.1785	3783.5929	2522.7310
1312.4616	1968.1888	3935.3703	37	L	66	7410.0774	3705.5423	2470.6973
1336.1407	2003.7073	4006.4074	38	A	65	7296.9933	3649.0003	2433.0026
1388.1744	2081.7579	4162.5085	39	R	64	7225.9562	3613.4818	2409.3236
1440.2081	2159.8085	4318.6096	40	R	63	7069.8551	3535.4312	2357.2899
1459.2152	2188.3192	4375.6311	41	G	62	6913.7540	3457.3806	2305.2562
1478.2224	2216.8299	4432.6526	42	G	61	6856.7325	3428.8699	2286.2490
1511.2452	2266.3641	4531.7210	43	V	60	6799.7111	3400.3592	2267.2419
1553.9435	2330.4116	4659.8159	44	K	59	6700.6427	3350.8250	2234.2191
1605.9772	2408.4622	4815.9171	45	R	58	6572.5477	3286.7775	2191.5208
1643.6719	2465.0042	4929.0011	46	I	57	6416.4466	3208.7269	2139.4870
1672.6826	2508.5202	5016.0332	47	S	56	6303.3625	3152.1849	2101.7924
1691.6897	2537.0309	5073.0546	48	G	55	6216.3305	3108.6689	2072.7817
1729.3844	2593.5730	5186.1387	49	L	54	6159.3090	3080.1582	2053.7745
1767.0791	2650.1150	5299.2227	50	I	53	6046.2250	3023.6161	2016.0798
1821.4335	2731.6467	5462.2861	51	Y	52	5933.1409	2967.0741	1978.3852

C

+3 c ions	+2 c ions	+1 c ions		Sequence		+1 z ions	+2 z ions	+3 z ions
1864.4477	2796.1680	5591.3287	52	E	51	5770.0776	2885.5424	1924.0307
1907.4619	2860.6893	5720.3713	53	E	50	5641.0350	2821.0211	1881.0165
1941.1445	2911.2131	5821.4189	54	T	49	5511.9924	2756.4998	1838.0023
1993.1782	2989.2637	5977.5200	55	R	48	5410.9447	2705.9760	1804.3198
2012.1854	3017.7744	6034.5415	56	G	47	5254.8436	2627.9254	1752.2860
2045.2082	3067.3086	6133.6099	57	V	46	5197.8221	2599.4147	1733.2789
2082.9028	3123.8506	6246.6940	58	L	45	5098.7537	2549.8805	1700.2561
2125.6012	3187.8981	6374.7890	59	K	44	4985.6697	2493.3385	1662.5614
2158.6240	3237.4323	6473.8574	60	V	43	4857.5747	2429.2910	1619.8631
2207.6468	3310.9665	6620.9258	61	F	42	4758.5063	2379.7568	1586.8403
2245.3415	3367.5086	6734.0098	62	L	41	4611.4379	2306.2226	1537.8175
2288.3557	3432.0299	6863.0524	63	E	40	4498.3538	2249.6805	1500.1228
2326.3700	3489.0513	6977.0954	64	N	39	4369.3112	2185.1592	1457.1086
2359.3928	3538.5855	7076.1638	65	V	38	4255.2683	2128.1378	1419.0943
2397.0875	3595.1276	7189.2478	66	I	37	4156.1999	2078.6036	1386.0715
2449.1212	3673.1781	7345.3490	67	R	36	4043.1158	2022.0615	1348.3768
2487.4635	3730.6916	7460.3759	68	D	35	3887.0147	1944.0110	1296.3431
2511.1425	3766.2101	7531.4130	69	A	34	3771.9877	1886.4975	1258.0008
2544.1653	3815.7444	7630.4814	70	V	33	3700.9506	1850.9790	1234.3217
2577.8479	3866.2682	7731.5291	71	T	32	3601.8822	1801.4447	1201.2989
2632.2023	3947.7999	7894.5924	72	Y	31	3500.8345	1750.9209	1167.6164
2665.8849	3998.3237	7995.6401	73	T	30	3337.7712	1669.3892	1113.2619
2708.8991	4062.8450	8124.6827	74	E	29	3236.7235	1618.8654	1079.5794
2754.5854	4131.3744	8261.7416	75	H	28	3107.6809	1554.3441	1036.5652
2778.2644	4166.8930	8332.7787	76	A	27	2970.6220	1485.8146	990.8789
2820.9628	4230.9405	8460.8737	77	K	26	2899.5849	1450.2961	967.1998
2872.9965	4308.9910	8616.9748	78	R	25	2771.4899	1386.2486	924.5015
2915.6948	4373.0385	8745.0698	79	K	24	2615.3888	1308.1981	872.4678
2949.3773	4423.5624	8846.1175	80	T	23	2487.2939	1244.1506	829.7695
2982.4001	4473.0966	8945.1859	81	V	22	2386.2462	1193.6267	796.0869
3016.0827	4523.6204	9046.2335	82	T	21	2287.1778	1144.0925	763.0641
3039.7617	4559.1390	9117.2707	83	A	20	2186.1301	1093.5687	729.3816
3083.4419	4624.6592	9248.3111	84	M	19	2115.0930	1058.0501	705.7025
3121.7842	4682.1727	9363.3381	85	D	18	1984.0525	992.5299	662.0224
3154.8070	4731.7069	9462.4065	86	V	17	1869.0256	935.0164	623.6800
3187.8298	4781.2411	9561.4749	87	V	16	1769.9571	885.4822	590.6572
3242.1843	4862.7728	9724.5382	88	Y	15	1670.8887	835.9480	557.6344
3265.8633	4898.2913	9795.5754	89	A	14	1507.8254	754.4163	503.2800
3303.5580	4954.8333	9908.6594	90	L	13	1436.7883	718.8978	479.6009
3346.2563	5018.8808	10036.7544	91	K	12	1323.7042	662.3557	441.9063
3398.2900	5096.9314	10192.8555	92	R	11	1195.6093	598.3083	399.2079
3440.9762	5160.9607	10320.9141	93	Q	10	1039.5081	520.2577	347.1742
3459.9834	5189.4714	10377.9355	94	G	9	911.4496	456.2284	304.4880
3512.0171	5267.5220	10534.0366	95	R	8	854.4281	427.7177	285.4809
3545.6996	5318.0458	10635.0843	96	T	7	698.3270	349.6671	233.4472
3583.3943	5374.5878	10748.1684	97	L	6	597.2793	299.1433	199.7646
3637.7488	5456.1195	10911.2317	98	Y	5	484.1953	242.6013	162.0699
3656.7559	5484.6302	10968.2532	99	G	4	321.1319	161.0696	107.7155
3705.7787	5558.1644	11115.3216	100	F	3	264.1105	132.5589	88.7083
3724.7859	5586.6752	11172.3431	101	G	2	117.0420	59.0247	39.6855
3744.1210	5615.6779	11230.3485	102	G	1	60.0206	30.5139	20.6784

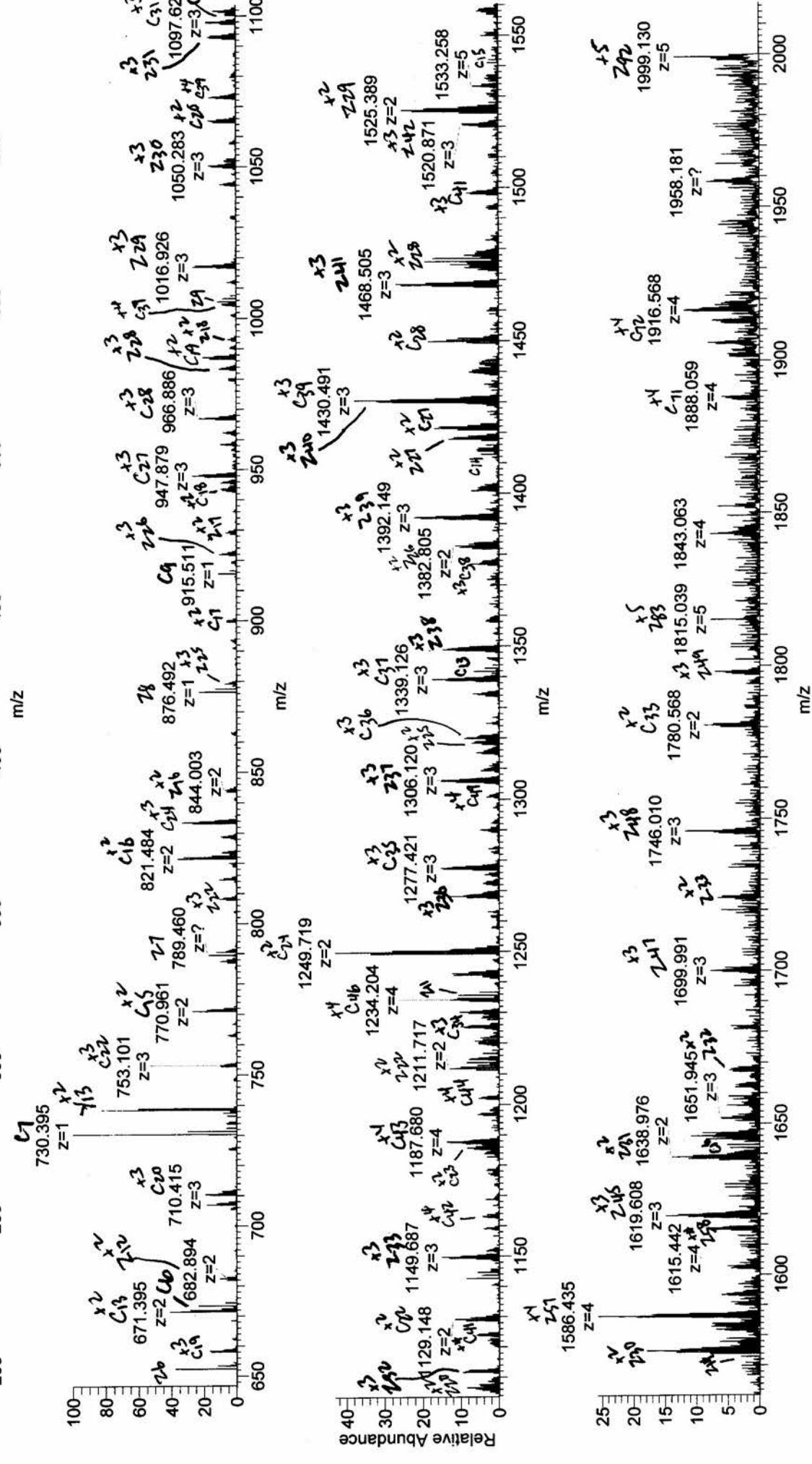
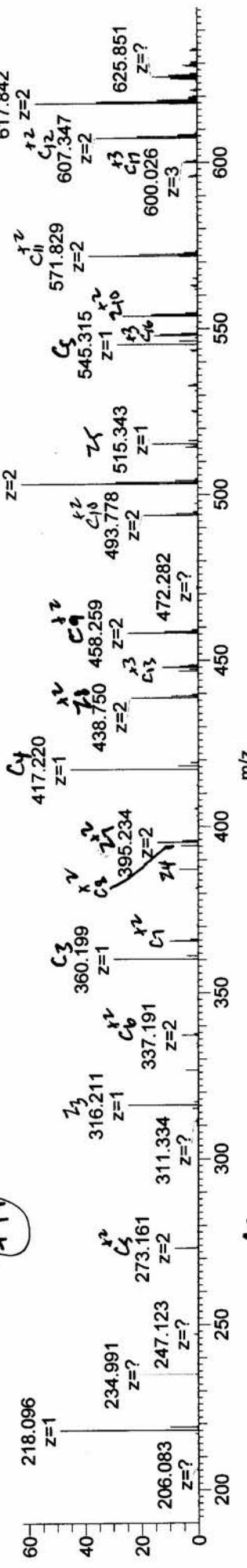
Supplemental Figure 3



Supplemental Figure 4

LCA_09192013_ButyrateH2A2_GarciaL....
 0-33% 10, 33-48% 70, 48-100% 80, 0% 85
 LCA_09192013_ButyrateH2A2_GarciaLab screen 130919200618 #453-531 RT: 36.42-41.06 AV: 6 NL: 4.83E5
 T: FTMS + p NSI sid=35.00 d Full ms2 738.04@etd4.00@ptr25.00 [190.00-2000.00]

H2A type 1



09/19/13 20:06:18 0.67 pmol H2A2, 125 fmol AV

*H2A type 1****SGRGKQGGKARAKAKTRSSRAGLQFPVGRVHRLLRK**

Charge	Monoisotopic Mass	Average Mass
1	13994.9263	14003.37
2	6997.9668	7002.19
3	4665.6469	4668.46
4	3499.4870	3501.60
5	2799.7911	2801.48
6	2333.3271	2334.74
7	2000.1386	2001.35
8	1750.2472	1751.30
9	1555.8872	1556.83
10	1400.3992	1401.24
11	1273.1817	1273.95
12	1167.1672	1167.87
13	1077.4626	1078.11
14	1000.5729	1001.18
15	933.9352	934.50
16	875.6272	876.16
17	824.1790	824.68
18	778.4472	778.92
19	737.5293	737.97
20	700.7032	701.13

Butyrate Hela...130919200618 # 453-531

Supplemental Figure 4 (cont)

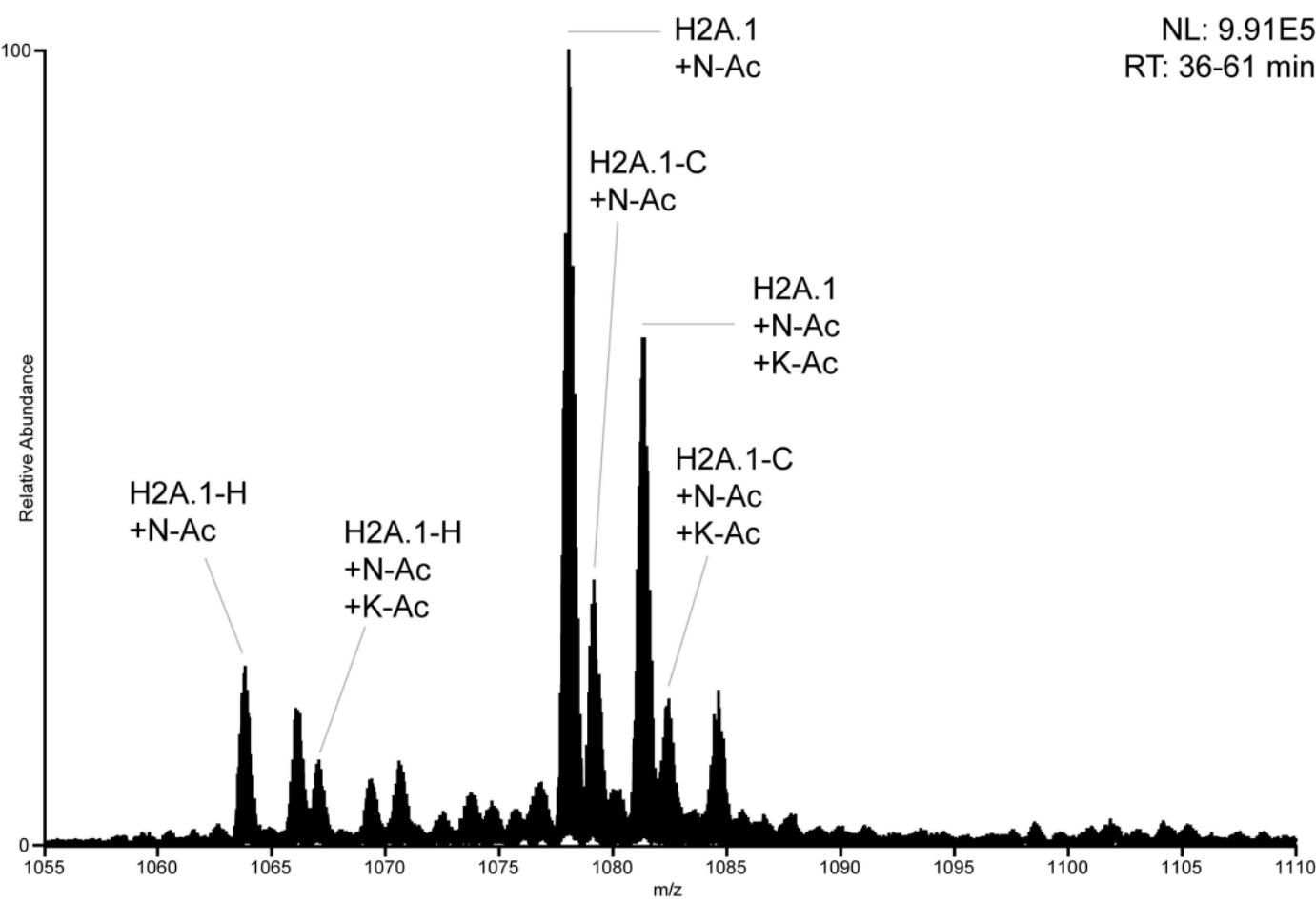
Fragment Masses

+5 c ions	+4 c ions	+3 c ions	+2 c ions	+1 c ions		Sequence (nterm + 42)		+1 z ions	+2 z ions	+3 z ions	+4 z ions	+5 z ions
30.2211	37.5246	49.6970	74.0419	147.0765	1	S	129	13994.9263	6997.9668	4665.6469	3499.4870	2799.7911
41.6254	51.7799	68.7042	102.5526	204.0979	2	G	128	13849.8649	6925.4361	4617.2932	3463.2217	2770.7788
72.8456	90.8052	120.7379	180.6032	360.1990 ✓	3	R	127	13792.8435	6896.9254	4598.2860	3448.9663	2759.3745
84.2499	105.0606	139.7450	209.1139	417.2205 ✓	4	G	126	13636.7424	6818.8748	4546.2523	3409.9410	2728.1543
109.8689	137.0843	182.4433	273.1614 ✓	545.3155 ✓	5	K	125	13579.7209	6790.3641	4527.2452	3395.6857	2716.7500
135.4806	169.0990	225.1295	337.1907 ✓	673.3740 ✓	6	Q	124	13451.6259	6726.3166	4484.5468	3363.6619	2691.1310
146.8849	183.3543	244.1367	365.7014 ✓	730.3955 ✓	7	G	123	13323.5674	6662.2873	4441.8606	3331.6473	2665.5193
158.2892	197.6097	263.1438	394.2121 ✓	787.4170	8	G	122	13266.5459	6633.7766	4422.8535	3317.3919	2654.1150
183.9082	229.6334	305.8422	458.2596 ✓	915.5119 ✓	9	K	121	13209.5244	6605.2659	4403.8463	3303.1366	2642.7107
198.1156	247.3927	329.5212	493.7782 ✓	986.5490	10	A	120	13081.4295	6541.2184	4361.1480	3271.1128	2617.0917
229.3359	286.4180	381.5549	571.8287 ✓	1142.6502	11	R	119	13010.3924	6505.6998	4337.4690	3253.3535	2602.8843
243.5433	304.1773	405.2339	607.3473 ✓	1213.6873	12	A	118	12854.2912	6427.6493	4285.4353	3214.3283	2571.6641
269.1623	336.2010	447.9323 ✓	671.3948 ✓	1341.7822 ✓	13	K	117	12783.2541	6392.1307	4261.7562	3196.5690	2557.4566
283.3697	353.9603	471.6113	706.9133	1412.8193 ✓	14	A	116	12655.1592	6328.0832	4219.0579	3164.5452	2531.8377
308.9887	385.9840	514.3096	770.9608 ✓	1504.9143 ✓	15	K	115	12584.1221	6292.5647	4195.3789	3146.7860	2517.6302
329.1982	411.2460	547.9922 ✓	821.4846 ✓	1641.9620 ✓	16	T	114	12456.0271	6228.5172	4152.6805	3114.7622	2492.0112
360.4184	450.2712	600.0259 ✓	899.5352 ✓	1798.0631	17	R	113	12354.9794	6177.9933	4118.9980	3089.5003	2471.8017
377.8248	472.0292	629.0366	943.0512 ✓	1885.0951	18	S	112	12198.8783	6099.9428	4066.9643	3050.4750	2440.5815
395.2313	493.7872	658.0472 ✓	986.5672 ✓	1972.1272	19	S	111	12111.8463	6056.4268	4037.9536	3028.7170	2423.1751
426.4515	532.8125	710.0809 ✓	1064.6178 ✓	2128.2283	20	R	110	12024.8142	6012.9108	4008.9429	3006.9590	2405.7687
440.6589	550.5718	733.7600	1100.1363 ✓	2199.2654	21	A	109	11868.7131	5934.8602	3956.9092	2967.9337	2374.5484
452.0632	564.8272	752.7671 ✓	1128.6471 ✓	2256.2868	22	G	108	11797.6760	5899.3416	3933.2302	2950.1745	2360.3410
474.6800	593.0982	790.4618 ✓	1185.1891 ✓	2369.3709	23	L	107	11740.6548	5870.8309	3914.2230	2935.9191	2348.9367
500.2917	625.1128	833.1480 ✓	1249.2184 ✓	2497.4295	24	Q	106	11627.5705	5814.2888	3876.5283	2907.6481	2326.3199
529.7054	661.8700	993.1709 ✓	1320.7426 ✓	2644.4970 ✓	25	F	105	11499.5119	5750.2596	3833.8422	2875.6334	2300.7082
549.1160	686.1431	914.5217	1371.2790	2741.5507	26	P	104	11426.4446	5670.7254	3764.6183	2838.5663	2271.2945
568.9296	710.9102	947.5445 ✓	1420.8132 ✓	2840.6191	27	V	103	11255.3907	5628.1990	3752.4684	2814.6031	2251.8840
580.3339	725.1656	966.5517 ✓	1449.3239 ✓	2897.6405	28	G	102	11156.3223	5578.6648	3719.4456	2789.8360	2232.0703
611.5542	764.1909	1018.5854	1527.3745	3053.7417	29	R	101	1099.3009	5550.1541	3700.4385	2775.5807	2220.6660
631.3678	788.9580	1051.6082	1576.9087	3152.8101	30	Y	100	10943.1997	5472.1035	3648.4048	2736.5554	2189.4458
658.7796	823.2227	1097.2945 ✓	1645.4381	3289.8860	31	H	99	10844.1313	5422.5693	3615.3820	2711.7883	2169.6321
689.9998	862.2480	1149.3282	1723.4887	3445.9701	32	R	98	10707.0724	5354.0398	3569.6957	2677.5236	2142.2203
712.6167	890.5190	1187.0229	1780.0307 ✓	3559.0542	33	L	97	10550.9713	5275.9893	3517.6620	2638.4983	2111.0001
735.2335	918.7900	1224.7176 ✓	1836.5727	3672.1382	34	L	96	10437.8872	5219.4473	3479.9673	2610.2273	2088.3833
766.4537	957.8153	1276.7513 ✓	1914.6233	3828.2393	35	R	95	10324.8032	5162.9052	3442.2726	2581.9563	2065.7665
792.0727	989.8390	1319.4496 ✓	1978.6708	3956.3343	36	K	94	10168.7021	5084.8547	3390.2389	2542.9310	2034.5462
803.4770	1004.0944 ✓	1338.4568 ✓	2007.1815	4013.3558	37	G	93	10040.6071	5020.8078	3347.5406	2510.9072	2008.9272
826.2856	1032.6051	1376.4711 ✓	2064.2030	4127.3987	38	N	92	9983.5856	4992.2965	3328.5334	2496.6519	1997.5229 ✓
858.8982	1073.3710 ✓	1430.8255 ✓	2145.7346	4290.4620	39	Y	91	9889.5427	4935.2750	3290.5191	2468.1411	1974.7144
873.1058	1091.1302	1454.5046	2181.2532	4361.4991	40	A	90	9706.4794	4853.7433	3236.1646	2427.3753	1942.1017
898.9142	1123.3909 ✓	1497.5188 ✓	2245.7745	4490.5417	41	E	89	9635.4423	4818.2248	3212.4856	2409.6160	1927.8943
930.1344	1162.4162 ✓	1549.5525	2323.8251	4646.6428	42	R	88	9506.3997	4753.7035	3169.4714	2377.3554	1902.0858
949.9481	1187.1833 ✓	1682.5753	2373.3593	4745.7112	43	V	87	9350.2986	4675.6529	3117.4377	2338.3301	1870.8655
961.3524	1201.4386	1601.5824	2401.8700	4802.7327	44	G	86	9251.2302	4626.1187	3084.4149	2313.5630	1851.0519
975.5598	1219.1979	1625.2615	2437.3885	4873.7698	45	A	85	9194.2087	4597.6080	3065.4077	2299.3076	1839.6476
986.9641	1233.4533 ✓	1644.2686	2465.8993	4930.7913	46	G	84	9123.1716	4562.0894	3041.7287	2281.5484	1825.4401
1001.7416	1254.2126	1667.0477	2501.0204	5031.4470	47	A	83	9066.1501	4533.5787	3022.7216	2267.2930	1814.0358 ✓
1020.5821	1275.4757	1700.2986	2549.9442	5098.8812	48	P	82	9066.1100	4488.0601	2940.8425	2240.5937	1700.0204
1040.3957	1300.2429 ✓	1733.3214	2599.4784	5197.9496	49	V	81	8898.0602	4449.5338	2966.6916	2225.2705	1780.4179
1073.0084	1341.0087	1787.6758	2681.0101	5361.0129	50	Y	80	8798.9911	4399.9995	2933.6688	2200.5034	1760.6042
1095.6252	1369.2797	1825.3705	2737.5521	5474.0970	51	L	79	8635.9285	4318.4679	2879.3143	2159.7376	1727.9915
1109.8326	1387.0390	1849.0495	2773.0707	5545.1341	52	A	78	8522.8444	4261.9259	2841.6197	2131.4666	1705.3747
1124.0401	1404.7983	1872.7286	2808.5892	5616.1712	53	A	77	8451.8073	4226.4073	2817.9406	2113.7073	1691.1673
1143.8537	1429.5654	1905.7514	2858.1234	5715.2398	54	V	76	8380.7702	4190.8887	2794.2616	2095.9480	1676.9599
1166.4476	1457.8364	1943.4461	2914.6655	5828.3237	55	L	75	8281.7018	4141.3545	2761.2388	2071.1809	1657.1462
1192.2791	1490.0970	1986.4803	2979.1868	5957.3663	56	E	74	8168.6177	4084.8125	2723.5441	2042.9099	1634.5294
1224.8917	1530.8629	2040.8147	3060.7184	6120.4296	57	Y	73	8039.5751	4020.2912	2680.5299	2010.6492	1608.7208
1247.5086	1559.1339	2078.5094	3117.2605	6233.5137	58	L	72	7876.5118	3938.7595	2626.1754	1969.8834	1576.1082
1267.7181	1584.3958	2112.1920	3167.7843	6334.5613	59	T	71	7763.4277	3882.2175	2588.4808	1941.6124	1553.4914
1281.9255	1602.1551	2135.8710	3203.3029	6405.5985	60	A	70	7662.3801	3831.6937	2554.7982	1916.3505	1533.2818
1307.7340	1634.4157	2178.8852	3267.8242	6534.6411	61	E	69	7591.3429	3796.1751	2531.1192	1899.5912	1519.0744
1330.3508	1682.6687	2216.5799	3324.3662	6647.7251	62	I	68	7462.3003	3731.6538	2488.1050	1866.3305	1493.2659
1352.9677	1690.9578	2254.2746	3380.9082	6760.8092	63	L	67	7349.2163	3675.1118	2450.4103	1838.0595	1470.6491
1378.7762	1723.2184	2297.2888	3445.4295	6889.8518	64	E	66	7236.1322	3618.5697	2412.7156	1809.7885	1448.0323
1401.3930	1751.4894	2334.9835	3501.9716	7002.9358	65	L	65	7107.0896	3554.04			

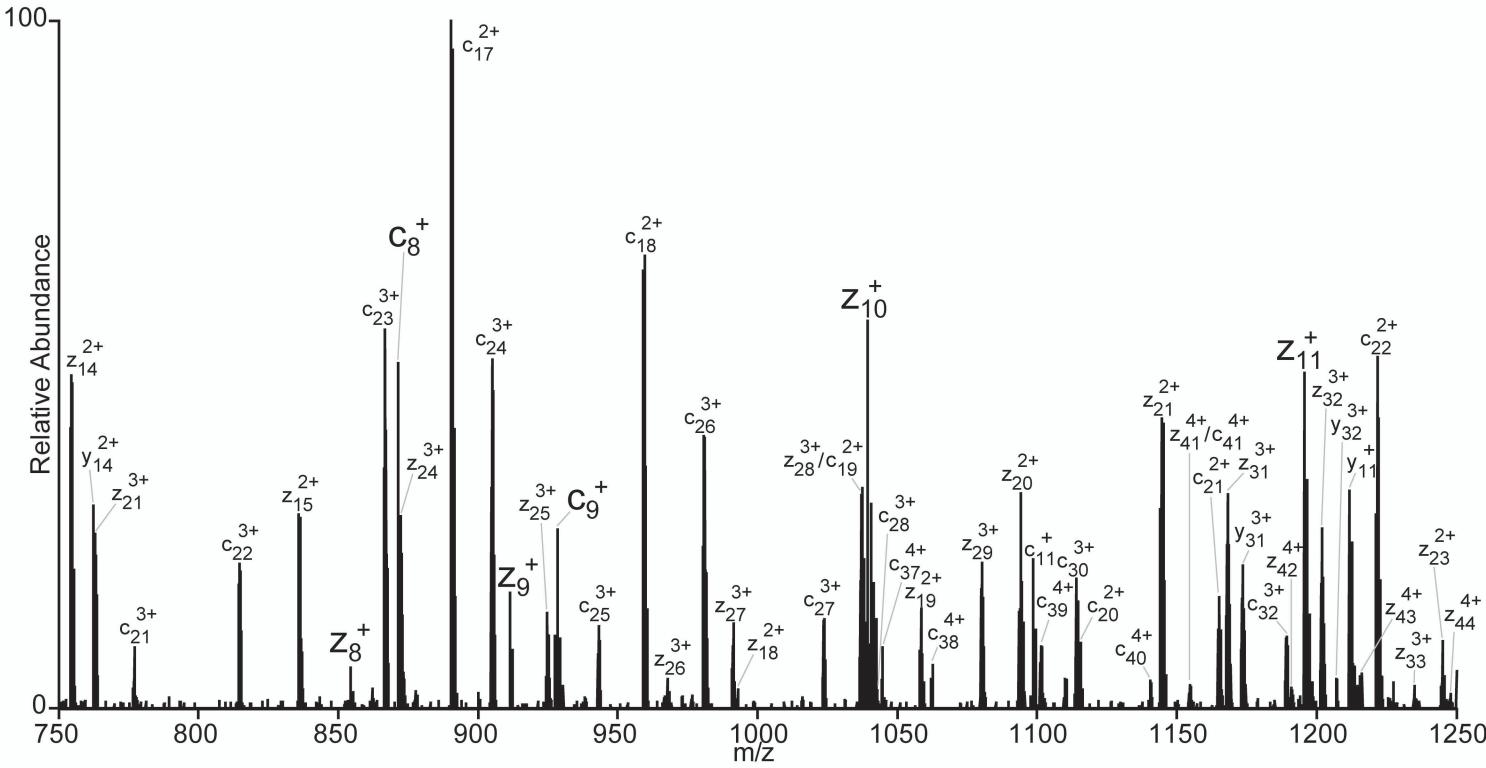
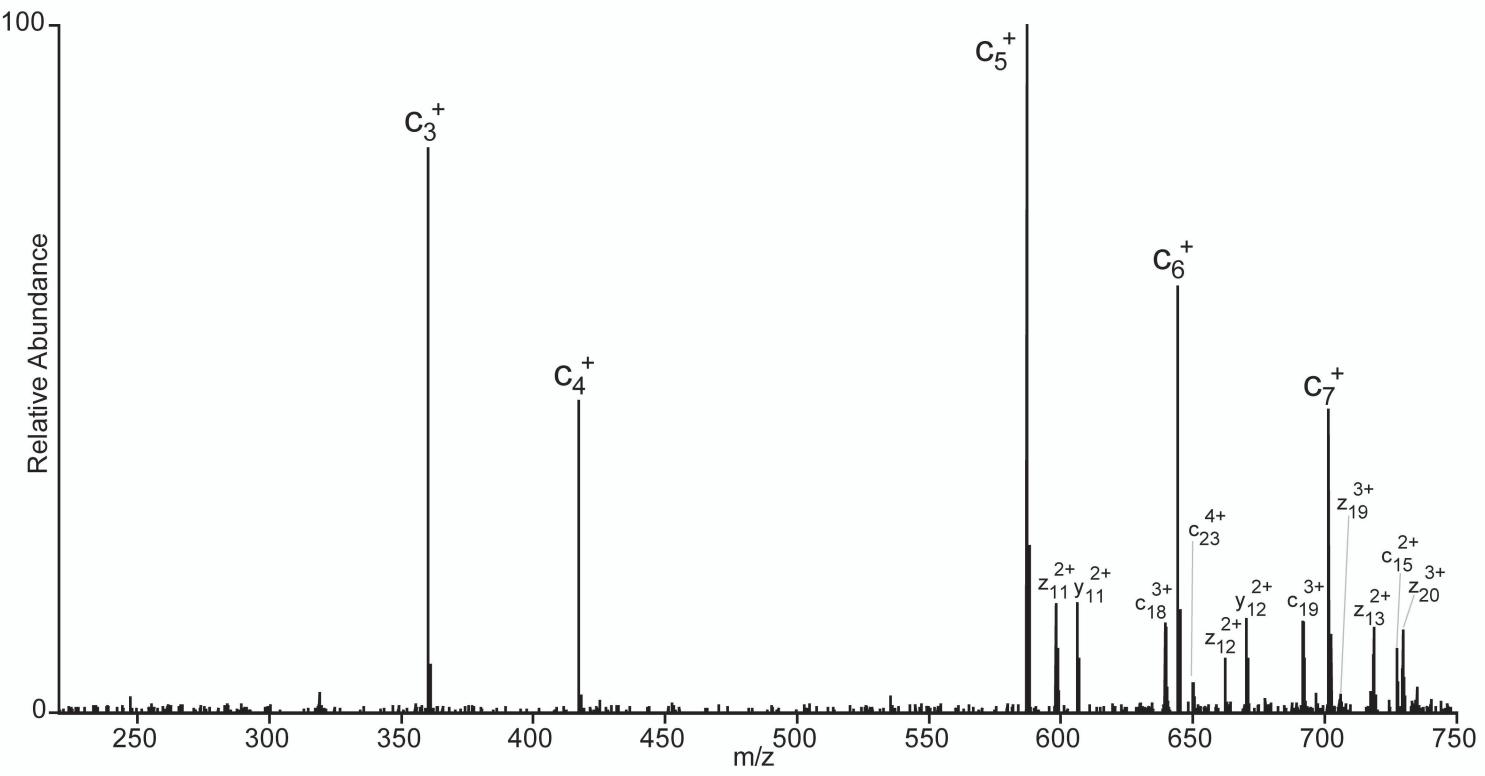
Fragment Masses

+5 z ions	+4 z ions	+3 z ions	+2 z ions	+1 z ions		Sequence		+1 z ions	+2 z ions	+3 z ions	+4 z ions	+5 z ions
1580.8813	1975.8498	2634.1307	3950.6924	7900.3775	74	K	56	6224.6588	3112.8331	2075.5578	1556.9202	1245.7376
1606.5003	2007.8736	2676.8290	4014.7399	8028.4725	75	K	55	6096.5639	3048.7856	2032.8595	1524.8984	1220.1186
1626.7099	2033.1355	2710.5116	4065.2637	8129.5202	76	T	54	5968.4689	2984.7381	1990.1612	1492.8727	1194.4996
1657.9301	2072.1608	2762.5453	4143.3143	8285.6213	77	R	53	5867.4212	2934.2143	1956.4786	1467.6108	1174.2901
1680.5469	2100.4318	2800.2400	4199.8563	8398.7053	78	I	52	5711.3201	2856.1637	1904.4449	1428.5855	1143.0698
1703.1667	2120.7926	2897.9940	4250.9965	8511.7694	79	—	51	5598.2361	2799.6217	1866.7502	1400.3145	1120.4530
1722.5743	2152.9660	2870.2856	4304.9247	8608.8422	80	P	60	5466.1526	2740.6790	1829.6555	1372.6435	1087.6662
1753.7945	2191.9913	2922.3193	4382.9753	8764.9433	81	R	49	5388.0992	2694.5533	1796.7046	1347.7803	1078.4257
1781.2063	2226.2560	2968.0056	4451.5047	8902.0022	82	H	48	5231.9981	2616.5027	1744.6709	1308.7550	1047.2054
1803.8231	2254.5270	3005.7003	4508.0468	9015.0862	83	L	47	5094.9392	2547.9732	1698.9846	1274.4903	1019.7937
1829.4348	2286.5417	3048.3865	4572.0761	9143.1448	84	Q	46	4981.8551	2491.4312	1661.2899	1246.2192	997.1769
1852.0516	2314.8127	3086.0811	4628.6181	9256.2289	85	L	45	4853.7966	2427.4019	1818.6037	1214.2046	971.5651
1866.2590	2332.5720	3109.7602	4664.1366	9327.2660	86	A	44	4740.7125	2370.8599	1580.9090	1185.9336	948.9483
1888.8758	2360.8430	3147.4549	4720.6787	9440.3501	87	I	43	4669.6754	2335.3413	1557.2300	1168.1743	934.7409
1920.0961	2399.8683	3199.4896	4798.7292	9596.4512	88	R	42	4556.5913	2278.7993	1519.5353	1139.9033	912.1241
1942.9046	2428.3790	3237.5029	4855.7507	9710.4941	89	N	41	4400.4902	2200.7487	1467.5016	1100.8780	880.9039
1965.9100	2457.1357	3275.8452	4913.2642	9825.5211	90	D	40	4286.4473	2143.7273	1429.4873	1072.3673	858.0953
1991.7186	2489.3964	3318.8594	4977.7855	9954.5636	91	E	39	4171.4203	2086.2138	1391.1450	1043.6105	835.0899
2017.5271	2521.6570	3361.8736	5042.3068	10083.6062	92	E	38	4042.3777	2021.6925	1348.1308	1011.3499	809.2814
2040.1439	2549.9280	3399.5683	5098.8488	10196.6903	93	L	37	3913.3352	1957.1712	1305.1166	979.0892	783.4729
2062.9525	2578.4388	3437.5826	5155.8703	10310.7332	94	N	36	3800.2511	1900.6292	1267.4219	950.8182	760.8560
2088.5715	2610.4625	3480.2809	5219.9177	10438.8282	95	K	35	3686.2082	1843.6077	1229.4076	922.3075	738.0475
2111.1883	2638.7335	3517.9756	5276.4598	10551.9123	96	L	34	3588.1132	1779.5602	1186.7093	890.2838	712.4285
2133.8051	2667.0045	3555.6703	5333.0018	10664.9963	97	L	33	3445.0291	1723.0182	1149.0146	862.0127	689.8116
2145.2094	2681.2599	3574.6774	5361.5125	10722.0178	98	G	32	3331.9451	1666.4762	1111.3199	833.7417	667.1948
2170.8284	2713.2836	3617.3758	5425.5600	10850.1127	99	K	31	3274.9236	1637.9654	1092.3127	819.4864	655.7905
2190.6421	2738.0507	3650.3986	5475.0942	10949.1812	100	V	30	3146.8286	1573.9180	1049.6144	787.4626	630.1715
2210.8516	2763.3127	3684.0811	5525.6181	11050.2288	101	T	29	3047.7602	1524.3838	1016.5916	762.6955	610.3579
2233.4684	2791.5837	3721.7758	5582.1601	11163.3129	102	I	28	2946.7126	1473.8599	982.9090	737.4336	590.1483
2247.6758	2809.3430	3745.4549	5617.6786	11234.3500	103	A	27	2833.6285	1417.3179	945.2143	709.1626	567.5315
2273.2875	2841.3576	3788.1411	5681.7079	11362.4086	104	Q	26	2762.5914	1381.7993	921.5353	691.4033	553.3241
2284.6918	2855.6130	3807.1482	5710.2187	11419.4301	105	G	25	2634.5328	1317.7700	878.8491	659.3887	527.7124
2296.0961	2869.8683	3826.1554	5738.7294	11476.4515	106	G	24	2577.5113	1289.2593	859.8420	645.1333	516.3081
2315.9098	2894.6354	3859.1782	5788.2636	11575.5199	107	V	23	2520.4899	1260.7486	840.8348	630.8779	504.9038
2338.6266	2922.0666	3896.0720	5844.0656	11666.0640	108	L	22	2421.4215	1211.2144	807.8120	606.1108	485.0901
2357.9372	2947.1696	3929.2238	5893.3320	11785.6568	109	P	21	2308.0074	1154.6720	770.1175	577.6396	402.4753
2380.7458	2975.6804	3967.2381	5950.3535	11899.6997	110	N	20	2211.2846	1106.1460	737.7664	553.5766	443.0627
2403.3626	3003.9514	4004.9328	6006.8955	12012.7838	111	I	19	2097.2417	1049.1245	699.7521	525.0659	420.2542
2428.9743	3035.9660	4047.6190	6070.9248	12140.8423	112	Q	18	1984.1576	992.5825	662.0574	496.7949	397.6373
2443.1817	3053.7253	4071.2980	6106.4434	12211.8795	113	A	17	1856.0911	928.5532	619.3712	464.8020	372.0256
2462.9954	3078.4924	4104.3208	6155.9776	12310.9479	114	V	16	1785.0619	893.0346	595.6922	447.0209	357.8182
2485.6122	3106.7634	4142.0155	6212.5196	12424.0319	115	L	15	1685.9935	843.5004	562.6694	422.2538	338.0045
2508.2290	3126.0345	4170.7402	6260.0646	12537.1160	116	L	14	1572.9095	786.9584	524.9747	393.9828	315.3877
2527.6396	3159.2976	4212.0611	6317.5880	12634.1688	117	P	13	1459.0254	706.4166	407.2000	605.7448	202.7700
2553.2586	3191.3214	4254.7594	6381.6355	12762.2637	118	K	12	1362.7726	681.8900	454.9291	341.4486	273.3603
2578.8776	3223.3451	4297.4577	6445.6830	12890.3587	119	K	11	1234.6777	617.8425	412.2307	309.4249	247.7414
2599.0871	3248.6070	4331.1403	6496.2068	12991.4064	120	T	10	1106.5827	553.7956	369.5324	277.4011	222.1224
2624.8956	3280.8677	4374.1545	6560.7281	13120.4490	121	E	9	1005.5350	503.2712	335.8499	252.1392	201.9128
2642.3020	3302.6257	4403.1652	6604.2441	13207.4810	122	S	8	876.4924	438.7499	292.8357	219.8786	176.1043
2669.7138	3336.8904	4448.8515	6672.7736	13344.5399	123	H	7	789.4604	395.2338	263.8250	198.1206	158.6979
2697.1256	3371.1552	4494.5378	6741.3030	13481.5988	124	H	6	652.4015	326.7044	218.1387	163.8558	131.2861
2722.7446	3403.1789	4537.2361	6805.3505	13609.6938	125	K	5	515.3426	258.1749	172.4524	129.5911	103.8743
2736.9520	3420.9382	4560.9151	6840.6861	13680.7309	126	A	4	387.2475	194.1274	129.7541	97.5674	78.2553
2762.5710	3452.9619	4603.6135	6904.9166	13808.8259	127	K	3	316.2105	158.6089	106.0750	79.8081	64.0479
2773.9753	3467.2173	4622.6206	6933.4273	13865.8473	128	G	2	188.1155	94.5614	63.3767	47.7843	38.4289
2799.7911	3499.4870	4665.6469	6997.9668	13994.9263	129	K	1	131.0941	66.0507	44.3695	33.5290	27.0246

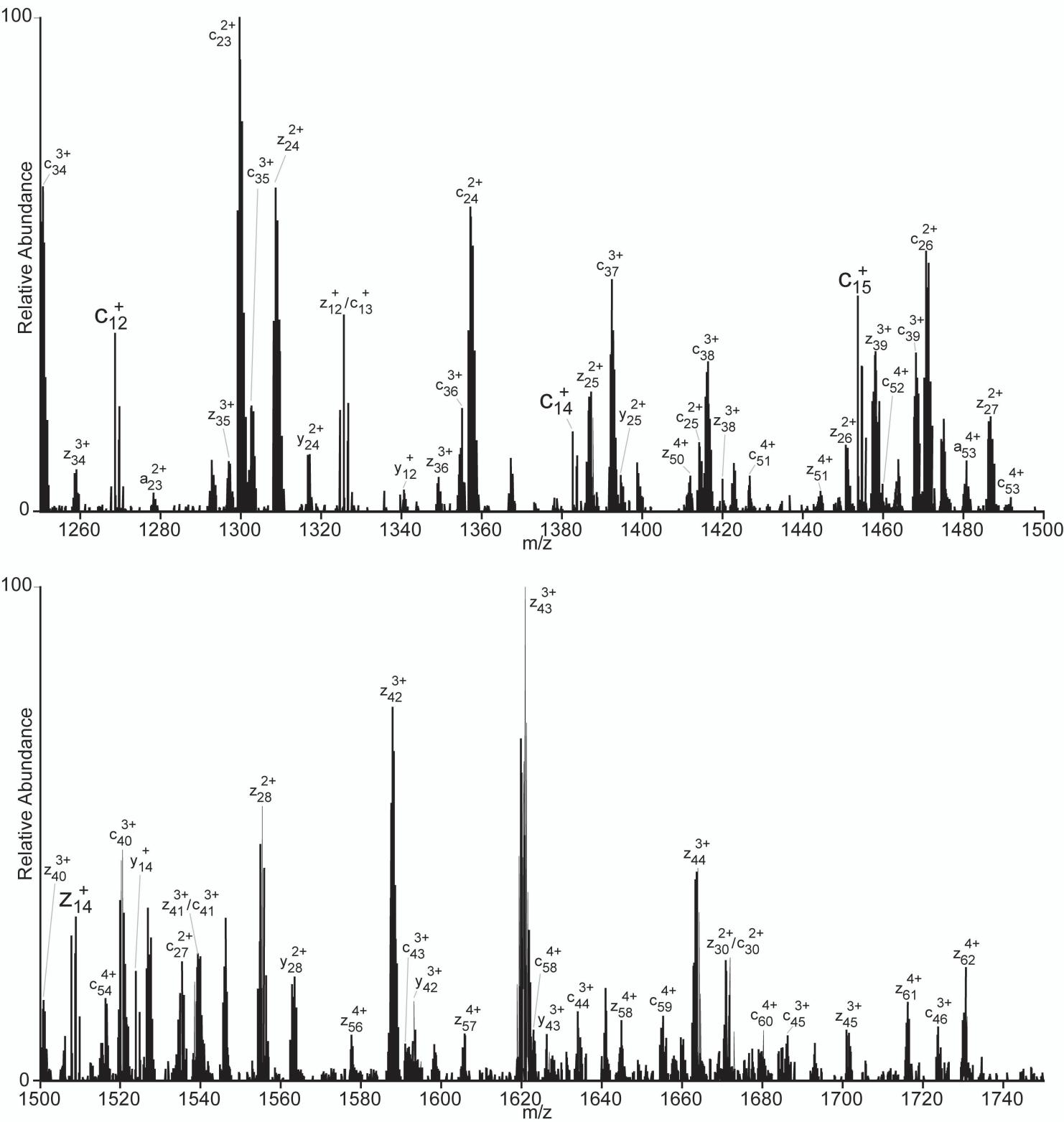
Supplemental Figure 5



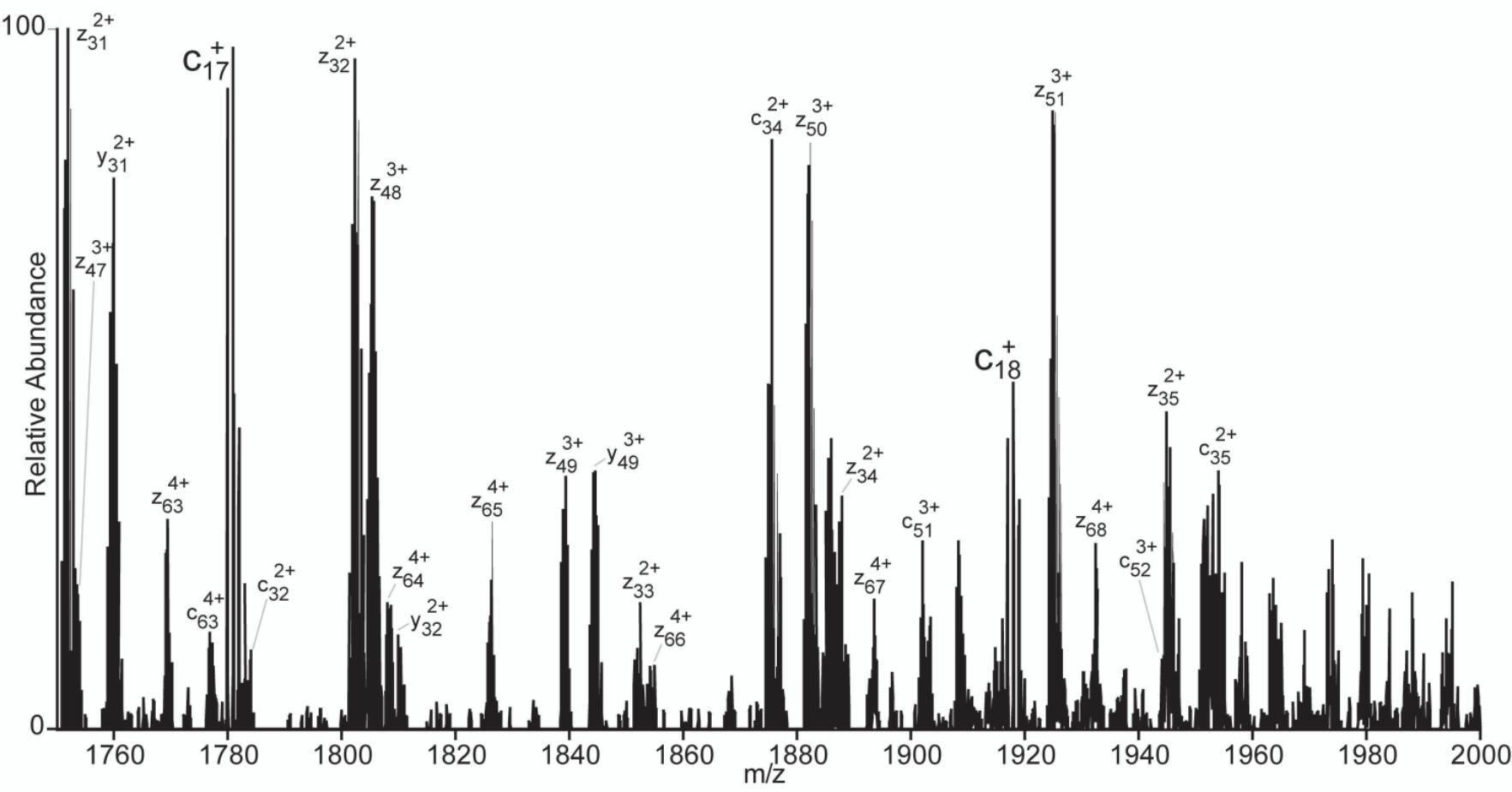
Supplemental Figure 6 A



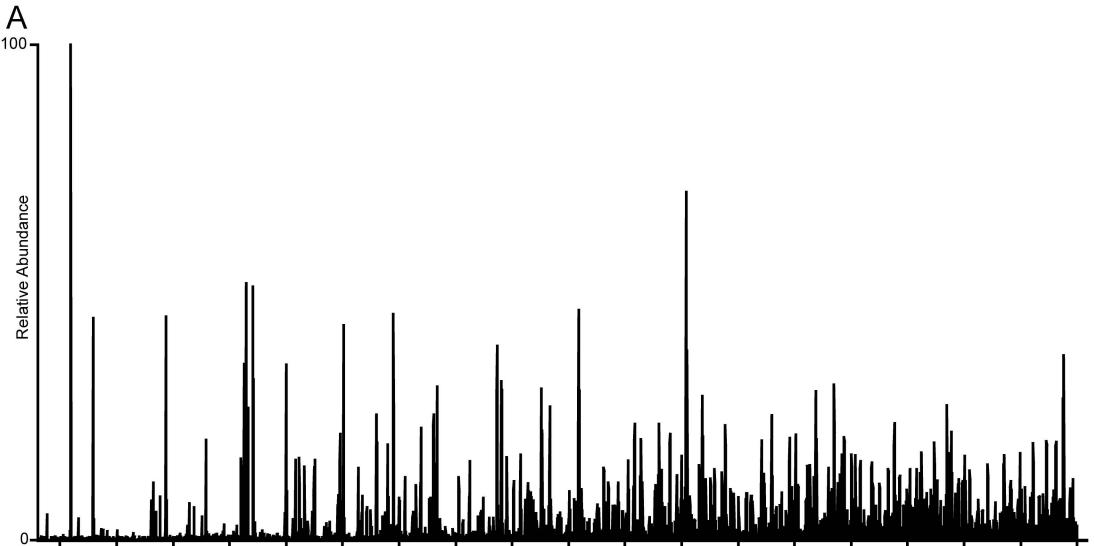
Supplemental Figure 6 B



Supplemental Figure 6 C



Supplemental Figure 7 A B



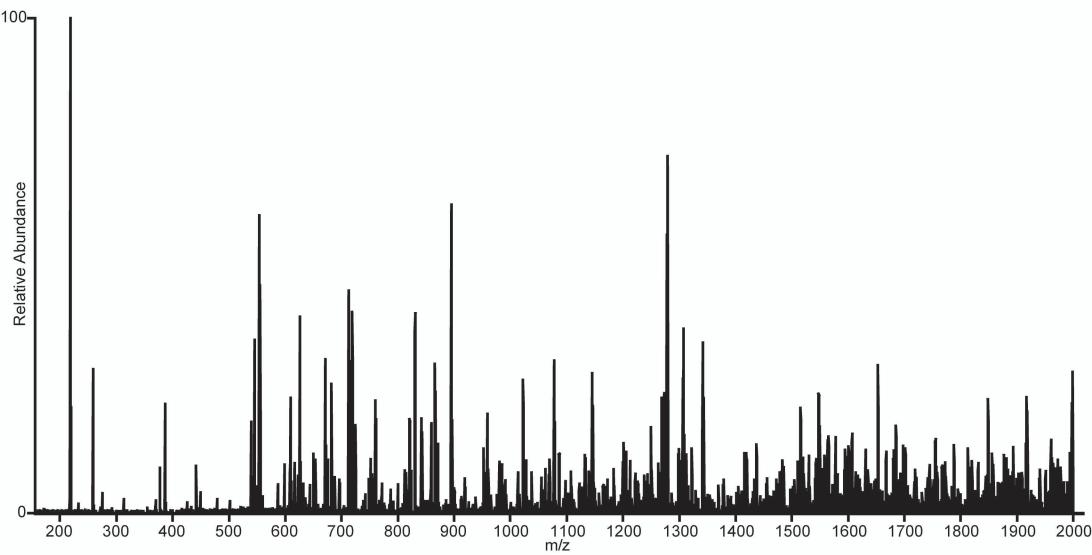
B

c-ions

Ac- α N-S E T A P A A P A A P A P A E K T P V K K K A R K S A G A A
K R K A S G P P V S E L I T K A V A A S K E R S G V S L A A
L K K A L A A A G Y D V E K N N S R I K L G L K S L V S K G
T L V Q T K G T G A S G S F K L N K K A A S G E A K P K A K
K A L G A A K A K K P A G A A K K P K K A T G A A T P K K S A
L K K L T P K K A K L K P A A A A G A K K A K L S P K K A K K A L K P
L K K A P K S P A K A K A V L K P K A A K P K T A K P K A A K P
L K K A A A K K z-ions

Supplemental Figure 7 C D

C



D

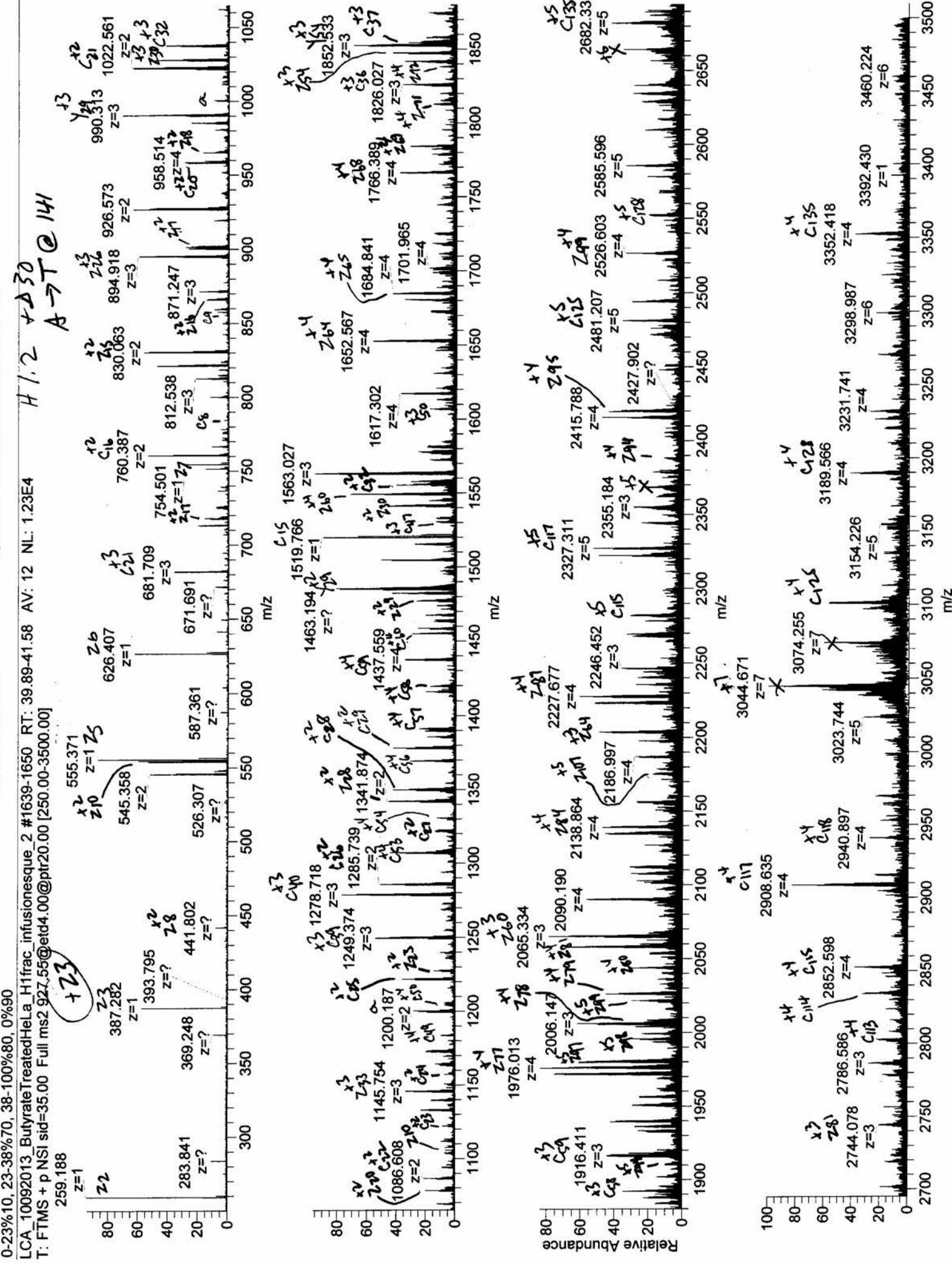
^{c-ions}
Ac- α N-S E T A P A TA P A TA P A P P A E KA P V K K K A A TK K A G G T
P R K A S G P P V S E L I T K A V A A S K E R S G V S I A A
L K K A L L A A A G Y D V E K N N S R I K L G L K S L V S K G
T L V Q T K G T G A S G S F K L N K K A A S G E A K P K V K
K A G G T K P K L K P V G A A K L K P K L A A G G A L T P K L K S A
L K K L T P K L K A L K L K P A A A L T V T L K K V L A K S P L K L K A L K V L A K
P L K L K A A L K S A A L K A V L K P L K A A L K P L K V V L K P L K L K A A P L K
L K K
z⁻ ions

Supplemental Figure 8

LCA 10092013 Butyrate Treated HeLa H1fr...
0-23% 10, 23-38% 70, 38-100% 80, 0% 90

10/09/13 17:56:31

2 pmol H1 frac 25 MF, variable ETD/PTR



141.2 A → T @ 141

***SETAPAAPAAAAPPAEKPVKKKAACKAGGTPRKASGI**

Charge	Monoisotopic Mass	Average Mass
1	21293.7355	21306.70
2	10647.3714	10653.85
3	7094.5834	7102.90
4	5324.1893	5327.43
5	4259.5529	4262.15
6	3549.7953	3551.96
7	3042.8256	3044.68
8	2662.5983	2664.22
9	2368.8660	2368.31
10	2130.2801	2131.58
11	1938.7098	1937.89
12	1775.4013	1776.48
13	1638.9094	1639.91
14	1521.9164	1522.84
15	1420.5225	1421.39
16	1331.8028	1332.61
17	1253.5207	1254.28
18	1183.9366	1184.68
19	1121.6772	1122.38
20	1065.6437	1066.29
21	1014.9467	1015.56
22	968.8588	969.45
23	926.7781	927.34
24	888.2043	888.74
25	852.7164	853.24

H1 fraction 10092013 - que 2
Batchrate - HeLa #1639-650 A → TQ 141

Supplemental Figure 8 (cont)

Fragment Masses

+6 z ions	+5 z ions	+4 z ions	+3 z ions	+2 z ions	+1 z ions	Sequence (item # + 42...)		+1 z ions	+2 z ions	+3 z ions	+4 z ions	+5 z ions	+6 z ions	
25.3521	30.2211	37.5246	49.8970	74.0419	147.0765	1	S	212	21293.7355	10847.3714	7088.5834	5324.1893	4259.5529	3549.7953
46.8592	56.0296	69.7852	92.7112	138.5632	276.1190	2	E	211	21148.6742	10574.8407	7050.2296	5267.9240	4230.5407	3525.6184
63.7005	76.2392	95.0471	126.3938	189.0870	377.1867	3	T	210	21019.6316	10510.3194	7007.2154	5255.6634	4204.7321	3504.1113
76.6400	90.1488	112.8084	160.0739	234.6059	448.2038	4	A	209	20918.5839	10459.7956	6973.5232	5230.4014	4184.5228	3467.2700
91.7155	109.8571	137.0698	182.4237	273.1319	545.2566	5	P	208	20847.5468	10424.2770	6949.0069	5212.0422	4170.5126	3475.0005
103.5550	124.0646	154.8289	206.1028	308.8505	616.2937	6	A	207	20750.4940	10375.7506	6917.5026	5188.3796	4150.9046	3459.2551
118.3945	138.3720	173.6882	230.7418	344.1891	687.9308	7	A	206	20679.4569	10340.2321	6893.8238	5170.6197	4136.8972	3447.4155
131.5700	157.8825	196.8514	262.1327	362.6954	788.3836	8	P	205	20608.4408	10301.7406	6870.1448	5166.0004	4122.4986	3455.5766
143.4095	171.8900	214.8106	285.8118	428.2140	855.4207	9	A	204	20511.3870	10258.1872	6837.7933	5128.5972	4103.0792	3419.4006
155.2490	186.0974	232.3699	309.4908	463.7326	926.4578	10	A	203	20440.3299	10220.8686	6814.1148	5110.8378	4088.8718	3407.5610
167.0888	200.3048	250.1292	333.1898	499.2511	987.4040	11	A	202	20389.2928	10185.1500	6870.4358	5093.0787	4074.8644	3395.7215
183.2846	210.7145	274.3924	366.6208	547.7744	1004.4477	12	P	201	20280.0467	10144.0016	6873.5194	5080.4370	3363.8820	
199.4355	239.1259	288.6556	387.8717	596.3039	1191.8005	13	P	200	20204.2039	10101.1051	6784.4068	5051.0502	4041.0404	3367.7008
211.2790	253.3333	316.4149	421.5507	631.8224	1262.8376	14	A	199	20104.1502	10052.5787	6782.0549	5026.7930	4021.6359	3351.5311
232.7881	279.1419	348.8755	564.5849	898.3437	1391.8802	15	E	198	20033.1130	10017.0602	6678.3759	5009.0337	4007.4284	3339.8916
254.1353	304.7608	360.6892	507.2632	760.3912	1519.7751	16	K	197	19904.0705	9952.5389	6635.3617	4978.7731	3981.8199	3318.1845
264.0746	240.0000	208.4585	300.0493	705.0000	1459.4493	17	A	196	19775.9755	9888.4914	6592.8633	4944.7493	3956.0009	3296.8353
282.1502	338.3785	422.7217	563.2932	844.4361	1687.8650	18	P	195	19704.9304	9852.9720	6500.0045	4920.9901	3941.7885	3264.9956
298.6616	358.1925	447.4888	596.3160	893.9704	1786.8334	19	V	194	19607.8856	9804.4464	6536.6334	4902.7269	3922.3829	3268.8203
320.1080	383.8115	479.5126	639.0143	958.0178	1915.0284	20	K	193	19508.8172	9754.9122	6503.6106	4877.9598	3902.5693	3252.3089
341.3800	408.4305	511.5363	681.7126	1022.0653	2043.1234	21	K	192	19380.7226	9690.8848	6460.9123	4845.9360	3876.9503	3230.9598
362.7091	435.0495	543.5800	724.4110	1086.1128	2171.2183	22	K	191	19252.6273	9626.8173	6418.2139	4813.9123	3851.3313	3209.6106
374.5484	449.2569	561.3193	748.0900	1121.8314	2242.2554	23	A	190	19124.5233	9562.7698	6375.5150	4781.8885	3825.7123	3188.2614
386.3882	463.4843	579.0786	771.7690	1157.1499	2313.2925	24	A	189	19053.4952	9527.2512	6351.8368	4784.1293	3811.5049	3178.4219
407.7373	489.0833	611.1023	814.4674	1221.1974	2441.3875	25	K	188	18982.4581	9491.7327	6288.1575	4746.3700	3797.2974	3164.5824
429.0868	514.7023	843.1261	857.1657	1285.2449	2569.4825	26	K	187	18854.3631	9427.6852	6285.4592	4714.3462	3771.6784	3143.2332
440.9260	528.9097	660.8854	880.8447	1320.7634	2640.5196	27	A	186	18726.2062	9363.6377	6242.7609	4682.3225	3746.0595	3121.8841
450.4286	540.3140	675.1407	889.8519	1349.2742	2697.5411	28	G	185	18655.2310	9328.1192	6219.0819	4664.5832	3731.8520	3110.0446
459.9331	551.1783	688.3981	918.8590	1377.7849	2754.5625	29	G	184	18598.2096	9299.6084	6200.0747	4650.3079	3720.4477	3100.5410
476.7744	574.0370	714.6880	962.6416	1436.3997	2944.8103	30	T	183	18541.1881	9217.0977	6181.0676	4636.0525	3709.0434	3091.0374
492.9499	511.3384	738.9212	984.8925	1476.8351	2952.8630	31	P	182	18444.1404	9190.7700	6147.0866	4610.7996	3666.8890	3074.4061
518.9667	622.5586	777.9485	1036.0262	1554.8857	3108.7841	32	R	181	18343.0877	9172.0475	6115.0341	4586.5274	3669.4234	3058.0207
540.3159	648.1776	809.9702	1079.6245	1618.9332	3236.8590	33	K	180	18188.9866	9093.9969	6083.0004	4547.5021	3638.2031	3032.0038
552.1554	662.3851	827.7295	1103.3036	1654.4517	3307.9861	34	A	179	18058.8916	9029.9494	6020.3020	4515.4784	3612.5841	3010.8547
566.6608	679.7915	849.4875	1132.3142	1697.9677	3394.9282	35	S	178	17987.8545	8994.4304	5996.8230	4497.7191	3598.3767	2998.8151
578.1643	694.1057	863.7420	1151.0214	1720.4705	3451.4460	36	G	177	17900.8225	8950.9149	5967.8123	4475.9811	3580.9703	2984.3098
582.3308	710.6083	884.0084	1184.4720	1776.0014	3540.0024	37	P	176	17840.8010	8822.4041	5948.0652	4464.7057	3560.5860	3024.8062
608.5153	730.0168	912.2692	1216.0232	1823.5312	3646.0552	38	P	175	17740.7468	8870.8778	5914.0543	4457.4495	3560.6866	3048.6908
625.2326	749.8305	937.0364	1249.0460	1873.0654	3745.1236	39	V	174	17649.6955	8825.3514	5813.9034	4413.1793	3530.7449	2942.4553
639.5320	767.2369	958.7844	1278.0567	1916.5814	3832.1558	40	S	173	17550.6270	8775.8172	5850.8805	4388.4122	3510.9312	2925.9439
661.0391	793.0455	991.0590	1321.0709	1981.1027	3961.1982	41	E	172	17463.5950	8732.3011	5821.8699	4386.6542	3493.5248	2911.4386
679.8864	815.6623	1019.3260	1358.7585	2037.8448	4074.2823	42	L	171	17334.5524	8667.7798	5778.8557	4334.3936	3467.7163	2889.9315
698.7338	838.2791	1047.5970	1396.4603	2094.1888	4187.3663	43	I	170	17221.4684	8611.2378	5741.6161	4306.1225	3445.0995	2871.0841
715.5751	858.4886	1072.5850	1430.1429	2144.7106	4288.4140	44	T	169	17108.3843	8554.6958	5703.4863	4277.8515	3422.4827	2852.2368
736.9244	884.1076	1104.8827	1472.8412	2208.7587	4416.5090	45	K	168	17007.3366	8504.1719	5669.7837	4252.5896	3402.2731	2835.3955
748.7837	888.3150	1226.6420	1496.5202	2244.2767	4487.5461	46	A	167	16879.2417	8440.1245	5627.0854	4220.5659	3376.8542	2814.0463
765.2751	918.1287	1147.4091	1529.5430	2293.8109	4588.6145	47	V	166	16808.2045	8404.0569	5603.4064	4202.8066	3362.4467	2802.2068
777.1147	932.3361	1165.1684	1553.2221	2329.3264	4657.6516	48	A	165	16709.1361	8355.0717	5570.3836	4178.0395	3342.6330	2785.8954
788.9542	946.5436	1182.9276	1576.9011	2364.8480	4726.6867	49	A	164	16638.0960	8319.5531	5546.7045	4160.2802	3328.4256	2773.8559
803.4595	963.9500	1204.8858	1605.9118	2408.3640	4815.7208	50	S	163	16587.0619	8284.0346	5523.0255	4142.5209	3314.2182	2762.0164
824.8087	989.5690	1236.7094	1648.6101	2474.4151	4943.8157	51	K	162	16480.0299	8240.5186	5494.0148	4120.7629	3296.8118	2747.5110
846.3158	1015.3775	1268.9700	1691.6243	2536.8328	5072.8583	52	E	161	16351.8349	8176.4711	5451.3165	4088.7392	3271.1928	2726.1619
872.3326	1046.5977	1307.9953	1743.8580	2614.9834	5228.8504	53	R	160	16222.8923	8111.9498	5408.3023	4056.4785	3245.3843	2704.6548
886.8380	1064.0041	1329.7533	1772.6867	2658.4994	5315.9915	54	S	159	16069.7912	8033.8992	5356.2868	4017.4533	3214.1641	2678.8379
898.3416	1075.4084	1344.0057	1791.6758	2687.0101	5373.0129	55	G	158	15979.7592	7990.3832	5327.2579	3995.6953	3198.7577	2664.1326
912.8530	1093.2221	1368.7758	1824.6986	2736.5443	5472.0813	56	V</							

H1 fraction 10092013...gue Z.

Supplemental Figure 8 (cont)

Butyrate - Hela #1639-1650

A → T @ 141

Fragment Masses

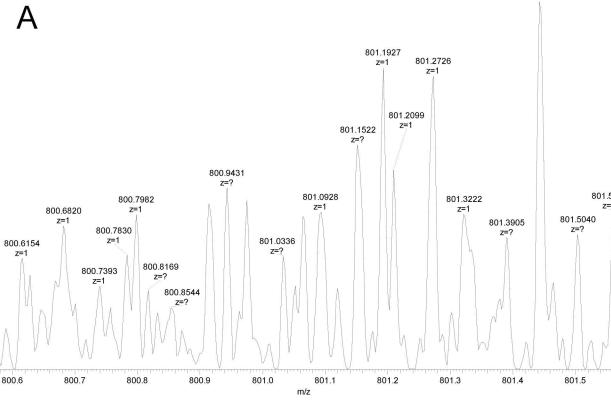
+6 c ions	+5 c ions	+4 c ions	+3 c ions	+2 c ions	+1 c ions	Sequence	+1 z ions	+2 z ions	+3 z ions	+4 z ions	+5 z ions	+6 z ions	
1433.4885	1719.9847	2149.7261	2865.9697	4298.4509	8595.8945	86	L	127	12812.9401	6406.9737	4271.6516	3203.9905	2563.3938
1449.9999	1739.7984	2174.4962	2898.9925	4347.9851	8694.9630	87	V	126	12899.8581	6350.4317	4233.9589	3175.7195	2540.7770
1464.5052	1757.2048	2196.2542	✓ 2928.0032	4391.5011	8781.9950	88	S	125	12600.7877	6300.8975	4200.9341	3150.9524	2520.9634
1485.8544	1782.8238	2228.2779	2970.7015	4455.5488	8910.0900	89	K	124	12513.7556	6257.3815	4171.9234	3129.1944	2503.5569
1495.3580	1794.2281	2242.5333	2989.7087	4484.0593	8987.1114	90	G	123	12385.6607	6163.3340	4129.2251	3097.1706	2477.9380
1512.1992	1814.4376	✓ 2287.7952	✓ 3023.3912	4534.5832	9068.1591	91	T	122	12328.6392	6164.8232	4110.2179	3082.9153	2466.5337
1531.0466	1837.0545	✓ 2298.0662	✓ 3061.0859	4581.1252	9181.2432	92	L	121	12227.5915	6114.2984	4076.5534	3057.6533	2446.3241
1547.5580	1854.8881	✓ 2320.8333	✓ 3094.1087	4640.6594	9280.3116	93	V	120	12114.5075	6057.7574	4038.8407	3029.3823	2423.7073
1588.9011	1882.4799	✓ 2352.8480	✓ 3136.7849	4704.8887	9408.3701	94	Q	119	12015.4391	6008.2232	4005.8179	3004.8152	2403.8936
1585.7424	1902.6894	✓ 2378.1099	✓ 3170.4775	4755.2126	9509.4178	95	T	118	11887.3805	5944.1938	3963.1317	2972.6006	2378.2819
1607.0915	1928.3084	✓ 2410.1337	✓ 3183.1758	4819.2600	9637.5128	98	K	117	11786.3328	5938.6700	3929.4491	2947.3387	2358.0724
1618.5591	1939.7127	✓ 2424.5890	✓ 3232.1829	4847.7708	9694.5343	97	G	116	11658.2378	5829.6229	3886.7508	2915.3149	2332.4534
1633.4384	1959.9222	✓ 2449.8509	✓ 3265.8655	4898.2946	9795.5819	98	T	115	11601.2184	5801.1118	3867.7436	2901.0598	2321.0491
1842.9400	1971.3285	✓ 2463.9063	✓ 3284.8727	4926.8053	9852.8034	99	G	114	11500.1687	5750.5880	3834.0611	2875.7978	2300.8396
1854.7795	1985.5339	✓ 2481.8658	✓ 3308.5517	4962.3239	9923.8405	100	A	113	11443.1472	5722.0773	3815.0539	2861.5423	2289.4353
1869.2448	2003.9403	✓ 2503.4236	✓ 3337.5624	5005.8399	10010.6725	101	S	112	11372.1101	5688.5587	3791.3749	2843.7830	2275.2278
1878.7884	2014.3446	✓ 2517.8790	✓ 3356.5895	5034.3506	10067.6940	102	G	111	11285.0781	5643.0427	3762.3642	2822.0250	2257.8214
1693.2937	2031.7510	✓ 2539.4370	✓ 3385.5802	5077.8867	10154.7260	103	S	110	11228.0586	5614.5319	3743.3571	2807.7896	2246.4171
1717.8051	2061.1847	✓ 2578.2041	✓ 3448.8030	5151.1409	10301.7944	104	F	109	11141.0246	5711.0519	3714.3464	2786.0118	2229.0107
1739.1543	2088.7837	✓ 2604.2278	✓ 3477.3013	5215.4483	10429.8894	105	K	108	10993.9562	5479.4817	3685.3236	2749.2445	2199.5971
1758.0016	2109.4005	✓ 2638.4988	✓ 3454.9980	5271.9904	10542.9735	106	L	107	10865.8612	5433.4342	3622.6253	2717.2208	2173.9781
1777.0888	2123.2091	✓ 2685.0098	✓ 3553.0103	5329.0118	10657.0184	107	N	106	10752.7772	5376.8922	3584.9306	2668.9497	2151.3613
1798.3580	2157.8281	✓ 2697.0333	✓ 3595.7088	5393.0593	10785.1114	108	K	105	10838.7342	5319.8708	3546.9183	2660.4390	2128.5527
1819.7071	2183.4471	✓ 2729.0570	✓ 3638.4070	5457.1088	10913.2063	109	K	104	10510.8393	5255.8233	3504.2179	2628.4153	2102.9337
1831.5466	2197.8545	✓ 2746.8163	✓ 3662.0860	5492.8254	10984.2434	110	A	103	10382.5443	5191.7758	3481.5196	2596.3915	2077.3147
1843.3862	2211.8819	✓ 2764.5758	✓ 3685.7650	5528.1439	11055.2806	111	A	102	10311.5072	5156.2572	3437.8406	2578.8323	2063.1073
1857.8915	2229.2683	✓ 2788.3336	✓ 3714.7757	5571.6599	11211.3126	112	S	101	10240.4701	5120.7387	3414.1815	2580.8730	2048.8998
1887.3951	2240.6726	✓ 2800.5890	✓ 3733.7828	5600.1707	11199.3341	113	G	100	10153.4380	5077.2227	3385.1508	2539.1150	2031.4934
1888.9022	✓ 2260.4811	✓ 2832.8496	✓ 3776.7971	5664.8920	11328.3768	114	E	99	10098.4186	5048.7119	3386.1437	2524.8596	✓ 2020.0891
1900.7417	✓ 2280.6886	✓ 2850.4769	✓ 3800.4761	5700.2105	11399.4138	115	A	98	9967.3740	4948.1908	3323.1295	2492.5980	✓ 1994.2806
1932.0000	✓ 2808.3078	✓ 3088.6236	✓ 3243.1744	✓ 3744.8690	11637.6987	116	K	97	9896.3369	4948.6721	3299.4508	2474.8597	✓ 1980.0732
1938.2663	✓ 2325.7181	✓ 2904.8958	✓ 3875.5253	5812.7844	11624.5615	117	P	96	✓ 0788.2410	4844.6246	✓ 0655.1222	✓ 2442.6136	✓ 1954.4542
1959.8155	✓ 2351.3371	✓ 2938.9196	✓ 3818.2237	5878.8319	11752.6564	118	K	95	9671.1891	4836.0982	✓ 3224.4012	2418.5527	✓ 1935.0438
1976.1269	✓ 2371.1508	✓ 2963.8867	✓ 3861.2465	5926.3861	11851.7249	119	V	94	9543.0942	4772.0507	3181.7029	2388.5280	✓ 1909.4247
1997.4760	✓ 2396.7698	✓ 2995.7104	✓ 3993.9448	5990.4136	11979.8198	120	K	93	944.0258	4722.5165	3148.8801	2381.7610	1889.6110
2018.8252	✓ 2242.3888	✓ 3027.7342	✓ 4036.6431	6054.4610	12107.9148	121	K	92	9315.9308	4658.4690	3105.9818	2329.7382	1863.9920
2030.8647	✓ 2436.5962	✓ 3045.4934	✓ 4060.3222	6089.8798	12178.9519	122	A	91	9187.8358	4594.4218	3083.2835	2297.7144	1838.3730
2040.1883	✓ 2448.0005	✓ 3059.7488	✓ 4079.3293	6118.4903	12235.9734	123	G	90	9116.7987	4585.9030	3039.6044	2279.9551	1824.1656
2049.8719	✓ 2459.4048	✓ 3074.0042	✓ 4098.3365	6147.0011	12292.9948	124	G	89	9059.7773	4530.3923	3020.5973	2265.8998	1812.7813
2066.5131	✓ 2479.6143	✓ 3099.2661	✓ 4132.0190	6197.5249	12394.0425	125	T	88	9002.7558	4501.8815	3030.1501	2251.4444	✓ 1801.3570
2087.8888	✓ 2505.6666	✓ 3141.0008	✓ 4141.7473	6204.6764	12662.1675	126	K	87	✓ 0801.7081	4451.3577	2967.9078	2226.1825	✓ 1781.1474
2104.0378	✓ 2524.8439	✓ 3155.5530	✓ 4207.0683	6310.9888	12619.1902	127	P	86	✓ 0773.6132	4467.3102	2926.2002	✓ 2104.1687	✓ 1766.6268
2125.3869	✓ 2550.2629	✓ 3187.5788	✓ 4249.7666	6374.1462	12747.2852	128	K	85	✓ 0876.5604	4338.7838	2892.8583	✓ 2169.8958	✓ 1736.1179
2140.7064	✓ 2575.0010	✓ 3210.0005	✓ 4260.1610	6400.1607	12975.0000	129	K	84	✓ 0848.4654	4274.7364	2850.1600	✓ 2137.8718	✓ 1710.4988
2162.9116	✓ 2595.2924	✓ 3243.8637	✓ 4242.8158	6486.7201	12972.4329	130	P	83	✓ 0820.0705	4210.0000	✓ 2007.4017	✓ 2105.0401	✓ 1684.0700
2179.4230	✓ 2615.1061	✓ 3268.8308	✓ 4268.2345	6536.2543	13071.5013	131	V	82	✓ 0833.3177	4162.1625	2725.1108	✓ 2081.5849	✓ 1665.4694
2188.9285	✓ 2628.5104	✓ 3282.8862	✓ 4276.8458	6564.7650	13128.5228	132	G	81	✓ 0824.2493	4162.6283	2742.0879	✓ 2056.8178	✓ 1645.6557
2200.7660	✓ 2640.7178	✓ 3300.6454	✓ 4400.5248	6600.2836	13199.5599	133	A	80	✓ 0817.2278	4084.1176	2723.0808	✓ 2042.5824	✓ 1634.2514
2212.6056	✓ 2654.9252	✓ 3318.4047	✓ 4424.2038	6635.8022	13270.5970	134	A	79	✓ 0806.1907	4086.5990	2699.4018	✓ 2024.8031	✓ 1620.0440
2233.9547	✓ 2680.5442	✓ 3320.4265	✓ 4466.8022	6699.8496	13308.8920	135	K	78	✓ 0825.1536	4013.0804	2675.7227	✓ 2007.0439	✓ 1605.8365
2255.3030	✓ 2708.4833	✓ 3342.4522	✓ 4500.4006	6763.8074	13438.7470	136	K	77	✓ 0879.0586	3949.0330	2633.0244	✓ 1975.0201	✓ 1580.2175
2271.4794	✓ 2725.5738	✓ 3406.7154	✓ 4541.9514	6812.4235	13623.8397	137	P	76	✓ 0768.0637	3884.0865	2600.3284	✓ 1942.0004	✓ 1666.6667
2292.8285	✓ 2751.1928	✓ 3438.7391	✓ 4584.8467	6875.4710	13751.9347	138	K	75	✓ 0767.1910	3876.4591	2557.9752	✓ 1918.7332	✓ 1535.1880
2314.1777	✓ 2776.8118	✓ 3470.7629	✓ 4621.3481	6940.5185	13880.0296	139	K	74	✓ 0743.8159	3772.4116	2515.2768	✓ 1888.7094	✓ 1509.5690
2326.0172	✓ 2791.0192	✓ 3488.5221	✓ 4651.0271	6976.0370	13951.0686	140	A	73	✓ 0745.7210	3707.3841	2472.5785	✓ 1854.6857	✓ 1483.9500
2342.8658	✓ 2811.2287	✓ 3513.7841	✓ 4684.7097	7026.5609	14052.1144	141	T	72	✓ 0744.6539	3672.4846	2448.8995	✓ 1836.9284	✓ 1469.7426
2352.3620	✓ 2822.6												

Fragment Masses

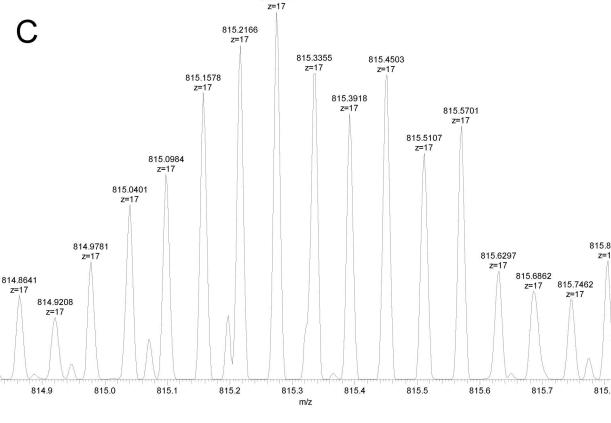
+6 c ions	+5 c ions	+4 c ions	+3 c ions	+2 c ions	+1 c ions	Sequence	+1 z ions	+2 z ions	+3 z ions	+4 z ions	+5 z ions	+6 z ions	
2857.6080	3428.6083	4086.7684	6744.0087	8670.5004	17430.0417	172	S 41	4242.7710	2121.8891	1414.9285	1061.4482	849.3600	707.9679
2873.6835	3448.2187	4310.0216	5746.3587	8619.0358	17237.0844	173	P 40	4156.7668	2070.0761	1305.9170	1059.0902	851.8550	685.4026
2895.0326	3473.8377	4342.0453	5789.0580	8683.0833	17365.1594	174	K 39	4058.6882	2028.8467	1353.5689	1015.4270	812.5431	677.2871
2916.3818	3499.4587	4374.0690	5831.7583	8747.1308	17493.2543	175	K 38	3930.5912	1965.7983	1310.8686	983.4033	786.9241	655.9379
2928.2213	3513.6641	4391.8263	5855.4353	8782.8494	17564.2915	176	A 37	3802.4963	1901.7514	1268.1703	951.3795	781.3051	634.5888
2949.5705	3539.2831	4423.8521	5898.1337	8846.6968	17892.3864	177	K 36	3731.4592	1866.2332	1244.4912	933.8202	747.0977	622.7493
2966.0819	3559.0968	4448.6192	5931.1565	8896.2311	17791.4548	178	V 35	3603.3642	1802.1857	1201.7929	901.5065	721.4787	601.4001
2977.9214	3573.3042	4468.3784	5954.8355	8931.7496	17862.4919	179	A 34	3504.2958	1752.6515	1168.7701	876.8294	701.6650	584.8887
2999.2705	3598.0232	4498.4022	5907.6324	8906.7073	17900.5880	180	K 33	3433.2587	1717.1334	1145.0911	859.0701	687.4576	573.0492
3015.4460	3618.3338	4522.6654	6029.8847	9044.3235	18087.8397	181	P 32	3305.1837	1663.0655	1102.0020	927.0404	801.8886	561.7000
3036.7952	3643.9527	4554.6891	6072.5831	9108.3710	18215.7346	182	K 31	3208.1110	1604.5591	1070.0418	802.7832	642.4280	535.5246
3058.1443	3669.5717	4586.7129	6115.2814	9172.4184	18343.8296	183	K 30	3080.0160	1540.5116	1027.3435	770.7595	616.8090	514.1754
3069.9838	3683.7702	4604.4721	6138.9604	9207.9370	18414.8667	184	A 29	2951.9210	1476.4642	984.6452	738.7357	591.1900	492.8262
3081.8234	3697.9866	4622.2314	6162.6395	9243.4556	18485.9038	185	A 28	2880.8839	1440.9456	960.9662	720.9764	576.9826	480.9867
3103.1725	3723.6056	4654.2552	6205.3378	9307.5030	18613.9988	186	K 27	2809.8468	1405.4270	937.2871	703.2172	562.7752	489.1472
3117.8779	3741.0120	4678.0132	6234.3485	9351.0190	18701.0308	187	S 28	2681.7518	1341.3795	994.5888	871.1934	537.1582	447.7980
3129.5174	3755.2194	4693.7724	6258.0275	9386.5376	18772.0679	188	A 25	2594.7198	1297.8635	865.5781	649.4354	519.7488	433.2927
3141.3589	3769.4268	4711.5317	6281.7065	9422.0562	18843.1051	189	A 24	2523.6827	1262.3450	841.8991	631.6761	505.5424	421.4532
3162.7061	3795.0458	4743.5555	6324.4049	9486.1038	18971.2000	190	K 23	2452.6456	1226.8264	818.2200	613.9169	491.3349	409.6137
3174.5456	3809.2532	4761.3147	6348.0839	9521.6222	19042.2371	191	A 22	2324.5506	1162.7789	775.5217	581.8931	465.7159	388.2645
3191.0570	3829.0669	4786.0818	6381.1067	9571.1584	19141.3055	192	V 21	2253.5135	1127.2604	751.8427	564.1338	451.5085	378.4250
3203.4084	3854.8850	4818.1056	6433.8650	9635.2030	19260.4095	193	K 20	2154.4451	1077.7262	718.8199	539.3667	431.8948	359.9136
3228.5816	3874.0965	4842.3688	6456.1559	9683.7303	19366.4533	194	P 19	2080.6601	1040.0761	678.1210	567.0460	400.0760	366.5044
3249.9308	3899.7155	4874.3925	6498.8543	9747.7778	19494.5482	195	K 18	1929.2974	965.1523	643.7706	483.0798	386.8653	322.3890
3261.7703	3913.9229	4892.1518	6522.5333	9783.2963	19565.5853	196	A 17	1801.2024	901.1048	5801.0723	451.0561	361.0463	301.0398
3273.8098	3928.1303	4909.9111	6546.2123	9818.6149	19636.6225	197	A 16	1730.1653	865.5863	577.3933	433.2968	348.8389	289.2003
3294.0500	3953.7403	4941.0348	6588.0107	9883.8633	19784.7174	198	K 15	1659.1262	830.0677	553.7142	415.5375	332.6315	277.3608
3311.1344	3973.1599	4968.1980	6621.2616	9931.3887	19861.7702	199	P 14	1534.0322	768.0200	511.0456	366.5166	267.0166	220.0116
3332.4836	3998.7759	4998.2217	6663.9599	9985.4362	19989.8651	200	K 13	1433.9804	717.4939	478.8650	359.2506	287.8019	239.8361
3348.9950	4018.5925	5022.8868	6696.8827	10044.9704	20088.9336	201	V 12	1305.6855	653.4464	435.9667	327.2268	261.8829	218.4870
3365.5064	4038.4062	5047.7580	6730.0055	10094.5044	20188.0208	202	V 11	1206.8171	603.9122	402.9439	302.4597	242.1692	201.9756
3400.0656	4084.0262	5070.7707	6772.7038	10458.6521	20318.0669	203	K 10	1107.7487	554.3780	369.9211	277.6926	222.3558	185.4842
3403.0310	4083.4358	5104.0429	6805.0548	10207.0785	20413.1497	204	P 9	970.6537	490.8805	397.0667	246.0000	199.7666	164.1106
3424.3802	4109.0548	5136.0866	6847.7531	10271.1260	20541.2447	205	K 8	882.8009	441.8041	294.8718	221.4057	177.3280	147.9396
3445.7293	4134.6737	5168.0904	6890.4514	10335.1735	20669.3396	206	K 7	754.5060	377.7566	252.1735	189.3819	151.7070	126.5904
3457.5689	4148.8812	5185.8496	6914.1304	10370.6920	20740.3767	207	A 6	626.4110	313.7091	209.4752	157.3582	126.0880	105.2412
3469.4094	4169.0866	5203.8039	6937.8006	10406.2406	20844.4430	208	A 5	555.3739	278.1906	185.7961	139.5989	111.8808	93.4017
3485.5838	4182.4991	5227.8721	6970.1804	10454.7369	20908.4686	209	P 4	494.8666	242.0720	162.1171	124.0006	91.0762	61.3022
3506.9330	4208.1181	5259.8959	7012.8587	10518.7844	21036.5816	210	K 3	387.2840	194.1456	129.7662	97.5785	78.2826	65.3867
3528.2822	4233.7371	5291.9196	7055.5570	10582.8319	21164.6565	211	K 2	259.1890	130.0982	87.0679	65.5527	52.6436	44.0376
3549.7953	4259.5529	5324.1893	7098.5834	10647.3714	21293.7355	212	K 1	131.0941	66.0507	44.3895	33.5290	27.0246	22.6884

Supplemental Figure 9

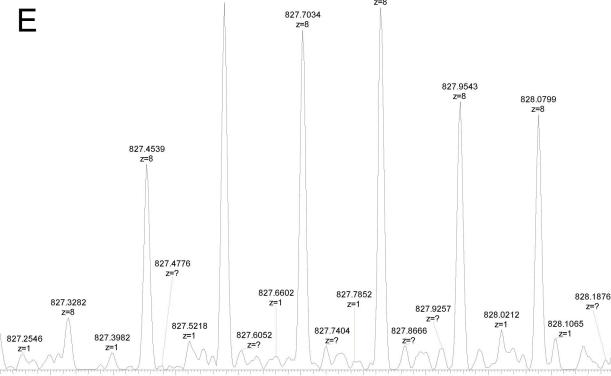
LCA SAU ButyrateTreatedHeLa H2B parking screen 150219111845 #2594-2636 RT: 53.63-54.34 AV: 5 NL: 4.88E5
F: FTMS + p NSI Full ms2 810.00@cd0.00 [625.00-2000.00]



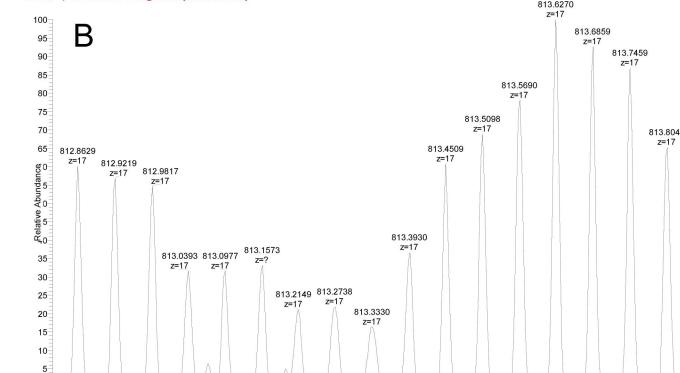
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F: FTMS + p NSI Full ms2 810.00@cd0.00 [625.00-2000.00]



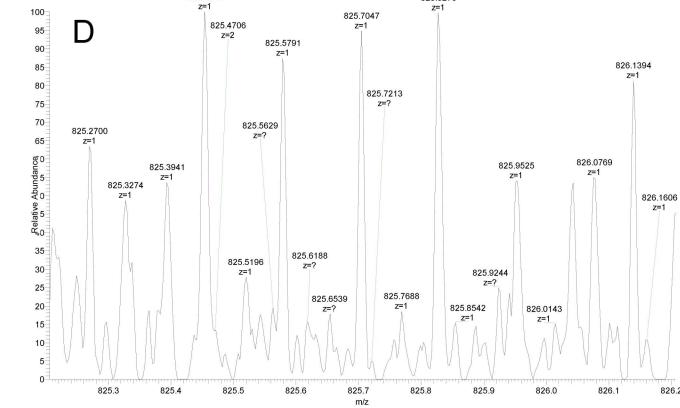
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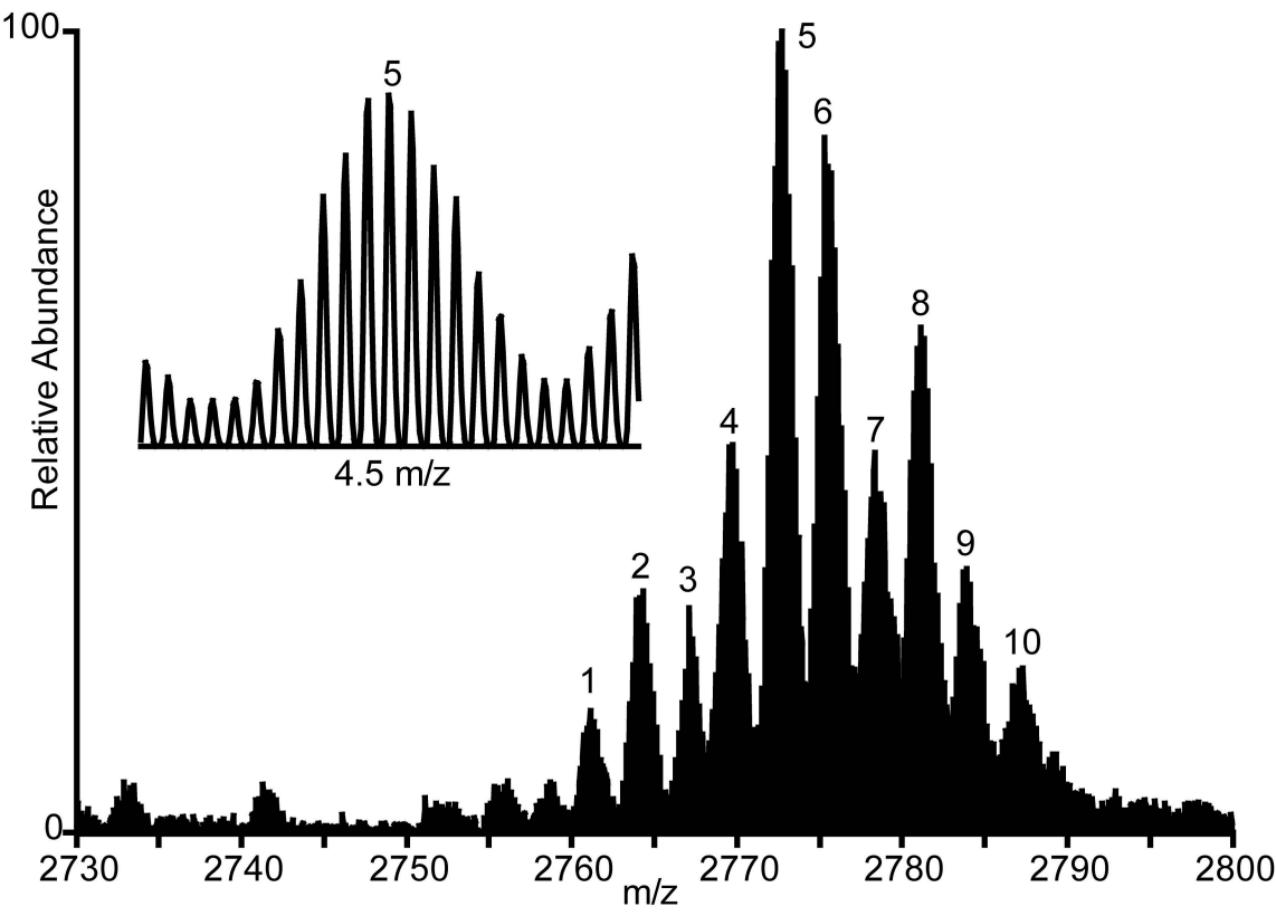
LCA SAU ButyrateTreatedHeLa H2B parking screen 150219111845 #2594-2636 RT: 53.63-54.34 AV: 5 NL: 5.15E6
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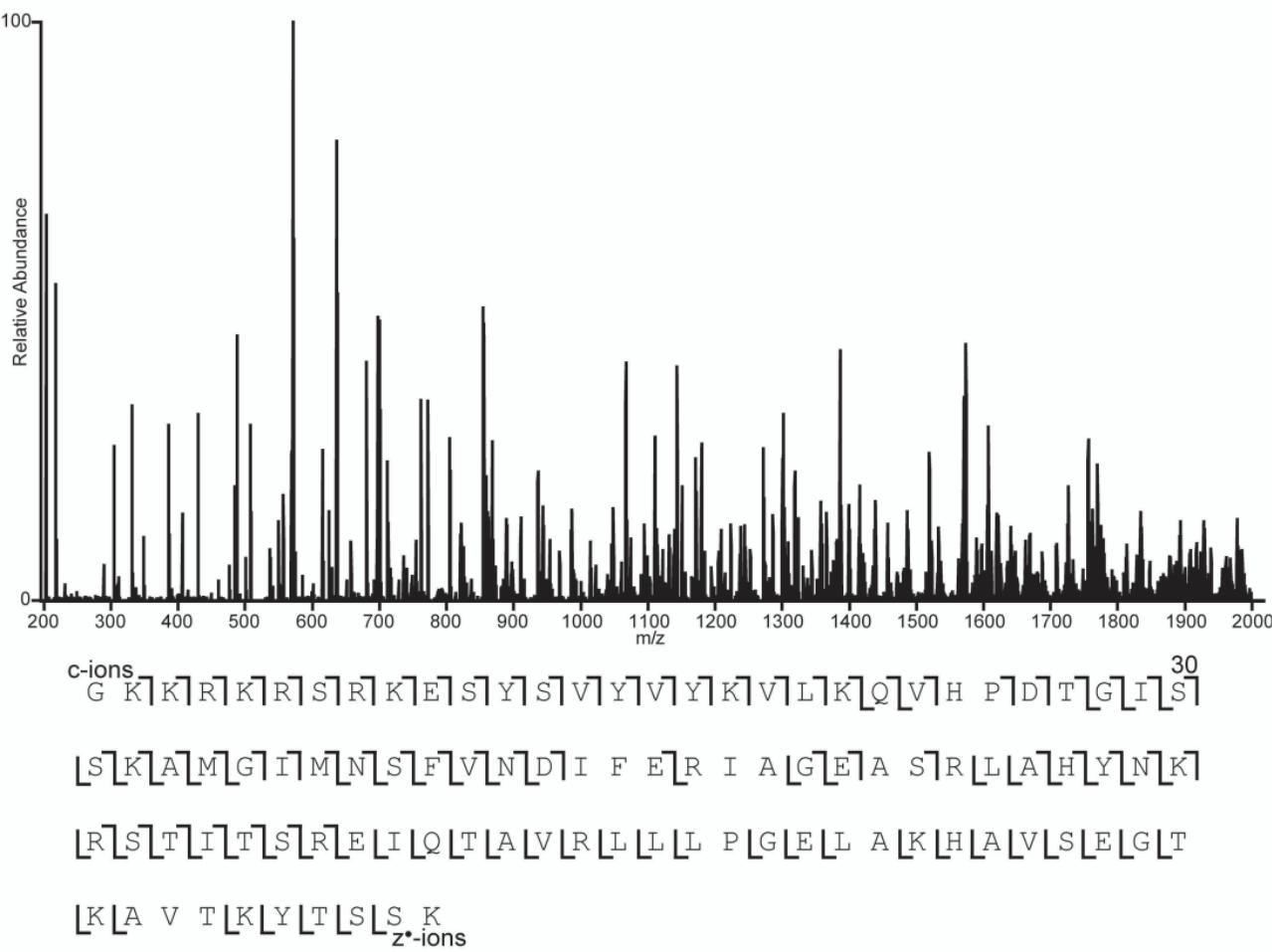
LCA SAU ButyrateTreatedHeLa H2B parking screen 150219111845 #2594-2636 RT: 53.63-54.34 AV: 5 NL: 5.16E5
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Supplemental Figure 10

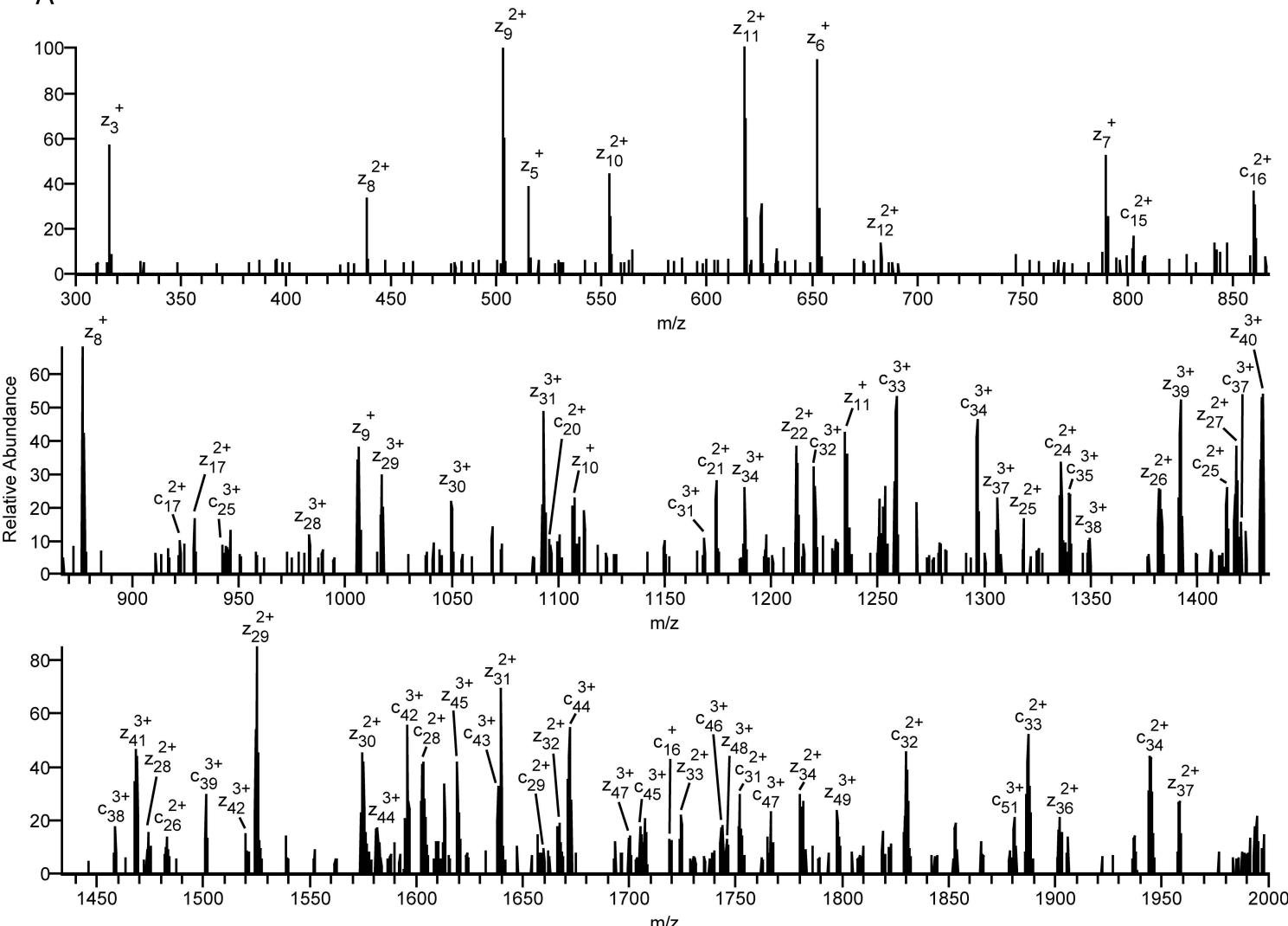


Supplemental Figure 11



Supplemental Figure 12 A

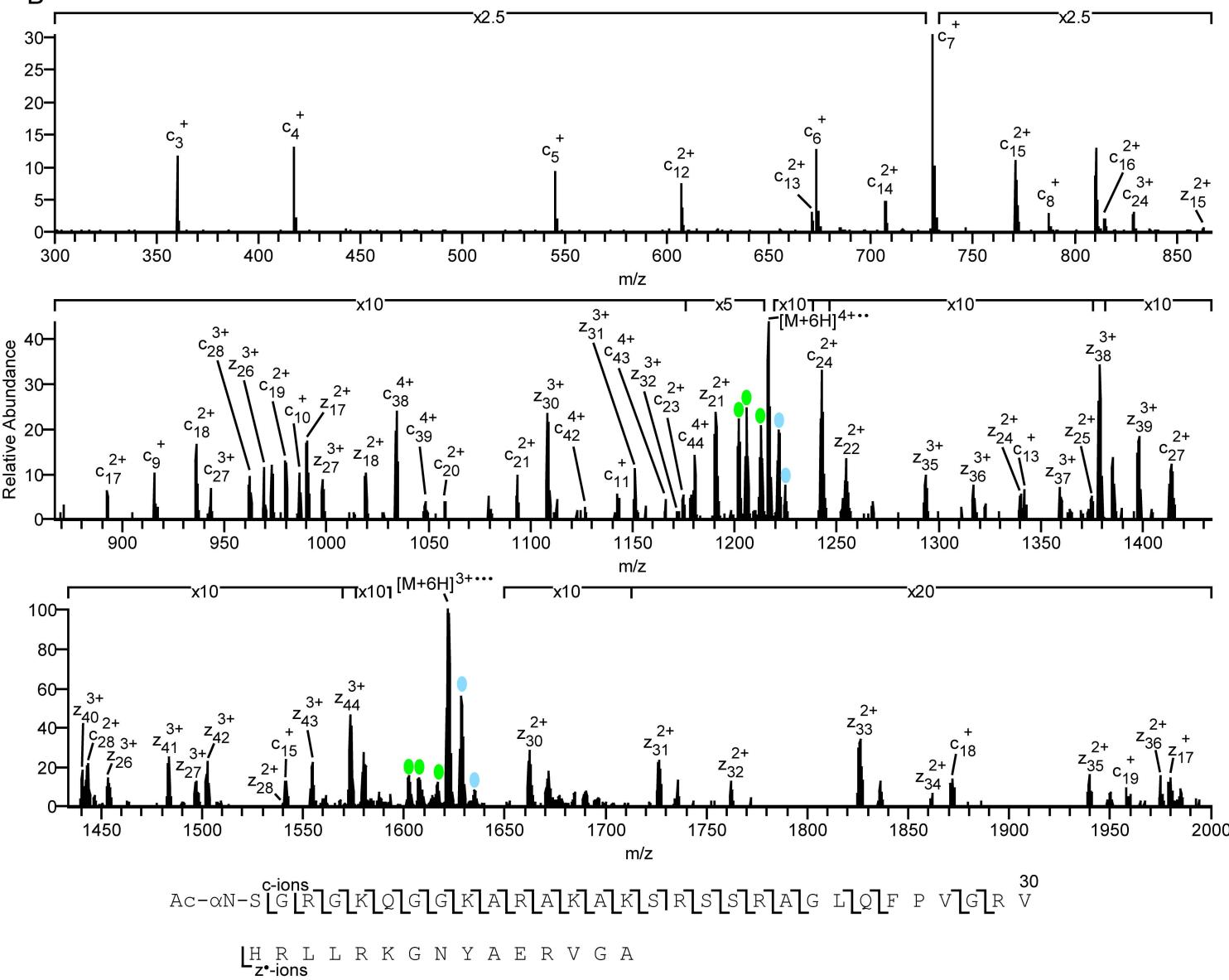
A



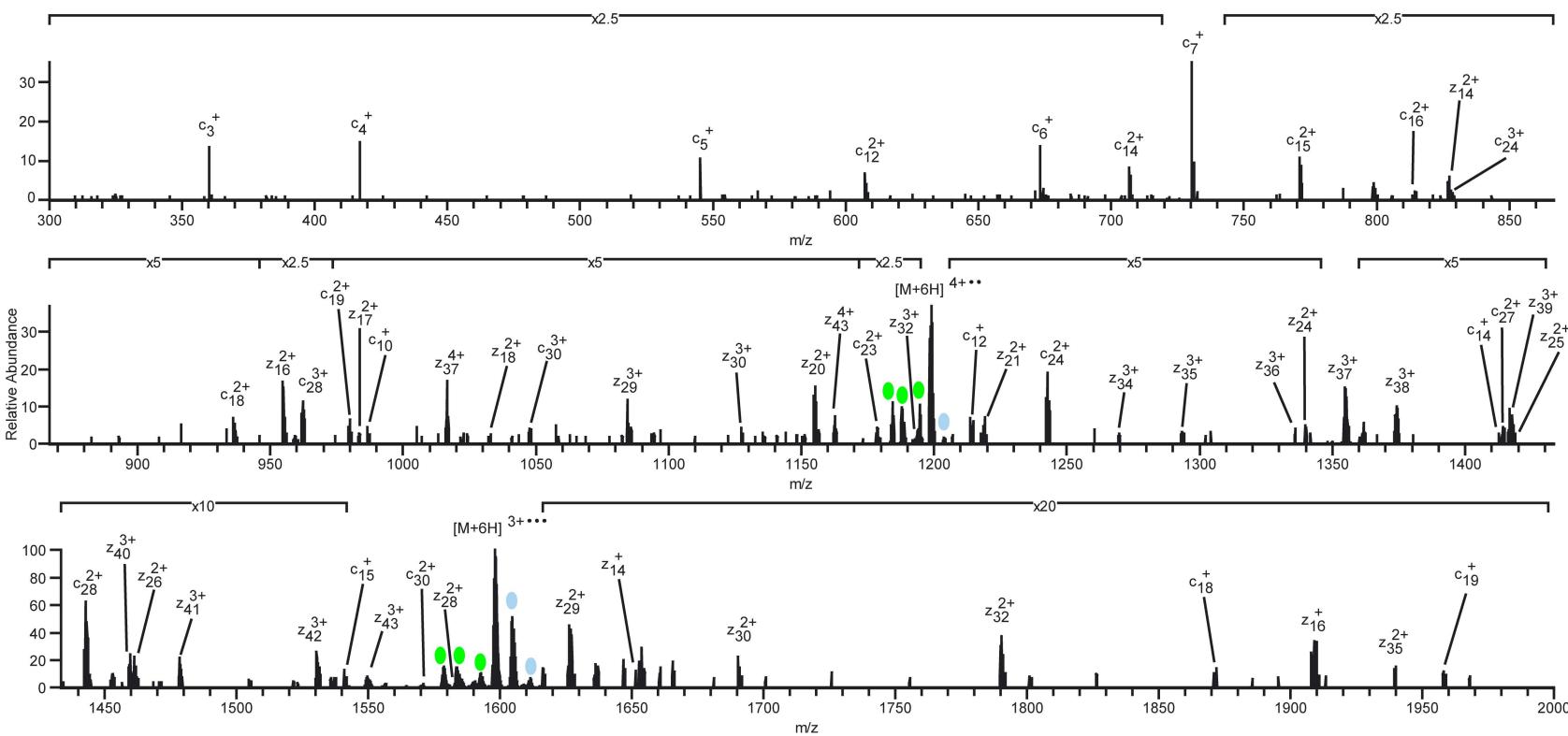
Y L T A E I L E L A G N A A R D N K K T R I I P R H L Q L L A
 I R N D E E L I N K L L G K V T I A Q L G G V L P N I Q L A V L L
 P K K L T E S H H K A L K G K
 z⁻-ions

Supplemental Figure 12 B

B

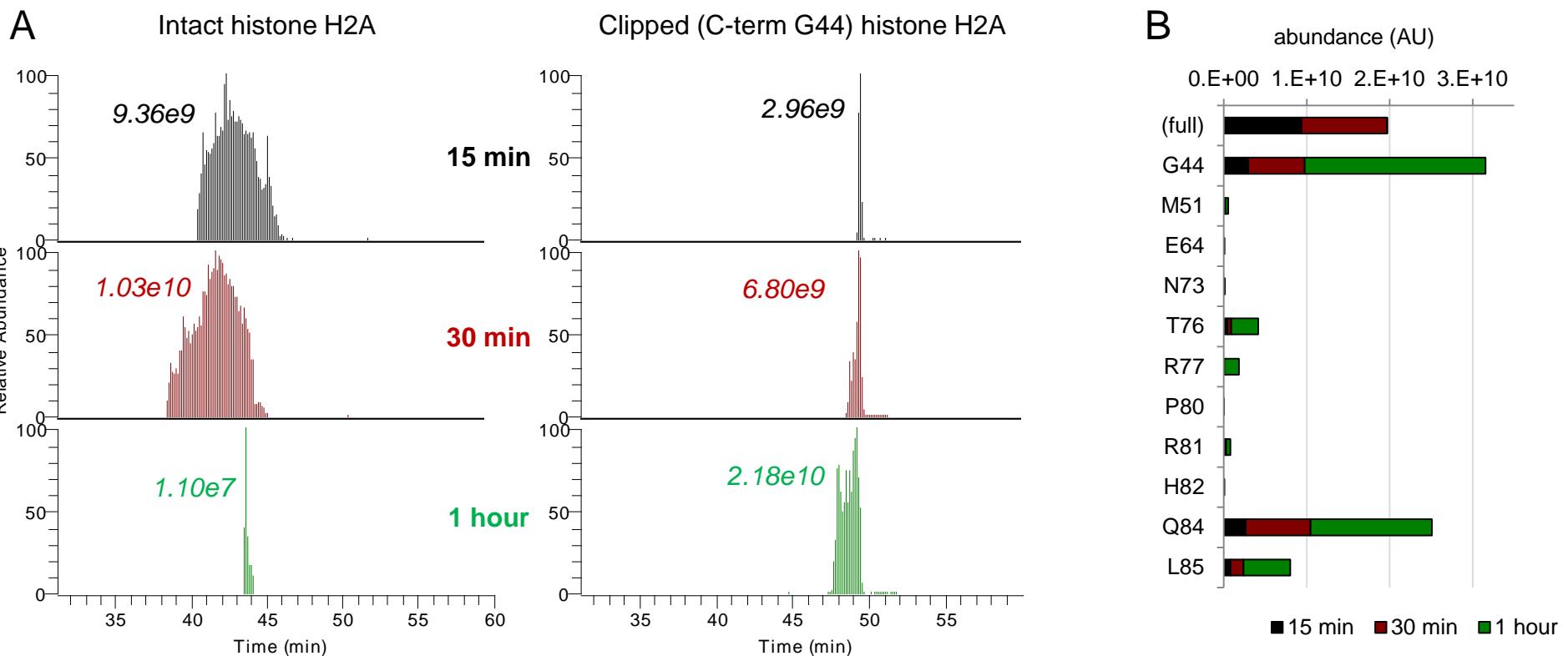


Supplemental Figure 12 C

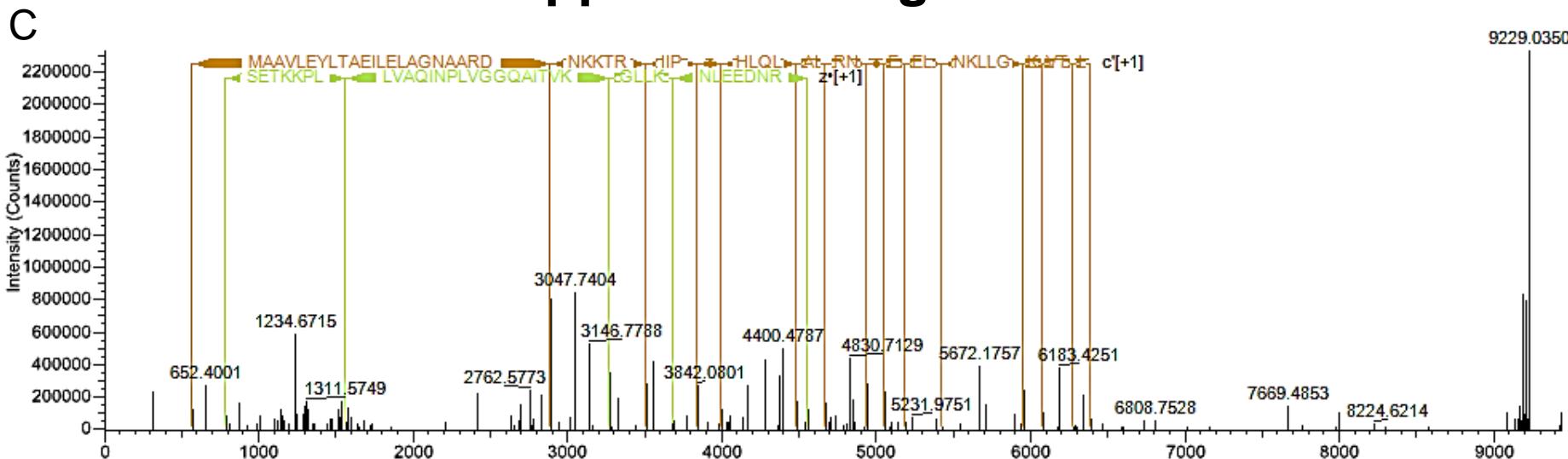


AC- α N-S³⁰ C-ions $\text{G-R-G-K-Q-G-G-K-A-R-A-K-A-K-S-R-S-S-R-A-G-L-Q-F-P-V-G-R-V}$

$\text{H}_\bullet \text{R-L-L-R-K-G-N-Y-A-E-R-V-G}$
 z-ions



Supplemental Figure 13



Supplemental Table 1

Sequence	Residues	AU
SGRKQGGKARAKAKSRSSRAGLQFPVGRVHRLRKGNYAERVGAGAPVYMAAVLE-56	Intact	6.671E+10
57-YLTAEILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVTTAQGGVLPNIQAVLLPKKTESHHKAKGK	1-129	
SGRKQGGKARAKAKSRSSRA	1-21	1.727E+07
SGRKQGGKARAKAKSRSSRAG	1-22	2.666E+07
SGRKQGGKARAKAKSRSSRAGL	1-23	1.189E+07
SGRKQGGKARAKAKSRSSRAGLQF	1-25	1.255E+07
SGRKQGGKARAKAKSRSSRAGLQFPVG	1-28	3.040E+07
SGRKQGGKARAKAKSRSSRAGLQFPVGRVHRLLRK	1-36	1.812E+07
SGRKQGGKARAKAKSRSSRAGLQFPVGRVHRLLRKG	1-37	6.719E+07
SGRKQGGKARAKAKSRSSRAGLQFPVGRVHRLLRKGNYA	1-40	1.484E+07
SGRKQGGKARAKAKSRSSRAGLQFPVGRVHRLLRKGNYAERVG	1-44	1.122E+08
SGRKQGGKARAKAKSRSSRAGLQFPVGRVHRLLRKGNYAERVG	1-45	5.379E+07
SGRKQGGKARAKAKSRSSRAGLQFPVGRVHRLLRKGNYAERVGAG	1-46	3.876E+07
SGRKQGGKARAKAKSRSSRAGLQFPVGRVHRLLRKGNYAERVGAGA	1-47	2.000E+07
SGRKQGGKARAKAKSRSSRAGLQFPVGRVHRLLRKGNYAERVGAGA	1-56	1.345E+07
YLTAEILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVTTAQGGVLPNIQAVLLPKKTESHHKAKGK	57-129	1.305E+07
LAGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVTTAQGGVLPNIQAVLLPKKTESHHKAKGK	65-129	1.336E+07
GNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVTTAQGGVLPNIQAVLLPKKTESHHKAKGK	67-129	1.874E+07
NAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVTTAQGGVLPNIQAVLLPKKTESHHKAKGK	68-129	6.762E+07
AARDNKKTRIIPRHLQLAIRNDEELNKLLGKVTTAQGGVLPNIQAVLLPKKTESHHKAKGK	69-129	1.024E+07
DNKKTRIIPRHLQLAIRNDEELNKLLGKVTTAQGGVLPNIQAVLLPKKTESHHKAKGK	72-129	1.281E+07
NKKTRIIPRHLQLAIRNDEELNKLLGKVTTAQGGVLPNIQAVLLPKKTESHHKAKGK	73-129	1.000E+08
KTRIIPRHLQLAIRNDEELNKLLGKVTTAQGGVLPNIQAVLLPKKTESHHKAKGK	75-129	1.218E+07
TRIIPRHLQLAIRNDEELNKLLGKVTTAQGGVLPNIQAVLLPKKTESHHKAKGK	76-129	1.689E+07
GKVTTAQGGVLPNIQAVLLPKKTESHHKAKGK	98-129	2.310E+07
KVTIAQGGVLPNIQAVLLPKKTESHHKAKGK	99-129	3.303E+07
GGVLPNIQAVLLPKKTESHHKAKGK	105-129	2.558E+07
GVLPNIQAVLLPKKTESHHKAKGK	106-129	6.375E+07
VLPNIQAVLLPKKTESHHKAKGK	107-129	2.406E+07
LPNIQAVLLPKKTESHHKAKGK	108-129	3.407E+07
PNIQAVLLPKKTESHHKAKGK	109-129	6.237E+07
QAVLLPKKTESHHKAKGK	112-129	1.283E+07
AVLLPKKTESHHKAKGK	113-129	2.142E+07
VLLPKKTESHHKAKGK	114-129	1.395E+07
LLPKKTESHHKAKGK	115-129	1.435E+07
PKKTESHHKAKGK	117-129	1.076E+07

Supplemental Table 2

Sequence	MH+ [Da]	Cleavage site	Motif	15 min	30 min	1 hour
SGRGKQGGKARAKAKSRSRAGLQFPVGRVHRLRKGNYAERVG-44						
45-AGAPVYMAAVLEYLTAEILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLKGKVTAQGGVLVLPNIQAVVLLPKKTESHHKAKGK	14412.07723	(intact)	NA	9.36E+09	1.03E+10	1.10E+07
AGAPVYMAAVLEYLTAEILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLKGKVTAQGGVLVLPNIQAVVLLPKKTESHHKAKGK	9228.20502	G44	YAERVG-AGAPV	2.96E+09	6.80E+09	2.18E+10
AAVLEYLTAEILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLKGKVTAQGGVLVLPNIQAVVLLPKKTESHHKAKGK	8538.84161	M51	GAPVYM-AAVLE	4.80E+06	2.05E+08	3.43E+08
LAGNAARDNKKTRIIPRHLQLAIRNDEELNKLKGKVTAQGGVLVLPNIQAVVLLPKKTESHHKAKGK	7123.1231	E64	TAEILE-LAGNA	6.55E+06	4.21E+07	5.66E+07
KKTRIIPRHLQLAIRNDEELNKLKGKVTAQGGVLVLPNIQAVVLLPKKTESHHKAKGK	6240.61681	N73	NAARDN-KKTRI	9.46E+06	7.32E+07	5.55E+07
RIIPRHLQLAIRNDEELNKLKGKVTAQGGVLVLPNIQAVVLLPKKTESHHKAKGK	5883.46855	T76	RDNKKT-RIIPR	4.55E+08	4.53E+08	3.25E+09
IIPRHLQLAIRNDEELNKLKGKVTAQGGVLVLPNIQAVVLLPKKTESHHKAKGK	5727.33432	R77	DNKKTR-IIPRH	3.14E+07	2.96E+07	1.77E+09
RHLQLAIRNDEELNKLKGKVTAQGGVLVLPNIQAVVLLPKKTESHHKAKGK	5404.12777	P80	KTRIIP-RHLQL	6.34E+06	2.66E+06	1.89E+07
HLQLAIRNDEELNKLKGKVTAQGGVLVLPNIQAVVLLPKKTESHHKAKGK	5248.01759	R81	TRIIIPR-HLQLA	2.45E+08	4.08E+07	5.33E+08
LQLAIRNDEELNKLKGKVTAQGGVLVLPNIQAVVLLPKKTESHHKAKGK	5110.95762	H82	RIIPRH-LQLAI	3.14E+07	1.44E+06	2.42E+06
LAIRNDEELNKLKGKVTAQGGVLVLPNIQAVVLLPKKTESHHKAKGK	4869.84071	Q84	IPRHLO-LAIRN	2.64E+09	7.84E+09	1.46E+10
AIRNDEELNKLKGKVTAQGGVLVLPNIQAVVLLPKKTESHHKAKGK	4756.73387	L85	PRHLQL-AIRND	8.54E+08	1.54E+09	5.62E+09
IRNDEELNKLKGKVTAQGGVLVLPNIQAVVLLPKKTESHHKAKGK	4685.69103	A86	RHLQLA-IRNDE	9.27E+08	1.23E+09	4.39E+10
RNDEELNKLKGKVTAQGGVLVLPNIQAVVLLPKKTESHHKAKGK	4572.5985	I87	HLQLAI-RNDEE	1.72E+08	7.91E+07	1.35E+08
DEELNKLKGKVTAQGGVLVLPNIQAVVLLPKKTESHHKAKGK	4302.45079	N89	QLAIRN-DEELN	3.71E+08	7.17E+07	2.06E+08
EELNKLKGKVTAQGGVLVLPNIQAVVLLPKKTESHHKAKGK	4187.43615	D90	LAIRND-EELNK	1.18E+07	1.25E+08	1.09E+07
KLLKGKVTAQGGVLVLPNIQAVVLLPKKTESHHKAKGK	3702.2246	N94	NDEELN-KLLGK	4.53E+07	1.42E+07	3.78E+07
LLGKVTAQGGVLVLPNIQAVVLLPKKTESHHKAKGK	3574.13171	K95	DEELNK-LLGKV	1.99E+07	8.87E+06	4.01E+07
LGKVTAQGGVLVLPNIQAVVLLPKKTESHHKAKGK	3461.05053	L96	EELNKL-LGKV	4.41E+06	4.34E+06	1.06E+07
GKVTAQGGVLVLPNIQAVVLLPKKTESHHKAKGK	3347.97448	L97	ELNKL-GKVTI	2.34E+08	3.98E+08	3.20E+09
KVTIAQGGVLVLPNIQAVVLLPKKTESHHKAKGK	3290.94445	G98	EELNKL-LGKV	1.30E+09	1.68E+09	1.07E+10
VTIAQGGVLVLPNIQAVVLLPKKTESHHKAKGK	3162.84833	K99	NKLLGK-VTIAQ	2.59E+07	3.20E+06	3.57E+07
TIAQGGVLVLPNIQAVVLLPKKTESHHKAKGK	3063.78051	V100	KLLGKV-TIAQG	3.42E+07	2.19E+07	3.78E+07
IAQGGVLVLPNIQAVVLLPKKTESHHKAKGK	2962.73119	T101	LLGKV-TIAQGG	3.34E+08	5.07E+08	2.07E+09
AQGGVLVLPNIQAVVLLPKKTESHHKAKGK	2849.65038	I102	LGKV-TIAQGGV	3.01E+07	2.47E+07	3.21E+07
QGGVLVLPNIQAVVLLPKKTESHHKAKGK	2778.61279	A103	GKVTIA-QGGVL	2.27E+08	1.46E+08	6.37E+08
GGVLVLPNIQAVVLLPKKTESHHKAKGK	2650.5523	Q104	KVTIAQ-GGVLP	6.98E+07	5.35E+07	1.82E+07
GVLVLPNIQAVVLLPKKTESHHKAKGK	2593.5296	G105	VTIAQG-GVLPN	4.91E+07	3.38E+07	7.35E+07