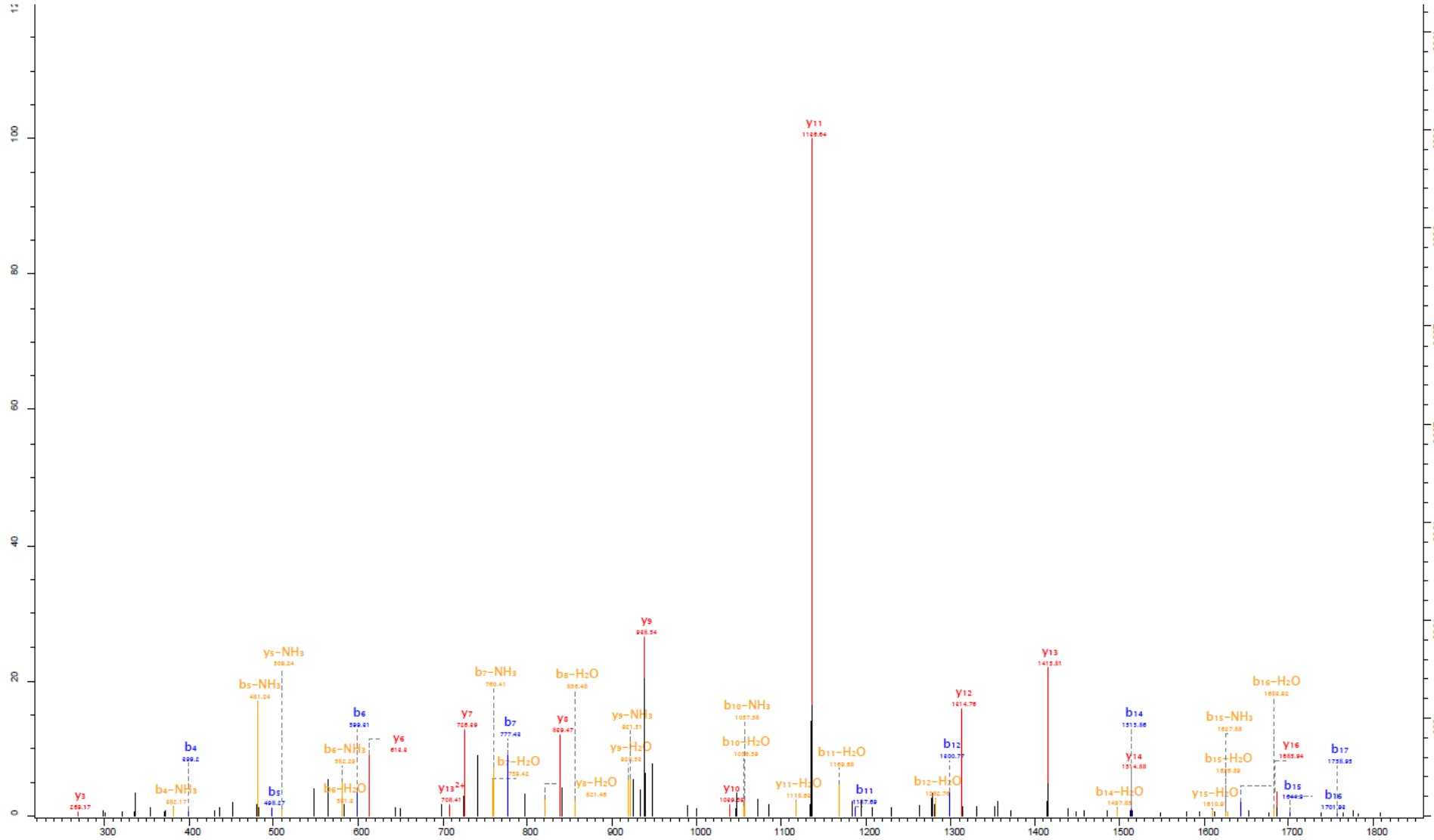
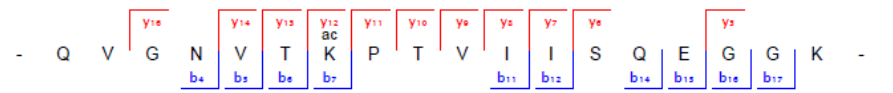
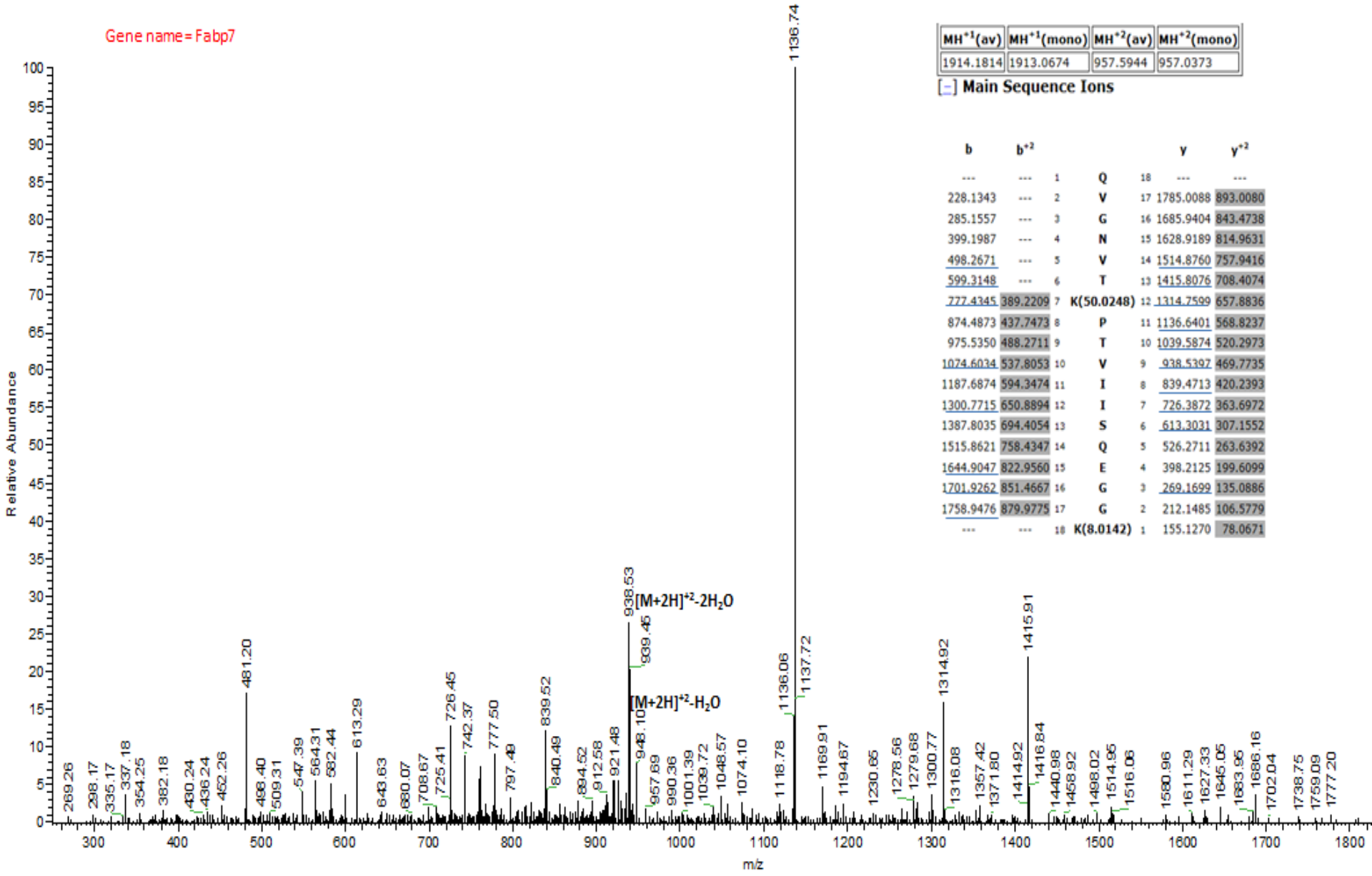
Raw file	Scan	Method	Score	m/z	Gene names
050813_SCW_II_29_19_4	17802	ITMS; CID	166.52	957.03	Fabp7





050813_SCW_II_29_19_4 #17802 RT: 75.95 AV: 1 NL: 3.45E3
T: ITMS + c NSI d Full ms2 957.03@cid35.00 [250.00-1925.00]

Gene name = Fabp7

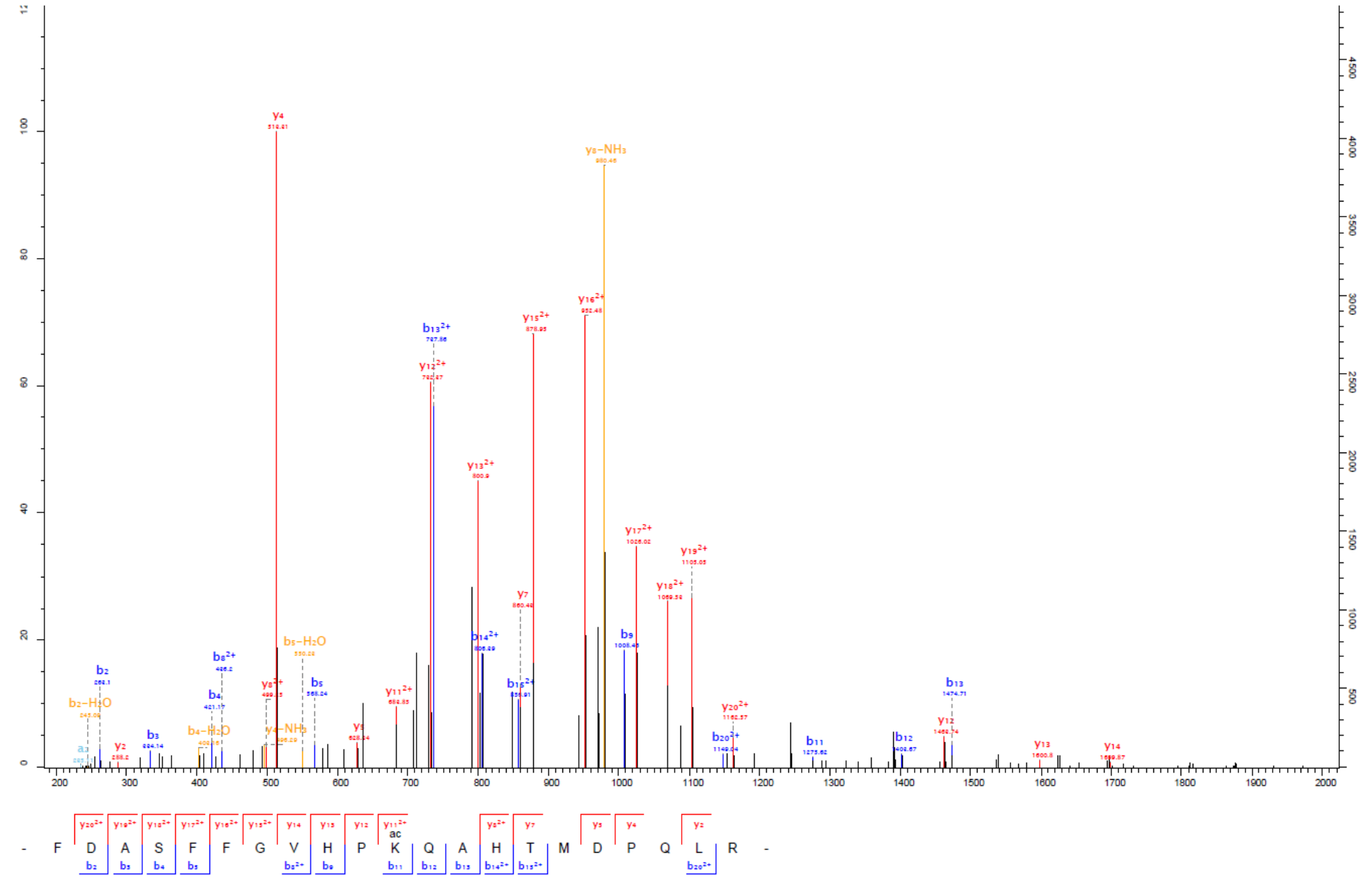


MH+1(av)	MH+1(mono)	MH+2(av)	MH+2(mono)
1914.1814	1913.0674	957.5944	957.0373

[–] Main Sequence Ions

b	b+2				y	y+2
---	---	1	Q	18	---	---
228.1343	---	2	V	17	1785.0088	893.0080
285.1557	---	3	G	16	1685.9404	843.4738
399.1987	---	4	N	15	1628.9189	814.9631
498.2671	---	5	V	14	1514.8760	757.9416
599.3148	---	6	T	13	1415.8076	708.4074
777.4345	389.2209	7	K(50.0248)	12	1314.7599	657.8836
874.4873	437.7473	8	P	11	1136.6401	568.8237
975.5350	488.2711	9	T	10	1039.5874	520.2973
1074.6034	537.8053	10	V	9	938.5397	469.7735
1187.6874	594.3474	11	I	8	839.4713	420.2393
1300.7715	650.8894	12	I	7	726.3872	363.6972
1387.8035	694.4054	13	S	6	613.3031	307.1552
1515.8621	758.4347	14	Q	5	526.2711	263.6392
1644.9047	822.9560	15	E	4	398.2125	199.6099
1701.9262	851.4667	16	G	3	269.1699	135.0886
1758.9476	879.9775	17	G	2	212.1485	106.5779
---	---	18	K(8.0142)	1	155.1270	78.0671

Raw file	Scan	Method	Score	m/z	Gene names
022814_SCW_II_68_10_2ndZT	23007	ITMS; CID	143.99	824.74	Fasn



- F D A S F F G V H P K ac Q A H T M D P Q L R -

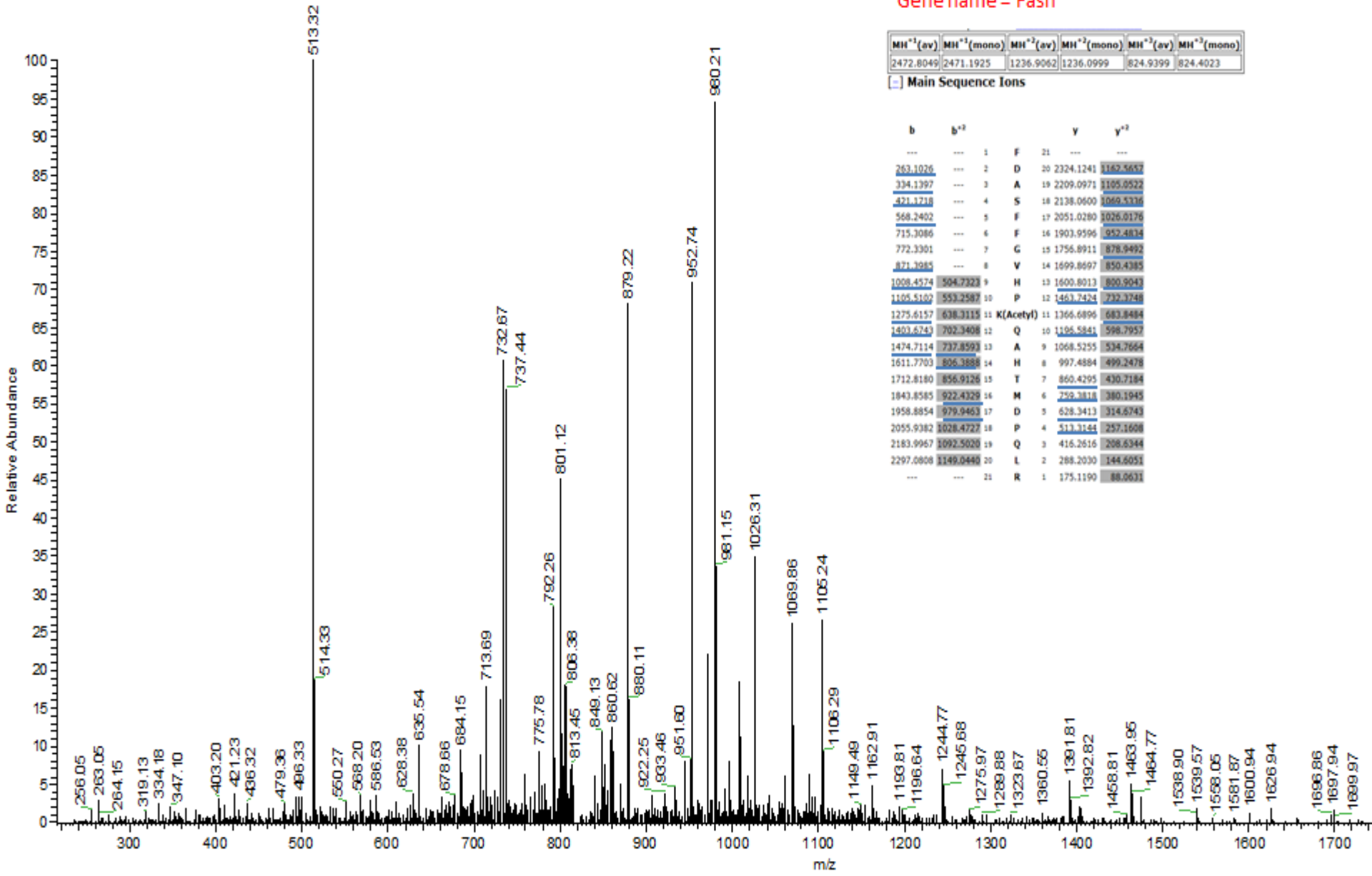
022814_SCW_II_68_10_2ndZT #23007 RT: 104.91 AV: 1 NL: 4.04E3
T: ITMS + c NSI d Full ms2 824.74@cid35.00 [215.00-2000.00]

Gene name = Fasn

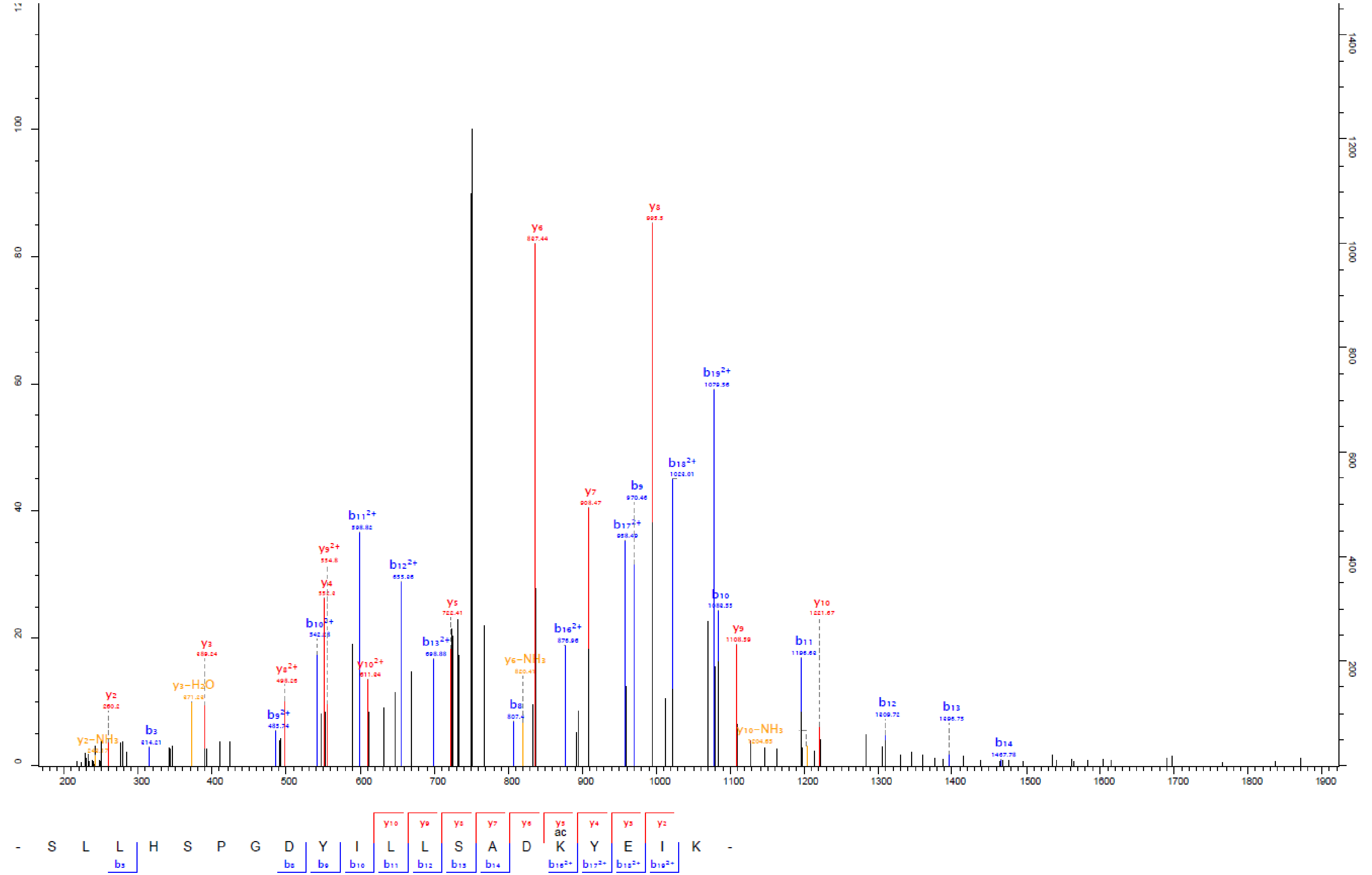
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)	MH^{+3}(av)	MH^{+3}(mono)
2472.8049	2471.1925	1236.9062	1236.0999	824.9399	824.4023

[-] Main Sequence Ions

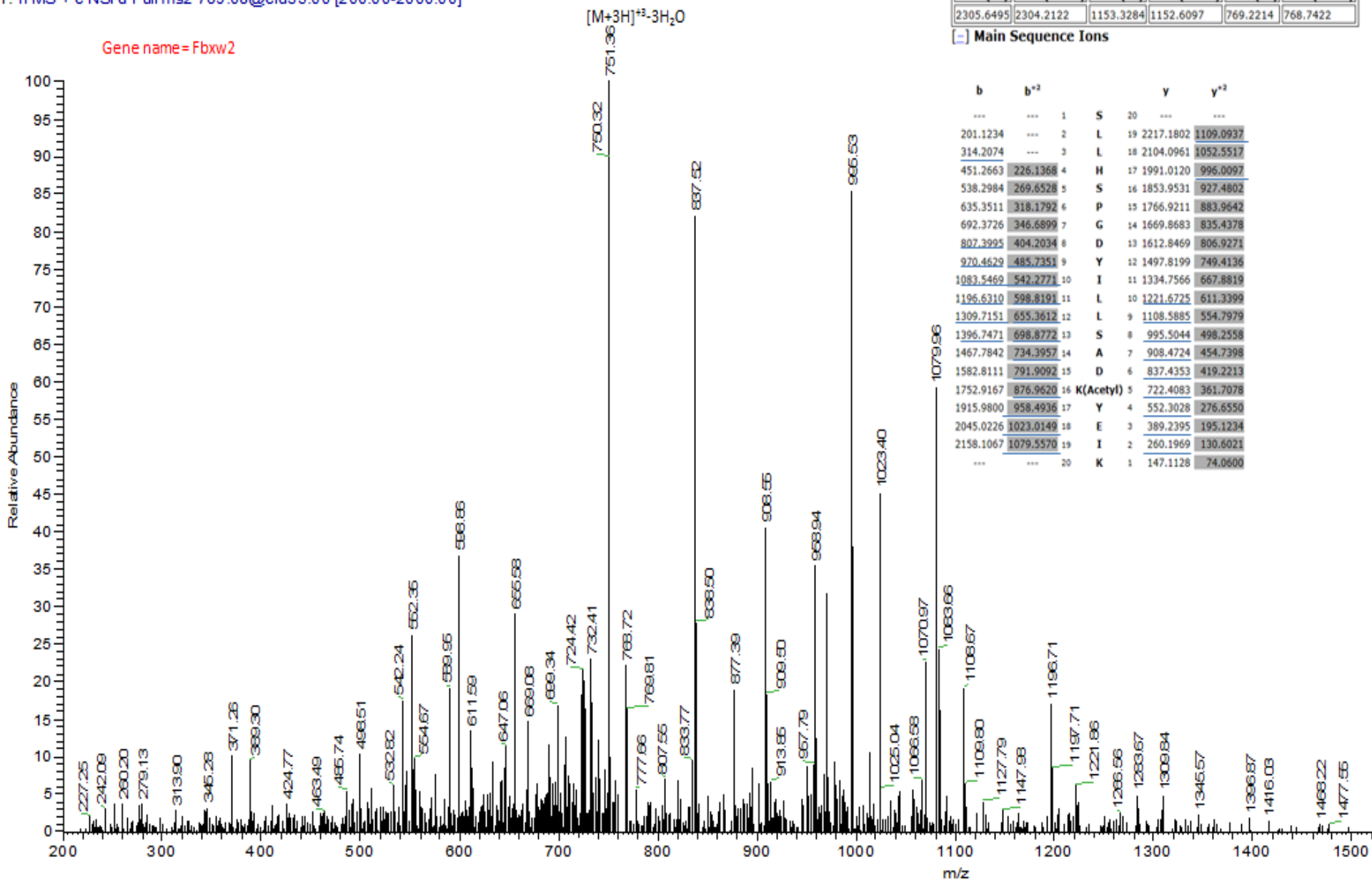
b	b^{+2}				y	y^{+2}
---	---	1	F	21	---	---
263.1026	---	2	D	20	2324.1241	1162.5657
334.1397	---	3	A	19	2209.0971	1105.0522
421.1718	---	4	S	18	2138.0600	1069.5336
568.2402	---	5	F	17	2051.0280	1026.0176
715.3086	---	6	F	16	1903.9596	952.4834
772.3301	---	7	G	15	1756.8911	878.9492
871.3985	---	8	V	14	1699.8697	850.4385
1008.4574	504.7323	9	H	13	1600.8013	800.9043
1105.5102	553.2587	10	P	12	1463.7424	732.3748
1275.6157	638.3115	11	K(Acetyl)	11	1366.6896	683.8484
1403.6743	702.3408	12	Q	10	1196.5841	598.7957
1474.7114	737.8593	13	A	9	1068.5255	534.7664
1611.7703	806.3888	14	H	8	997.4884	499.2478
1712.8180	856.9126	15	T	7	860.4295	430.7184
1843.8585	922.4329	16	M	6	759.3818	380.1945
1958.8854	979.9463	17	D	5	628.3413	314.6743
2055.9382	1028.4727	18	P	4	513.3144	257.1608
2183.9967	1092.5020	19	Q	3	416.2616	208.6344
2297.0808	1149.0440	20	L	2	288.2030	144.6051
---	---	21	R	1	175.1190	88.0631



Raw file	Scan	Method	Score	m/z	Gene names
062513_SCW_II_53_7_Vargas_Enriched	23241	ITMS; CID	132.51	769.08	Fbxw2



062513_SCW_II_53_7_Vargas_Enriched #23241 RT: 101.18 AV: 1 NL: 1.22E3
T: ITMS + c NSI d Full ms2 769.08@cid35.00 [200.00-2000.00]

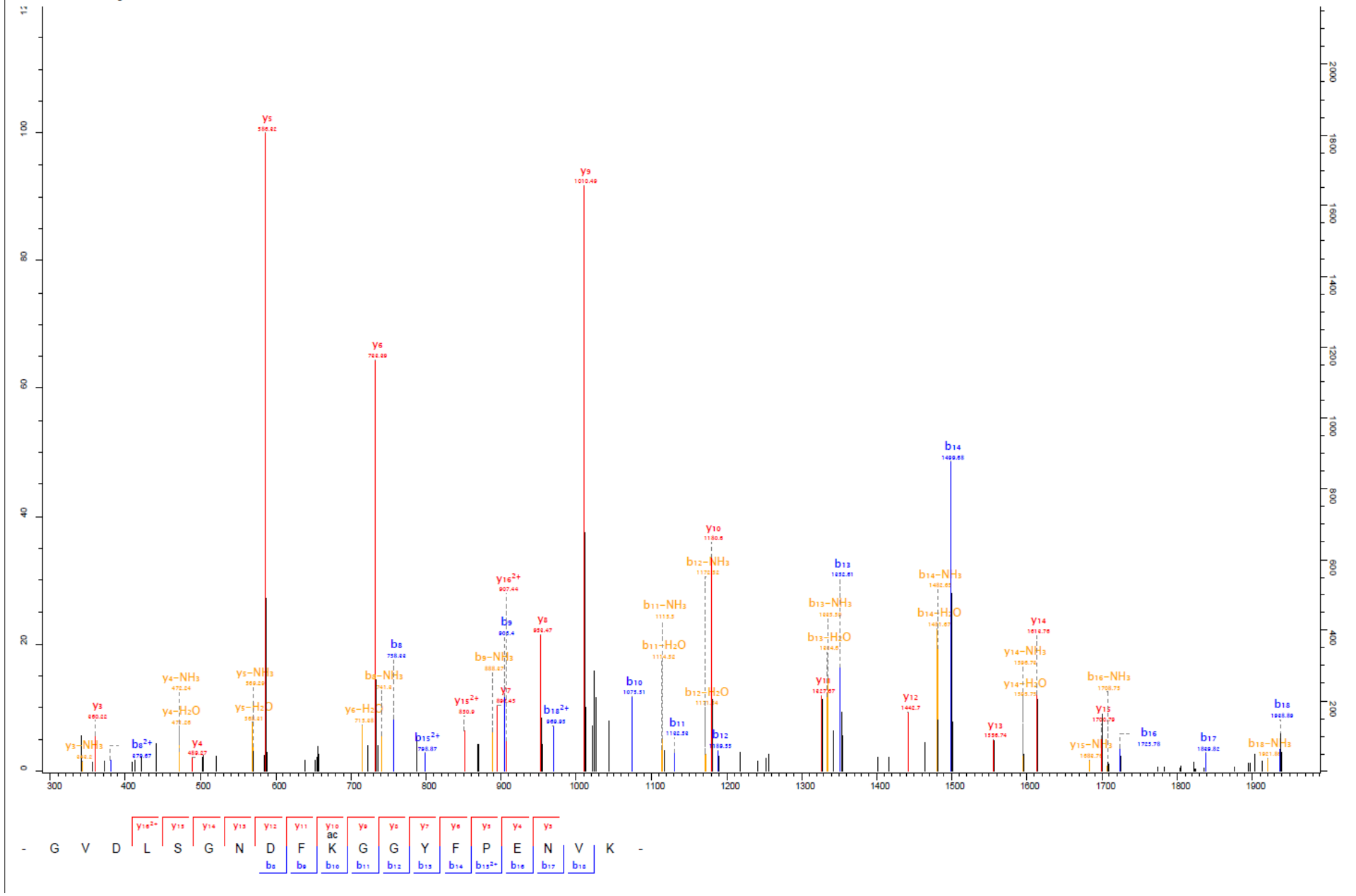


MH+1(av)	MH+1(mono)	MH+2(av)	MH+2(mono)	MH+3(av)	MH+3(mono)
2305.6495	2304.2122	1153.3284	1152.6097	769.2214	768.7422

[-] Main Sequence Ions

b	b+2				y	y+2
---	---	1	S	20	---	---
201.1234	---	2	L	19	2217.1802	1109.0937
314.2074	---	3	L	18	2104.0961	1052.5517
451.2663	226.1368	4	H	17	1991.0120	996.0097
538.2984	269.6528	5	S	16	1853.9531	927.4802
635.3511	318.1792	6	P	15	1766.9211	883.9642
692.3726	346.6899	7	G	14	1669.8683	835.4378
807.3995	404.2034	8	D	13	1612.8469	806.9271
970.4629	485.7351	9	Y	12	1497.8199	749.4136
1083.5469	542.2771	10	I	11	1334.7566	667.8819
1196.6310	598.8191	11	L	10	1221.6725	611.3399
1309.7151	655.3612	12	L	9	1108.5885	554.7979
1396.7471	698.8772	13	S	8	995.5044	498.2558
1467.7842	734.3957	14	A	7	908.4724	454.7398
1582.8111	791.9092	15	D	6	837.4353	419.2213
1752.9167	876.9620	16	K(Acetyl)	5	722.4083	361.7078
1915.9800	958.4936	17	Y	4	552.3028	276.6550
2045.0226	1023.0149	18	E	3	389.2395	195.1234
2158.1067	1079.5570	19	I	2	260.1969	130.6021
---	---	20	K	1	147.1128	74.0600

Raw file	Scan	Method	Score	m/z	Gene names
062513_SCW_II_53_4_Vargas_Enriched	21023	ITMS; CID	205	1043.5	Flii



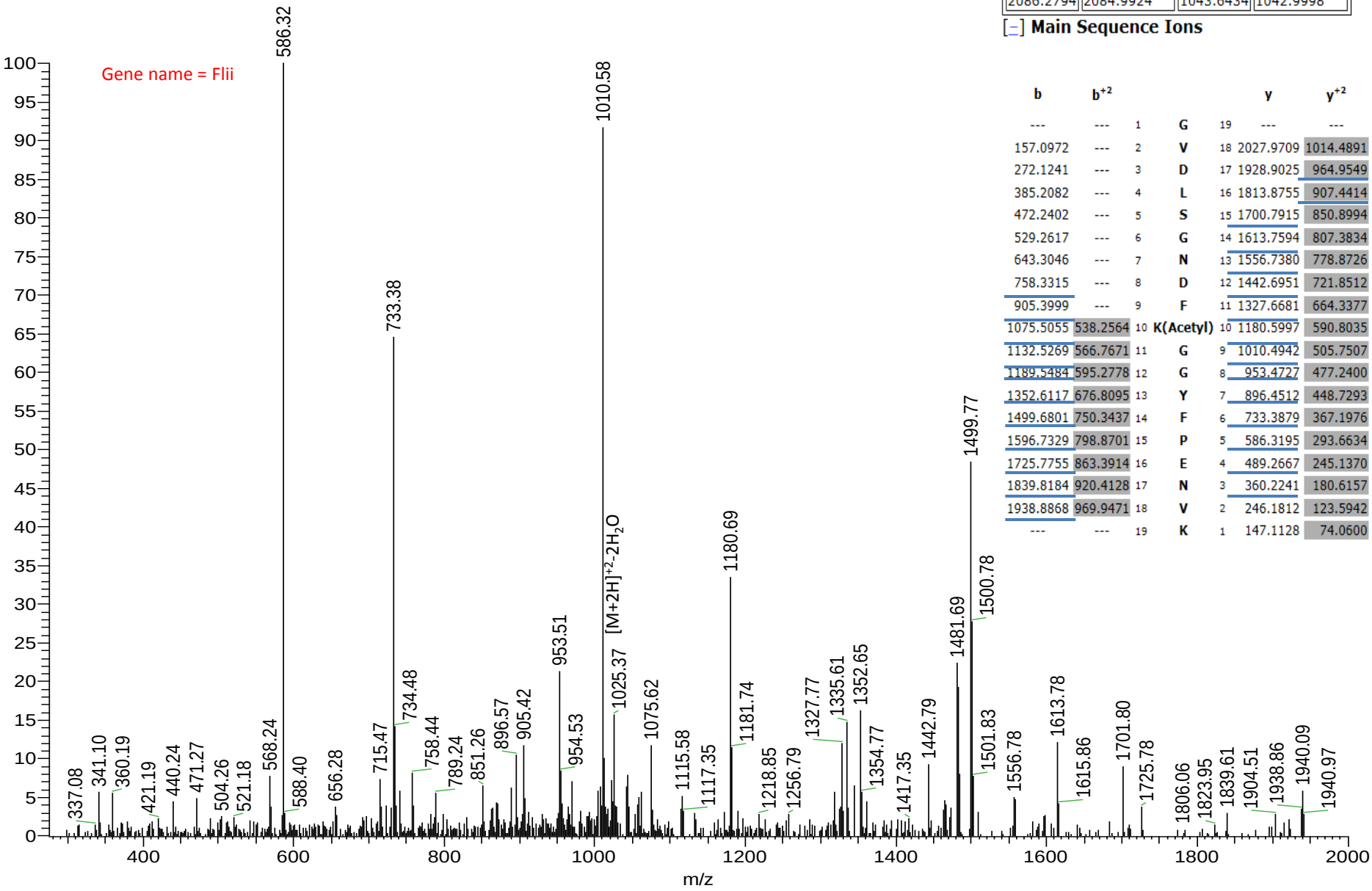
- G V D L S G N D F K(ac) G G Y F P E N V K -

062513_SCW_II_53_4_Vargas_Enriched #21023 RT: 91.55 AV: 1 NL: 1.81E3
T: ITMS + c NSI d Full ms2 1043.50@cid35.00 [275.00-2000.00]

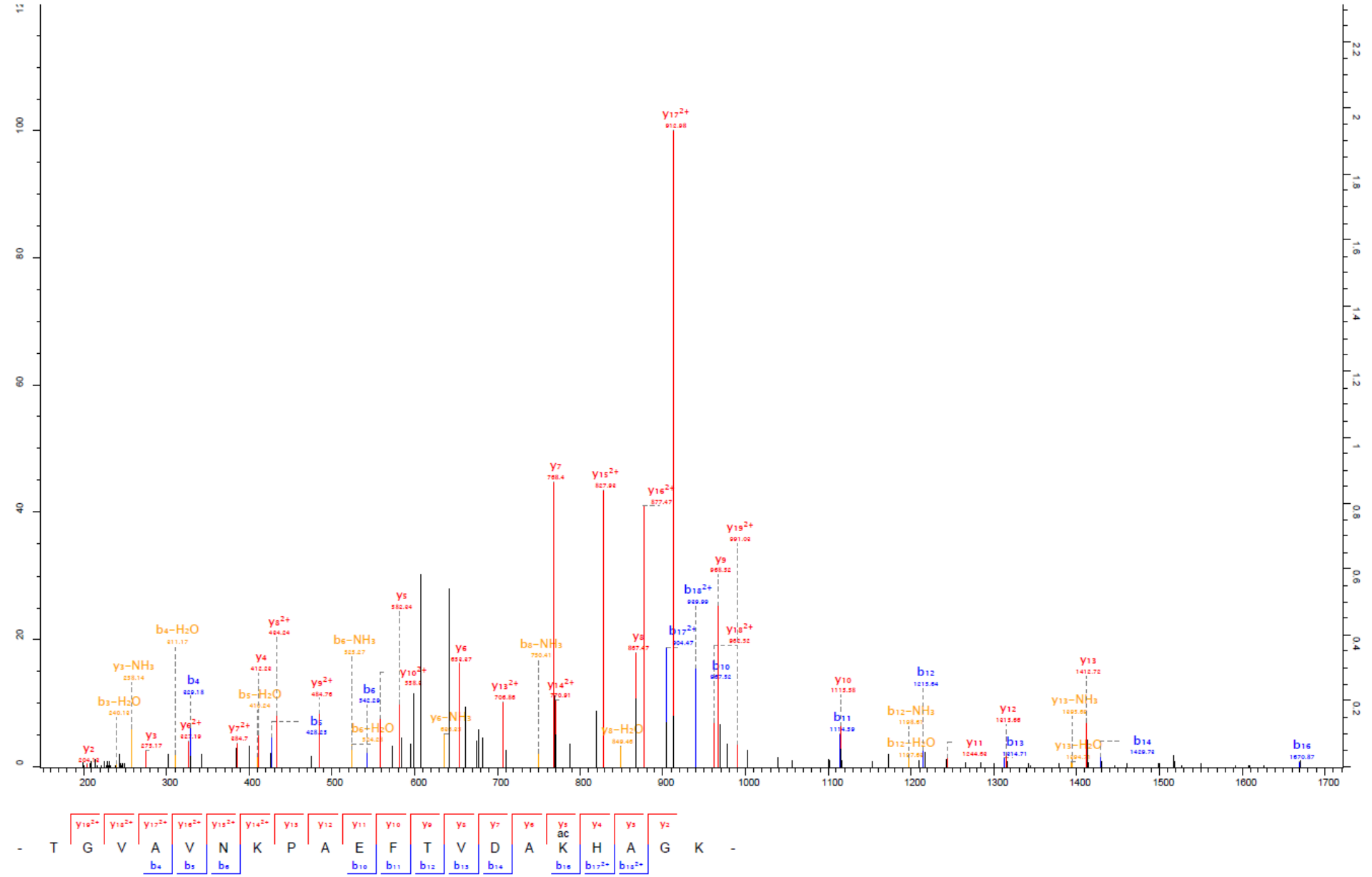
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)
2086.2794	2084.9924	1043.6434	1042.9998

[–] **Main Sequence Ions**

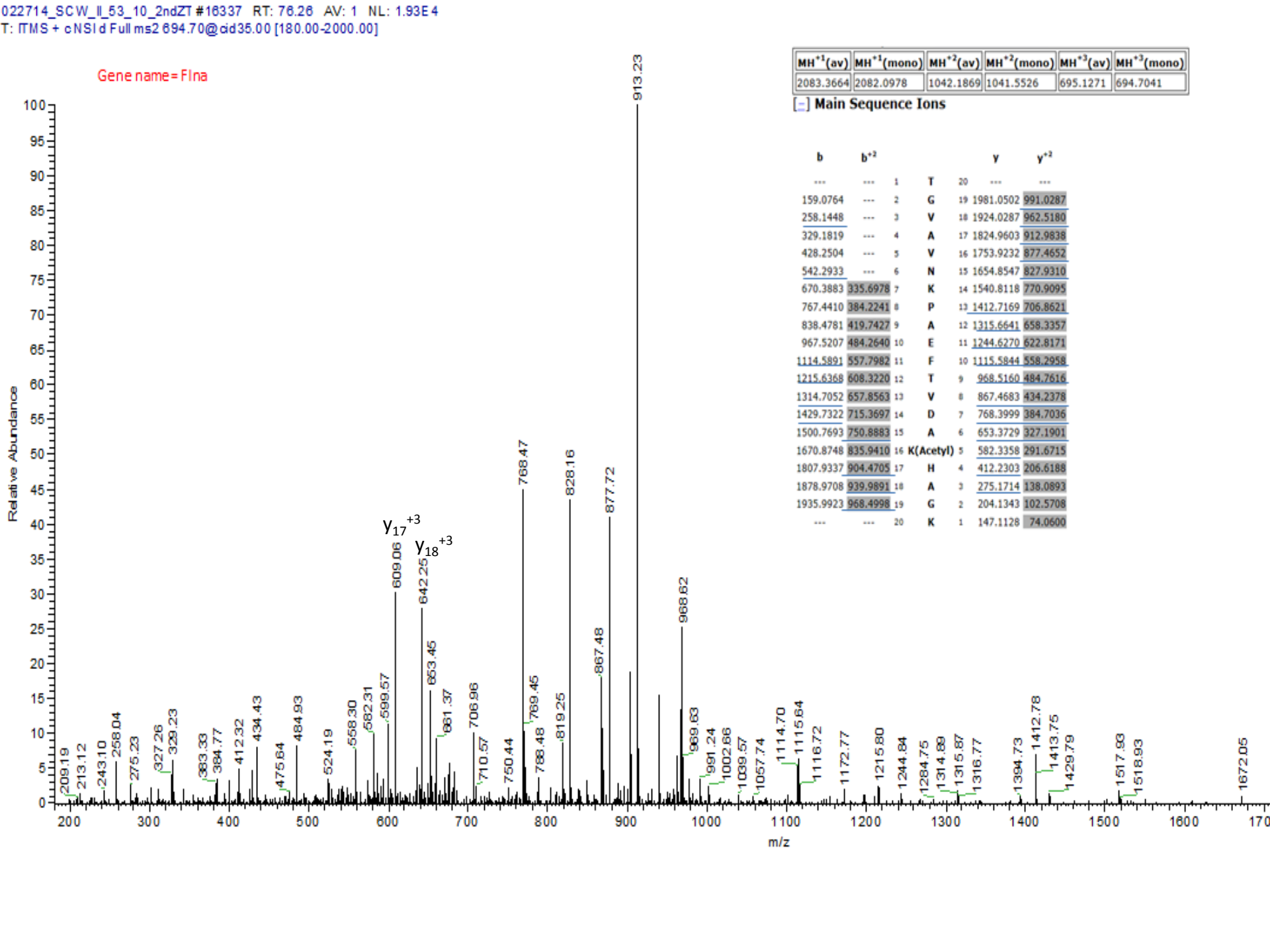
b	b^{+2}				y	y^{+2}
---	---	1	G	19	---	---
157.0972	---	2	V	18	2027.9709	1014.4891
272.1241	---	3	D	17	1928.9025	964.9549
385.2082	---	4	L	16	1813.8755	907.4414
472.2402	---	5	S	15	1700.7915	850.8994
529.2617	---	6	G	14	1613.7594	807.3834
643.3046	---	7	N	13	1556.7380	778.8726
758.3315	---	8	D	12	1442.6951	721.8512
905.3999	---	9	F	11	1327.6681	664.3377
1075.5055	538.2564	10	K(Acetyl)	10	1180.5997	590.8035
1132.5269	566.7671	11	G	9	1010.4942	505.7507
1189.5484	595.2778	12	G	8	953.4727	477.2400
1352.6117	676.8095	13	Y	7	896.4512	448.7293
1499.6801	750.3437	14	F	6	733.3879	367.1976
1596.7329	798.8701	15	P	5	586.3195	293.6634
1725.7755	863.3914	16	E	4	489.2667	245.1370
1839.8184	920.4128	17	N	3	360.2241	180.6157
1938.8868	969.9471	18	V	2	246.1812	123.5942
---	---	19	K	1	147.1128	74.0600



Raw file	Scan	Method	Score	m/z	Gene names
022714_SCW_II_53_10_2ndZT	16337	ITMS; CID	210.43	694.7	Flna



- T G V A V N K P A E F T V D A K H A G K -

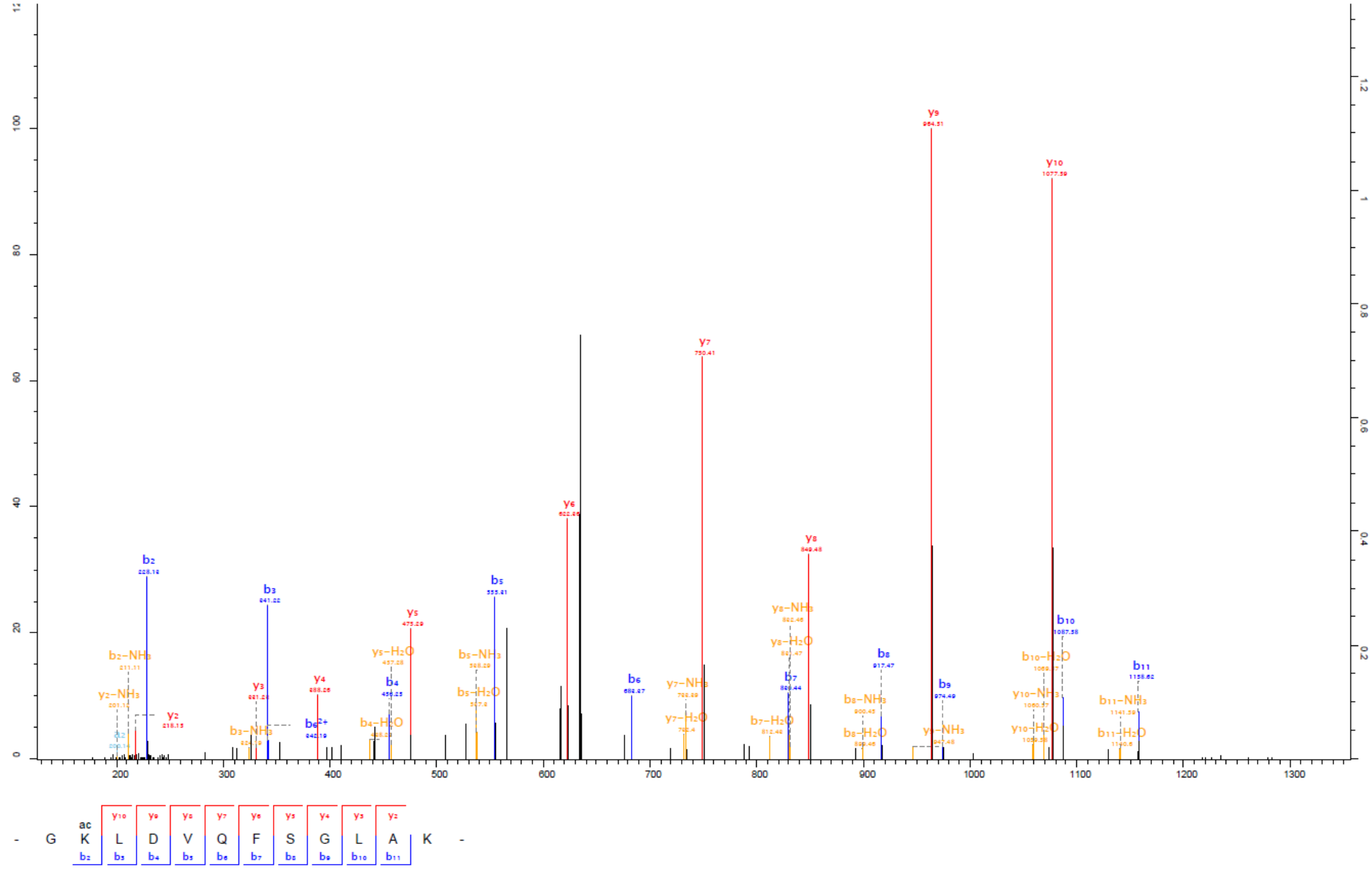


MH+1(av)	MH+1(mono)	MH+2(av)	MH+2(mono)	MH+3(av)	MH+3(mono)
2083.3664	2082.0978	1042.1869	1041.5526	695.1271	694.7041

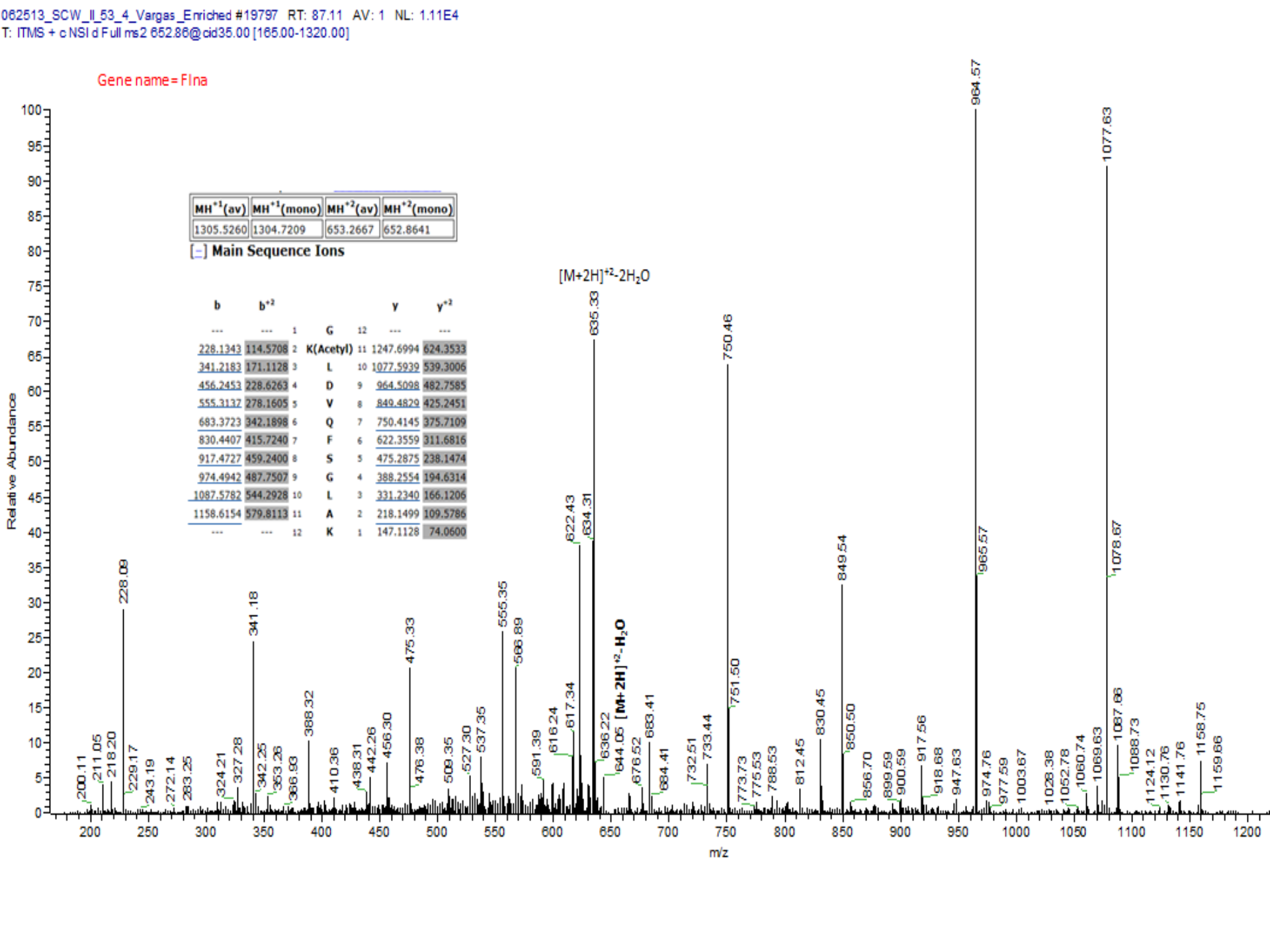
[-] Main Sequence Ions

b	b+2				y	y+2
---	---	1	T	20	---	---
159.0764	---	2	G	19	1981.0502	991.0287
258.1448	---	3	V	18	1924.0287	962.5180
329.1819	---	4	A	17	1824.9603	912.9838
428.2504	---	5	V	16	1753.9232	877.4652
542.2933	---	6	N	15	1654.8547	827.9310
670.3883	335.6978	7	K	14	1540.8118	770.9095
767.4410	384.2241	8	P	13	1412.7169	706.8621
838.4781	419.7427	9	A	12	1315.6641	658.3357
967.5207	484.2640	10	E	11	1244.6270	622.8171
1114.5891	557.7982	11	F	10	1115.5844	558.2958
1215.6368	608.3220	12	T	9	968.5160	484.7616
1314.7052	657.8563	13	V	8	867.4683	434.2378
1429.7322	715.3697	14	D	7	768.3999	384.7036
1500.7693	750.8883	15	A	6	653.3729	327.1901
1670.8748	835.9410	16	K(Acetyl)	5	582.3358	291.6715
1807.9337	904.4705	17	H	4	412.2303	206.6188
1878.9708	939.9891	18	A	3	275.1714	138.0893
1935.9923	968.4998	19	G	2	204.1343	102.5708
---	---	20	K	1	147.1128	74.0600

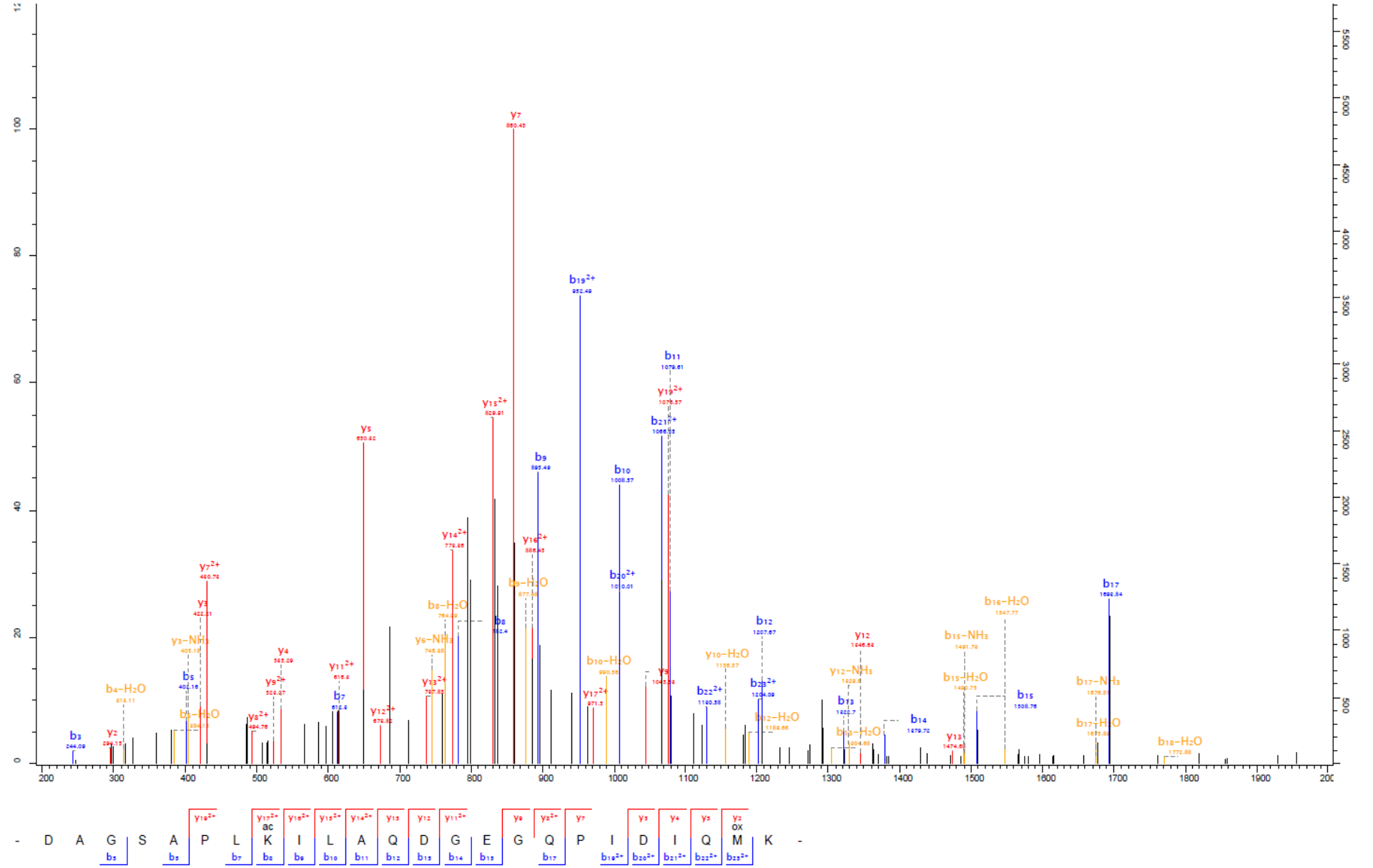
Raw file	Scan	Method	Score	m/z	Gene names
062513_SCW_II_53_4_Vargas_Enriched	19797	ITMS; CID	194.86	652.86	Flna



-	G	ac K	L	D	V	Q	F	S	G	L	A	K	-
		b2	b3	b4	b5	b6	b7	b8	b9	b10	b11		
			y10	y9	y8	y7	y6	y5	y4	y3	y2		


062513_SCW_II_53_4_Vargas_Enriched #19797 RT: 87.11 AV: 1 NL: 1.11E4
T: ITMS + c NSI d Full ms2 652.86@cid35.00 [165.00-1320.00]
Gene name = Flna
MH+1(av) MH+1(mono) MH+2(av) MH+2(mono)
1305.5260 1304.7209 653.2667 652.8641
[-] Main Sequence Ions
b b+2 y y+2
--- --- 1 G 12 --- ---
228.1343 114.5708 2 K(Acetyl) 11 1247.6994 624.3533
341.2183 171.1128 3 L 10 1077.5939 539.3006
456.2453 228.6263 4 D 9 964.5098 482.7585
555.3137 278.1605 5 V 8 849.4829 425.2451
683.3723 342.1898 6 Q 7 750.4145 375.7109
830.4407 415.7240 7 F 6 622.3559 311.6816
917.4727 459.2400 8 S 5 475.2875 238.1474
974.4942 487.7507 9 G 4 388.2554 194.6314
1087.5782 544.2928 10 L 3 331.2340 166.1206
1158.6154 579.8113 11 A 2 218.1499 109.5786
--- --- 12 K 1 147.1128 74.0600
[M+2H]+2-2H2O
[M+2H]+2-H2O
Relative Abundance
m/z

Raw file	Scan	Method	Score	m/z	Gene names
050813_SCW_II_29_16_3	20531	ITMS; CID	181.51	852.1	Flnb

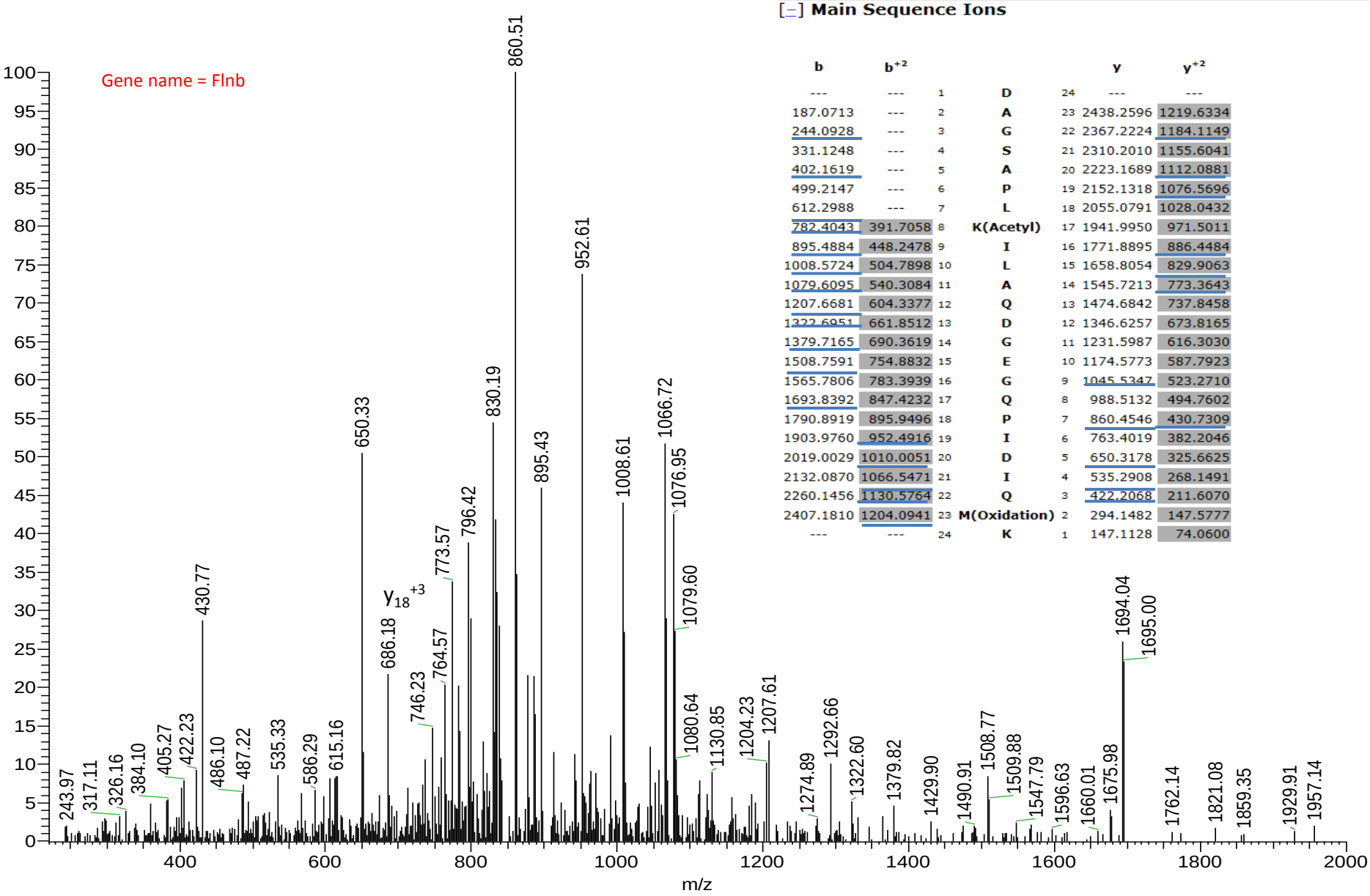


050813_SCW_II_29_16_3 #20531 RT: 91.05 AV: 1 NL: 4.77E3
T: ITMS + c NSI d Full ms2 852.10@cid35.00 [220.00-2000.00]

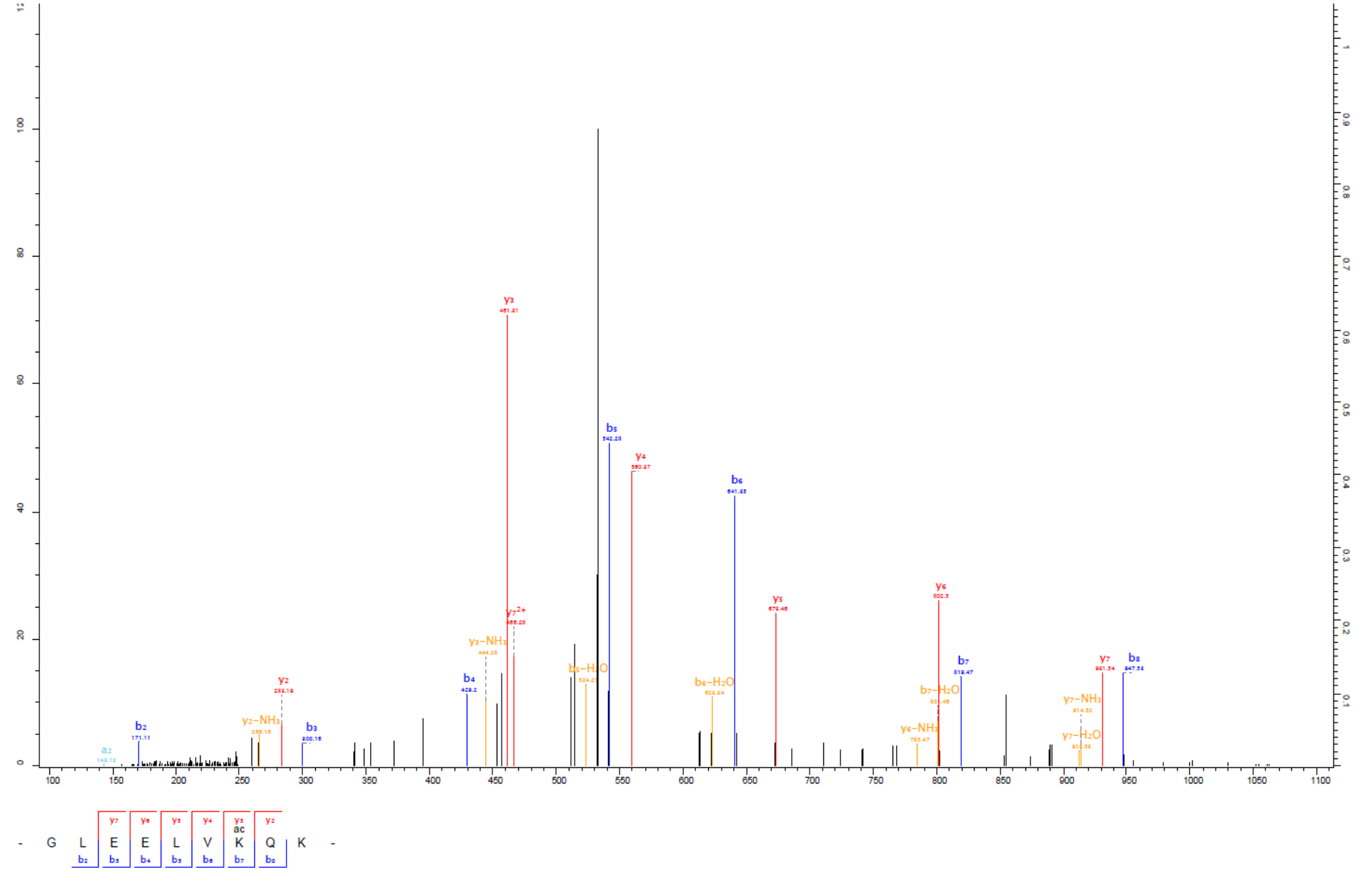
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)	MH^{+3}(av)	MH^{+3}(mono)
2554.8967	2553.2865	1277.9520	1277.1469	852.3038	851.7670

[–] Main Sequence Ions

b	b^{+2}				y	y^{+2}
---	---	1	D	24	---	---
187.0713	---	2	A	23	2438.2596	1219.6334
244.0928	---	3	G	22	2367.2224	1184.1149
331.1248	---	4	S	21	2310.2010	1155.6041
402.1619	---	5	A	20	2223.1689	1112.0881
499.2147	---	6	P	19	2152.1318	1076.5696
612.2988	---	7	L	18	2055.0791	1028.0432
782.4043	391.7058	8	K(Acetyl)	17	1941.9950	971.5011
895.4884	448.2478	9	I	16	1771.8895	886.4484
1008.5724	504.7898	10	L	15	1658.8054	829.9063
1079.6095	540.3084	11	A	14	1545.7213	773.3643
1207.6681	604.3377	12	Q	13	1474.6842	737.8458
1322.6951	661.8512	13	D	12	1346.6257	673.8165
1379.7165	690.3619	14	G	11	1231.5987	616.3030
1508.7591	754.8832	15	E	10	1174.5773	587.7923
1565.7806	783.3939	16	G	9	1045.5347	523.2710
1693.8392	847.4232	17	Q	8	988.5132	494.7602
1790.8919	895.9496	18	P	7	860.4546	430.7309
1903.9760	952.4916	19	I	6	763.4019	382.2046
2019.0029	1010.0051	20	D	5	650.3178	325.6625
2132.0870	1066.5471	21	I	4	535.2908	268.1491
2260.1456	1130.5764	22	Q	3	422.2068	211.6070
2407.1810	1204.0941	23	M(Oxidation)	2	294.1482	147.5777
---	---	24	K	1	147.1128	74.0600



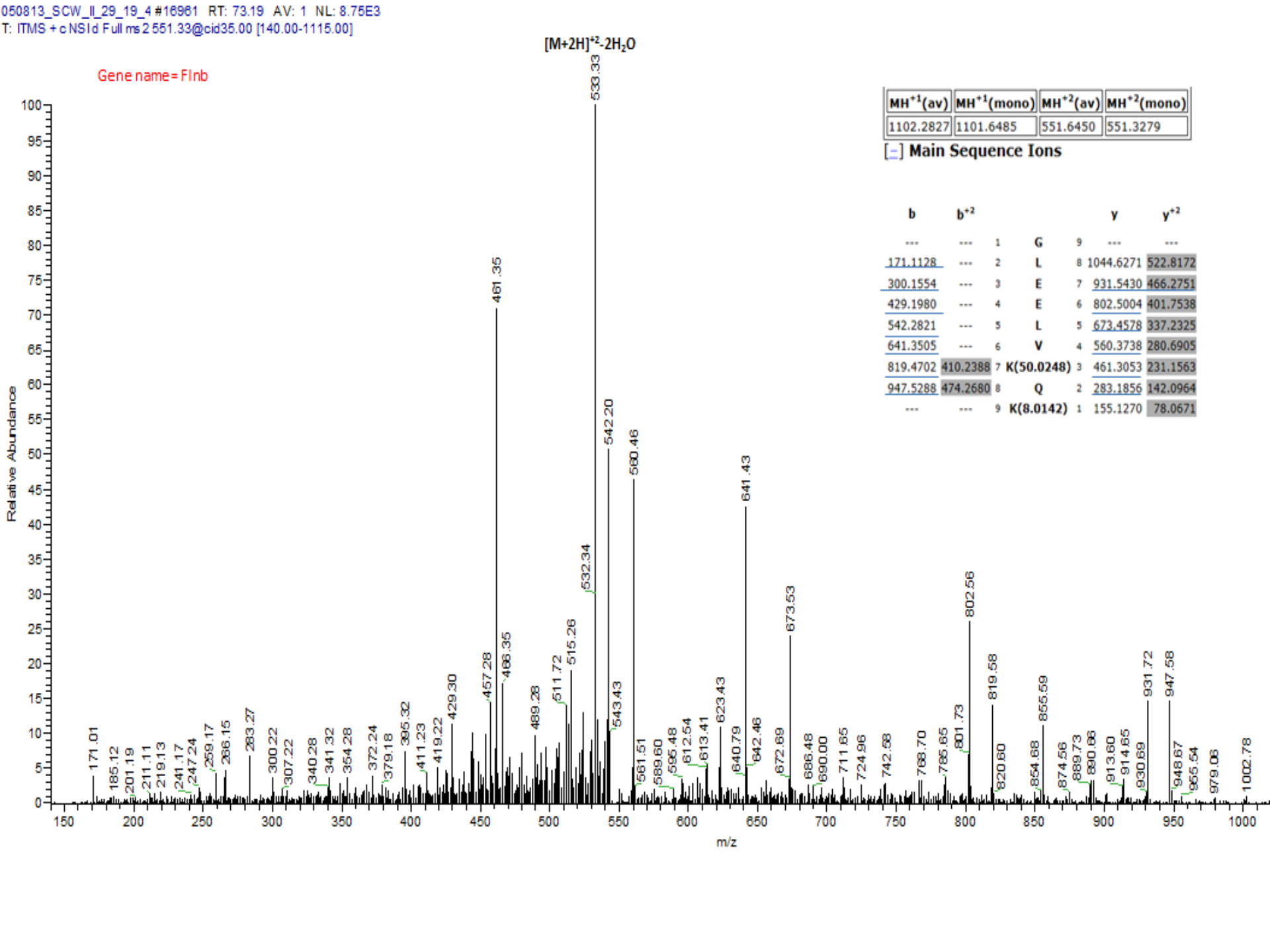
Raw file	Scan	Method	Score	m/z	Gene names
050813_SCW_II_29_19_4	16961	ITMS; CID	144.77	551.33	Flnb

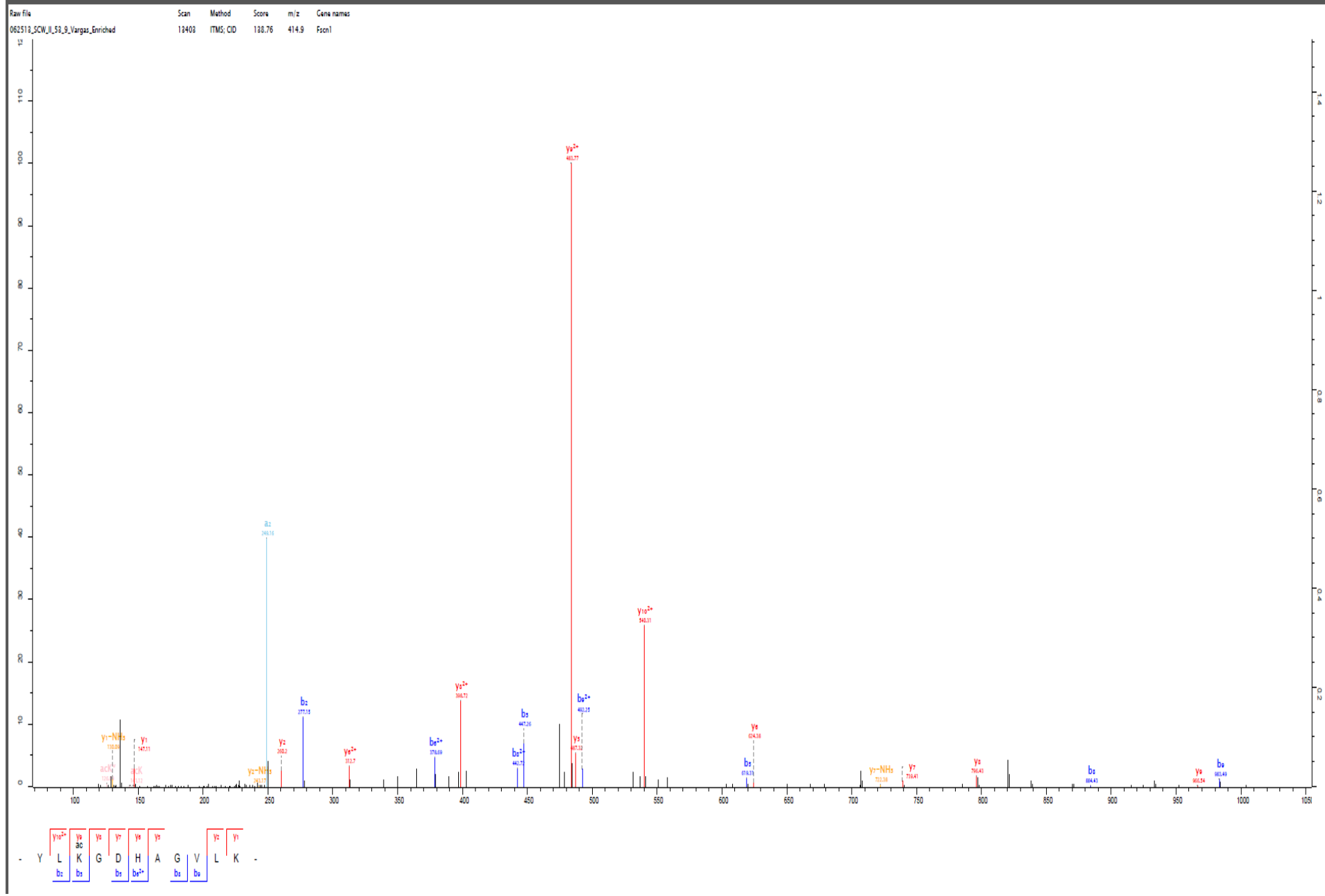


- G L E E L V K Q K -

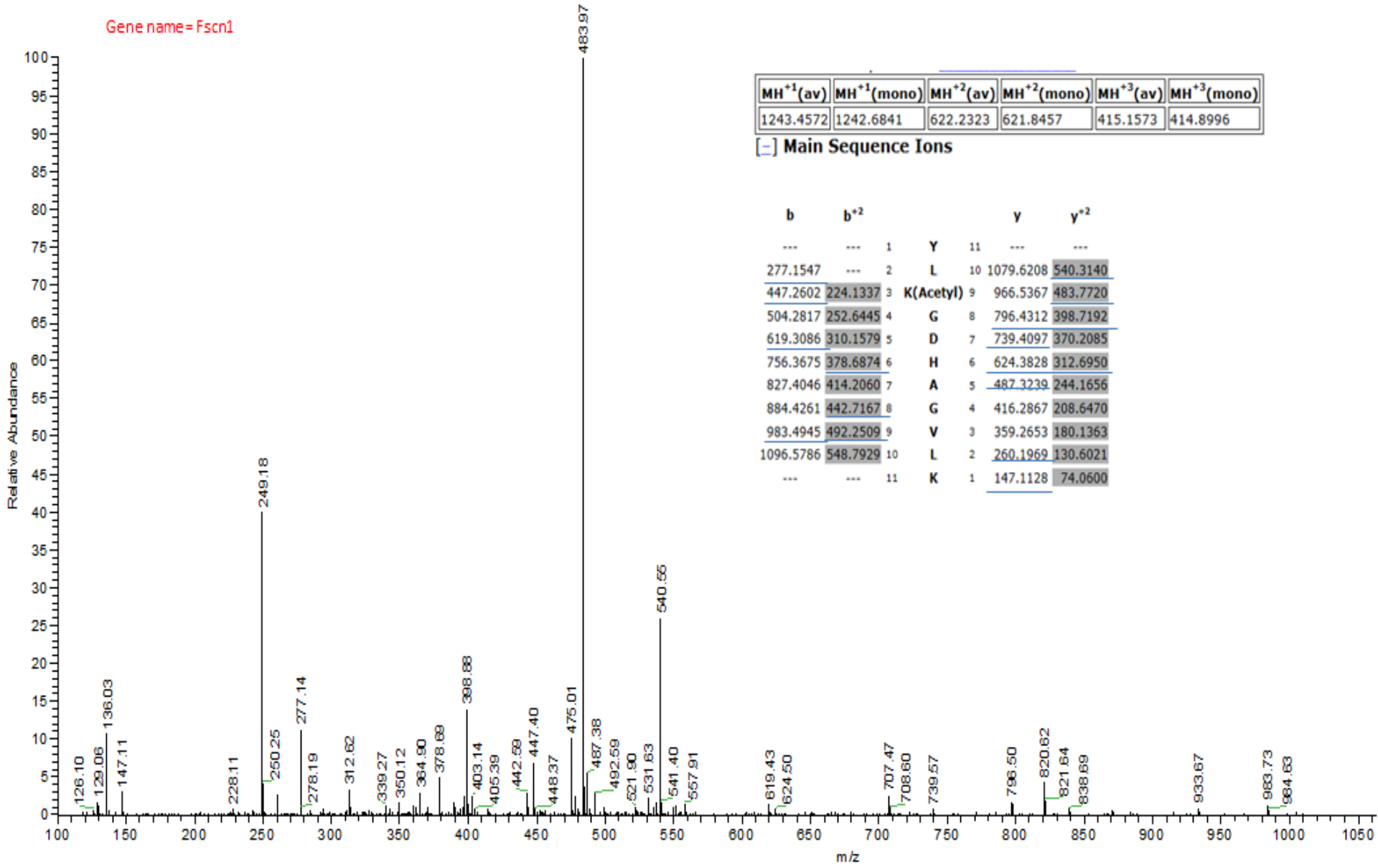
b2 b3 b4 b5 b6 b7 b8

y7 y6 y5 y4 y3 ac y2


050813_SCW_II_29_19_4 #16961 RT: 73.19 AV: 1 NL: 8.75E3
T: ITMS + c NSI d Full ms2 551.33@cid35.00 [140.00-1115.00]
[M+2H]+2-2H2O
Gene name = Flnb
MH+1(av) MH+1(mono) MH+2(av) MH+2(mono)
1102.2827 1101.6485 551.6450 551.3279
[-] Main Sequence Ions
b b+2 y y+2
--- --- 1 G 9 --- ---
171.1128 --- 2 L 8 1044.6271 522.8172
300.1554 --- 3 E 7 931.5430 466.2751
429.1980 --- 4 E 6 802.5004 401.7538
542.2821 --- 5 L 5 673.4578 337.2325
641.3505 --- 6 V 4 560.3738 280.6905
819.4702 410.2388 7 K(50.0248) 3 461.3053 231.1563
947.5288 474.2680 8 Q 2 283.1856 142.0964
--- --- 9 K(8.0142) 1 155.1270 78.0671
Relative Abundance
m/z


Raw file
Scan
Method
Score
m/z
Gene names
062513_SCW_II_53_9_Vargas_Enriched
13408
ITMS; CID
138.76
414.9
Fscn1
- Y L K G D H A G V L K -

062513_SCW_II_53_9_Vargas_Enriched #13403 RT: 63.60 AV: 1 NL: 1.26E5
T: ITMS + c NSI d Full ms2 414.90@cid35.00 [100.00-1255.00]

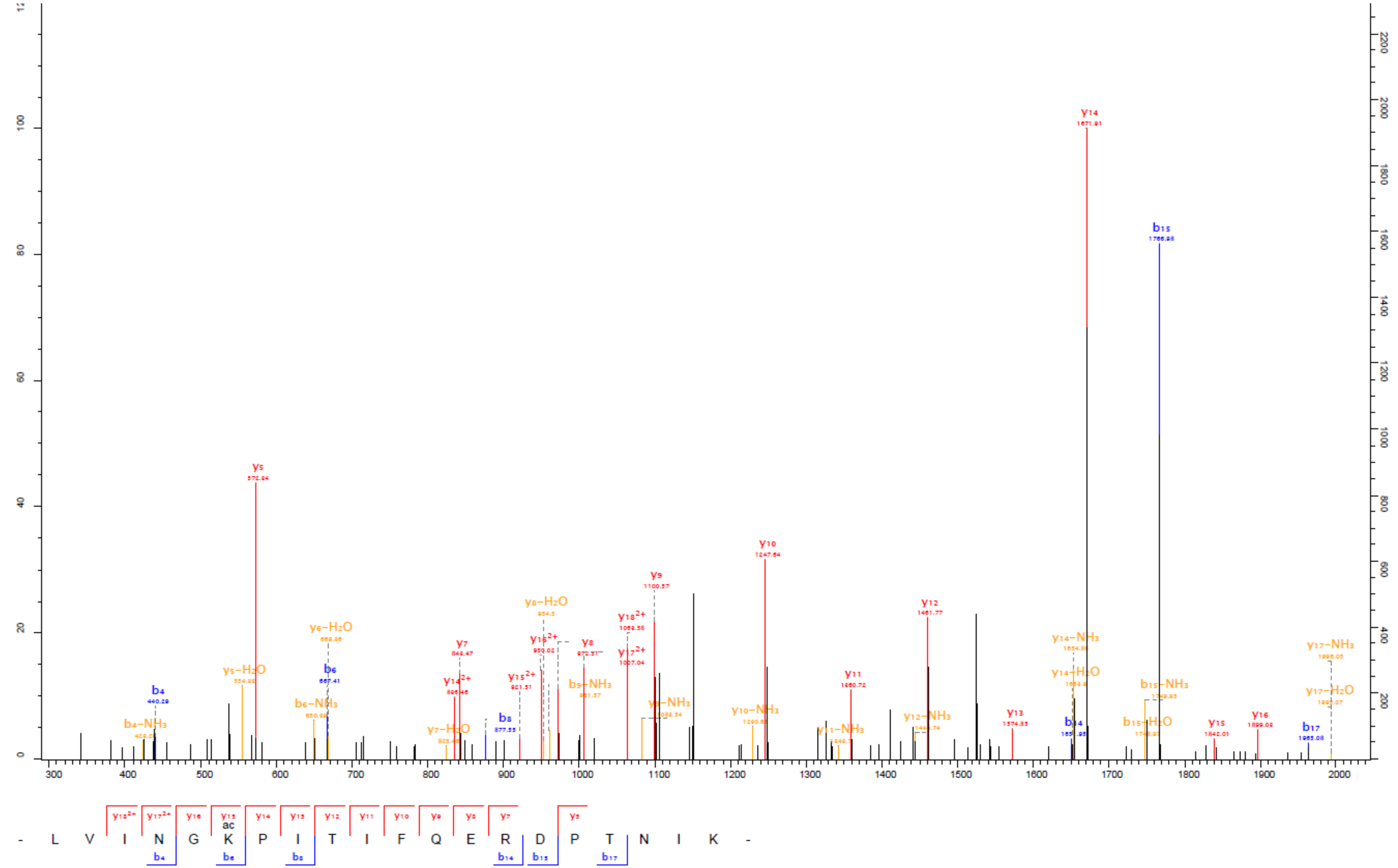


MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)	MH^{+3}(av)	MH^{+3}(mono)
1243.4572	1242.6841	622.2323	621.8457	415.1573	414.8996

[–] **Main Sequence Ions**

b	b^{+2}				y	y^{+2}
---	---	1	Y	11	---	---
277.1547	---	2	L	10	1079.6208	540.3140
447.2602	224.1337	3	K(Acetyl)	9	966.5367	483.7720
504.2817	252.6445	4	G	8	796.4312	398.7192
619.3086	310.1579	5	D	7	739.4097	370.2085
756.3675	378.6874	6	H	6	624.3828	312.6950
827.4046	414.2060	7	A	5	487.3239	244.1656
884.4261	442.7167	8	G	4	416.2867	208.6470
983.4945	492.2509	9	V	3	359.2653	180.1363
1096.5786	548.7929	10	L	2	260.1969	130.6021
---	---	11	K	1	147.1128	74.0600

Raw file	Scan	Method	Score	m/z	Gene names
062513_SCW_II_53_6_Vargas_Enriched	22084	ITMS; CID	139.81	1169.66	Gapdh



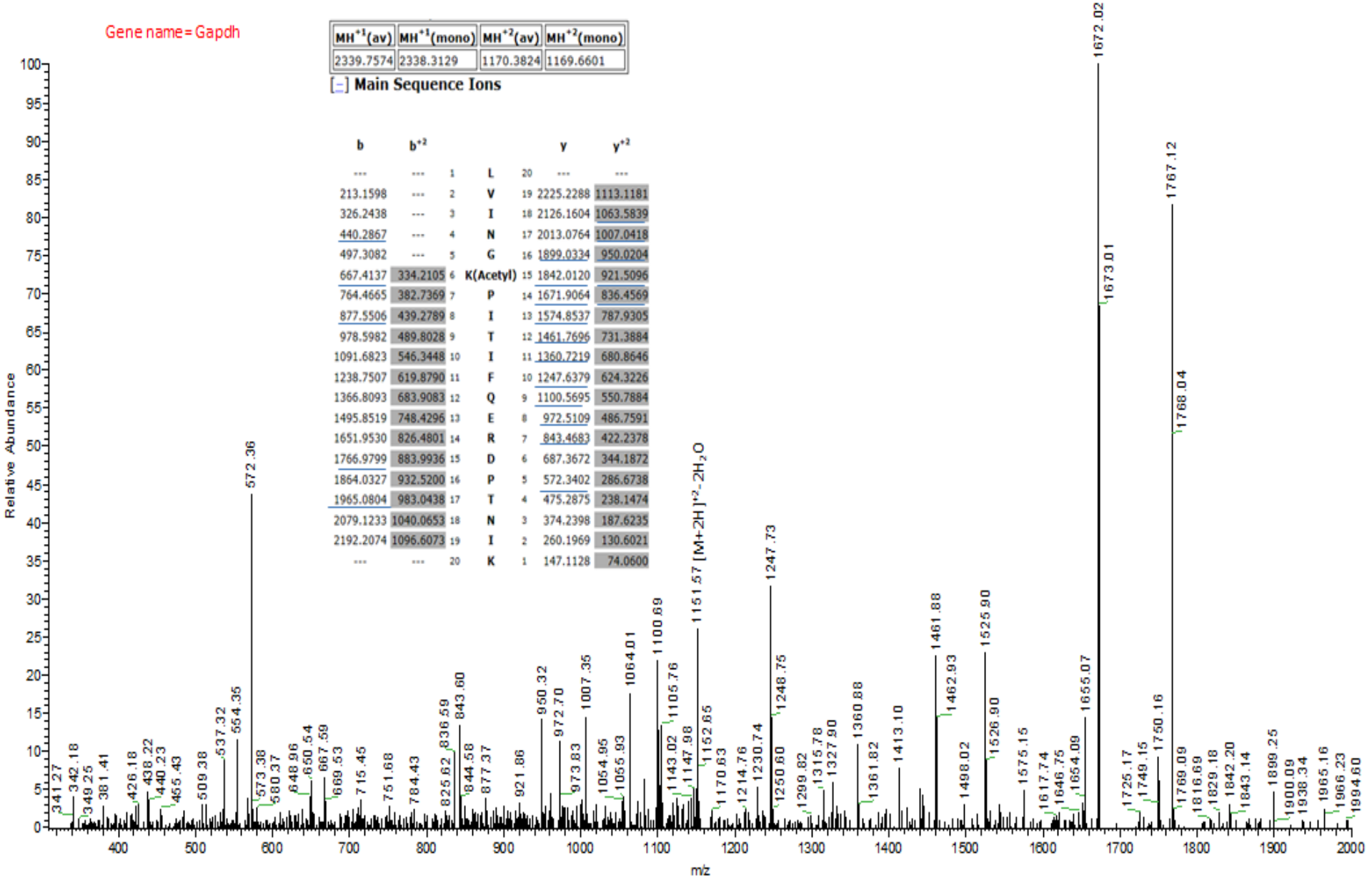
062513_SCW_II_53_6_Vargas_Enrichec #22084 RT: 94.49 AV: 1 NL: 1.91E3
T: ITMS + cNSI d Full ms2 1169.66@cid35.00 [310.00-2000.00]

Gene name = Gapdh

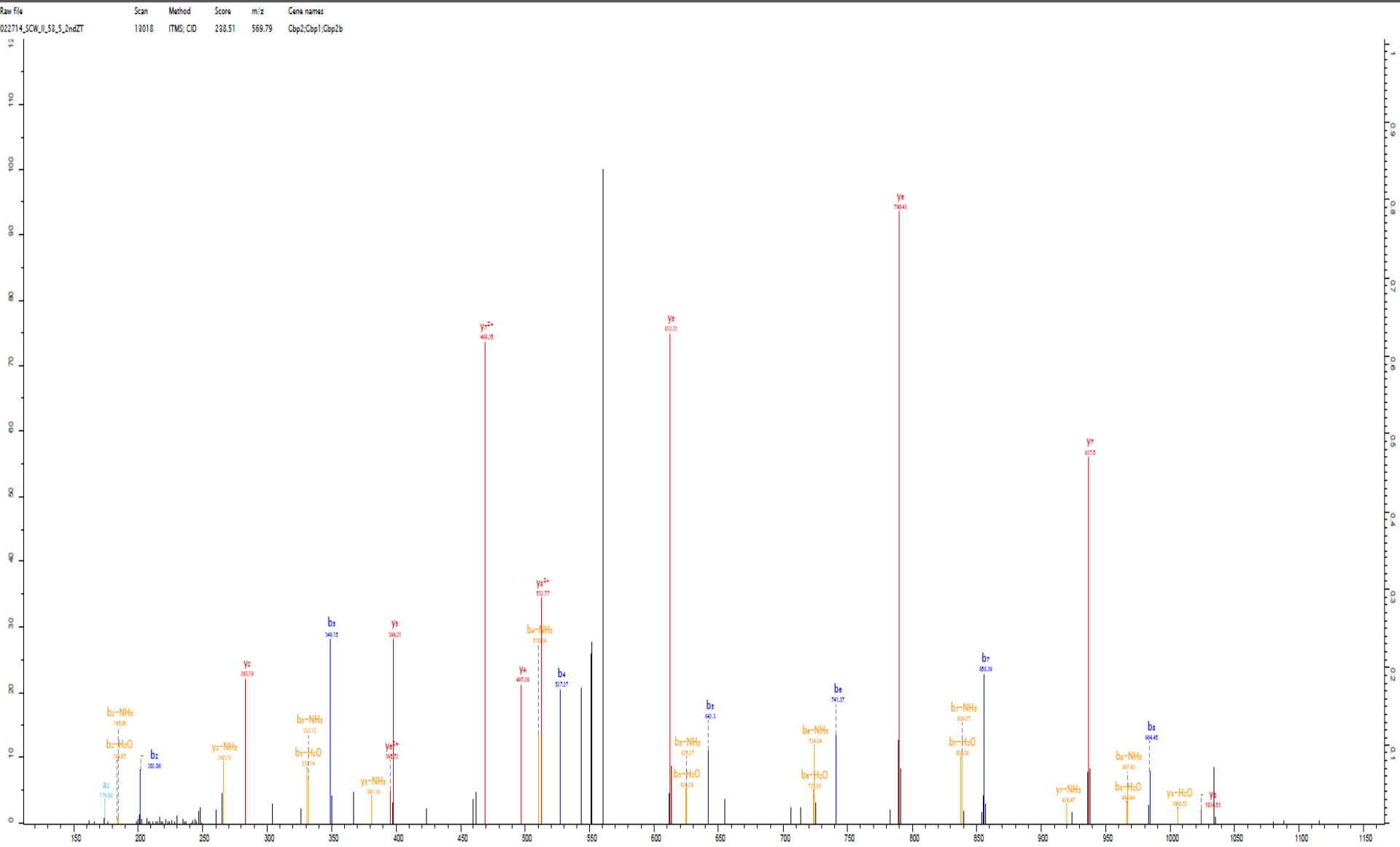
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)
2339.7574	2338.3129	1170.3824	1169.6601

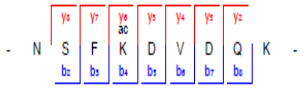
[–] **Main Sequence Ions**

b	b^{+2}				y	y^{+2}
---	---	1	L	20	---	---
213.1598	---	2	V	19	2225.2288	1113.1181
326.2438	---	3	I	18	2126.1604	1063.5839
440.2867	---	4	N	17	2013.0764	1007.0418
497.3082	---	5	G	16	1899.0334	950.0204
667.4137	334.2105	6	K(Acetyl)	15	1842.0120	921.5096
764.4665	382.7369	7	P	14	1671.9064	836.4569
877.5506	439.2789	8	I	13	1574.8537	787.9305
978.5982	489.8028	9	T	12	1461.7696	731.3884
1091.6823	546.3448	10	I	11	1360.7219	680.8646
1238.7507	619.8790	11	F	10	1247.6379	624.3226
1366.8093	683.9083	12	Q	9	1100.5695	550.7884
1495.8519	748.4296	13	E	8	972.5109	486.7591
1651.9530	826.4801	14	R	7	843.4683	422.2378
1766.9799	883.9936	15	D	6	687.3672	344.1872
1864.0327	932.5200	16	P	5	572.3402	286.6738
1965.0804	983.0438	17	T	4	475.2875	238.1474
2079.1233	1040.0653	18	N	3	374.2398	187.6235
2192.2074	1096.6073	19	I	2	260.1969	130.6021
---	---	20	K	1	147.1128	74.0600



Raw file	Scan	Method	Score	m/z	Gene names
022714_SCW_II_53_5_2ndZT	13018	ITMS; CID	238.51	569.79	Cbp2;Cbp1;Cbp2b





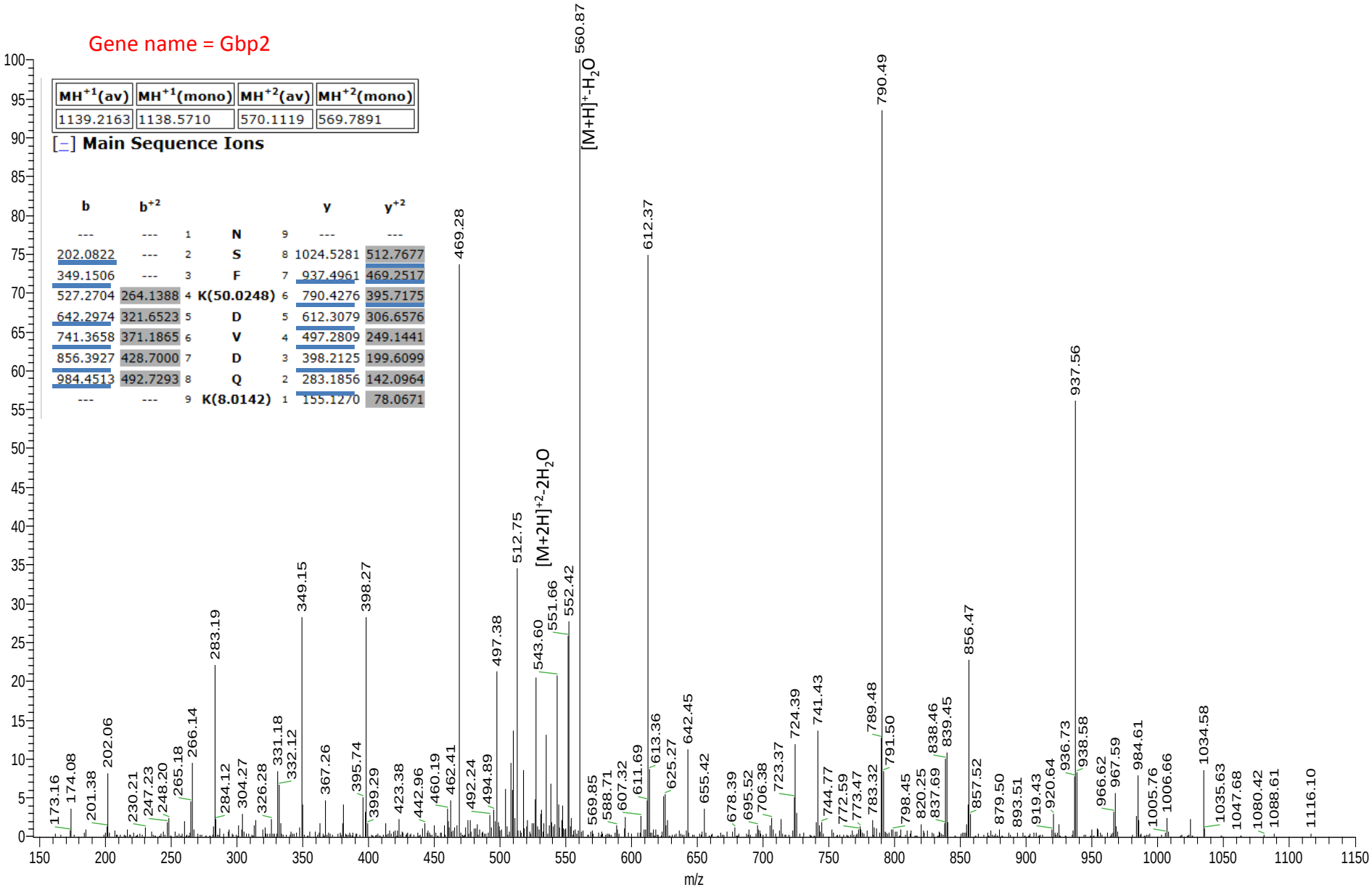
022714_SCW_II_53_5_2ndZT #13018 RT: 61.41 AV: 1 NL: 8.39E3
T: ITMS + c NSI d Full ms2 569.79@cid35.00 [145.00-1150.00]

Gene name = Gbp2

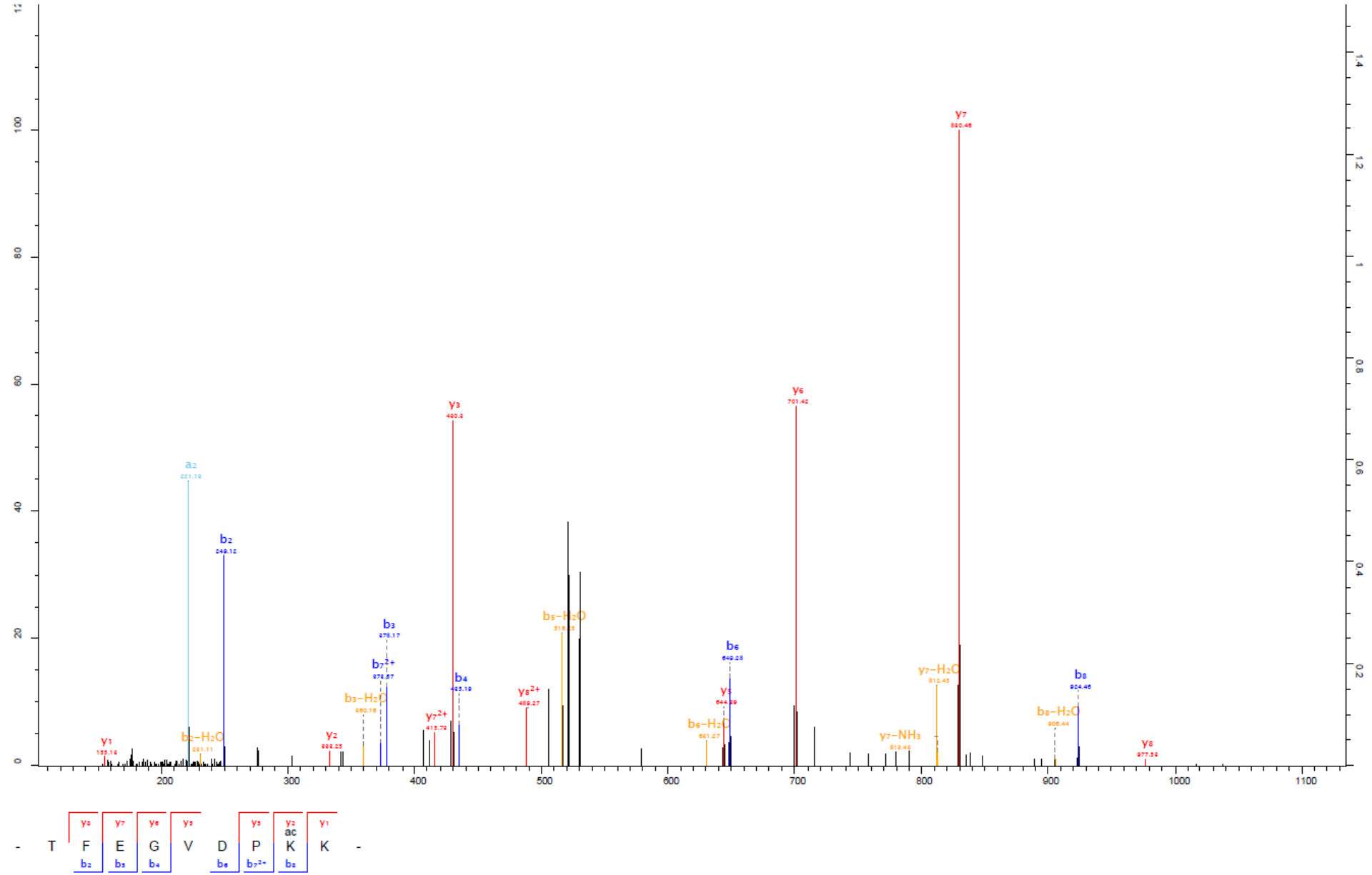
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)
1139.2163	1138.5710	570.1119	569.7891

[–] Main Sequence Ions

b	b^{+2}				y	y^{+2}
---	---	1	N	9	---	---
202.0822	---	2	S	8	1024.5281	512.7677
349.1506	---	3	F	7	937.4961	469.2517
527.2704	264.1388	4	K(50.0248)	6	790.4276	395.7175
642.2974	321.6523	5	D	5	612.3079	306.6576
741.3658	371.1865	6	V	4	497.2809	249.1441
856.3927	428.7000	7	D	3	398.2125	199.6099
984.4513	492.7293	8	Q	2	283.1856	142.0964
---	---	9	K(8.0142)	1	155.1270	78.0671



Raw file	Scan	Method	Score	m/z	Gene names
050813_SCW_II_29_22_5	13591	ITMS; CID	122.96	539.79	Gdi2



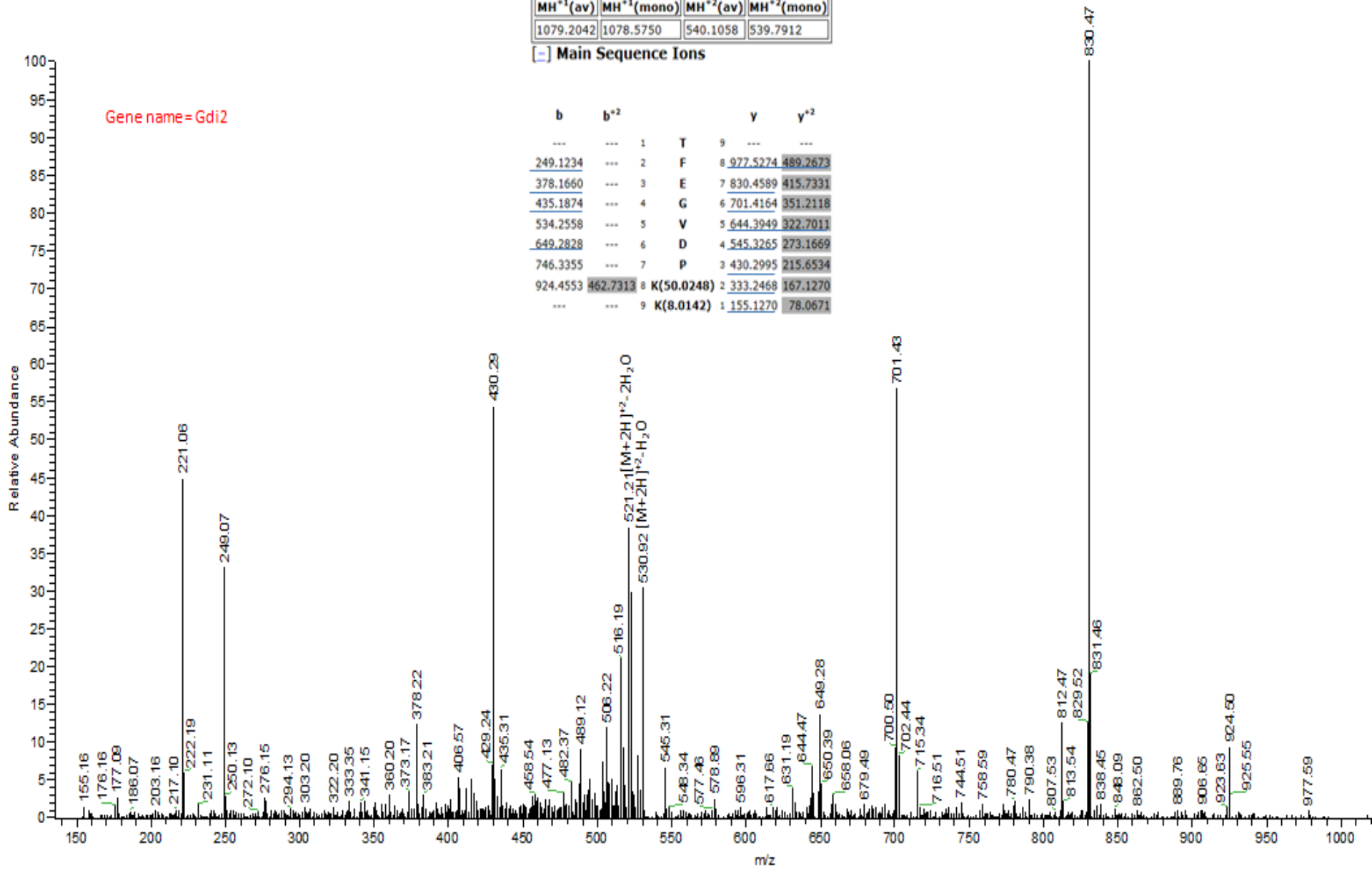
050813_SCW_II_29_22_5 #13591 RT: 61.94 AV: 1 NL: 1.25E4
T: ITMS + c NSI d Full ms2 539.79@cid35.00 [135.00-1090.00]

MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)
1079.2042	1078.5750	540.1058	539.7912

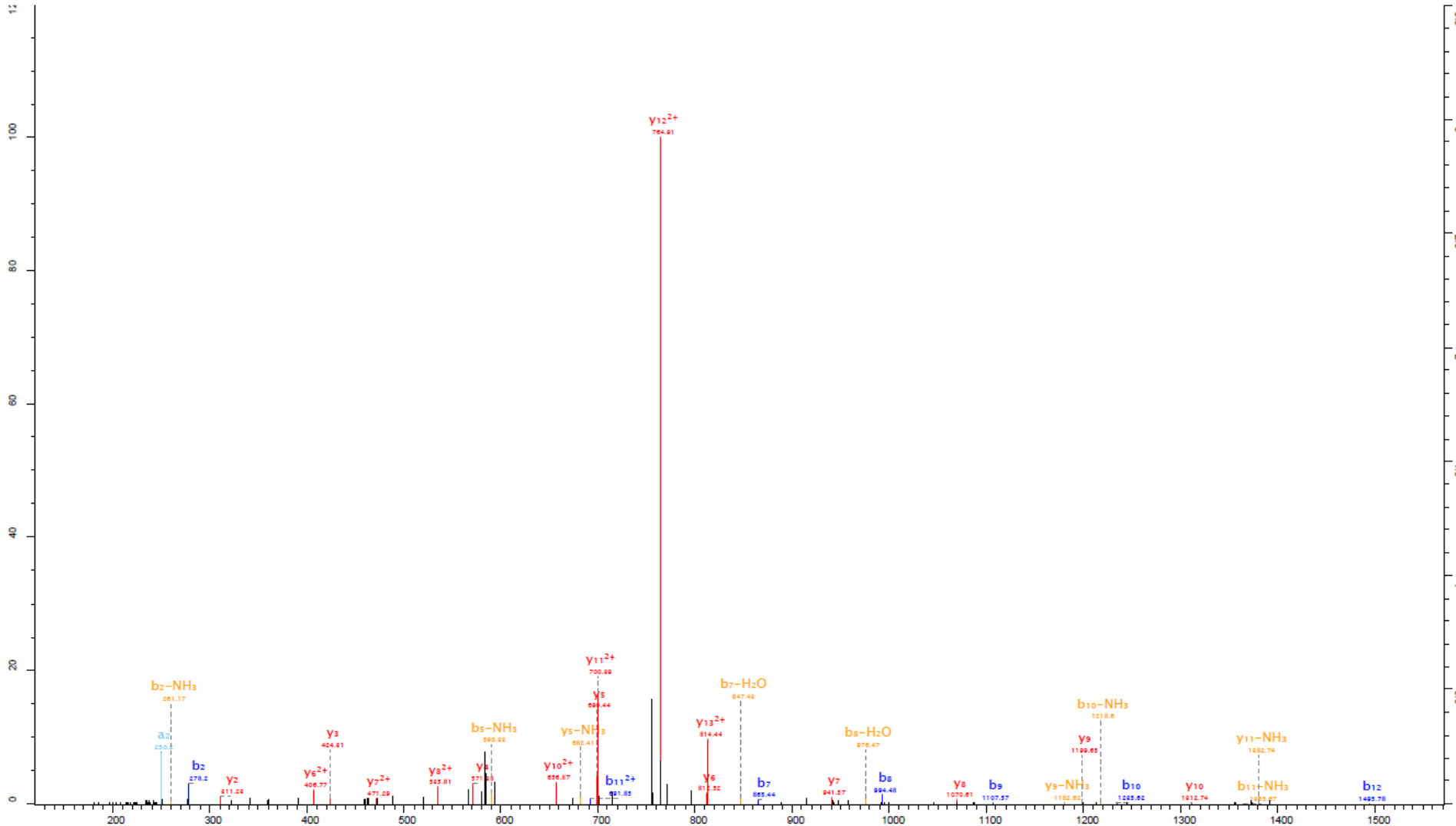
[–] Main Sequence Ions

b	b^{+2}				y	y^{+2}
---	---	1	T	9	---	---
249.1234	---	2	F	8	977.5274	489.2673
378.1660	---	3	E	7	830.4589	415.7331
435.1874	---	4	G	6	701.4164	351.2118
534.2558	---	5	V	5	644.3949	322.7011
649.2828	---	6	D	4	545.3265	273.1669
746.3355	---	7	P	3	430.2995	215.6534
924.4553	462.7313	8	K(50.0248)	2	333.2468	167.1270
---	---	9	K(8.0142)	1	155.1270	78.0671

Gene name = Gdi2

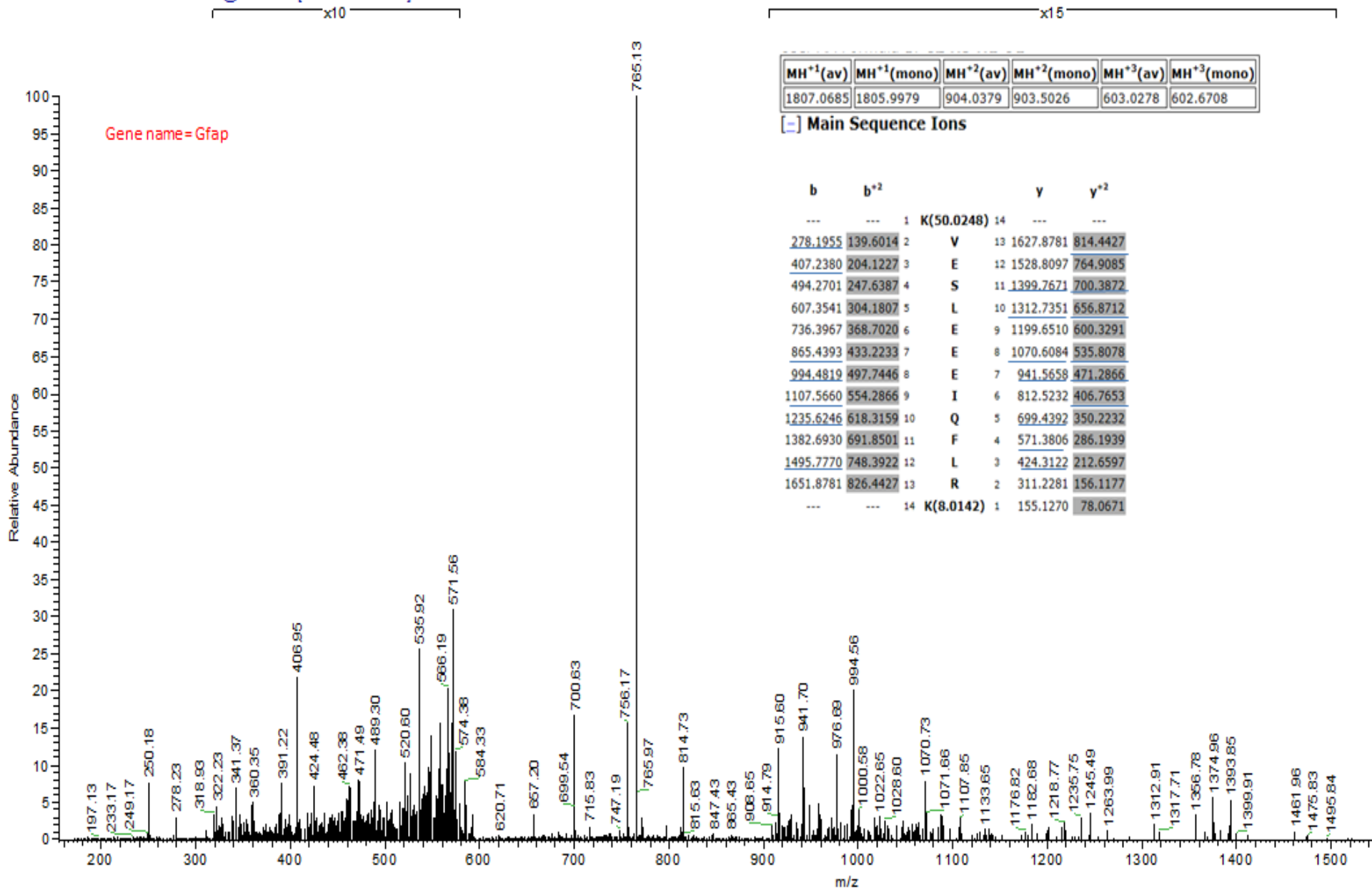


aw file	Scan	Method	Score	m/z	Gene names
22714_SCW_II_53_8_2ndZT	25033	ITMS; CID	147.39	602.67	Gfap



- ac K V E S L E E E I Q F L R K -

022714_SCW_II_53_8_2ndZT #25033 RT: 110.82 AV: 1 NL: 2.92E4
T: ITMS + c NSI d Full ms2 602.67@cid35.00 [155.00-1820.00]

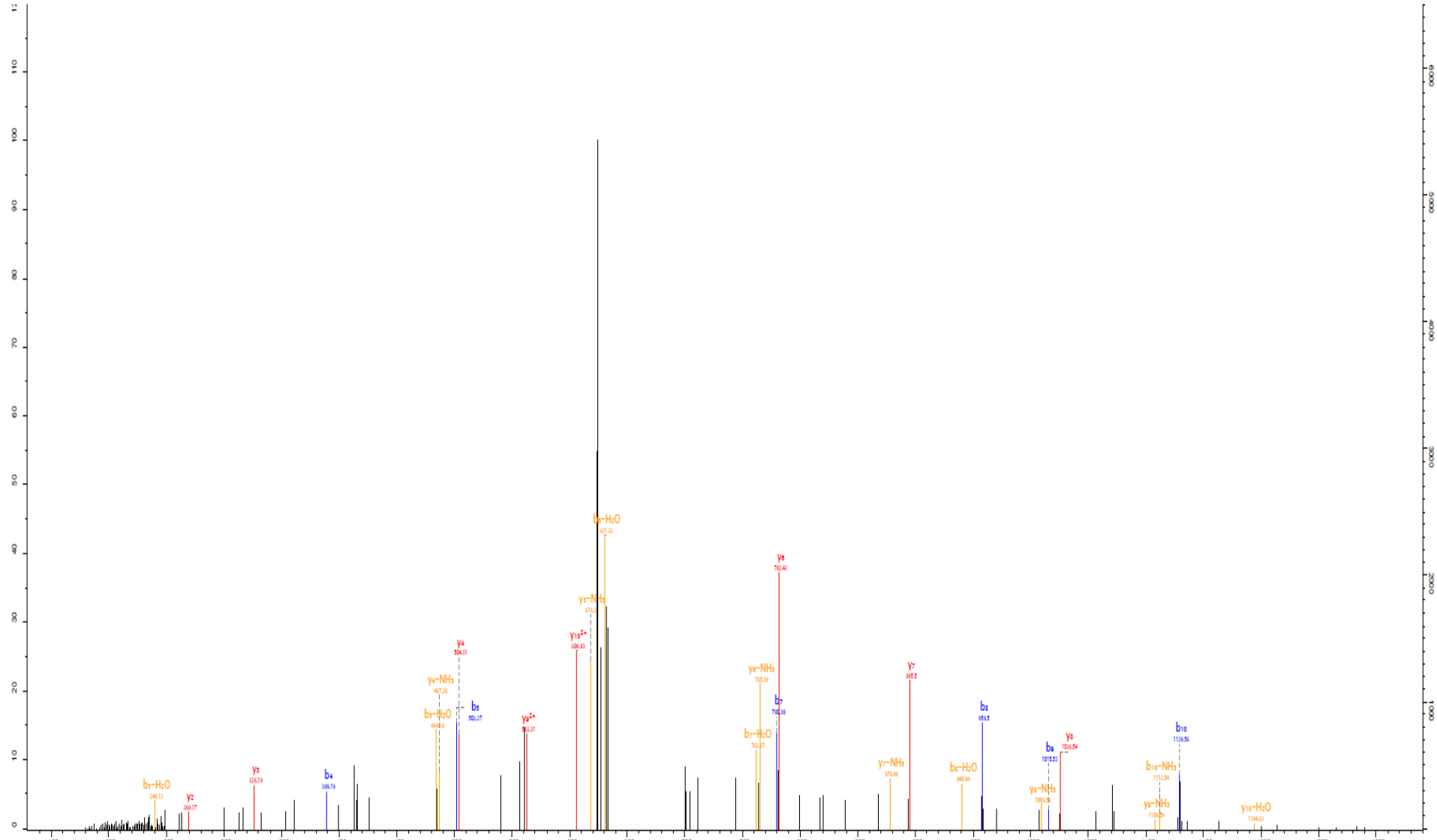


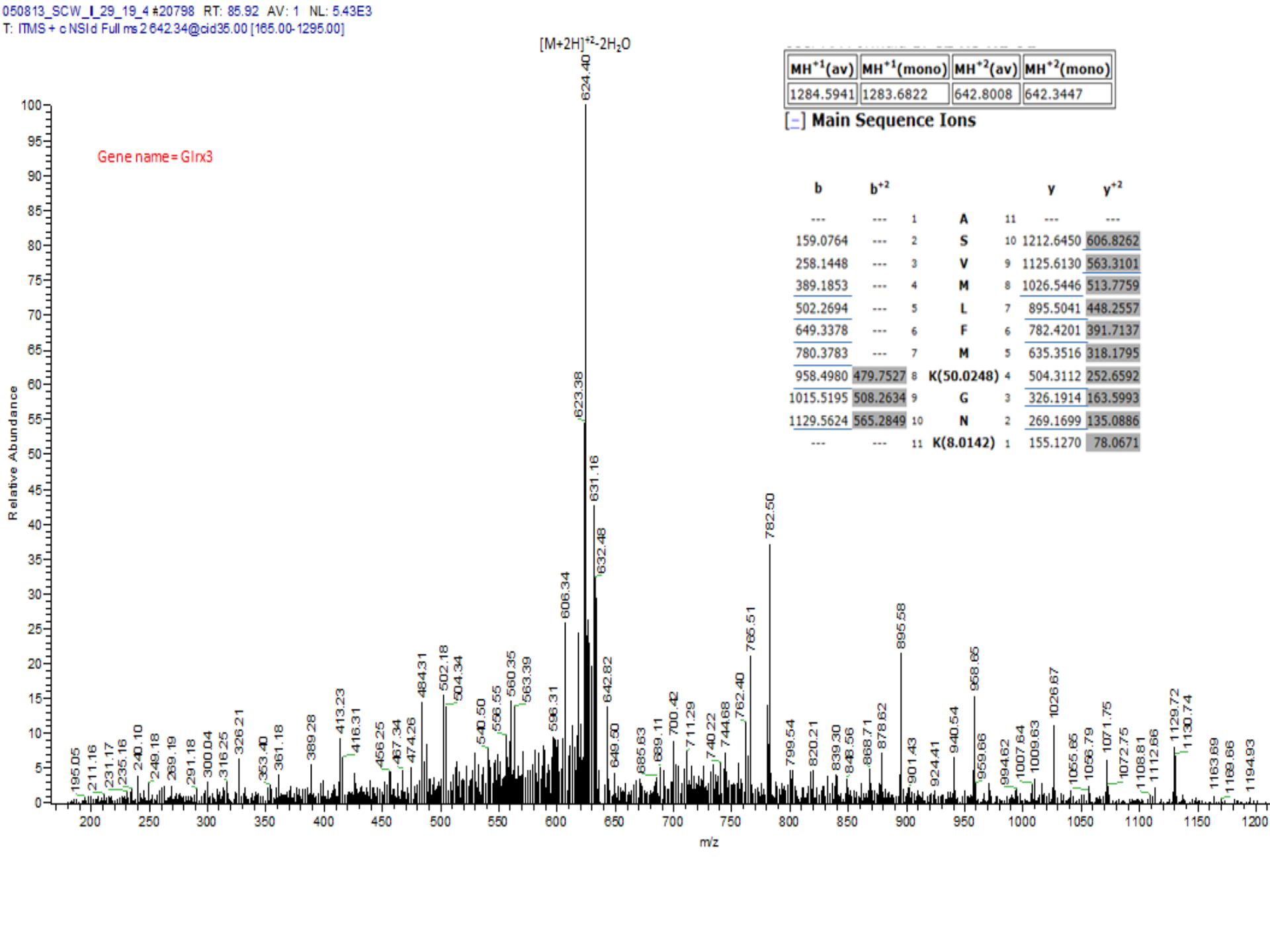
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)	MH^{+3}(av)	MH^{+3}(mono)
1807.0685	1805.9979	904.0379	903.5026	603.0278	602.6708

[–] **Main Sequence Ions**

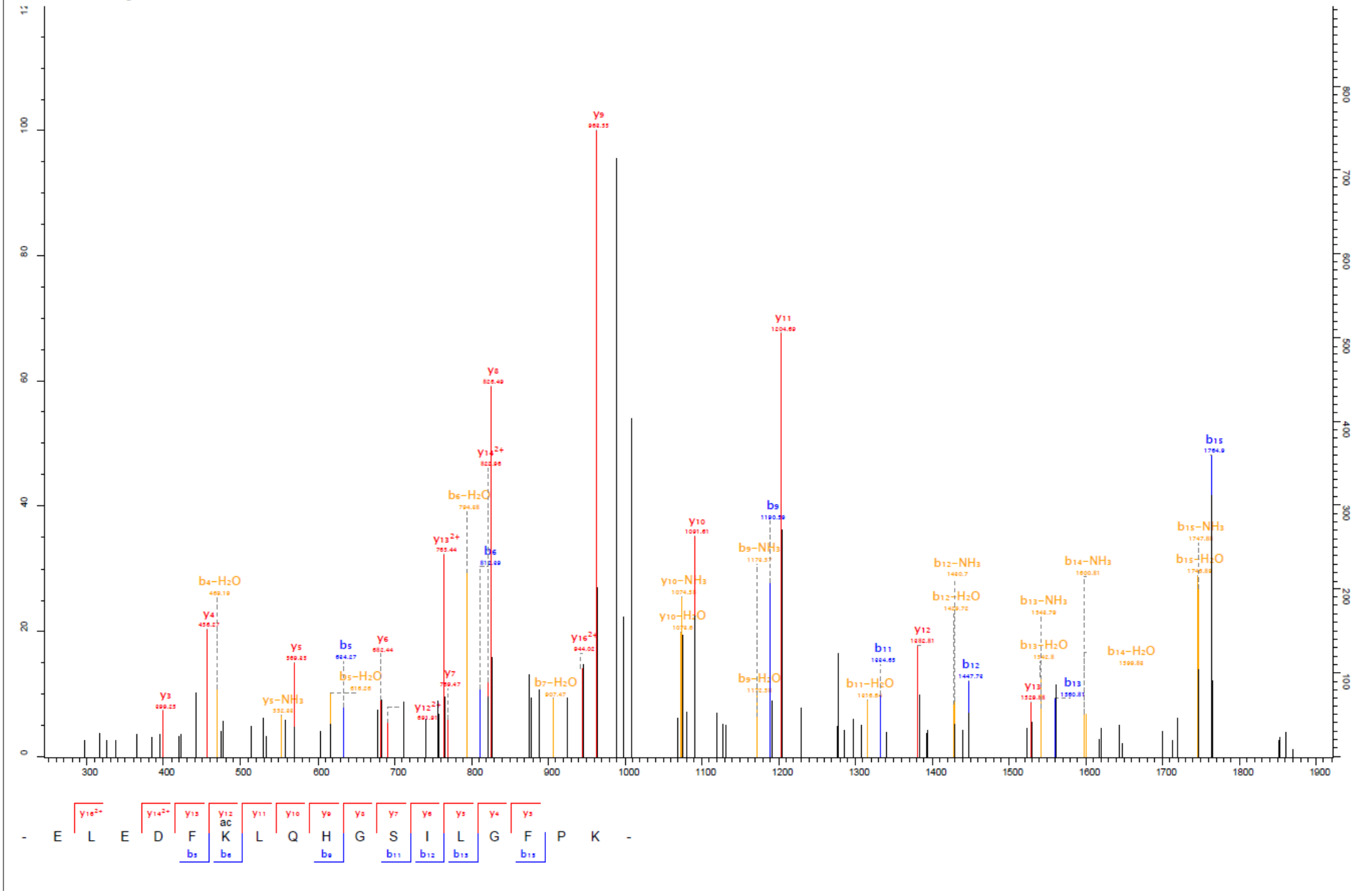
b	b^{+2}				y	y^{+2}
---	---	1	K(50.0248)	14	---	---
278.1955	139.6014	2	V	13	1627.8781	814.4427
407.2380	204.1227	3	E	12	1528.8097	764.9085
494.2701	247.6387	4	S	11	1399.7671	700.3872
607.3541	304.1807	5	L	10	1312.7351	656.8712
736.3967	368.7020	6	E	9	1199.6510	600.3291
865.4393	433.2233	7	E	8	1070.6084	535.8078
994.4819	497.7446	8	E	7	941.5658	471.2866
1107.5660	554.2866	9	I	6	812.5232	406.7653
1235.6246	618.3159	10	Q	5	699.4392	350.2232
1382.6930	691.8501	11	F	4	571.3806	286.1939
1495.7770	748.3922	12	L	3	424.3122	212.6597
1651.8781	826.4427	13	R	2	311.2281	156.1177
---	---	14	K(8.0142)	1	155.1270	78.0671

Raw file	Scan	Method	Score	m/z	Gene names
050813_SCW_JI_29_19_4	20798	ITMS; CID	129.89	642.34	Glrx3




050813_SCW_I_29_19_4 #20798 RT: 85.92 AV: 1 NL: 5.43E3
T: ITMS + c NSI d Full ms2 642.34@cid35.00 [165.00-1295.00]
[M+2H]+2-2H2O
Gene name = Glrx3
Relative Abundance
m/z
MH+1(av) MH+1(mono) MH+2(av) MH+2(mono)
1284.5941 1283.6822 642.8008 642.3447
[-] Main Sequence Ions
b b+2 y y+2
--- --- 1 A 11 --- ---
159.0764 --- 2 S 10 1212.6450 606.8262
258.1448 --- 3 V 9 1125.6130 563.3101
389.1853 --- 4 M 8 1026.5446 513.7759
502.2694 --- 5 L 7 895.5041 448.2557
649.3378 --- 6 F 6 782.4201 391.7137
780.3783 --- 7 M 5 635.3516 318.1795
958.4980 479.7527 8 K(50.0248) 4 504.3112 252.6592
1015.5195 508.2634 9 G 3 326.1914 163.5993
1129.5624 565.2849 10 N 2 269.1699 135.0886
--- --- 11 K(8.0142) 1 155.1270 78.0671

Raw file	Scan	Method	Score	m/z	Gene names
062513_SCW_II_53_7_Vargas_Enriched	21955	ITMS; CID	166.62	1009.04	Glud1

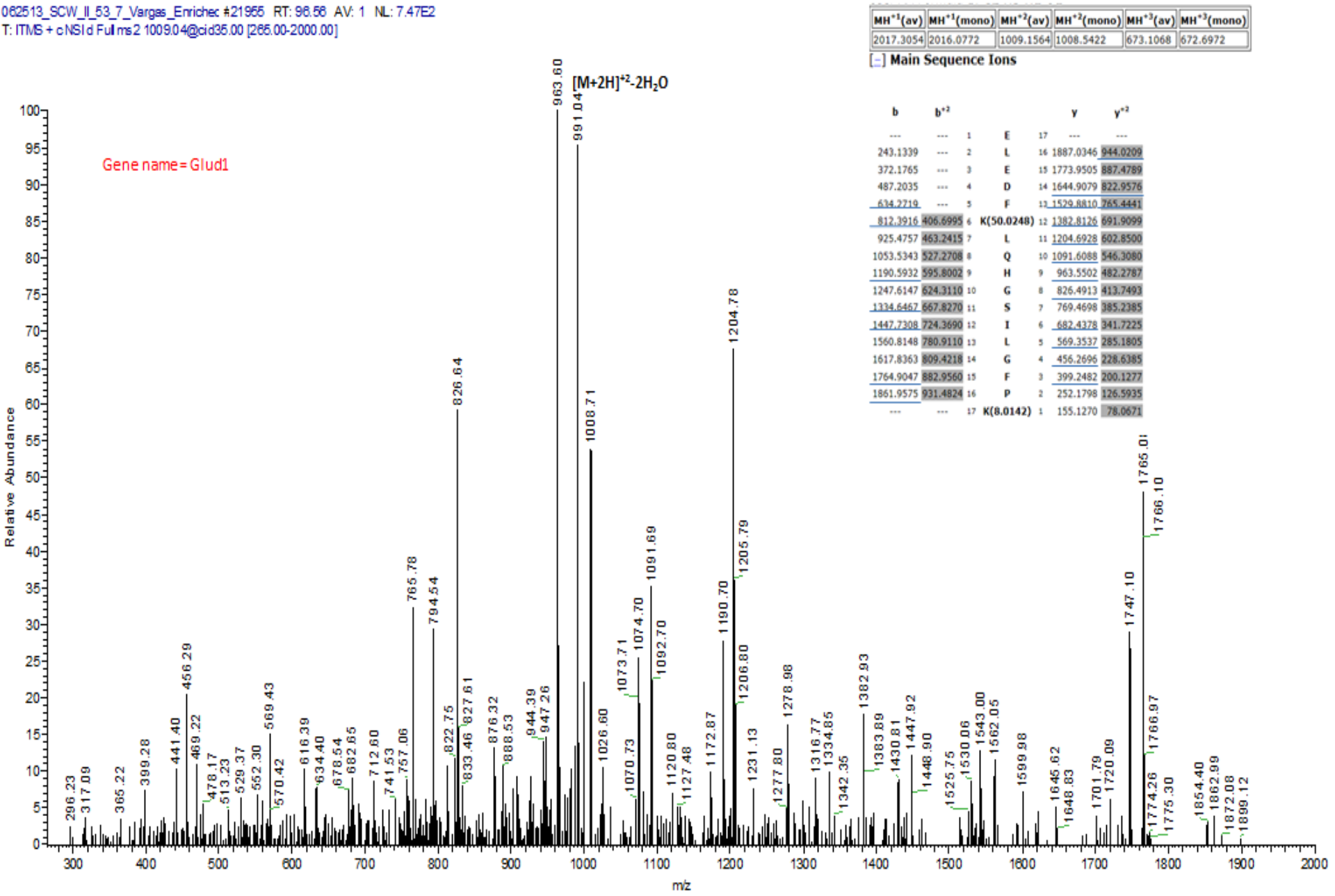


062513_SCW_II_53_7_Vargas_Enrichec #21955 RT: 96.56 AV: 1 NL: 7.47E2
T: ITMS + c NSI d Full ms2 1009.04@cid35.00 [265.00-2000.00]

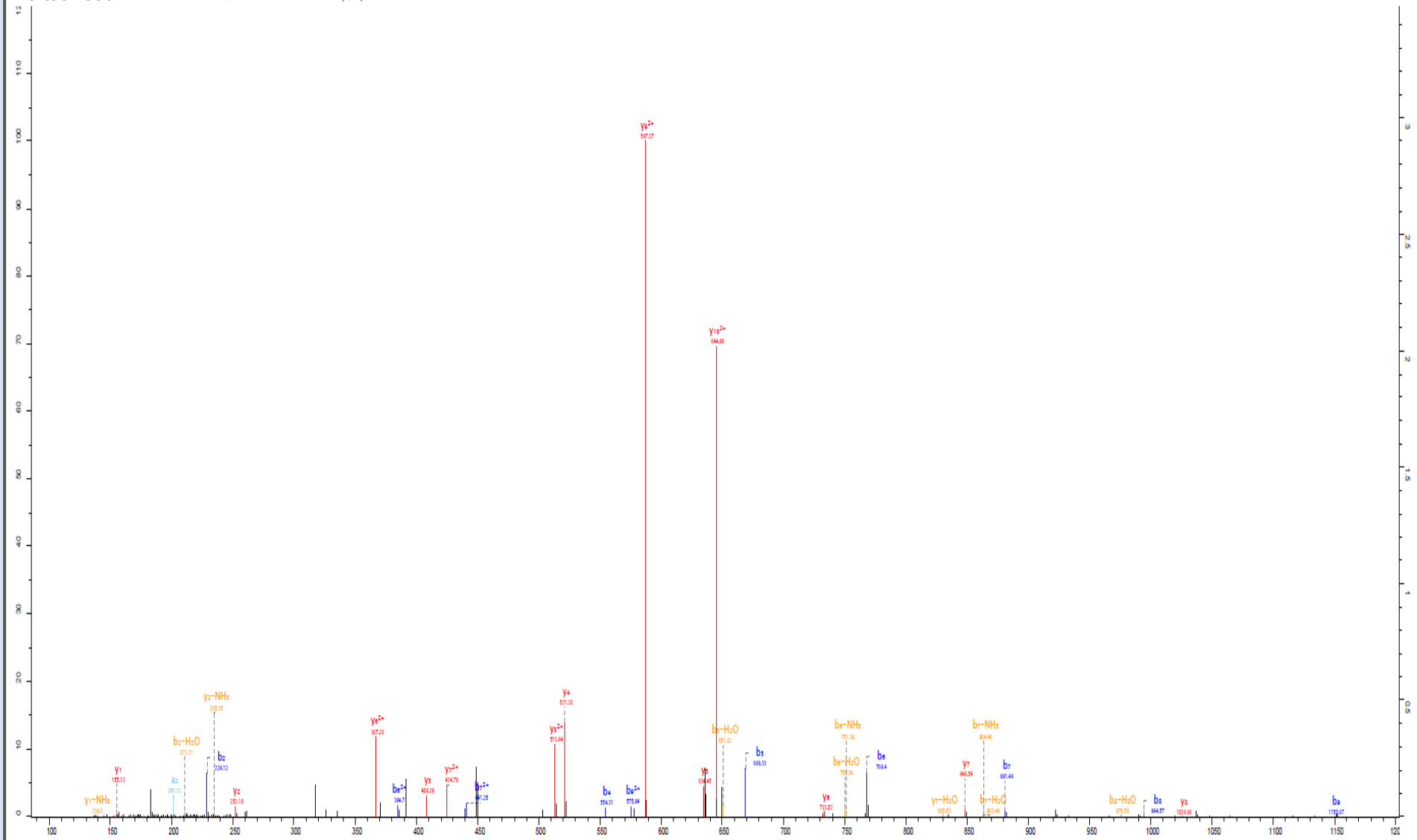
MH+1(av)	MH+1(mono)	MH+2(av)	MH+2(mono)	MH+3(av)	MH+3(mono)
2017.3054	2016.0772	1009.1564	1008.5422	673.1068	672.6972

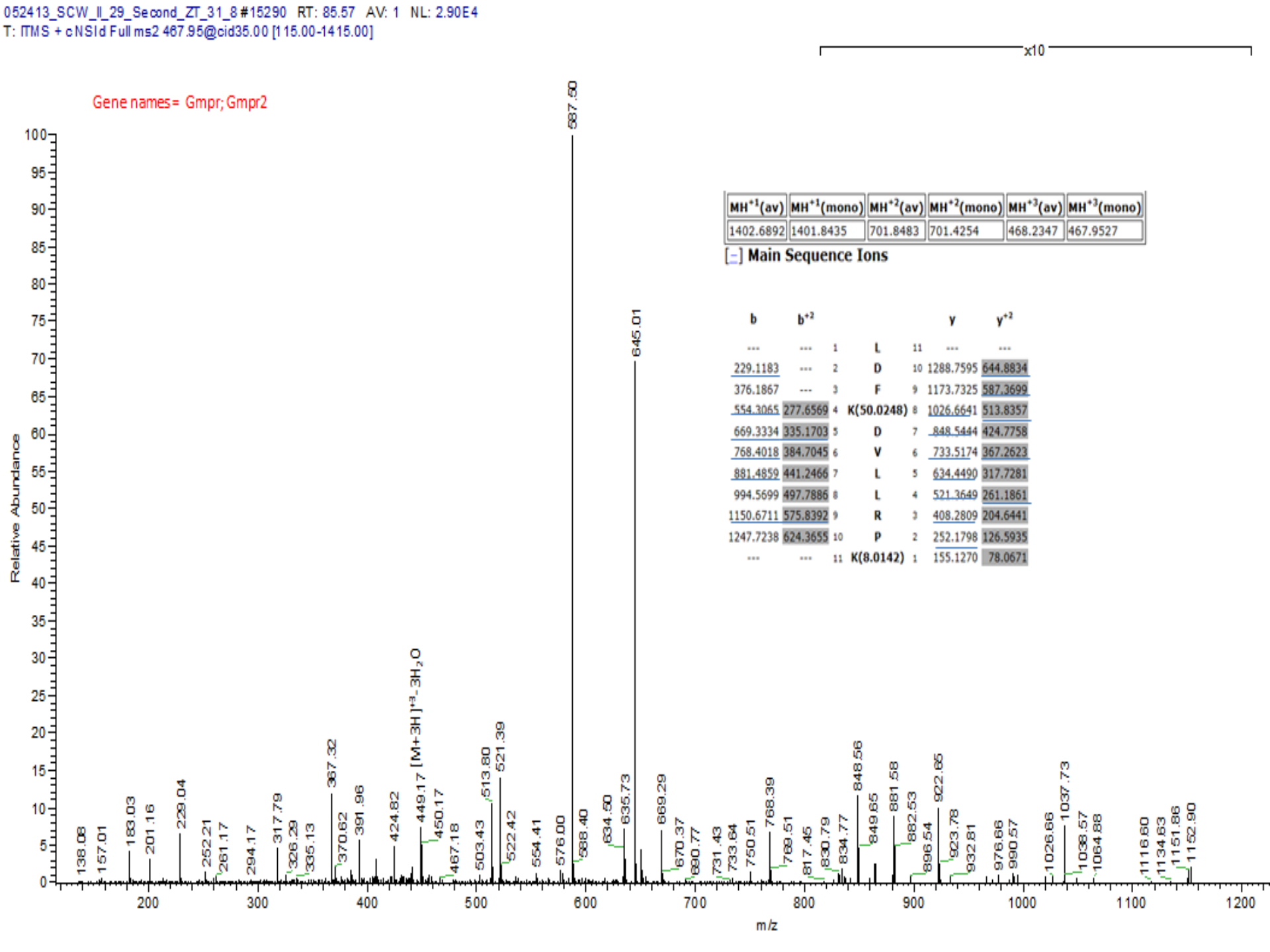
[-] Main Sequence Ions

b	b+2				y	y+2
---	---	1	E	17	---	---
243.1339	---	2	L	16	1887.0346	944.0209
372.1765	---	3	E	15	1773.9505	887.4789
487.2035	---	4	D	14	1644.9079	822.9576
634.2719	---	5	F	13	1529.8810	765.4441
812.3916	406.6995	6	K(50.0248)	12	1382.8126	691.9099
925.4757	463.2415	7	L	11	1204.6928	602.8500
1053.5343	527.2708	8	Q	10	1091.6088	546.3080
1190.5932	595.8002	9	H	9	963.5502	482.2787
1247.6147	624.3110	10	G	8	826.4913	413.7493
1334.6467	667.8270	11	S	7	769.4698	385.2385
1447.7308	724.3690	12	I	6	682.4378	341.7225
1560.8148	780.9110	13	L	5	569.3537	285.1805
1617.8363	809.4218	14	G	4	456.2696	228.6385
1764.9047	882.9560	15	F	3	399.2482	200.1277
1861.9575	931.4824	16	P	2	252.1798	126.5935
---	---	17	K(8.0142)	1	155.1270	78.0671

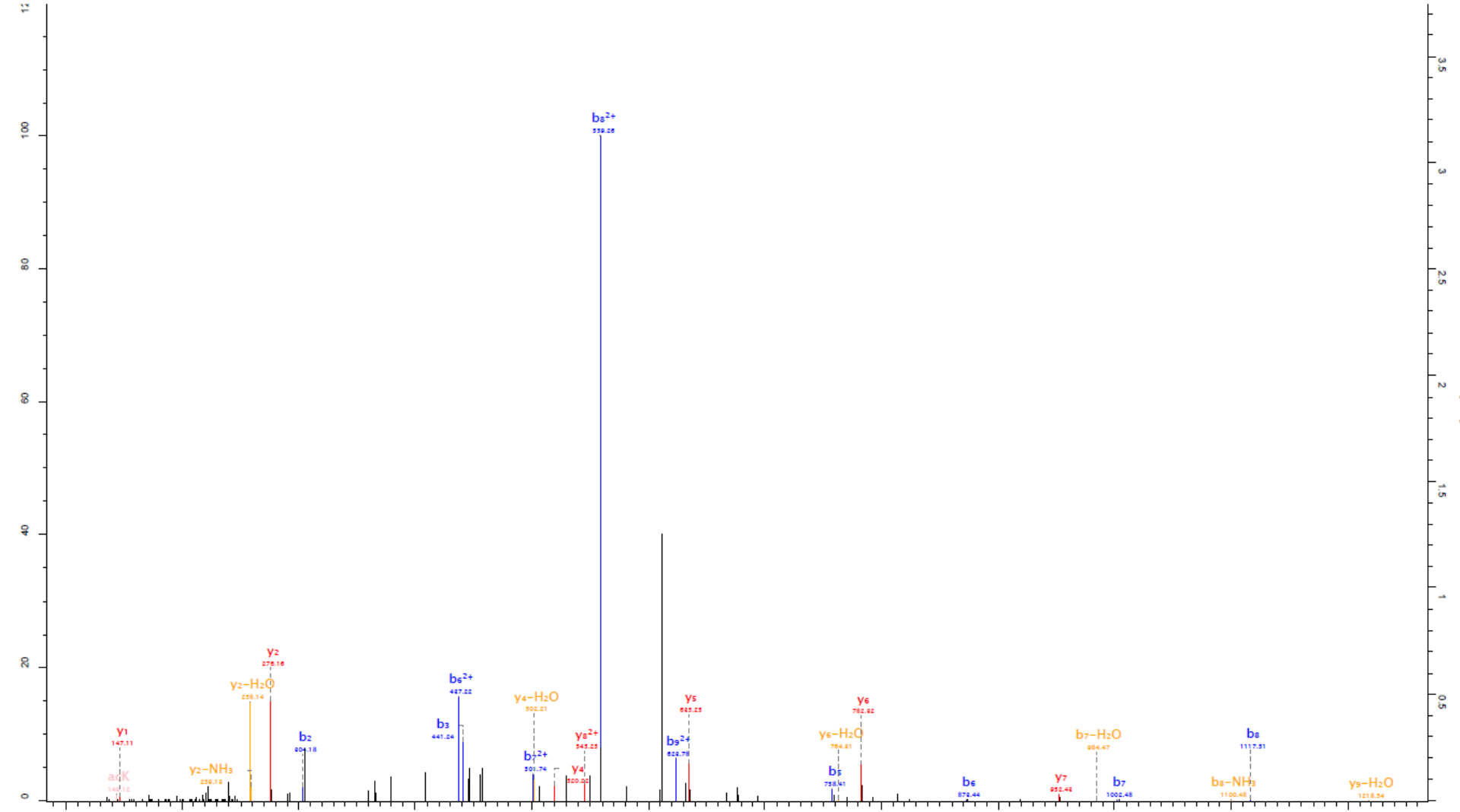


Raw file	Scan	Method	Score	m/z	Gene names
052413_SCW_II_29_Second_ZT_31_8	15290	ITMS; CID	171.67	467.95	Cmpr;Cmpr2



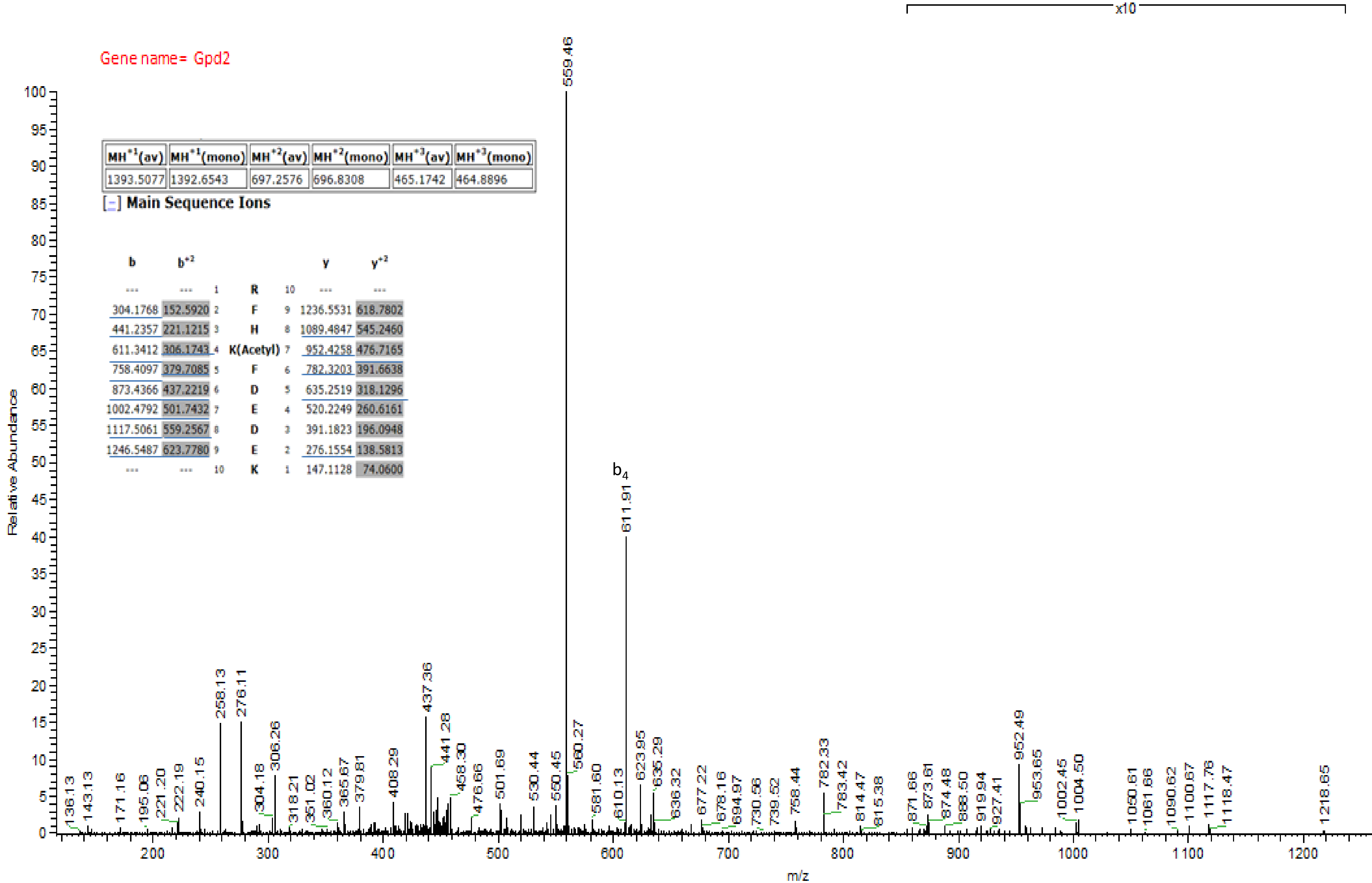

052413_SCW_II_29_Second_ZT_31_8 #15290 RT: 85.57 AV: 1 NL: 2.90E4
T: ITMS + c NSI d Full ms2 467.95@cid35.00 [115.00-1415.00]
x10
Gene names= Gmpr; Gmpr2
MH+1(av) MH+1(mono) MH+2(av) MH+2(mono) MH+3(av) MH+3(mono)
1402.6892 1401.8435 701.8483 701.4254 468.2347 467.9527
[-] Main Sequence Ions
b b+2 y y+2
... ... 1 L 11 ... ...
229.1183 ... 2 D 10 1288.7595 644.8834
376.1867 ... 3 F 9 1173.7325 587.3699
554.3065 277.6569 4 K(50.0248) 8 1026.6641 513.8357
669.3334 335.1703 5 D 7 848.5444 424.7758
768.4018 384.7045 6 V 6 733.5174 367.2623
881.4859 441.2466 7 L 5 634.4490 317.7281
994.5699 497.7886 8 L 4 521.3649 261.1861
1150.6711 575.8392 9 R 3 408.2809 204.6441
1247.7238 624.3655 10 P 2 252.1798 126.5935
... ... 11 K(8.0142) 1 155.1270 78.0671
Relative Abundance
m/z
[M+3H]+3 - 3H2O

Raw file	Scan	Method	Score	m/z	Gene names
050713_SCW_II_29_50_12	10975	ITMS; CID	130.01	464.89	Gpd2



		y5 2+	y7	y6	y5	y4	y3	y2	y1				
-	R	F	H	ac K	F	D	E	D	E	K	-		
		b2	b3		b5	b6	b7	b8	b9 2+				

050713_SCW_II_29_50_12 #10975 RT: 54.39 AV: 1 NL: 3.13E4
T: ITMS + c NSI d Full ms2 464.89@cid35.00 [115.00-1405.00]

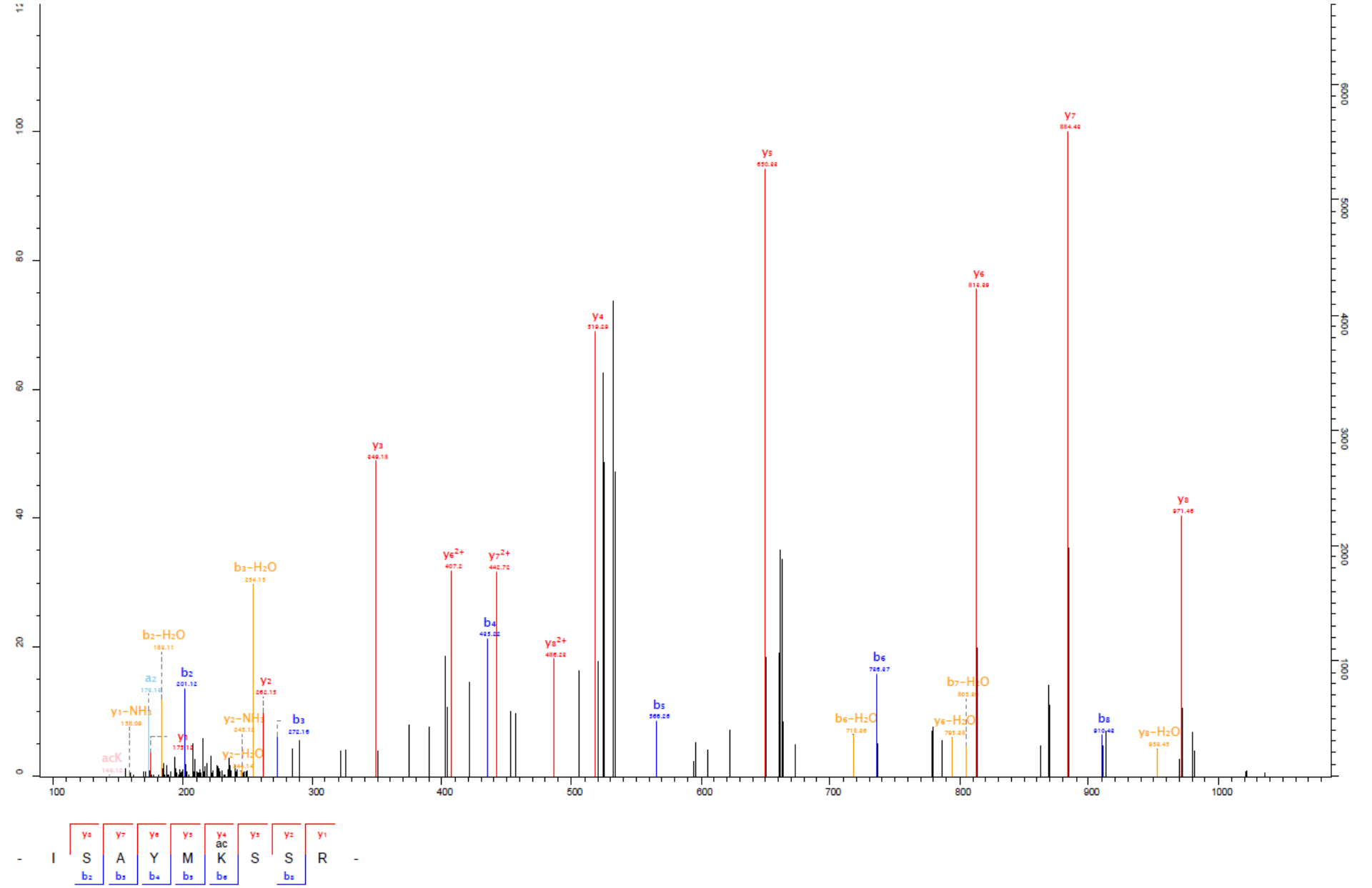


MH+1(av)	MH+1(mono)	MH+2(av)	MH+2(mono)	MH+3(av)	MH+3(mono)
1393.5077	1392.6543	697.2576	696.8308	465.1742	464.8896

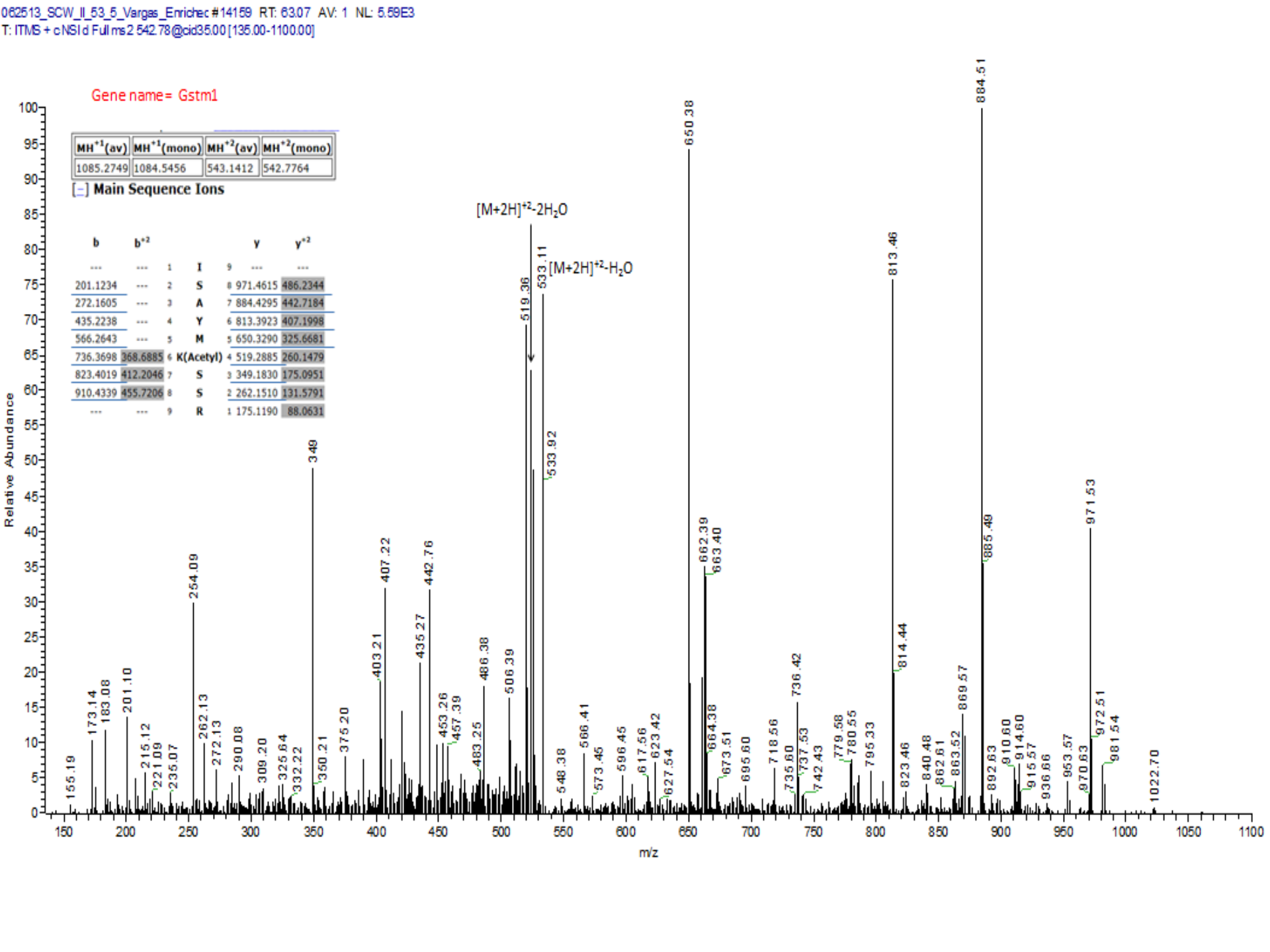
[-] **Main Sequence Ions**

b	b^{+2}				y	y^{+2}
---	---	1	R	10	---	---
304.1768	152.5920	2	F	9	1236.5531	618.7802
441.2357	221.1215	3	H	8	1089.4847	545.2460
611.3412	306.1743	4	K(Acetyl)	7	952.4258	476.7165
758.4097	379.7085	5	F	6	782.3203	391.6638
873.4366	437.2219	6	D	5	635.2519	318.1296
1002.4792	501.7432	7	E	4	520.2249	260.6161
1117.5061	559.2567	8	D	3	391.1823	196.0948
1246.5487	623.7780	9	E	2	276.1554	138.5813
---	---	10	K	1	147.1128	74.0600

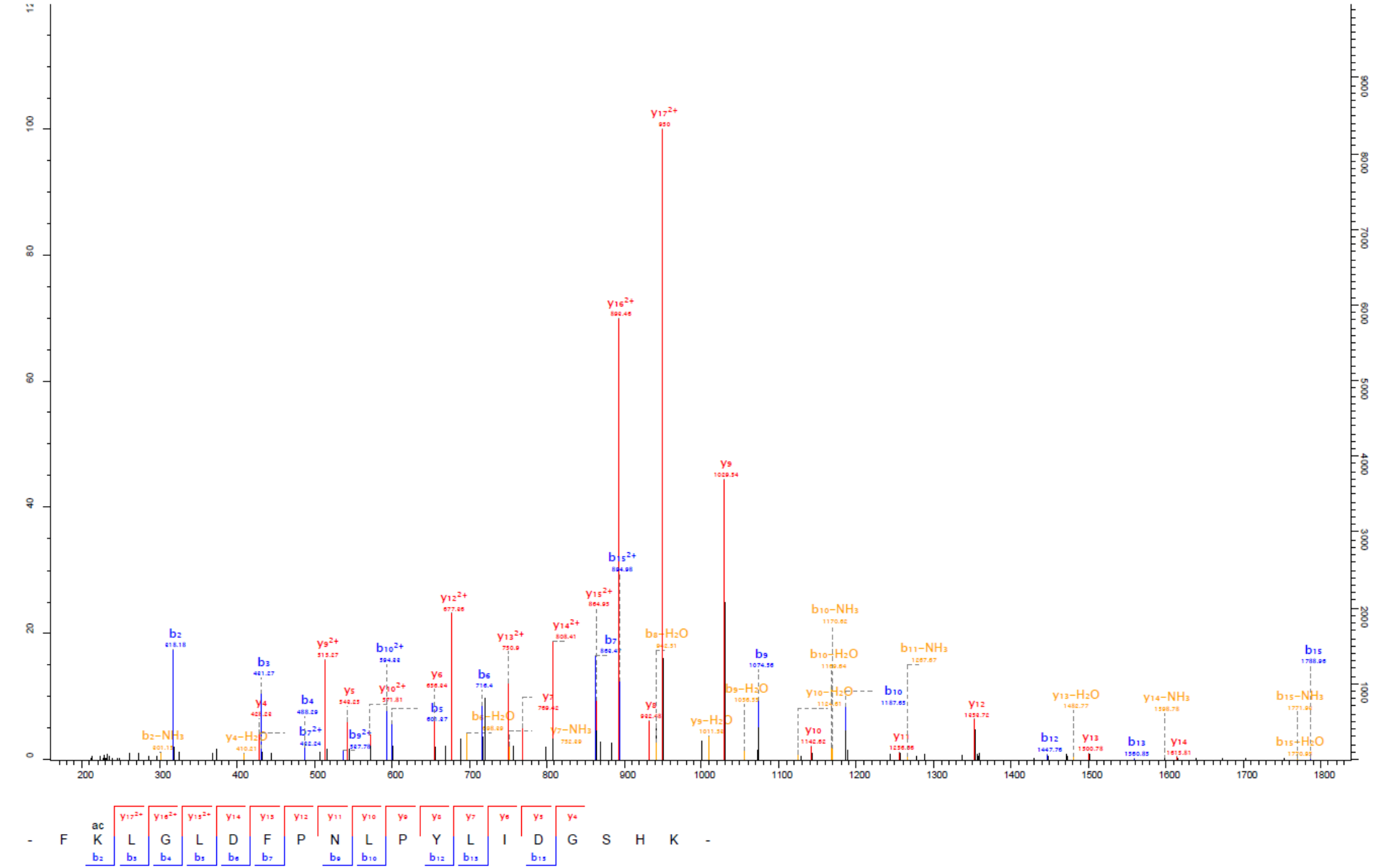
Raw file	Scan	Method	Score	m/z	Gene names
062513_SCW_II_53_5_Vargas_Enriched	14159	ITMS; CID	121.36	542.78	Gstm1



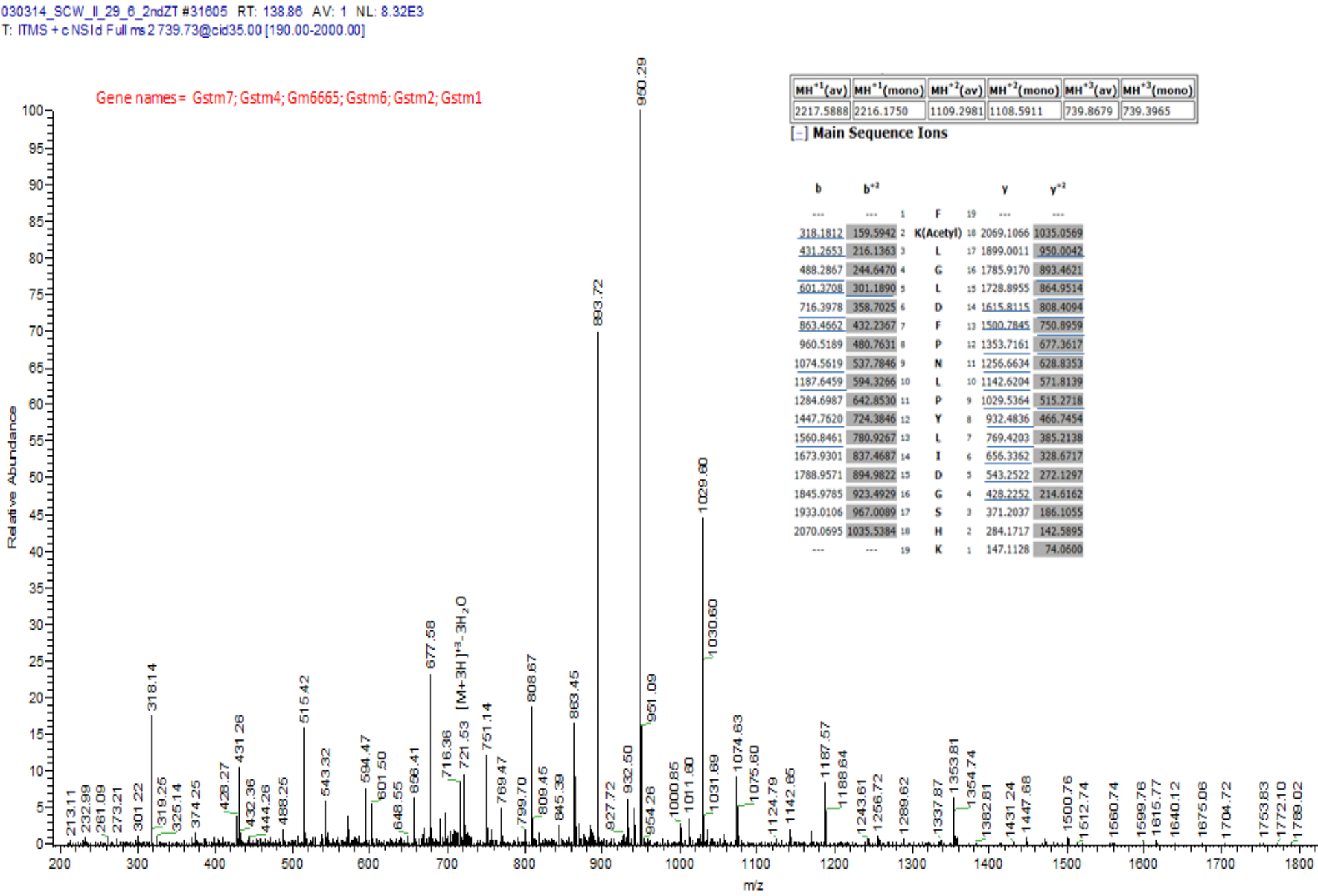
- I S A Y M ac K S S R -


062513_SCW_II_53_5_Vargas_Enrichec #14159 RT: 63.07 AV: 1 NL: 5.59E3
T: ITMS + c NSI d Full ms2 542.78@cid35.00 [135.00-1100.00]
Gene name= Gstm1
MH+1(av) MH+1(mono) MH+2(av) MH+2(mono)
1085.2749 1084.5456 543.1412 542.7764
[-] Main Sequence Ions
b b+2 y y+2
--- --- 1 I 9 --- ---
201.1234 --- 2 S 8 971.4615 486.2344
272.1605 --- 3 A 7 884.4295 442.7184
435.2238 --- 4 Y 6 813.3923 407.1998
566.2643 --- 5 M 5 650.3290 325.6681
736.3698 368.6885 6 K(Acetyl) 4 519.2885 260.1479
823.4019 412.2046 7 S 3 349.1830 175.0951
910.4339 455.7206 8 S 2 262.1510 131.5791
--- --- 9 R 1 175.1190 88.0631
[M+2H]+2-2H2O
[M+2H]+2-H2O
Relative Abundance
m/z

Raw file	Scan	Method	Score	m/z	Gene names
030314_SCW_II_29_6_2ndZT	31605	ITMS; CID	225.54	739.73	Gstm7;Gstm4;Gm6665;Gstm6;Gstm2;Gstm1



ac
- F K L G L D F P N L P Y L I D G S H K -

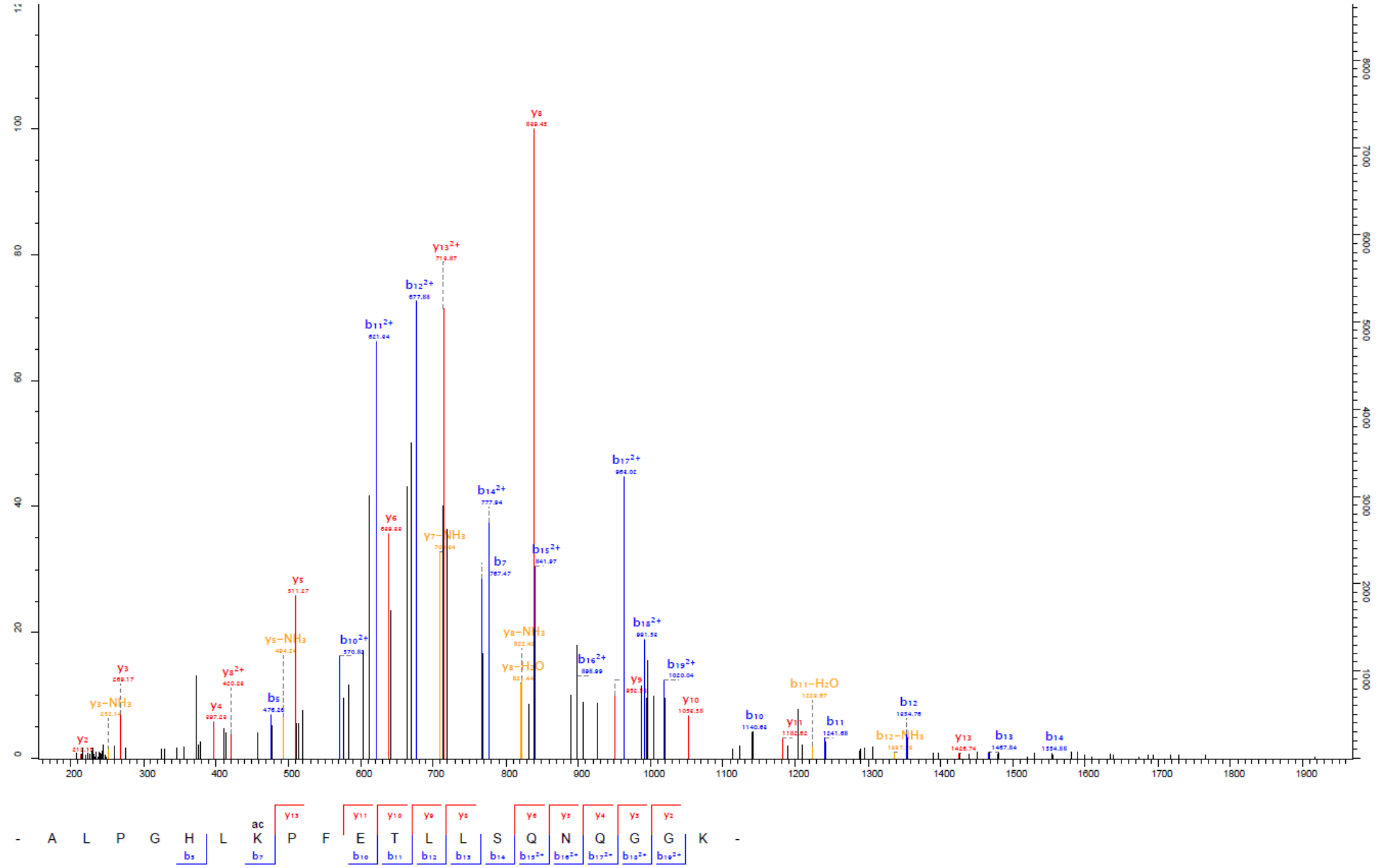


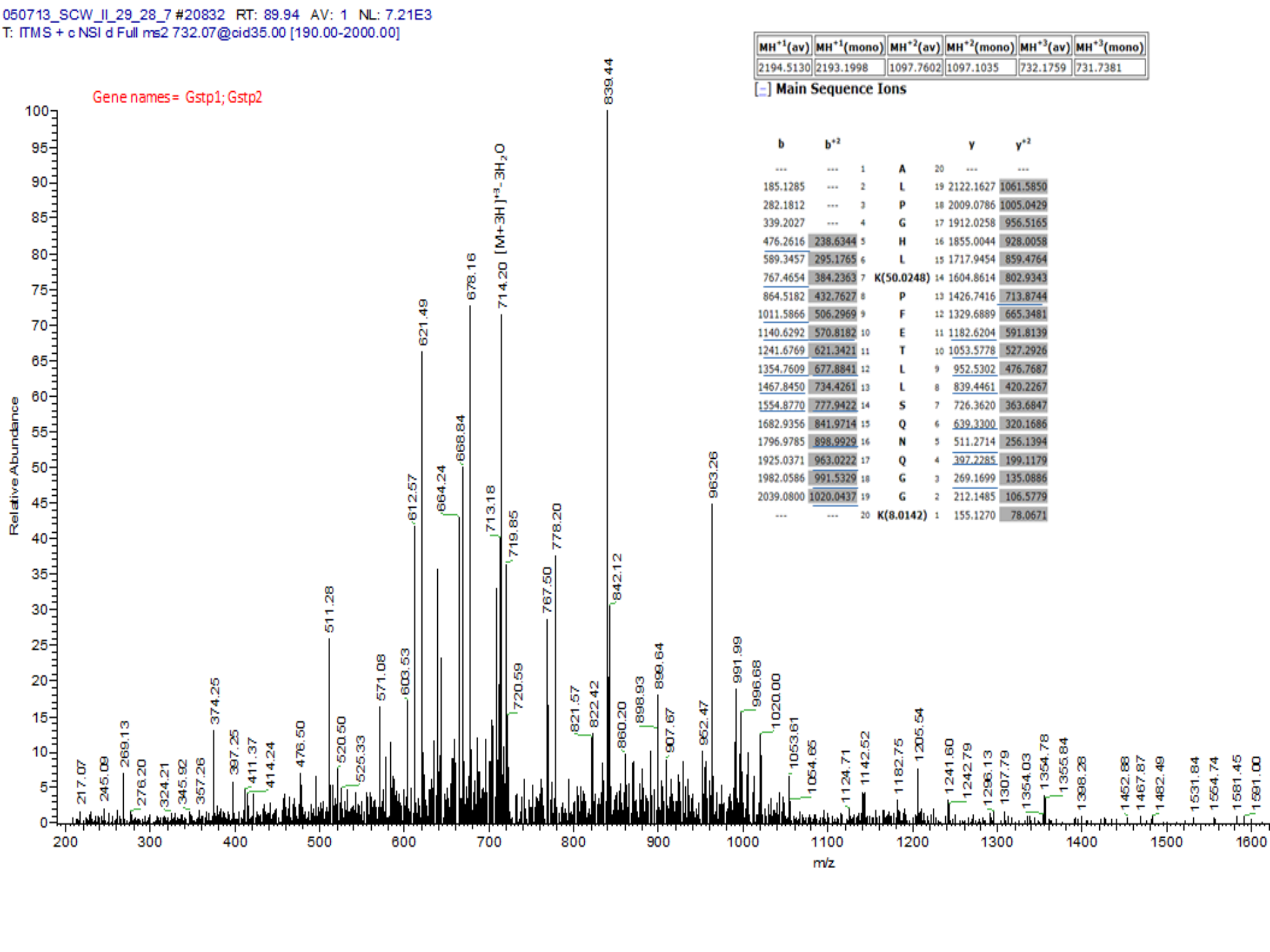
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)	MH^{+3}(av)	MH^{+3}(mono)
2217.5888	2216.1750	1109.2981	1108.5911	739.8679	739.3965

[–] **Main Sequence Ions**

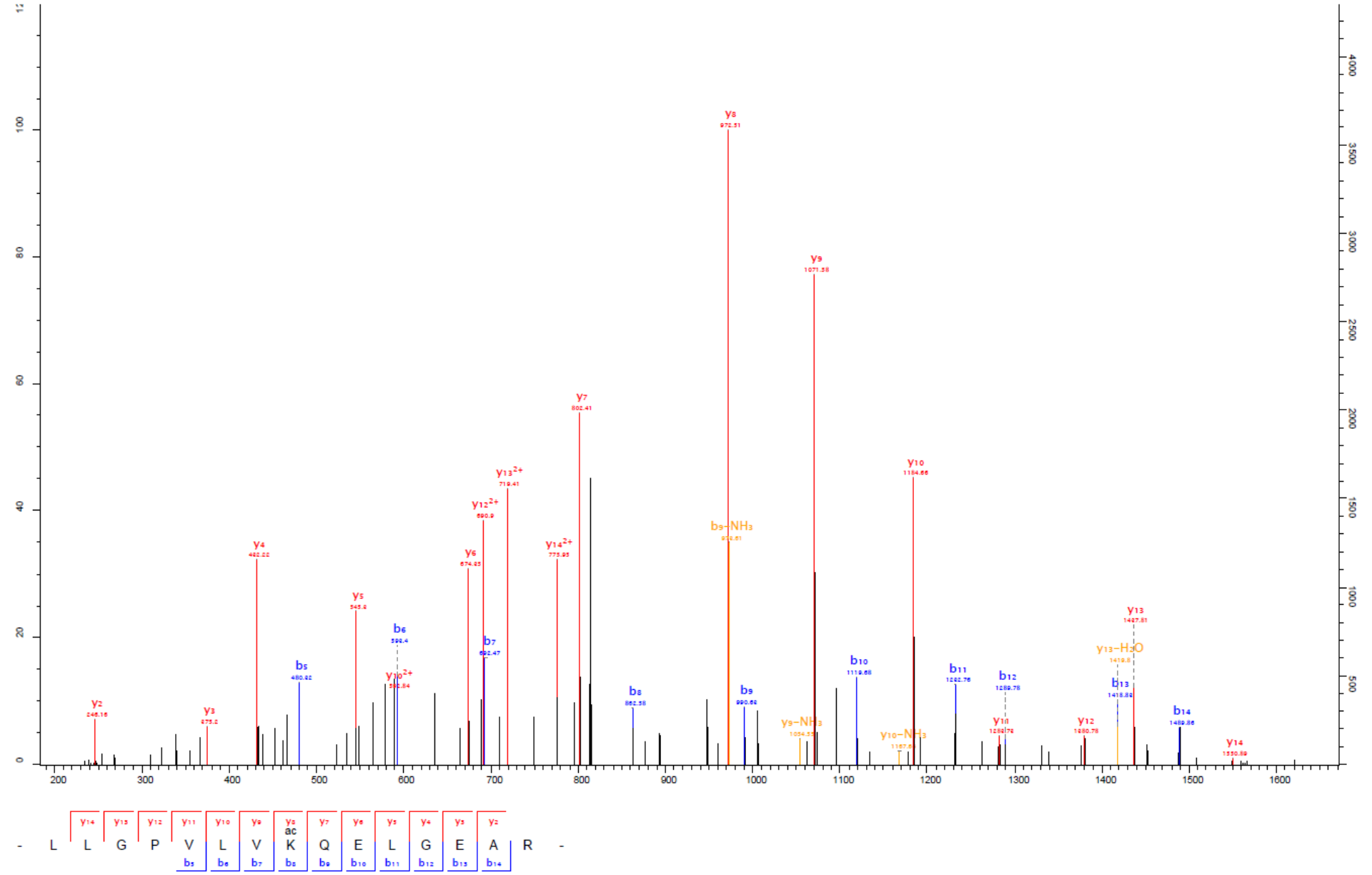
b	b^{+2}				y	y^{+2}
---	---	1	F	19	---	---
318.1812	159.5942	2	K(Acetyl)	18	2069.1066	1035.0569
431.2653	216.1363	3	L	17	1899.0011	950.0042
488.2867	244.6470	4	G	16	1785.9170	893.4621
601.3708	301.1890	5	L	15	1728.8955	864.9514
716.3978	358.7025	6	D	14	1615.8115	808.4094
863.4662	432.2367	7	F	13	1500.7845	750.8959
960.5189	480.7631	8	P	12	1353.7161	677.3617
1074.5619	537.7846	9	N	11	1256.6634	628.8353
1187.6459	594.3266	10	L	10	1142.6204	571.8139
1284.6987	642.8530	11	P	9	1029.5364	515.2718
1447.7620	724.3846	12	Y	8	932.4836	466.7454
1560.8461	780.9267	13	L	7	769.4203	385.2138
1673.9301	837.4687	14	I	6	656.3362	328.6717
1788.9571	894.9822	15	D	5	543.2522	272.1297
1845.9785	923.4929	16	G	4	428.2252	214.6162
1933.0106	967.0089	17	S	3	371.2037	186.1055
2070.0695	1035.5384	18	H	2	284.1717	142.5895
---	---	19	K	1	147.1128	74.0600

Raw file	Scan	Method	Score	m/z	Gene names
050713_SCW_II_29_28_7	20832	ITMS; CID	128.94	732.07	Gstp1;Gstp2




050713_SCW_II_29_28_7 #20832 RT: 89.94 AV: 1 NL: 7.21E3
T: ITMS + c NSI d Full ms2 732.07@cid35.00 [190.00-2000.00]
Gene names= Gstp1; Gstp2
MH+1(av) MH+1(mono) MH+2(av) MH+2(mono) MH+3(av) MH+3(mono)
2194.5130 2193.1998 1097.7602 1097.1035 732.1759 731.7381
[-] Main Sequence Ions
b b*2 y y*2
--- --- 1 A 20 --- ---
185.1285 --- 2 L 19 2122.1627 1061.5850
282.1812 --- 3 P 18 2009.0786 1005.0429
339.2027 --- 4 G 17 1912.0258 956.5165
476.2616 238.6344 5 H 16 1855.0044 928.0058
589.3457 295.1765 6 L 15 1717.9454 859.4764
767.4654 384.2363 7 K(50.0248) 14 1604.8614 802.9343
864.5182 432.7627 8 P 13 1426.7416 713.8744
1011.5866 506.2969 9 F 12 1329.6889 665.3481
1140.6292 570.8182 10 E 11 1182.6204 591.8139
1241.6769 621.3421 11 T 10 1053.5778 527.2926
1354.7609 677.8841 12 L 9 952.5302 476.7687
1467.8450 734.4261 13 L 8 839.4461 420.2267
1554.8770 777.9422 14 S 7 726.3620 363.6847
1682.9356 841.9714 15 Q 6 639.3300 320.1686
1796.9785 898.9929 16 N 5 511.2714 256.1394
1925.0371 963.0222 17 Q 4 397.2285 199.1179
1982.0586 991.5329 18 G 3 269.1699 135.0886
2039.0800 1020.0437 19 G 2 212.1485 106.5779
--- --- 20 K(8.0142) 1 155.1270 78.0671
Relative Abundance
m/z
839.44
714.20 [M+3H]+3-3H2O
678.16
621.49
668.84
664.24
612.57
963.26
713.18
719.85
778.20
511.28
767.50
842.12
571.08
603.53
720.59
991.99
996.68
899.64
898.93
1020.00
374.25
822.42
821.57
860.20
907.67
952.47
1053.61
1054.85
1124.71
1142.52
1182.75
1205.54
1241.60
1242.79
1296.13
1307.79
1354.03
1354.78
1355.84
1398.28
1452.88
1467.87
1482.49
1531.84
1554.74
1581.45
1591.00
217.07
245.09
269.13
276.20
324.21
345.92
357.26
397.25
411.37
414.24
476.50
520.50
525.33

Raw file	Scan	Method	Score	m/z	Gene names
062513_SCW_II_53_4_Vargas_Enriched	23264	ITMS; CID	156.49	832.49	H2-Ke2;Pfdn6



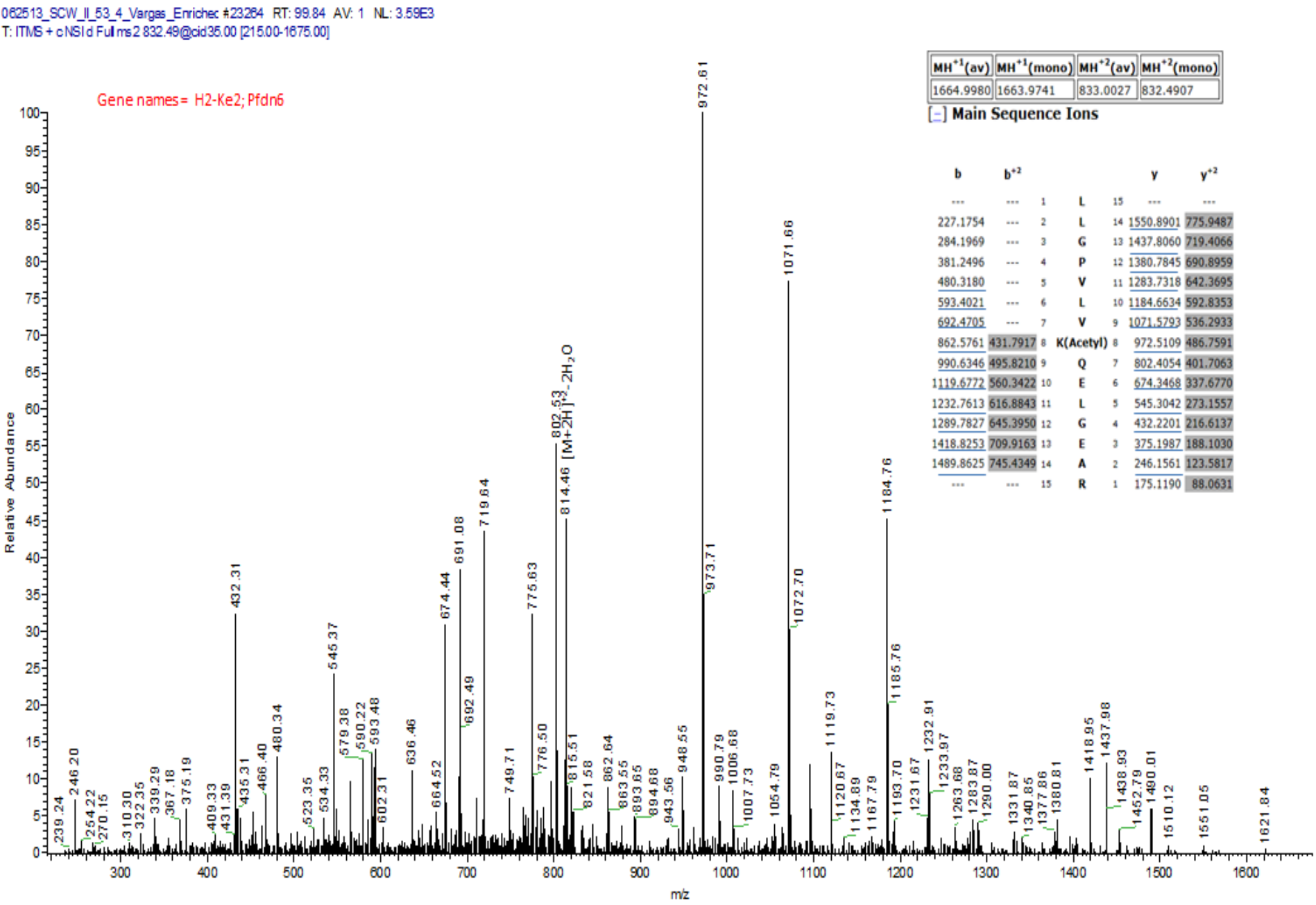
062513_SCW_II_53_4_Vargas_Enrichec #23264 RT: 99.84 AV: 1 NL: 3.59E3
T: ITMS + cNSI d Full ms2 832.49@cid35.00 [215.00-1675.00]

Gene names= H2-Ke2; Pfdn6

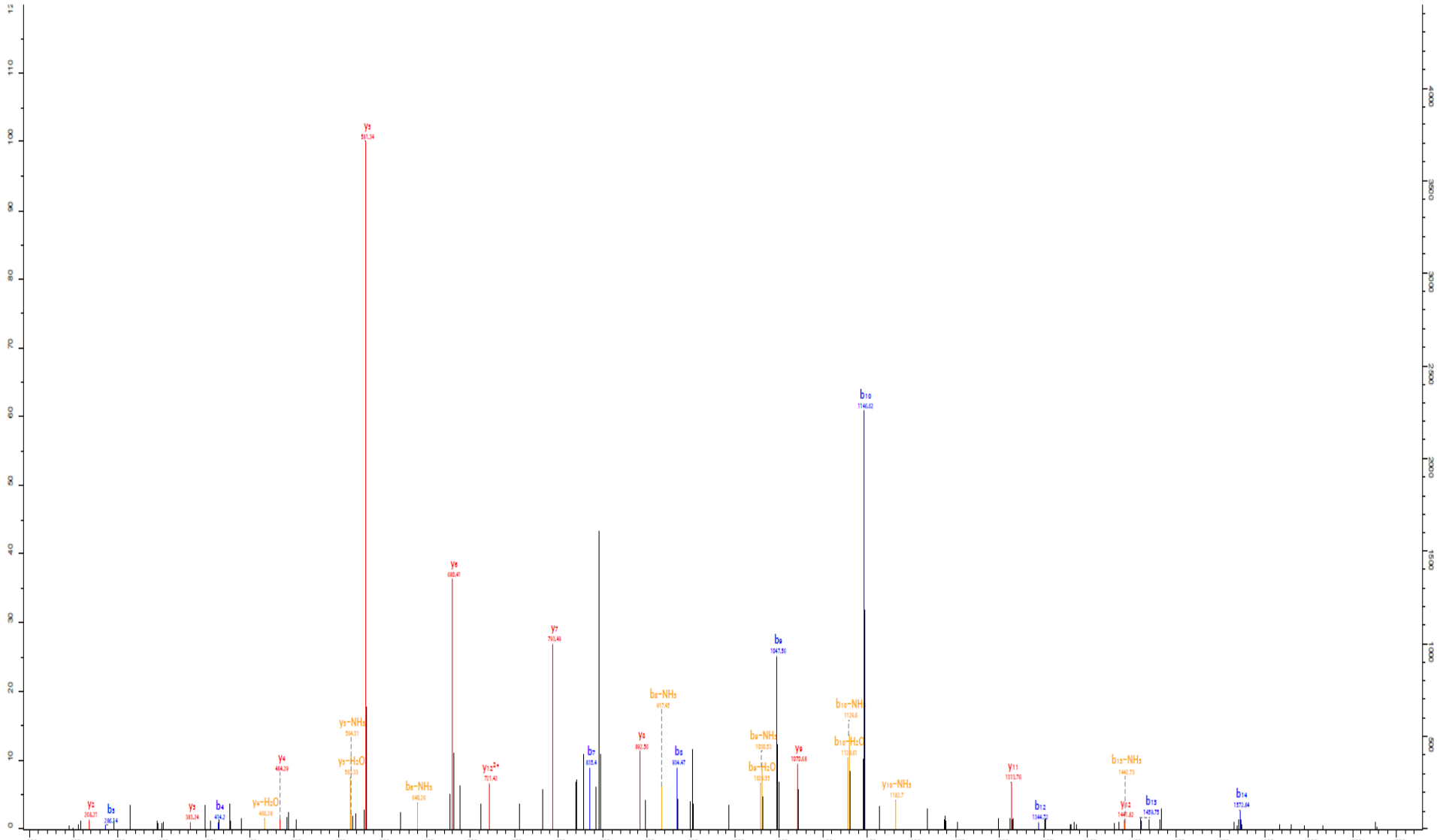
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)
1664.9980	1663.9741	833.0027	832.4907

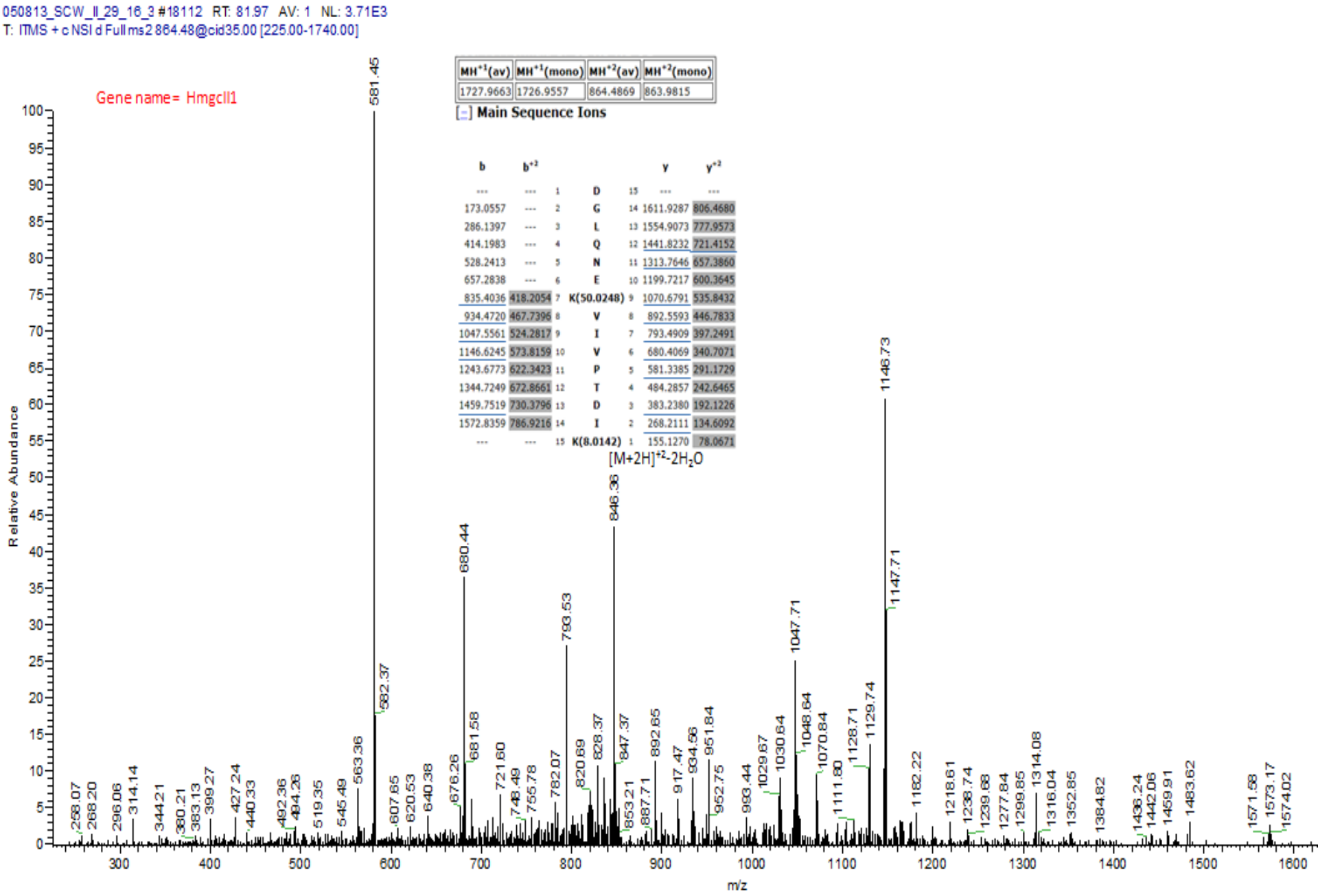
[-] Main Sequence Ions

b	b^{+2}				y	y^{+2}
---	---	1	L	15	---	---
227.1754	---	2	L	14	1550.8901	775.9487
284.1969	---	3	G	13	1437.8060	719.4066
381.2496	---	4	P	12	1380.7845	690.8959
480.3180	---	5	V	11	1283.7318	642.3695
593.4021	---	6	L	10	1184.6634	592.8353
692.4705	---	7	V	9	1071.5793	536.2933
862.5761	431.7917	8	K(Acetyl)	8	972.5109	486.7591
990.6346	495.8210	9	Q	7	802.4054	401.7063
1119.6772	560.3422	10	E	6	674.3468	337.6770
1232.7613	616.8843	11	L	5	545.3042	273.1557
1289.7827	645.3950	12	G	4	432.2201	216.6137
1418.8253	709.9163	13	E	3	375.1987	188.1030
1489.8625	745.4349	14	A	2	246.1561	123.5817
---	---	15	R	1	175.1190	88.0631

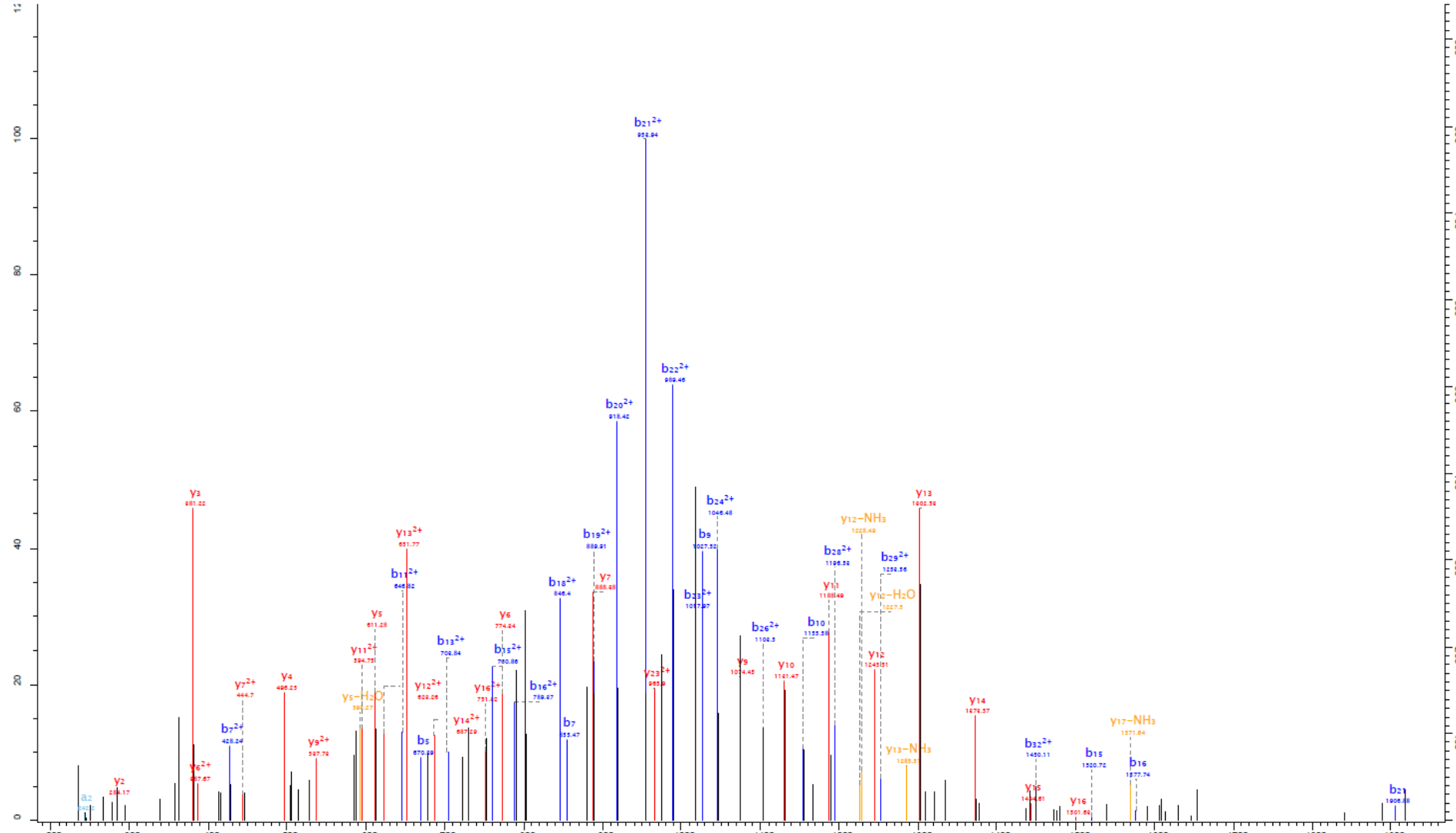


Raw file	Scan	Method	Score	m/z	Gene names
050813_SCW_II_29_16_3	18112	ITMS; CID	97.21	864.48	Hmgcll1




050813_SCW_II_29_16_3 #18112 RT: 81.97 AV: 1 NL: 3.71E3
T: ITMS + c NSI d Full ms2 864.48@cid35.00 [225.00-1740.00]
Gene name= Hmgcll1
MH+1(av) MH+1(mono) MH+2(av) MH+2(mono)
1727.9663 1726.9557 864.4869 863.9815
[-] Main Sequence Ions
b b+2 y y+2
--- --- 1 D 15 --- ---
173.0557 --- 2 G 14 1611.9287 806.4680
286.1397 --- 3 L 13 1554.9073 777.9573
414.1983 --- 4 Q 12 1441.8232 721.4152
528.2413 --- 5 N 11 1313.7646 657.3860
657.2838 --- 6 E 10 1199.7217 600.3645
835.4036 418.2054 7 K(50.0248) 9 1070.6791 535.8432
934.4720 467.7396 8 V 8 892.5593 446.7833
1047.5561 524.2817 9 I 7 793.4909 397.2491
1146.6245 573.8159 10 V 6 680.4069 340.7071
1243.6773 622.3423 11 P 5 581.3385 291.1729
1344.7249 672.8661 12 T 4 484.2857 242.6465
1459.7519 730.3796 13 D 3 383.2380 192.1226
1572.8359 786.9216 14 I 2 268.2111 134.6092
--- --- 15 K(8.0142) 1 155.1270 78.0671
[M+2H]+2-2H2O
Relative Abundance
m/z

Raw file	Scan	Method	Score	m/z	Gene names
072613_SCW_II_68_Enriched_11	11950	ITMS; CID	129.57	821.37	Hnrnpl



- R L K T E N A G D Q H G G G G G G S G A A G G G G E N Y D D P H K -

ac

a2 b5 b7 b9 b10 b11 2+ b13 2+ b15 b16 b18 2+ b19 2+ b20 2+ b21 b22 2+ b23 2+ b24 2+ b26 2+ b28 2+ b29 2+ b32 2+

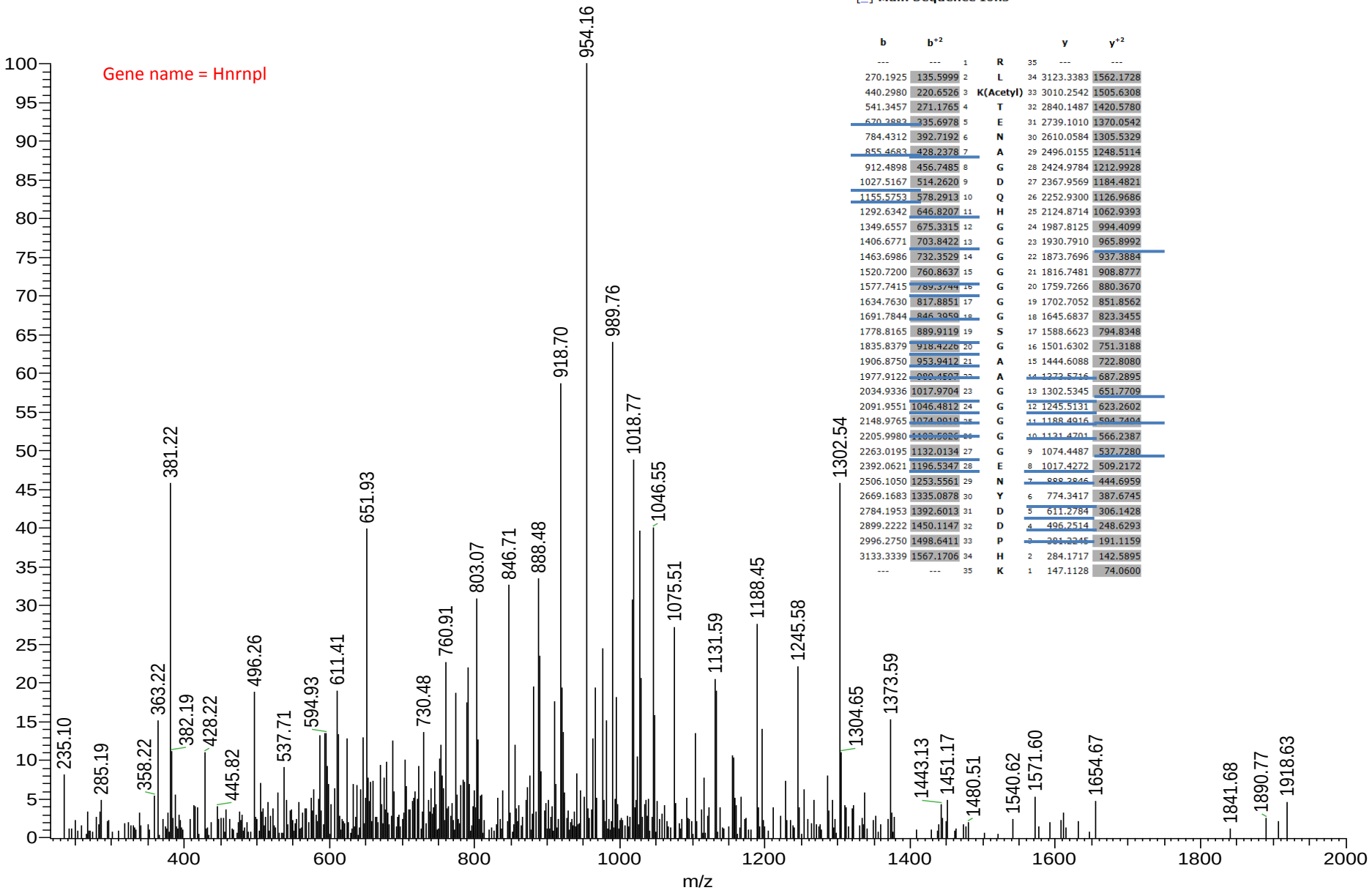
y23 2+ y16 y15 y14 y13 y12 y11 y10 y9 y7 y6 y5 y4 y3 y2

072613 SCW II 68 Enriched 11 #11950 RT: 55.36 AV: 1 NL: 7.85E2
T: ITMS + c NSI d Full ms2 821.37@cid35.00 [215.00-2000.00]

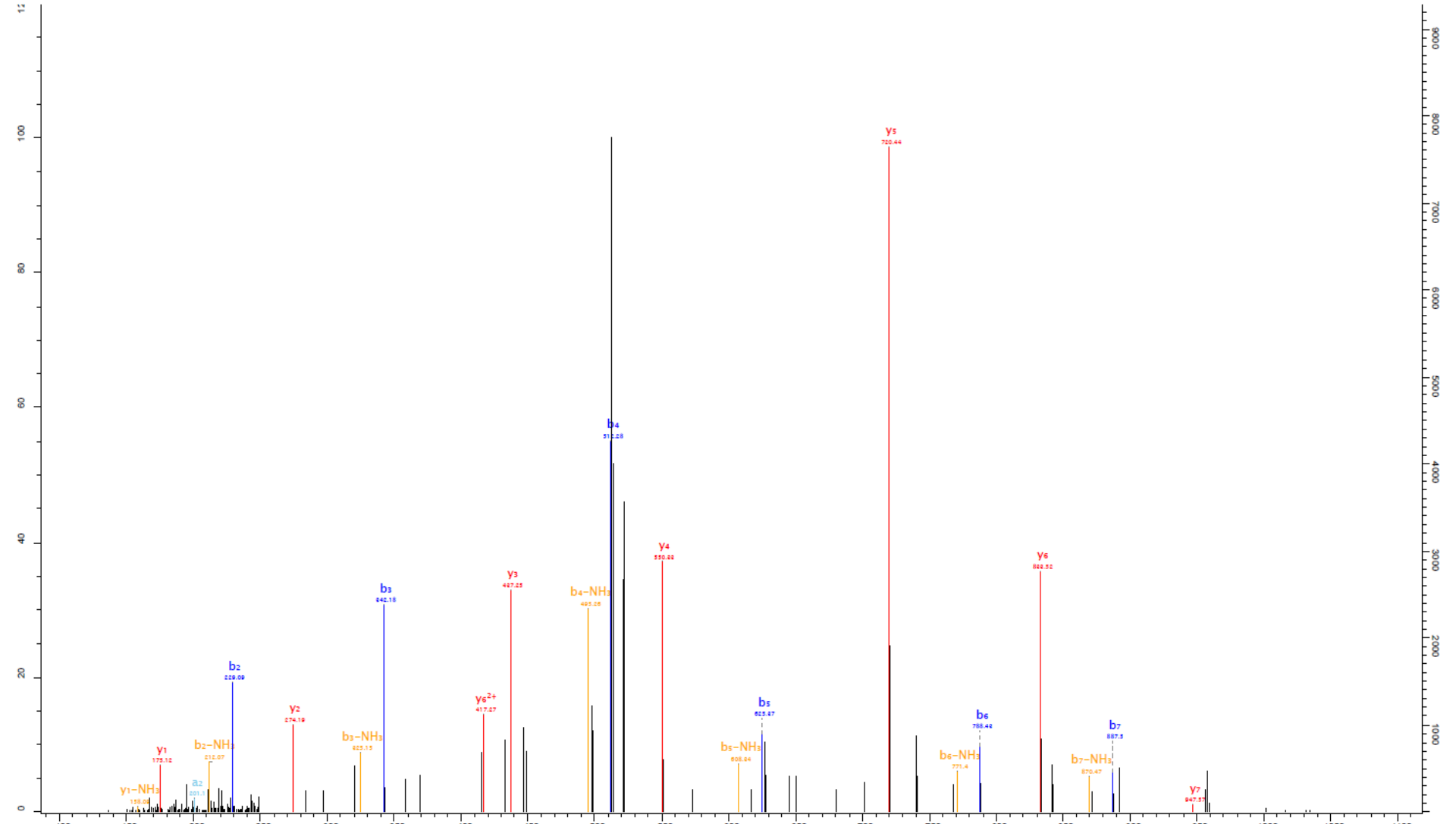
MH+1(av)	MH+1(mono)	MH+2(av)	MH+2(mono)	MH+3(av)	MH+3(mono)	MH+4(av)	MH+4(mono)
3281.3325	3279.4394	1641.1699	1640.2233	1094.4491	1093.8180	821.0887	820.6153

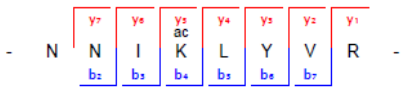
[–] Main Sequence Ions

b	b+2			y	y+2
---	---	1	R	35 ---	---
270.1925	135.5999	2	L	34 3123.3383	1562.1728
440.2980	220.6526	3	K(Acetyl)	33 3010.2542	1505.6308
541.3457	271.1765	4	T	32 2840.1487	1420.5780
670.3883	335.6978	5	E	31 2739.1010	1370.0542
784.4312	392.7192	6	N	30 2610.0584	1305.5329
855.4683	428.2378	7	A	29 2496.0155	1248.5114
912.4898	456.7485	8	G	28 2424.9784	1212.9928
1027.5167	514.2620	9	D	27 2367.9569	1184.4821
1155.5753	578.2913	10	Q	26 2252.9300	1126.9686
1292.6342	646.8207	11	H	25 2124.8714	1062.9393
1349.6557	675.3315	12	G	24 1987.8125	994.4099
1406.6771	703.8422	13	G	23 1930.7910	965.8992
1463.6986	732.3529	14	G	22 1873.7696	937.3884
1520.7200	760.8637	15	G	21 1816.7481	908.8777
1577.7415	789.3744	16	G	20 1759.7266	880.3670
1634.7630	817.8851	17	G	19 1702.7052	851.8562
1691.7844	846.3958	18	G	18 1645.6837	823.3455
1778.8165	889.9119	19	S	17 1588.6623	794.8348
1835.8379	918.4226	20	G	16 1501.6302	751.3188
1906.8750	953.9412	21	A	15 1444.6088	722.8080
1977.9122	989.4597	22	A	14 1373.5716	687.2895
2034.9336	1017.9704	23	G	13 1302.5345	651.7709
2091.9551	1046.4812	24	G	12 1245.5131	623.2602
2148.9765	1074.9919	25	G	11 1188.4916	594.7494
2205.9980	1103.5026	26	G	10 1131.4701	566.2387
2263.0195	1132.0134	27	G	9 1074.4487	537.7280
2392.0621	1196.5347	28	E	8 1017.4272	509.2172
2506.1050	1253.5561	29	N	7 888.3846	444.6959
2669.1683	1335.0878	30	Y	6 774.3417	387.6745
2784.1953	1392.6013	31	D	5 611.2784	306.1428
2899.2222	1450.1147	32	D	4 496.2514	248.6293
2996.2750	1498.6411	33	P	3 381.2245	191.1159
3133.3339	1567.1706	34	H	2 284.1717	142.5895
---	---	35	K	1 147.1128	74.0600

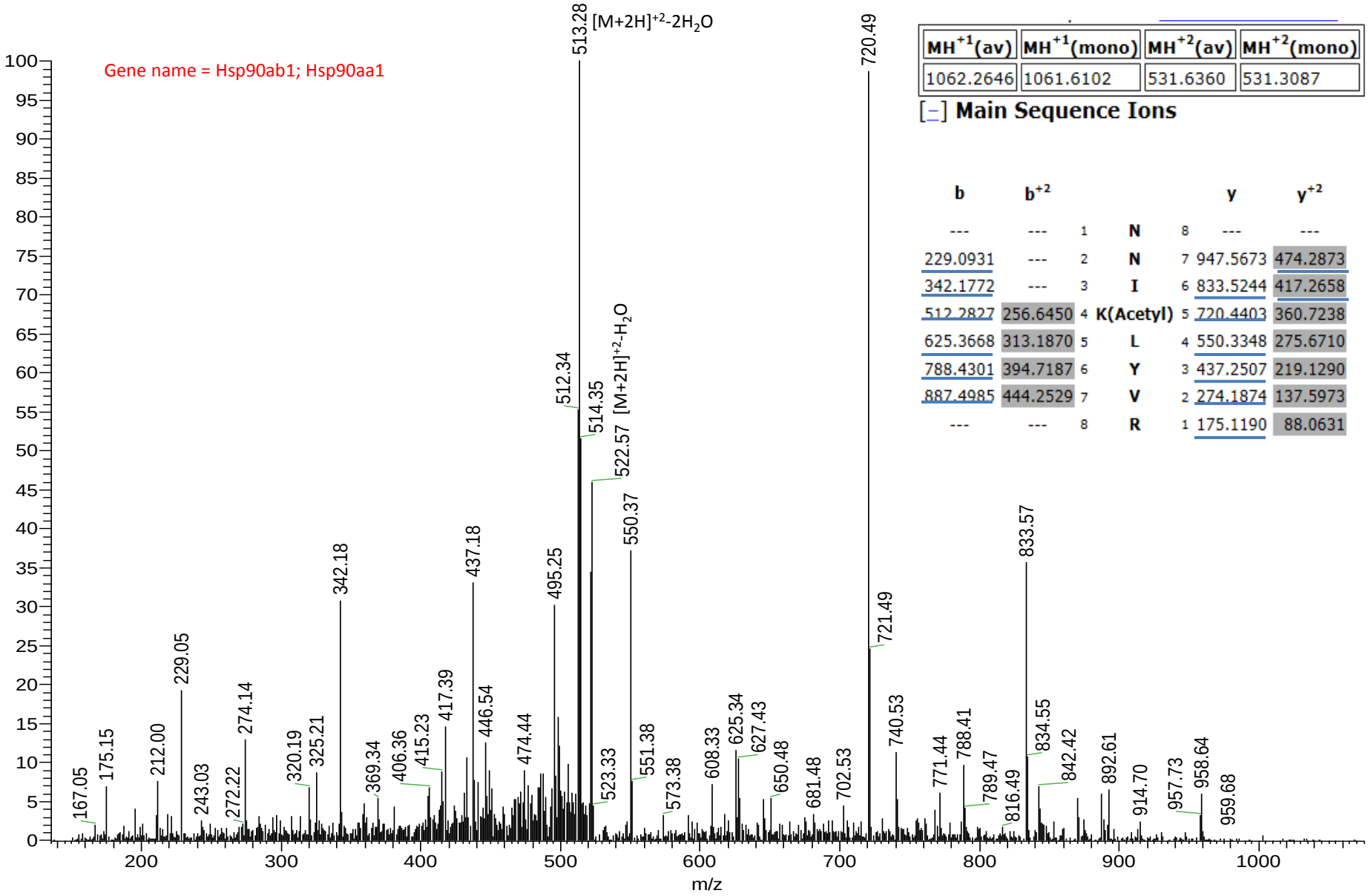


Raw file	Scan	Method	Score	m/z	Gene names
050813_SCW_II_29_22_5	16616	ITMS; CID	134.48	531.31	Hsp90ab1;Hsp90aa1





050813_SCW_II_29_22_5 #16616 RT: 72.12 AV: 1 NL: 7.74E3
T: ITMS + c NSI d Full ms2 531.31@cid35.00 [135.00-1075.00]

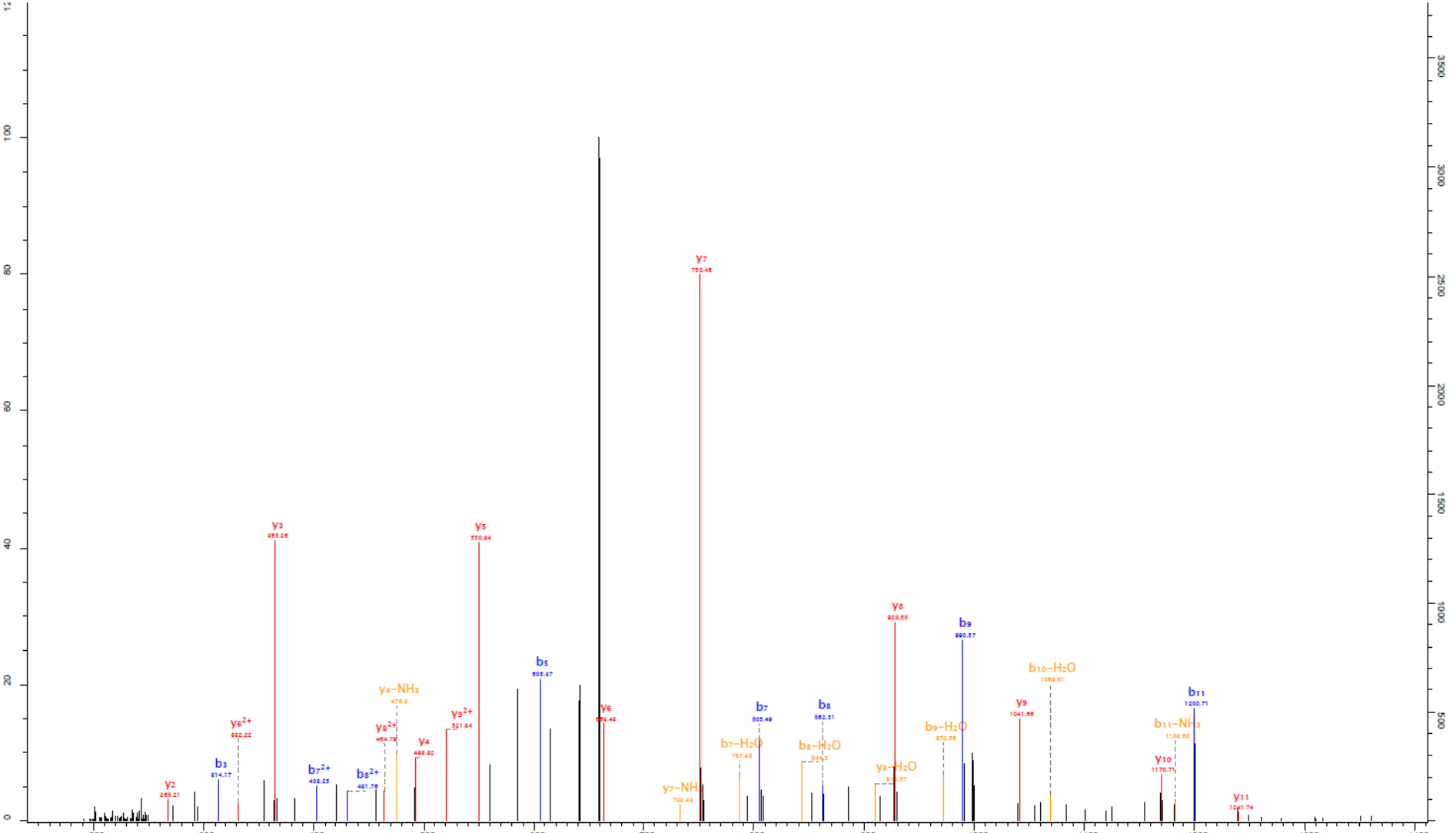


MH+1(av)	MH+1(mono)	MH+2(av)	MH+2(mono)
1062.2646	1061.6102	531.6360	531.3087

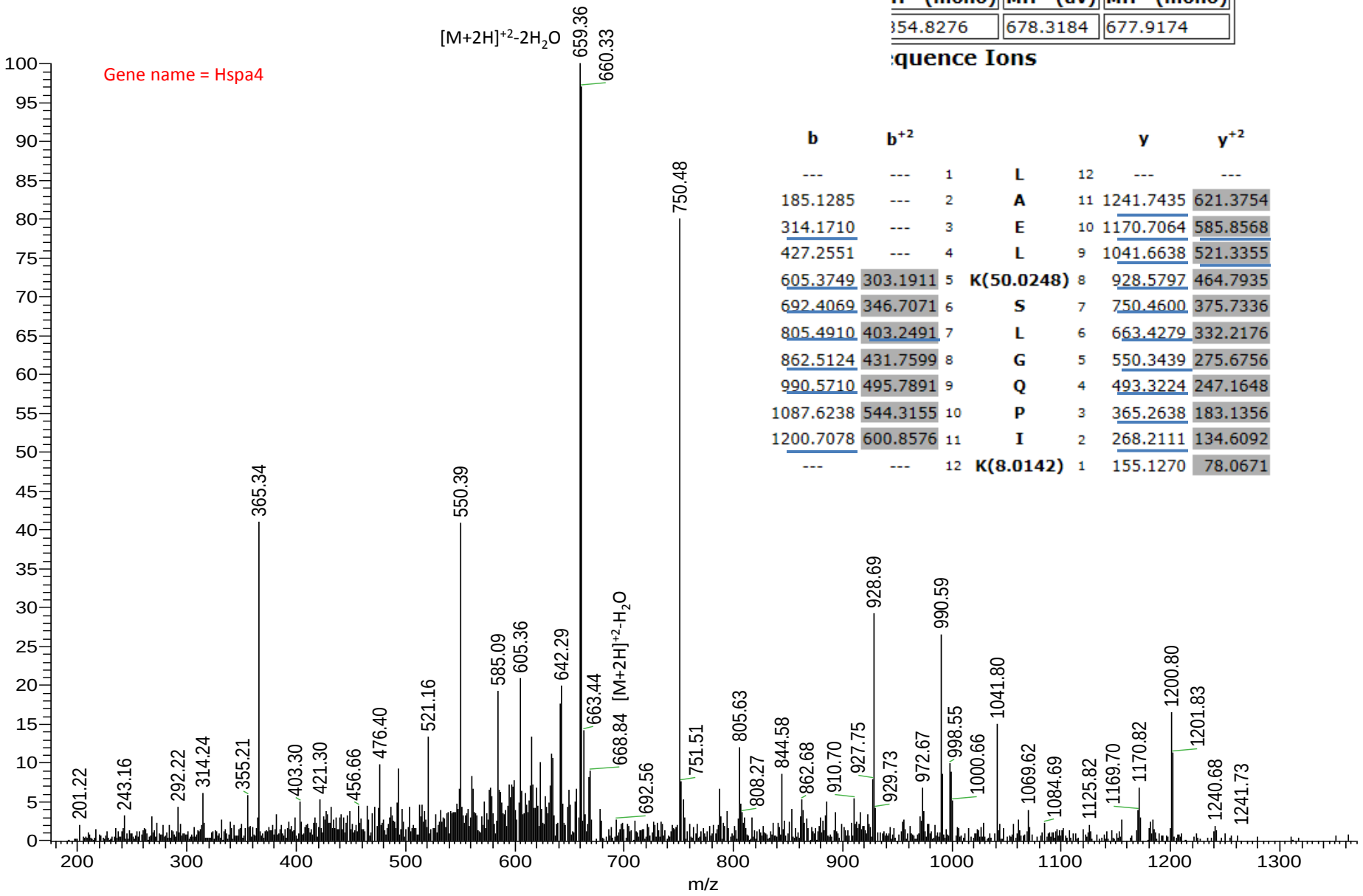
[–] Main Sequence Ions

b	b+2				y	y+2
---	---	1	N	8	---	---
229.0931	---	2	N	7	947.5673	474.2873
342.1772	---	3	I	6	833.5244	417.2658
512.2827	256.6450	4	K(Acetyl)	5	720.4403	360.7238
625.3668	313.1870	5	L	4	550.3348	275.6710
788.4301	394.7187	6	Y	3	437.2507	219.1290
887.4985	444.2529	7	V	2	274.1874	137.5973
---	---	8	R	1	175.1190	88.0631

Raw file	Scan	Method	Score	m/z	Gene names
062513_SCW_II_53_4_Vargas_Enriched	19093	ITMS; CID	129.37	677.92	Hspa4



062513_SCW_II_53_4_Vargas_Enriched #19093 RT: 84.58 AV: 1 NL: 3.13E3
T: ITMS + c NSI d Full ms2 677.92@cid35.00 [175.00-1370.00]

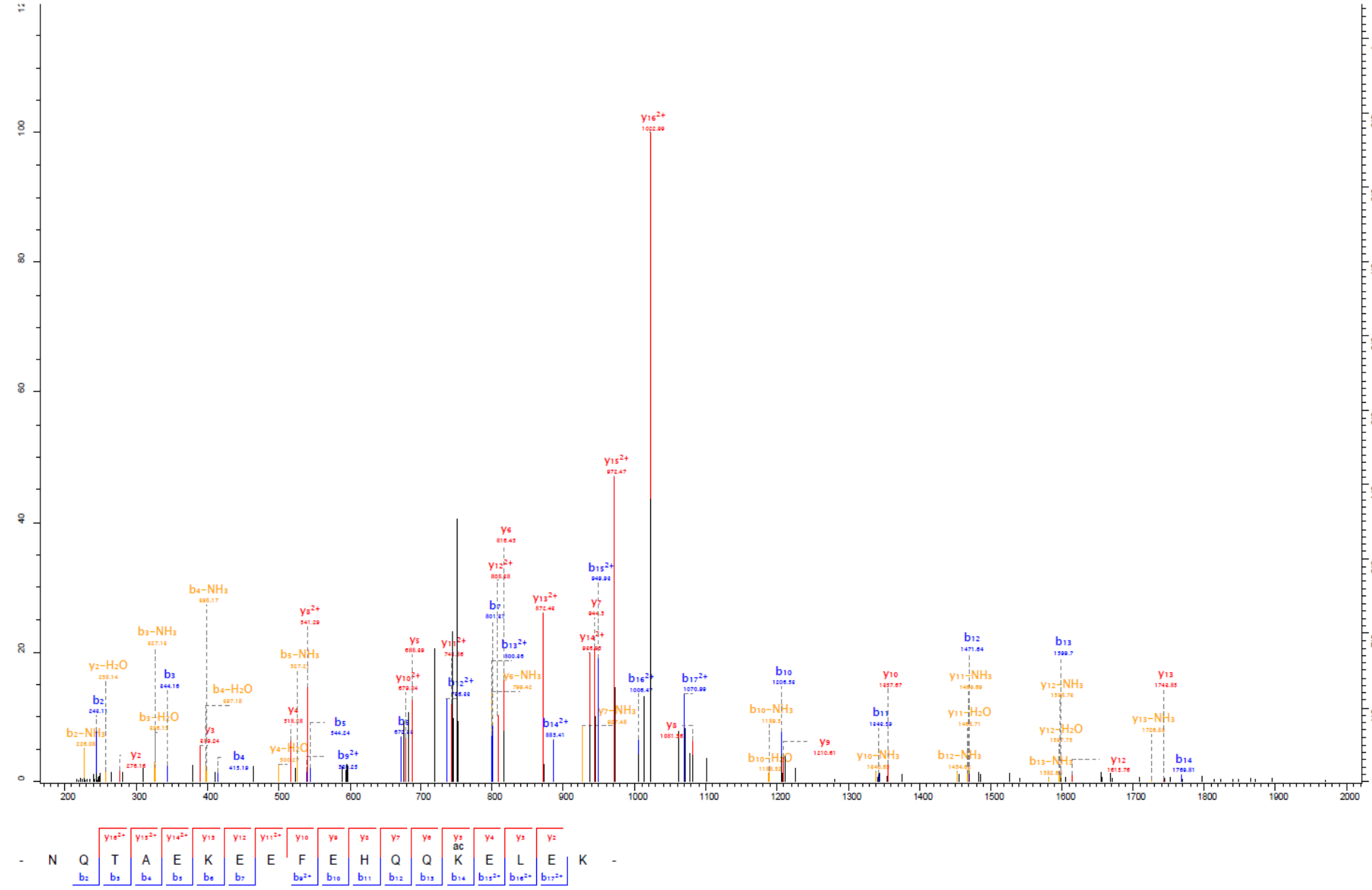


MH+1(mono)	MH+2(av)	MH+2(mono)
354.8276	678.3184	677.9174

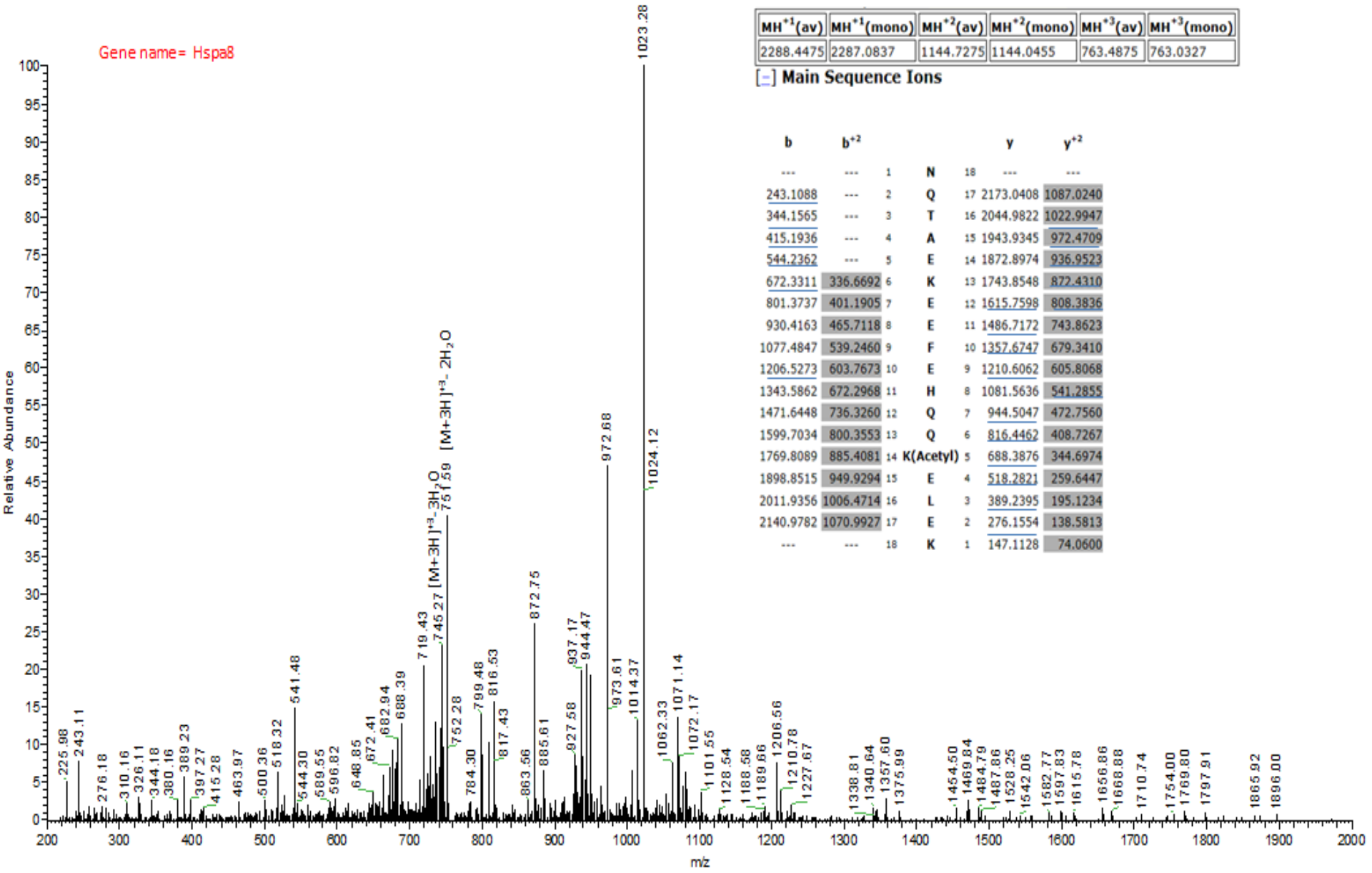
Sequence Ions

b	b+2				y	y+2
---	---	1	L	12	---	---
185.1285	---	2	A	11	1241.7435	621.3754
314.1710	---	3	E	10	1170.7064	585.8568
427.2551	---	4	L	9	1041.6638	521.3355
605.3749	303.1911	5	K(50.0248)	8	928.5797	464.7935
692.4069	346.7071	6	S	7	750.4600	375.7336
805.4910	403.2491	7	L	6	663.4279	332.2176
862.5124	431.7599	8	G	5	550.3439	275.6756
990.5710	495.7891	9	Q	4	493.3224	247.1648
1087.6238	544.3155	10	P	3	365.2638	183.1356
1200.7078	600.8576	11	I	2	268.2111	134.6092
---	---	12	K(8.0142)	1	155.1270	78.0671

Raw file	Scan	Method	Score	m/z	Gene names
072613_SCW_II_68_Enriched_11	15556	ITMS; CID	268.42	763.37	Hspa8



072613_SCW_II_68_Enriched_11#15556 RT: 68.13 AV: 1 NL: 8.74E3
T: ITMS + c NSI d Full ms2 763.37@cid35.00 [200.00-2000.00]

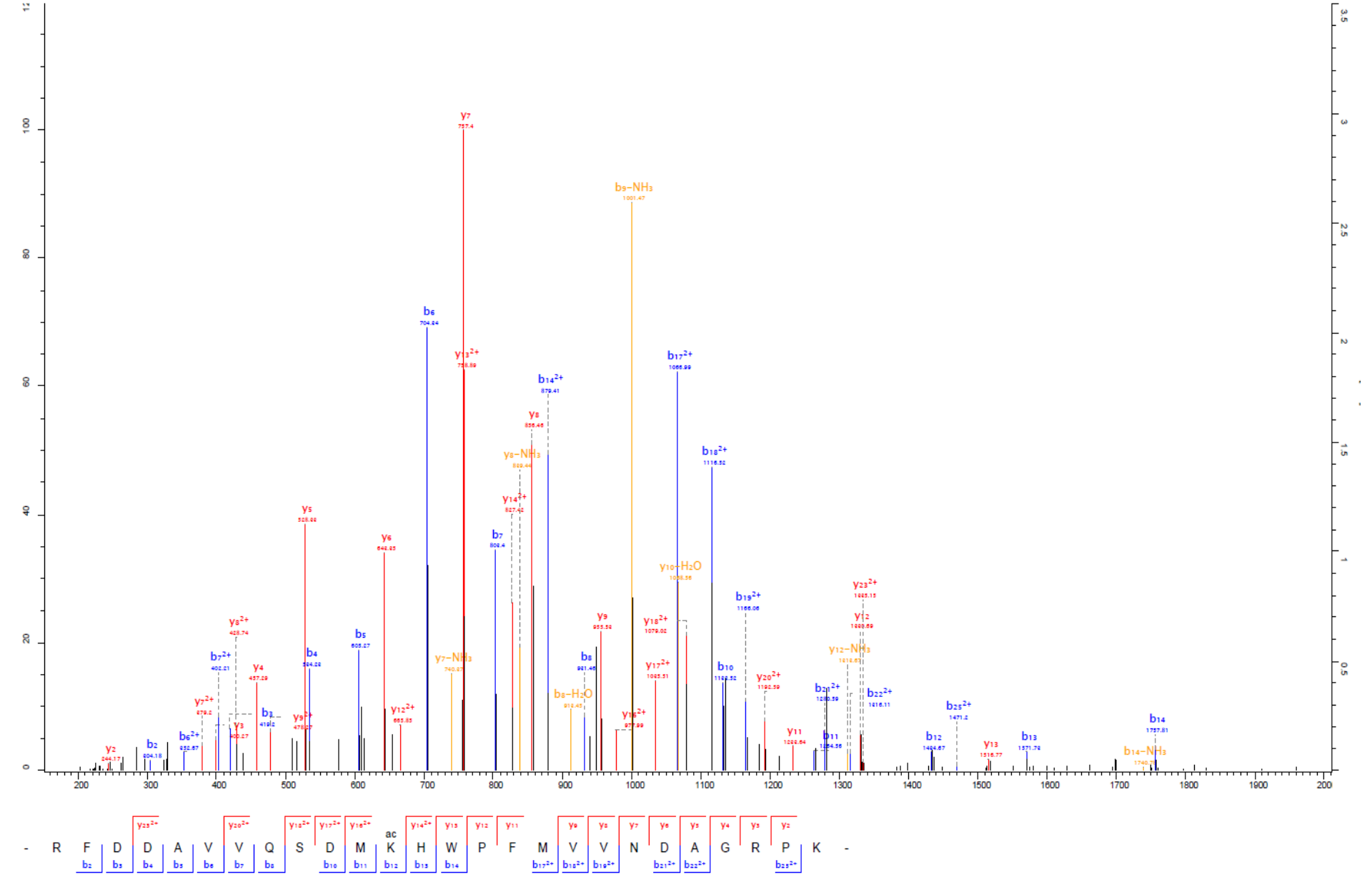


MH+1(av)	MH+1(mono)	MH+2(av)	MH+2(mono)	MH+3(av)	MH+3(mono)
2288.4475	2287.0837	1144.7275	1144.0455	763.4875	763.0327

[-] Main Sequence Ions

b	b+2				y	y+2
---	---	1	N	18	---	---
243.1088	---	2	Q	17	2173.0408	1087.0240
344.1565	---	3	T	16	2044.9822	1022.9947
415.1936	---	4	A	15	1943.9345	972.4709
544.2362	---	5	E	14	1872.8974	936.9523
672.3311	336.6692	6	K	13	1743.8548	872.4310
801.3737	401.1905	7	E	12	1615.7598	808.3836
930.4163	465.7118	8	E	11	1486.7172	743.8623
1077.4847	539.2460	9	F	10	1357.6747	679.3410
1206.5273	603.7673	10	E	9	1210.6062	605.8068
1343.5862	672.2968	11	H	8	1081.5636	541.2855
1471.6448	736.3260	12	Q	7	944.5047	472.7560
1599.7034	800.3553	13	Q	6	816.4462	408.7267
1769.8089	885.4081	14	K(Acetyl)	5	688.3876	344.6974
1898.8515	949.9294	15	E	4	518.2821	259.6447
2011.9356	1006.4714	16	L	3	389.2395	195.1234
2140.9782	1070.9927	17	E	2	276.1554	138.5813
---	---	18	K	1	147.1128	74.0600

Raw file	Scan	Method	Score	m/z	Gene names
062513_SCW_II_53_11_Vargas_Enriched	24258	ITMS; CID	166.43	773.13	Hspa8



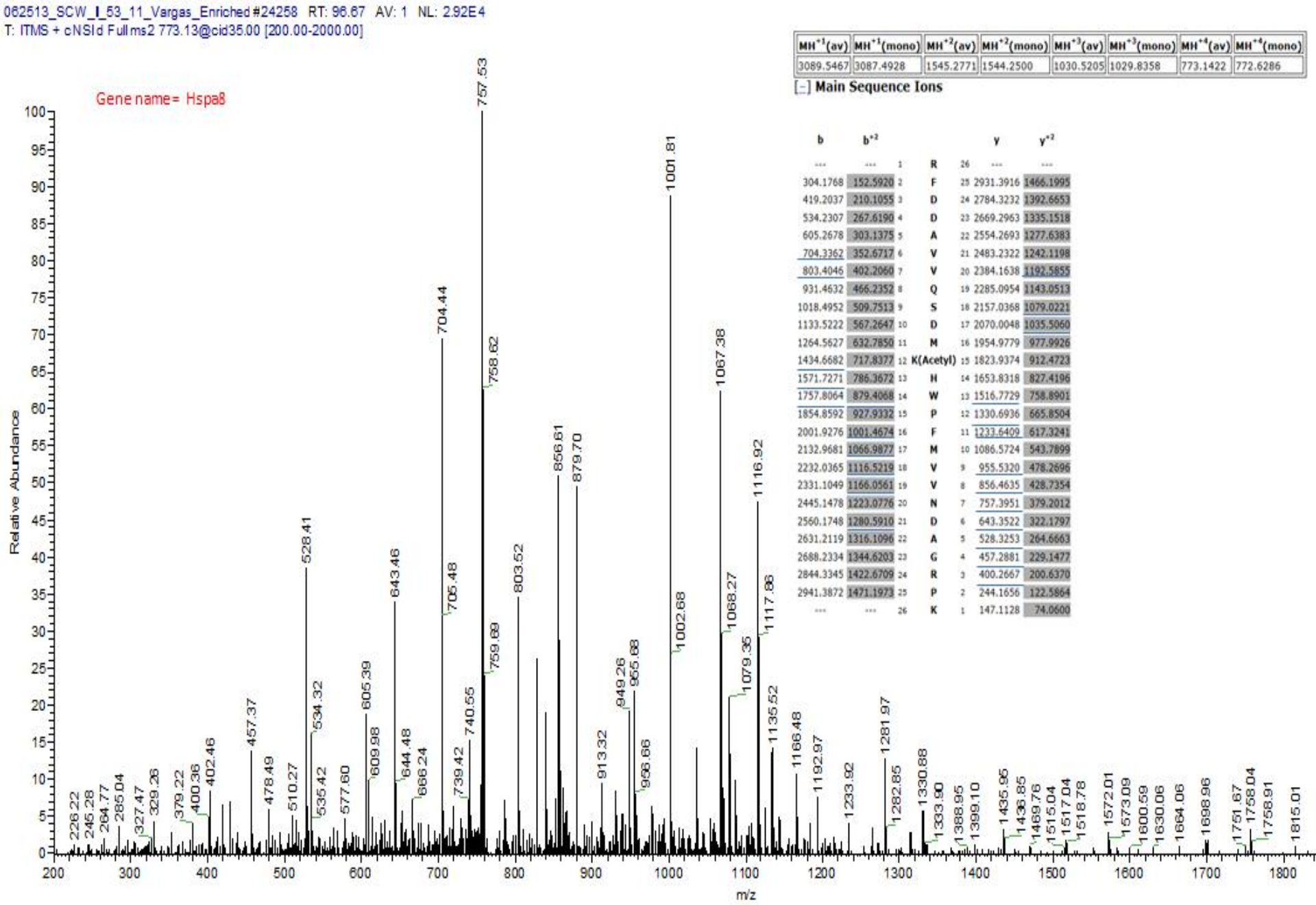
062513_SCW_I_53_11_Vargas_Enriched #24258 RT: 96.67 AV: 1 NL: 2.92E4
T: ITMS + cNSId Full ms2 773.13@cid35.00 [200.00-2000.00]

Gene name= Hspa8

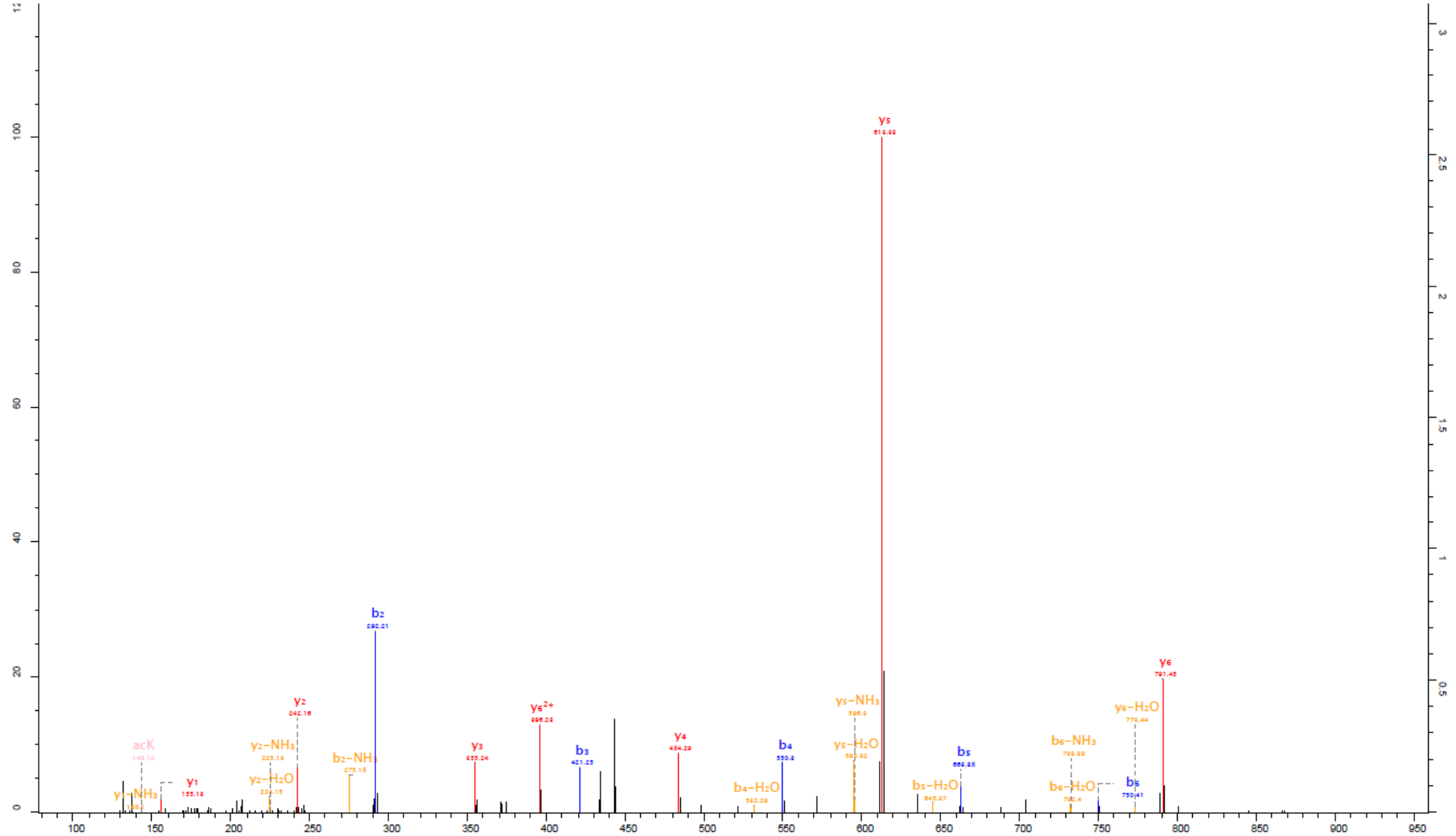
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)	MH^{+3}(av)	MH^{+3}(mono)	MH^{+4}(av)	MH^{+4}(mono)
3089.5467	3087.4928	1545.2771	1544.2500	1030.5205	1029.8358	773.1422	772.6286

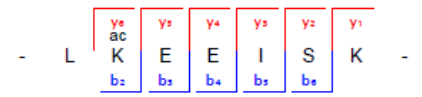
[-] Main Sequence Ions

b	b^{+2}				y	y^{+2}
...	...	1	R	26	...	...
304.1768	152.5920	2	F	25	2931.3916	1466.1995
419.2037	210.1055	3	D	24	2784.3232	1392.6653
534.2307	267.6190	4	D	23	2669.2963	1335.1518
605.2678	303.1375	5	A	22	2554.2693	1277.6383
704.3362	352.6717	6	V	21	2483.2322	1242.1198
803.4046	402.2060	7	V	20	2384.1638	1192.5855
931.4632	466.2352	8	Q	19	2285.0954	1143.0513
1018.4952	509.7513	9	S	18	2157.0368	1079.0221
1133.5222	567.2647	10	D	17	2070.0048	1035.5060
1264.5627	632.7850	11	M	16	1954.9779	977.9926
1434.6682	717.8377	12	K(Acetyl)	15	1823.9374	912.4723
1571.7271	786.3672	13	H	14	1653.8318	827.4196
1757.8064	879.4068	14	W	13	1516.7729	758.8901
1854.8592	927.9332	15	P	12	1330.6936	665.8504
2001.9276	1001.4674	16	F	11	1233.6409	617.3241
2132.9681	1066.9877	17	M	10	1086.5724	543.7899
2232.0365	1116.5219	18	V	9	955.5320	478.2696
2331.1049	1166.0561	19	V	8	856.4635	428.7354
2445.1478	1223.0776	20	N	7	757.3951	379.2012
2560.1748	1280.5910	21	D	6	643.3522	322.1797
2631.2119	1316.1096	22	A	5	528.3253	264.6663
2688.2334	1344.6203	23	G	4	457.2881	229.1477
2844.3345	1422.6709	24	R	3	400.2667	200.6370
2941.3872	1471.1973	25	P	2	244.1656	122.5864
...	...	26	K	1	147.1128	74.0600



Raw file	Scan	Method	Score	m/z	Gene names
050813_SCW_II_29_22_5	10642	ITMS; CID	137.14	452.77	Hspa9





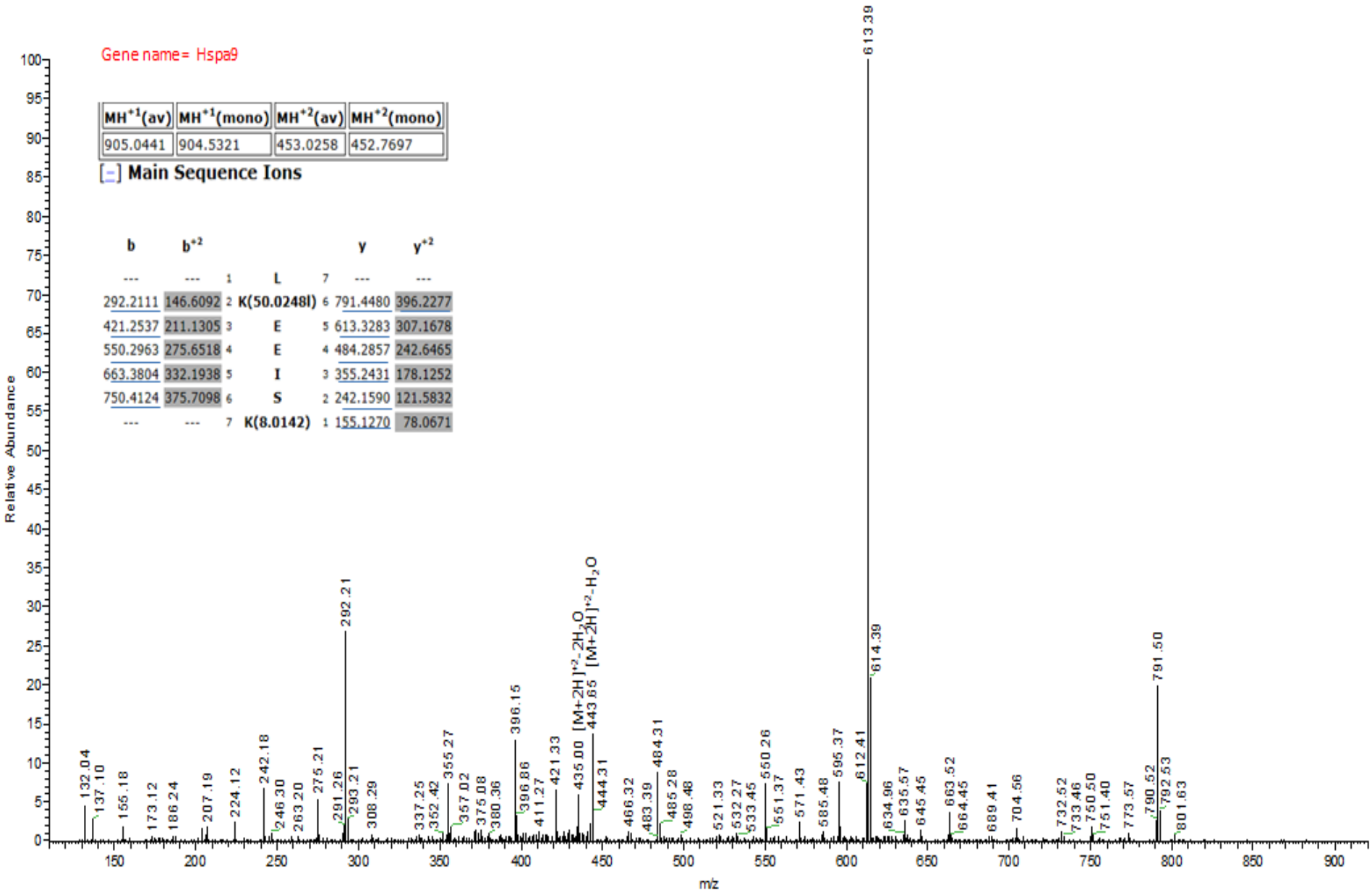
050813_SCW_II_29_22_5 #10642 RT: 51.70 AV: 1 NL: 2.57E4
T: ITMS + c NSI d Full ms2 452.77@cid35.00 [110.00-920.00]

Gene name= Hspa9

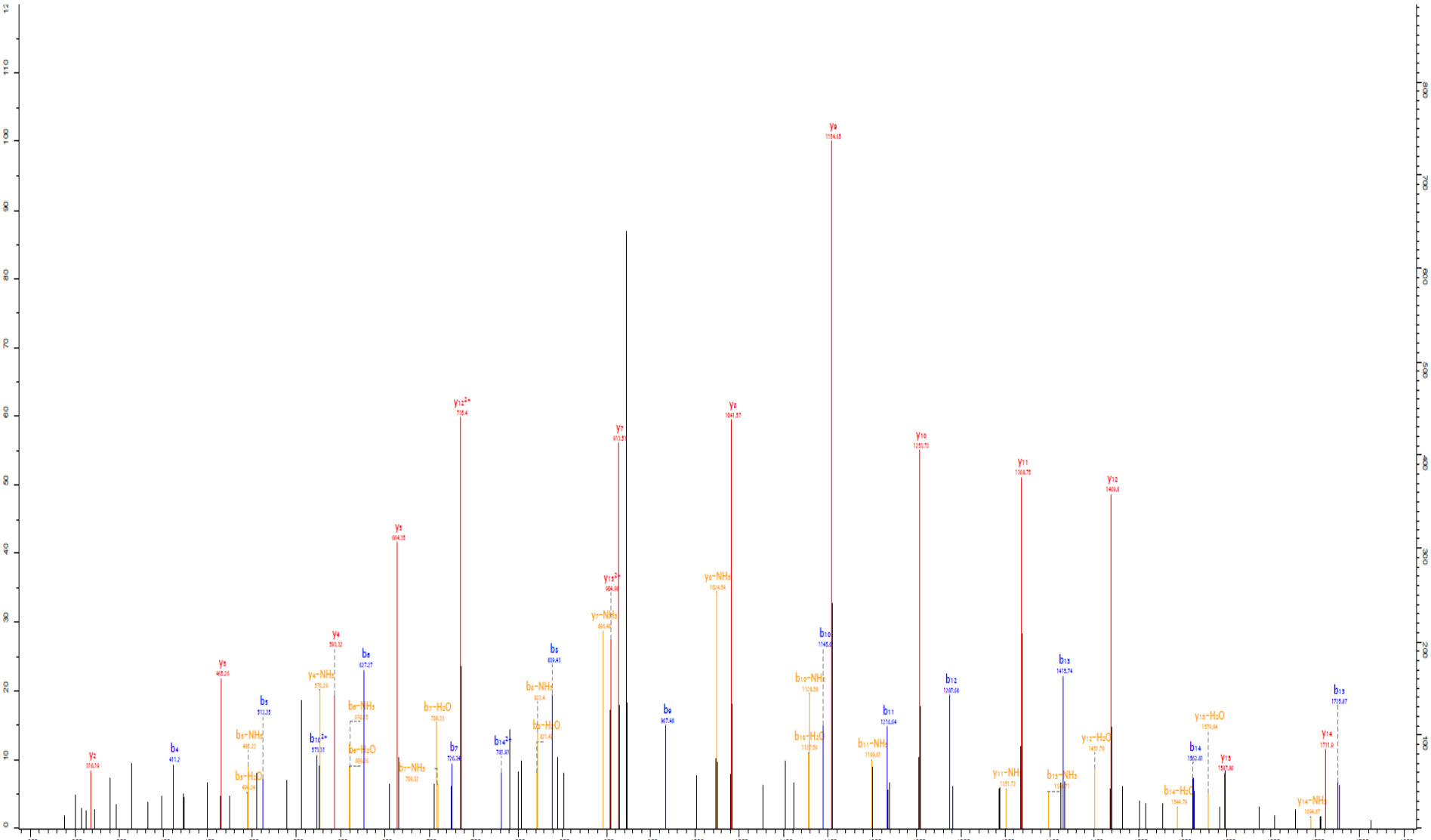
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)
905.0441	904.5321	453.0258	452.7697

[–] **Main Sequence Ions**

b	b^{+2}				y	y^{+2}
---	---	1	L	7	---	---
292.2111	146.6092	2	K(50.0248l)	6	791.4480	396.2277
421.2537	211.1305	3	E	5	613.3283	307.1678
550.2963	275.6518	4	E	4	484.2857	242.6465
663.3804	332.1938	5	I	3	355.2431	178.1252
750.4124	375.7098	6	S	2	242.1590	121.5832
---	---	7	K(8.0142)	1	155.1270	78.0671



Raw file	Scan	Method	Score	m/z	Gene names
062513_SCW_II_53_4_Vargas_Enriched	22099	ITMS; CID	254.72	940.5	I830012O16Rik;Ifit3



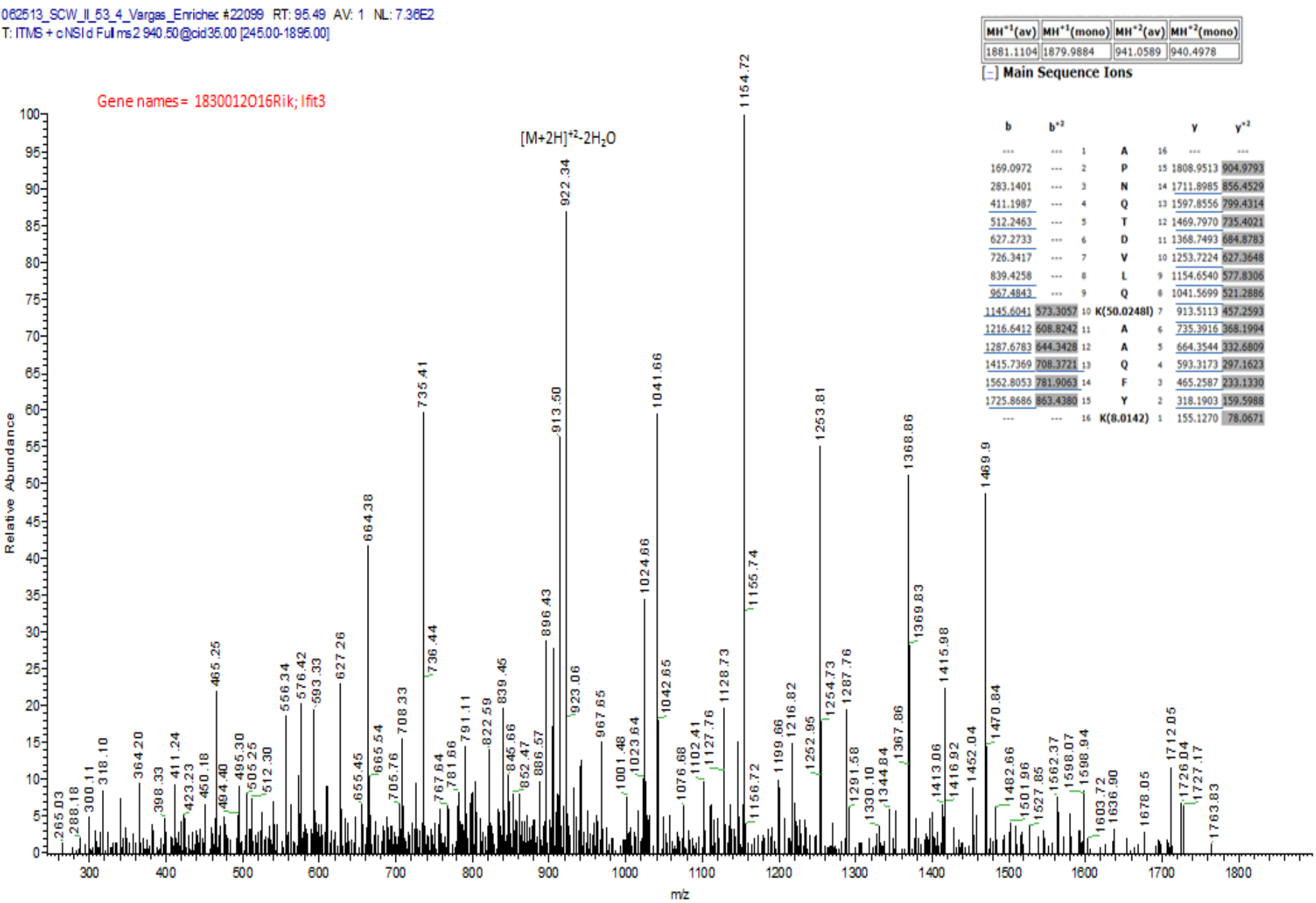
062513_SCW_II_53_4_Vargas_Enrichec #22099 RT: 95.49 AV: 1 NL: 7.36E2
T: ITMS + c NSI d Full ms2 940.50@cid35.00 [245.00-1895.00]

MH+1(av)	MH+1(mono)	MH+2(av)	MH+2(mono)
1881.1104	1879.9884	941.0589	940.4978

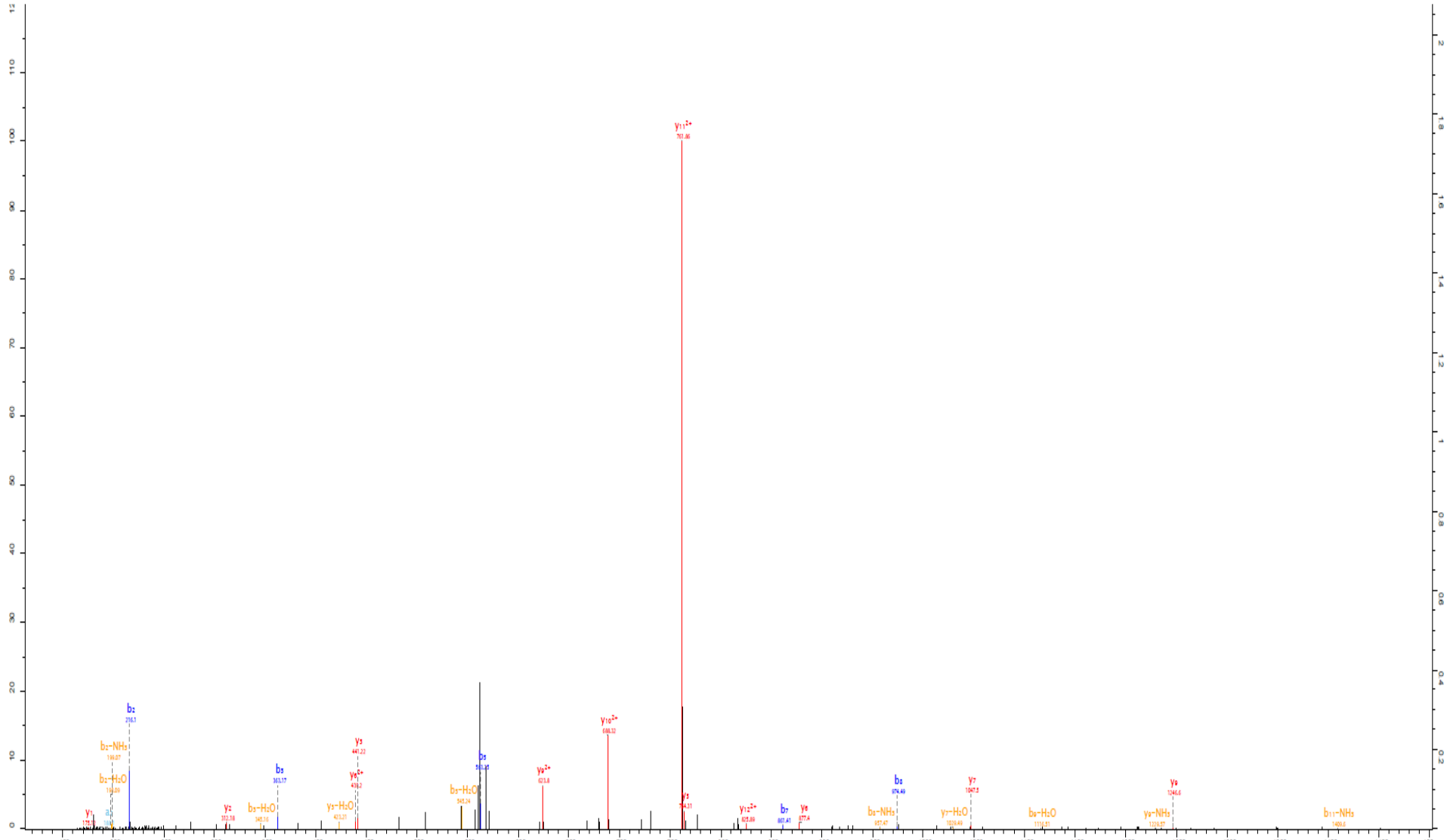
[-] Main Sequence Ions

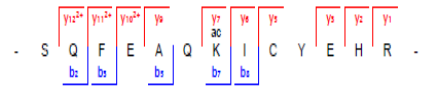
b	b+2				y	y+2
---	---	1	A	16	---	---
169.0972	---	2	P	15	1808.9513	904.9793
283.1401	---	3	N	14	1711.8985	856.4529
411.1987	---	4	Q	13	1597.8556	799.4314
512.2463	---	5	T	12	1469.7970	735.4021
627.2733	---	6	D	11	1368.7493	684.8783
726.3417	---	7	V	10	1253.7224	627.3648
839.4258	---	8	L	9	1154.6540	577.8306
967.4843	---	9	Q	8	1041.5699	521.2886
1145.6041	573.3057	10	K(50.0248l)	7	913.5113	457.2593
1216.6412	608.8242	11	A	6	735.3916	368.1994
1287.6783	644.3428	12	A	5	664.3544	332.6809
1415.7369	708.3721	13	Q	4	593.3173	297.1623
1562.8053	781.9063	14	F	3	465.2587	233.1330
1725.8686	863.4380	15	Y	2	318.1903	159.5988
---	---	16	K(8.0142)	1	155.1270	78.0671

Gene names= 1830012O16Rik; Ifit3

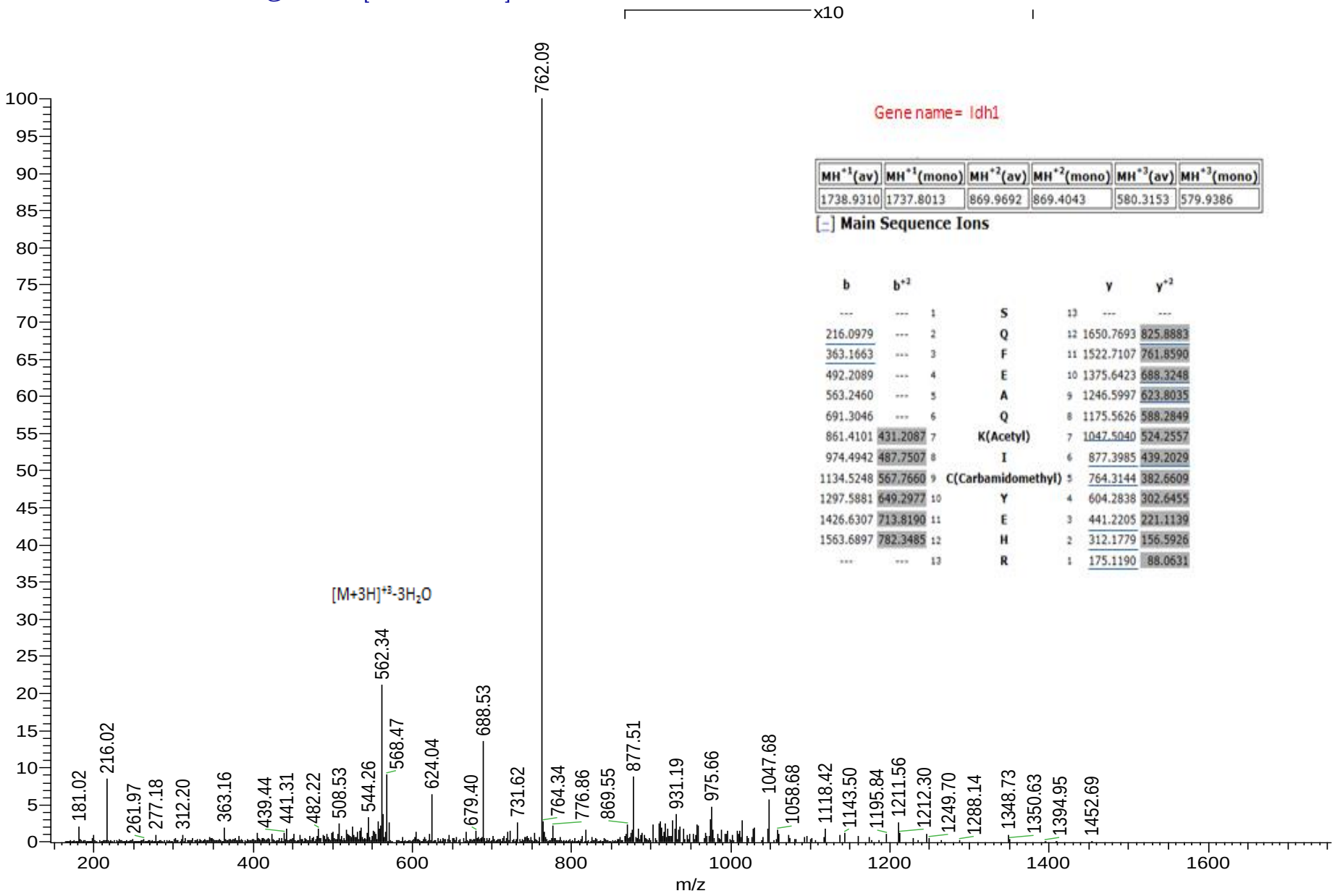


Raw file	Scan	Method	Score	m/z	Gene names
062513_SCW_II_53_9_Vargas_Enriched	15284	ITMS; CID	123.28	580.27	Idh1





062513_SCW_II_53_9_Vargas_Enriched #15284 RT: 70.68 AV: 1 NL: 1.73E4
T: ITMS + c NSI d Full ms2 580.27@cid35.00 [145.00-1755.00]



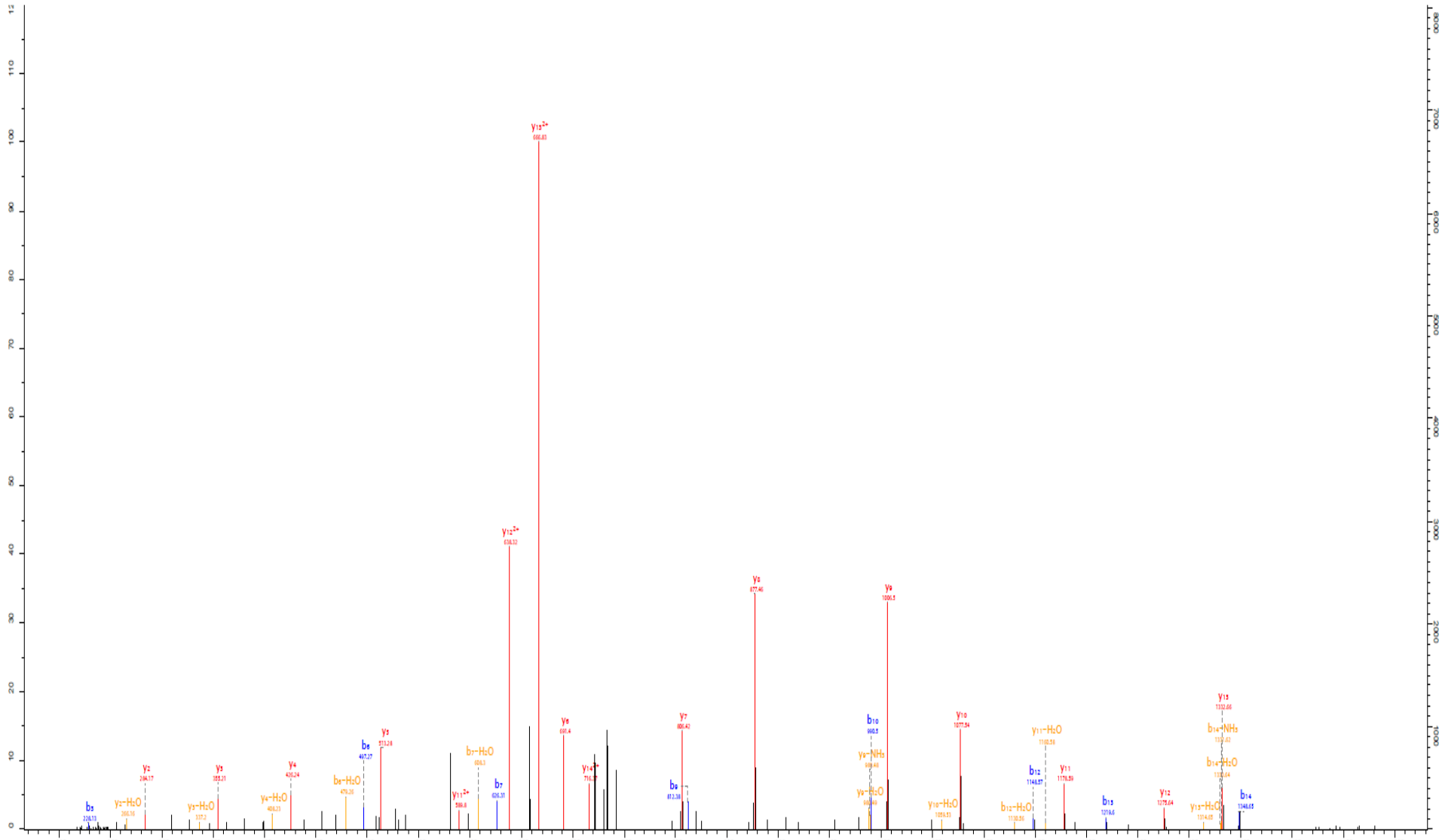
Gene name= Idh1

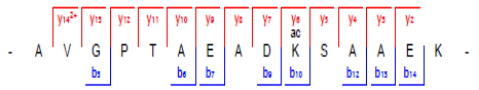
MH+1(av)	MH+1(mono)	MH+2(av)	MH+2(mono)	MH+3(av)	MH+3(mono)
1738.9310	1737.8013	869.9692	869.4043	580.3153	579.9386

[-] Main Sequence Ions

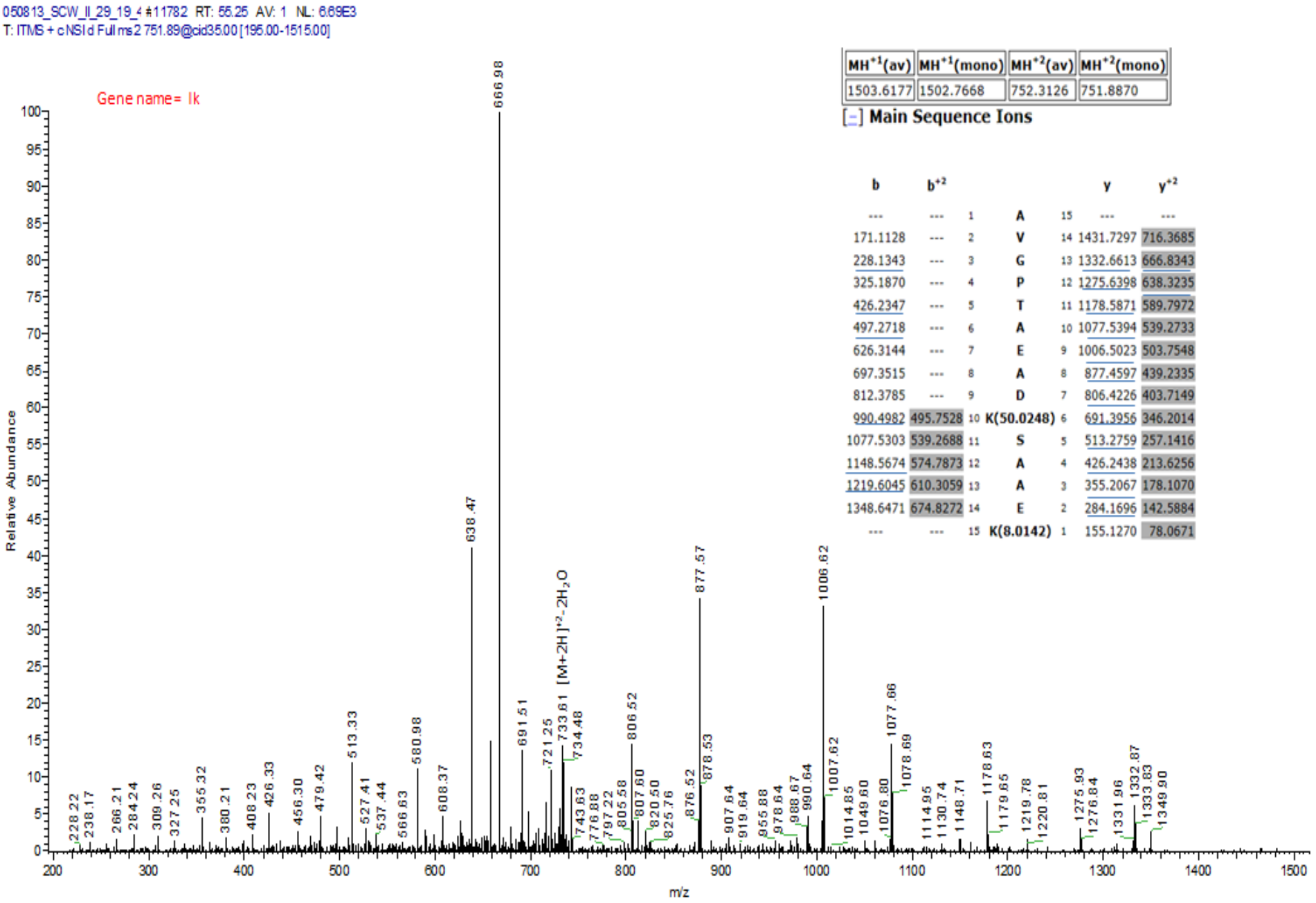
b	b+2				y	y+2
---	---	1	S	13	---	---
216.0979	---	2	Q	12	1650.7693	825.8883
363.1663	---	3	F	11	1522.7107	761.8590
492.2089	---	4	E	10	1375.6423	688.3248
563.2460	---	5	A	9	1246.5997	623.8035
691.3046	---	6	Q	8	1175.5626	588.2849
861.4101	431.2087	7	K(Acetyl)	7	1047.5040	524.2557
974.4942	487.7507	8	I	6	877.3985	439.2029
1134.5248	567.7660	9	C(Carbamidomethyl)	5	764.3144	382.6609
1297.5881	649.2977	10	Y	4	604.2838	302.6455
1426.6307	713.8190	11	E	3	441.2205	221.1139
1563.6897	782.3485	12	H	2	312.1779	156.5926
---	---	13	R	1	175.1190	88.0631

law file	Scan	Method	Score	m/z	Gene names
)50813_SCW_II_29_19_4	11782	ITMS; CID	160.03	751.89	Ik





050813_SCW_II_29_19_4 #11782 RT: 55.25 AV: 1 NL: 6.69E3
T: ITMS + c NSI d Full ms2 751.89@cid35.00 [195.00-1515.00]

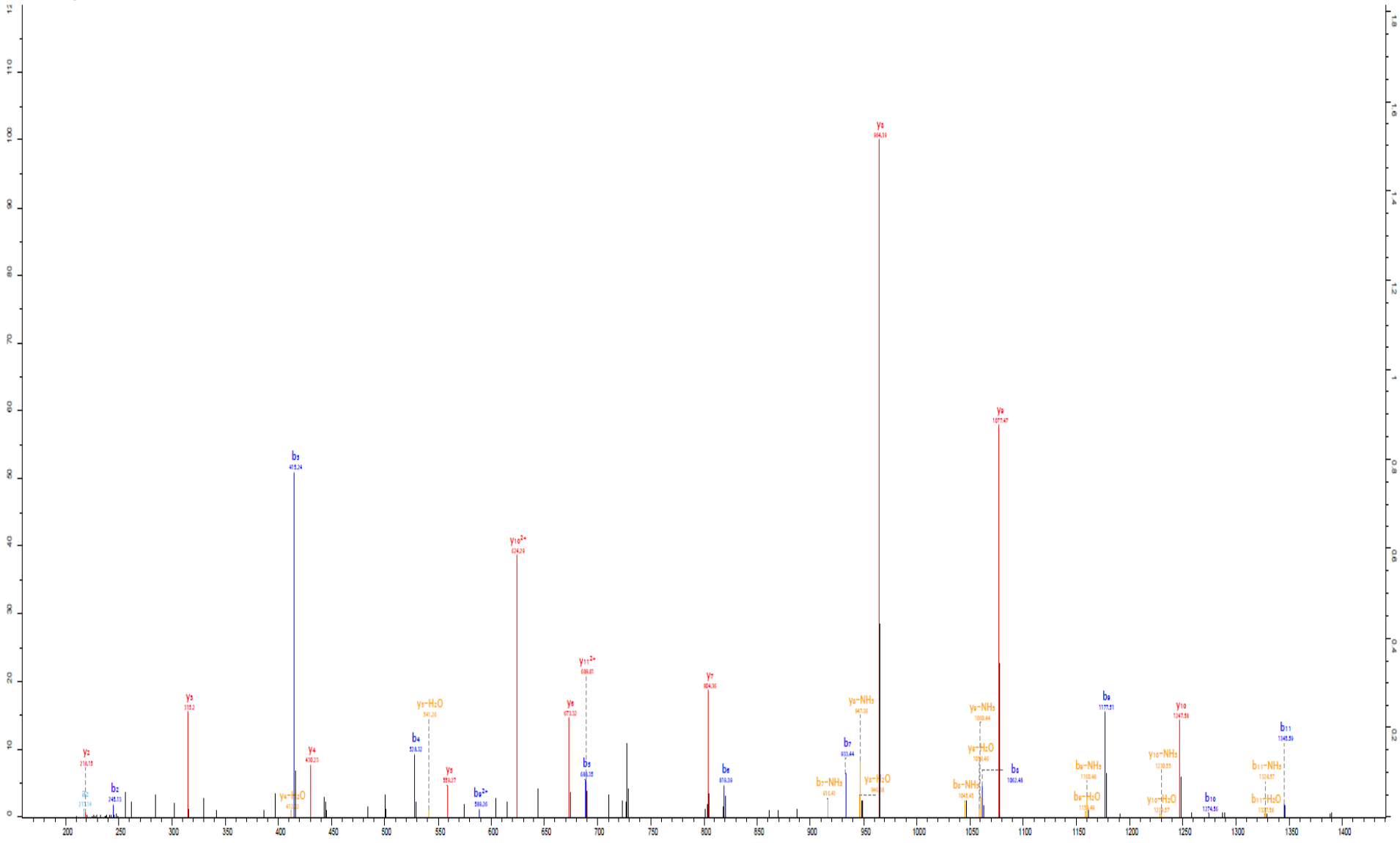


MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)
1503.6177	1502.7668	752.3126	751.8870

[–] **Main Sequence Ions**

b	b^{+2}				y	y^{+2}
---	---	1	A	15	---	---
171.1128	---	2	V	14	1431.7297	716.3685
228.1343	---	3	G	13	1332.6613	666.8343
325.1870	---	4	P	12	1275.6398	638.3235
426.2347	---	5	T	11	1178.5871	589.7972
497.2718	---	6	A	10	1077.5394	539.2733
626.3144	---	7	E	9	1006.5023	503.7548
697.3515	---	8	A	8	877.4597	439.2335
812.3785	---	9	D	7	806.4226	403.7149
990.4982	495.7528	10	K(50.0248)	6	691.3956	346.2014
1077.5303	539.2688	11	S	5	513.2759	257.1416
1148.5674	574.7873	12	A	4	426.2438	213.6256
1219.6045	610.3059	13	A	3	355.2067	178.1070
1348.6471	674.8272	14	E	2	284.1696	142.5884
---	---	15	K(8.0142)	1	155.1270	78.0671

Raw file	Scan	Method	Score	m/z	Gene names
062513_SCW_II_53_4_Vargas_Enriched	17778	ITMS; CID	187.62	746.35	Ilk



	y11 2+	y10 ac	y9	y8	y7	y6	y5	y4	y3	y2
-	L	M	K	I	C	M	N	E	D	P	A	K	-
	b2	b3	b4	b5	b6	b7	b8	b9	b10	b11			

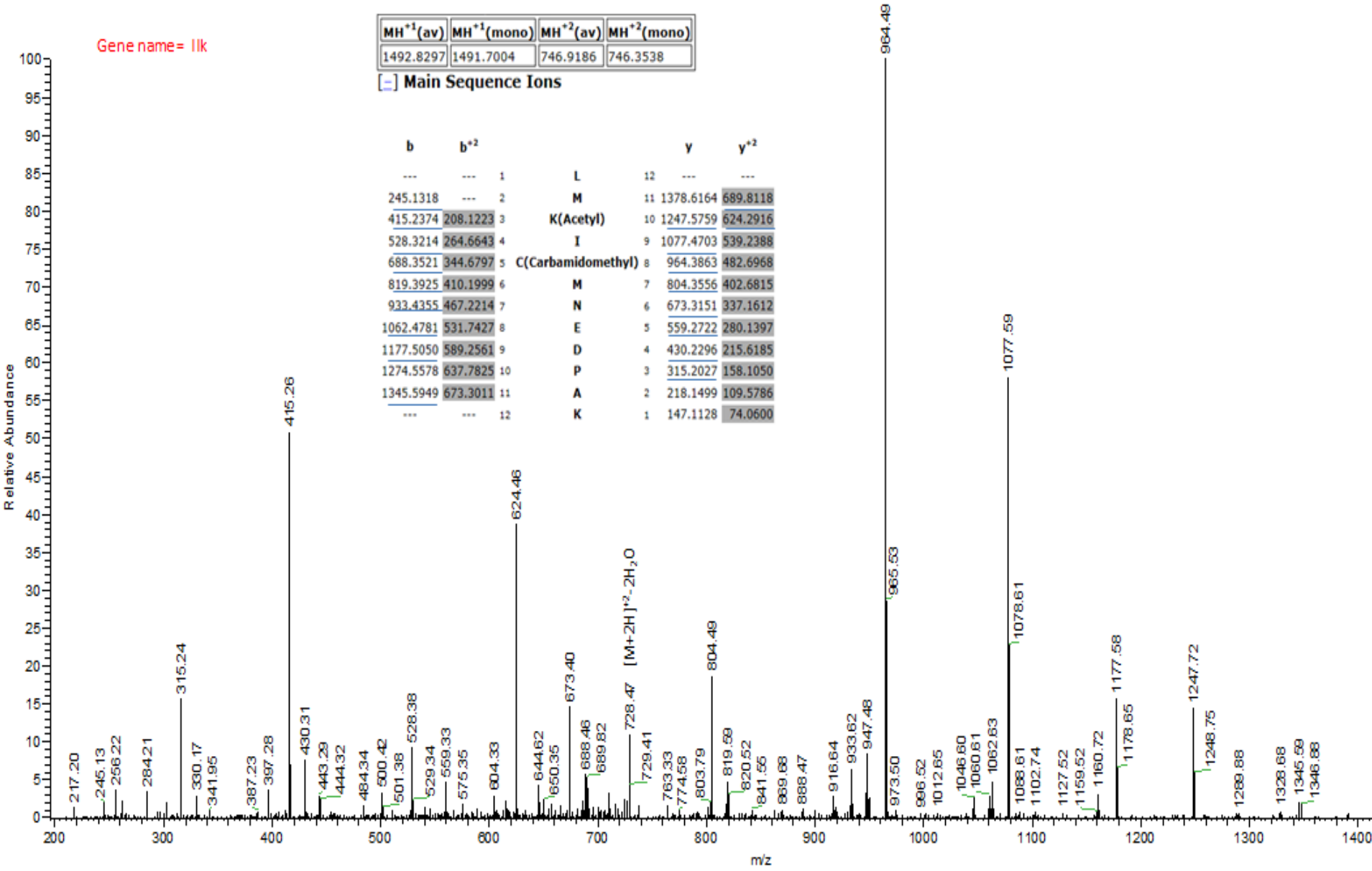
062513_SCW_II_53_4_Vargas_Enriched #17778 RT: 79.77 AV: 1 NL: 1.51E4
T: ITMS + c NSI d Full ms2 746.35@cid35.00 [195.00-1505.00]

Gene name= Ilk

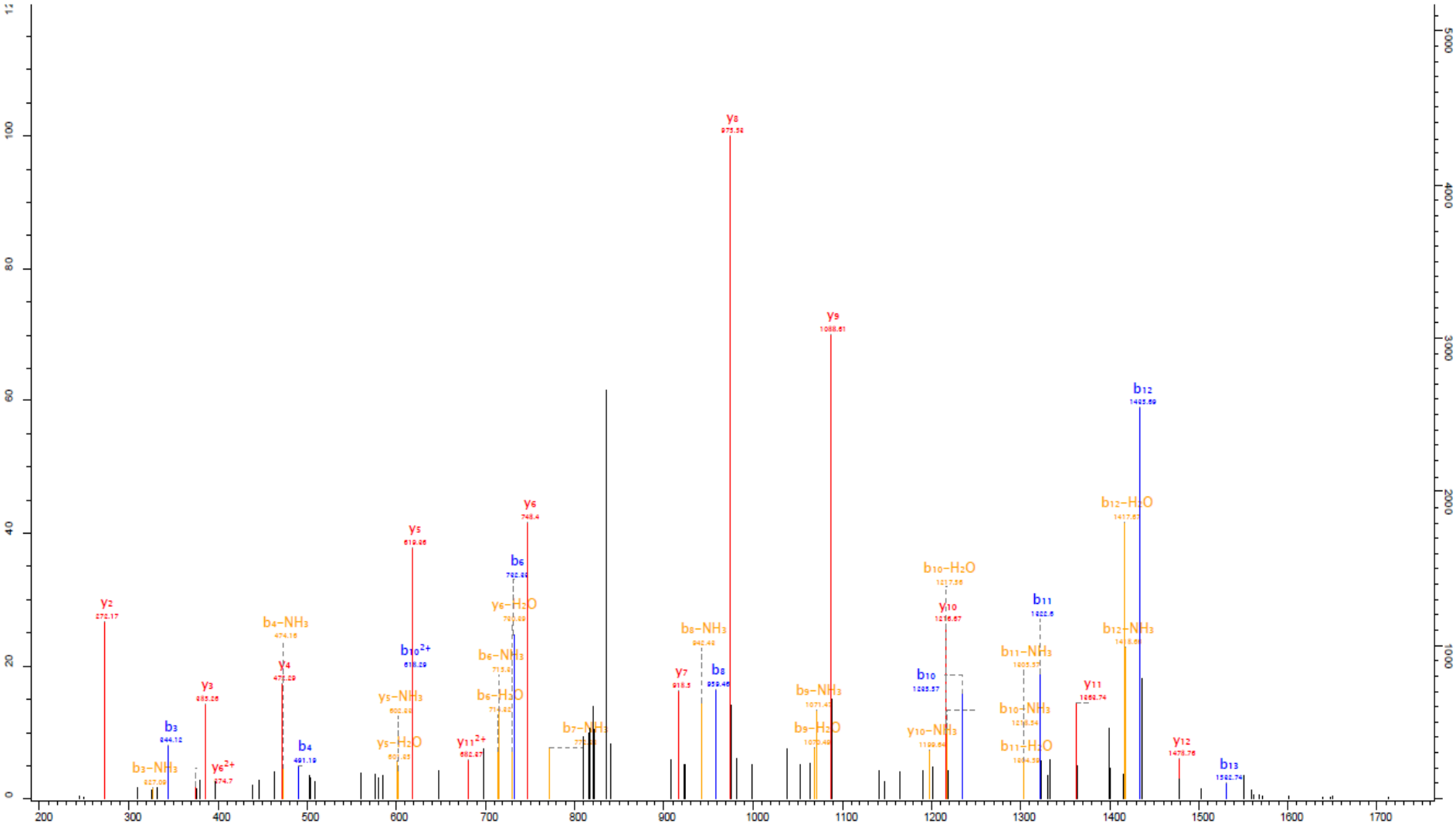
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)
1492.8297	1491.7004	746.9186	746.3538

[-] Main Sequence Ions

b	b^{+2}				y	y^{+2}
---	---	1	L	12	---	---
245.1318	---	2	M	11	1378.6164	689.8118
415.2374	208.1223	3	K(Acetyl)	10	1247.5759	624.2916
528.3214	264.6643	4	I	9	1077.4703	539.2388
688.3521	344.6797	5	C(Carbamidomethyl)	8	964.3863	482.6968
819.3925	410.1999	6	M	7	804.3556	402.6815
933.4355	467.2214	7	N	6	673.3151	337.1612
1062.4781	531.7427	8	E	5	559.2722	280.1397
1177.5050	589.2561	9	D	4	430.2296	215.6185
1274.5578	637.7825	10	P	3	315.2027	158.1050
1345.5949	673.3011	11	A	2	218.1499	109.5786
---	---	12	K	1	147.1128	74.0600



Raw file	Scan	Method	Score	m/z	Gene names
050813_SCW_II_29_19_4	22222	ITMS; CID	217.48	853.93	lng3



- N N D F Q L G K E F S I P R -

b3 b4 b6 b8 b10 b11 b12 b13

y12 y11 y10 y9 y8 y7 ac y6 y5 y4 y3 y2

050813_SCW_II_29_19_4 #22222 RT: 90.38 AV: 1 NL: 4.32E3
T: ITMS + c NSI d Full ms2 853.93@cid35.00 [225.00-1720.00]

Gene name= Ing3

MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)
1707.8950	1706.8497	854.4512	853.9285

[-] Main Sequence Ions

b	b^{+2}				y	y^{+2}
---	---	1	N	14	---	---
229.0931	---	2	N	13	1592.8067	796.9070
344.1201	---	3	D	12	1478.7638	739.8855
491.1885	---	4	F	11	1363.7369	682.3721
619.2471	---	5	Q	10	1216.6684	608.8379
732.3311	---	6	L	9	1088.6099	544.8086
789.3526	---	7	G	8	975.5258	488.2665
959.4581	480.2327	8	K(Acetyl)	7	918.5043	459.7558
1088.5007	544.7540	9	E	6	748.3988	374.7030
1235.5691	618.2882	10	F	5	619.3562	310.1817
1322.6012	661.8042	11	S	4	472.2878	236.6475
1435.6852	718.3462	12	I	3	385.2558	193.1315
1532.7380	766.8726	13	P	2	272.1717	136.5895
---	---	14	R	1	175.1190	88.0631