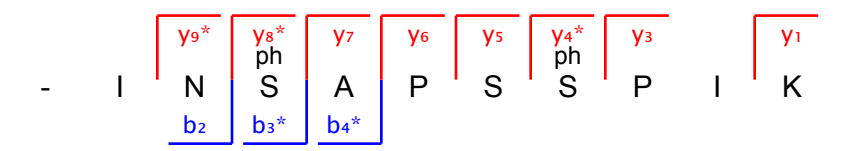
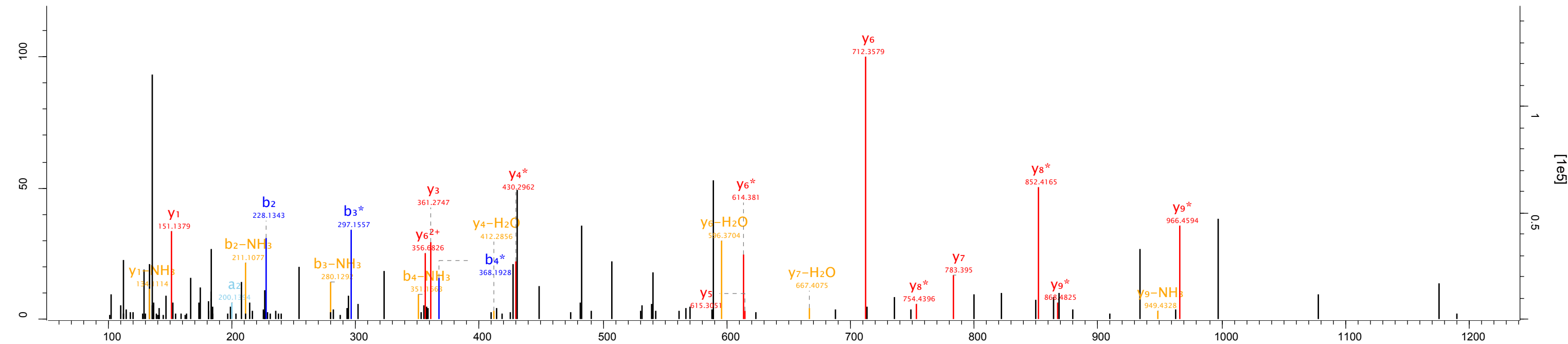
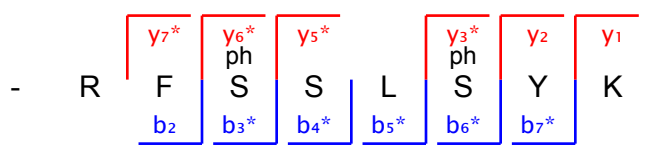
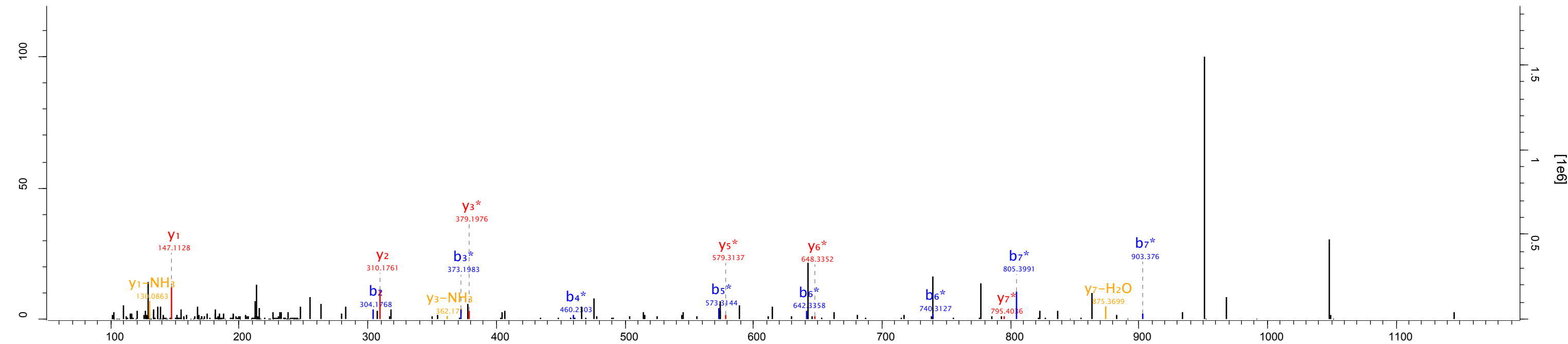


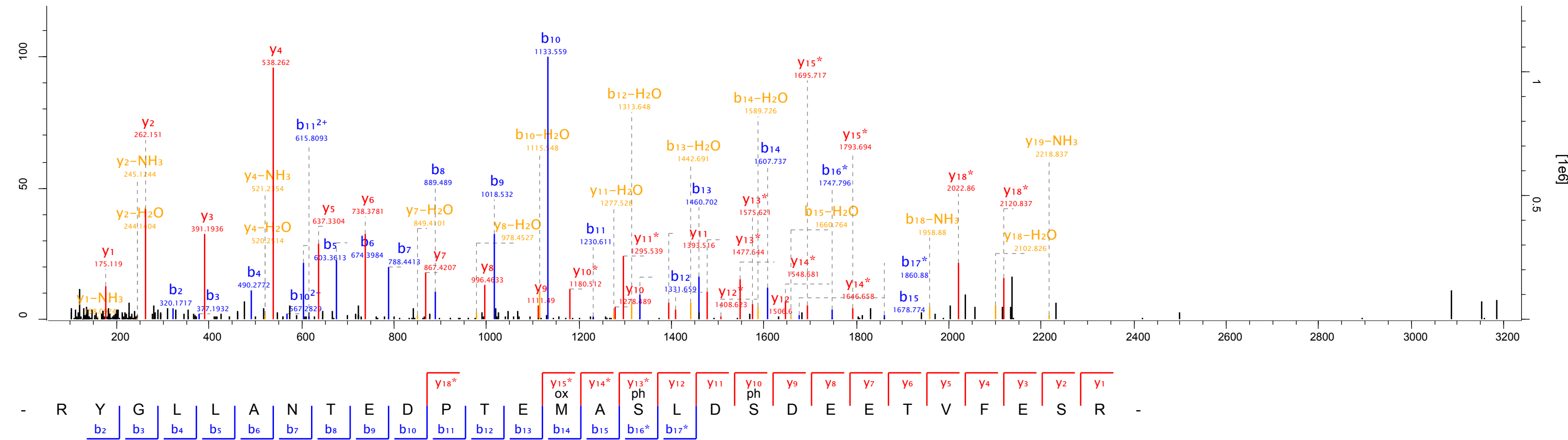
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 Scan: 7860 Method: FTMS; HCD Score: 68.86 m/z: 589.27 Gene names: E2F8



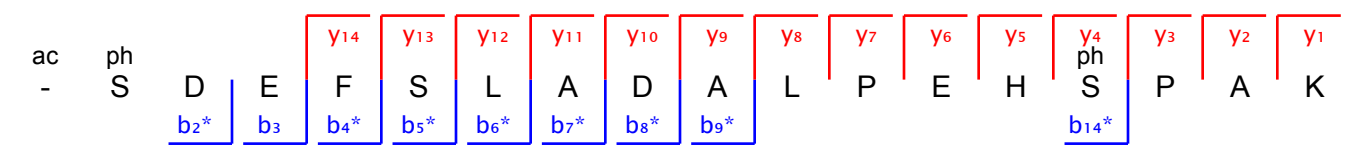
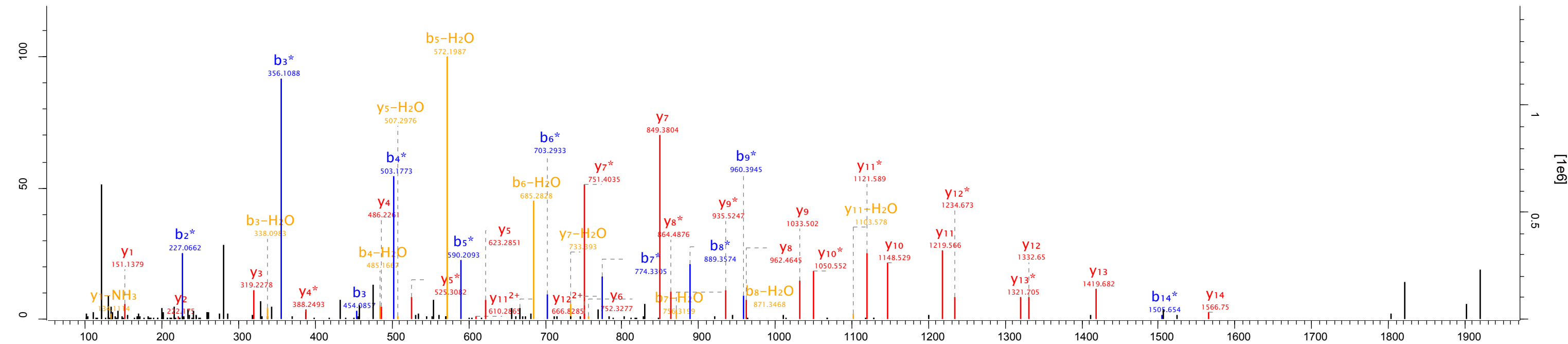
Raw file Scan Method Score m/z Gene names
 20150812_A375SR_Phospho_BR1_03 13760 FTMS; HCD 47.82 574.23 PAG1



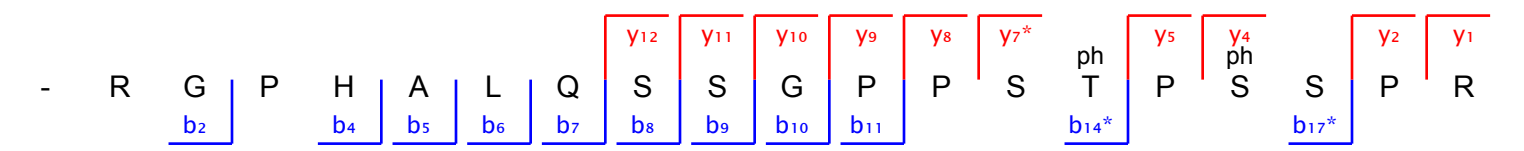
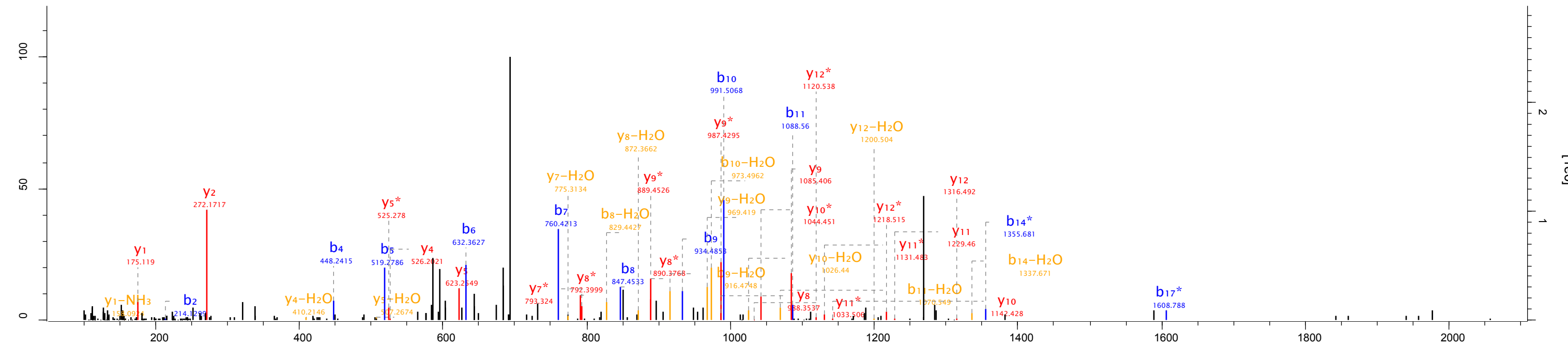
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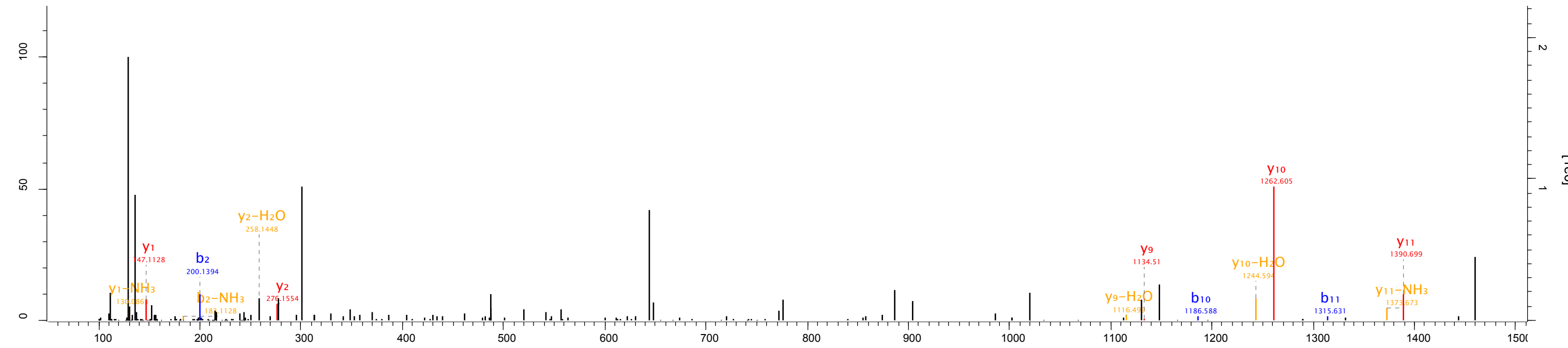
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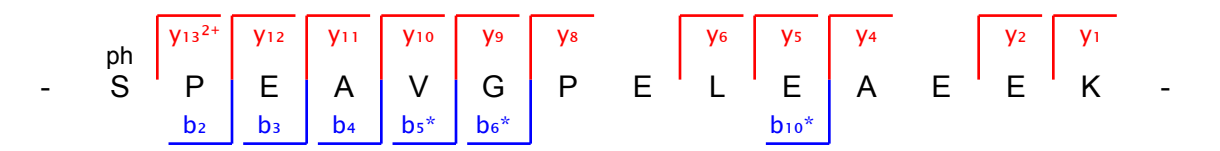
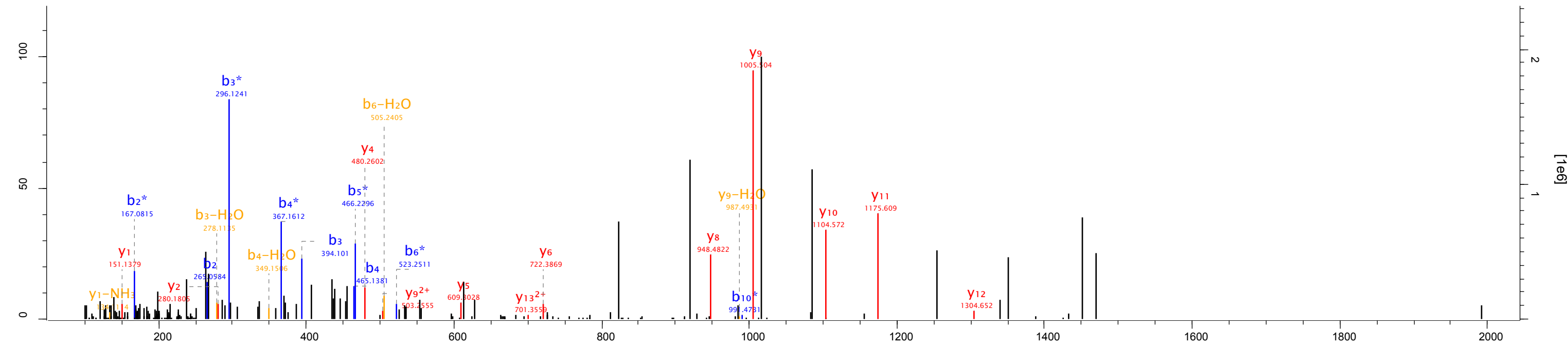
Raw file: 20150812_A375SR_Phospho_BR1_03
 Scan: 8400 Method: FTMS; HCD Score: 96.31 m/z: 692.98 Gene names: HIVEP2

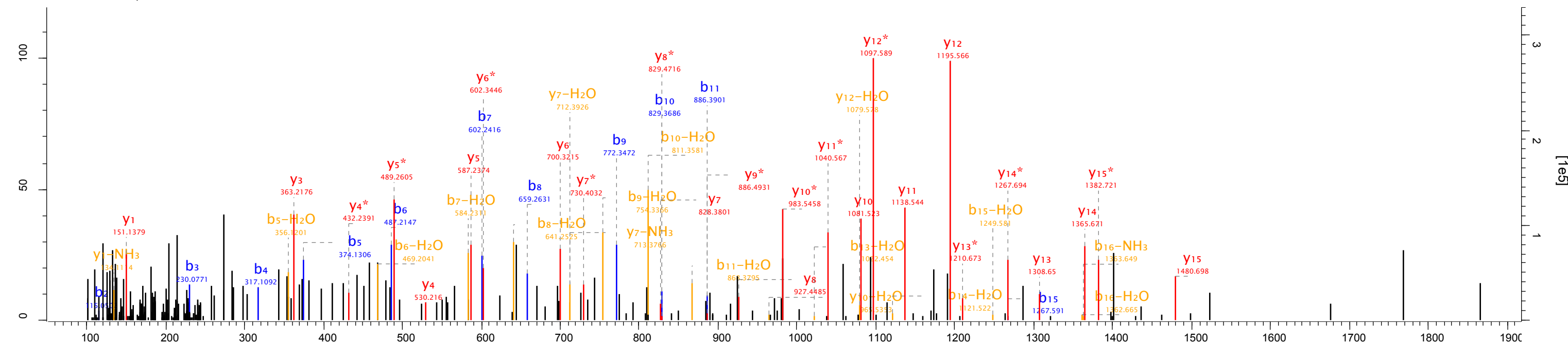


Raw file: 20150812_A375SR_Phospho_BR1_04
 Scan: 1290 Method: FTMS; HCD Score: 47.06 m/z: 488.25



Raw file 20150812_A375SR_Phospho_BR1_04 Scan 13990 Method FTMS; HCD Score 67.15 m/z 784.86 Gene names PWWP2A





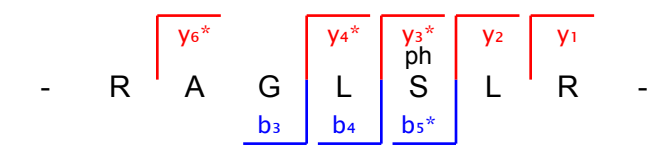
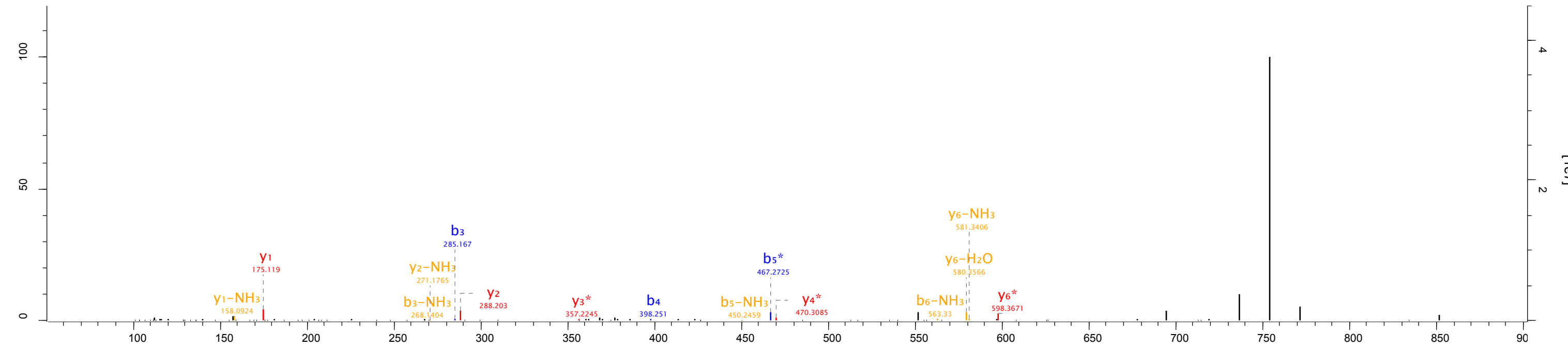
- G G D S G L D G L G G P G V Q L G S P D K -

b₂ b₃ b₄ b₅ b₆ b₇ b₈ b₉ b₁₀ b₁₁ b₁₅

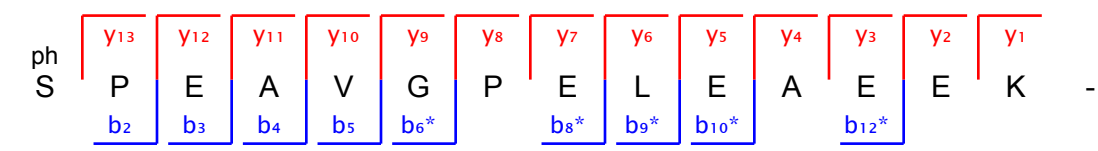
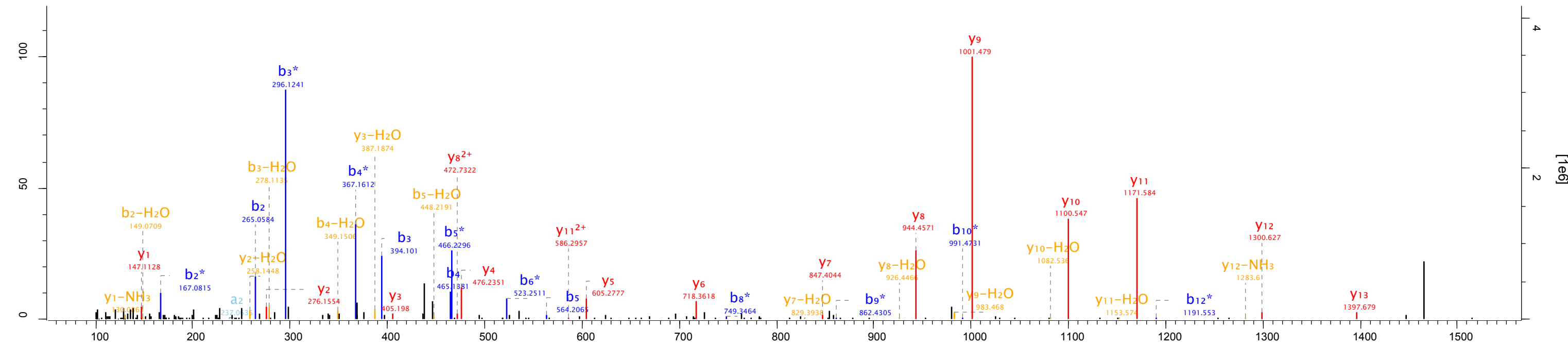
y₁₅ y₁₄ y₁₃ y₁₂ y₁₁ y₁₀ y₉* y₈ y₇ y₆ y₅ y₄ y₃ y₁

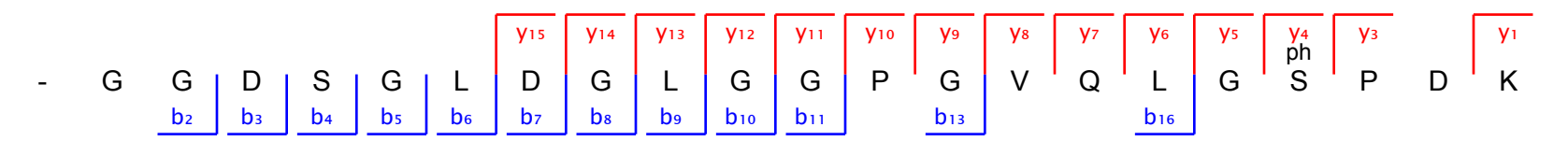
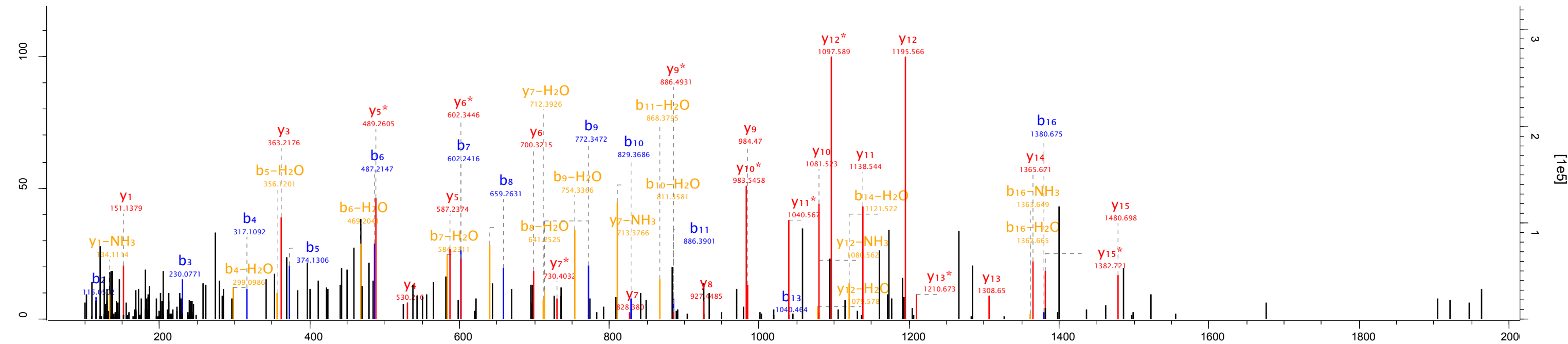
ph

Raw file 20150812_A375SR_Phospho_BR1_04 Scan 6310 Method FTMS; HCD Score 72.93 m/z 426.73

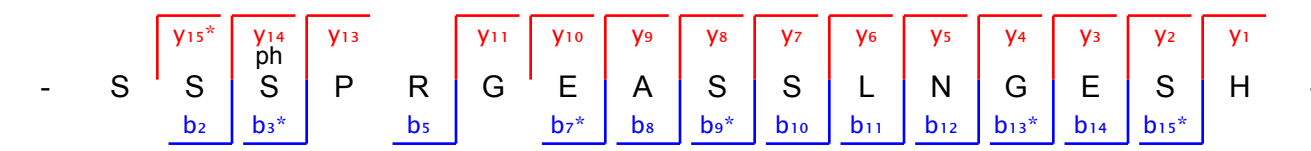
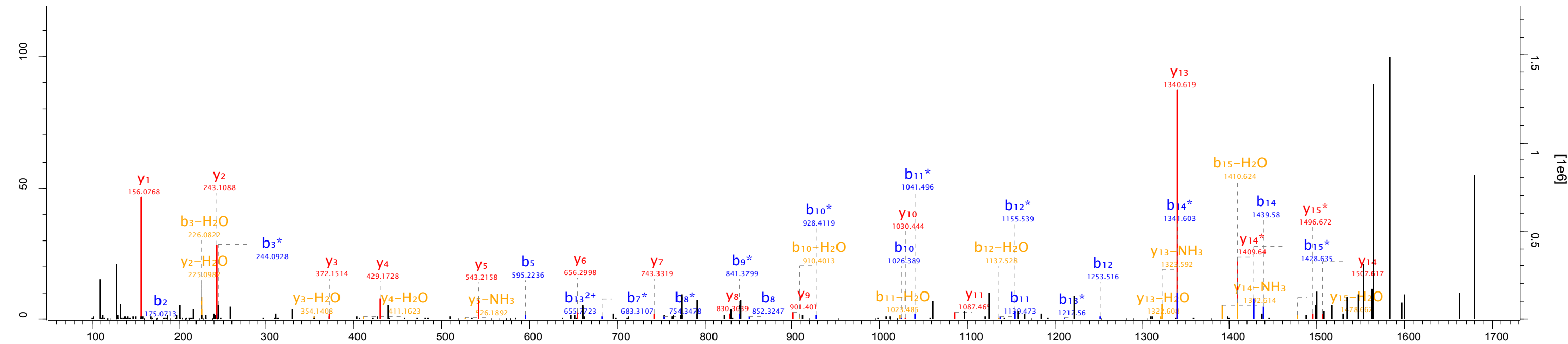


Raw file: 20150812_A375SR_Phospho_BR1_05
 Scan: 13940 Method: FTMS; HCD Score: 174.21 m/z: 782.85 Gene names: PWWP2A

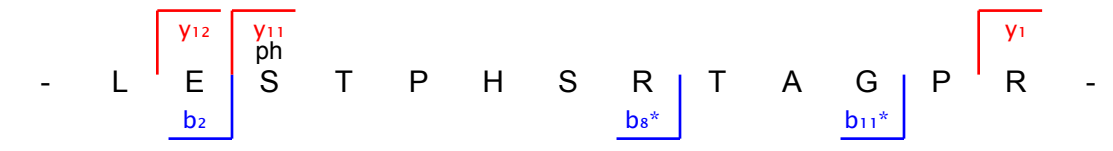
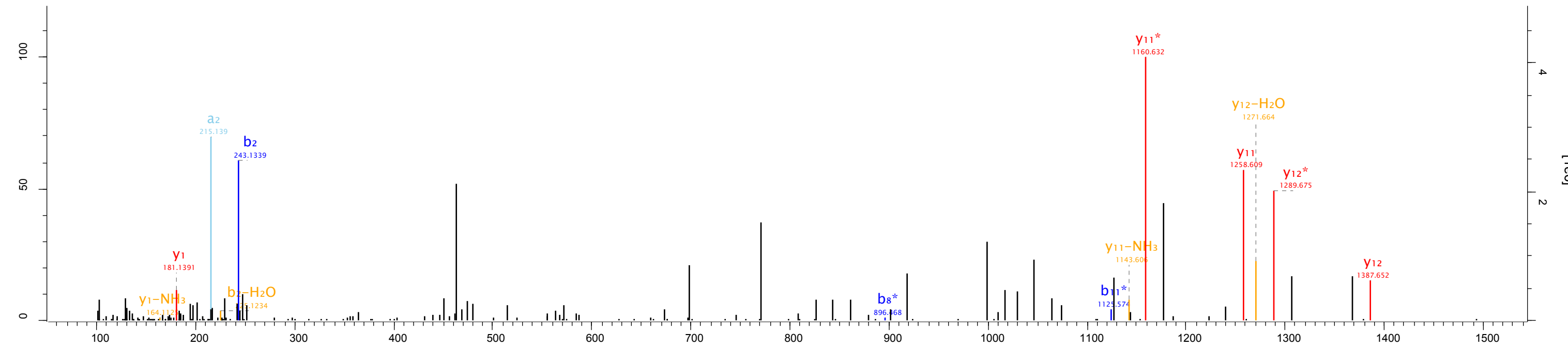




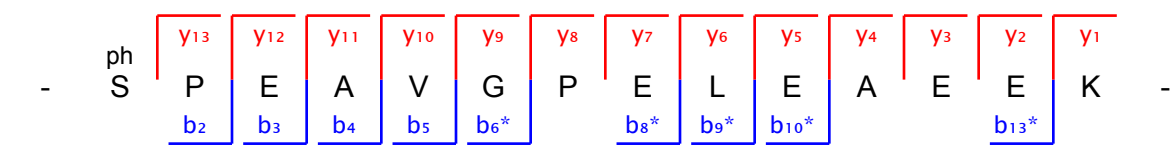
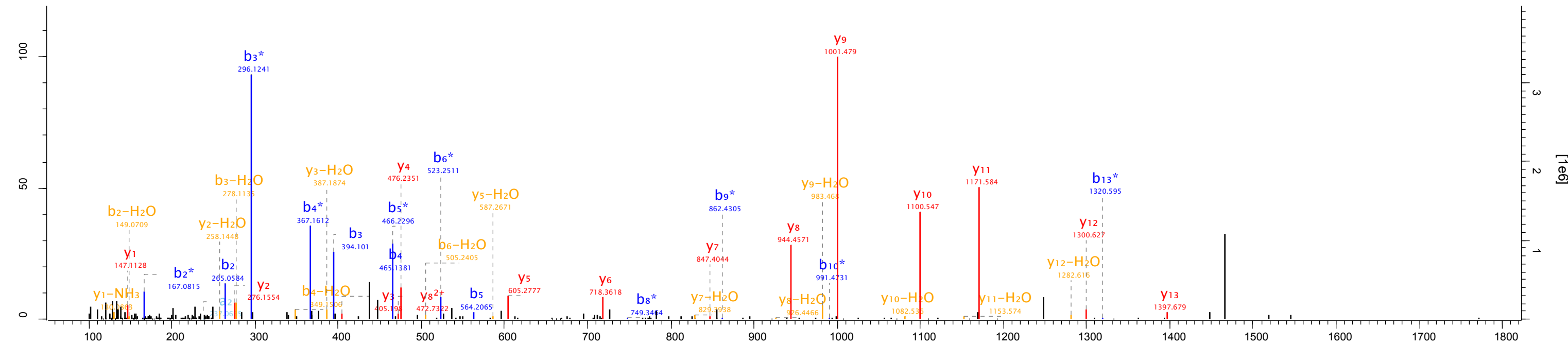
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 Scan: 6000 Method: FTMS; HCD Score: 126.88 m/z: 841.35 Gene names: YAF2



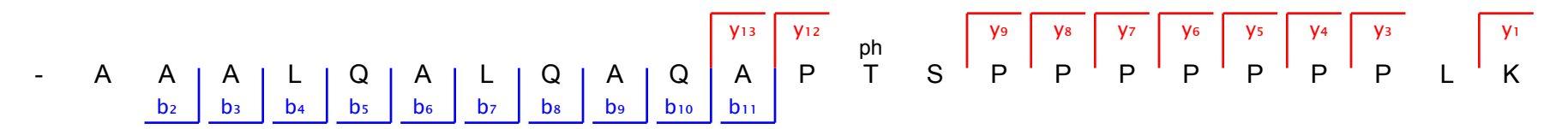
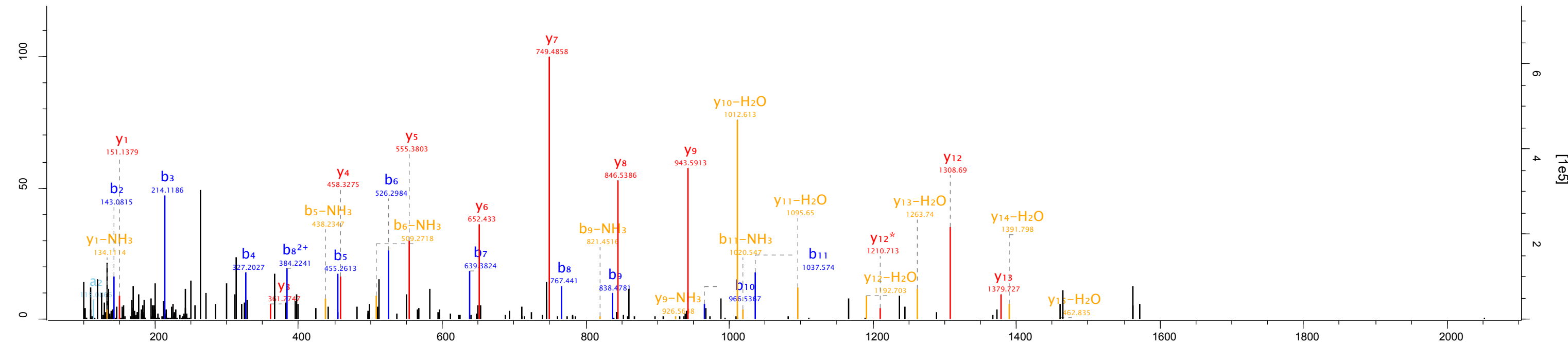
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 20150812_A375SR_Phospho_BR1_05 8640 FTMS; HCD 41.54 500.92



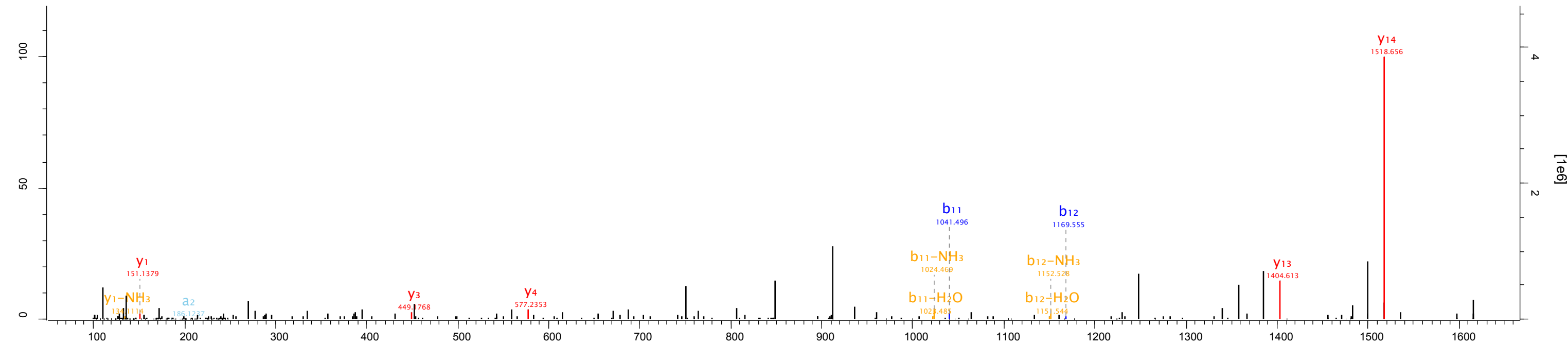
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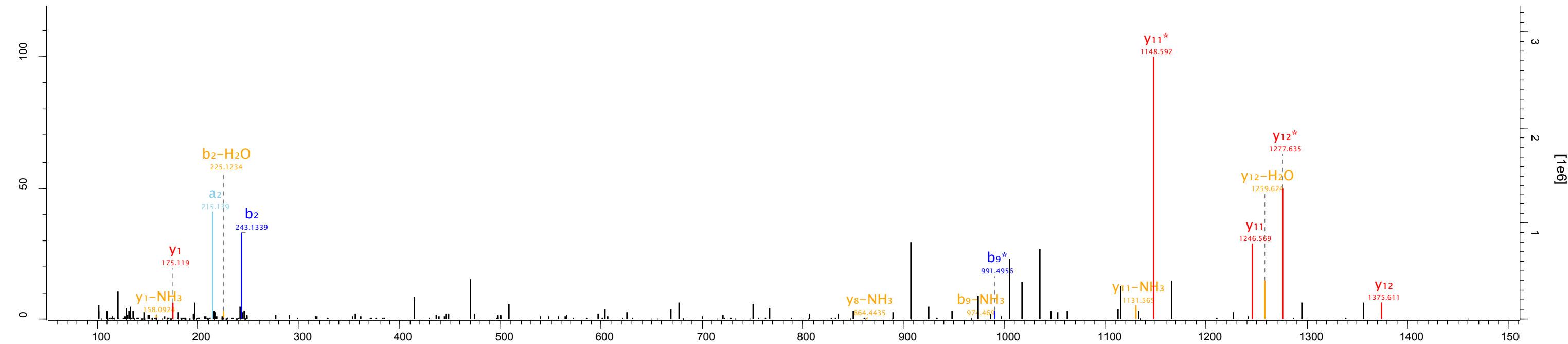
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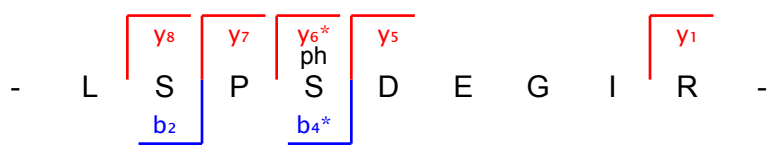
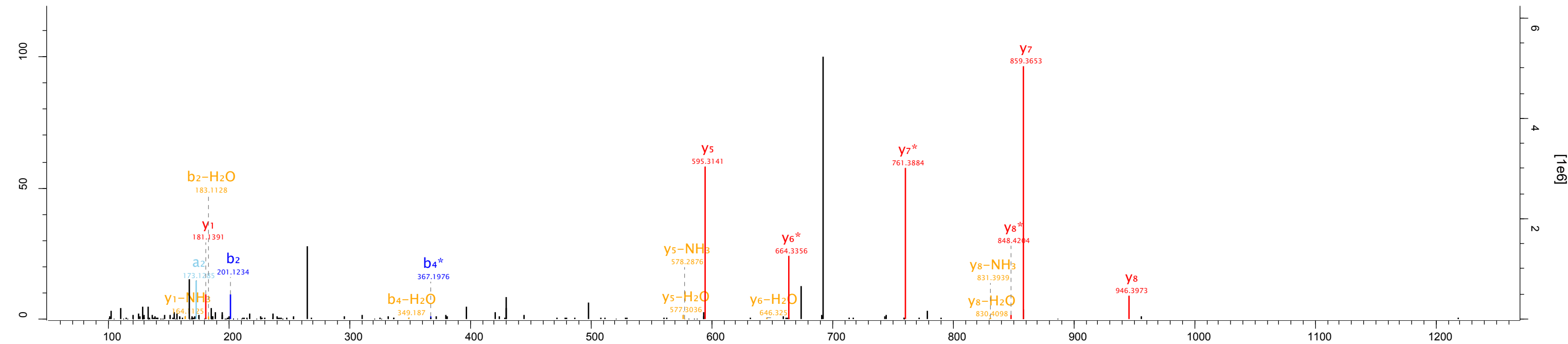
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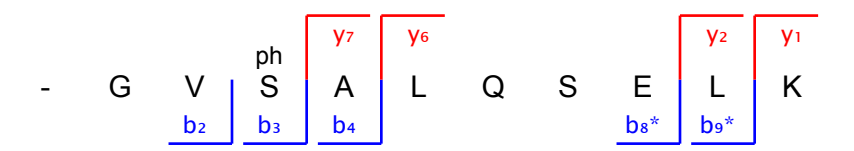
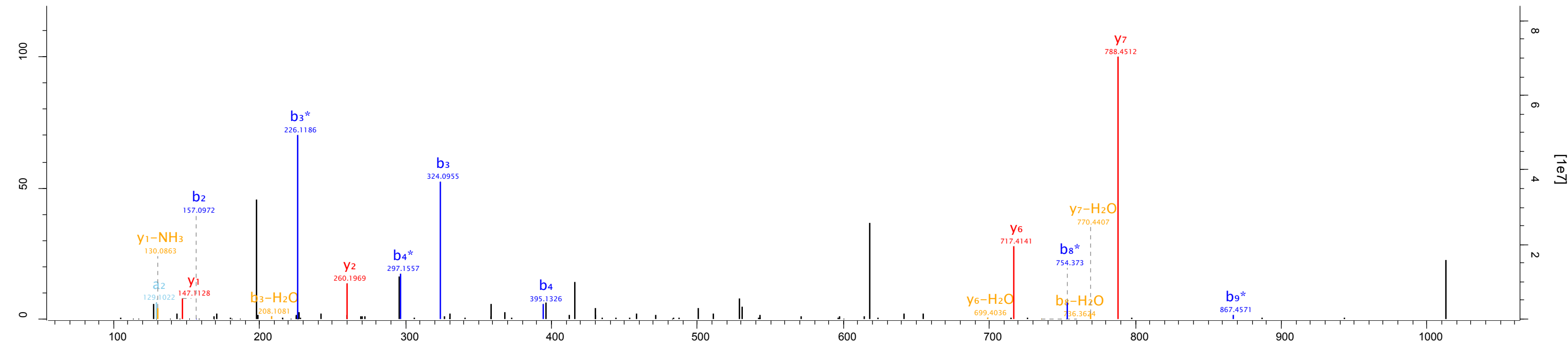
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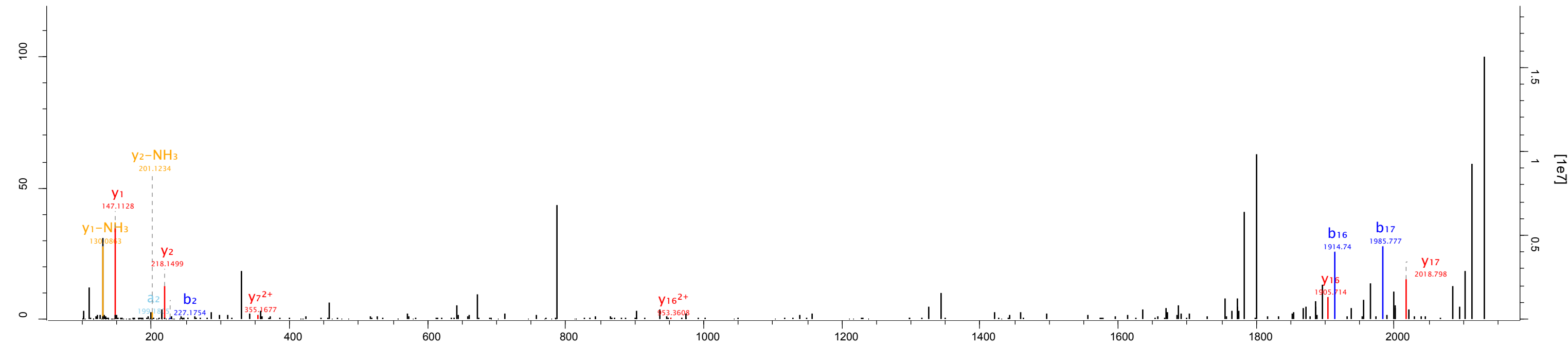
Raw file Scan Method Score m/z
 20150812_A375SR_Phospho_BR1_08 5080 FTMS; HCD 48.94 530.24



Raw file 20150812_A375SR_Phospho_BR1_09 Scan 12400 Method FTMS; HCD Score 62.34 m/z 556.27



Raw file Scan Method Score m/z Gene names
 20150812_A375SR_Phospho_BR1_09 15520 FTMS; HCD 46.16 711.63 LINC00614



- L L L E C T Y G A L E S A G V P A K -

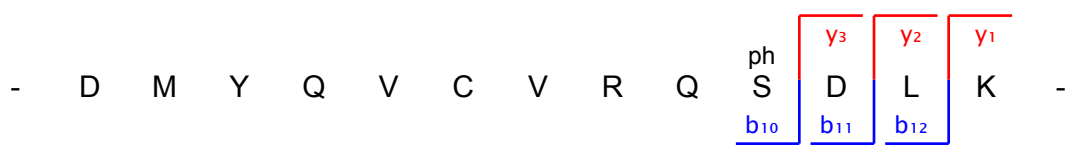
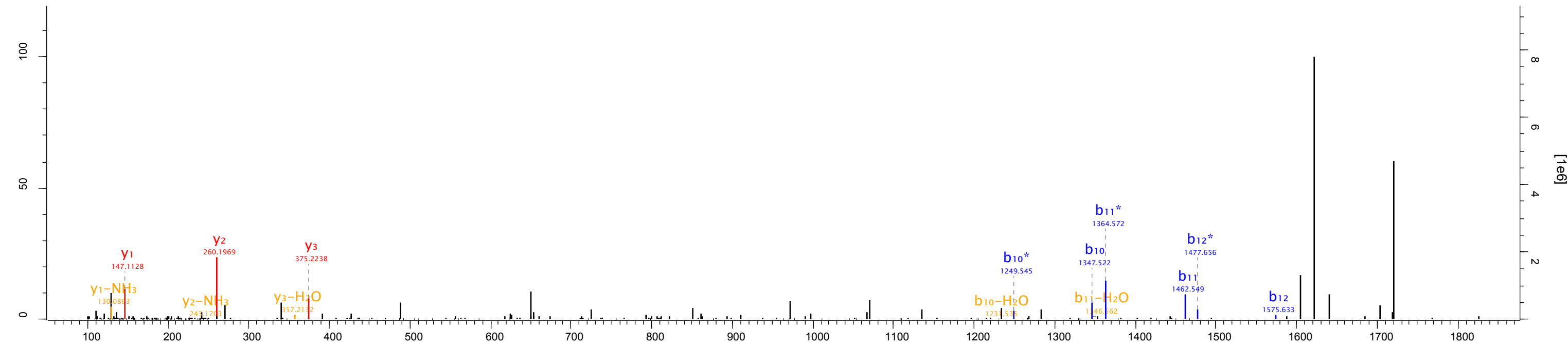
Annotations above the sequence:

- y_{17} above the first L
- y_{16} above the second L
- y_7^{2+} above the S
- y_2 above the A
- y_1 above the K

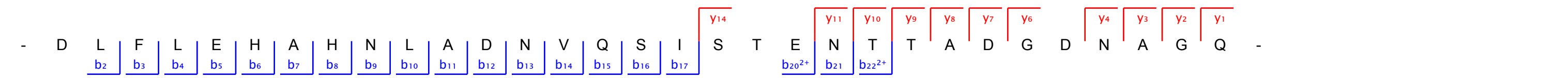
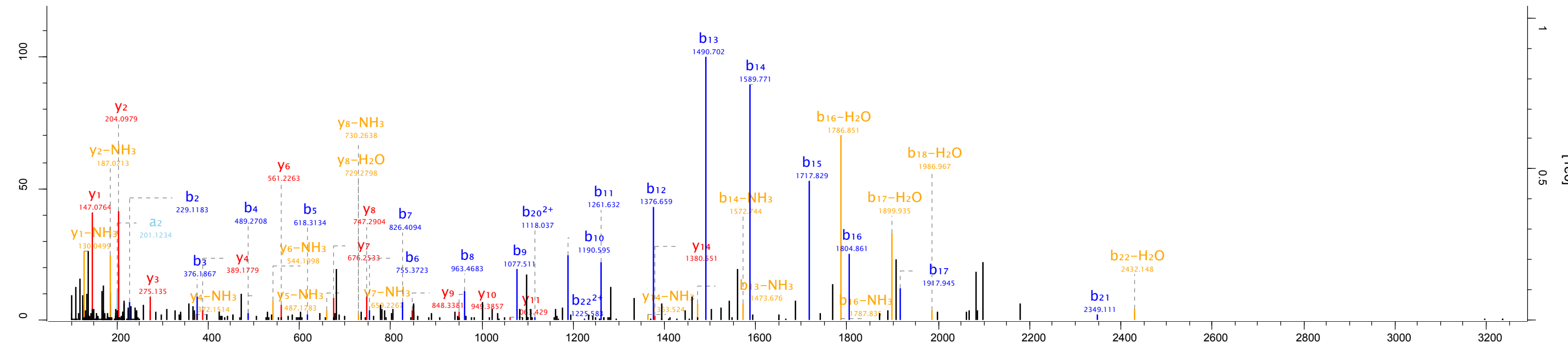
Annotations below the sequence:

- b_2 below the first L
- b_{16} below the P
- b_{17} below the A

Raw file 20150812_A375SR_Phospho_BR1_09 Scan 17200 Method FTMS; HCD Score 53.98 m/z 861.37

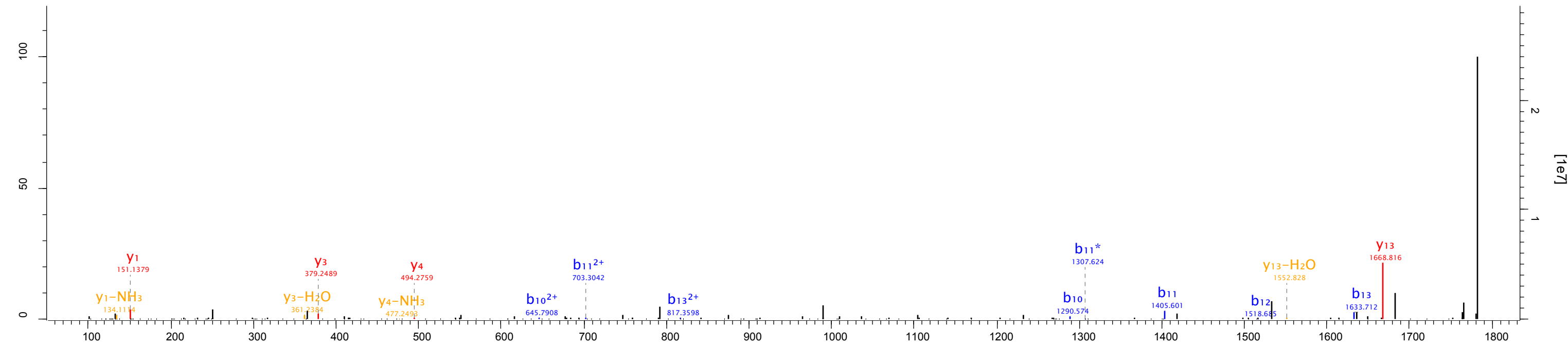


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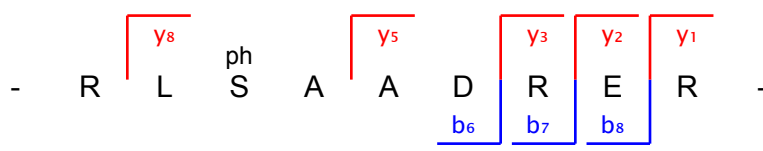
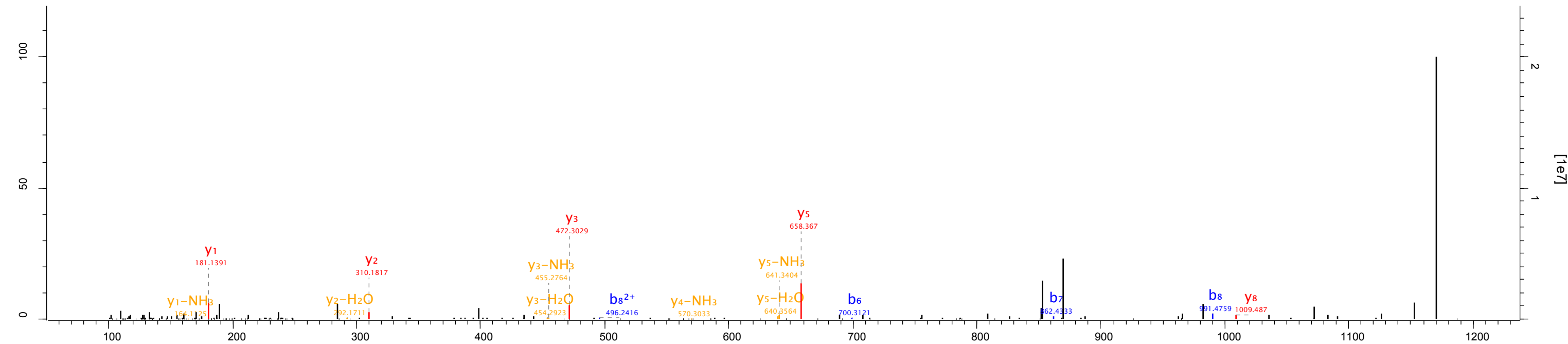


Raw file
20150812_A375SR_Phospho_BR1_09

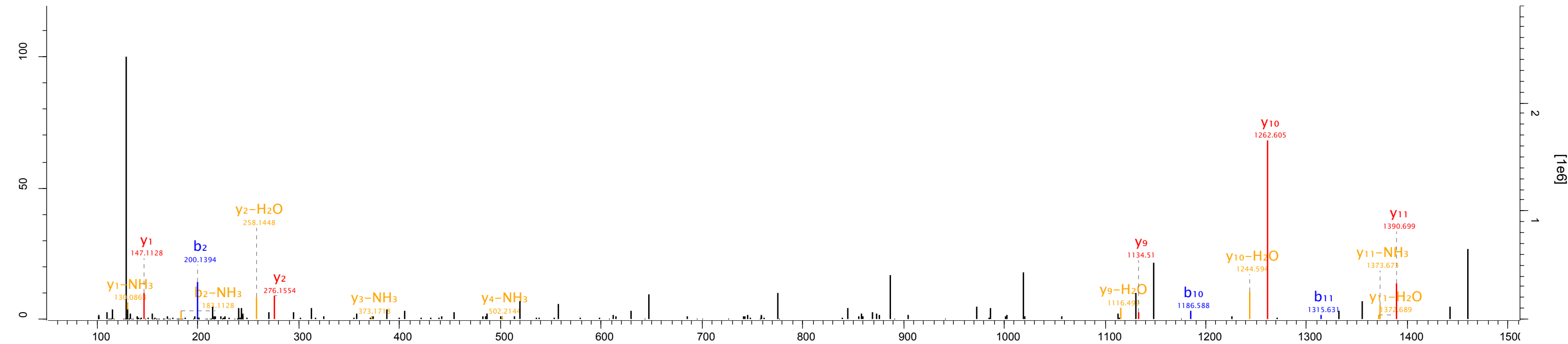
Scan 2980 Method FTMS; HCD Score 70.44 m/z 892.43



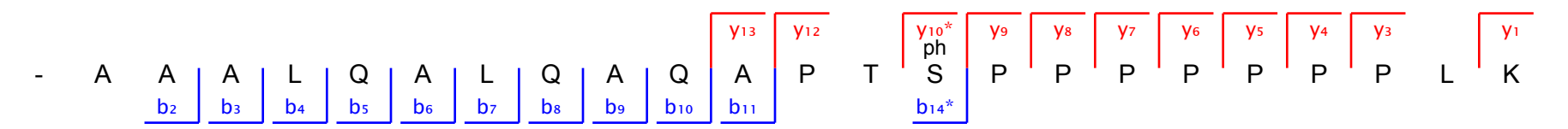
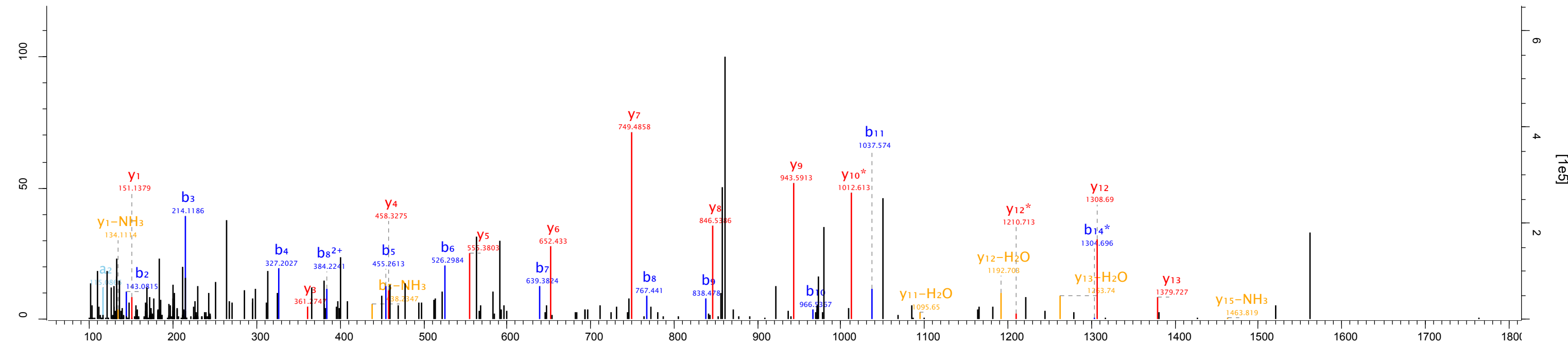
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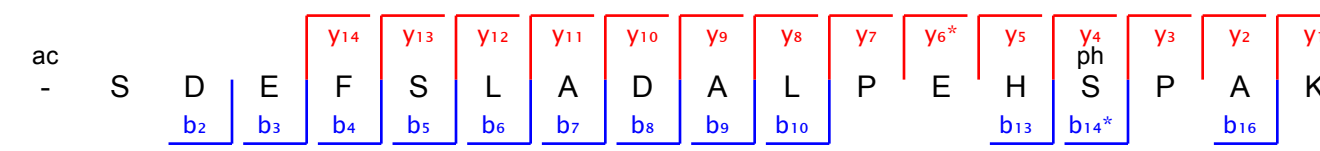
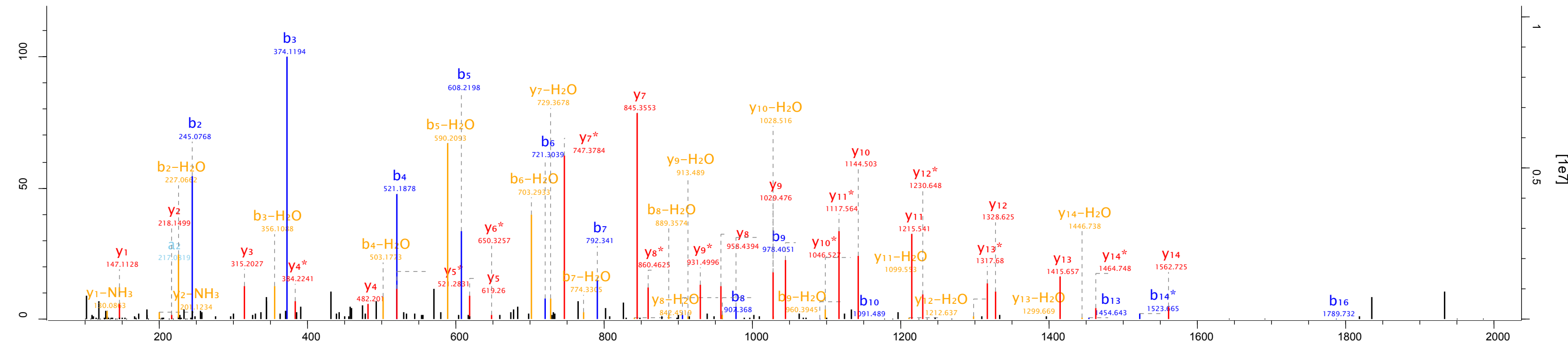
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 Scan: 1210 Method: FTMS; HCD Score: 72.34 m/z: 487.92



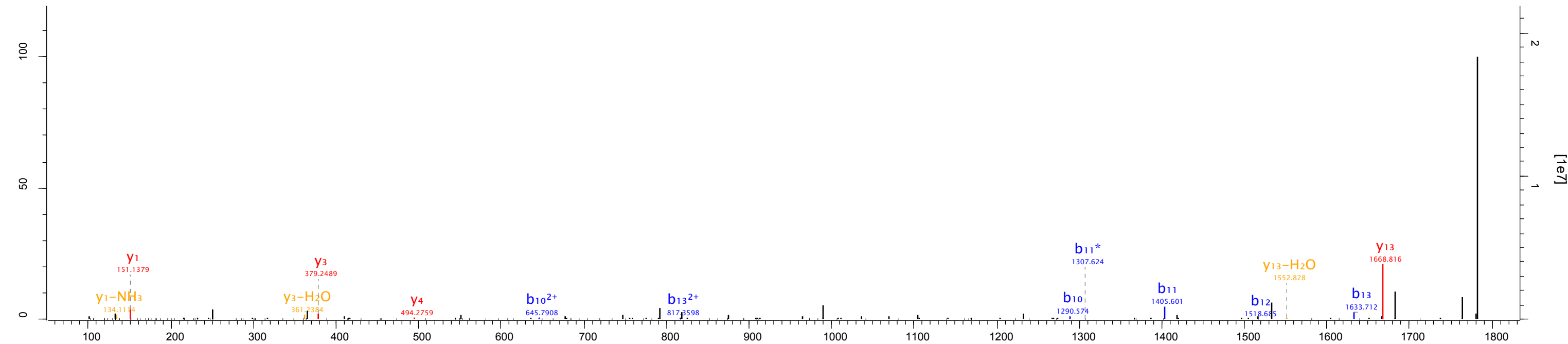
Raw file: 20150812_A375SR_Phospho_BR1_10
 Scan: 21000 Method: FTMS; HCD Score: 42.42 m/z: 782.76 Gene names: ZNF579



Raw file
 20150812_A375SR_Phospho_BR1_10
 Scan 24160 Method FTMS; HCD Score 293.33 m/z 968.92 Gene names MAPK11P1L



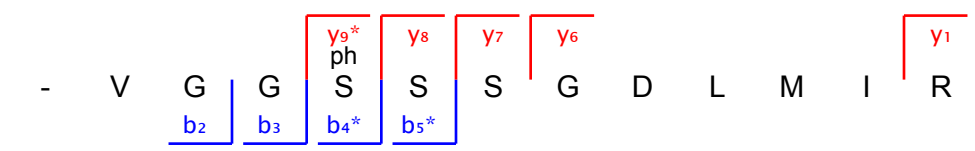
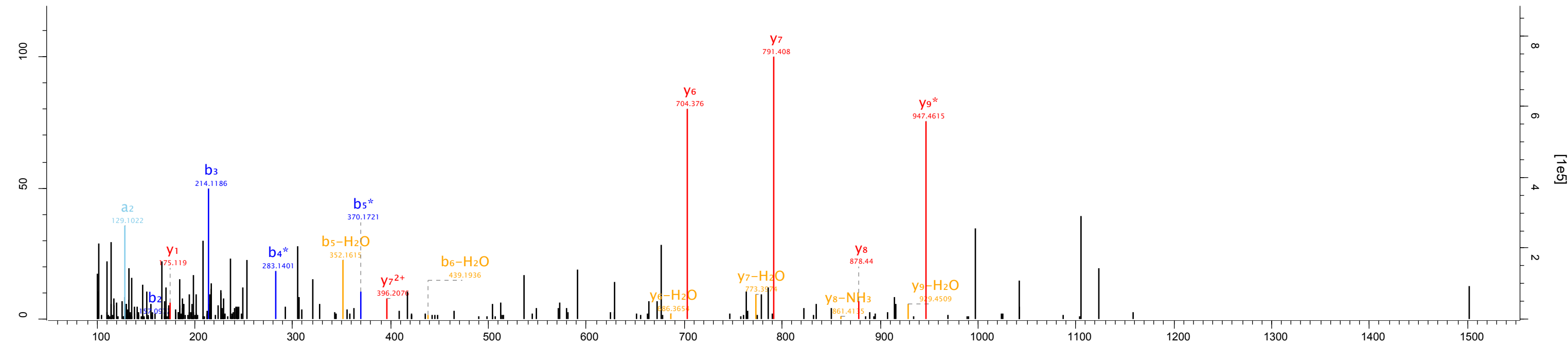
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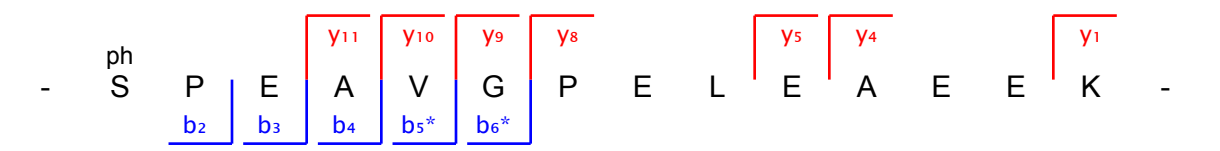
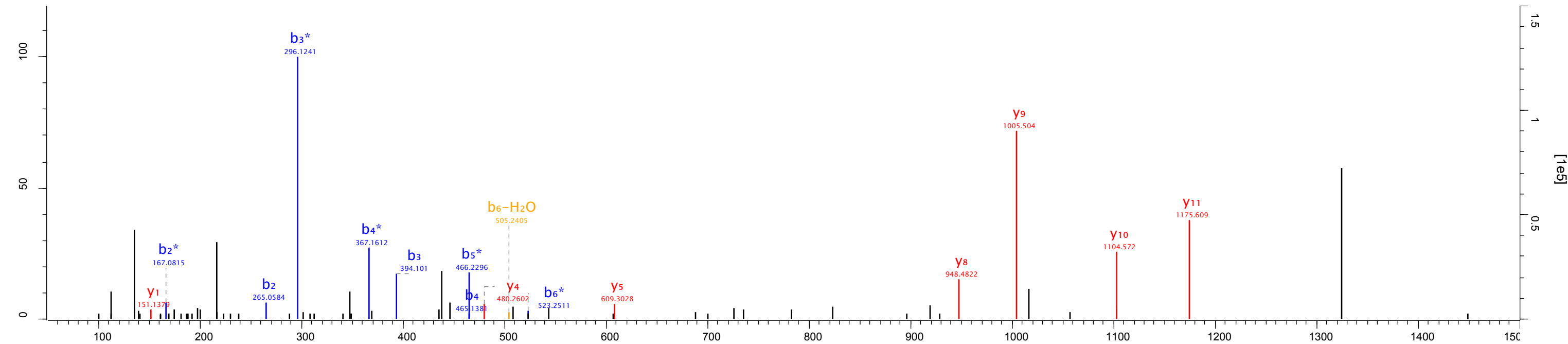
- D M S T E L E L L R D L D K -

y₁₃ox ph
b₁₀ y₄ y₃ b₁₁ b₁₂ b₁₃ y₁

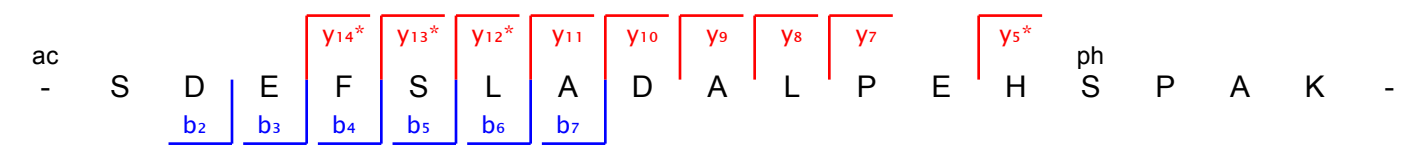
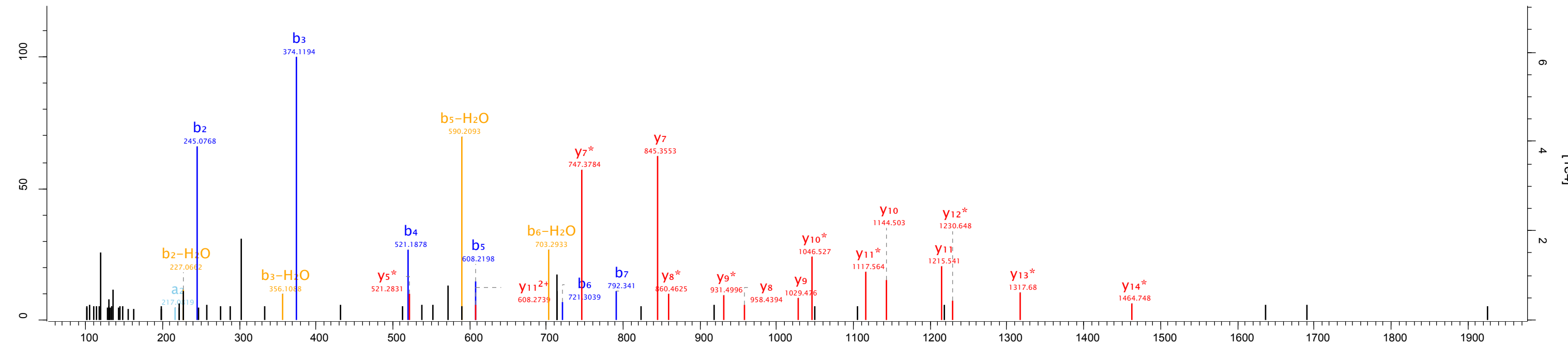
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 Scan: 8010 Method: FTMS; HCD Score: 46.7 m/z: 629.78 Gene names: CNTN3



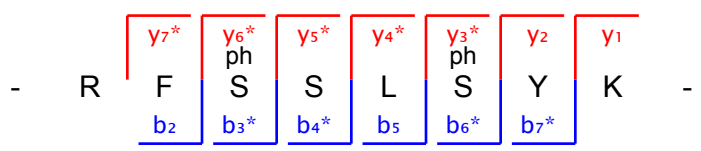
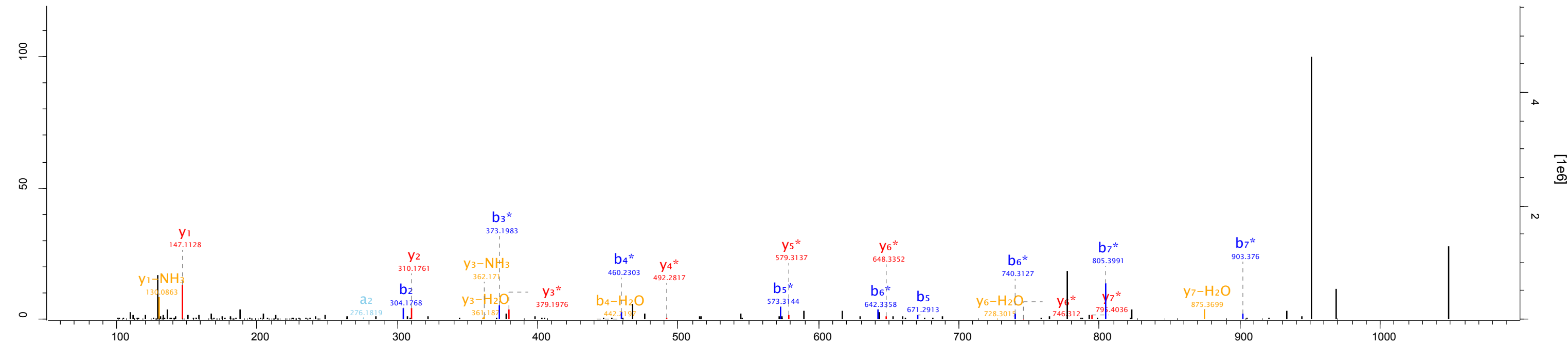
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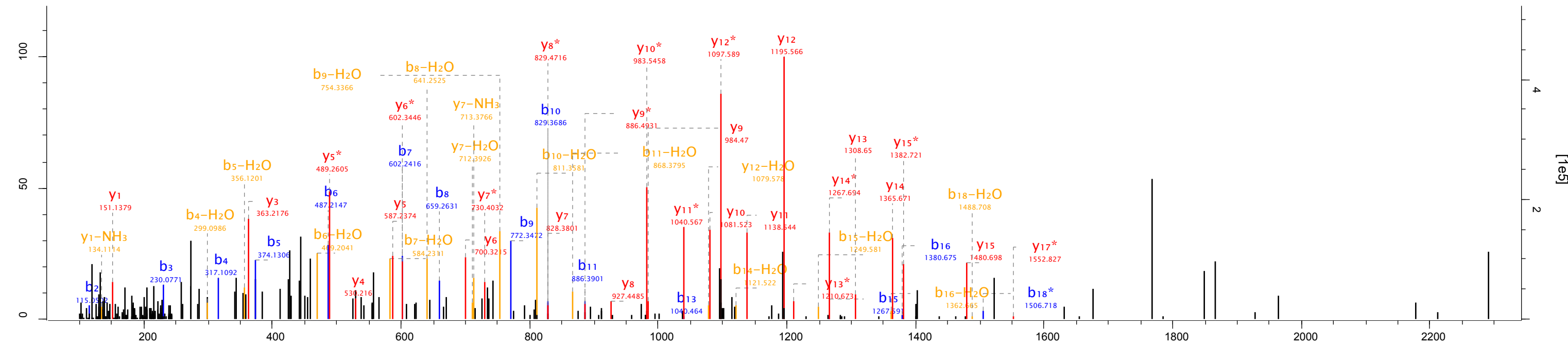
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 Scan: 17620 Method: FTMS; HCD Score: 98.54 m/z: 968.43 Gene names: MAPK11P1L



Raw file Scan Method Score m/z Gene names
 20150814_A375SR_Phospho_BR2_03 12070 FTMS; HCD 83.45 574.23 PAG1



Raw file 20150814_A375SR_Phospho_BR2_03 Scan 19120 Method FTMS; HCD Score 203.5 m/z 983.96



- G G D S G L D G L G G P G V Q L G S P D K -

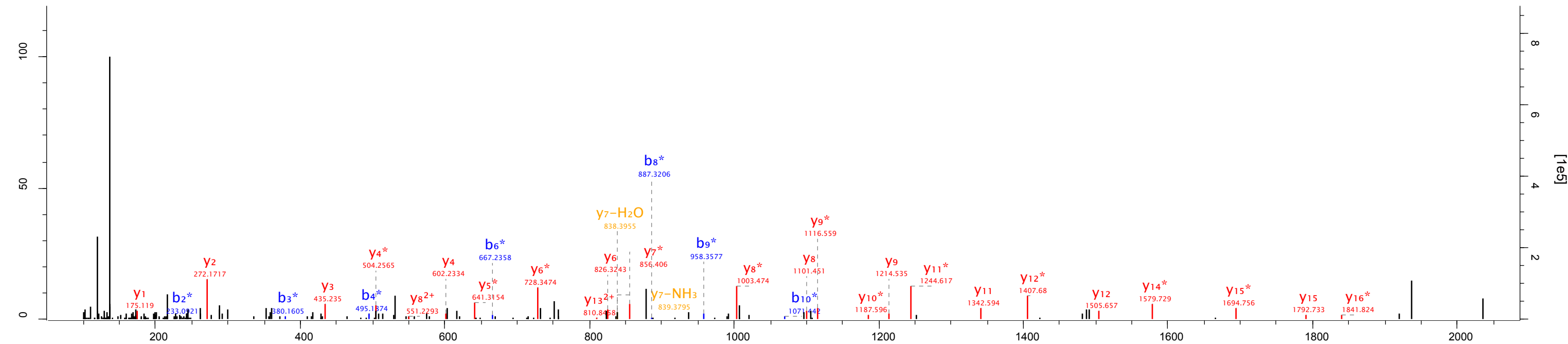
Fragmentation mapping (b and y ions) is shown below the sequence:

- b₂ (under G)
- b₃ (under G)
- b₄ (under D)
- b₅ (under S)
- b₆ (under G)
- b₇ (under L)
- b₈ (under D)
- b₉ (under G)
- b₁₀ (under L)
- b₁₁ (under G)
- b₁₃ (under P)
- b₁₅ (under V)
- b₁₆ (under Q)
- b₁₈* (under S)

Fragmentation mapping (b and y ions) is shown above the sequence:

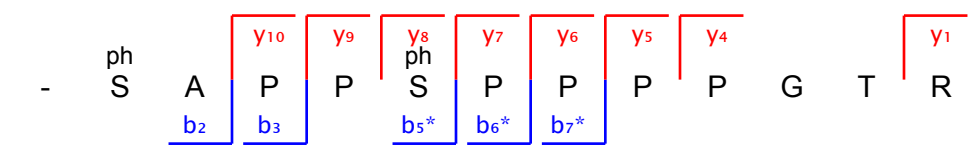
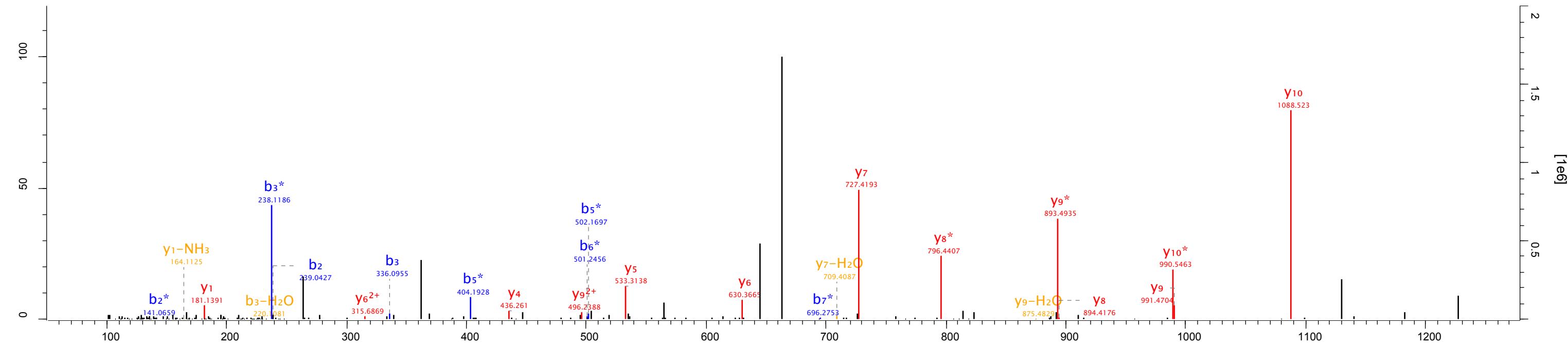
- y₁₇* (above S)
- y₁₅ (above D)
- y₁₄ (above G)
- y₁₃ (above L)
- y₁₂ (above G)
- y₁₁ (above G)
- y₁₀ (above P)
- y₉ (above G)
- y₈ (above V)
- y₇ (above Q)
- y₆ (above L)
- y₅ (above G)
- y₄ (above S)
- y₃ (above P)
- y₁ (above K)

Raw file
 20150814_A375SR_Phospho_BR2_03
 Scan 25440 Method FTMS; HCD Score 75.7 m/z 757.63 Gene names LRFN1

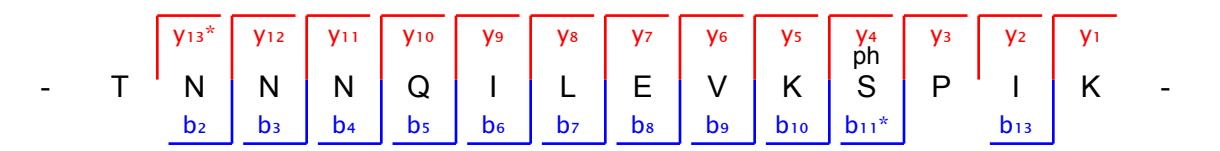
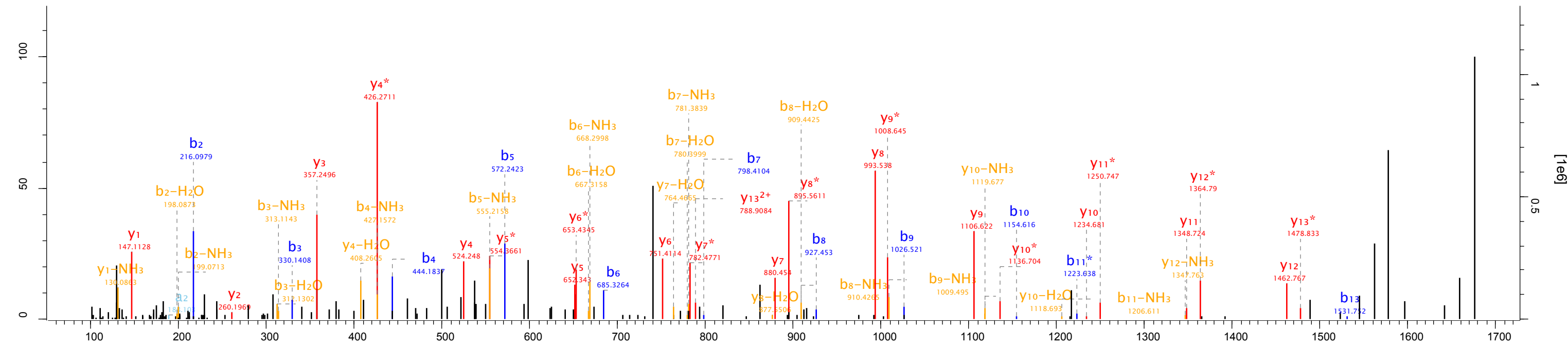


- Y ph S Y₁₆* Y₁₅* Y₁₄* Y₁₃²⁺ Y₁₂ Y₁₁ Y₁₀* Y₉ Y₈ Y₇* Y₆ Y₅* Y₄ Y₃ Y₂ Y₁ -
 b₂* b₃* b₄* b₆* b₈* b₉* b₁₀*

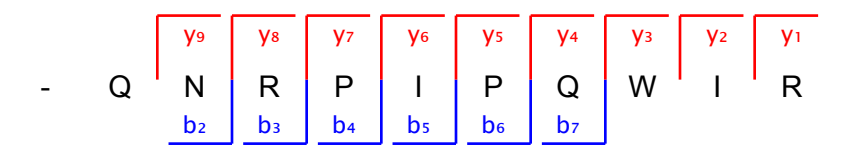
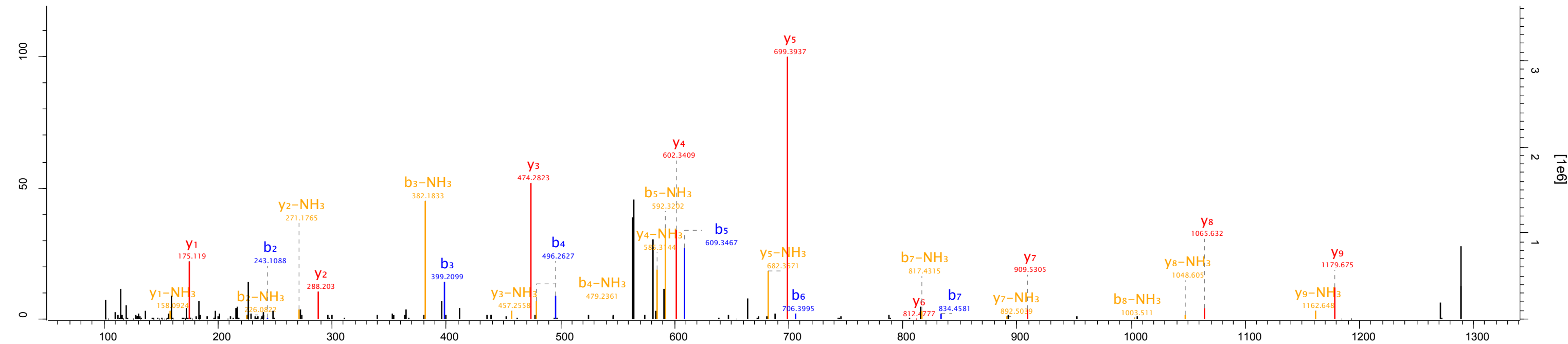
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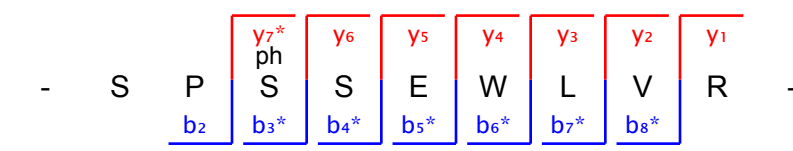
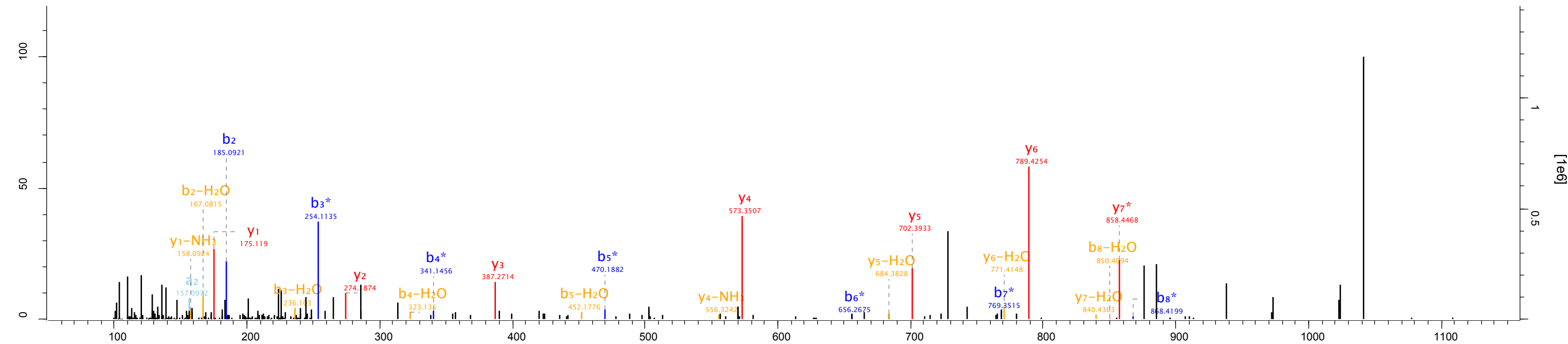
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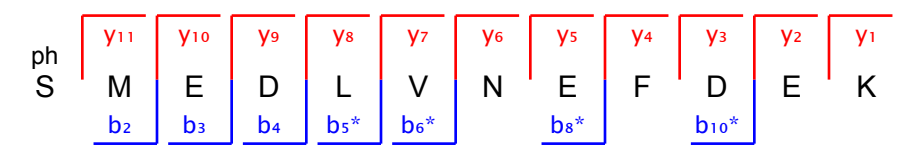
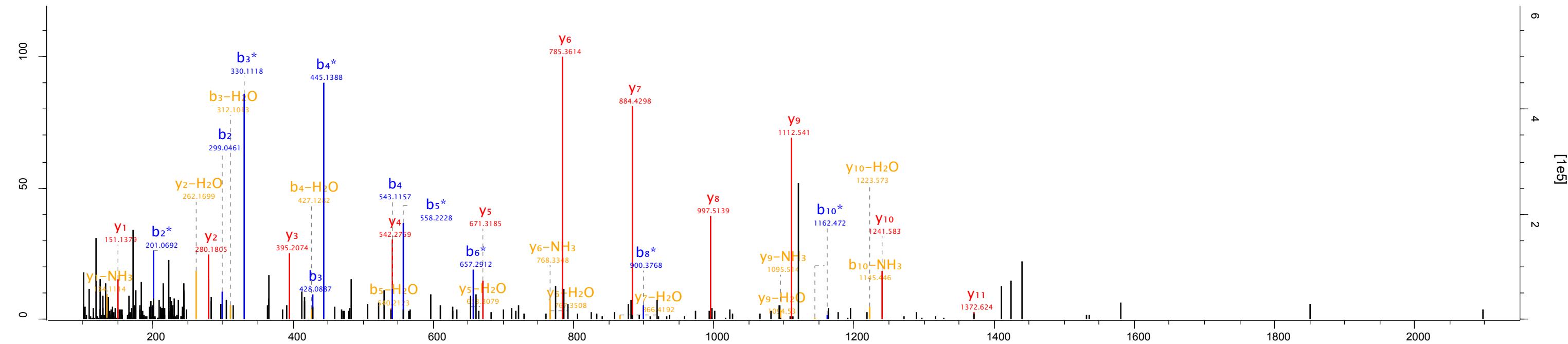
Raw file: 20150814_A375SR_Phospho_BR2_04
 Scan: 13480 Method: FTMS; HCD Score: 185.81 m/z: 436.58 Gene names: RPL39P5;RPL39



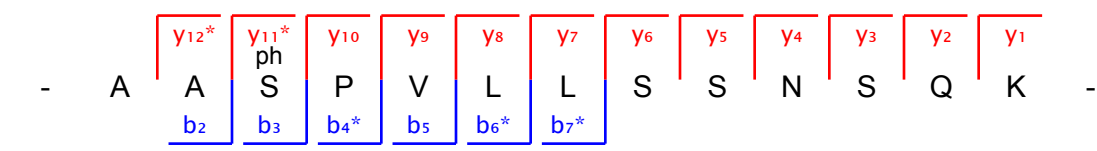
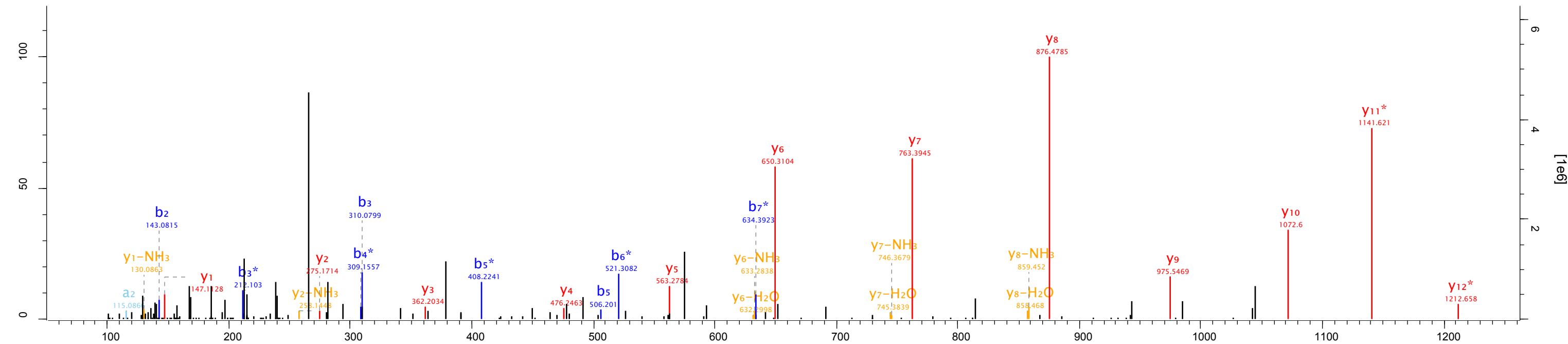
Raw file: 20150814_A375SR_Phospho_BR2_04
 Scan: 17310 Method: FTMS; HCD Score: 101.12 m/z: 570.76 Gene names: GPATCH2L



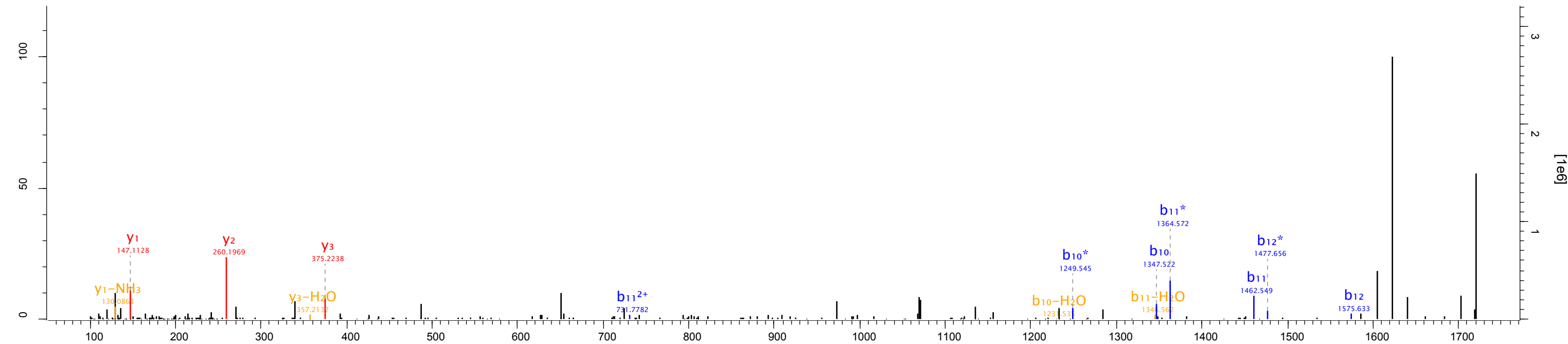
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 Scan: 23110 Method: FTMS; HCD Score: 123.02 m/z: 770.32 Gene names: FEZ1



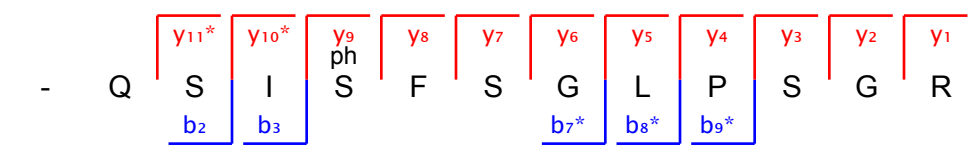
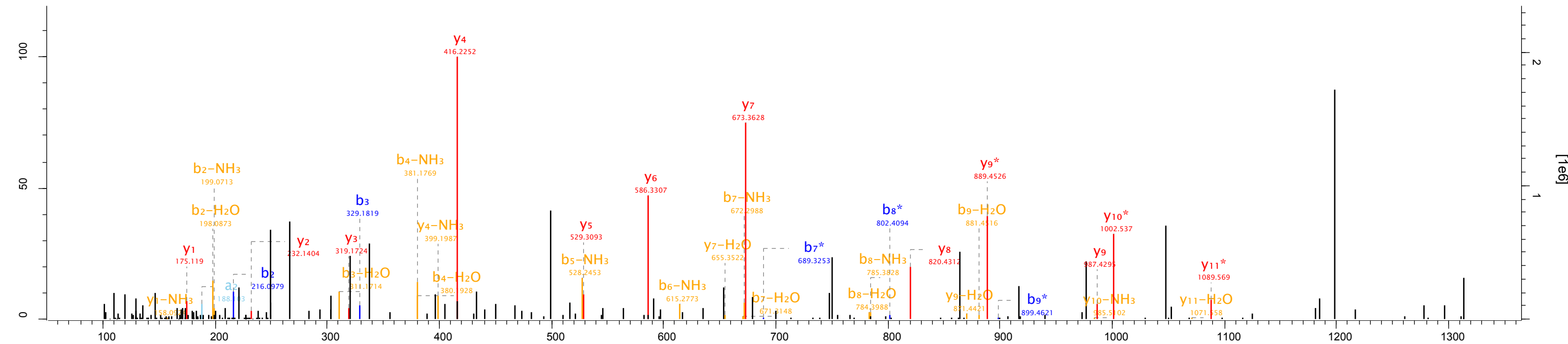
Raw file 20150814_A375SR_Phospho_BR2_05 Scan 10930 Method FTMS; HCD Score 98.51 m/z 691.34 Gene names ELK3



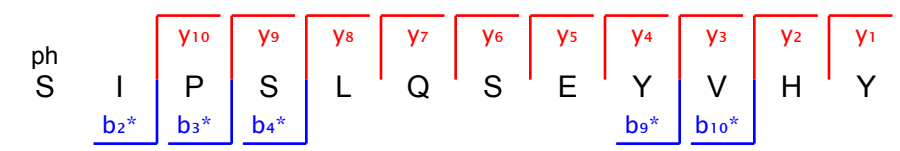
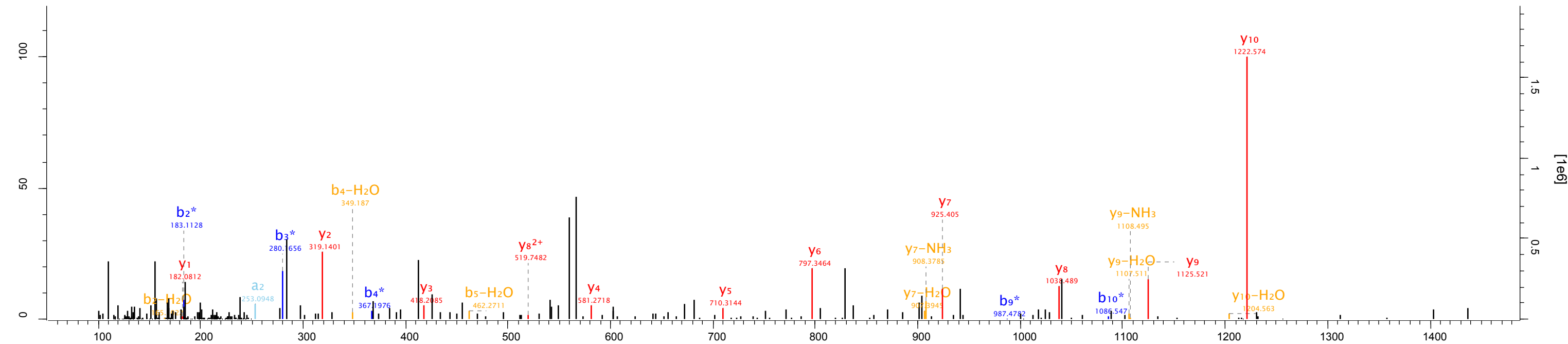
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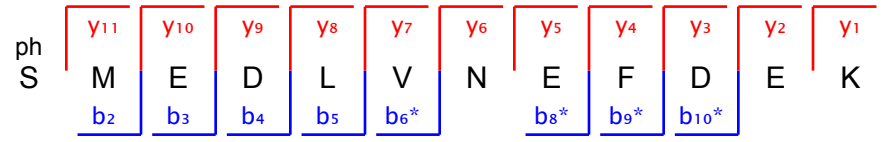
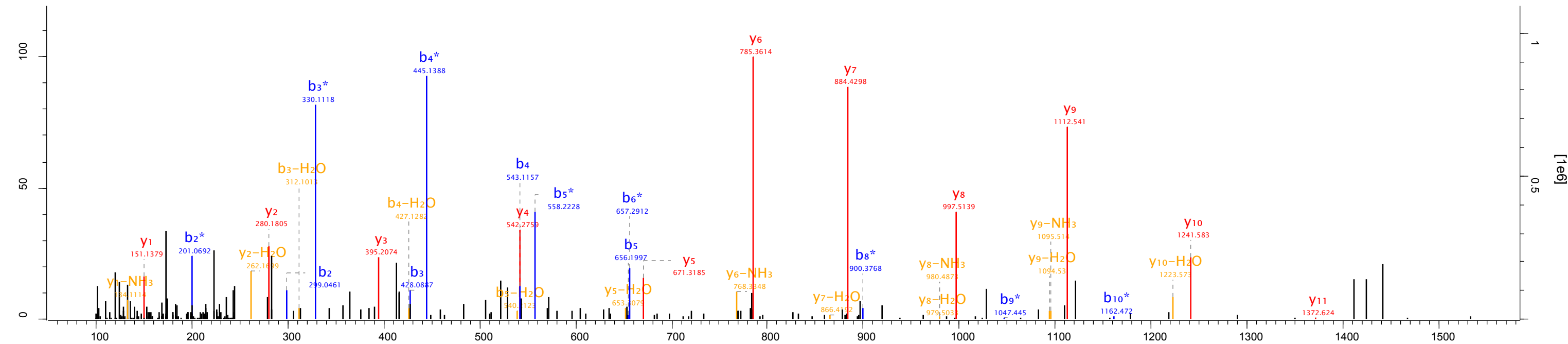
Raw file 20150814_A375SR_Phospho_BR2_05 Scan 18000 Method FTMS; HCD Score 97.22 m/z 658.31 Gene names ZFP36



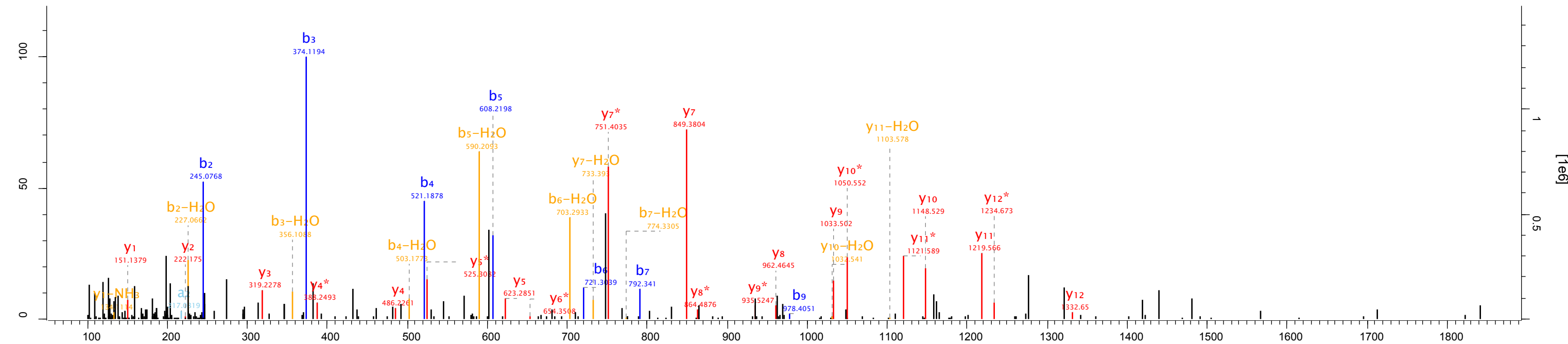
Raw file: 20150814_A375SR_Phospho_BR2_05
 Scan: 21490 Method: FTMS; HCD Score: 79.66 m/z: 751.83 Gene names: CDC14A



Raw file: 20150814_A375SR_Phospho_BR2_05
 Scan: 23290 Method: FTMS; HCD Score: 130.21 m/z: 770.32 Gene names: FEZ1



Raw file: 20150814_A375SR_Phospho_BR2_05
 Scan: 23880 Method: FTMS; HCD Score: 125.45 m/z: 971.45 Gene names: MAPK11P1L

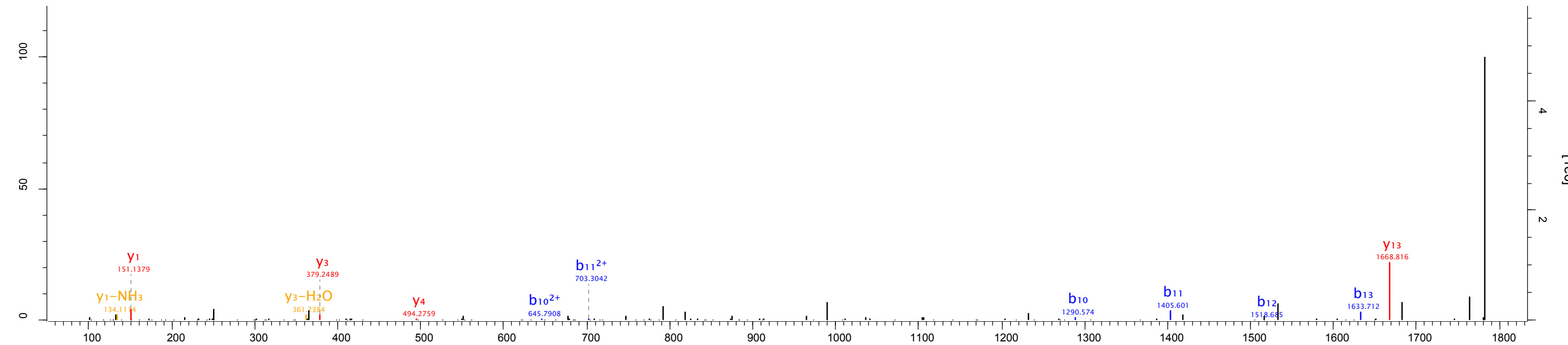


ac - S D E F S L A D A L P E H S P A K -

Fragmentation mapping (b and y ions):

- b2: D
- b3: E
- b4: F
- b5: S
- b6: L
- b7: A
- b9: S
- y1: K
- y2: A
- y3: P
- y4: S
- y5: H
- y6*: E
- y7: P
- y8: L
- y9: A
- y10: D
- y11: A
- y12: L

Raw file 20150814_A375SR_Phospho_BR2_05 Scan 3100 Method FTMS; HCD Score 62.16 m/z 892.43

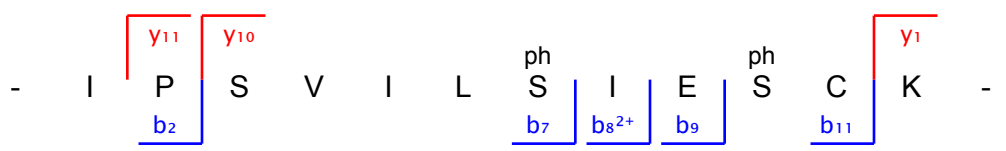
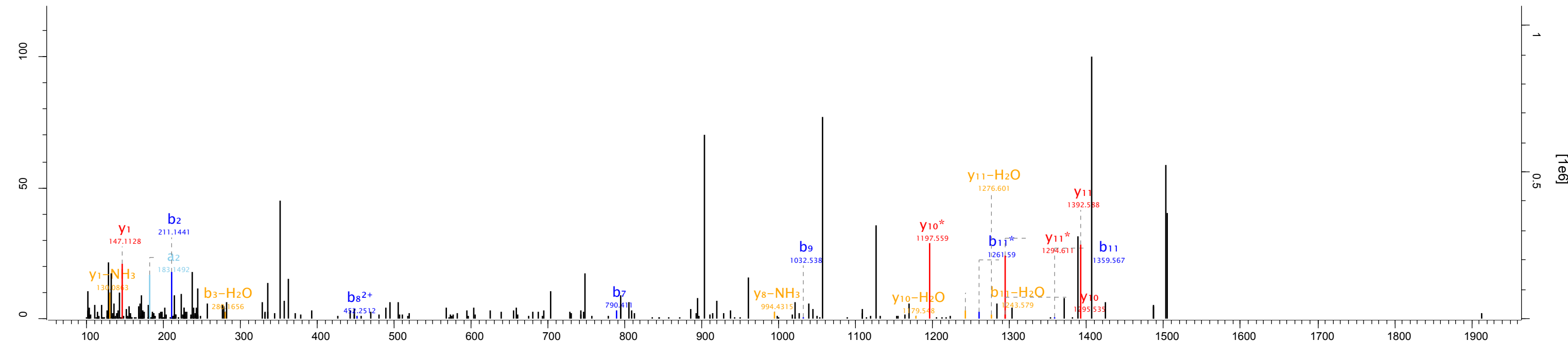


- D M S T E L E L L R D L D K -

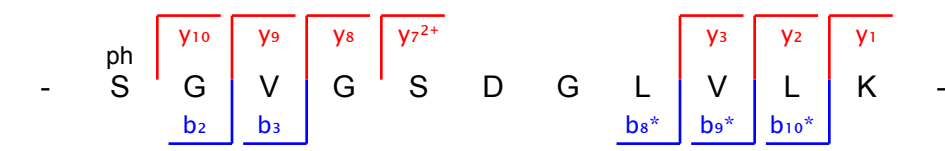
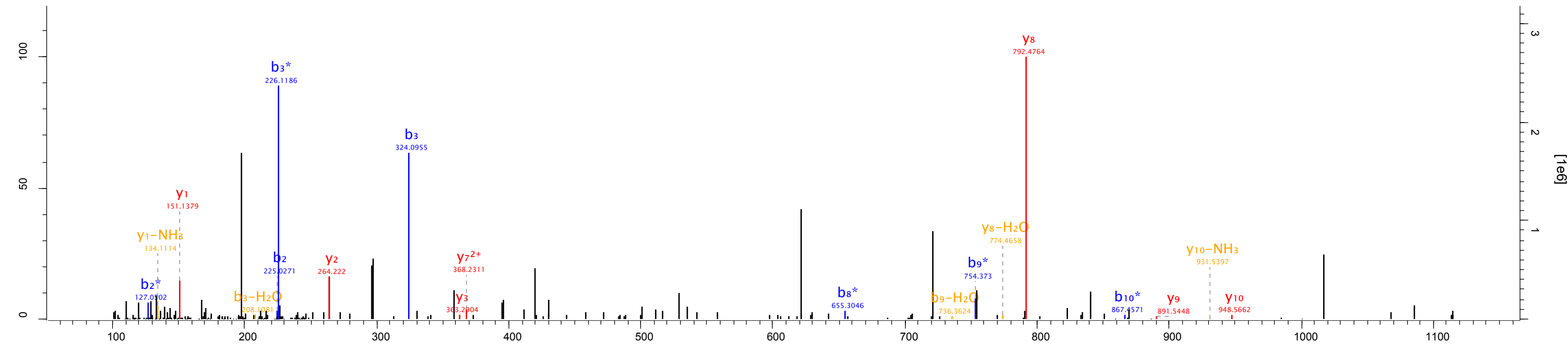
y13
ox
ph
y4
y3
y1

b10
b11
b12
b13

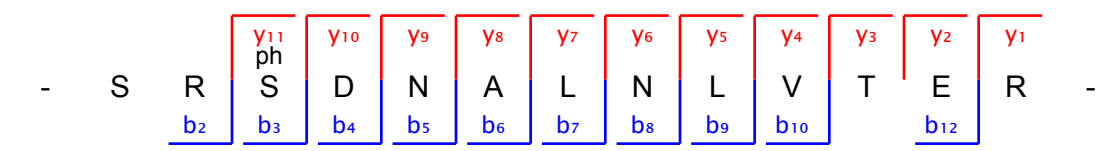
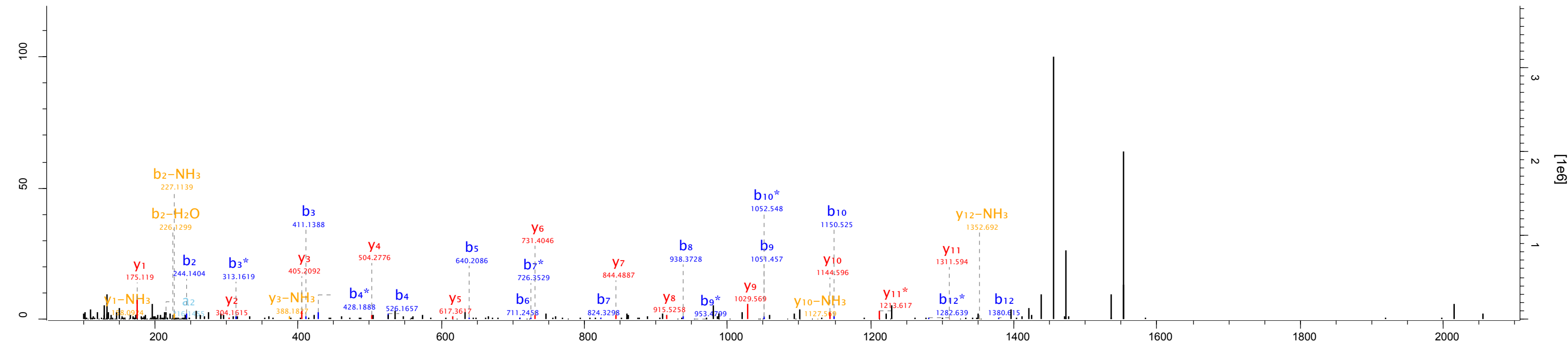
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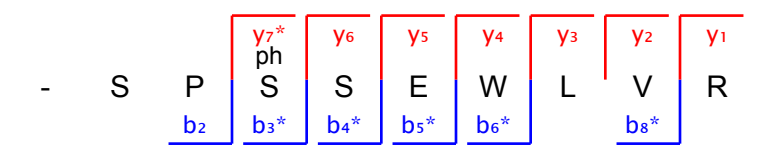
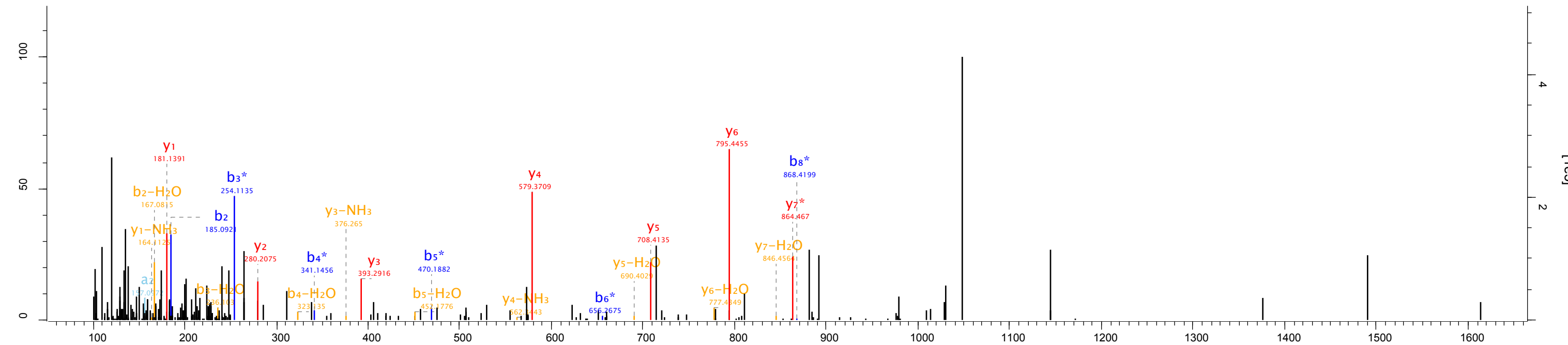
Raw file 20150814_A375SR_Phospho_BR2_06 Scan 12910 Method FTMS; HCD Score 53.05 m/z 558.29



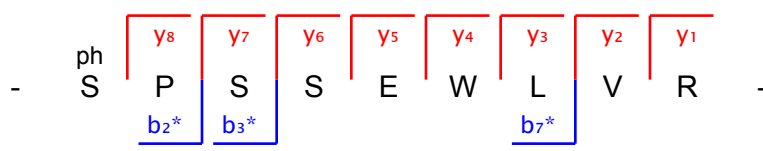
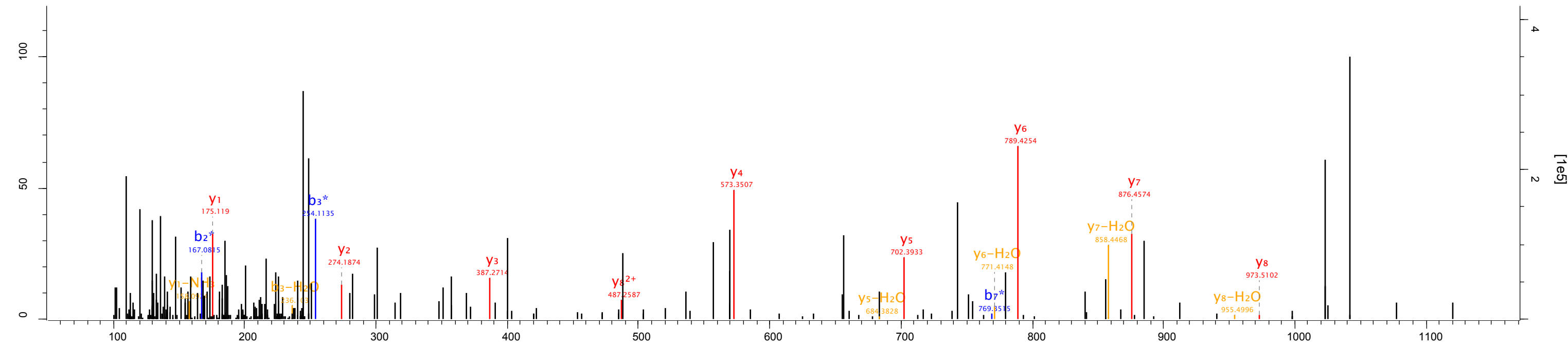
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 Scan: 15260 Method: FTMS; HCD Score: 72.56 m/z: 778.37 Gene names: PRICKLE1

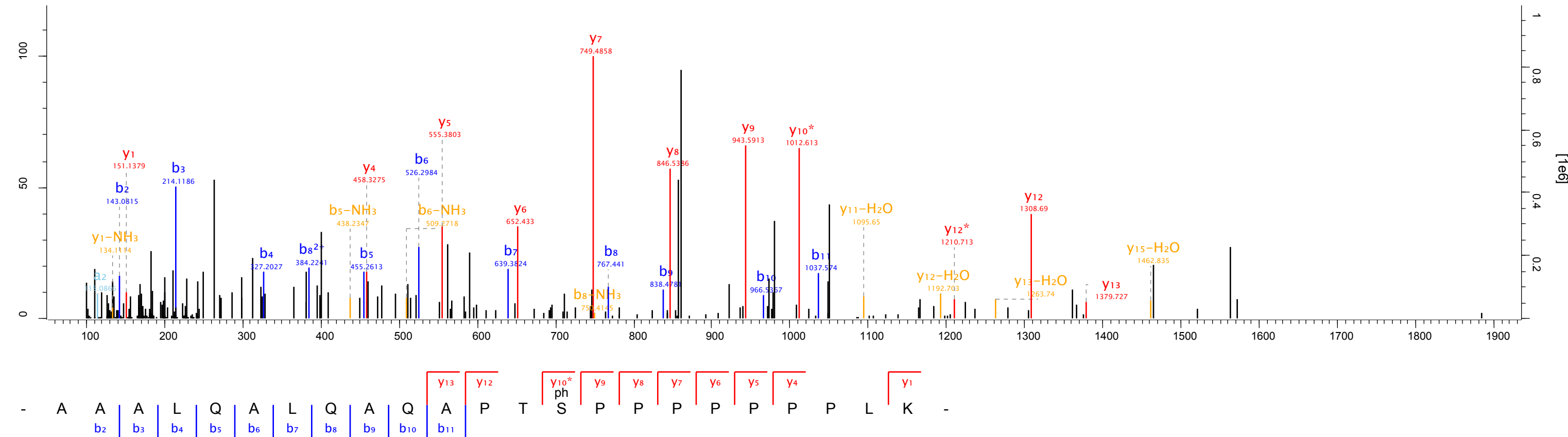


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 Scan: 17830 Method: FTMS; HCD Score: 73.95 m/z: 573.77 Gene names: GPATCH2L

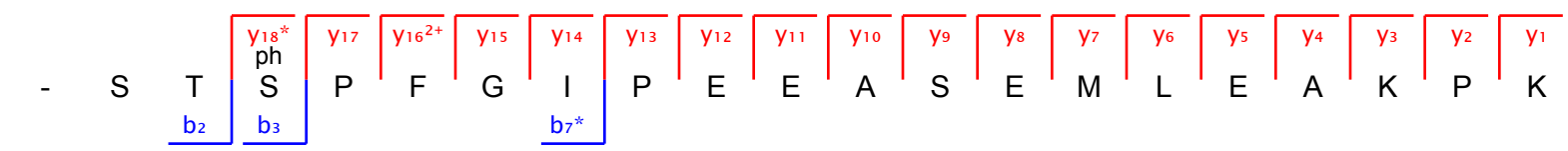
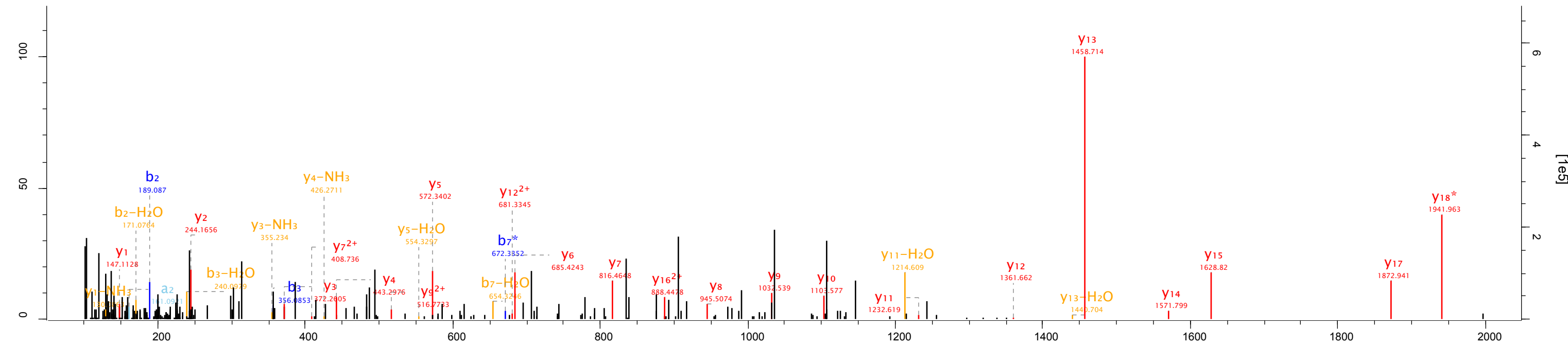


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 Scan: 17840 Method: FTMS; HCD Score: 49.06 m/z: 570.76 Gene names: GPATCH2L



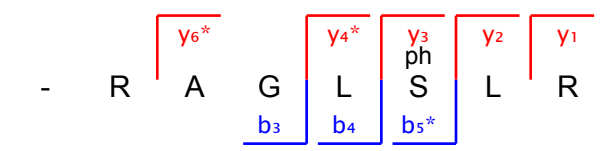
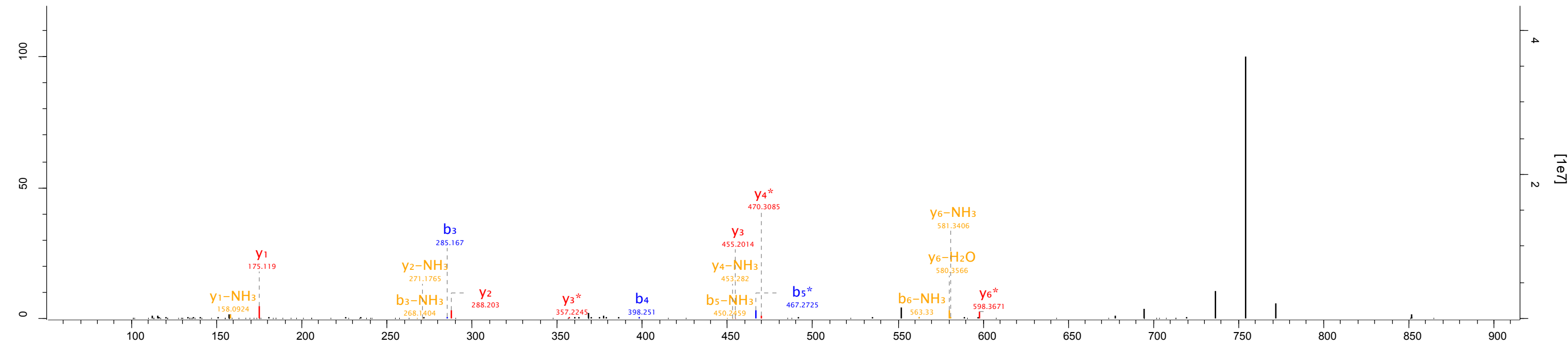


Raw file: 20150814_A375SR_Phospho_BR2_06
 Scan: 26280 Method: FTMS; HCD Score: 60.32 m/z: 743.68 Gene names: GPRASP2

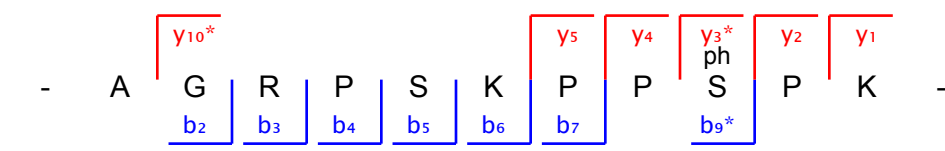
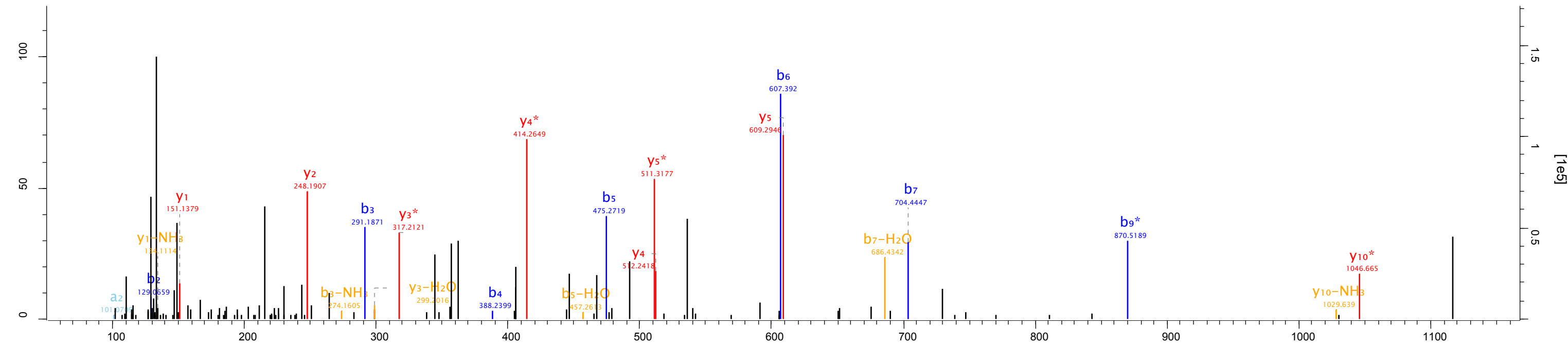


Raw file
20150814_A375SR_Phospho_BR2_06

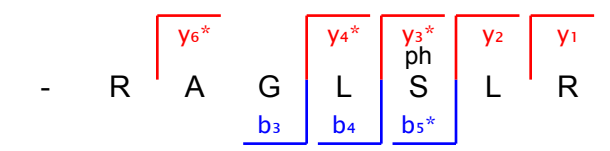
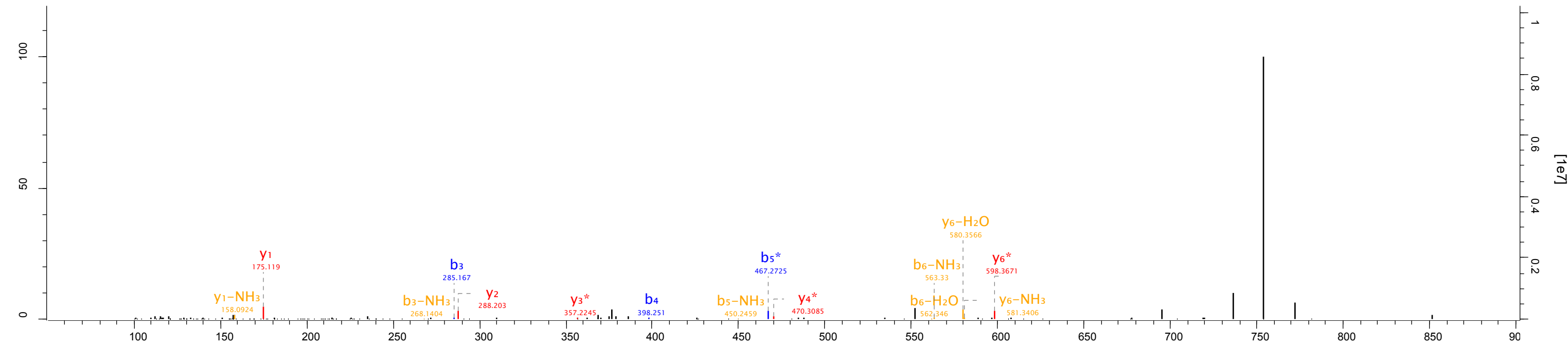
Scan 6330 Method FTMS; HCD Score 60.4 m/z 426.73



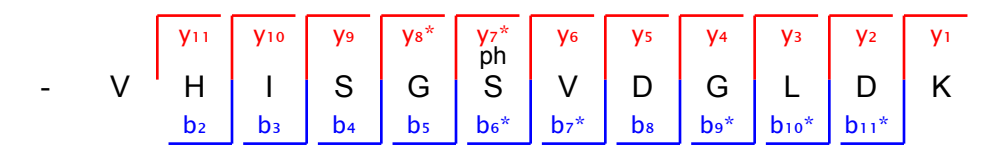
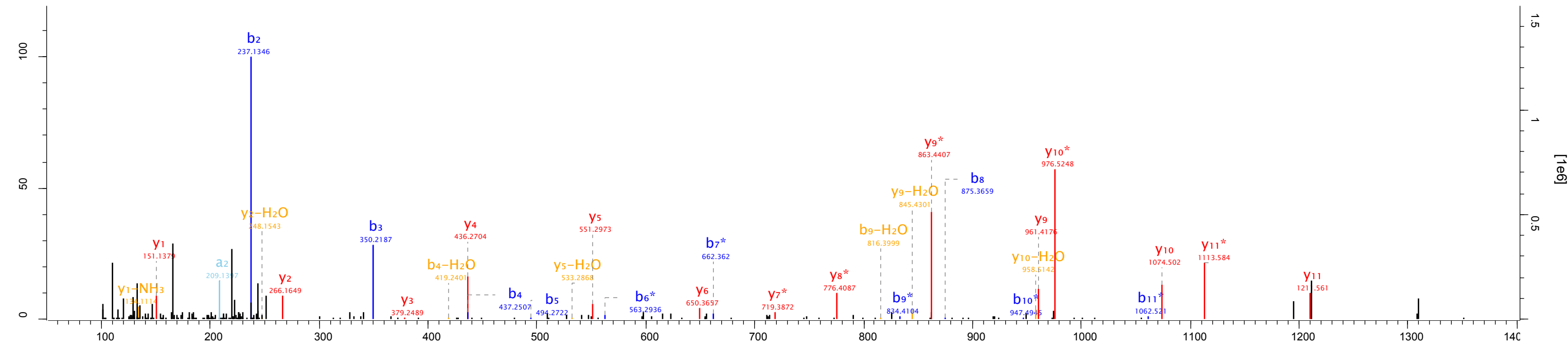
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 Scan: 1880 Method: FTMS; HCD Score: 71.28 m/z: 405.9 Gene names: TBC1D14



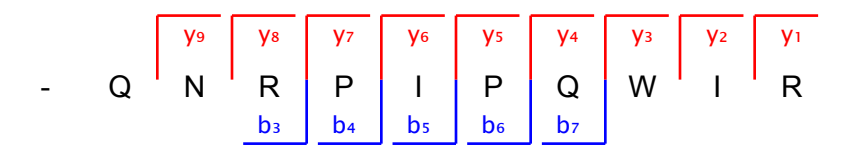
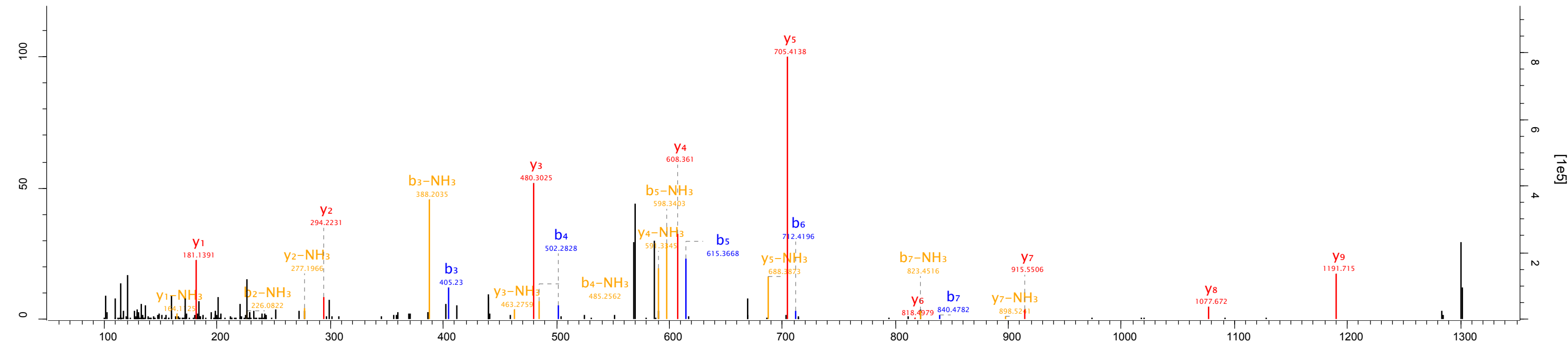
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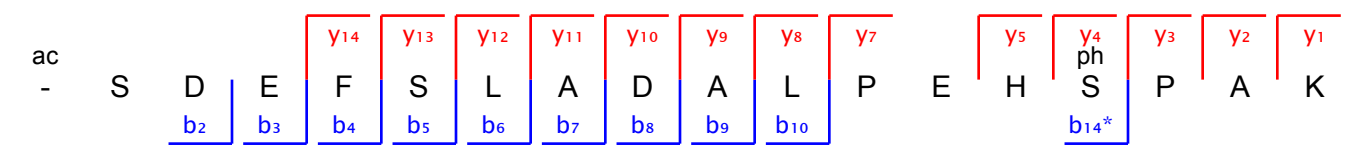
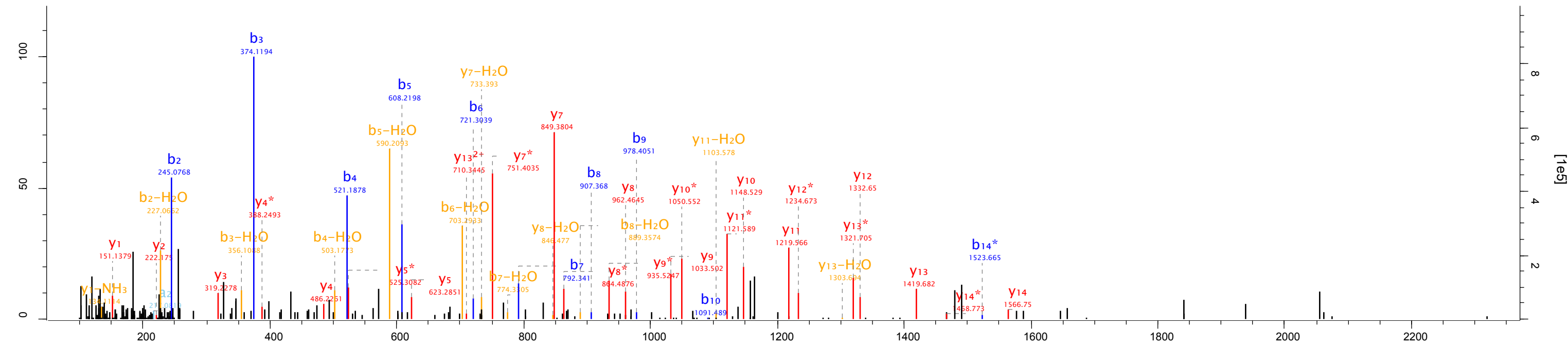
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 Scan: 12010 Method: FTMS; HCD Score: 122.08 m/z: 655.82 Gene names: PHACTR2



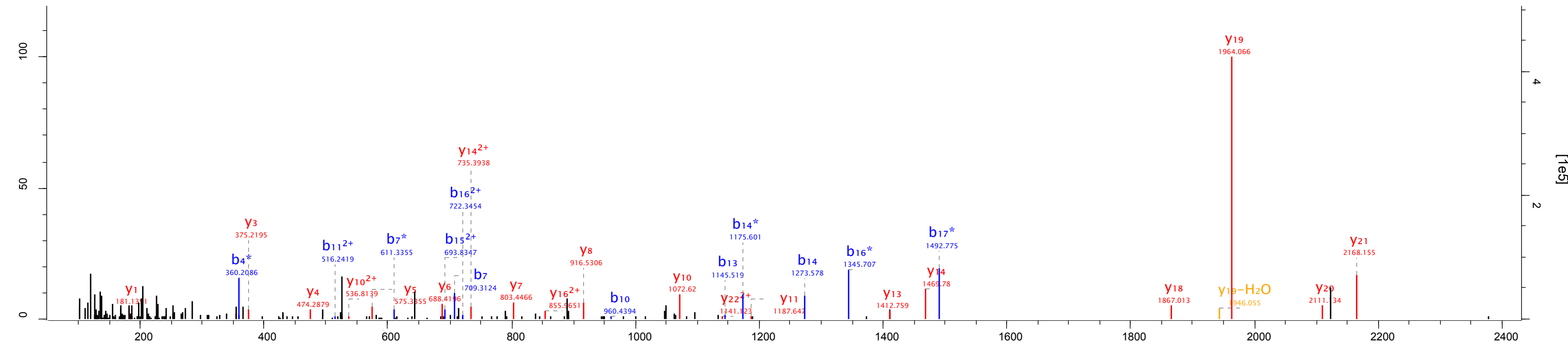
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 Scan: 14270 Method: FTMS; HCD Score: 148.94 m/z: 440.6 Gene names: RPL39P5;RPL39



Raw file
 20150814_A375SR_Phospho_BR2_08
 Scan 24010 Method FTMS; HCD Score 184.68 m/z 970.94 Gene names MAPK11P1L



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 Scan: 27400 Method: FTMS; HCD Score: 58.6 m/z: 889.46 Gene names: SOBP

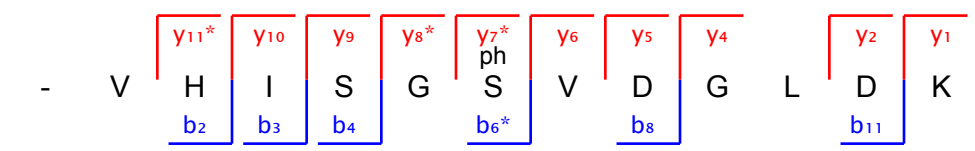
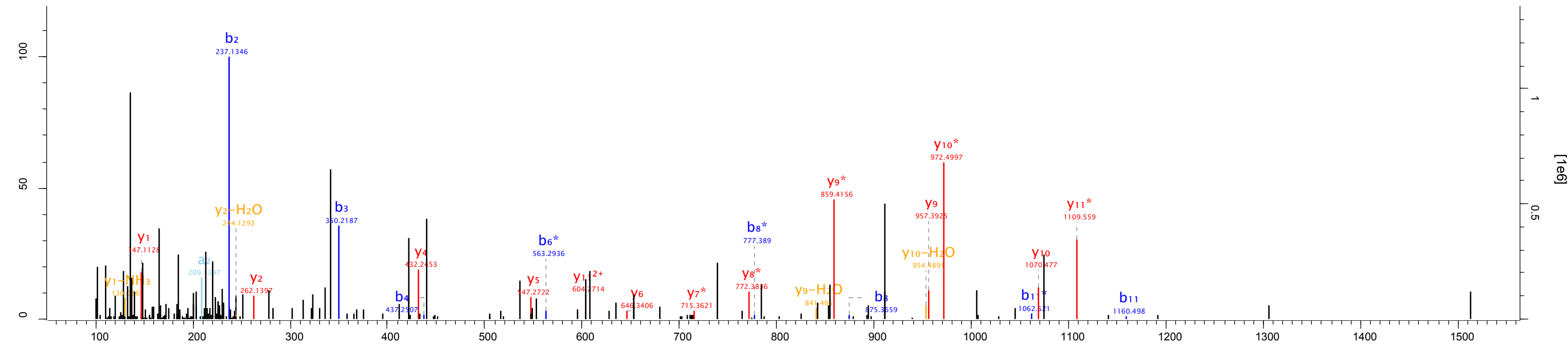


Sequence: - R A G S P P G P P G A G G Q L G F P G V L Q G P Q D G V I D L T V G H R -

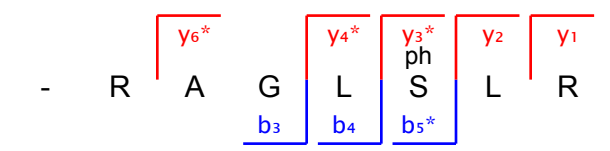
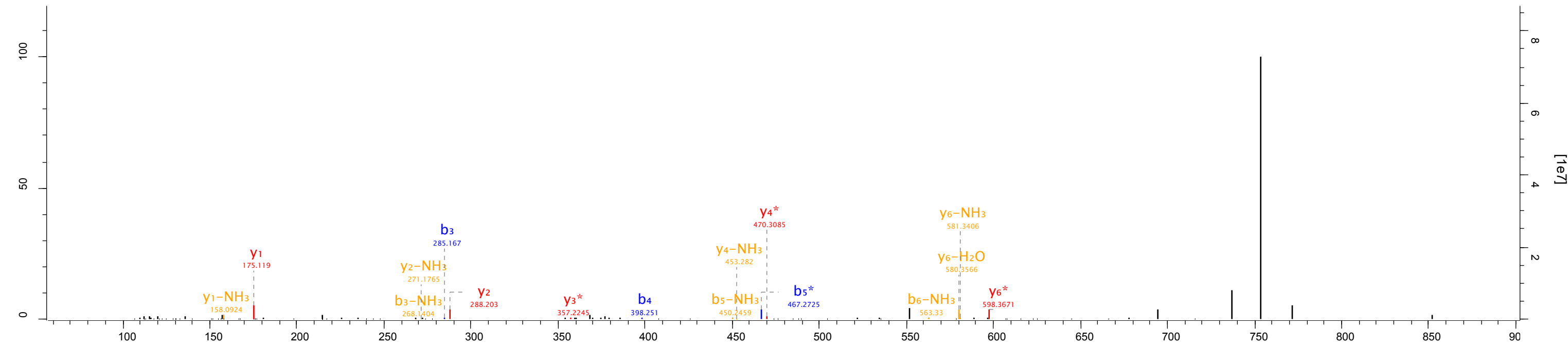
Fragmentation sites (b and y ions) are indicated by brackets below the sequence:

- b4* (under S)
- b7 (under G)
- b10 (under G)
- b11²⁺ (under A)
- b13 (under G)
- b14 (under Q)
- b15²⁺ (under L)
- b16* (under G)
- b17* (under F)
- y1 (under R)
- y3 (under G)
- y4 (under V)
- y5 (under T)
- y6 (under L)
- y7 (under D)
- y8 (under I)
- y10 (under G)
- y11 (under D)
- y13 (under P)
- y14 (under G)
- y16²⁺ (under L)
- y18 (under G)
- y19 (under P)
- y20 (under F)
- y21 (under G)
- y22²⁺ (under L)

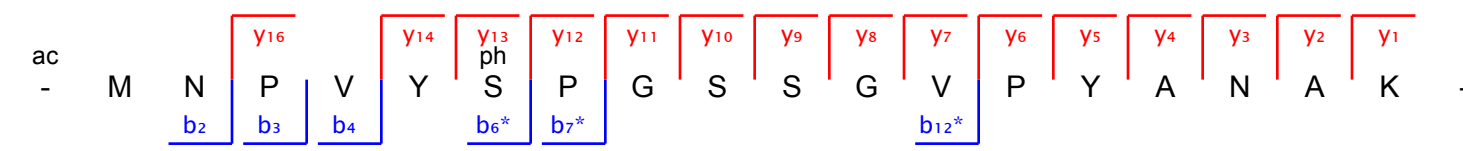
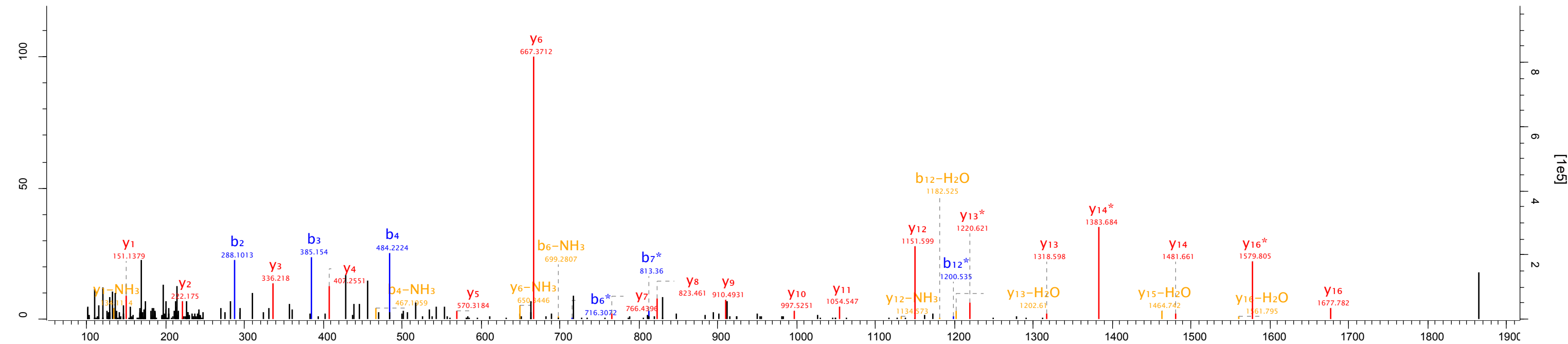
Raw file 20150814_A375SR_Phospho_BR2_09 Scan 11870 Method FTMS; HCD Score 63.03 m/z 653.81 Gene names PHACTR2



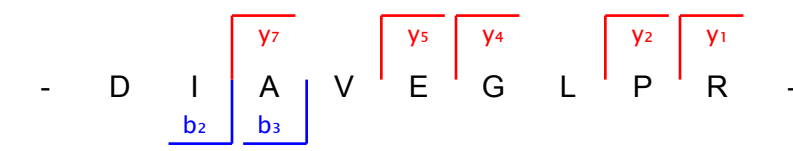
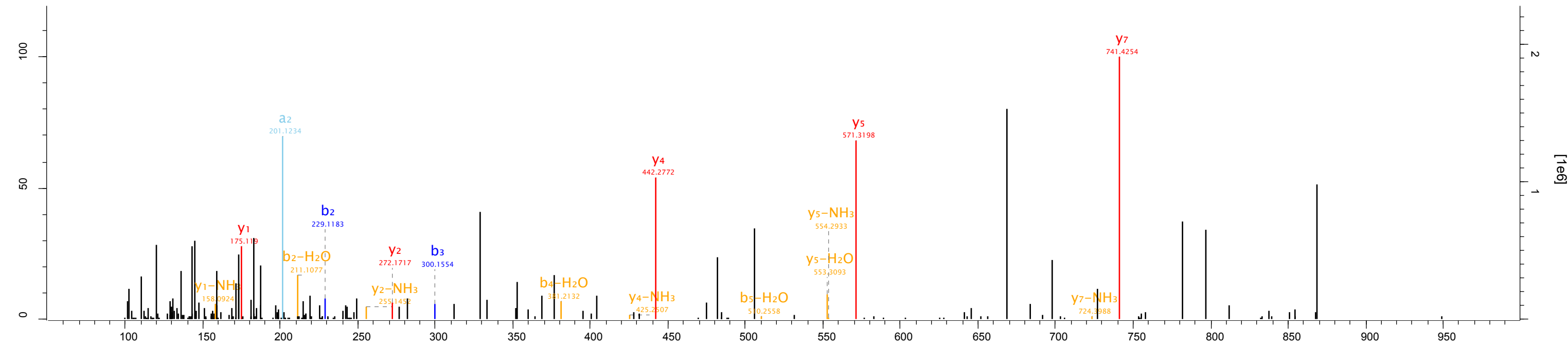
Raw file 20150814_A375SR_Phospho_BR2_09 Scan 6260 Method FTMS; HCD Score 62.56 m/z 426.73



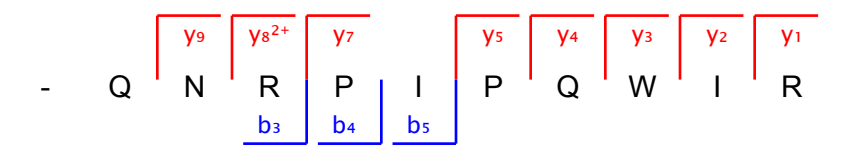
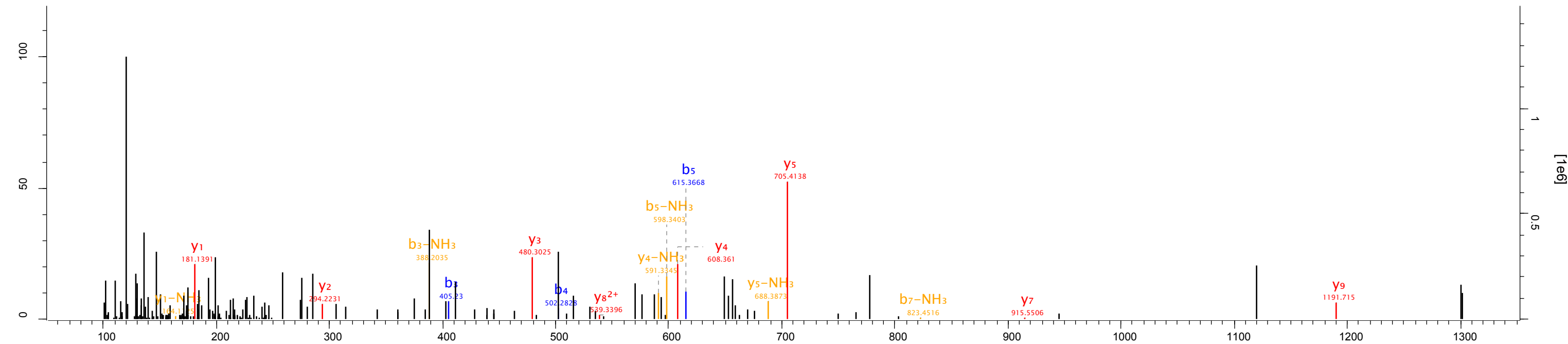
Raw file
 20150814_A375SR_Phospho_BR2_10
 Scan 20980 Method FTMS; HCD Score 92.01 m/z 983.44 Gene names FAM168B



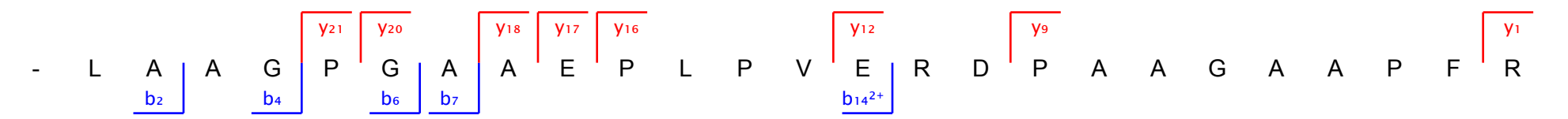
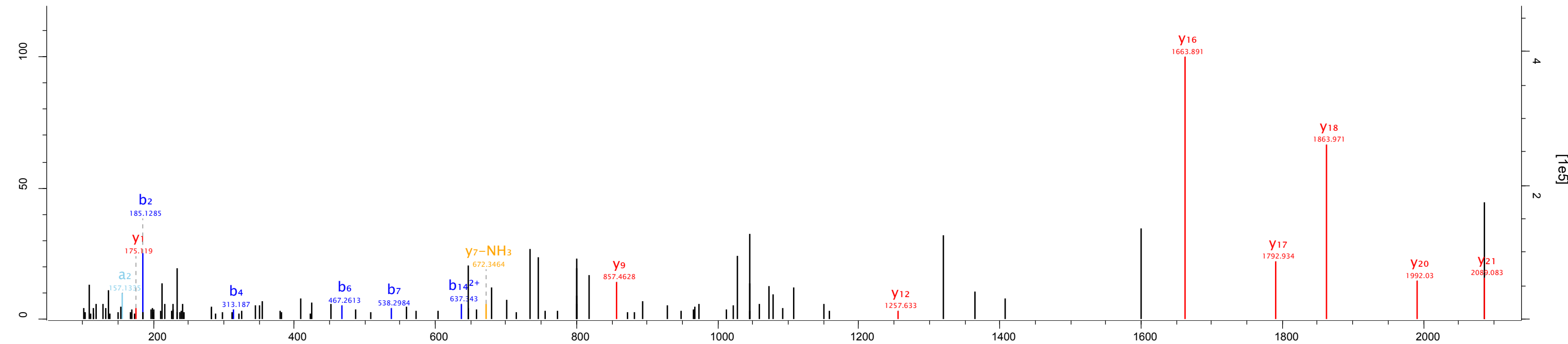
Raw file 20150818_A375SR-Proteome_BR1 Scan 38280 Method FTMS; HCD Score 39.62 m/z 485.27



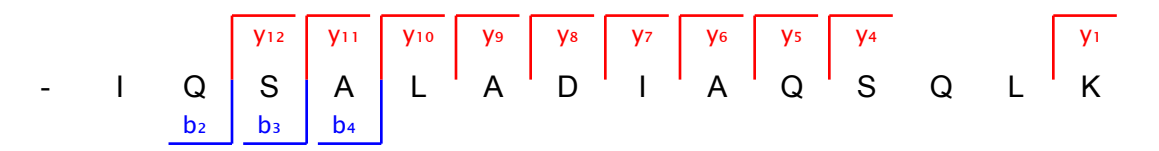
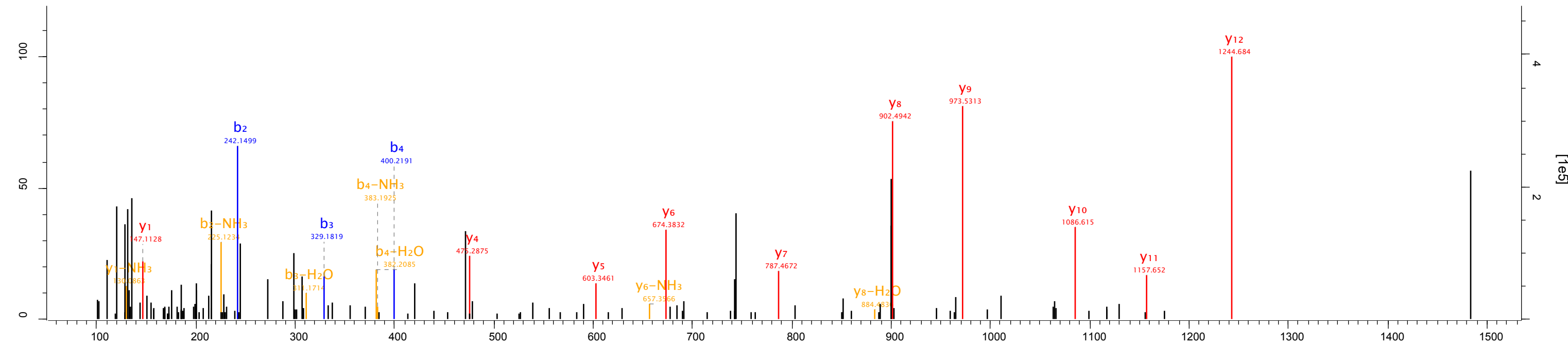
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 Scan: 38430 Method: FTMS; HCD Score: 70.91 m/z: 440.6 Gene names: RPL39P5;RPL39



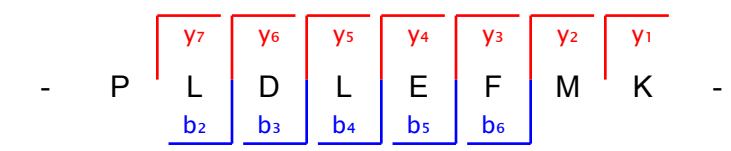
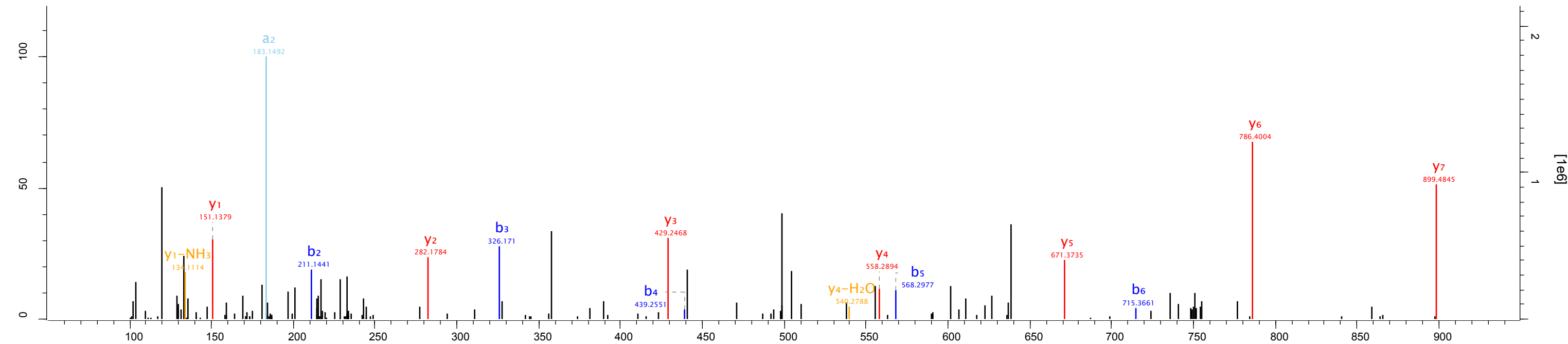
Raw file Scan Method Score m/z Gene names
 20150818_A375SR-Proteome_BR1 64860 FTMS; HCD 26.5 801.64 ZNF511



Raw file 20150818_A375SR-Proteome_BR1 Scan 67220 Method FTMS; HCD Score 82.65 m/z 743.42 Gene names MED21

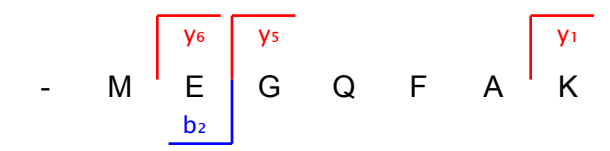
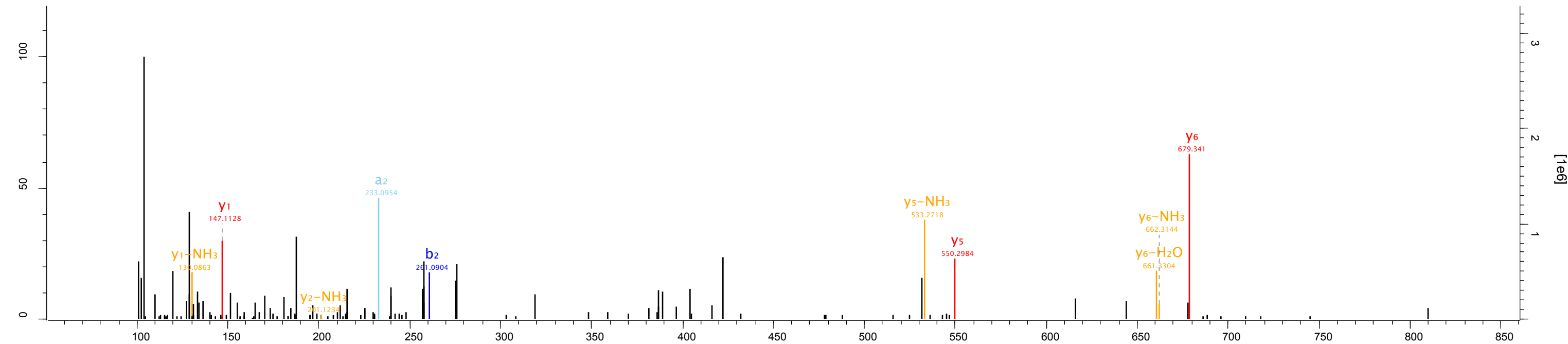


Raw file: 20150818_A375SR-Proteome_BR1
 Scan: 68150 Method: FTMS; HCD Score: 67.51 m/z: 498.77 Gene names: SEPT3

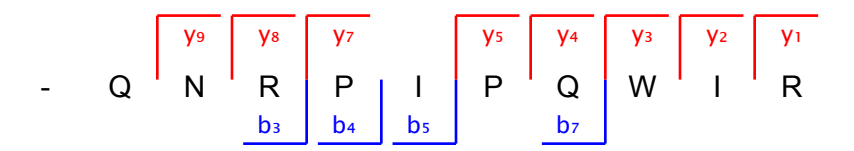
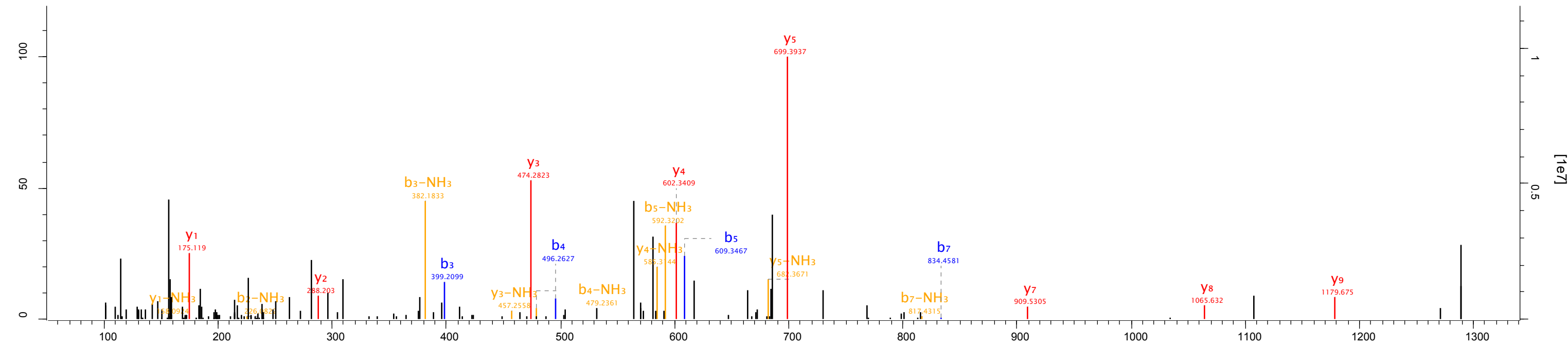


Raw file
20150818_A375SR-Proteome_BR1

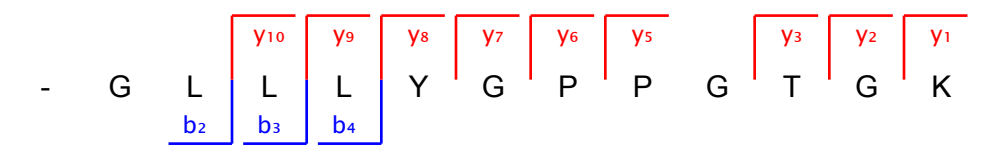
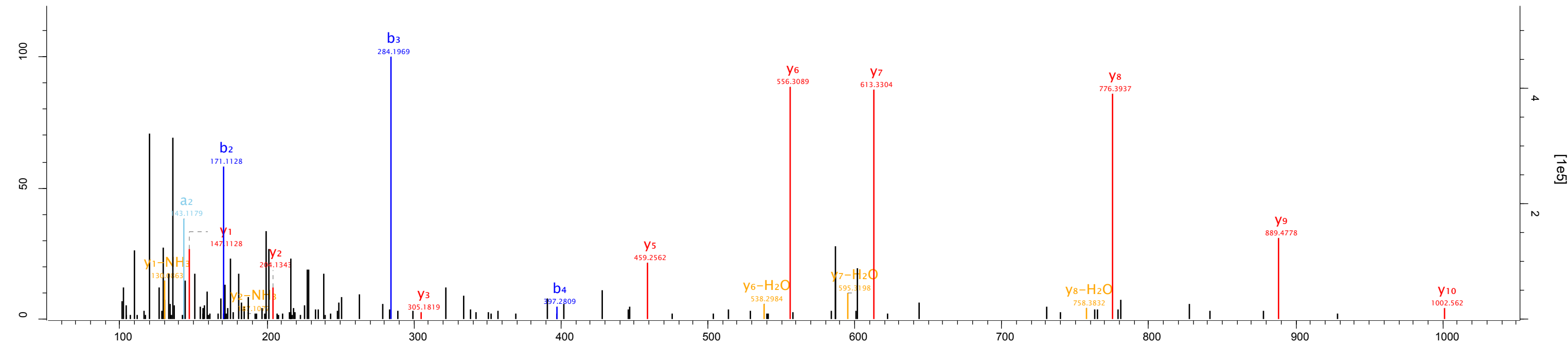
Scan	Method	Score	m/z
7190	FTMS; HCD	64.78	405.69



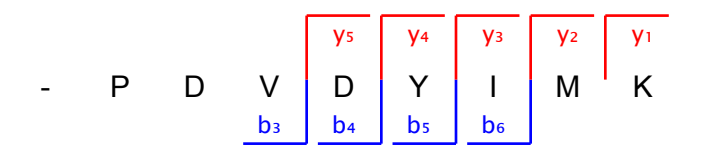
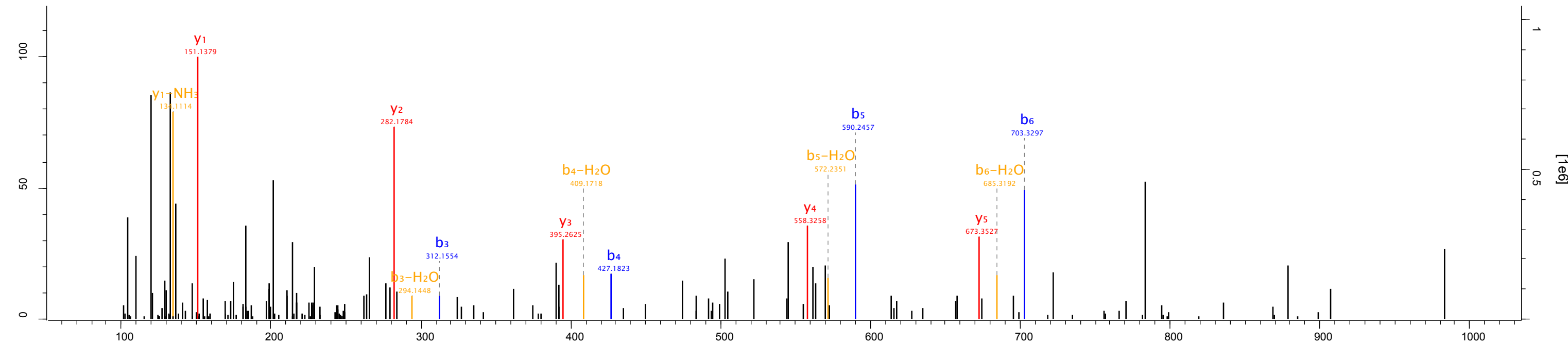
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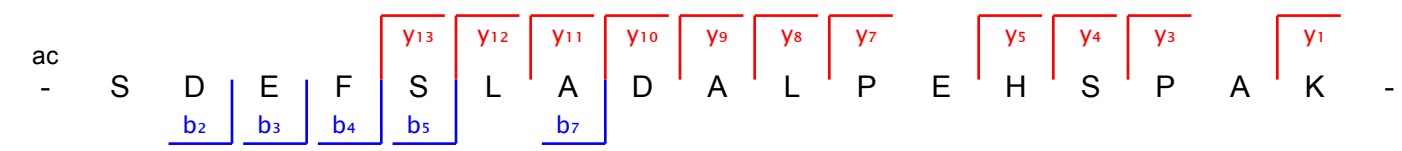
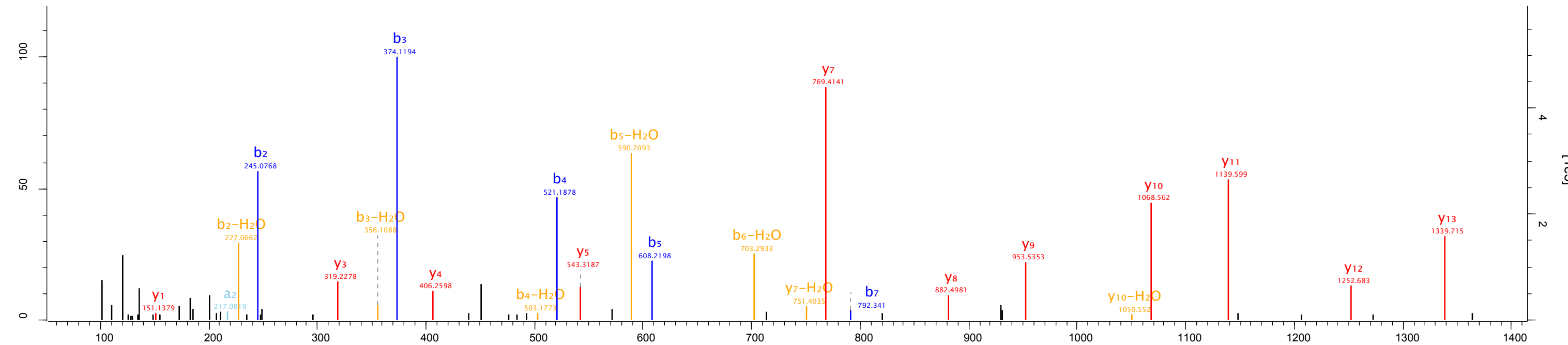
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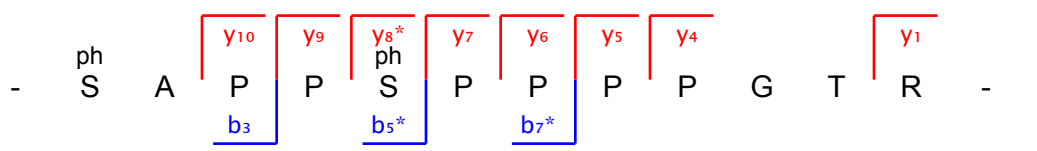
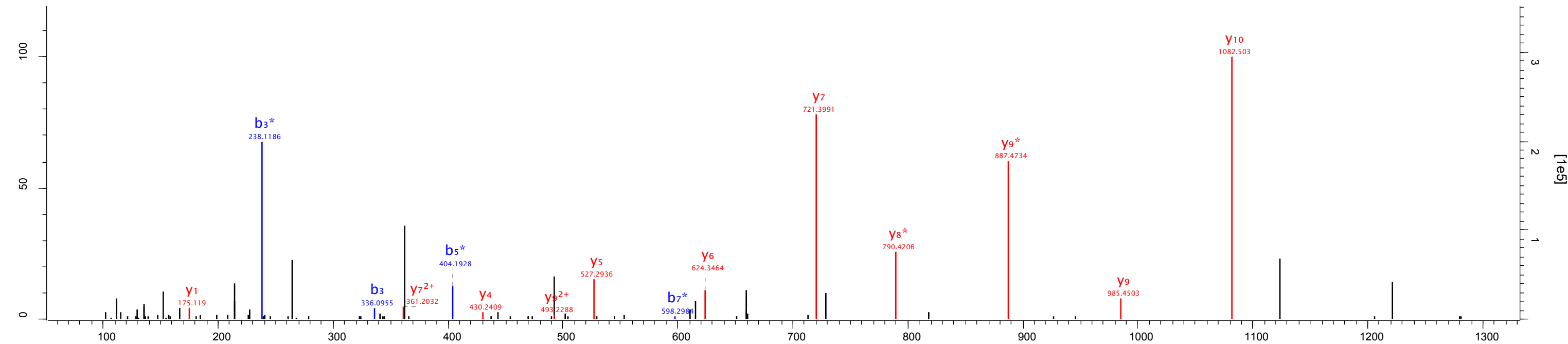
Raw file Scan Method Score m/z
20150818_A375SR-Proteome_BR2 68460 FTMS; HCD 83.21 492.75



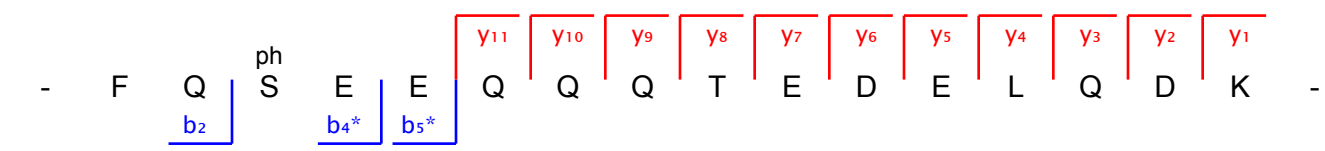
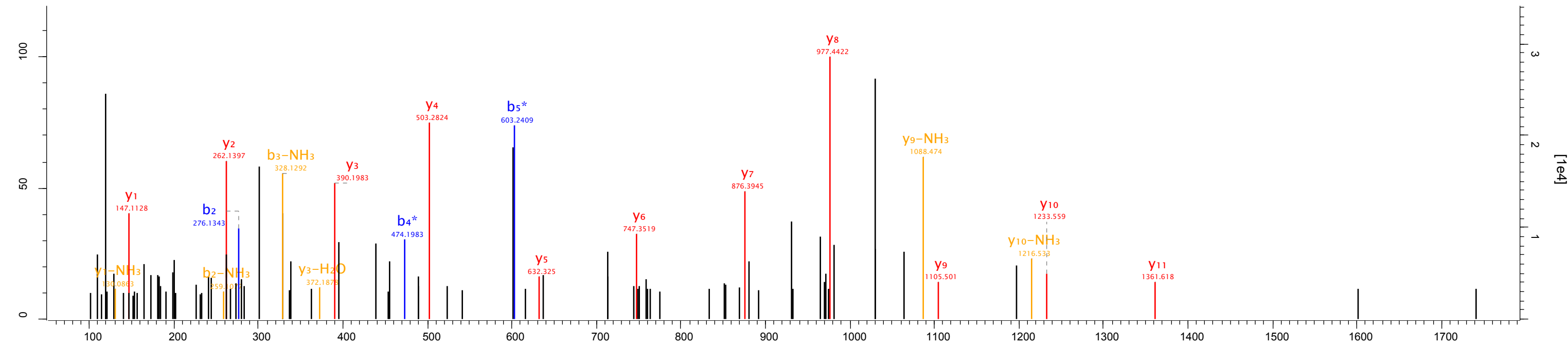
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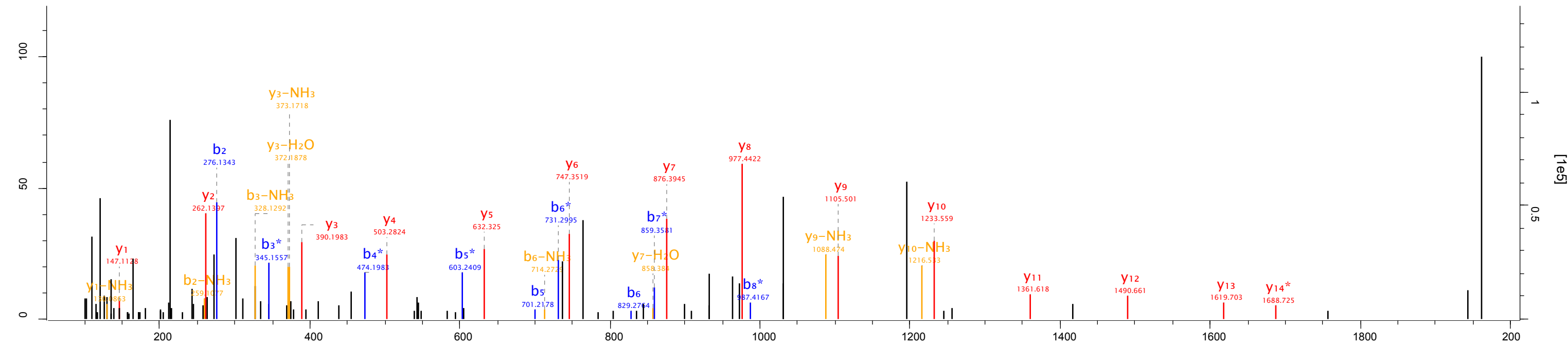
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 Scan: 5260 Method: FTMS; HCD Score: 40.8 m/z: 660.77 Gene names: GPSM3



Raw file: 20150822_A375SR_Phospho_BR3_03
 Scan: 11060 Method: FTMS; HCD Score: 60.62 m/z: 1031.41



Raw file: 20150822_A375SR_Phospho_BR3_05
 Scan: 12390 Method: FTMS; HCD Score: 101.89 m/z: 1031.42

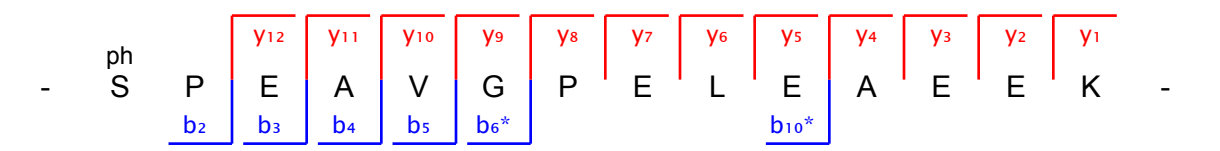
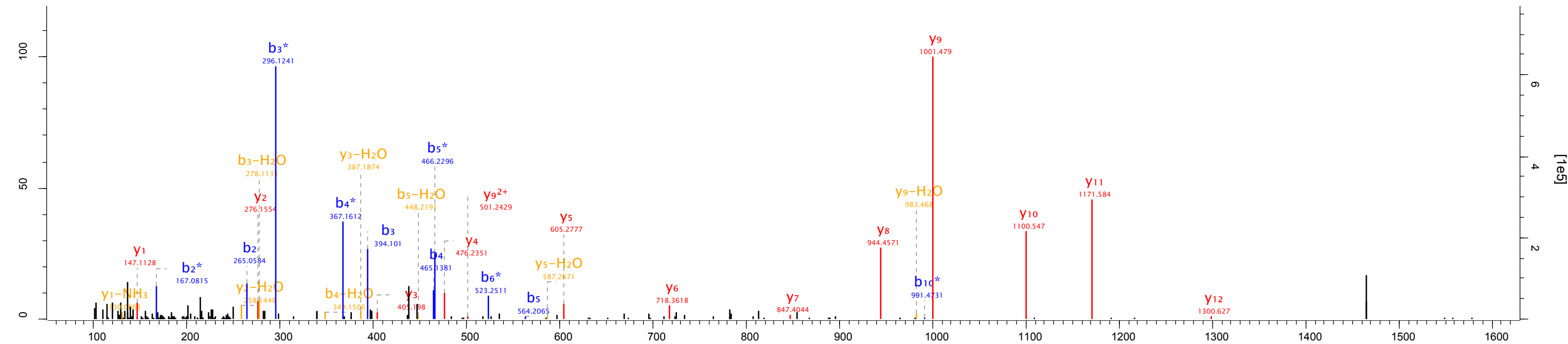


Peptide sequence: - F Q S E E Q Q Q T E D E L Q D K -

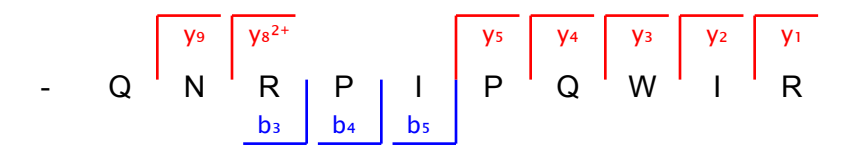
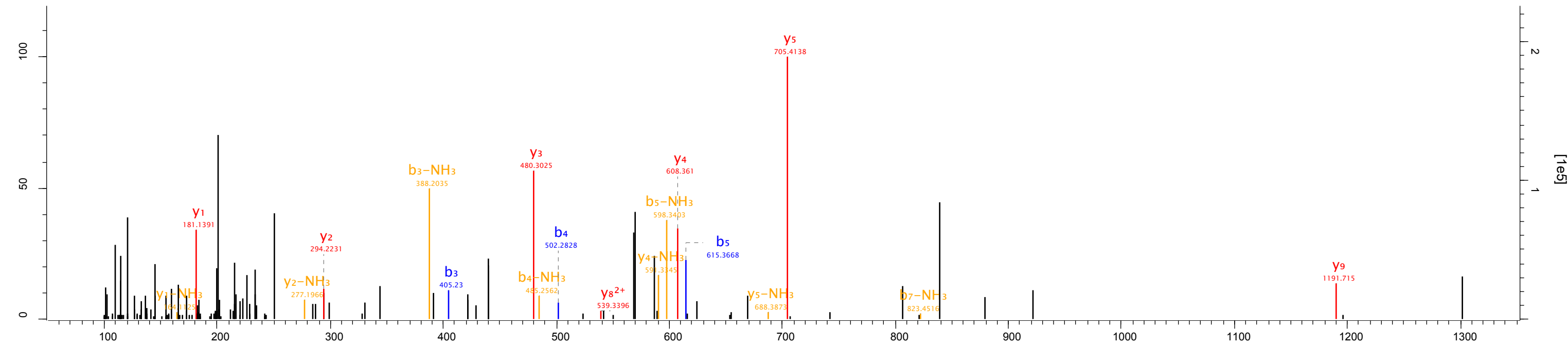
Fragmentation sites are indicated by boxes below the sequence:

- Red boxes (y-series): y14* (S), y13 (E), y12 (E), y11 (Q), y10 (Q), y9 (Q), y8 (T), y7 (E), y6 (D), y5 (E), y4 (L), y3 (Q), y2 (D), y1 (K).
- Blue boxes (b-series): b2 (Q), b3* (S), b4* (E), b5 (E), b6 (Q), b7* (Q), b8* (Q).

Raw file 20150822_A375SR_Phospho_BR3_06 Scan 13880 Method FTMS; HCD Score 113.88 m/z 783.35 Gene names PWWP2A

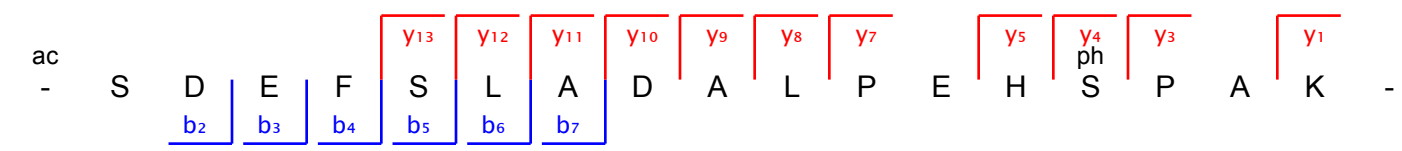
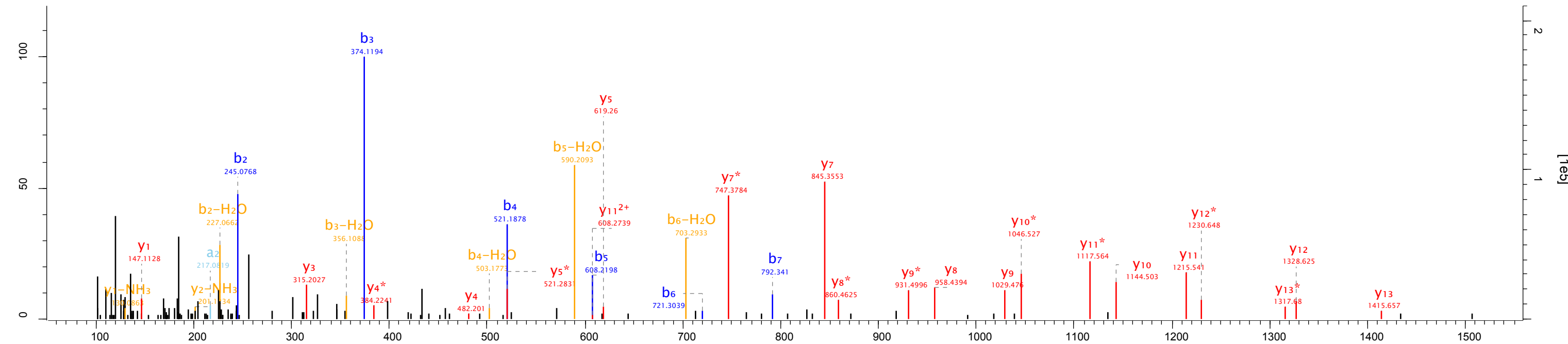


Raw file: 20150822_A375SR_Phospho_BR3_06
 Scan: 14710 Method: FTMS; HCD Score: 66.96 m/z: 440.6 Gene names: RPL39P5;RPL39

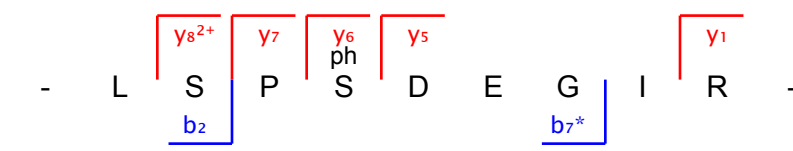
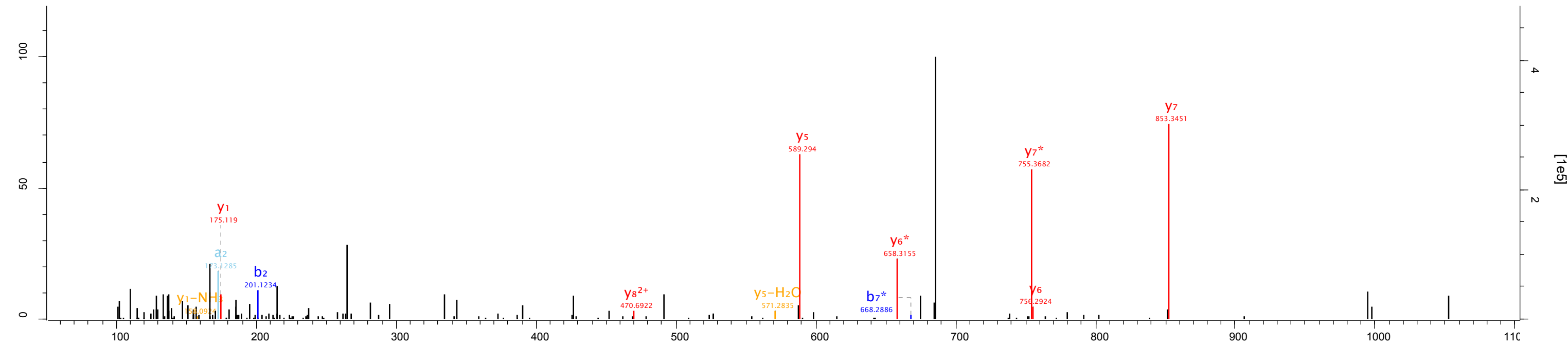


Raw file
20150822_A375SR_Phospho_BR3_06

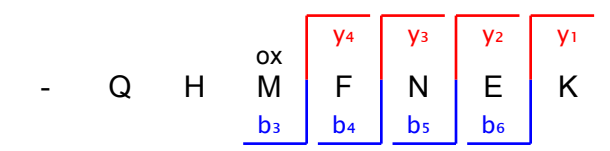
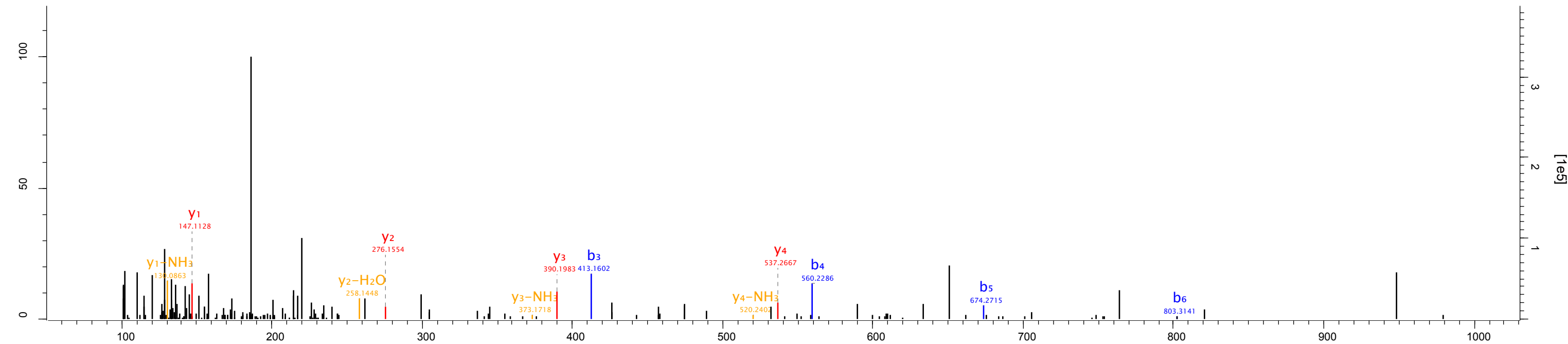
Scan 24070 Method FTMS; HCD Score 131.82 m/z 968.42 Gene names MAPK11P1L



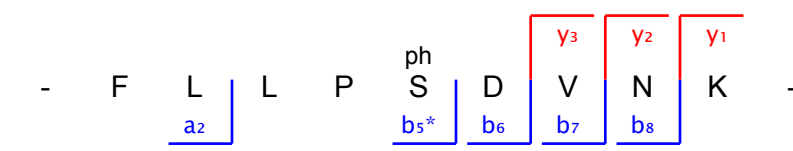
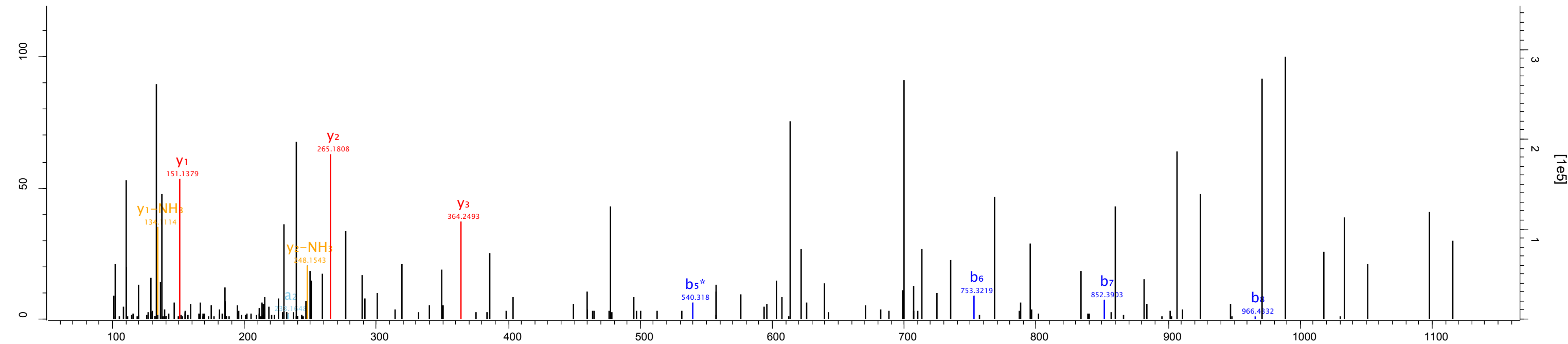
Raw file Scan Method Score m/z
 20150822_A375SR_Phospho_BR3_06 4990 FTMS; HCD 44.61 527.23



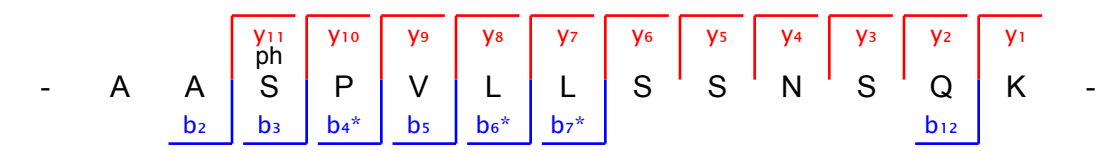
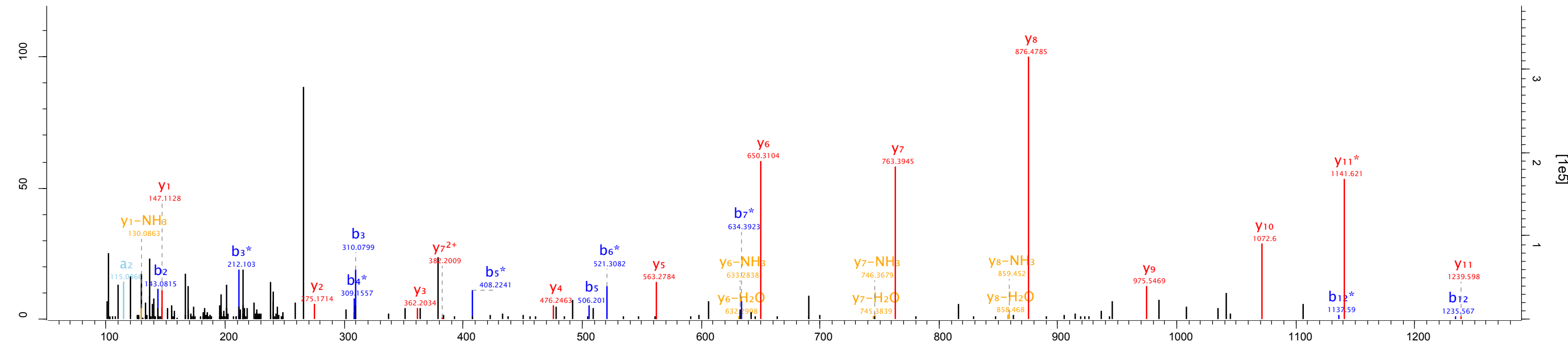
Raw file 20150822_A375SR_Phospho_BR3_07 Scan 10230 Method FTMS; HCD Score 43.22 m/z 475.21 Gene names GPR64



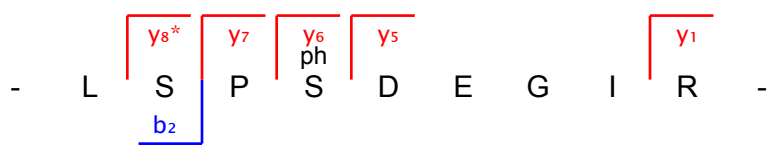
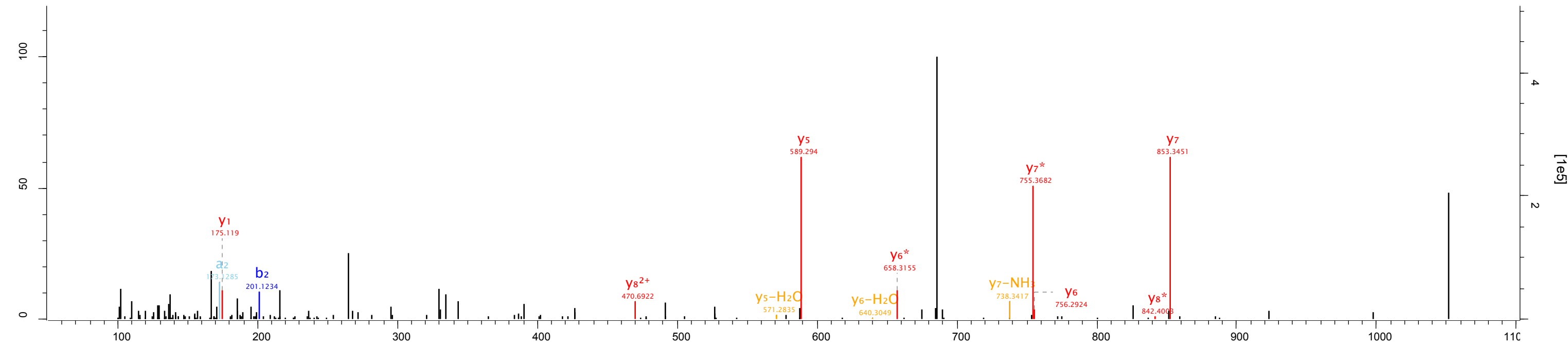
Raw file 20150822_A375SR_Phospho_BR3_08 Scan 10090 Method FTMS; HCD Score 60.12 m/z 558.79



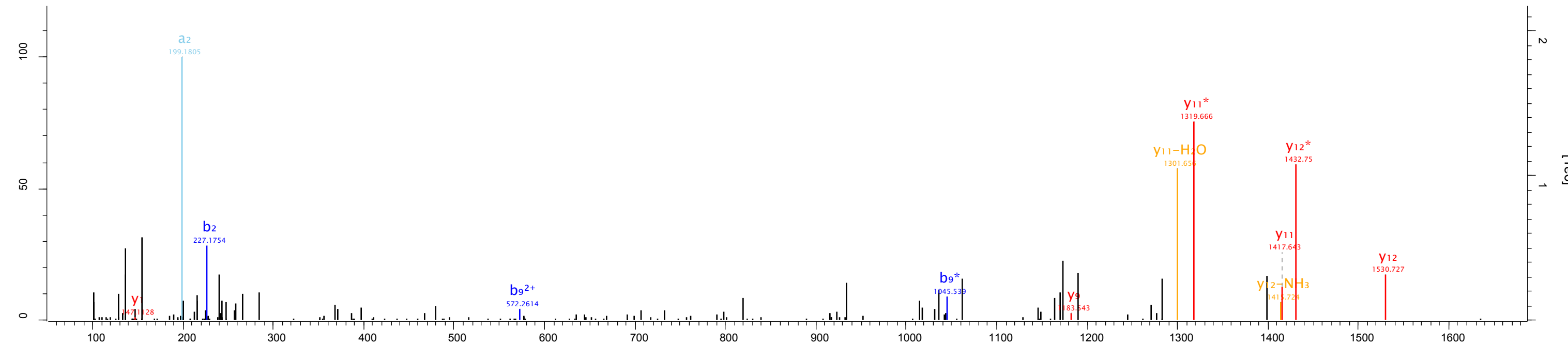
Raw file 20150822_A375SR_Phospho_BR3_08 Scan 11790 Method FTMS; HCD Score 93.77 m/z 691.34 Gene names ELK3



Raw file: 20150822_A375SR_Phospho_BR3_09
 Scan: 5280 Method: FTMS; HCD Score: 53.01 m/z: 527.23



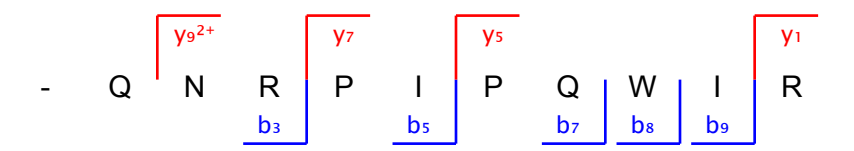
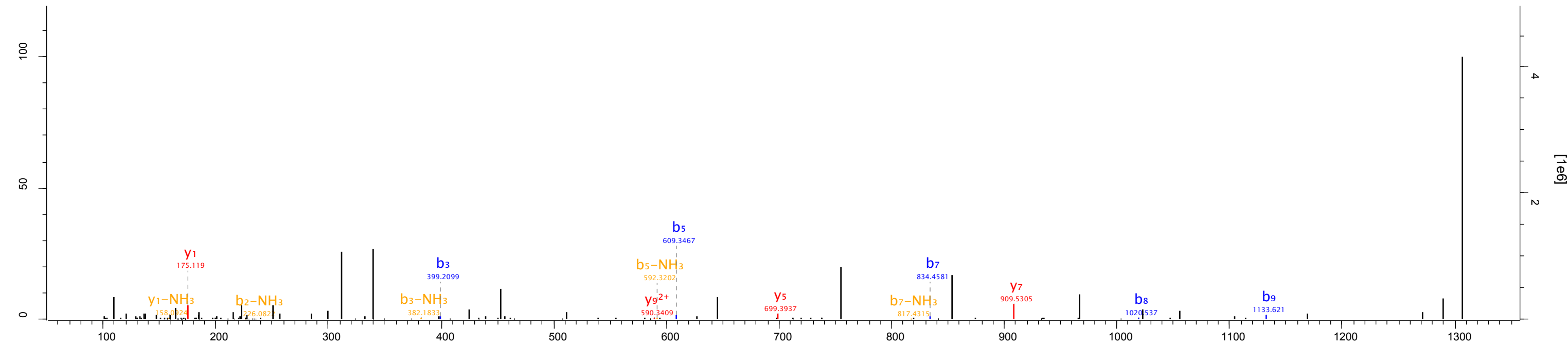
Raw file 20150822_A375SR_Phospho_BR3_09 Scan 7060 Method FTMS; HCD Score 52.53 m/z 548.61



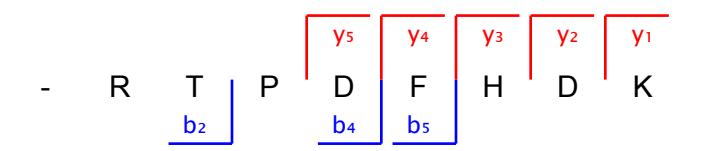
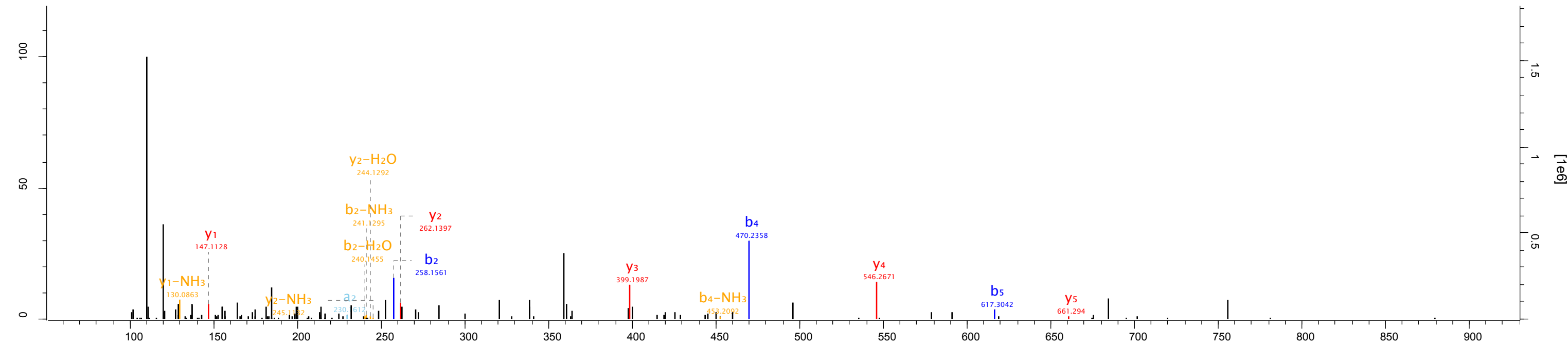
- I L S F E L C S L E K P K -

Fragmentation labels: y_{12} , y_{11} , y_9 , y_1 , b_2 , b_9^*

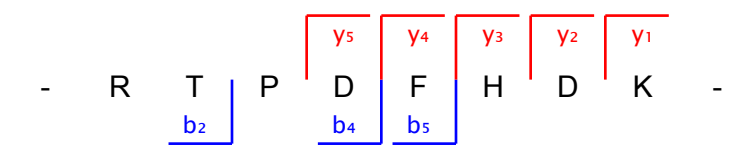
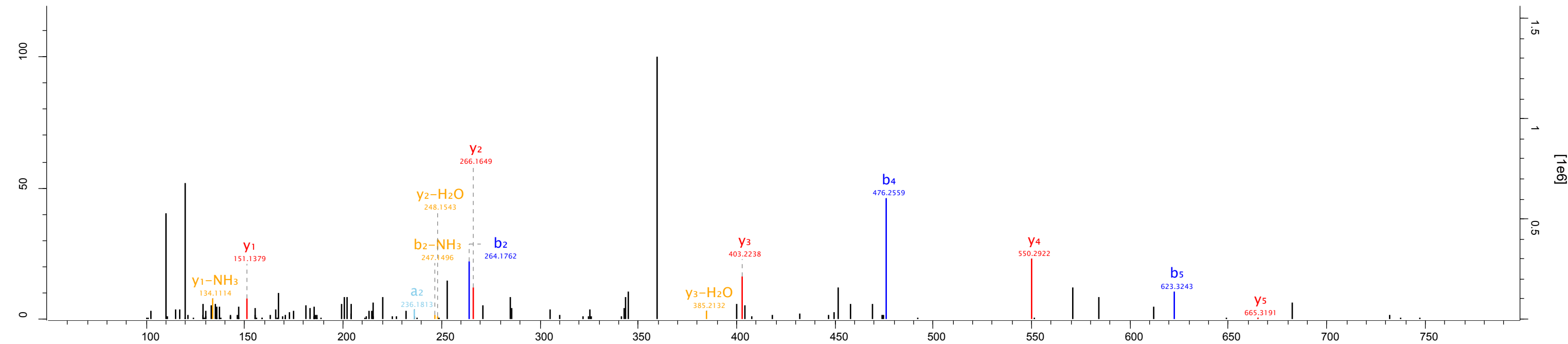
Raw file: 20150822_A375SR-Proteome_BR3
 Scan: 44730 Method: FTMS; HCD Score: 46.82 m/z: 654.37 Gene names: RPL39P5;RPL39



Raw file: 20150822_A375SR-Proteome_BR3
 Scan: 4740 Method: FTMS; HCD Score: 44.32 m/z: 339.17 Gene names: COX7B

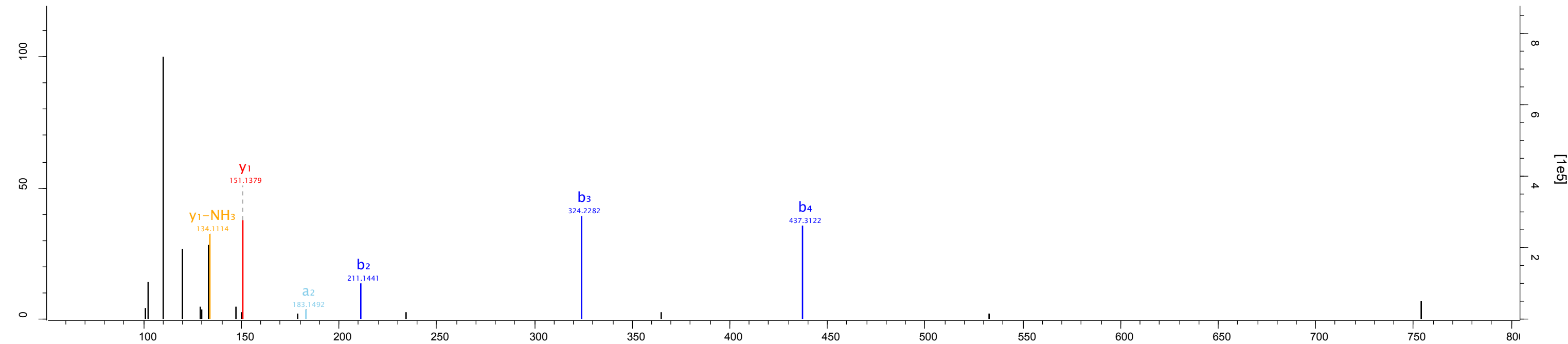


Raw file: 20150822_A375SR_Proteome_BR3
 Scan: 4750 Method: FTMS; HCD Score: 39.85 m/z: 342.52 Gene names: COX7B

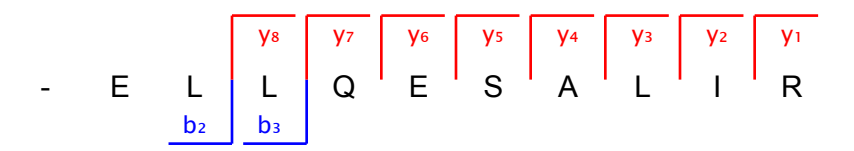
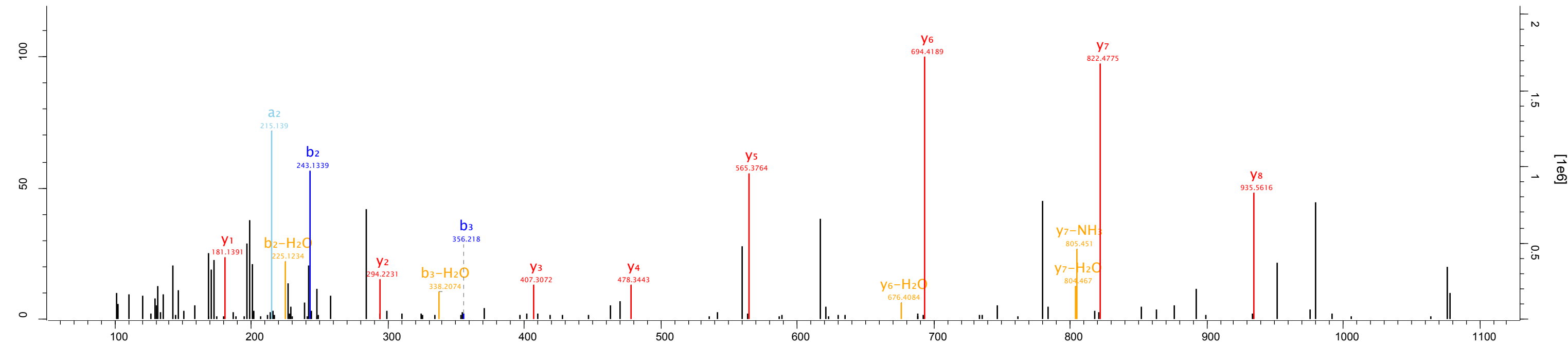


Raw file
20180707_MaS_A375SR_LM_proteome_04

Scan: 23850
Method: FTMS; HCD
Score: 11.58
m/z: 486.29
Gene names: IL1R1

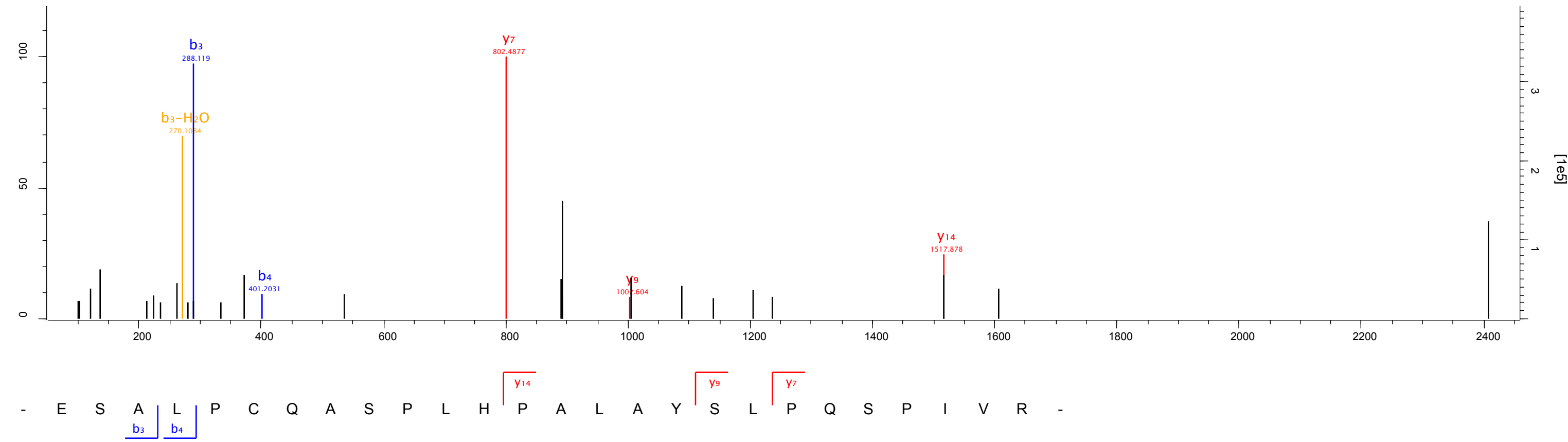


Raw file 20180707_MaS_A375SR_LM_proteome_06 Scan 21400 Method FTMS; HCD Score 96.34 m/z 589.35 Gene names TRAP1

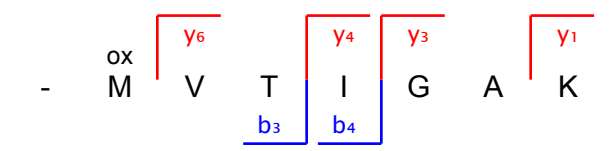
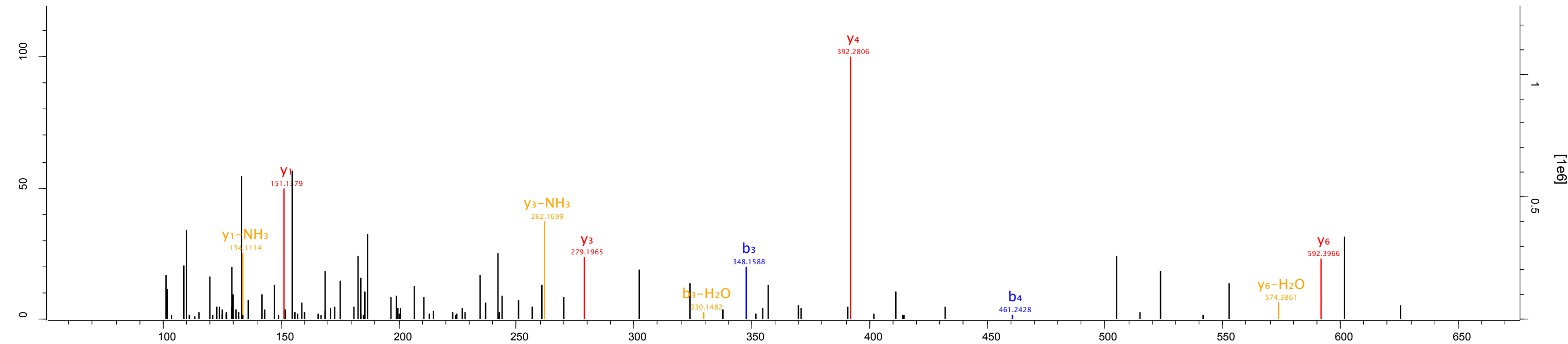


Raw file
20180707_MaS_A375SR_LM_proteome_06

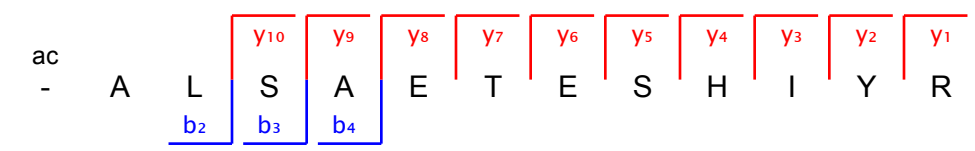
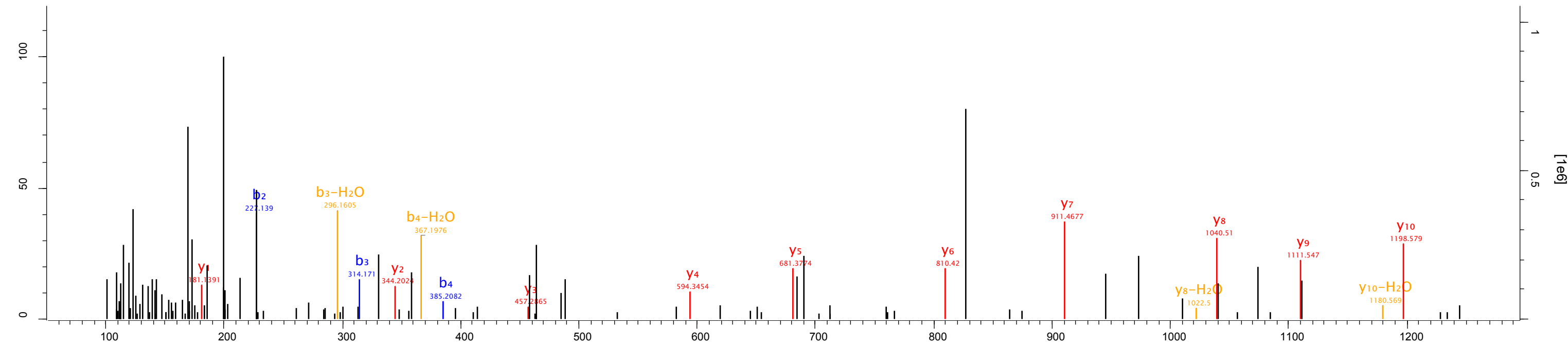
Scan Method Score m/z Gene names
26380 FTMS; HCD 7.01 937.5 C1orf85



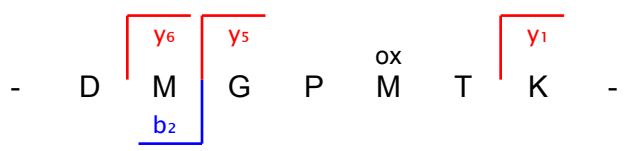
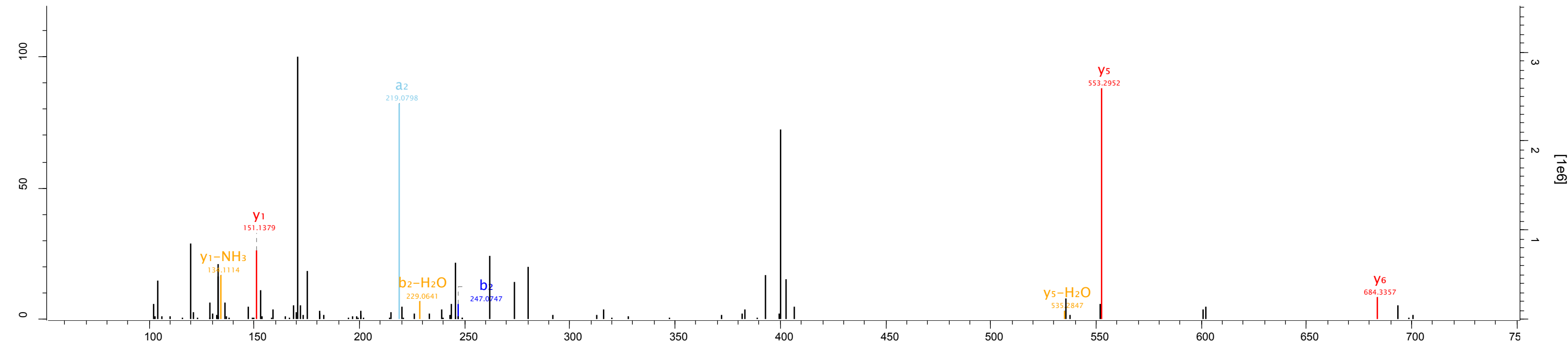
Raw file 20180707_MaS_A375SR_LM_proteome_10 Scan 7340 Method FTMS; HCD Score 58.17 m/z 370.22



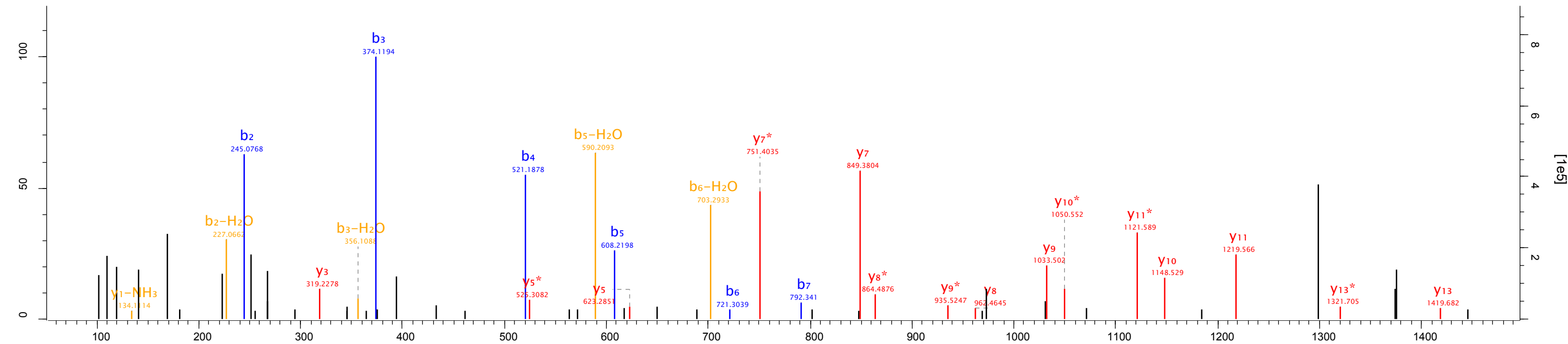
Raw file: 20180707_MaS_A375SR_LM_proteome_14
 Scan: 16940 Method: FTMS; HCD Score: 67.52 m/z: 712.86 Gene names: CYB561D2



Raw file 20180707_MaS_A375SR_LM_proteome_17 Scan 9470 Method FTMS; HCD Score 44.72 m/z 400.18



Raw file 20180707_MaS_A375SR_LM_proteome_18 Scan 27670 Method FTMS; HCD Score 102.43 m/z 970.44 Gene names MAPK11P1L

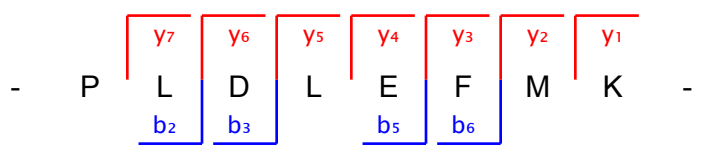
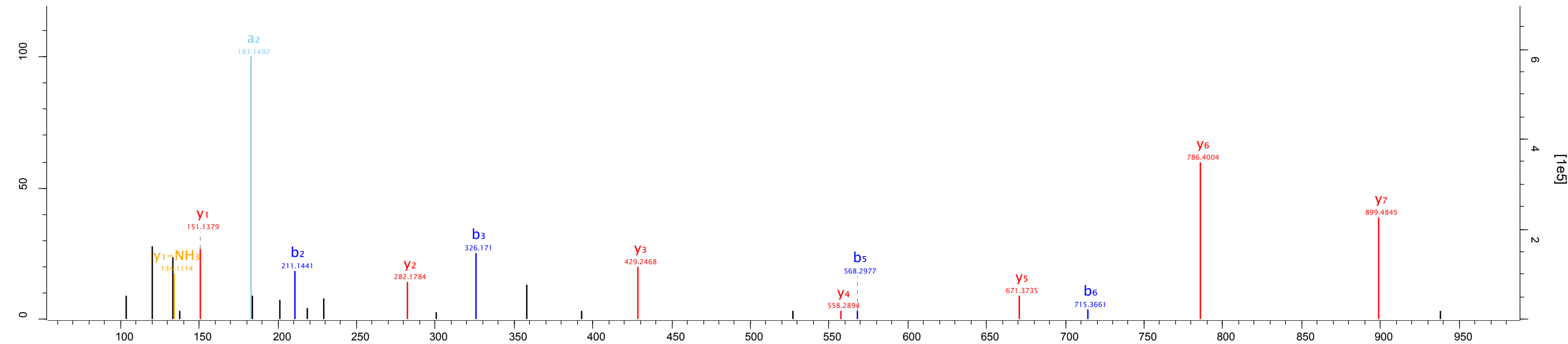


ac - S D E F S L A D A L P E H S P A K -

Fragmentation mapping: b2 (D), b3 (E), b4 (F), b5 (S), b6 (L), b7 (A), y3 (P), y5 (H), y7 (P), y8 (L), y9 (A), y10 (D), y11 (A), y13 (S)

Raw file
20180707_MaS_A375SR_LM_proteome_21

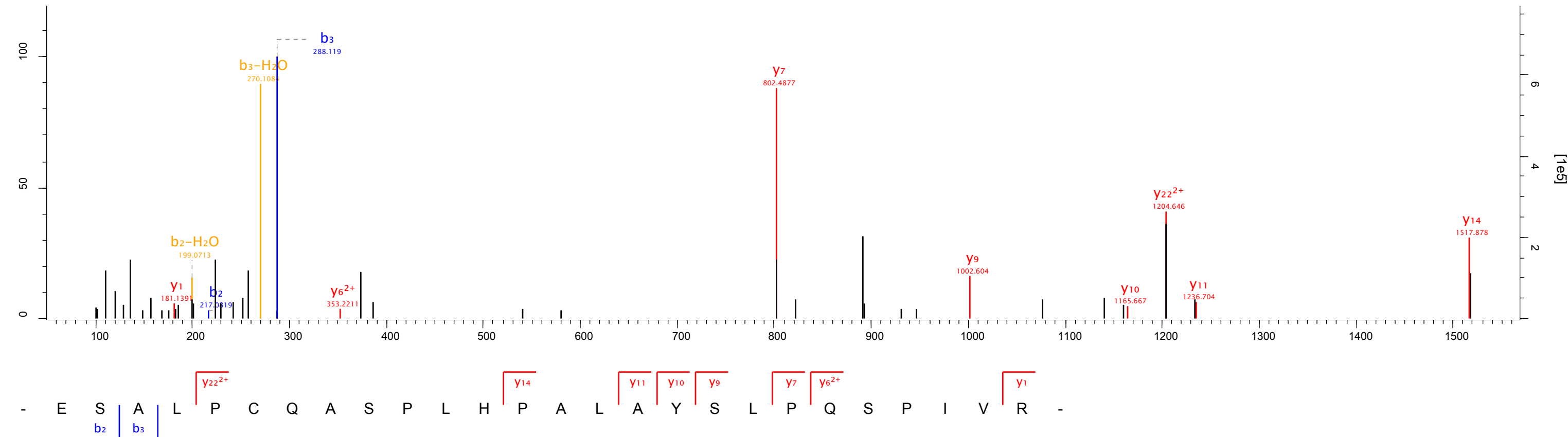
Scan: 25090
Method: FTMS; HCD
Score: 78.15
m/z: 499.27
Gene names: SEPT3



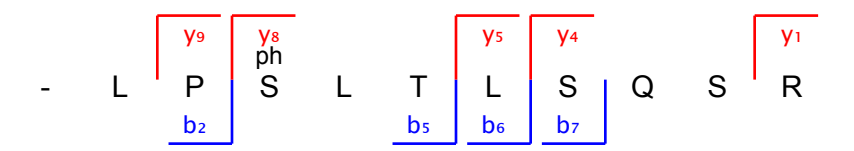
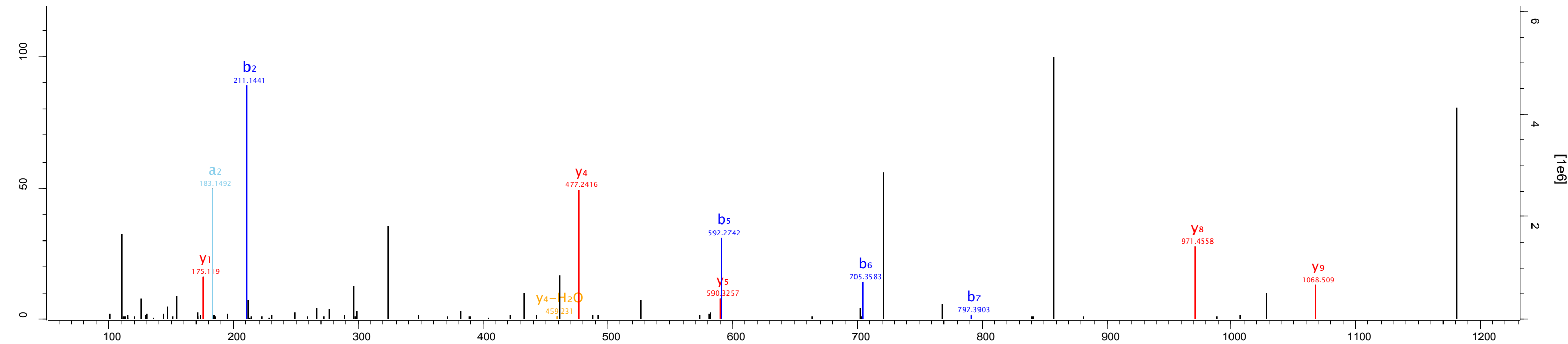
Raw file

20180707_MaS_A375SR_LM_proteome_21

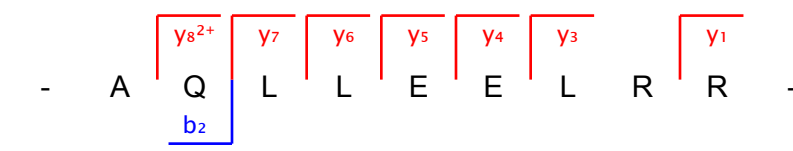
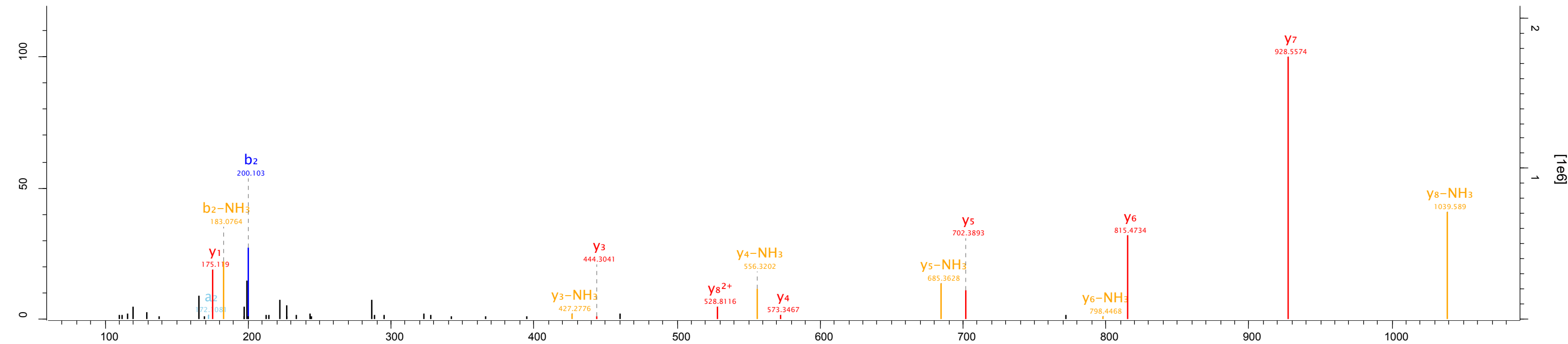
Scan	Method	Score	m/z	Gene names
26750	FTMS; HCD	9.23	937.17	C1orf85



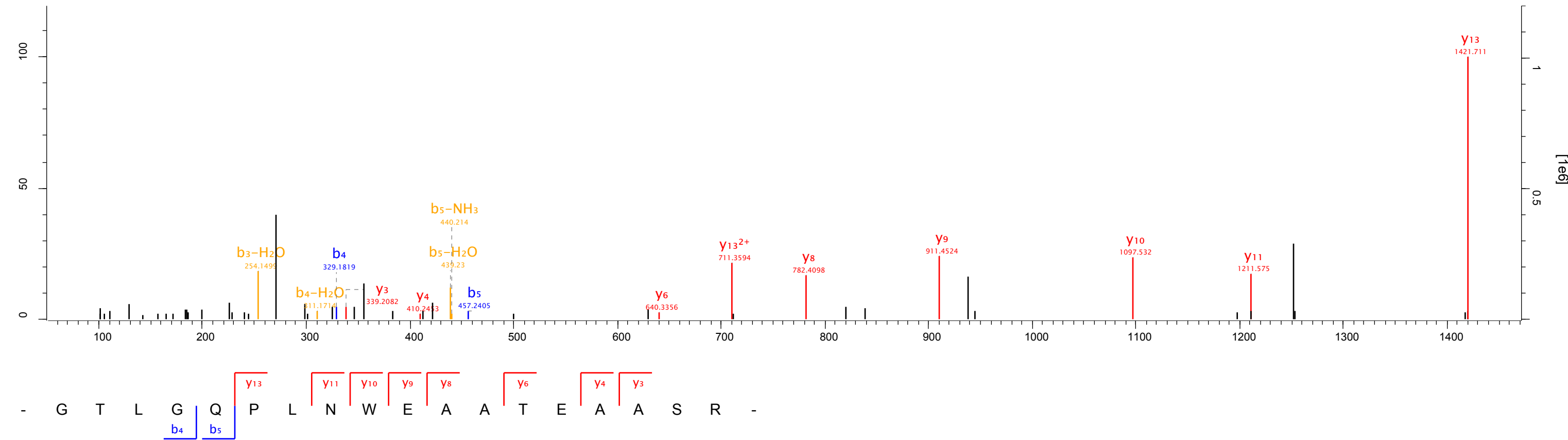
Raw file 20180707_MaS_A375SR_LM_proteome_24 Scan 8660 Method FTMS; HCD Score 58.7 m/z 591.3



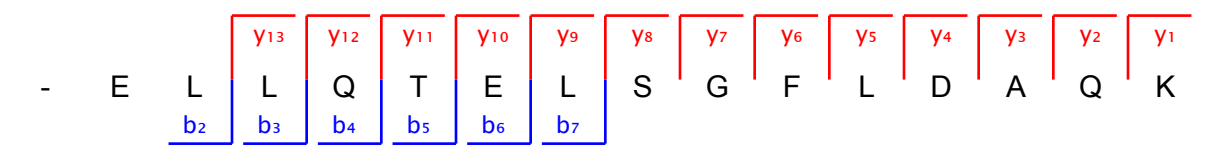
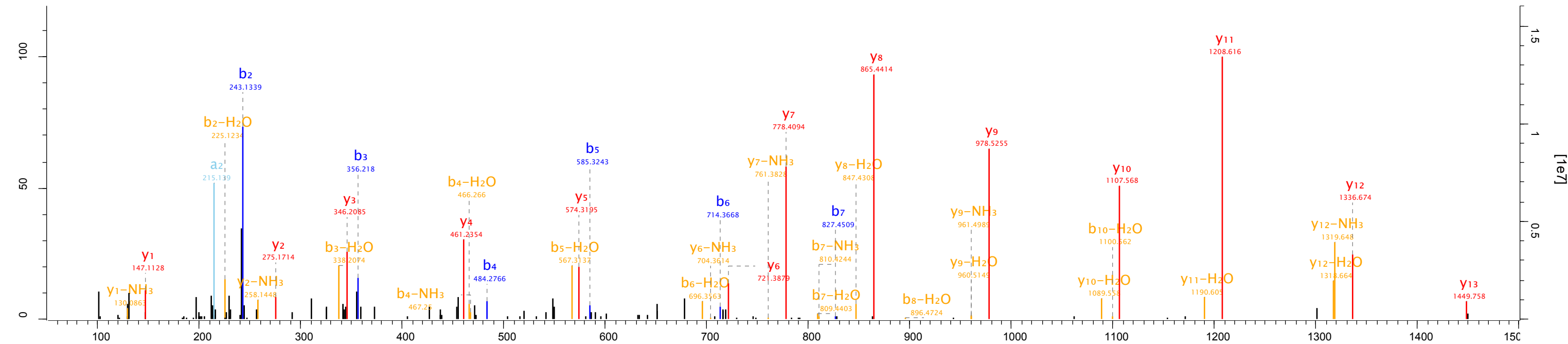
Raw file: 20180707_MaS_A375SR_ML_proteome_01
 Scan: 15050 Method: FTMS; HCD Score: 97.43 m/z: 376.56 Gene names: PNKD



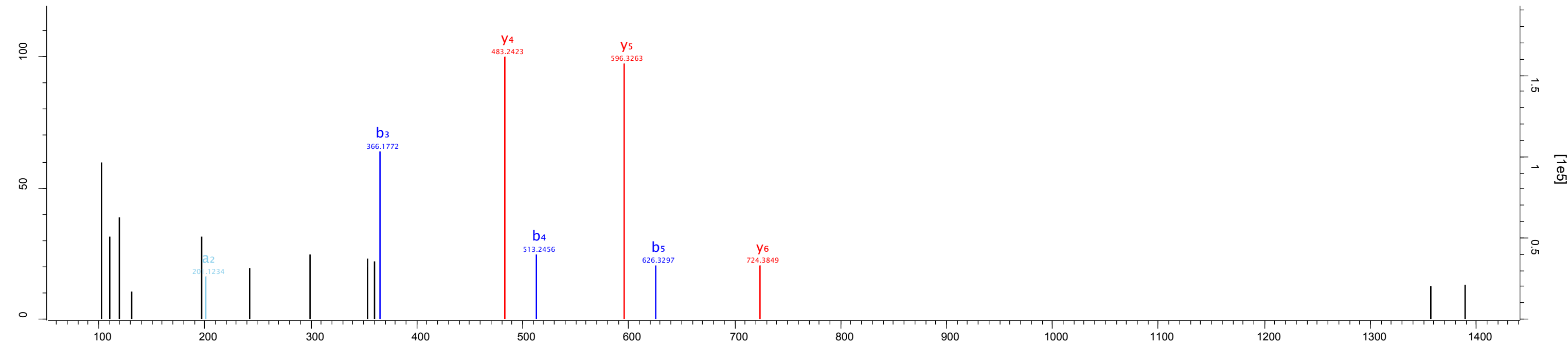
Raw file 20180707_MaS_A375SR_ML_proteome_01 Scan 23650 Method FTMS; HCD Score 41.51 m/z 939.47 Gene names SIRT7



Raw file 20180707_MaS_A375SR_ML_proteome_01 Scan 27380 Method FTMS; HCD Score 210.34 m/z 846.45 Gene names S100A1

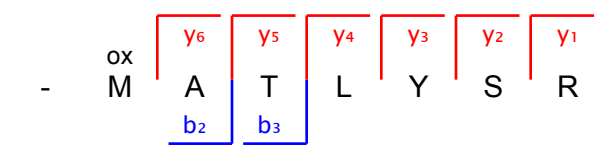
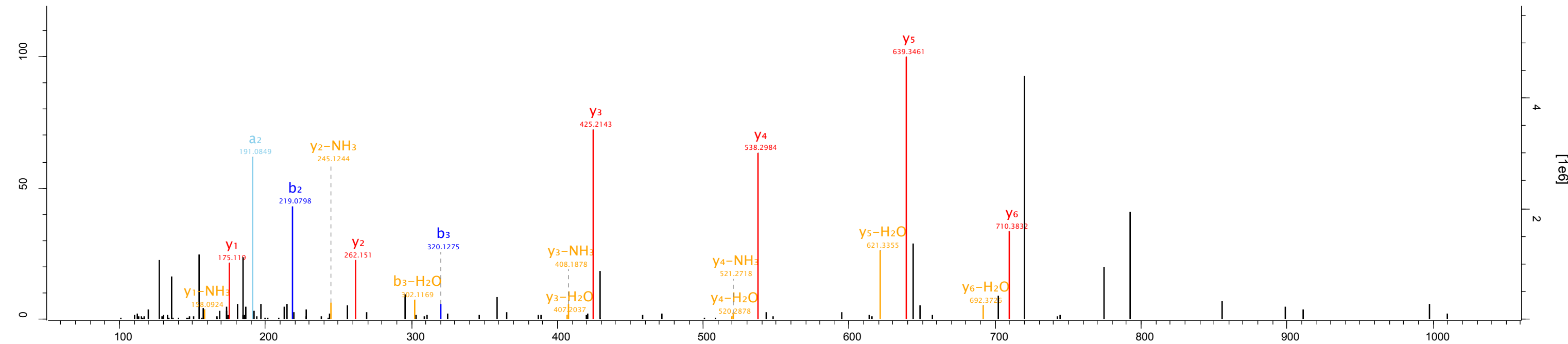


Raw file 20180707_MaS_A375SR_ML_proteome_02
 Scan 23900 Method FTMS; HCD Score 19.24 m/z 431.23 Gene names IGFALS

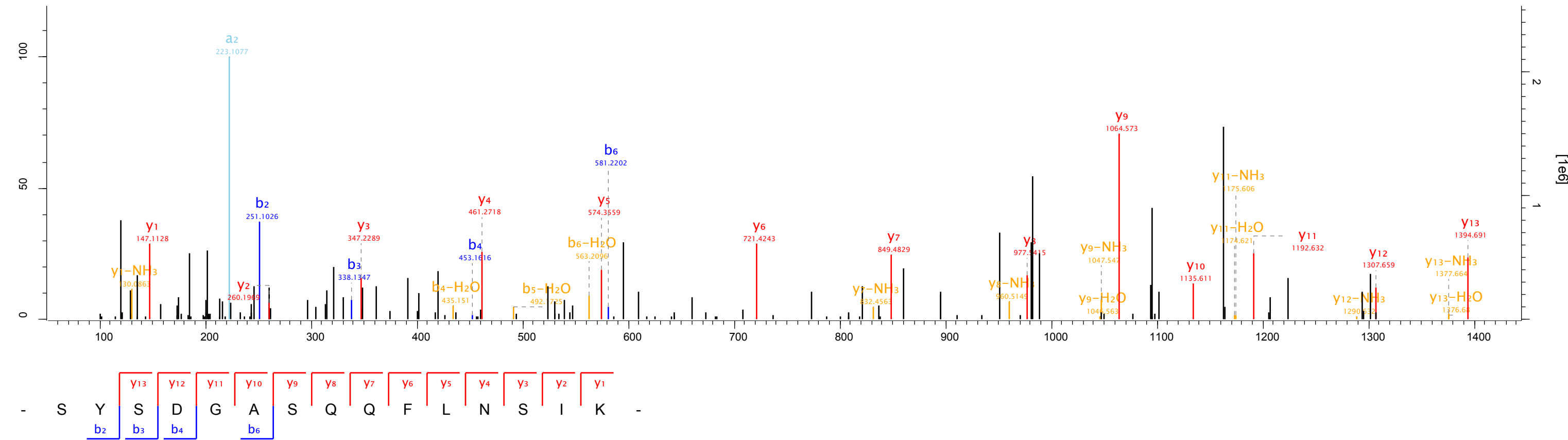


Raw file
20180707_MaS_A375SR_ML_proteome_02

Scan Method Score m/z Gene names
6440 FTMS; HCD 128.57 429.21 PTGDS

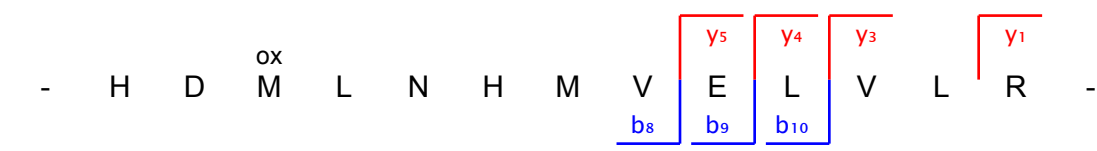
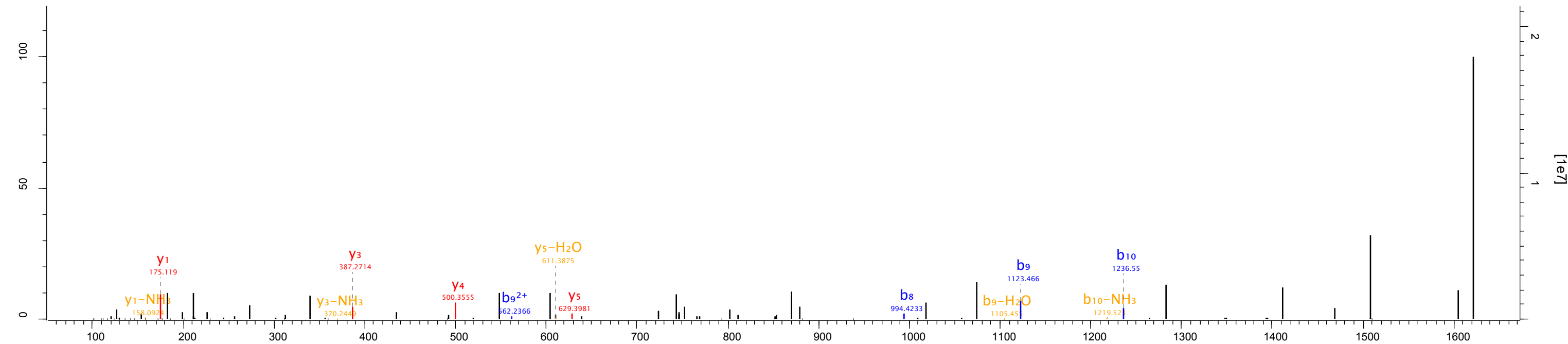


Raw file 20180707_MaS_A375SR_ML_proteome_03 Scan 18170 Method FTMS; HCD Score 104.86 m/z 822.9 Gene names UBXN2A

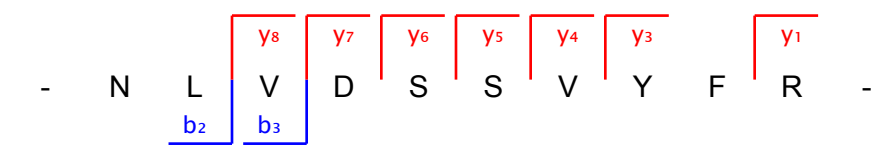
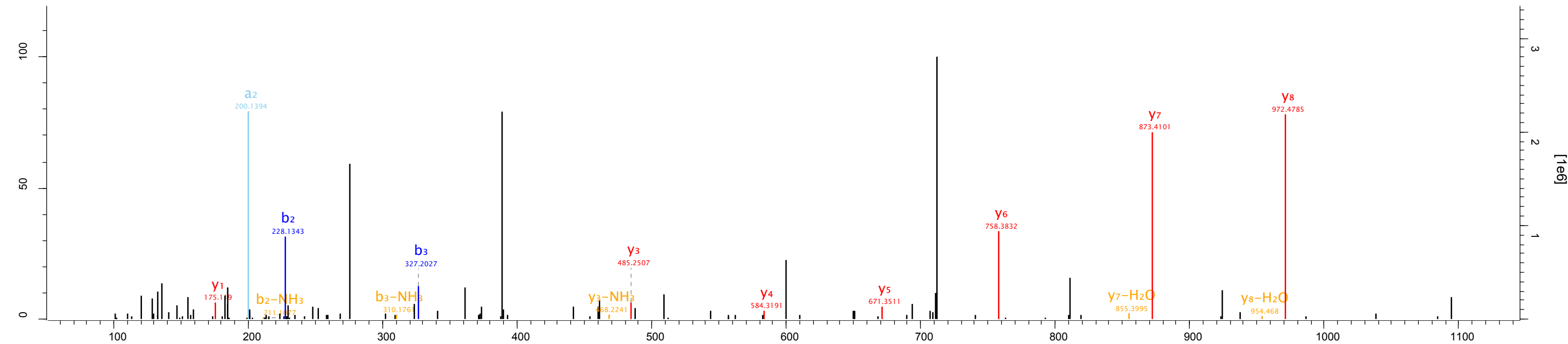


Raw file
20180707_MaS_A375SR_ML_proteome_03

Scan Method Score m/z
24740 FTMS; HCD 46.06 811.91

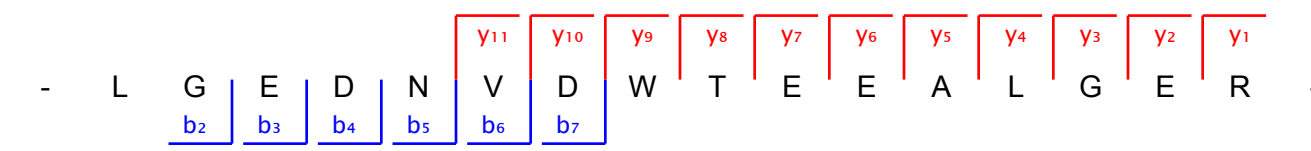
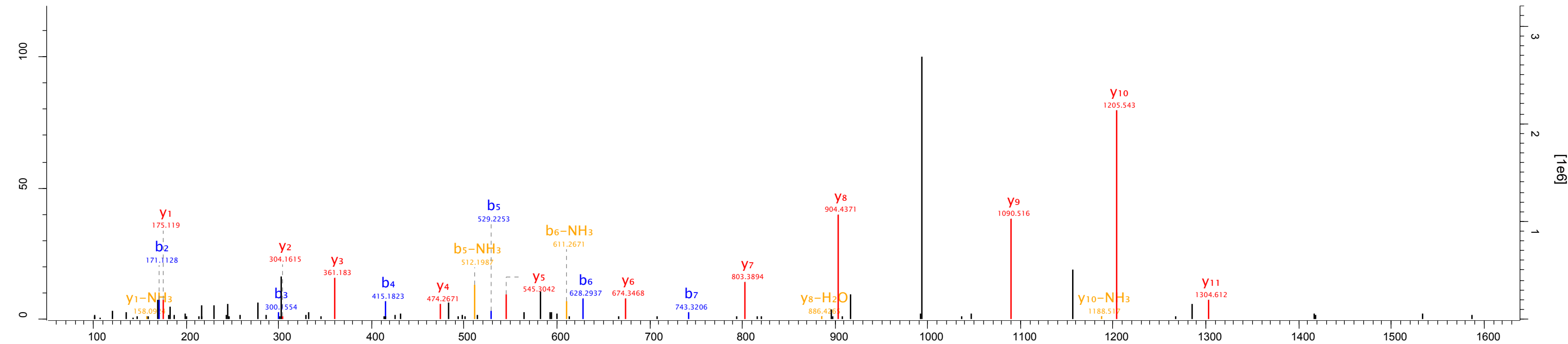


Raw file: 20180707_MaS_A375SR_ML_proteome_04
 Scan: 22030 Method: FTMS; HCD Score: 56.55 m/z: 600.32 Gene names: MEF2BNB



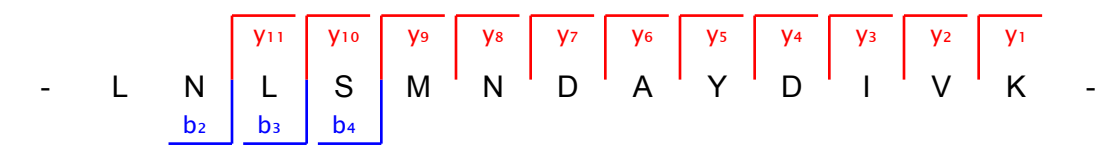
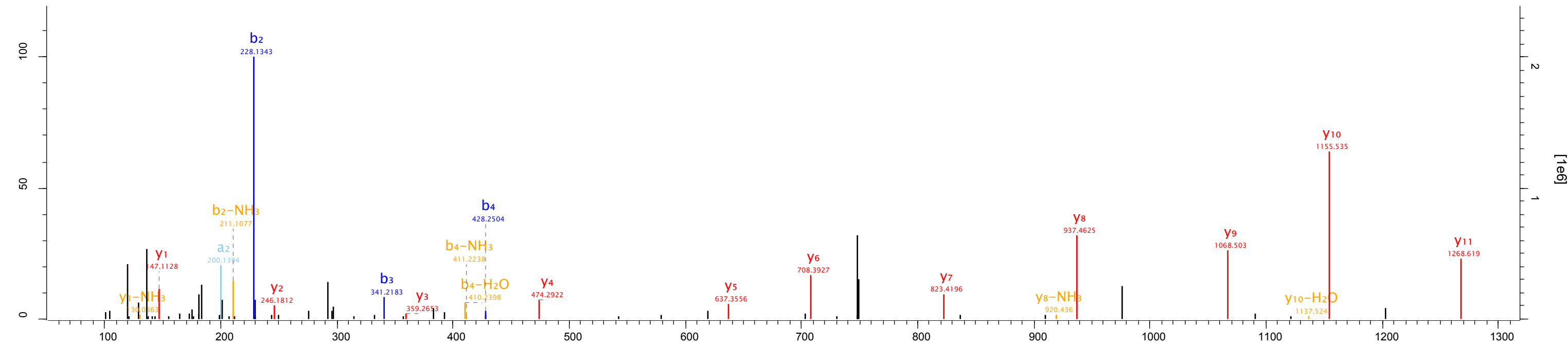
Raw file
20180707_MaS_A375SR_ML_proteome_04

Scan: 24770
Method: FTMS; HCD
Score: 78.95
m/z: 917.42
Gene names: MIEF2

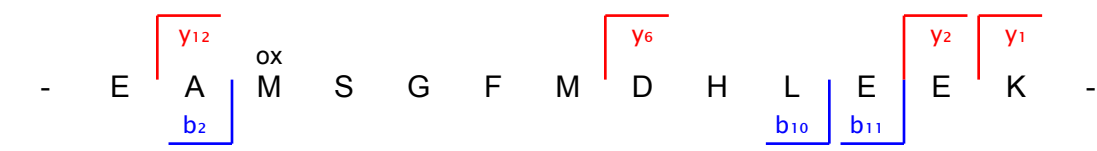
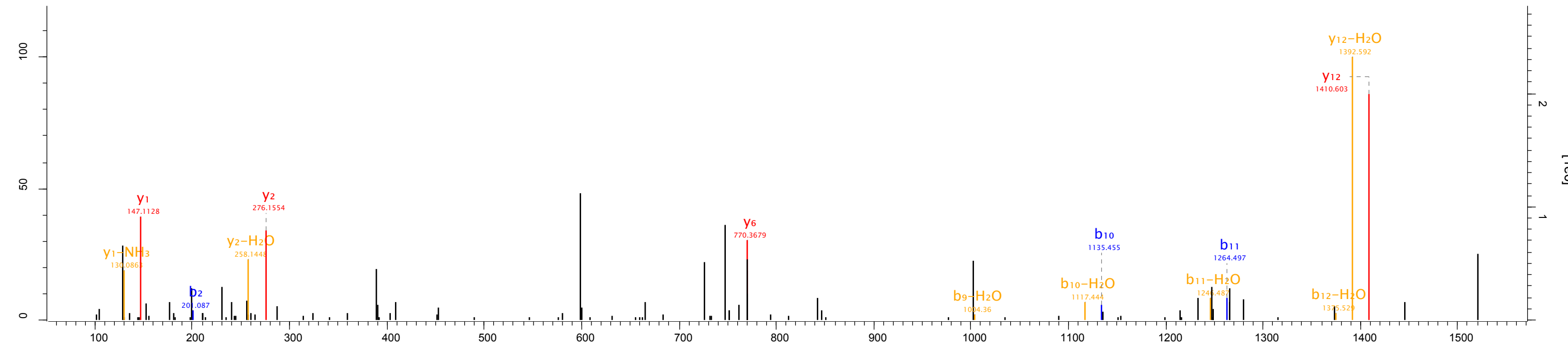


Raw file
20180707_MaS_A375SR_ML_proteome_05

Scan: 26770
Method: FTMS; HCD
Score: 80.75
m/z: 748.88
Gene names: PGS1;DUSP6

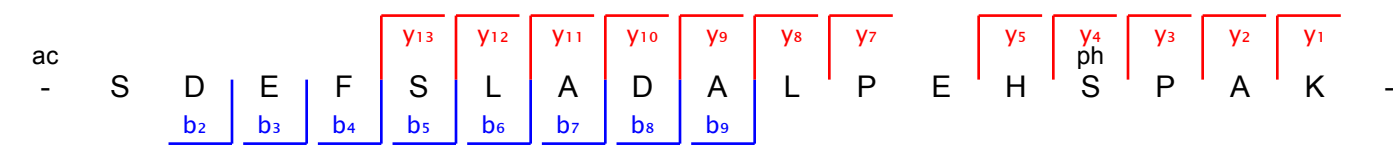
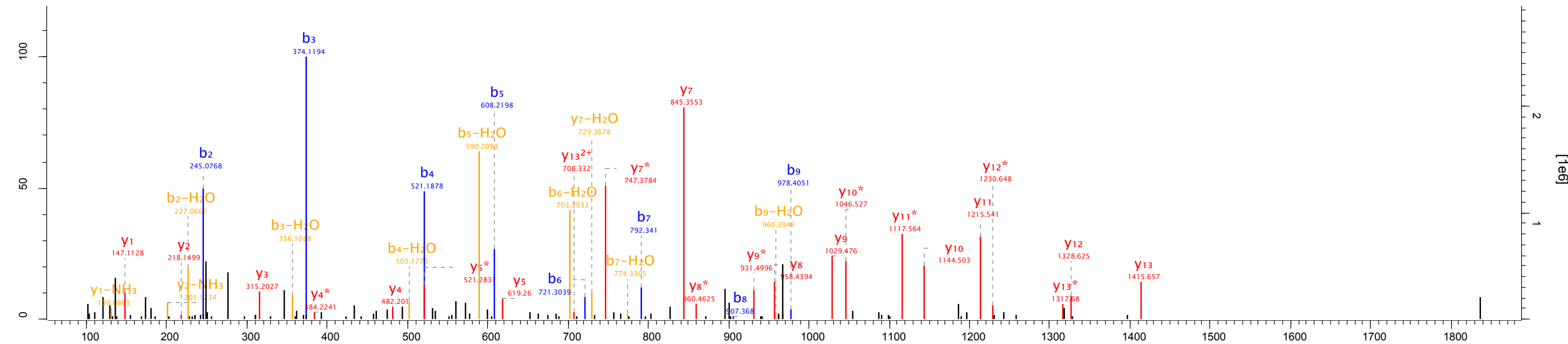


Raw file 20180707_MaS_A375SR_ML_proteome_05 Scan 8990 Method FTMS; HCD Score 56.2 m/z 770.83 Gene names GOLGA8F;GOLGA8DP



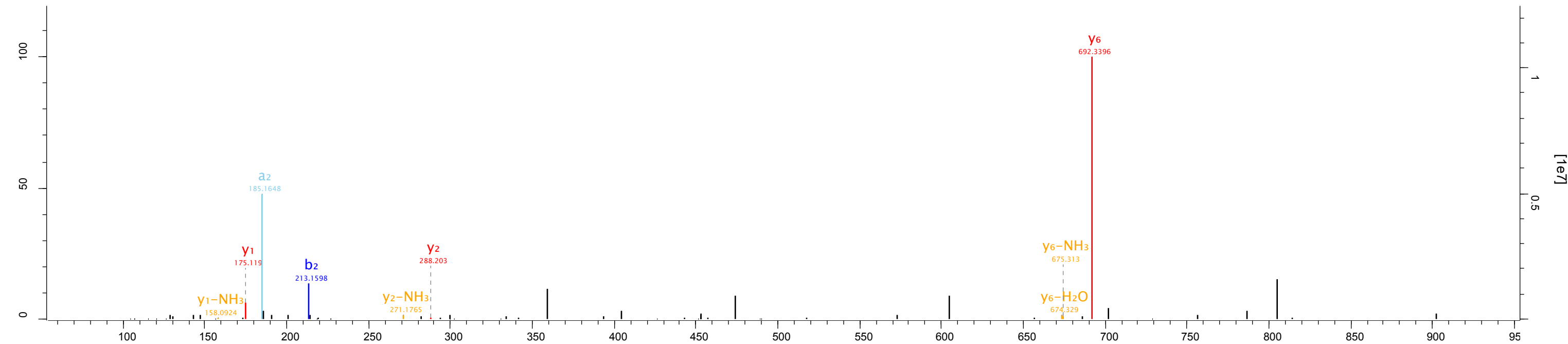
Raw file
20180707_MaS_A375SR_ML_proteome_06

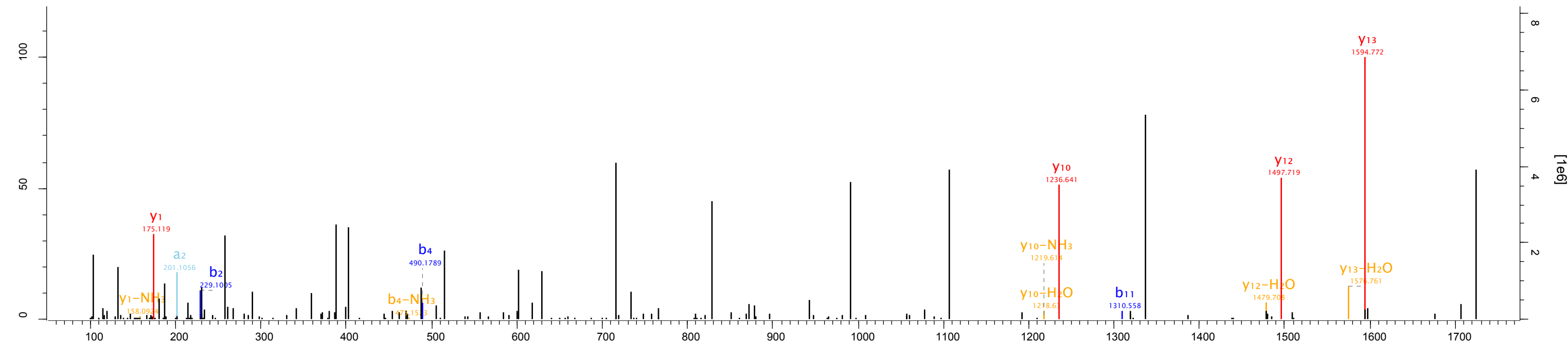
Scan 27790 Method FTMS; HCD Score 183.24 m/z 968.42 Gene names MAPK11P1L



Raw file
20180707_MaS_A375SR_ML_proteome_07

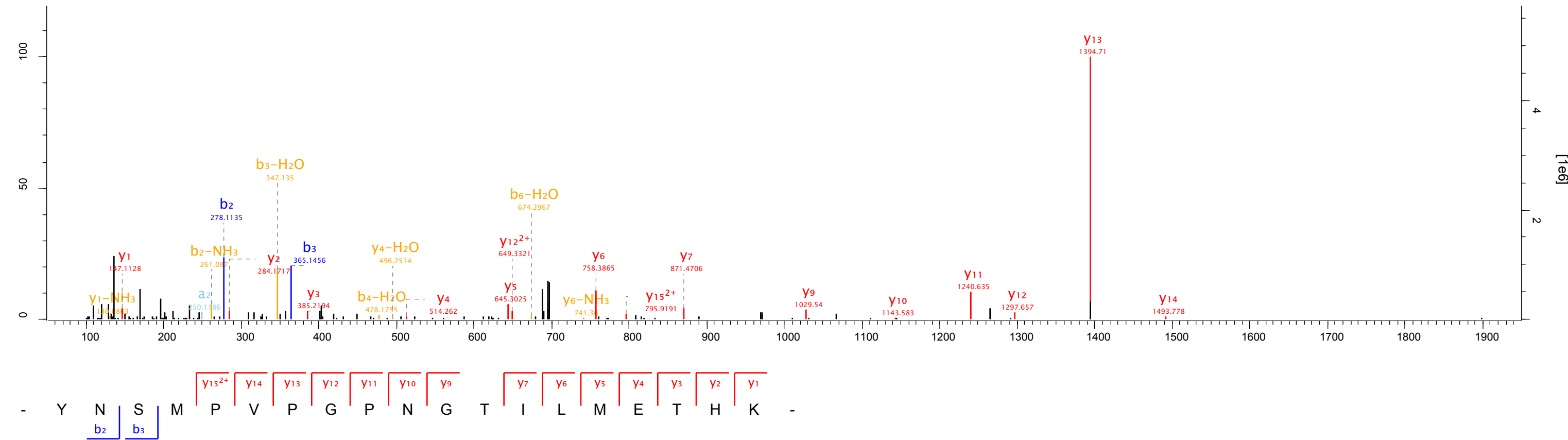
Scan 15290 Method FTMS; HCD Score 46.02 m/z 452.75





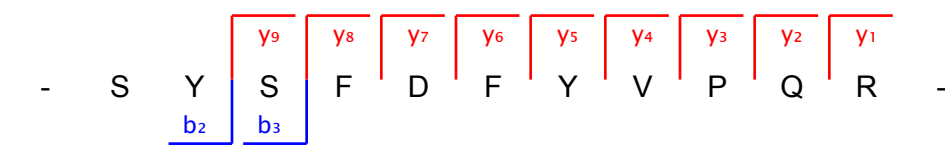
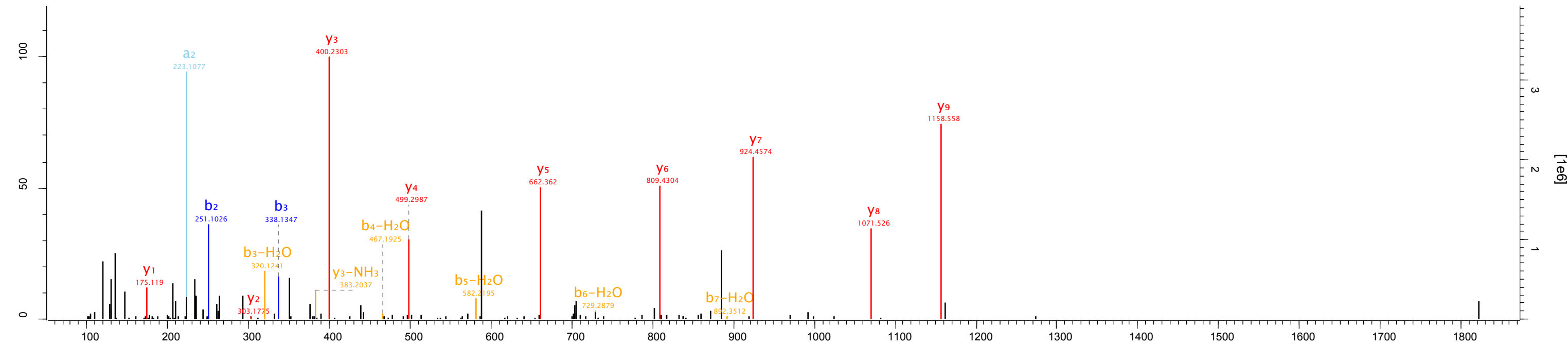
Raw file
20180707_MaS_A375SR_ML_proteome_09

Scan Method Score m/z Gene names
20770 FTMS; HCD 70.84 696.34 SLC31A1



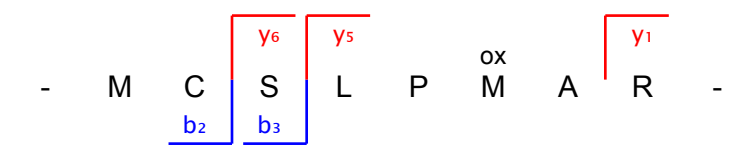
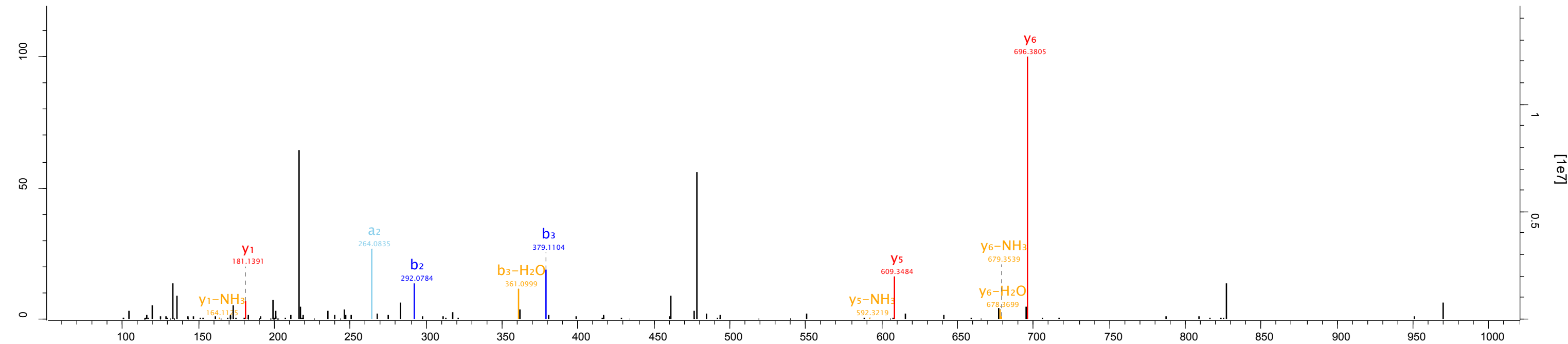
Raw file
20180707_MaS_A375SR_ML_proteome_09

Scan 25410 Method FTMS; HCD Score 69.72 m/z 705.33 Gene names OAF



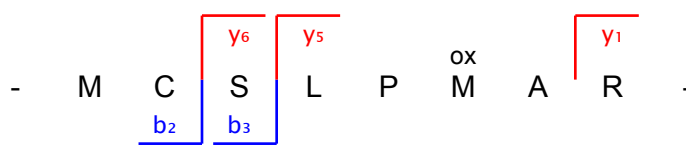
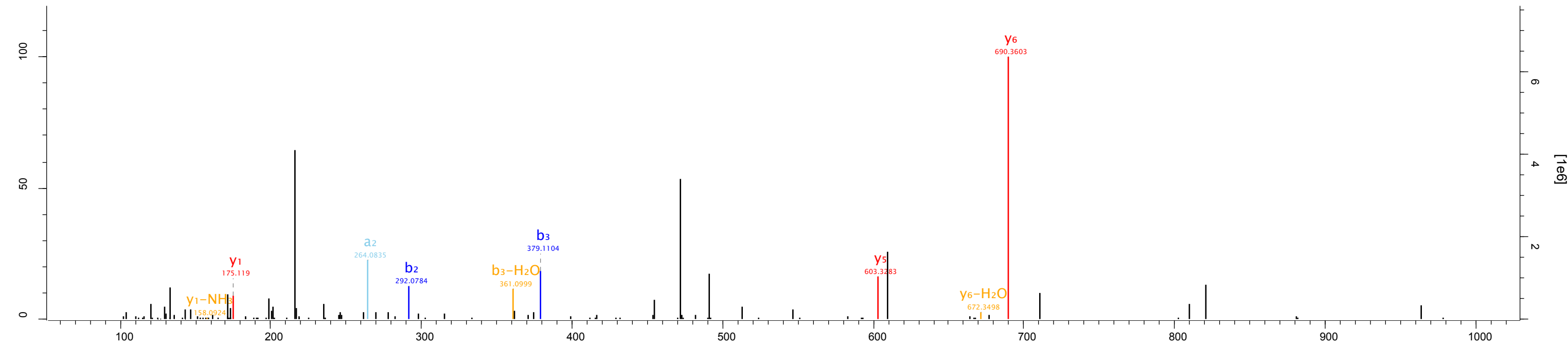
Raw file
20180707_MaS_A375SR_ML_proteome_10

Scan 13830 Method FTMS; HCD Score 64.76 m/z 494.23 Gene names IL1F10

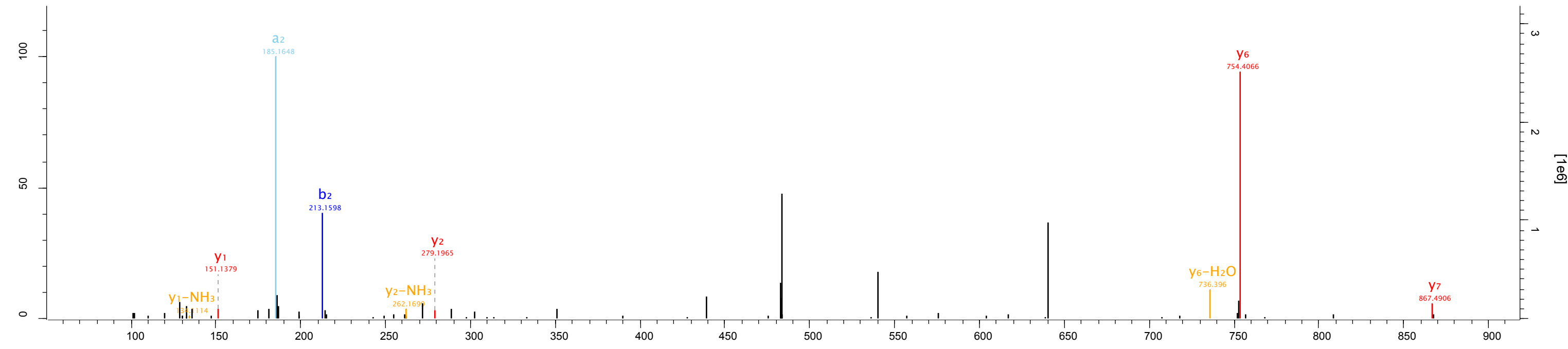


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20180707_MaS_A375SR_ML_proteome_10

Scan Method Score m/z Gene names
13860 FTMS; HCD 50.13 491.22 IL1F10

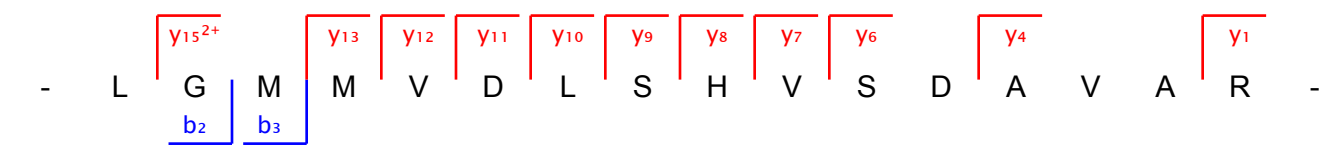
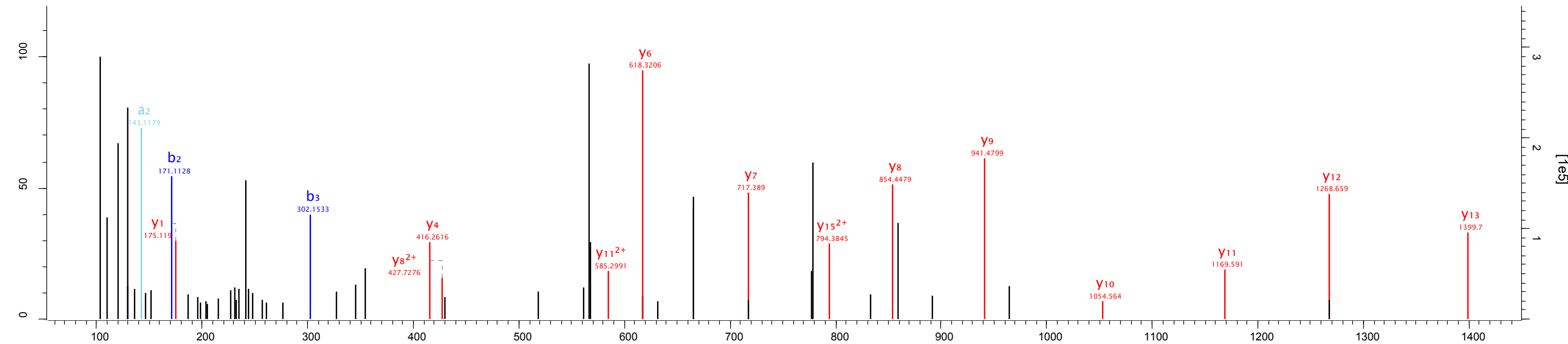


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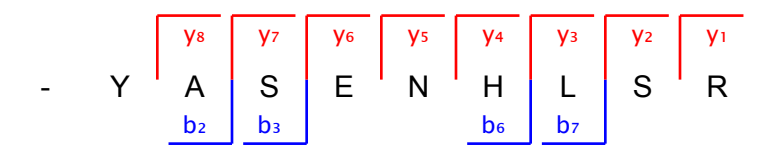
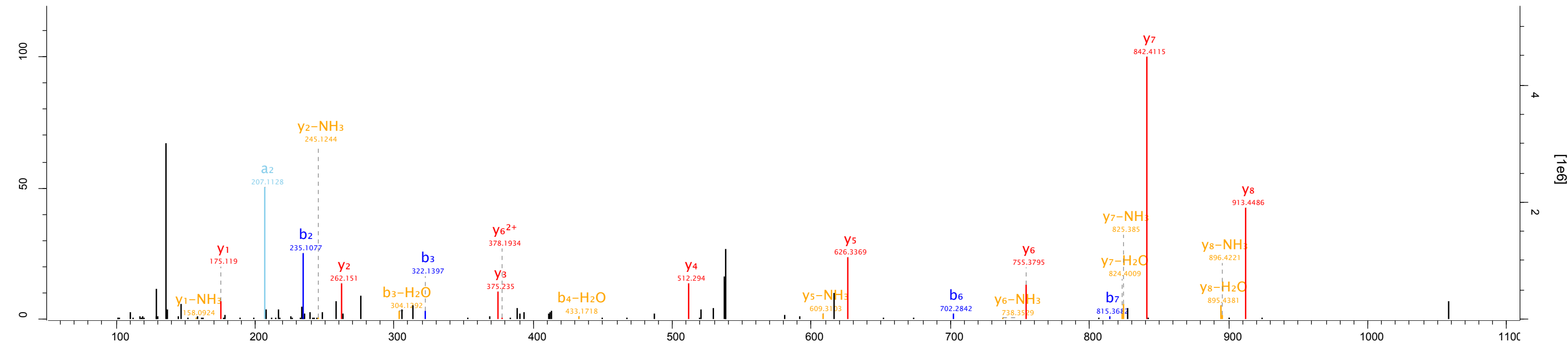


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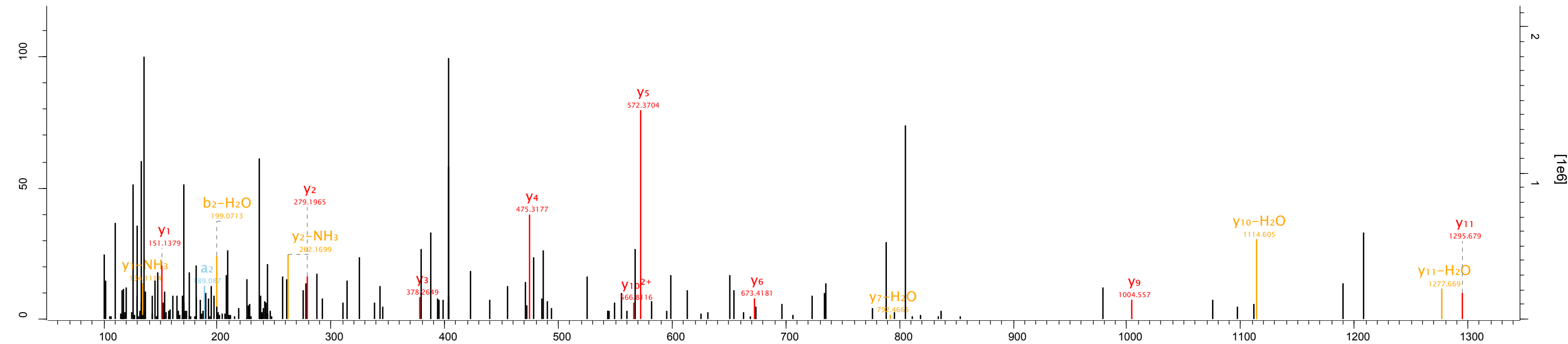
Scan 26990 Method FTMS; HCD Score 59.67 m/z 567.62 Gene names DPEP2



Raw file: 20180707_MaS_A375SR_ML_proteome_11
 Scan: 3160 Method: FTMS; HCD Score: 115.78 m/z: 538.76 Gene names: TM4SF1



Raw file 20180707_MaS_A375SR_ML_proteome_11 Scan 3310 Method FTMS; HCD Score 18.4 m/z 403.96 Gene names MT-CO3



- E S T Y Q G H H T P P V Q K -

Fragmentation mapping (red boxes):

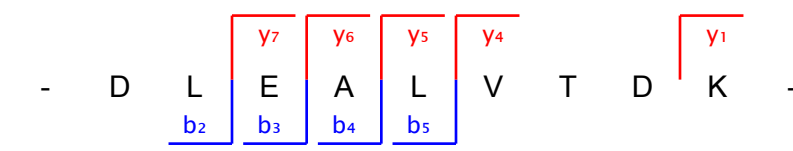
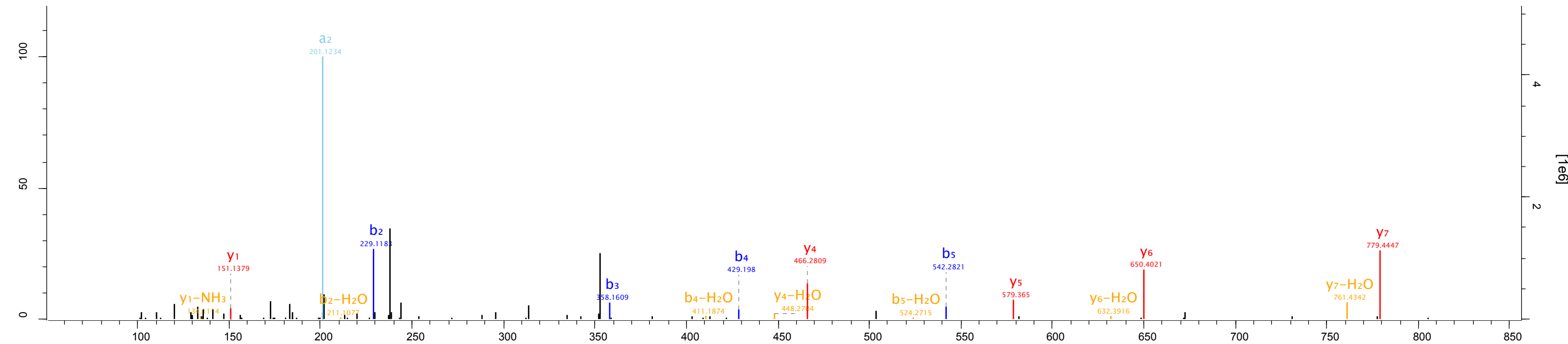
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- Q: y10²⁺
- G: y9
- T: y6
- P: y5
- P: y4
- V: y3
- Q: y2
- K: y1

Additional label (blue box):

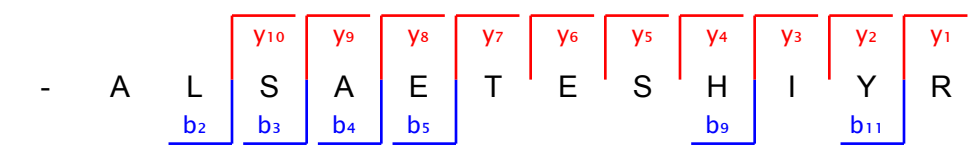
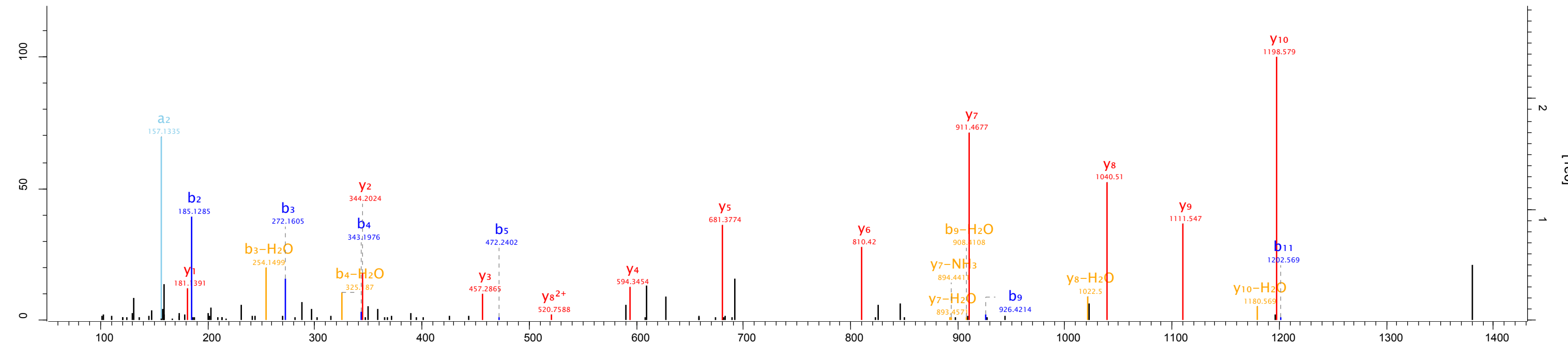
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20180707_MaS_A375SR_ML_proteome_12

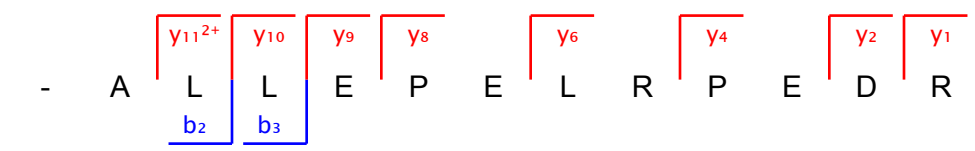
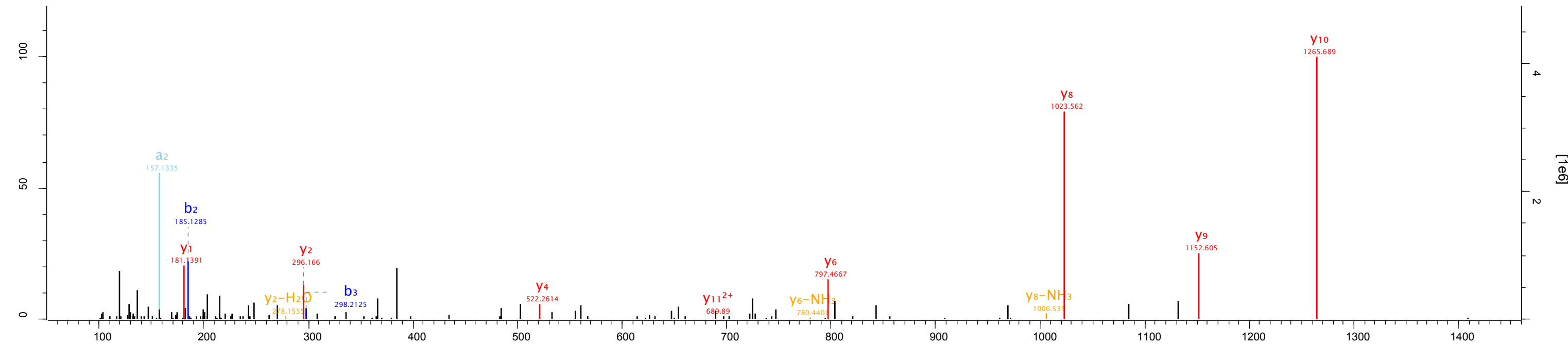
Scan 23750 Method FTMS; HCD Score 84 m/z 504.28 Gene names PGM5

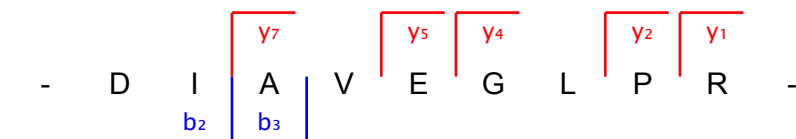
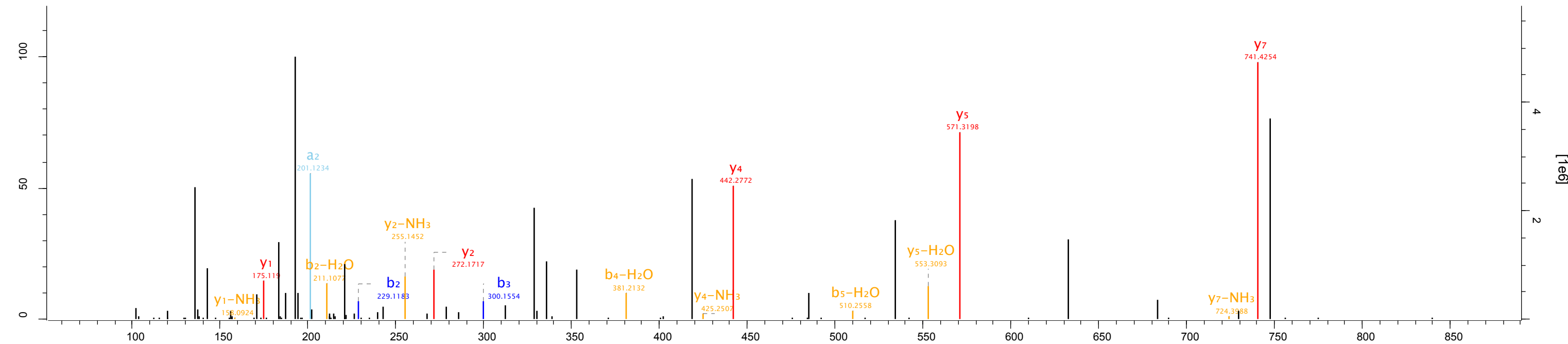


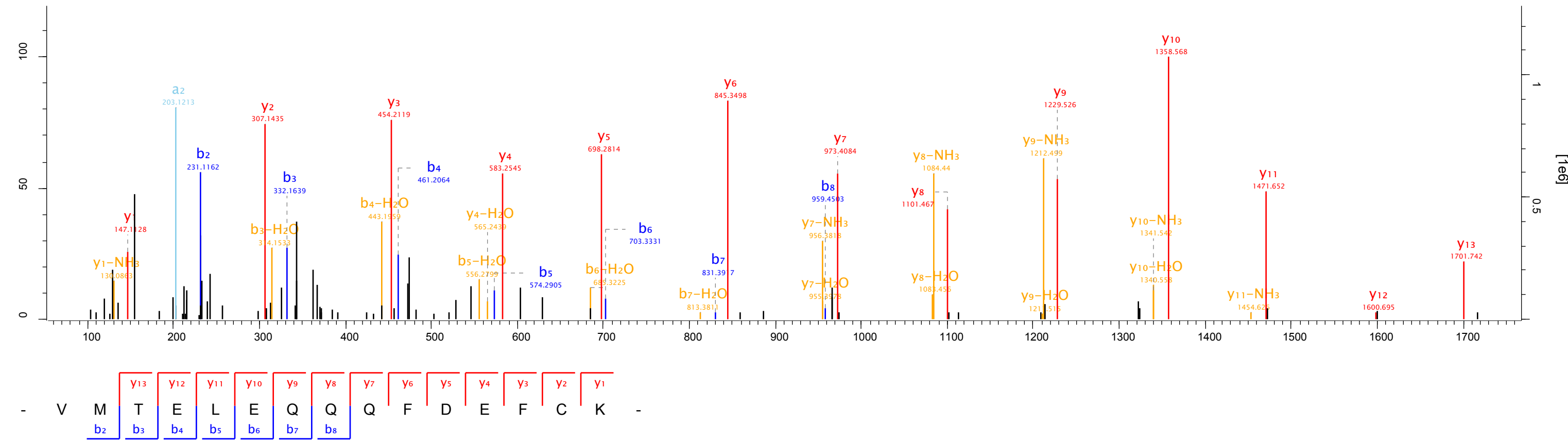
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 Scan: 9470 Method: FTMS; HCD Score: 131.17 m/z: 691.85 Gene names: CYB561D2



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 Scan 16910 Method FTMS; HCD Score 48.57 m/z 483.94 Gene names ECE2

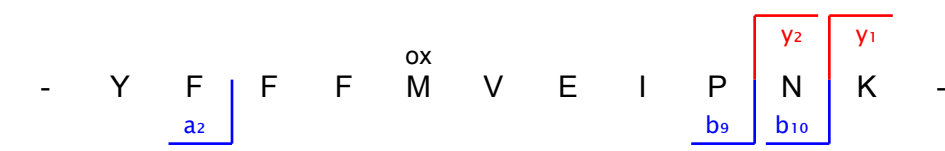
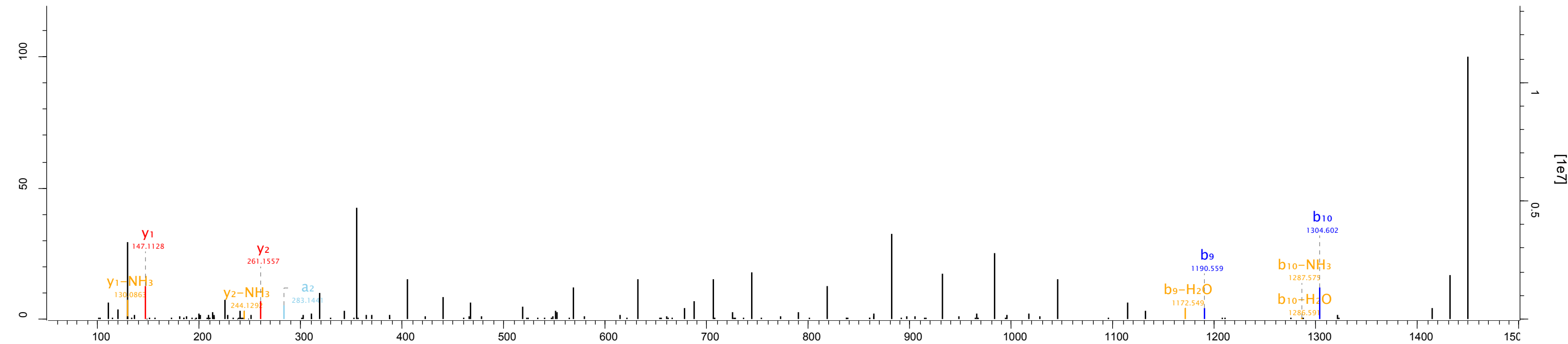






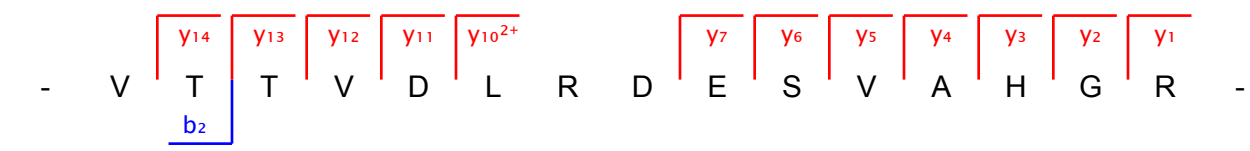
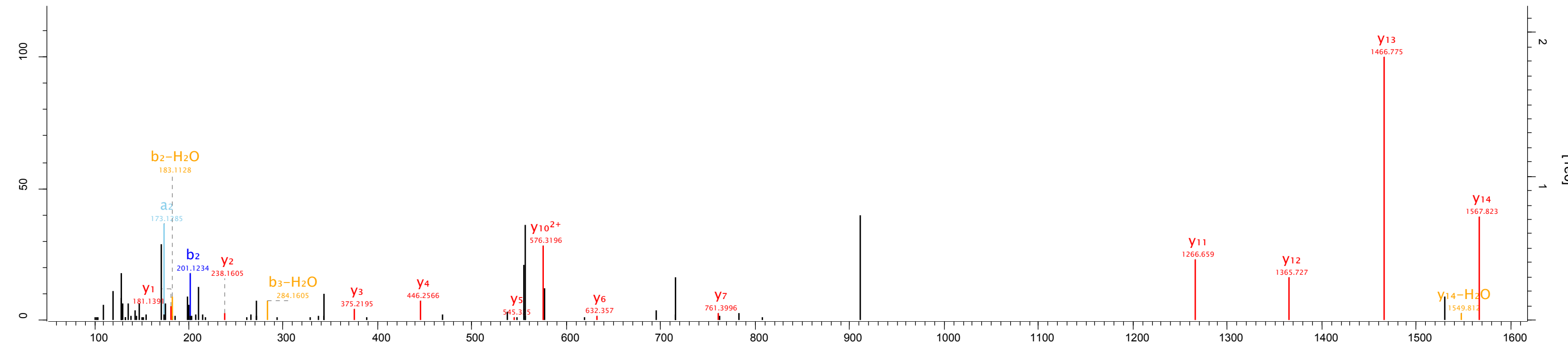
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20180707_MaS_A375SR_ML_proteome_17

Scan 22500 Method FTMS; HCD Score 43.77 m/z 725.86



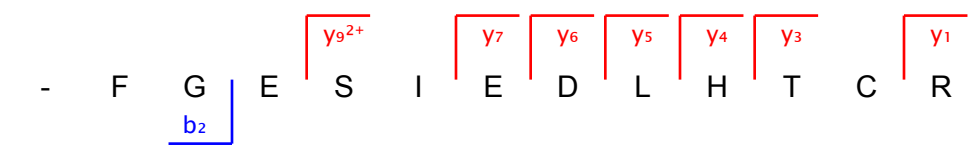
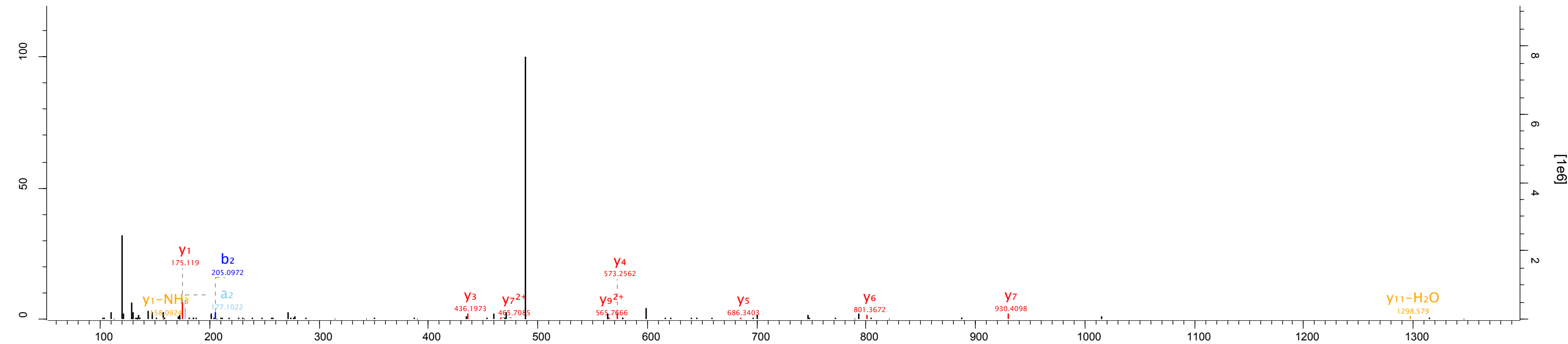
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20180707_MaS_A375SR_ML_proteome_17

Scan: 9980
Method: FTMS; HCD
Score: 58.89
m/z: 556.3
Gene names: LSM10

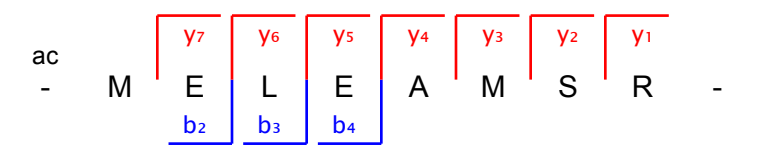
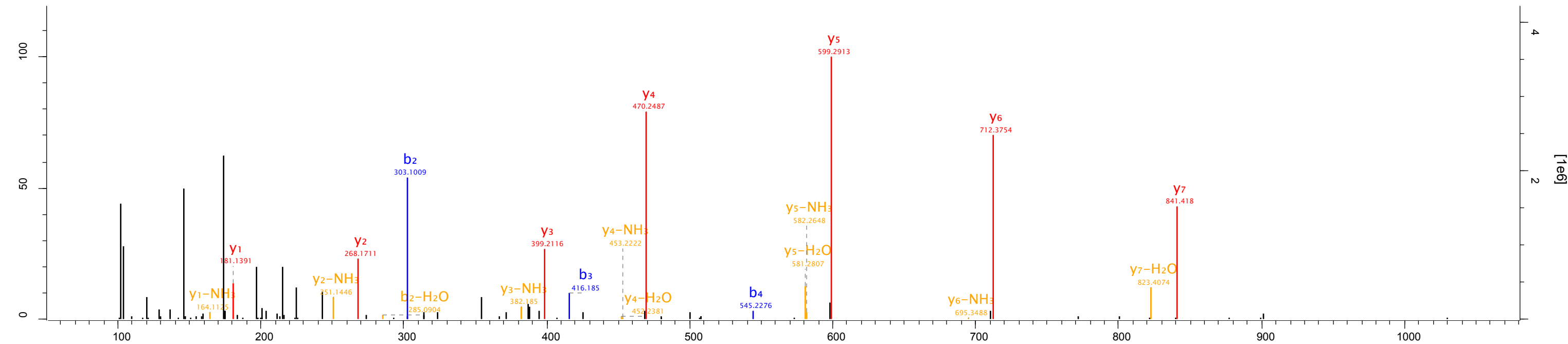


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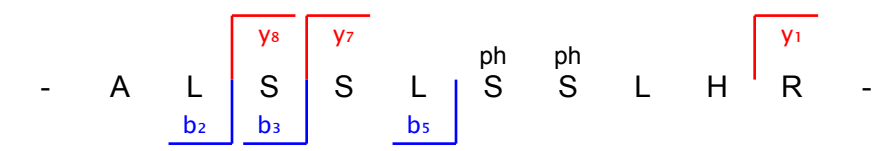
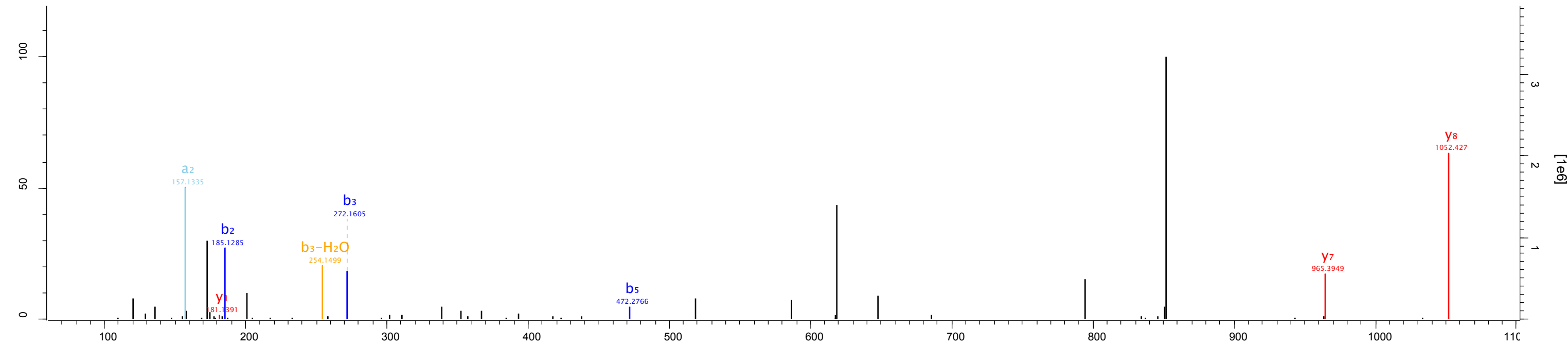
Scan	Method	Score	m/z	Gene names
14740	FTMS; HCD	35.59	488.56	PIGX



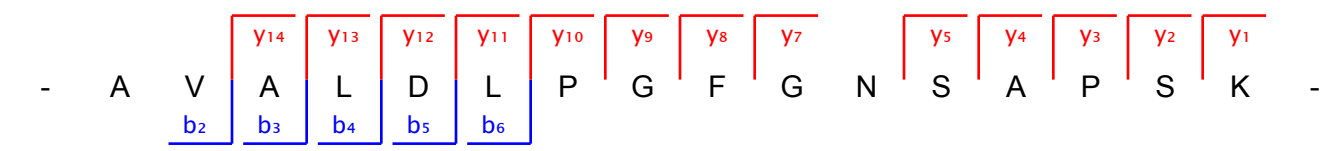
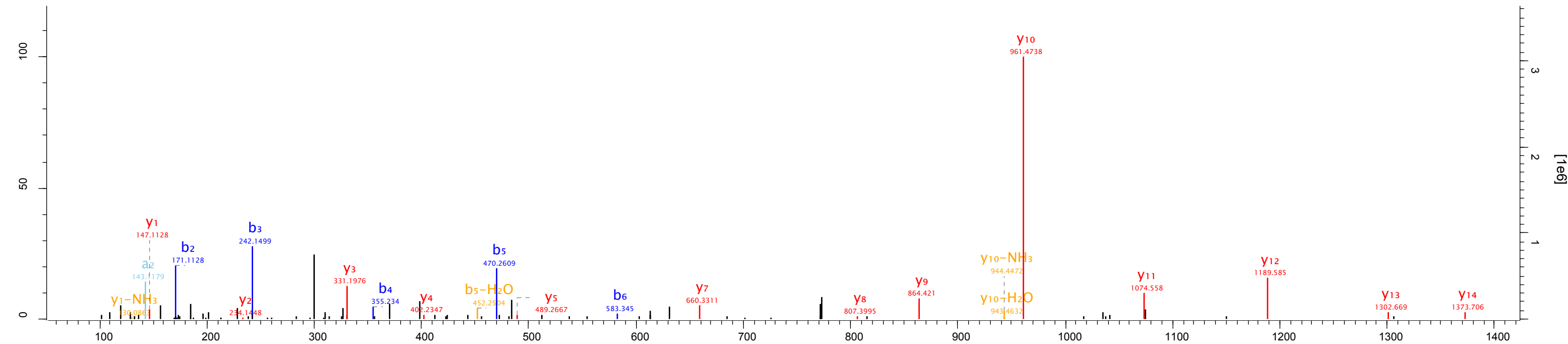
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 Scan: 25420 Method: FTMS; HCD Score: 106.6 m/z: 507.74 Gene names: TMEM258



Raw file 20180707_MaS_A375SR_ML_proteome_2_01 Scan 25430 Method FTMS; HCD Score 44.32 m/z 618.78 Gene names ZNF442

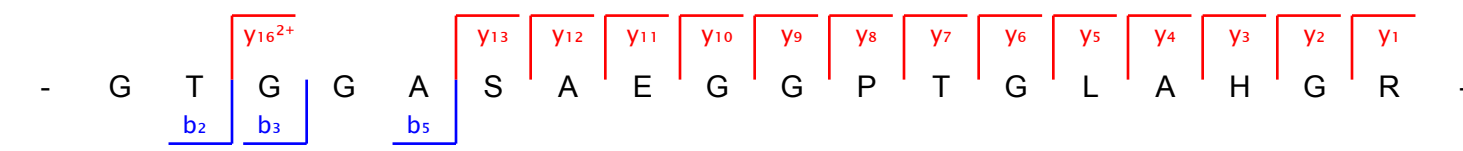
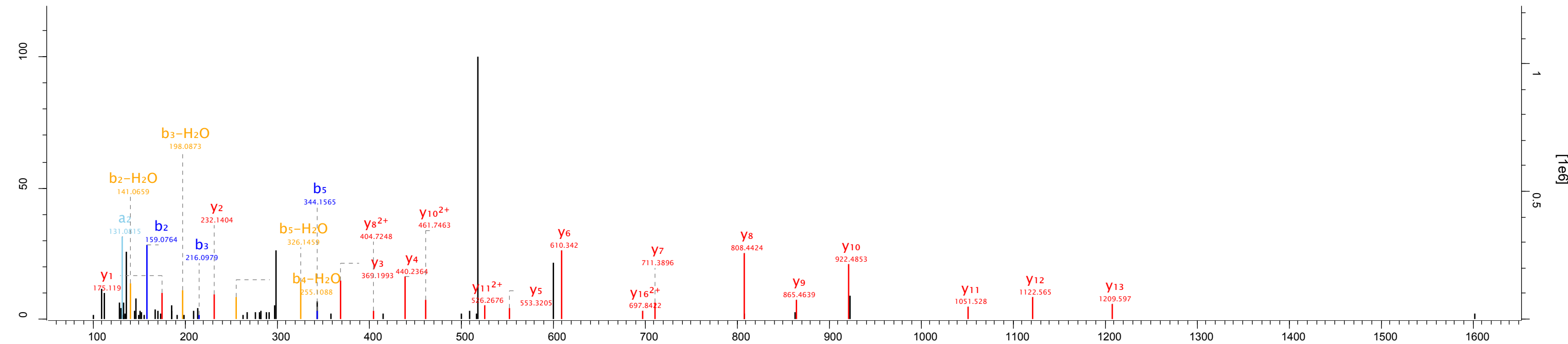


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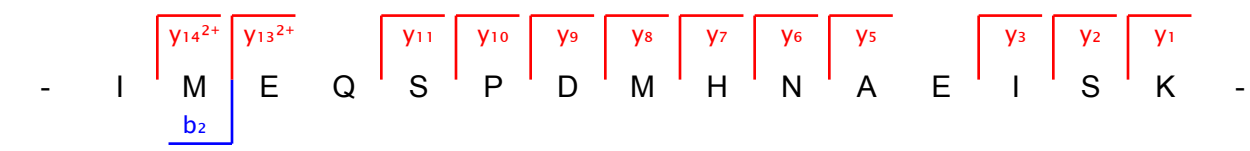
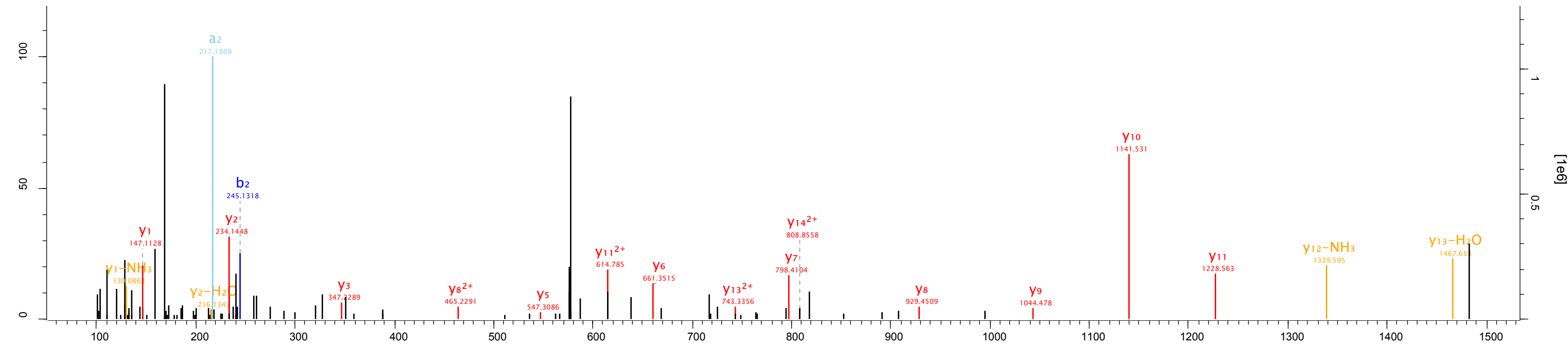


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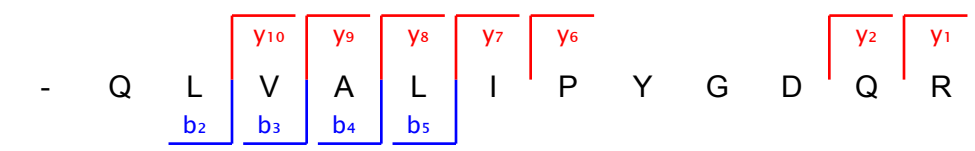
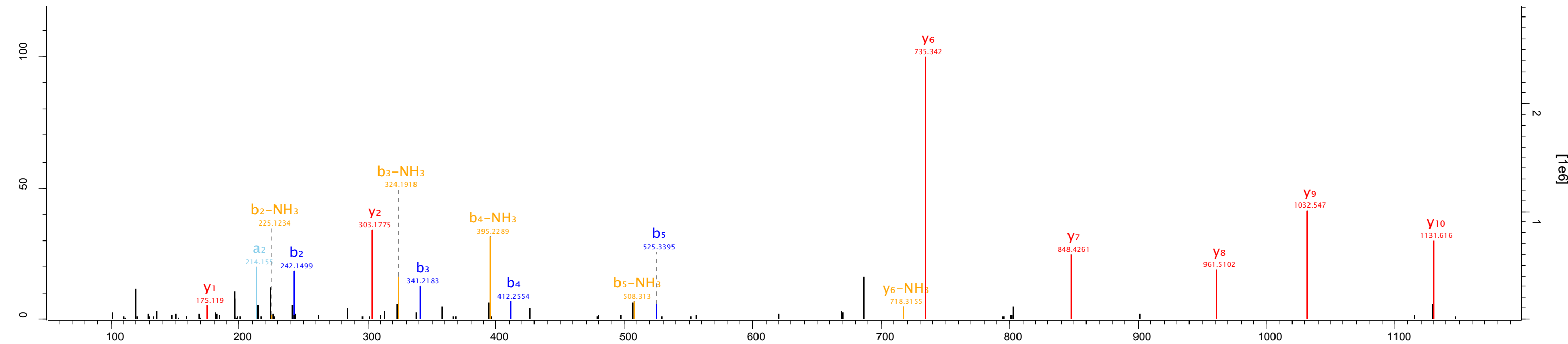
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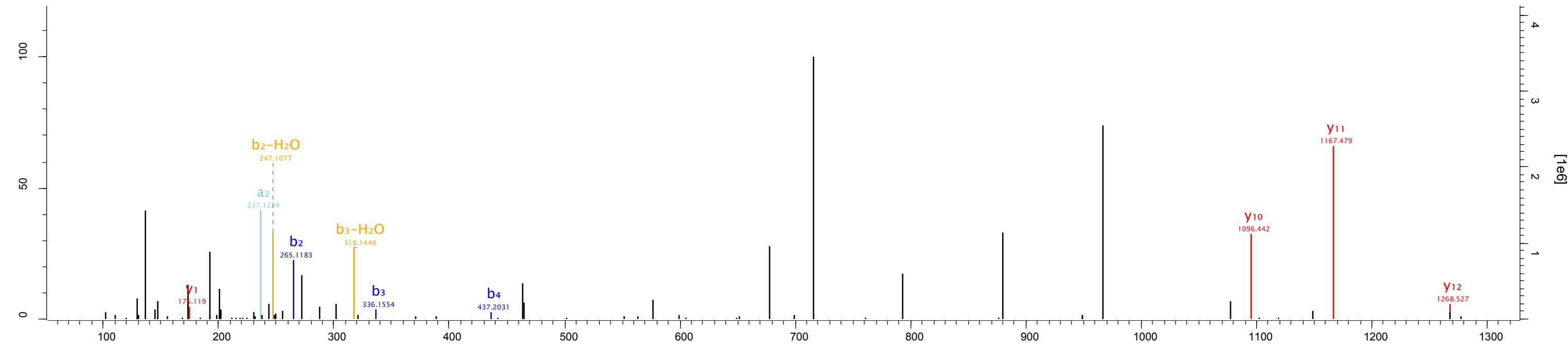
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 Scan: 10510 Method: FTMS; HCD Score: 66.25 m/z: 577.27 Gene names: SOX11;SOX4



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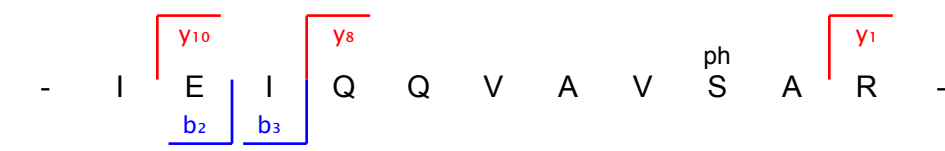
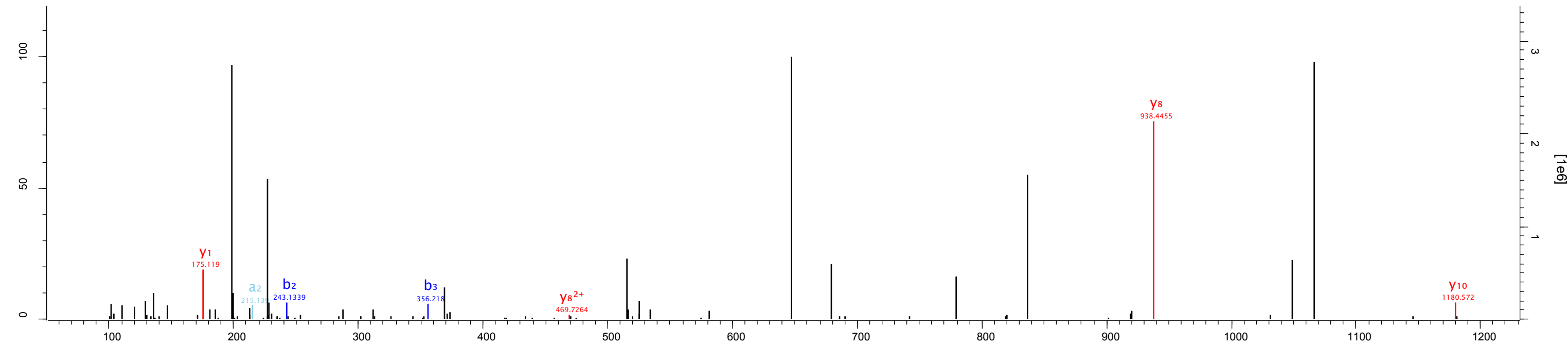


Raw file 20180707_MaS_A375SR_ML_proteome_2_04 Scan 11060 Method FTMS; HCD Score 56.2 m/z 716.3



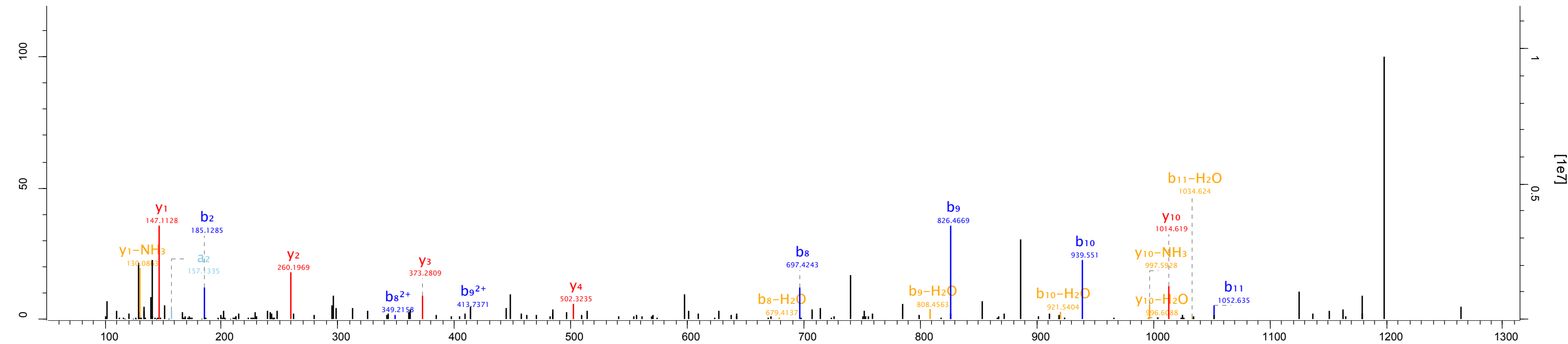
Raw file
20180707_MaS_A375SR_ML_proteome_2_04

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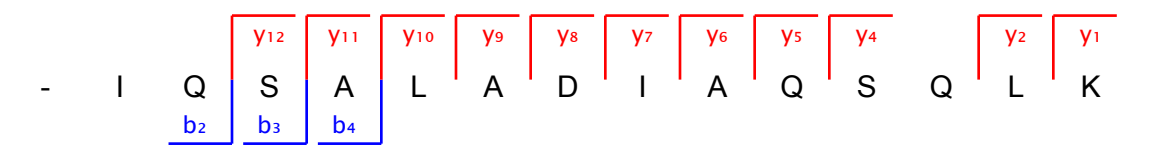
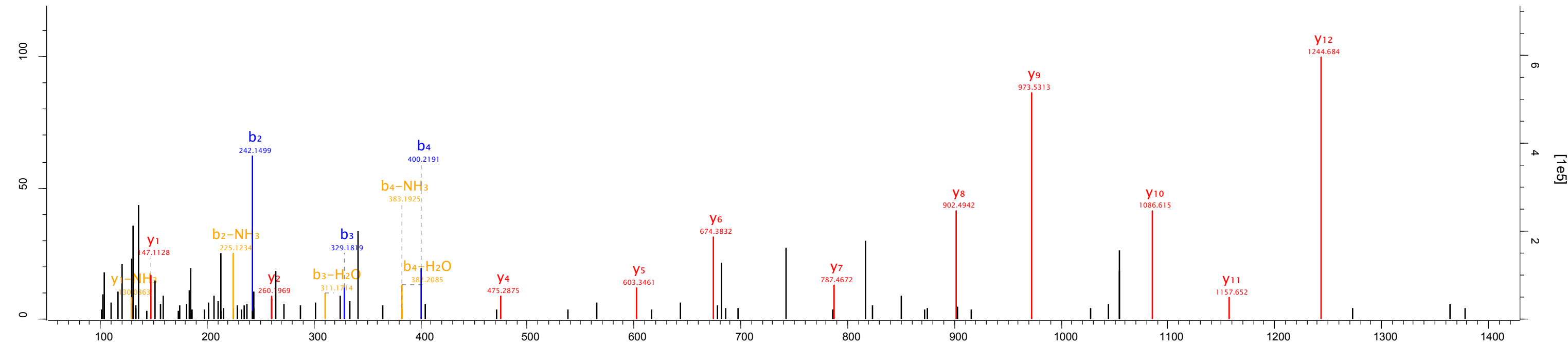


Raw file
20180707_MaS_A375SR_ML_proteome_2_04

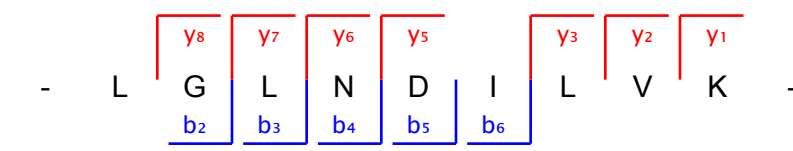
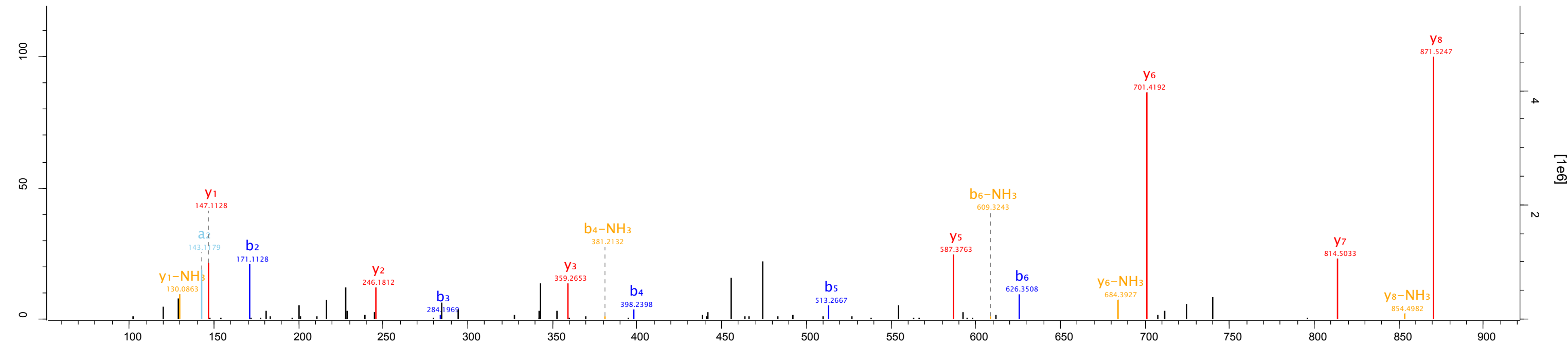
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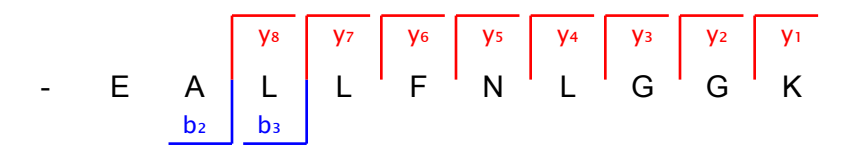
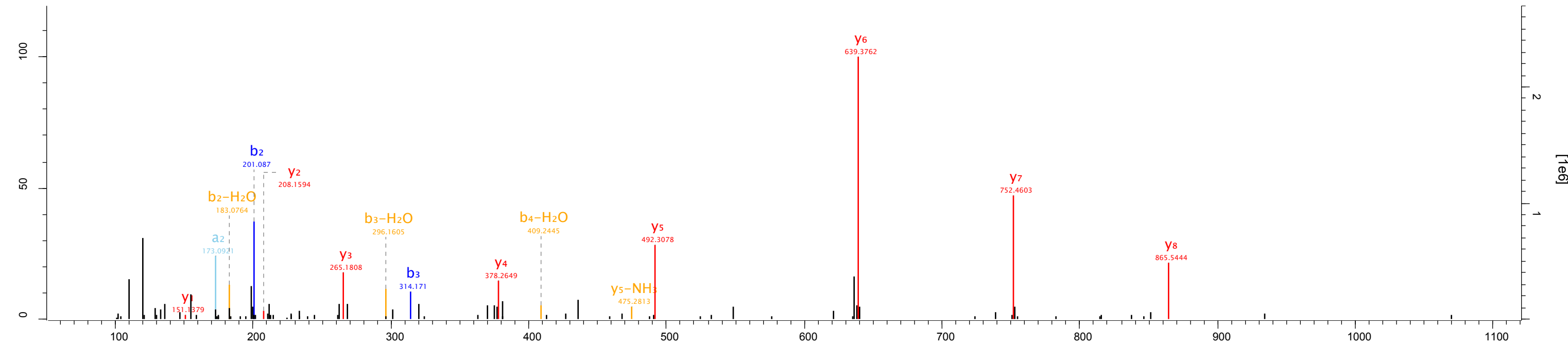
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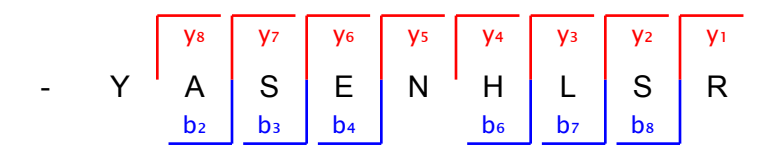
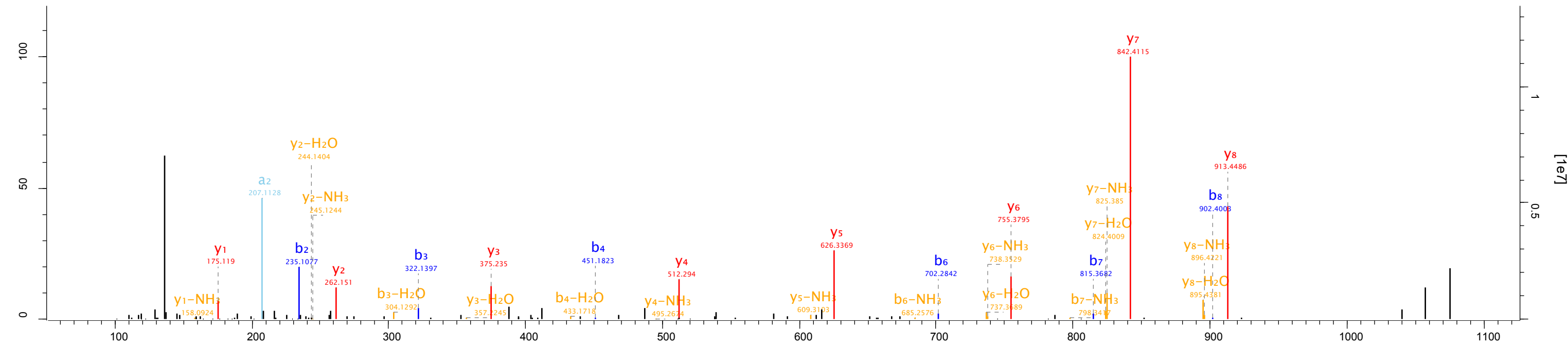


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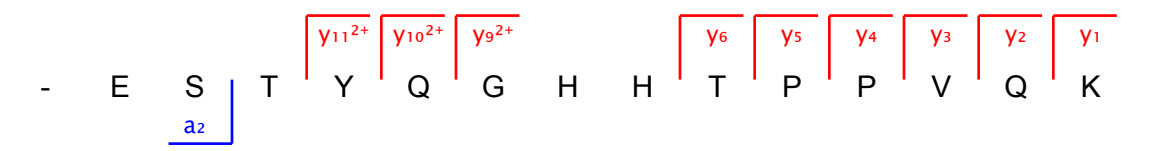
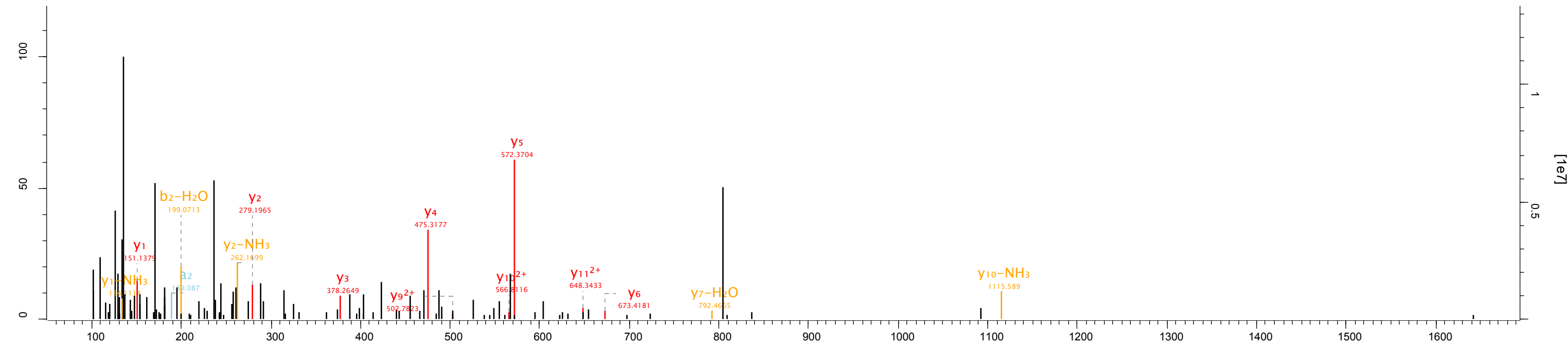


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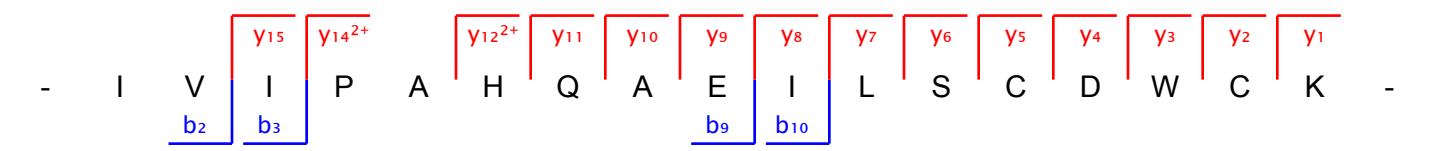
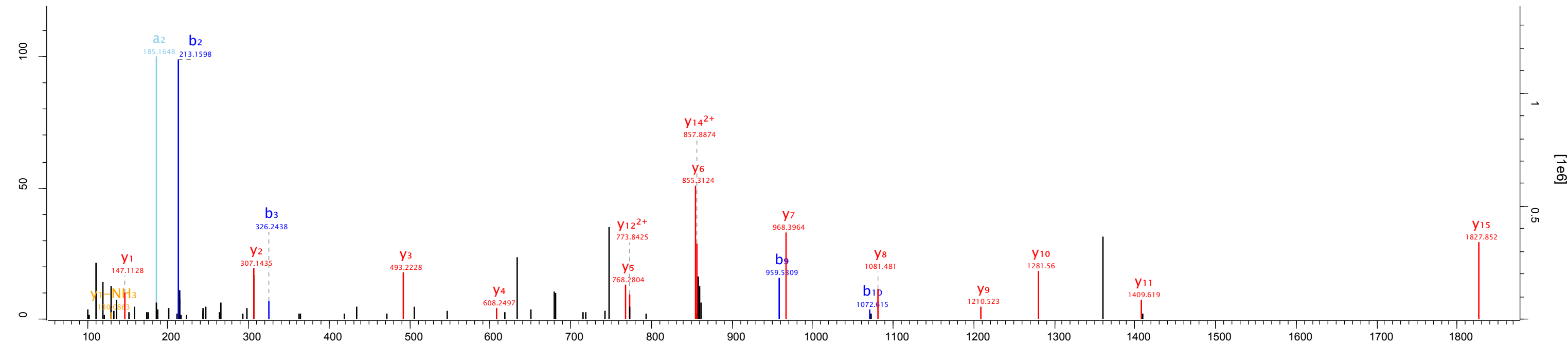
Scan 2890 Method FTMS; HCD Score 146.48 m/z 538.76 Gene names TM4SF1



Raw file 20180707_MaS_A375SR_ML_proteome_2_04
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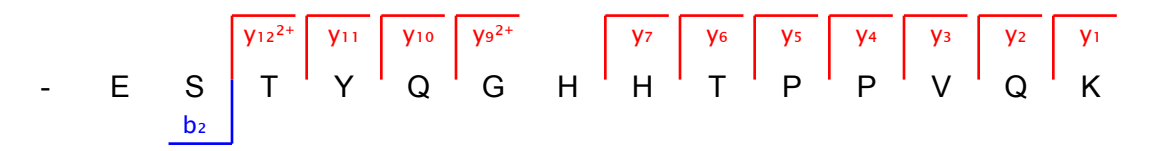
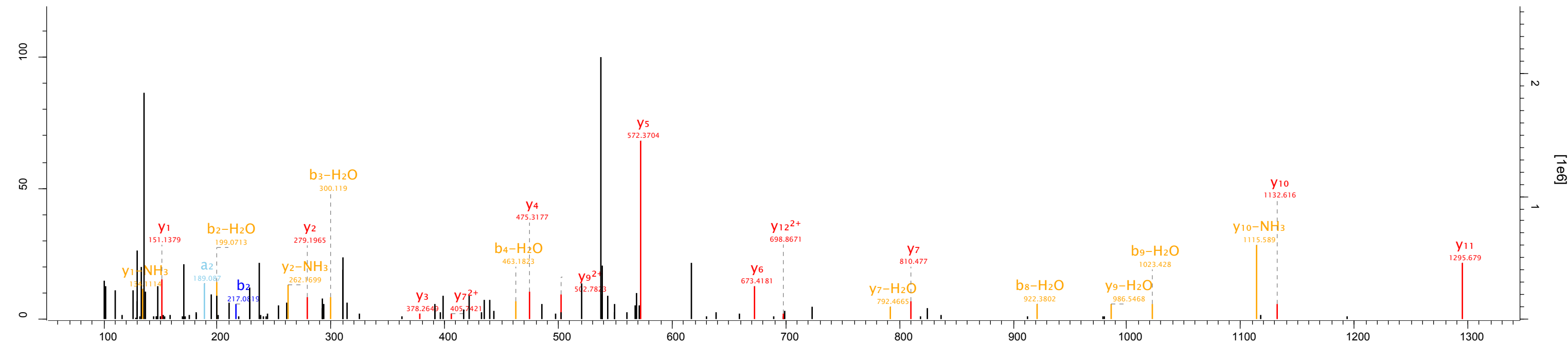


Raw file 20180707_MaS_A375SR_ML_proteome_2_05 Scan 23910 Method FTMS; HCD Score 78.95 m/z 681.01 Gene names PEX7

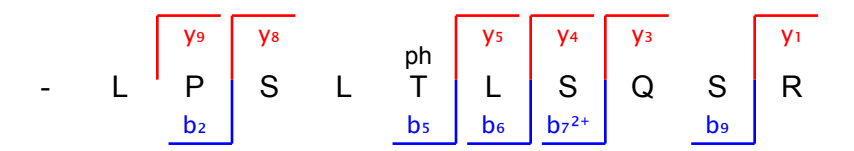
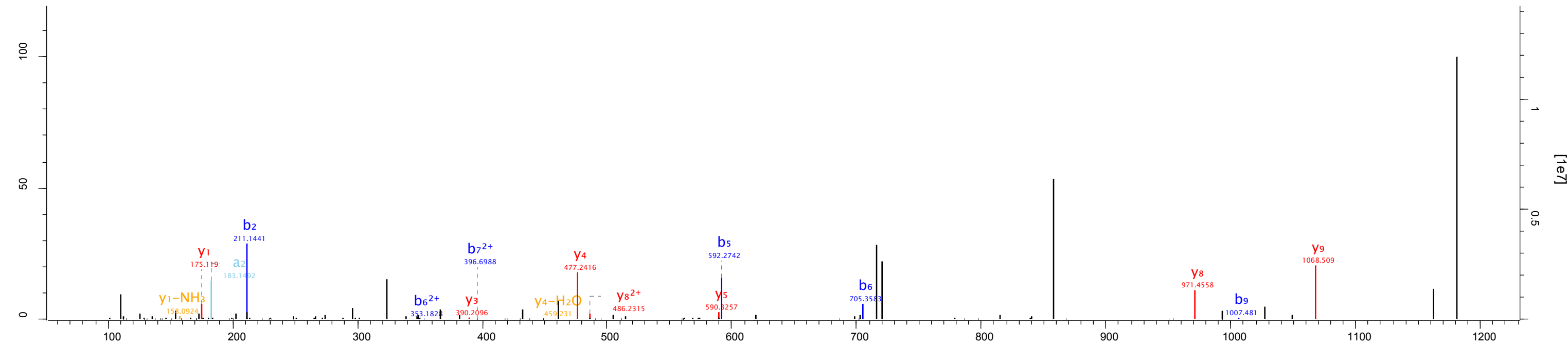


Raw file
20180707_MaS_A375SR_ML_proteome_2_05

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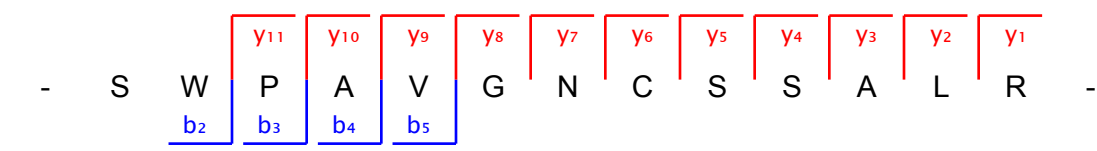
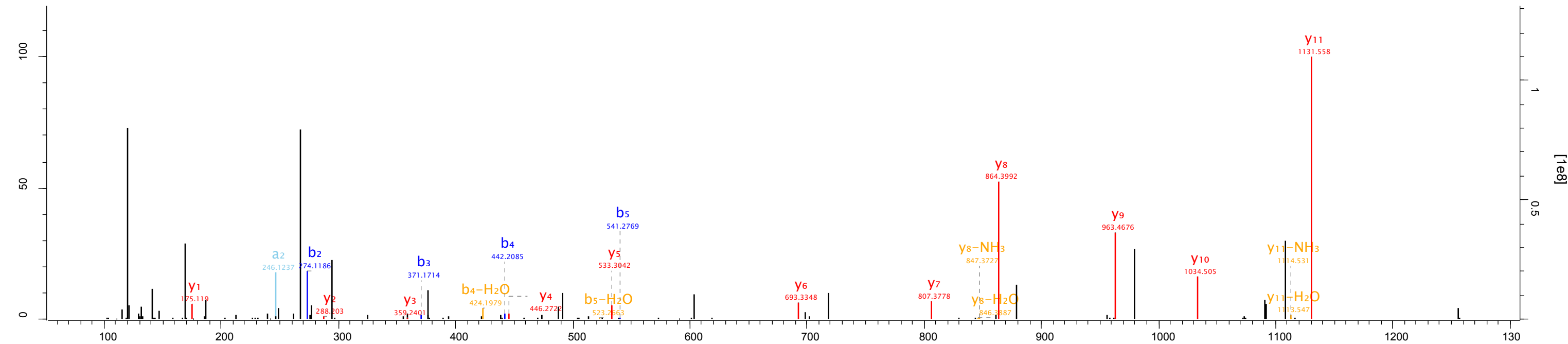


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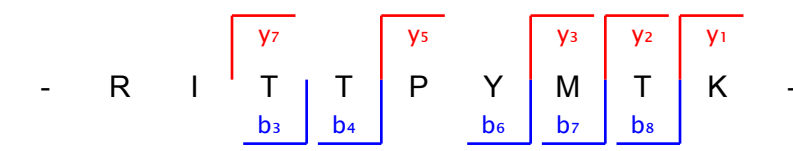
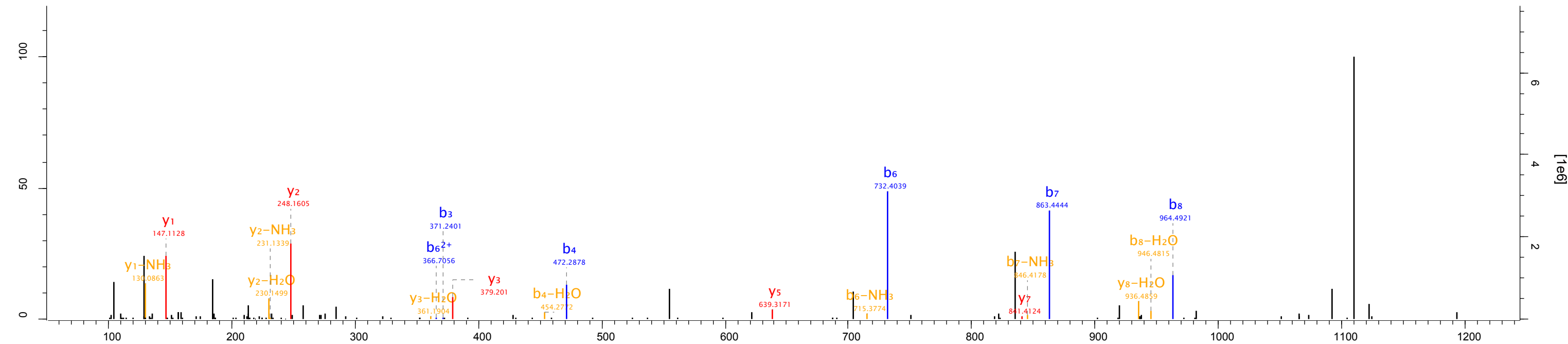


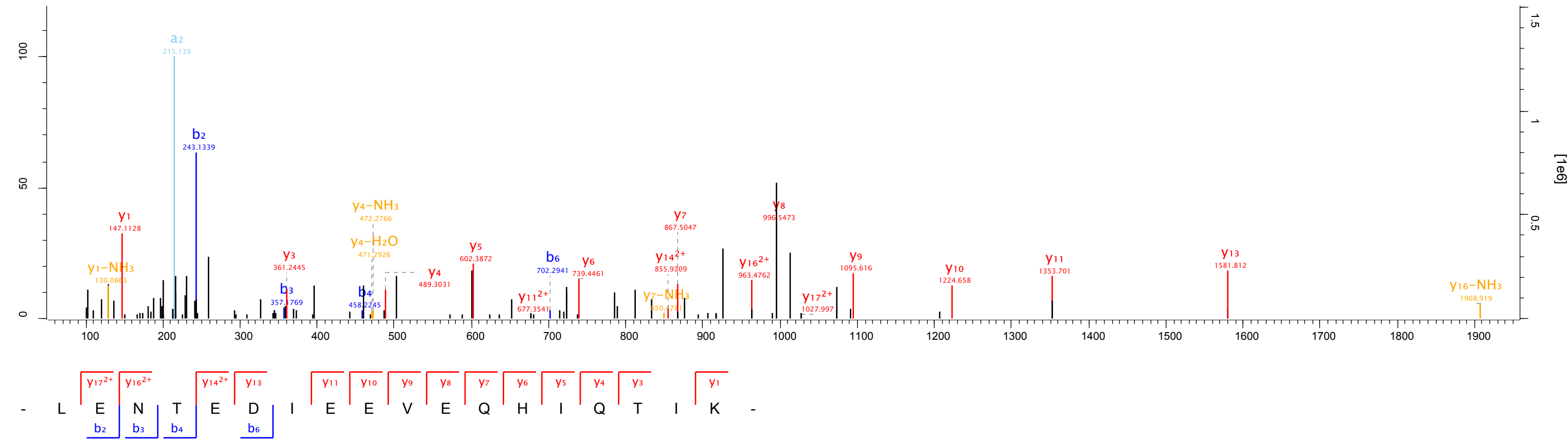
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20180707_MaS_A375SR_ML_proteome_2_06

Scan 17830 Method FTMS; HCD Score 67.08 m/z 702.84 Gene names HPX

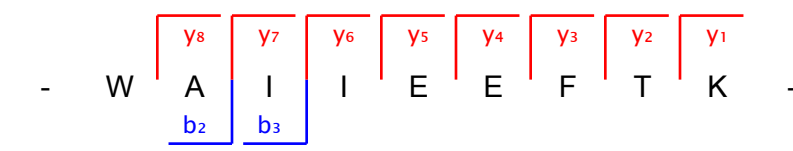
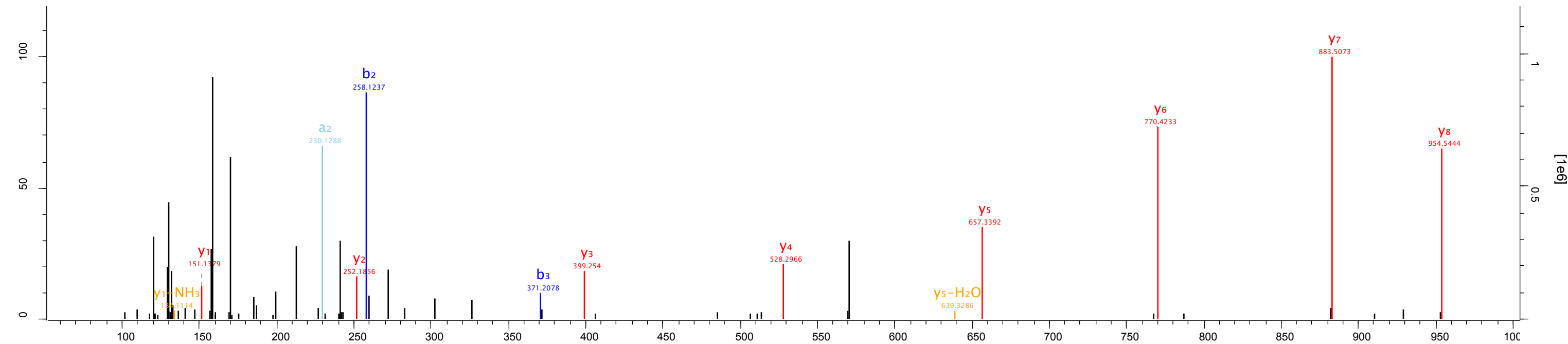


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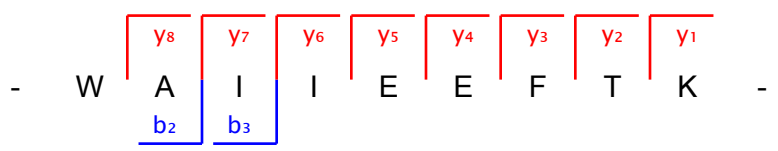
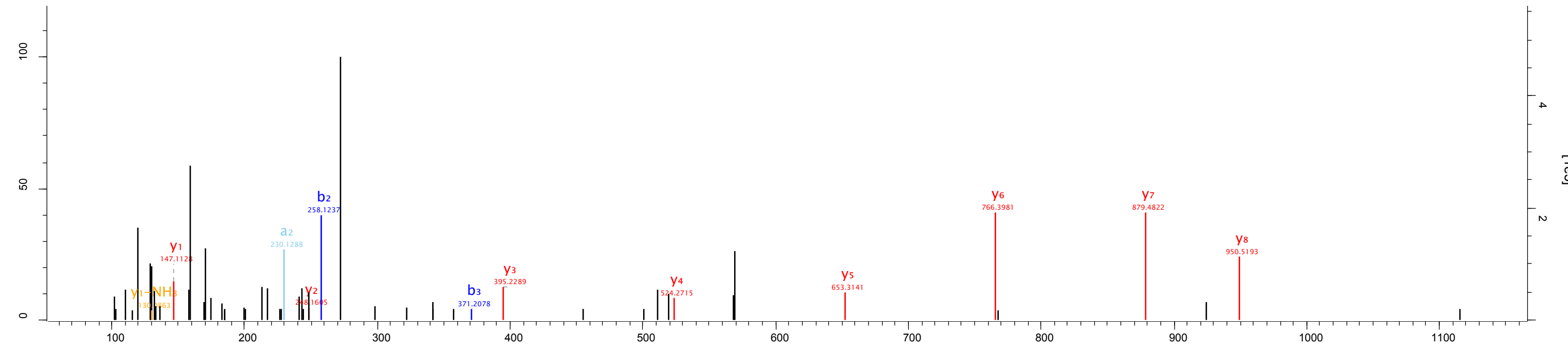


Raw file 20180707_MaS_A375SR_ML_proteome_2_07 Scan 27940 Method FTMS; HCD Score 51.44 m/z 570.82 Gene names MT-ND2



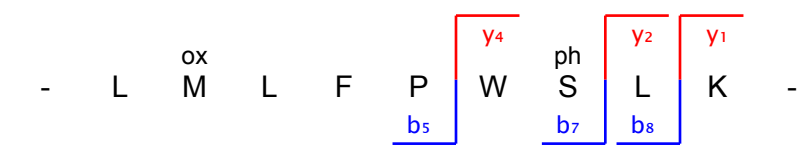
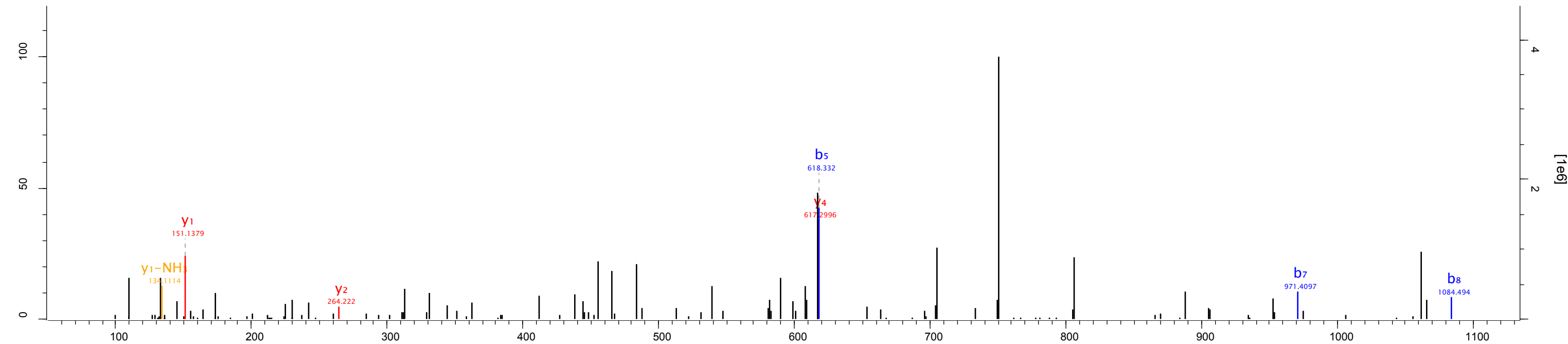
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20180707_MaS_A375SR_ML_proteome_2_07

Scan 27960 Method FTMS; HCD Score 43.3 m/z 568.8 Gene names MT-ND2

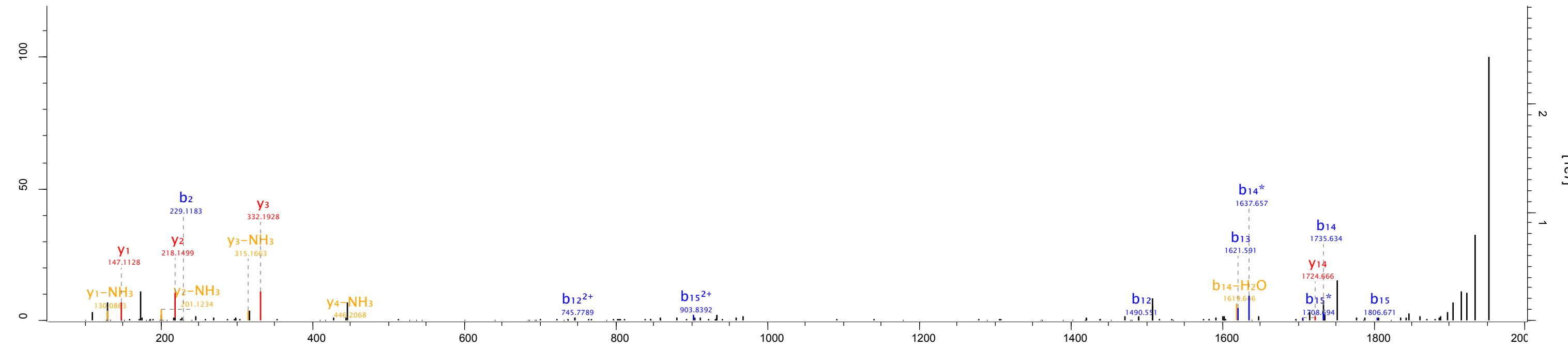


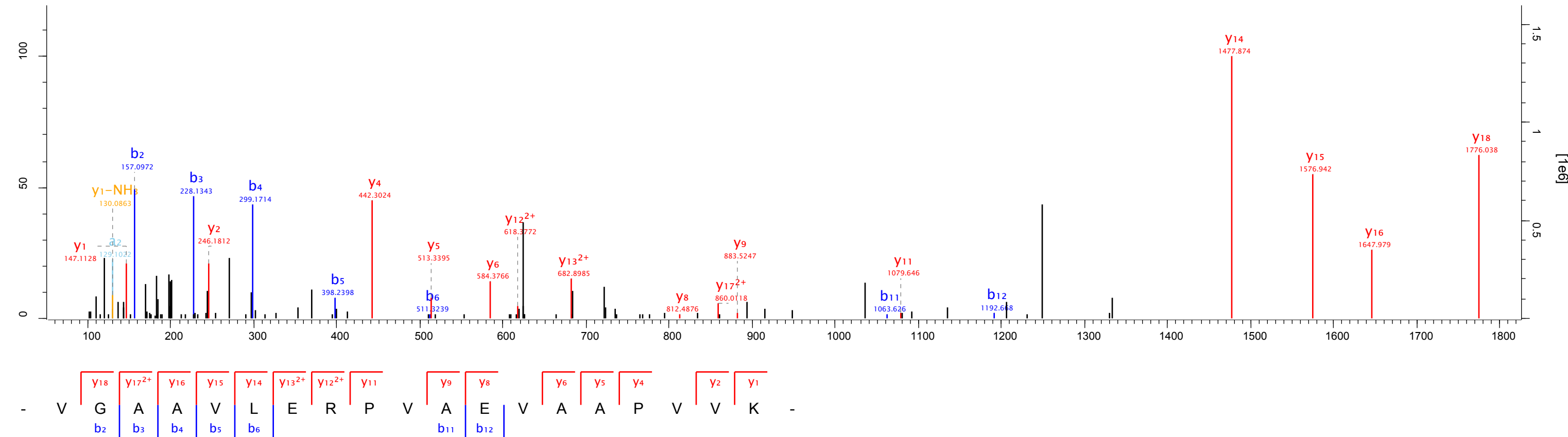
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20180707_MaS_A375SR_ML_proteome_2_07

Scan	Method	Score	m/z
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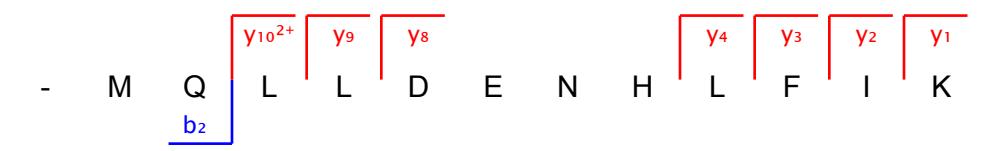
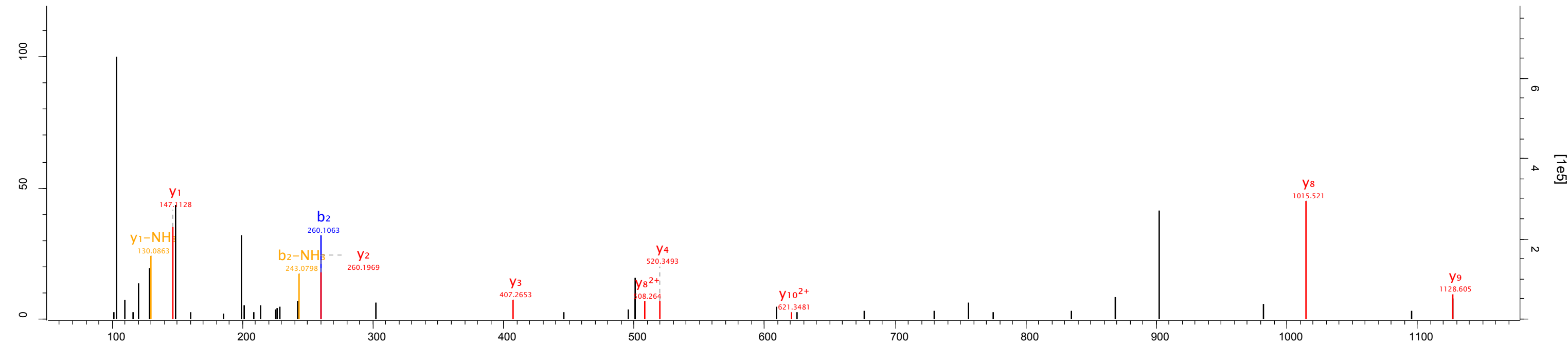


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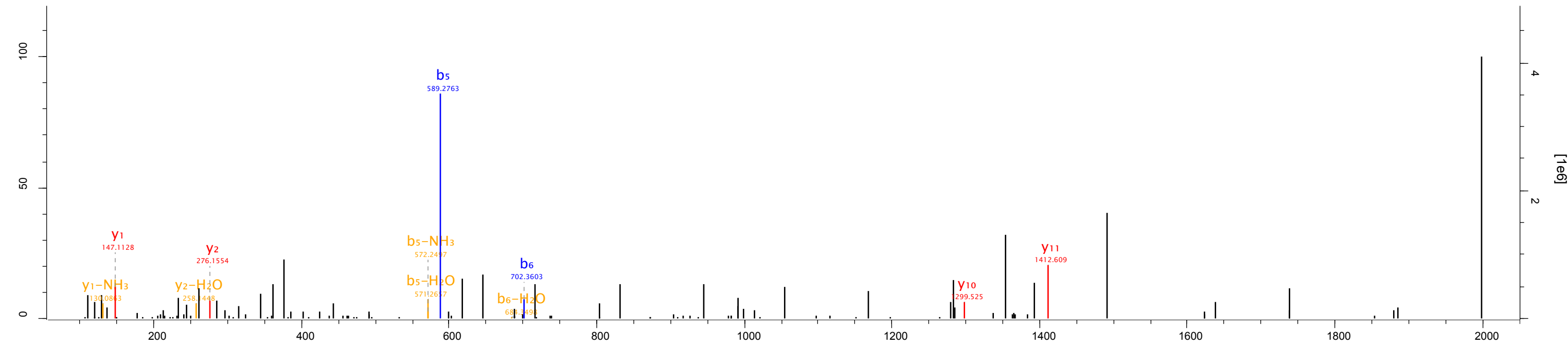




Raw file 20180707_MaS_A375SR_ML_proteome_2_08 Scan 25600 Method FTMS; HCD Score 52.25 m/z 501.27 Gene names DET1



Raw file
 20180707_MaS_A375SR_ML_proteome_2_08
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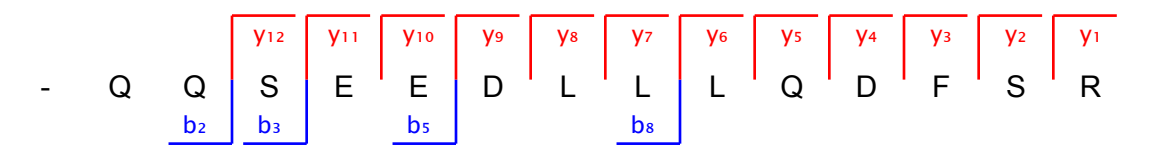
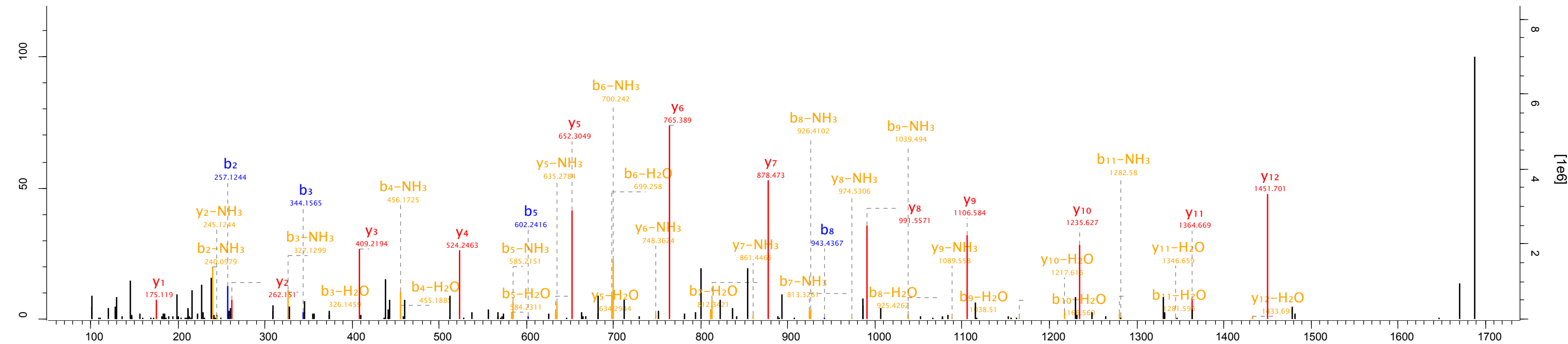


ac
 - M G T R T L Q F E I S D S H E K -

Fragmentation mapping:
 - b₅ (under T)
 - b₆ (under L)
 - y₁₁ (over L)
 - y₁₀ (over Q)
 - y₂ (over E)
 - y₁ (over K)

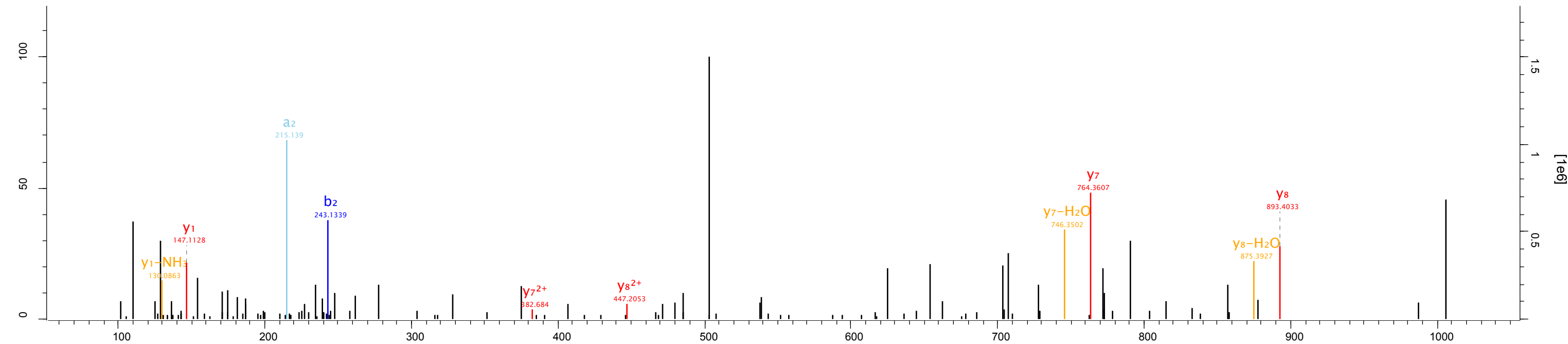
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20180707_MaS_A375SR_ML_proteome_2_08

Scan 27830 Method FTMS; HCD Score 124.62 m/z 854.41 Gene names SSR3

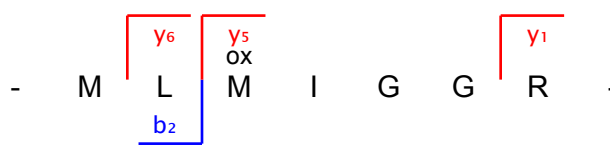
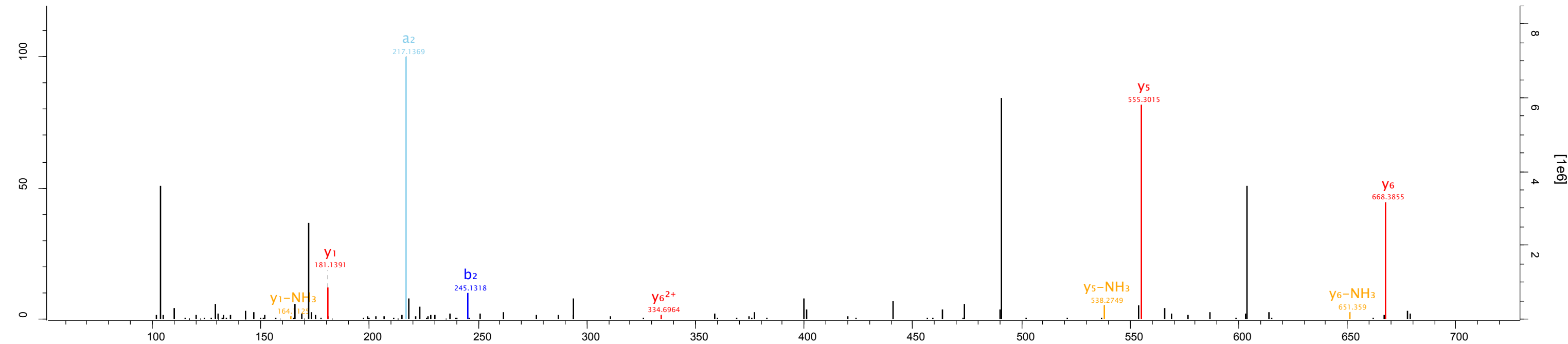


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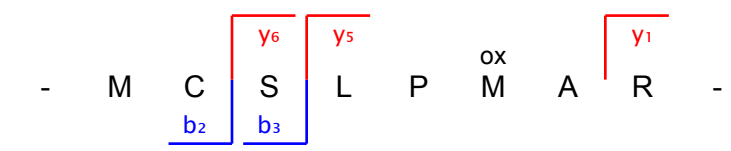
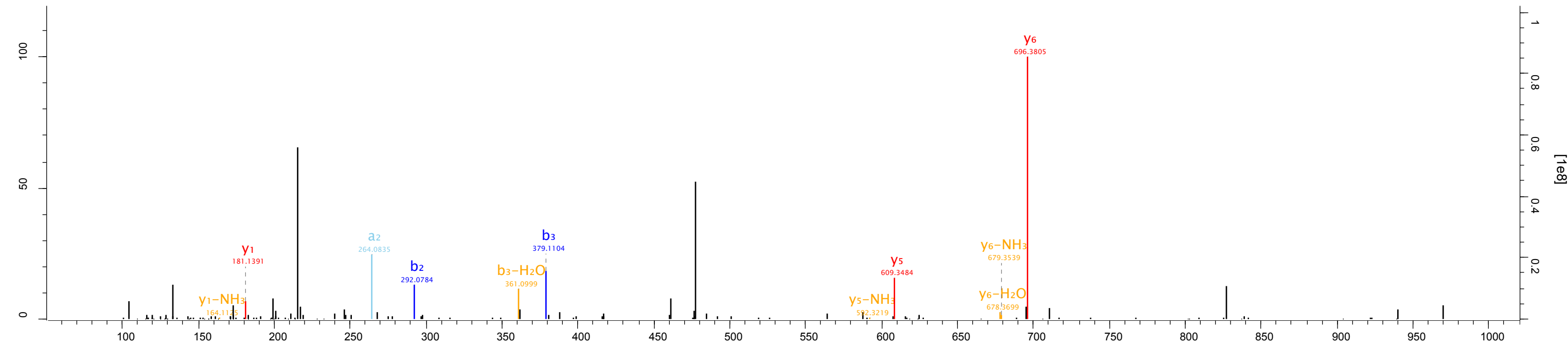
Scan 3300 Method FTMS; HCD Score 62.55 m/z 503.75 Gene names NRXN2

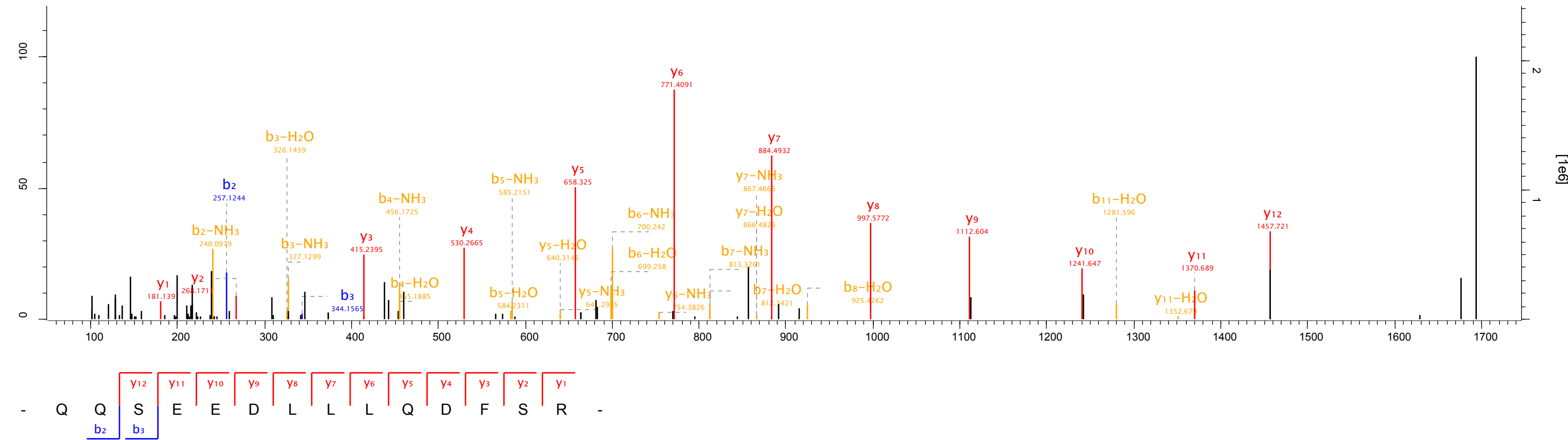


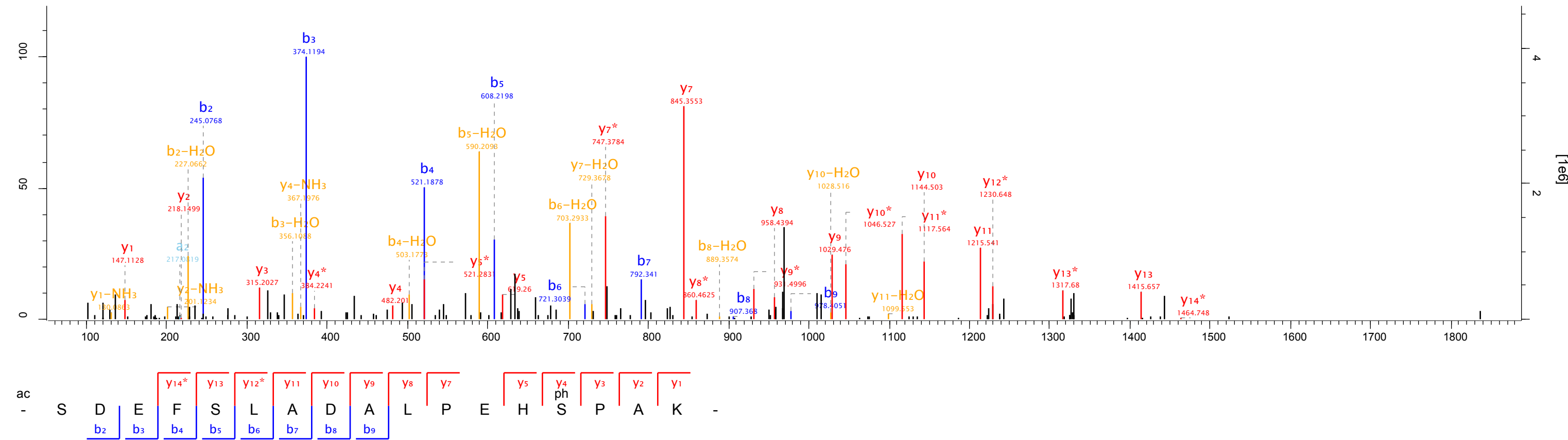
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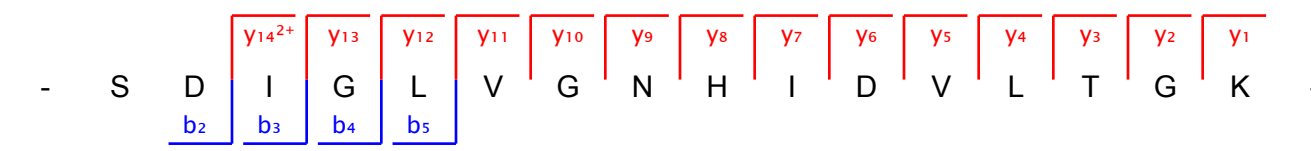
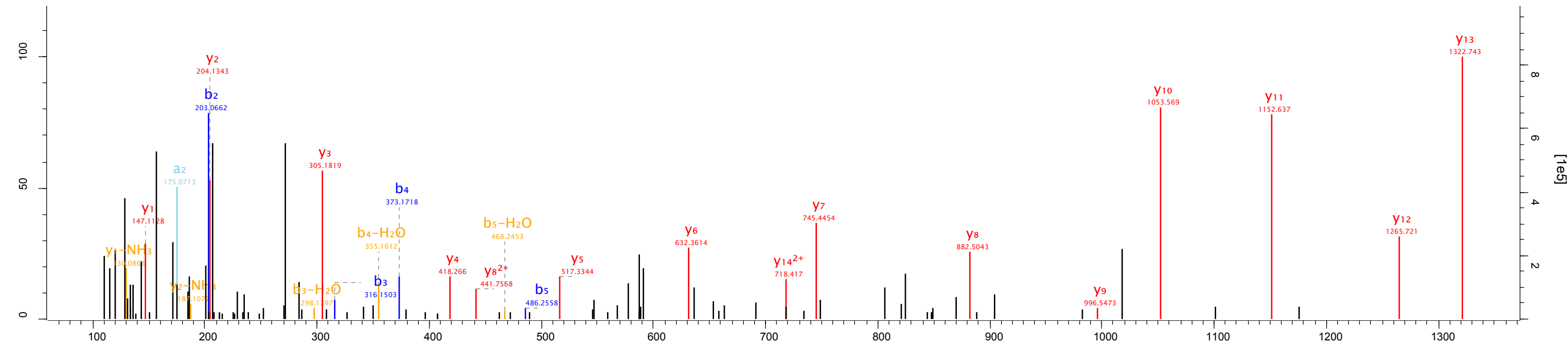
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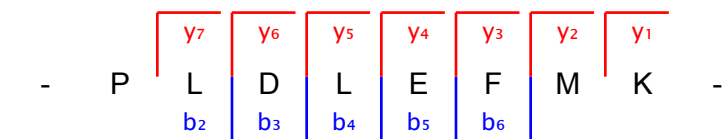
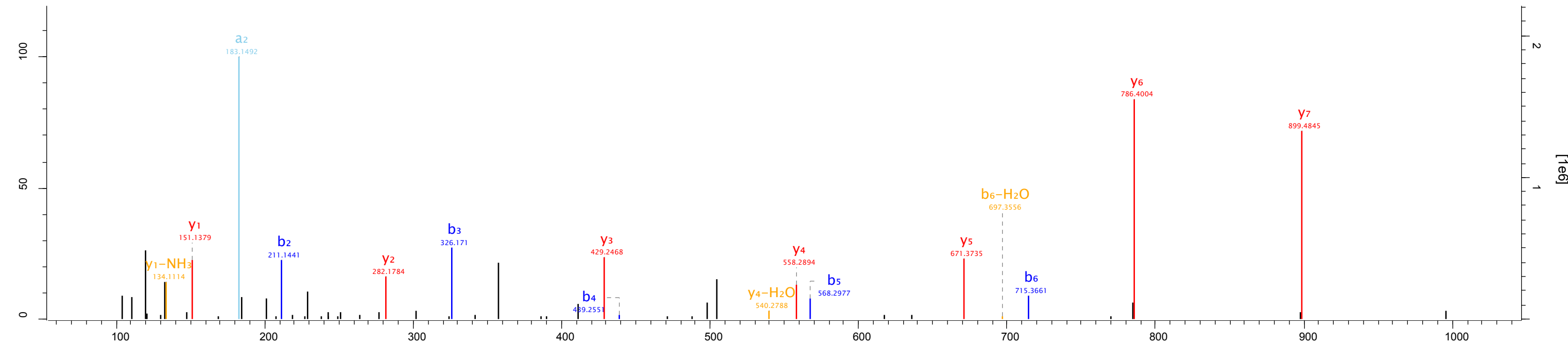




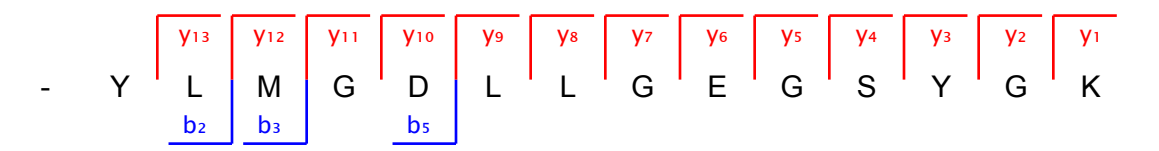
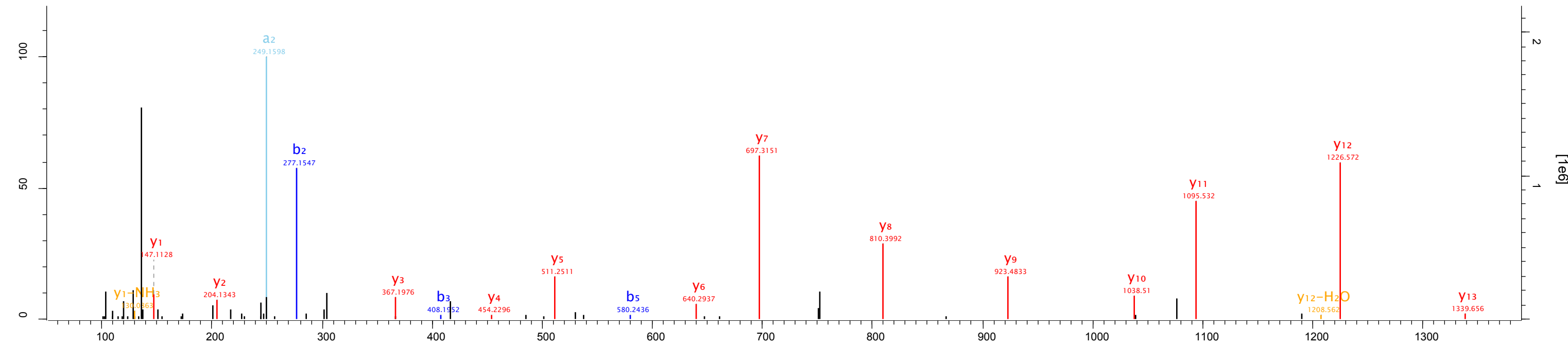


Raw file 20180707_MaS_A375SR_ML_proteome_2_10 Scan 23300 Method FTMS; HCD Score 88.39 m/z 546.97 Gene names EDEM2

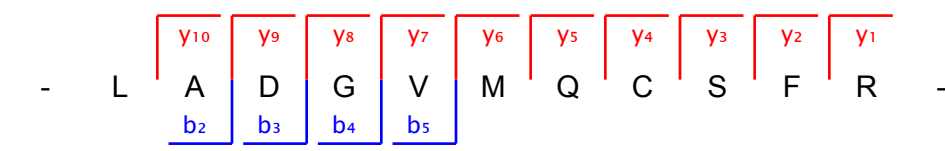
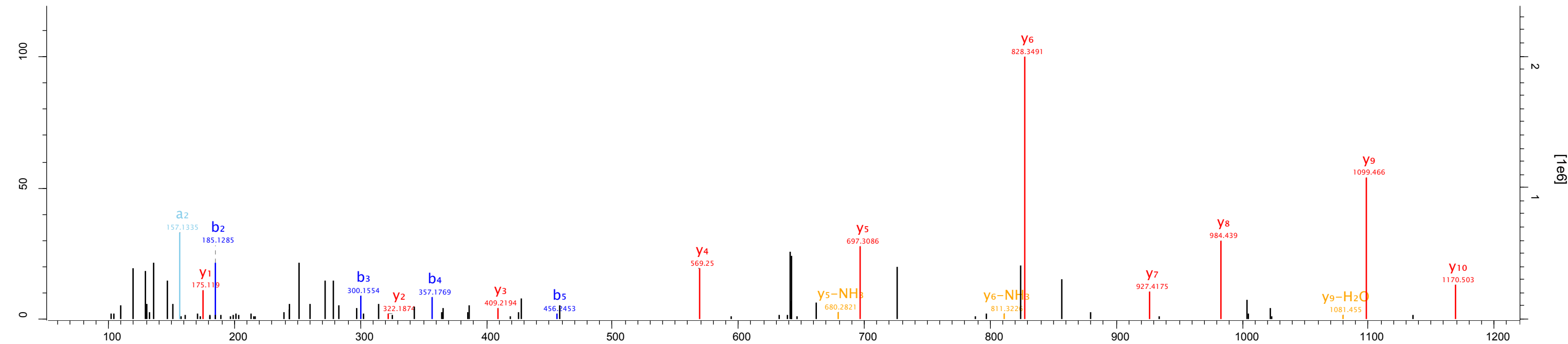




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 Scan: 17600 Method: FTMS; HCD Score: 75.74 m/z: 642.3 Gene names: FRRS1



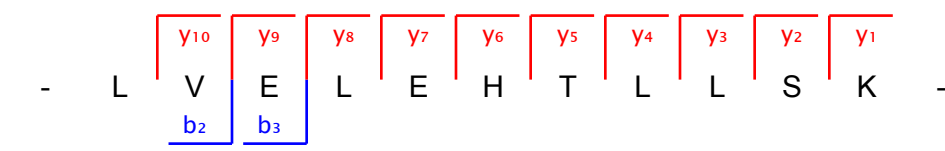
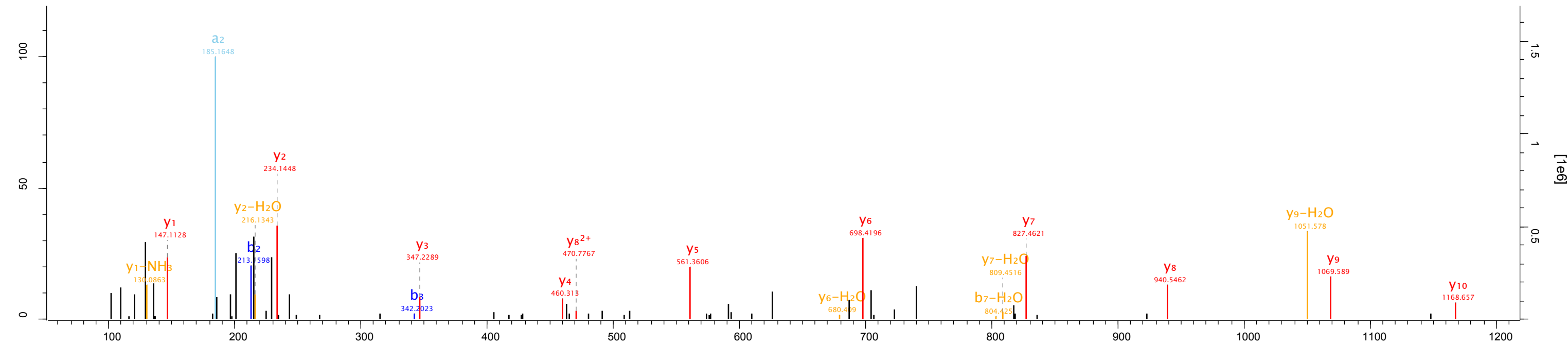
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ac - L Y Q L P A A D ph S A ph T A S V V I T K -

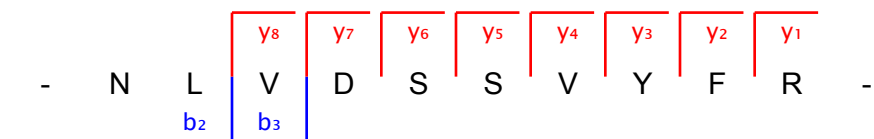
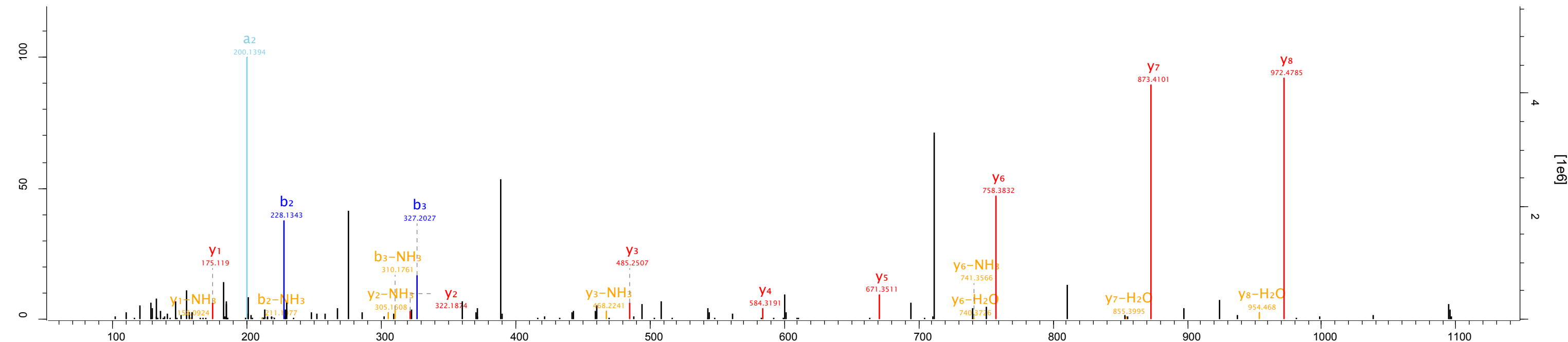
b15
y3
I
T
y2
K
y1

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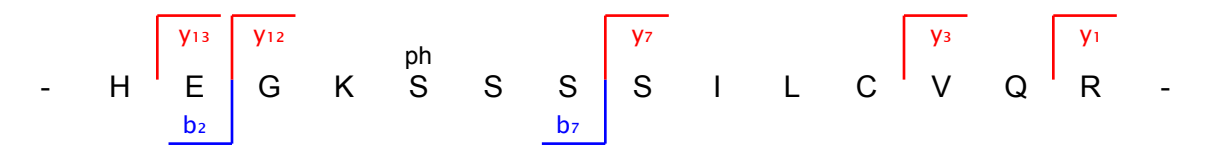
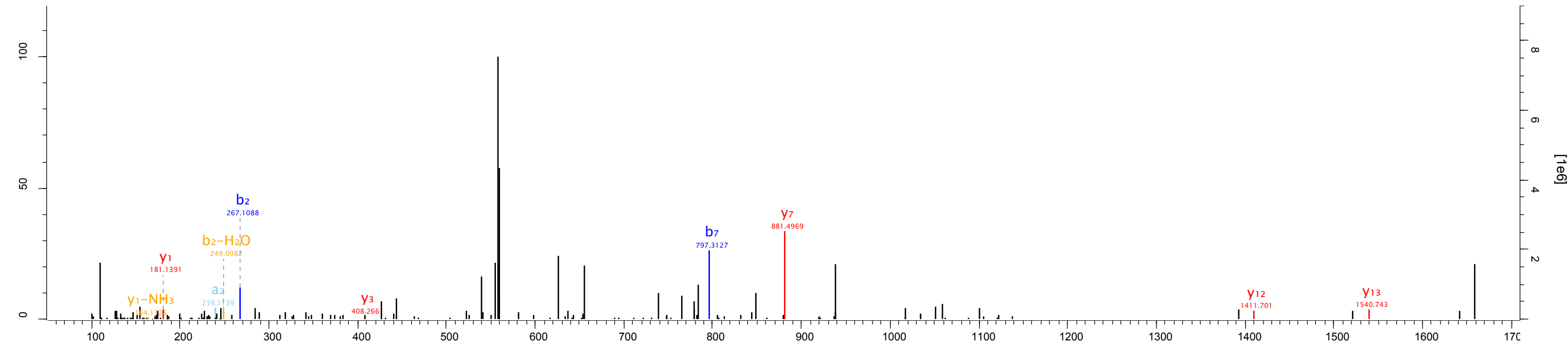


Raw file
20180707_MaS_A375SR_ML_proteome_2_11

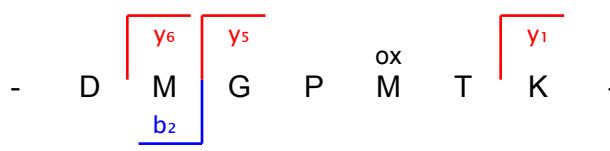
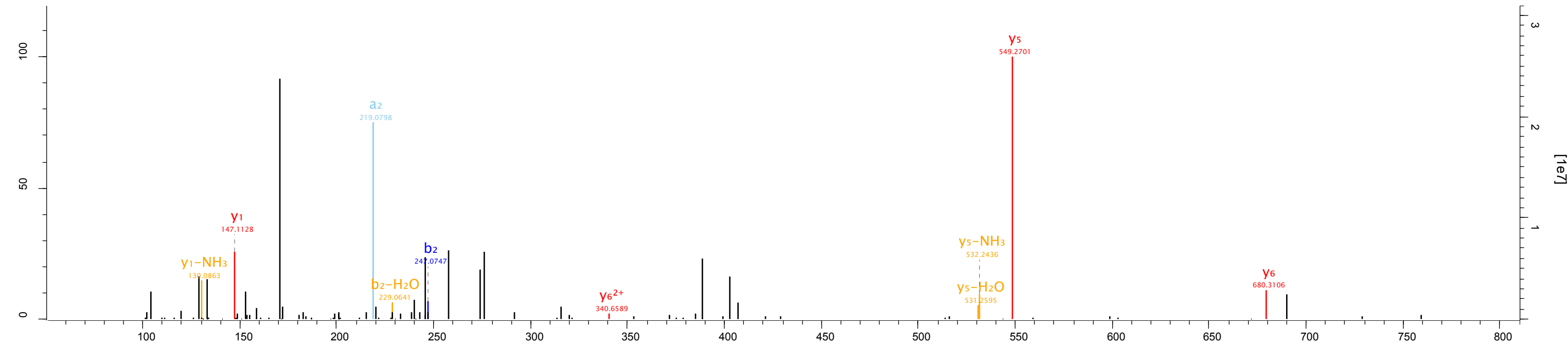
Scan 22250 Method FTMS; HCD Score 78.93 m/z 600.82 Gene names MEF2BNB



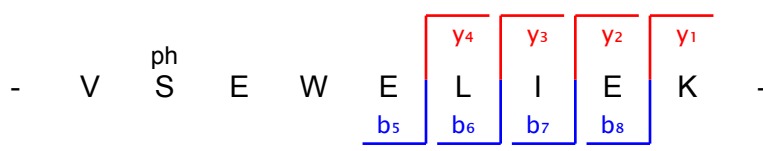
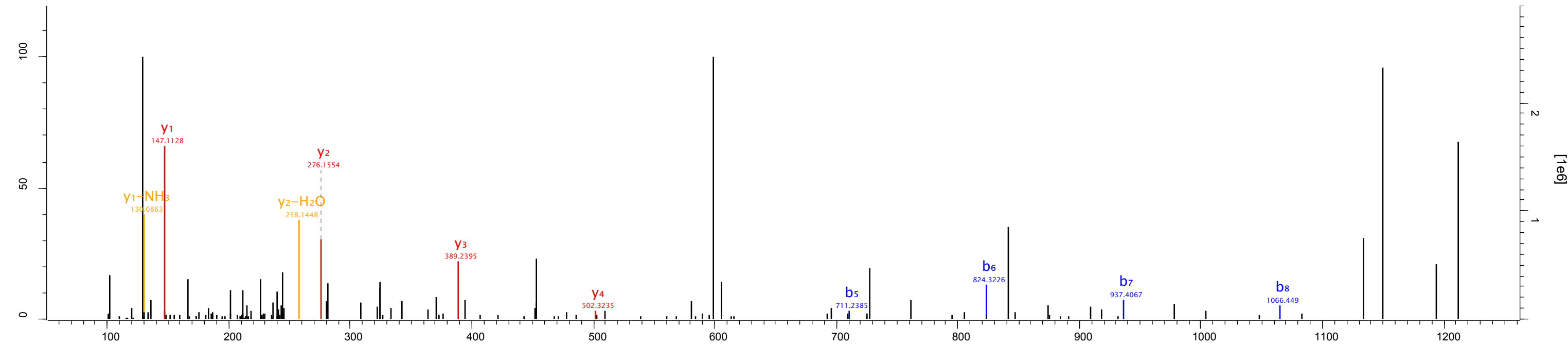
Raw file 20180707_MaS_A375SR_ML_proteome_2_11 Scan 3800 Method FTMS; HCD Score 42.78 m/z 559.94



Raw file 20180707_MaS_A375SR_ML_proteome_2_12 Scan 11040 Method FTMS; HCD Score 60.29 m/z 398.17

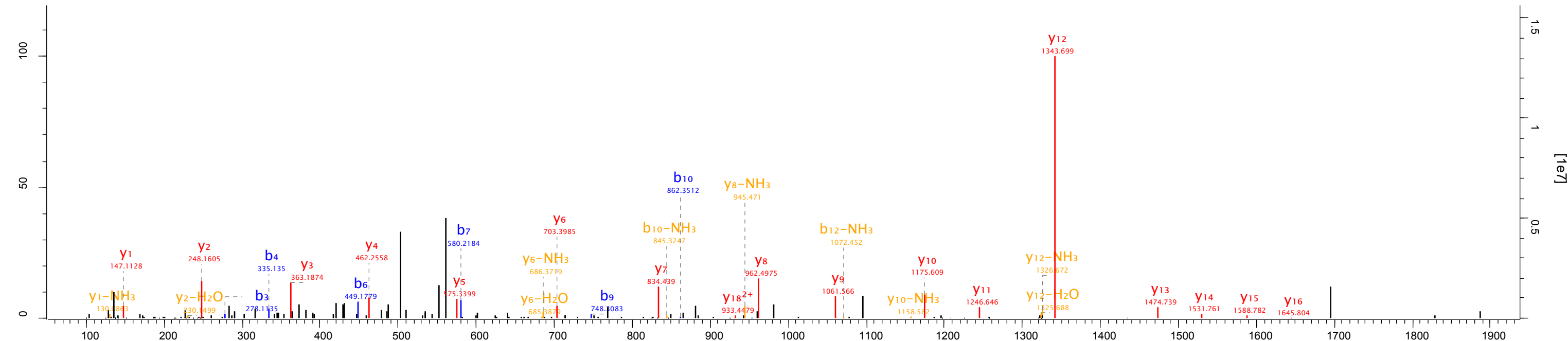


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Raw file
20180707_MaS_A375SR_ML_proteome_2_12

Scan 25850 Method FTMS; HCD Score 129.43 m/z 961.96 Gene names CDC42SE2



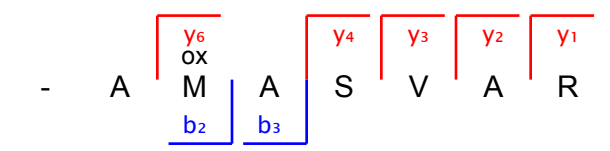
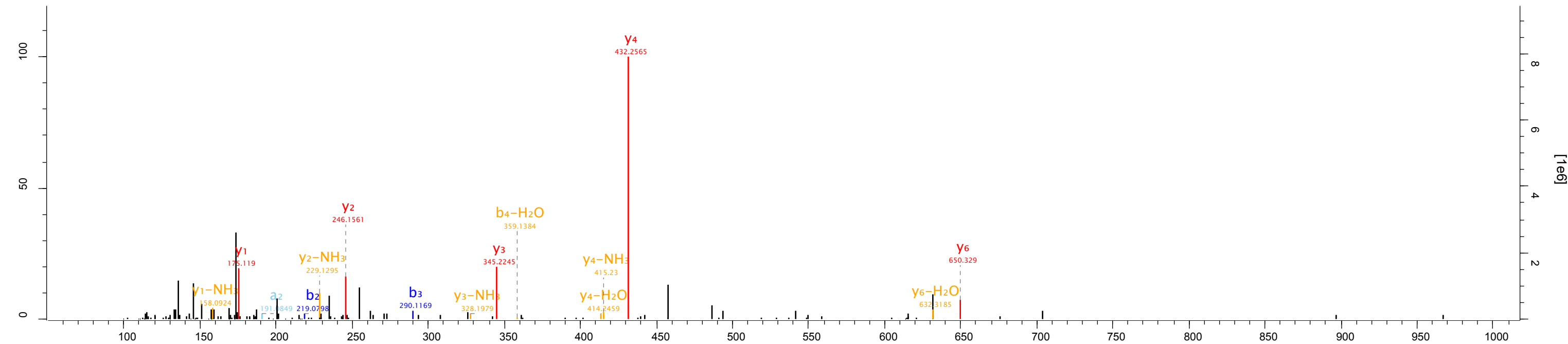
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Fragmentation mapping:

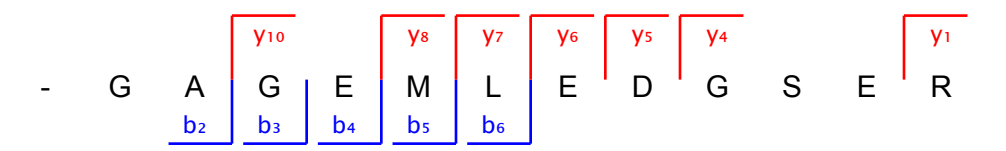
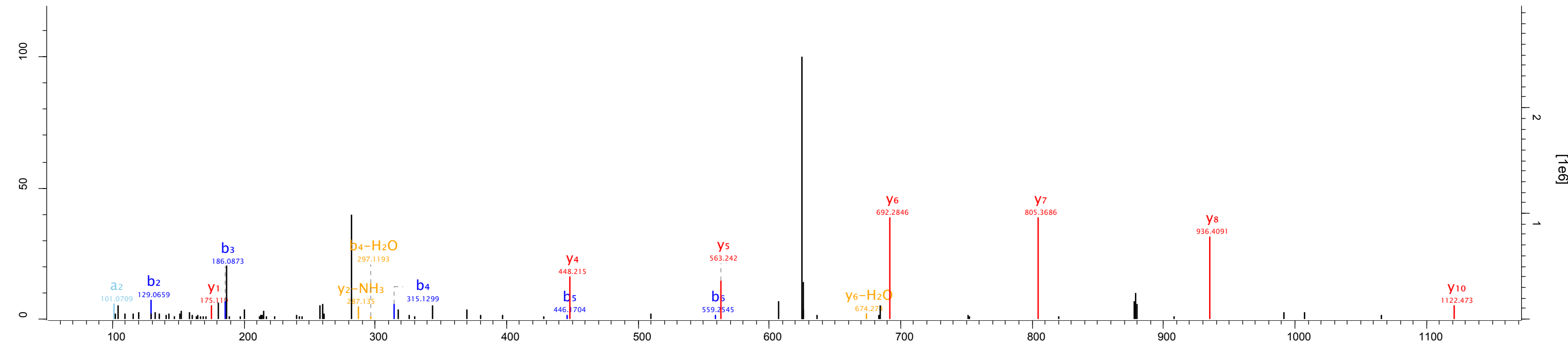
- Red boxes (y ions): y₁₈²⁺ (G), y₁₆ (G), y₁₅ (G), y₁₄ (G), y₁₃ (M), y₁₂ (P), y₁₁ (A), y₁₀ (N), y₉ (V), y₈ (Q), y₇ (M), y₆ (Q), y₅ (L), y₄ (V), y₃ (D), y₂ (T), y₁ (K).
- Blue boxes (b ions): b₃ (Y), b₄ (G), b₆ (G), b₇ (M), b₉ (A), b₁₀ (N).

Raw file
20180707_MaS_A375SR_ML_proteome_2_13

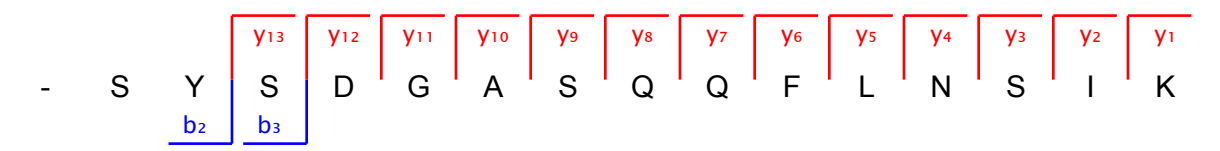
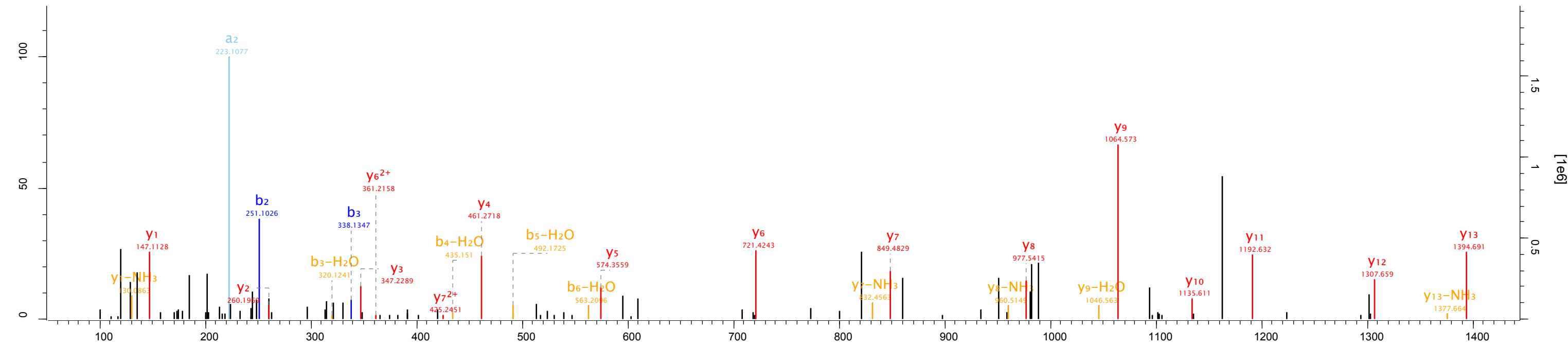
Scan Method Score m/z Gene names
10150 FTMS; HCD 92.19 361.19 ART4



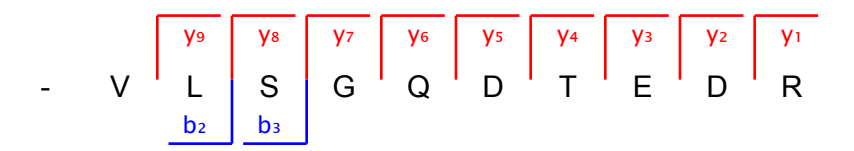
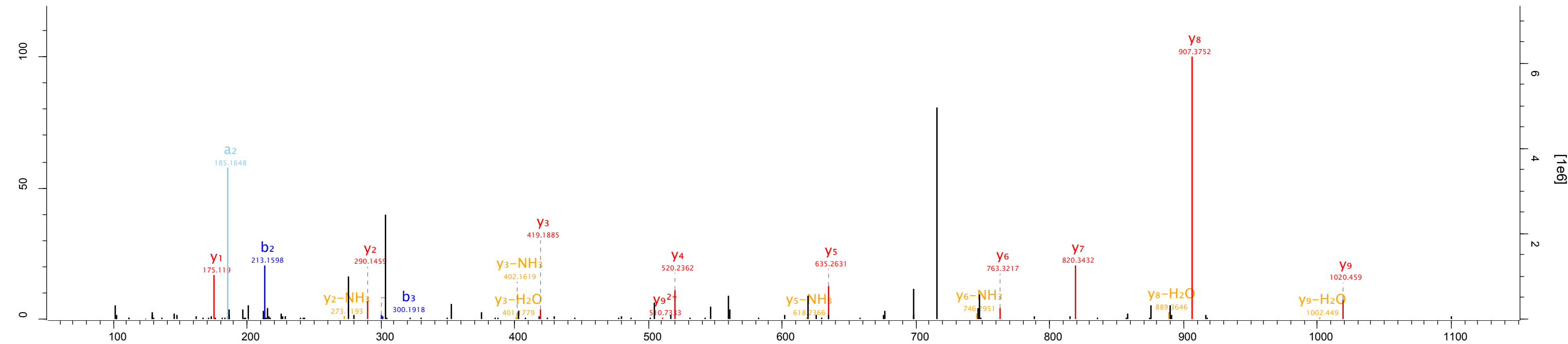
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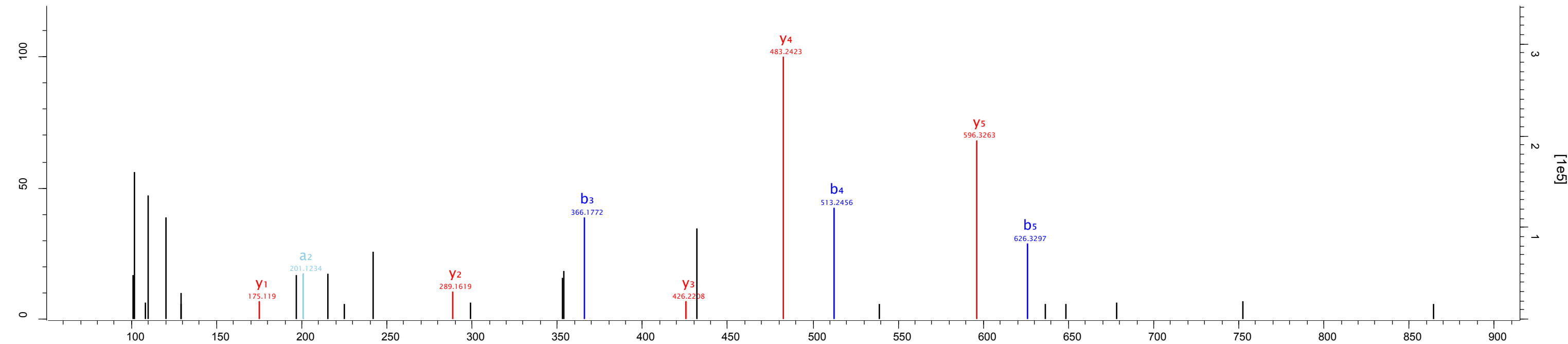
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 Scan: 21520 Method: FTMS; HCD Score: 76.82 m/z: 822.9 Gene names: UBXN2A



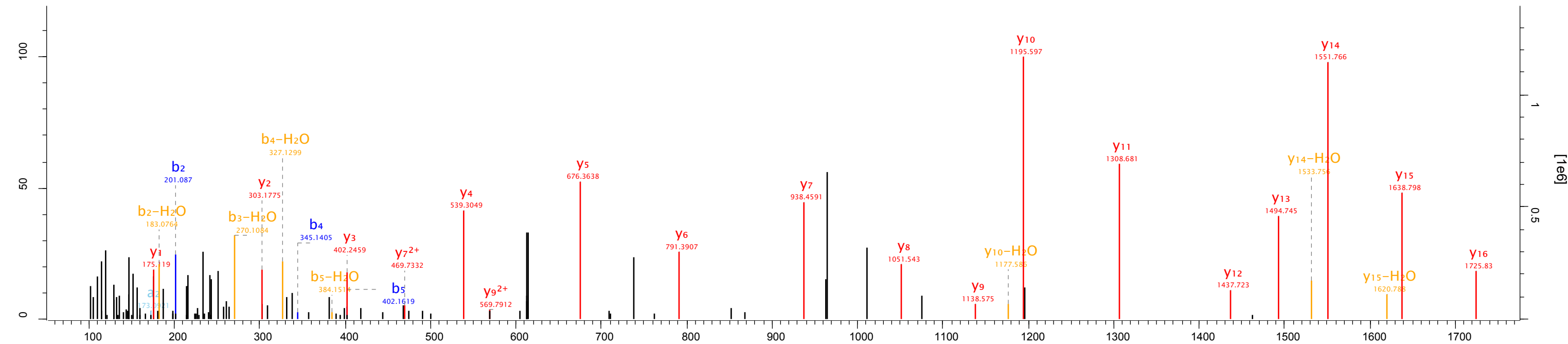
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 Scan: 4890 Method: FTMS; HCD Score: 90.05 m/z: 560.27 Gene names: SFT2D2



Raw file 20180707_MaS_A375SR_ML_proteome_2_14 Scan 25800 Method FTMS; HCD Score 24.96 m/z 431.23 Gene names IGFALS



Raw file: 20180707_MaS_A375SR_ML_proteome_2_15
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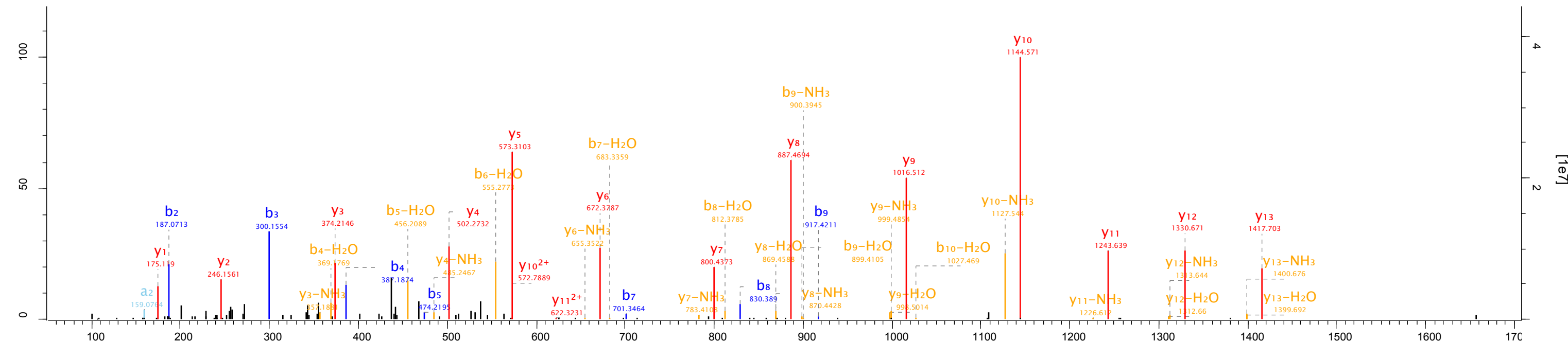


ac - A S S G G E L G S L F D H H V Q R -

Fragmentation mapping:
 - b2 (under S)
 - b4 (under G)
 - b5 (under G)

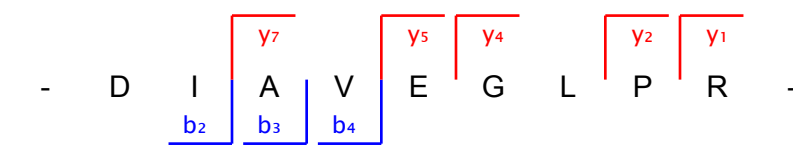
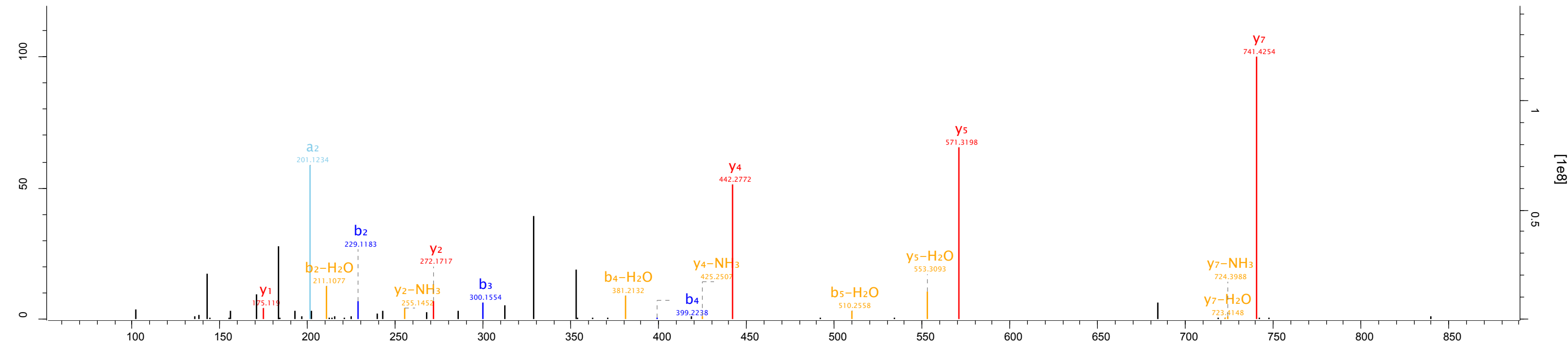
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20180707_MaS_A375SR_ML_proteome_2_16

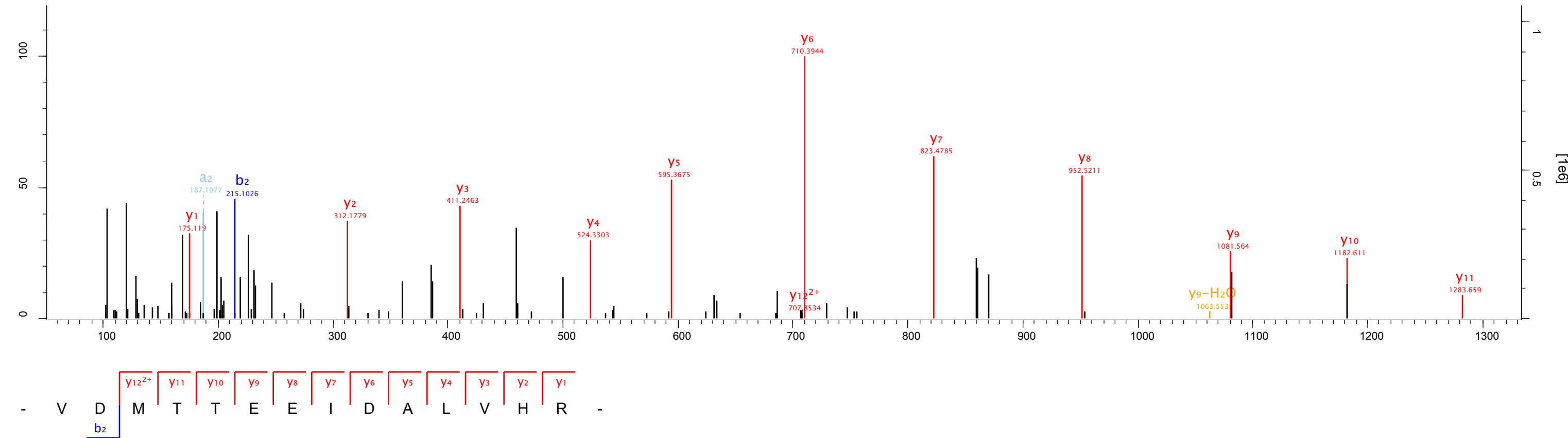
Scan 14700 Method FTMS; HCD Score 251.68 m/z 858.93 Gene names APOC3



- D A L S S V Q E S Q V A Q Q A R -
b2 b3 b4 b5 b7 b8 b9

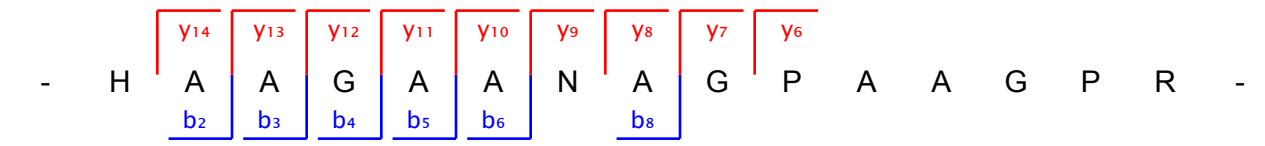
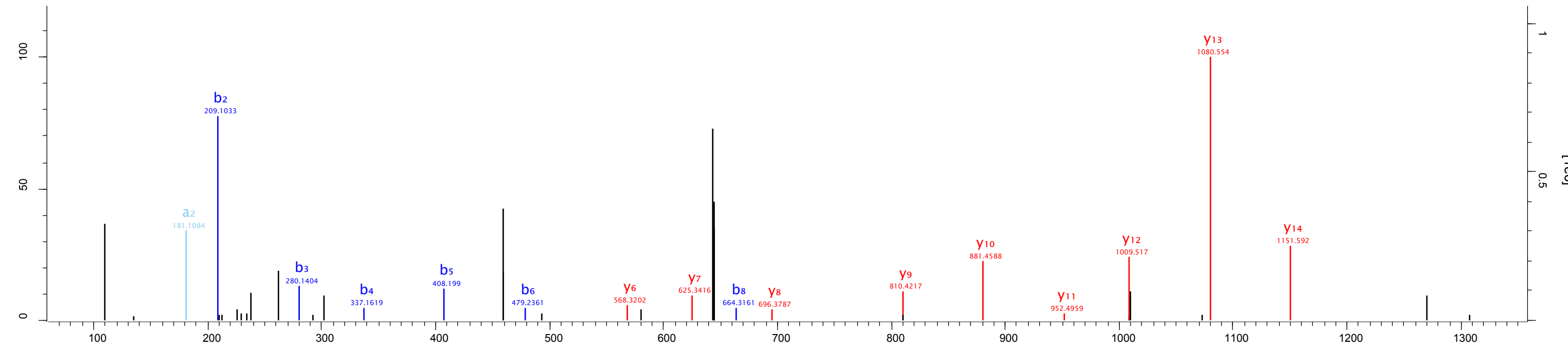
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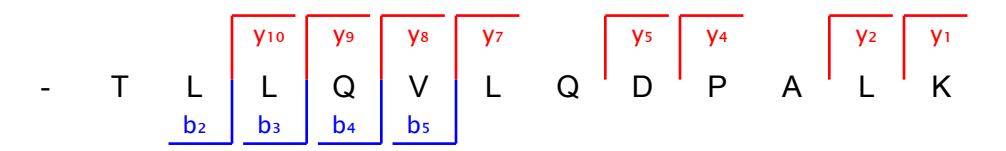
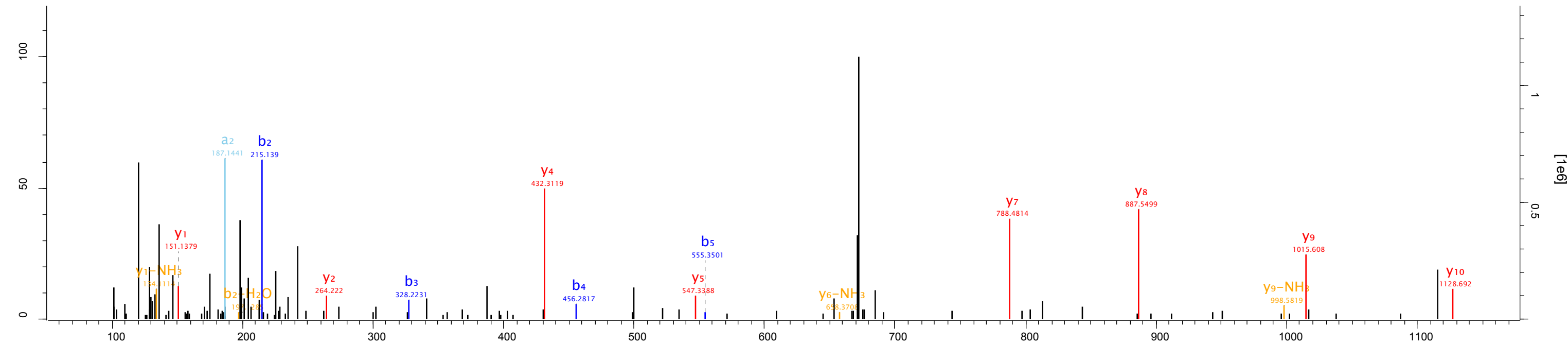


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20180707_MaS_A375SR_ML_proteome_2_16

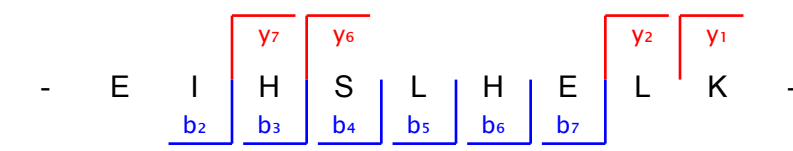
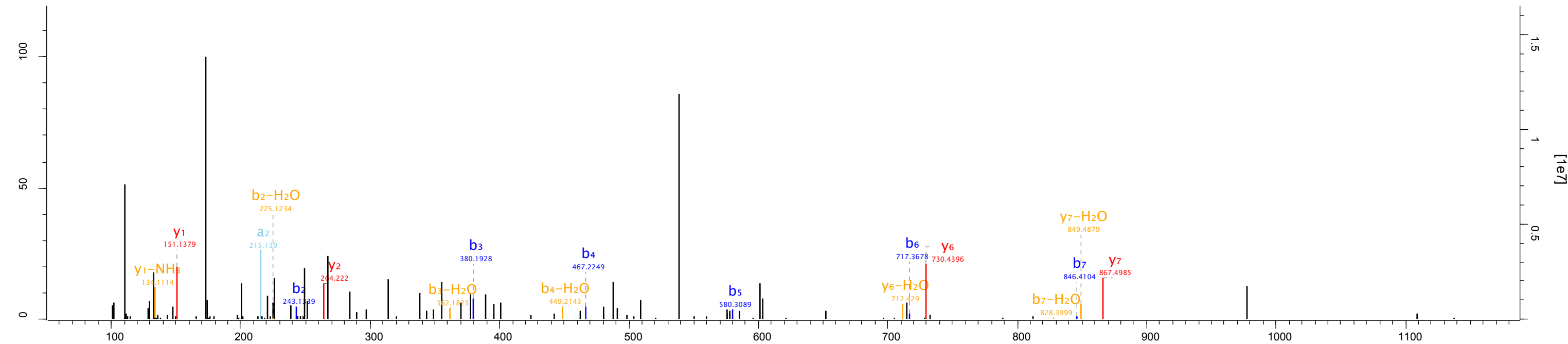
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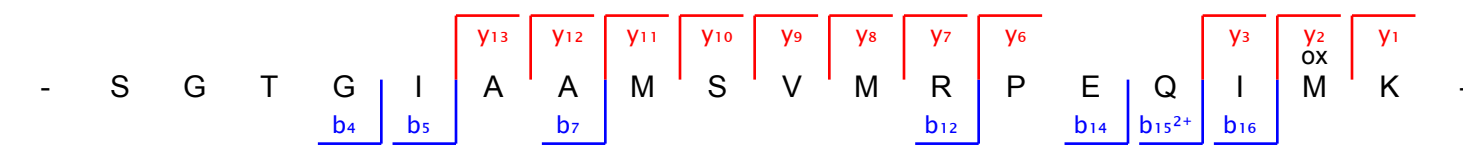
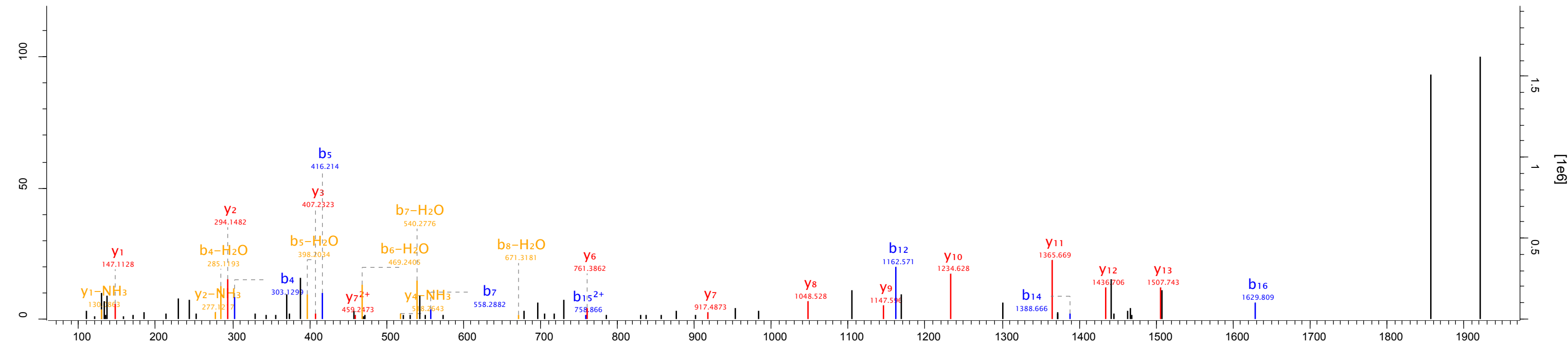
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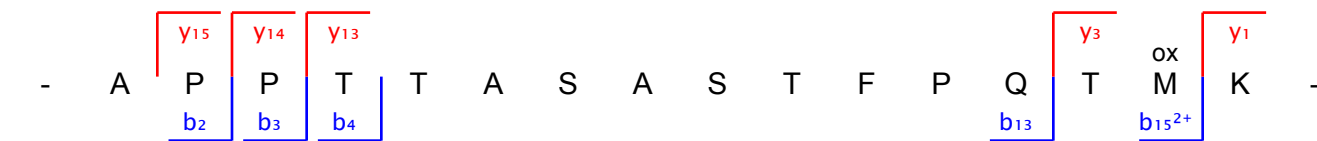
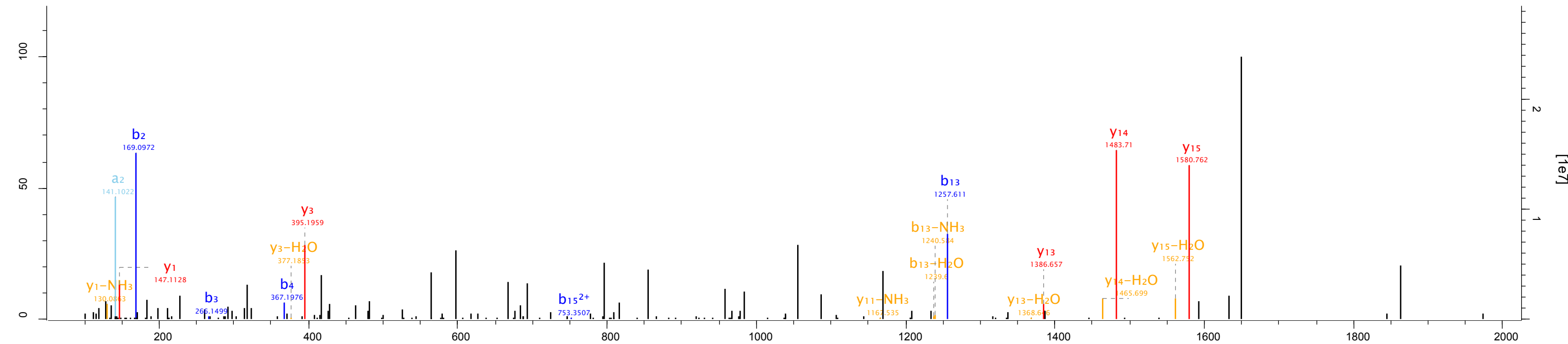


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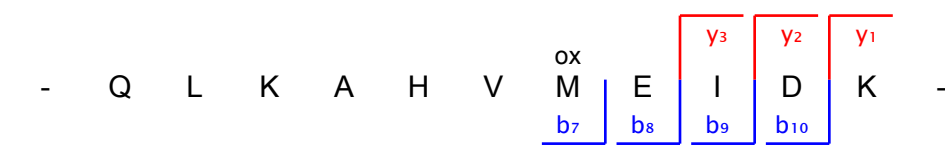
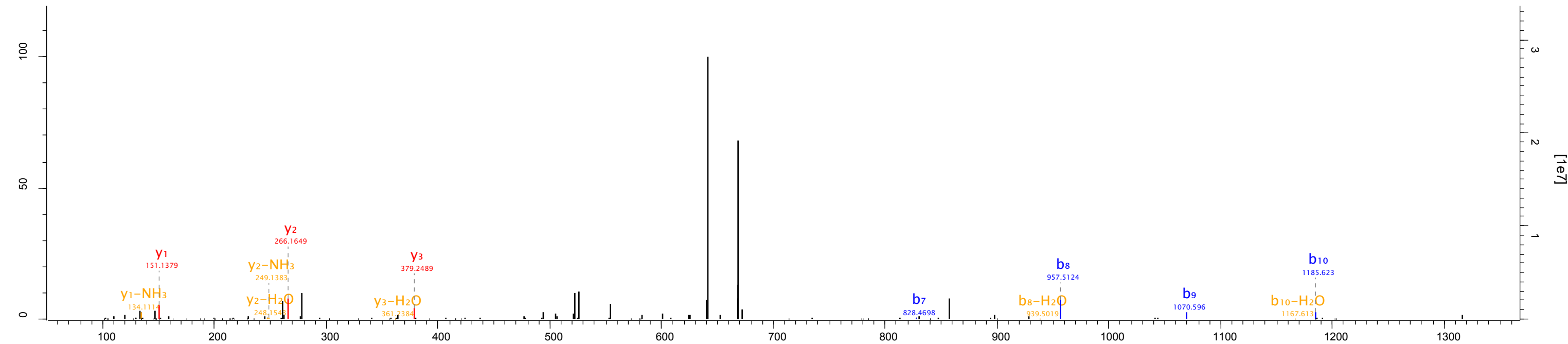


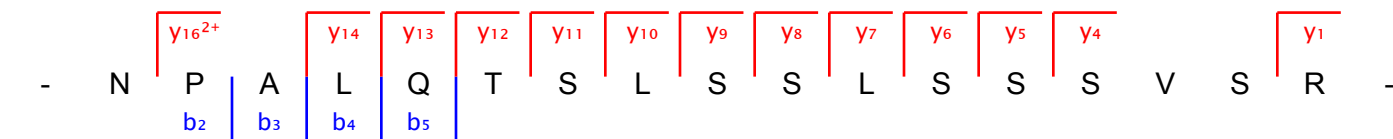
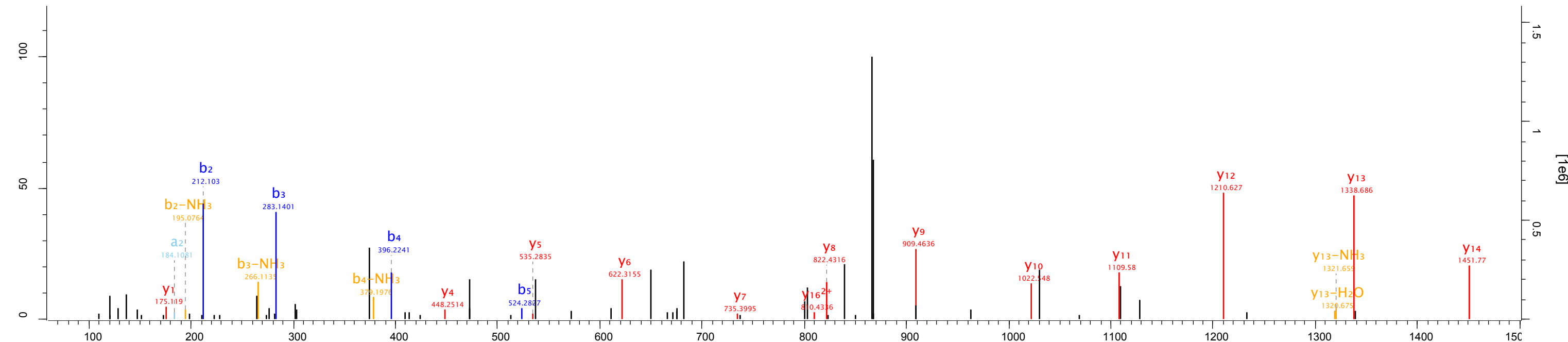
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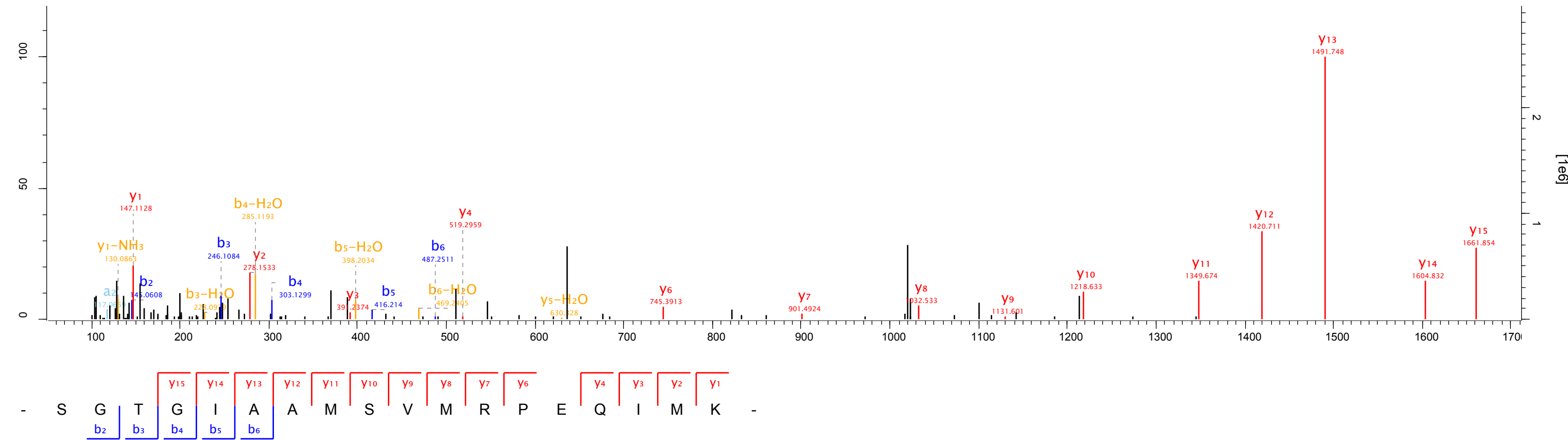


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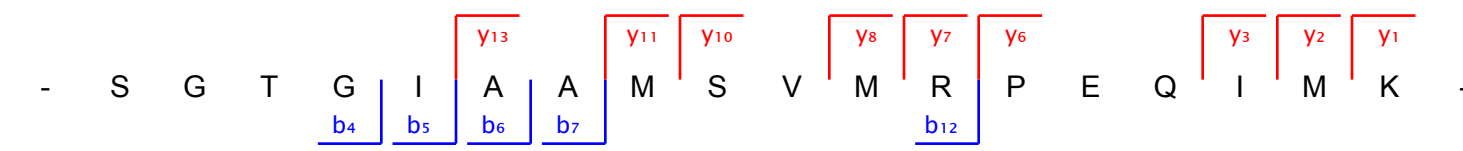
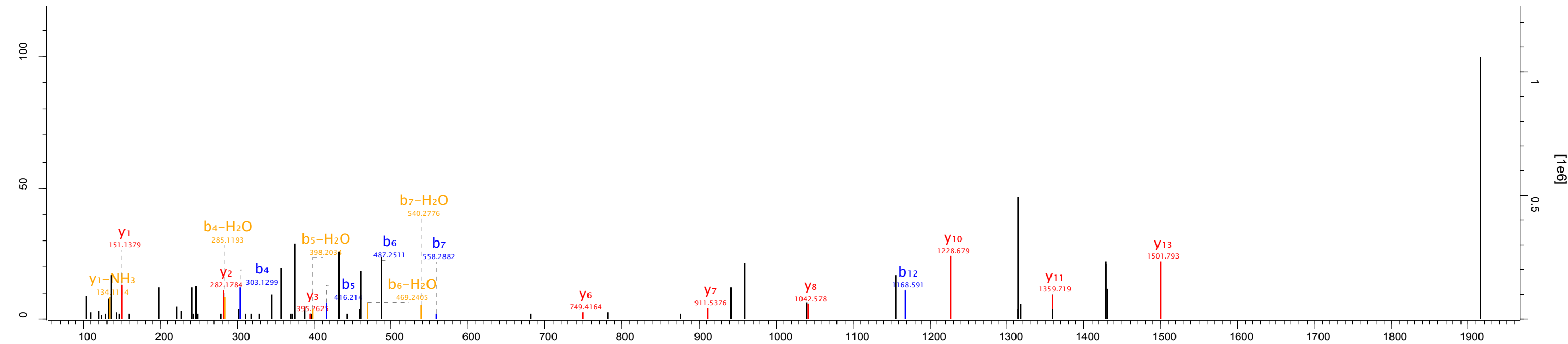




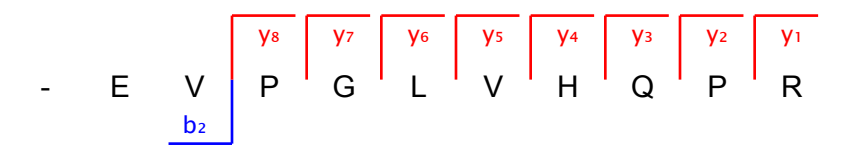
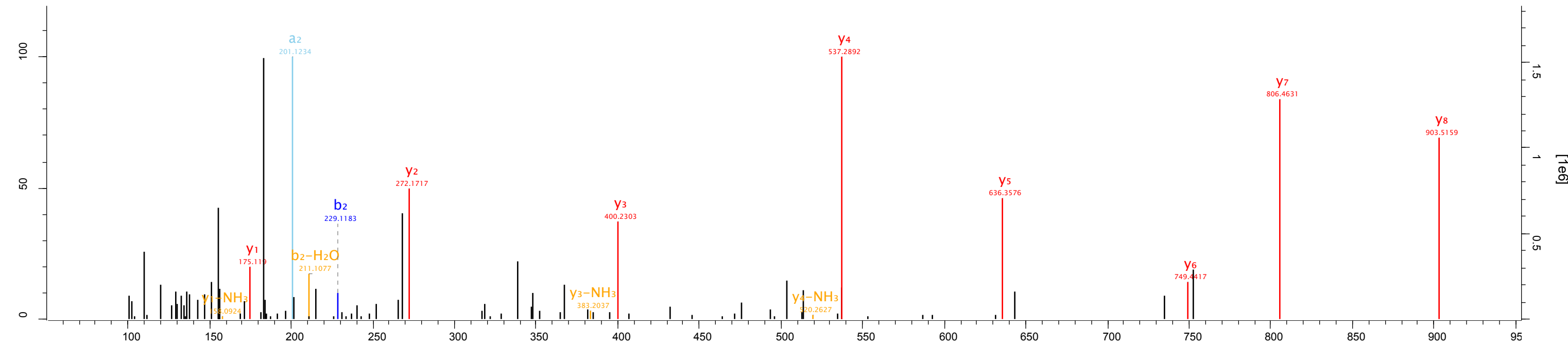
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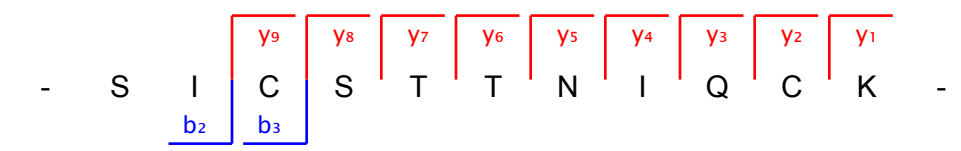
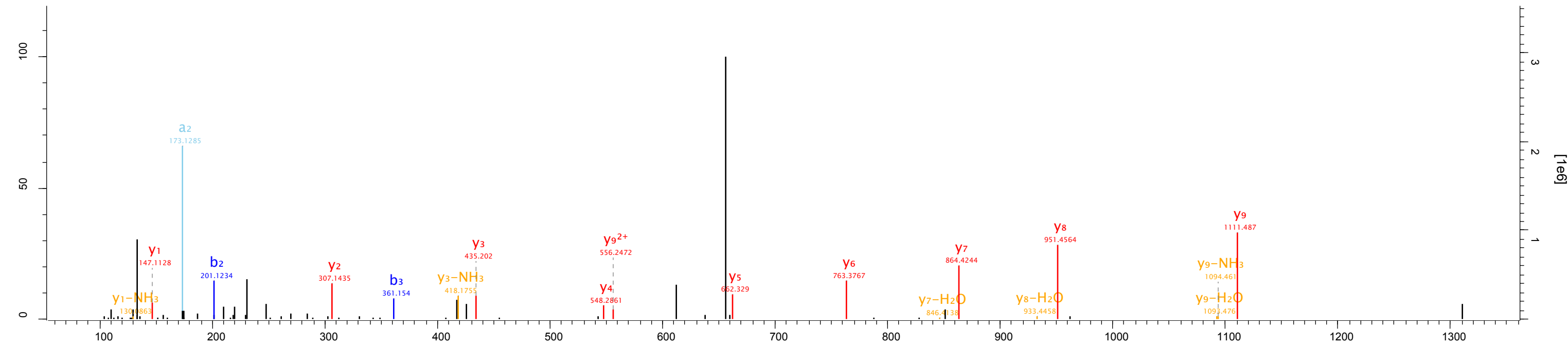
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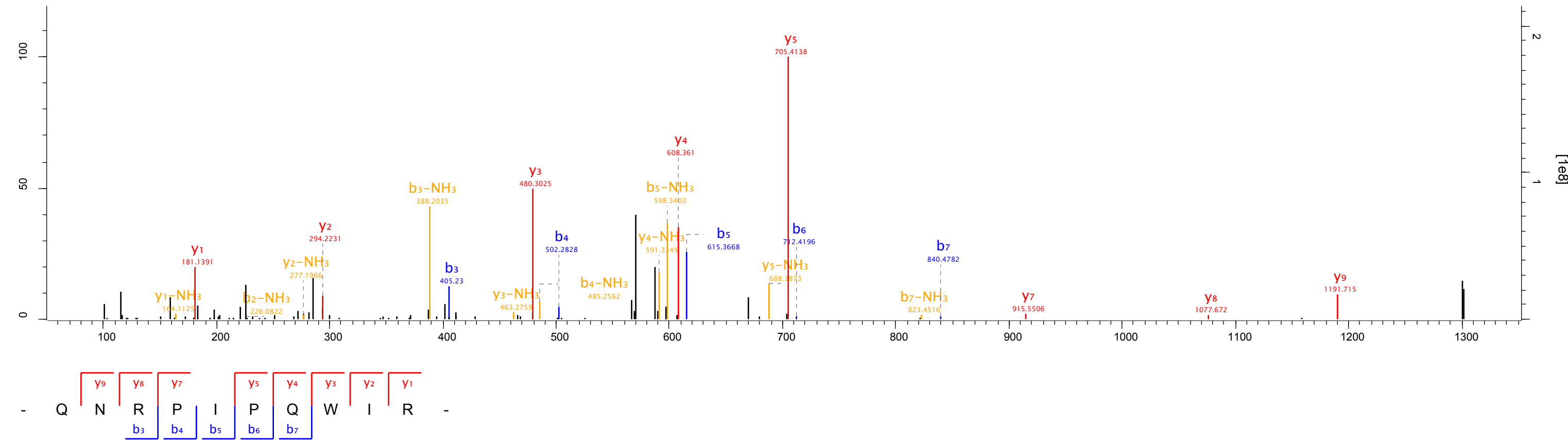


Raw file

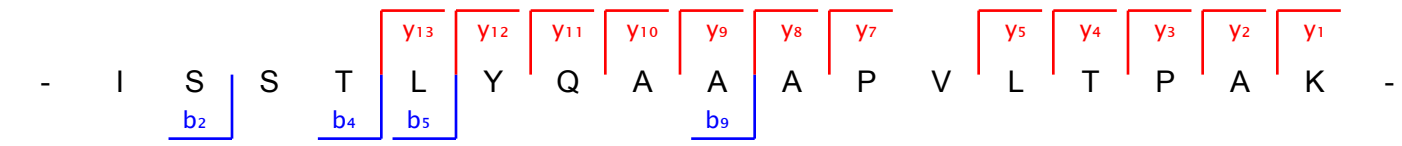
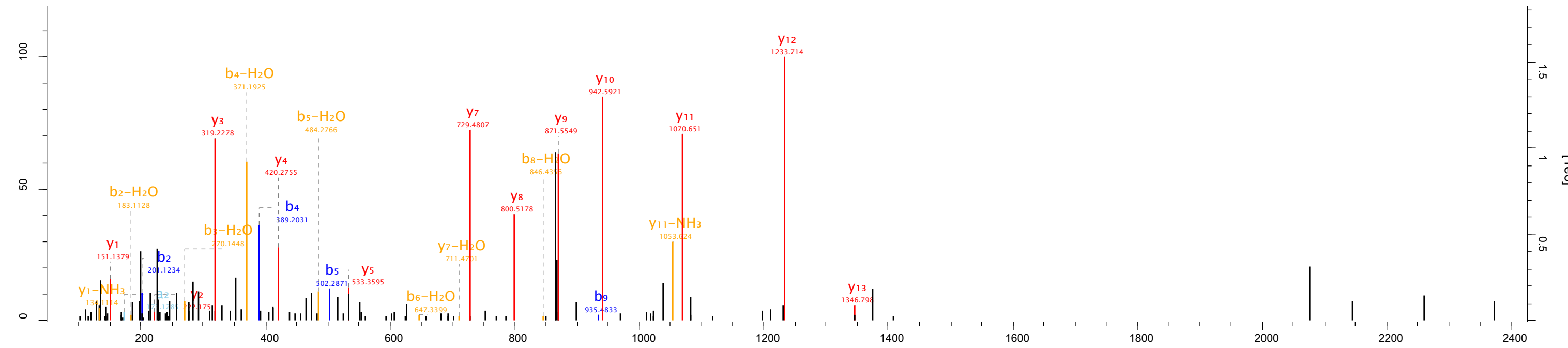
20180707_MaS_A375SR_ML_proteome_2_22

Scan	Method	Score	m/z	Gene names
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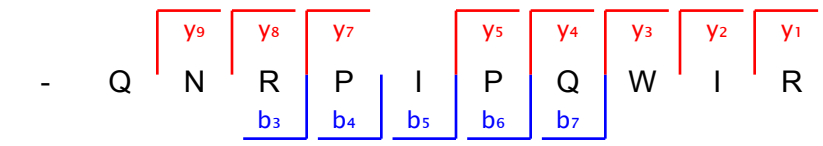
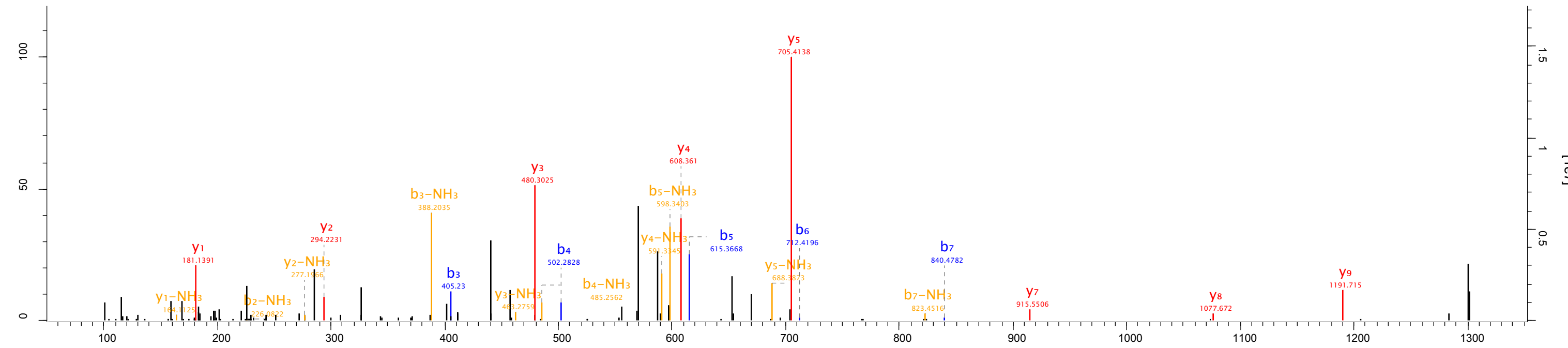
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 Scan: 23160 Method: FTMS; HCD Score: 78.08 m/z: 868 Gene names: KRTCAP2



Raw file

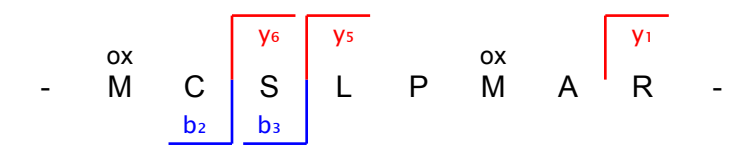
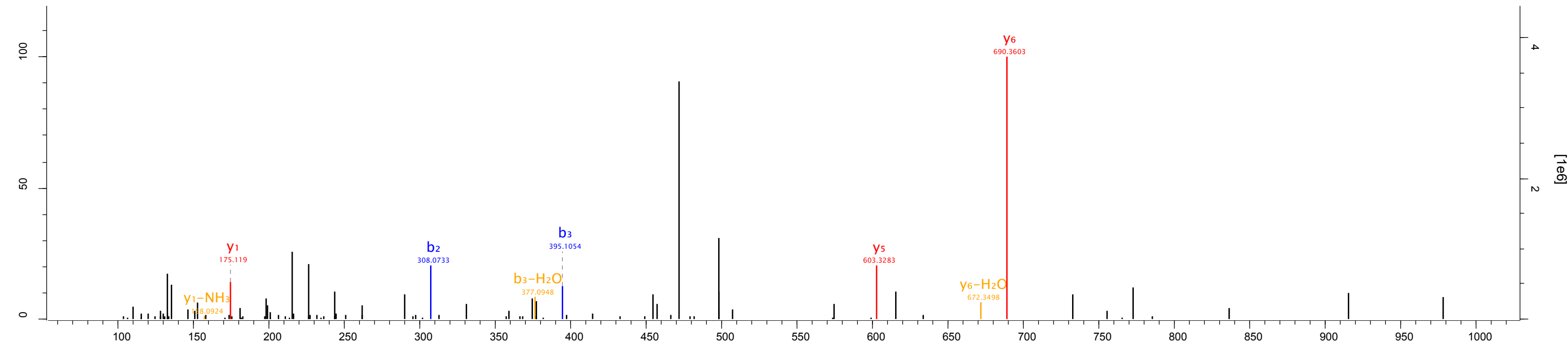
20180707_MaS_A375SR_ML_proteome_2_25

Scan	Method	Score	m/z	Gene names
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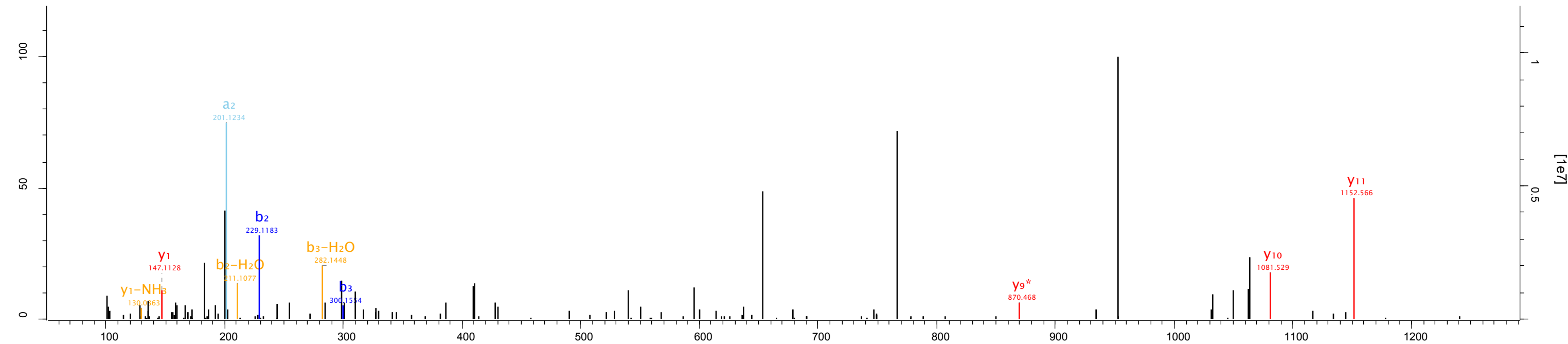


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20180707_MaS_A375SR_ML_proteome_2_25

Scan 8940 Method FTMS; HCD Score 46.43 m/z 499.22 Gene names IL1F10

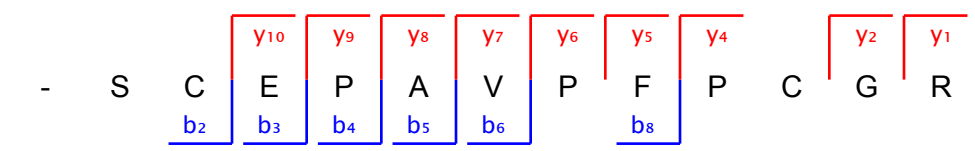
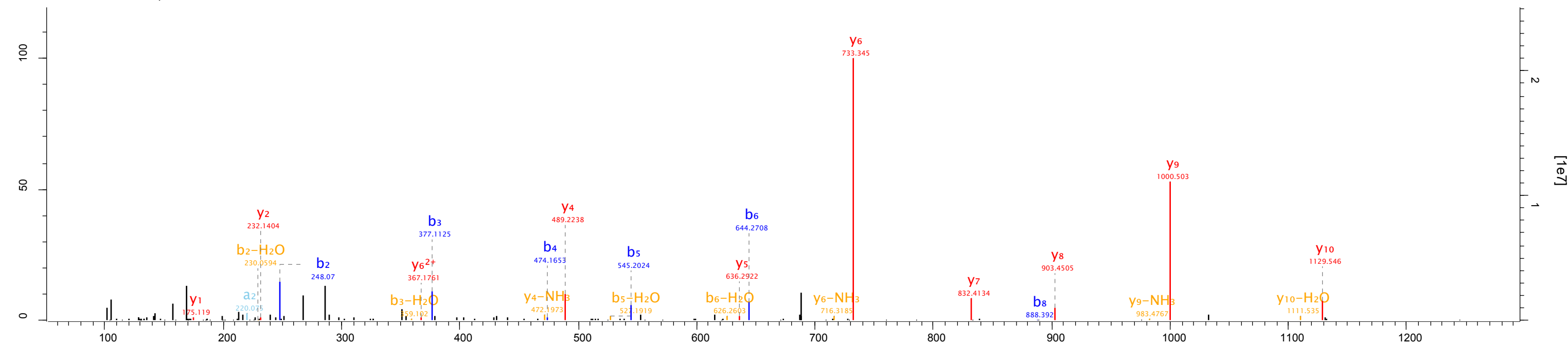


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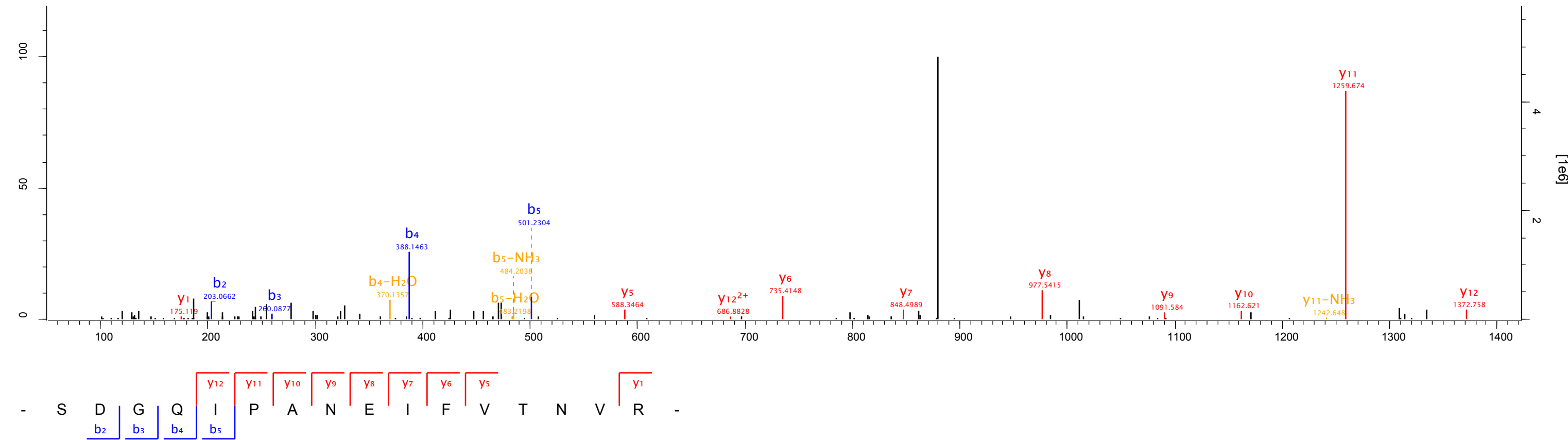


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20180707_MaS_A375SR_ML_proteome_2_27

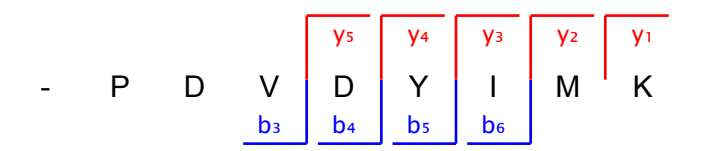
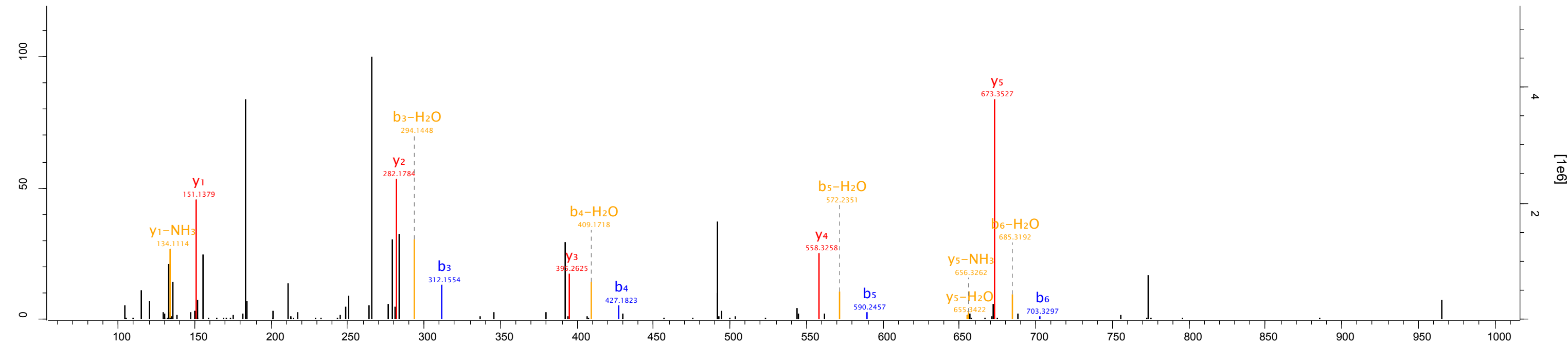
Scan 17330 Method FTMS; HCD Score 125.72 m/z 688.81 Gene names F9



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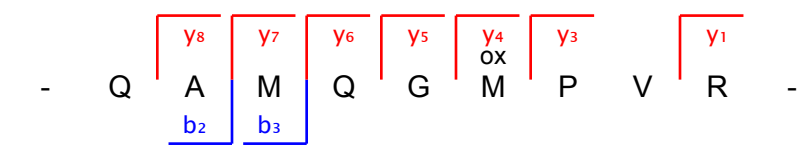
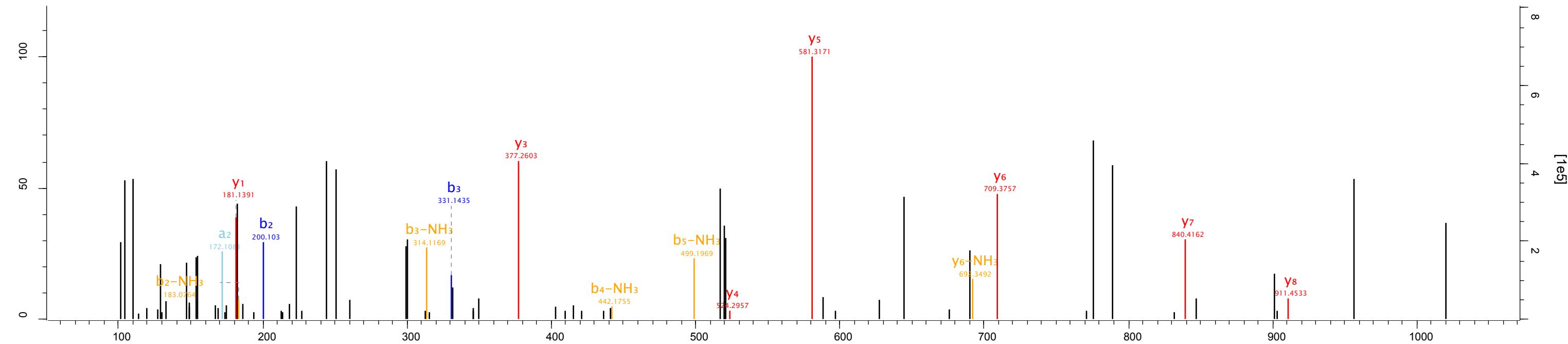


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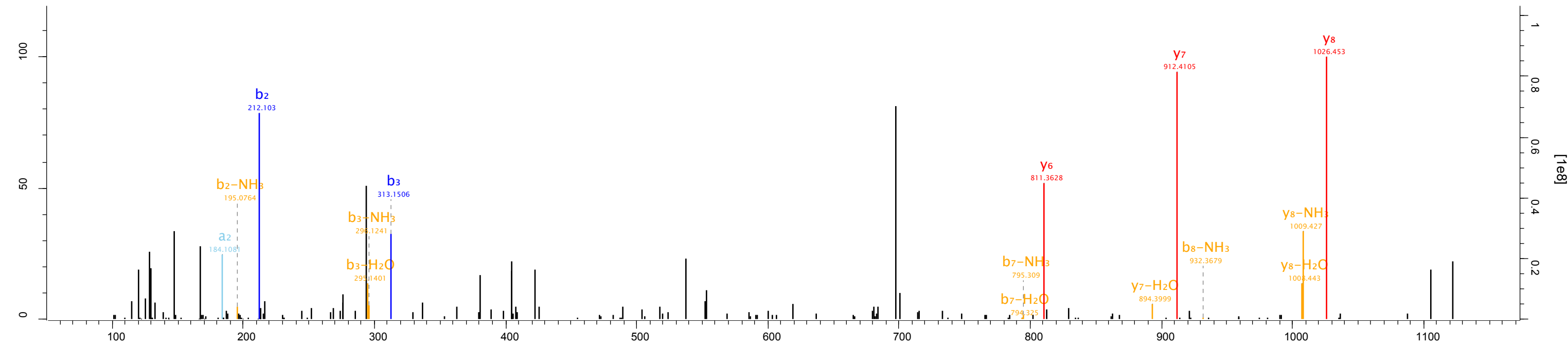


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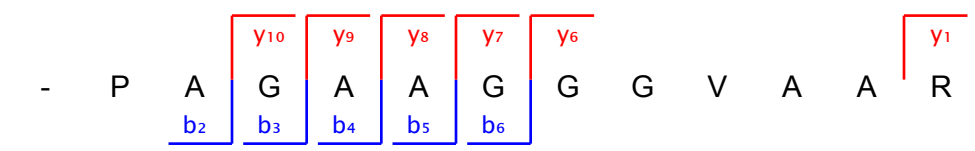
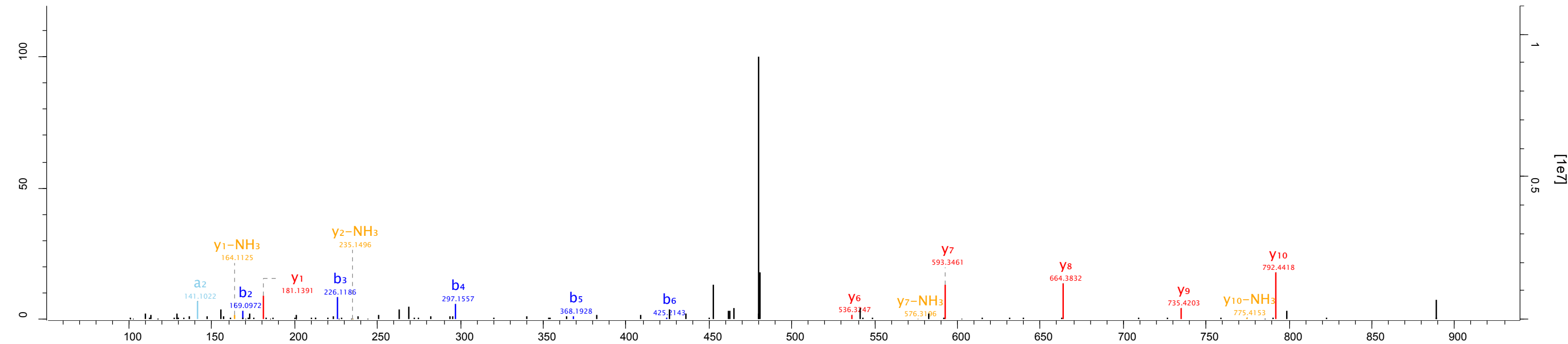
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Method: FTMS; HCD
Score: 53.49
m/z: 520.26
Gene names: MTA3



Raw file 20180707_MaS_A375SR_ML_proteome_2_28 Scan 13160 Method FTMS; HCD Score 66.69 m/z 562.26

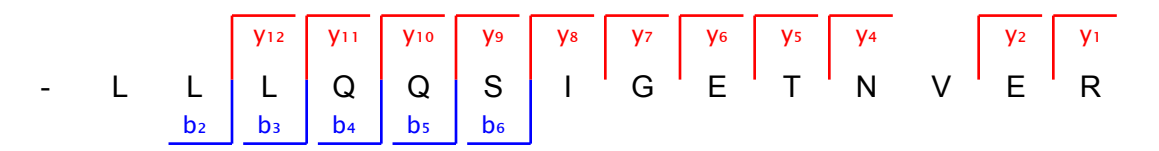
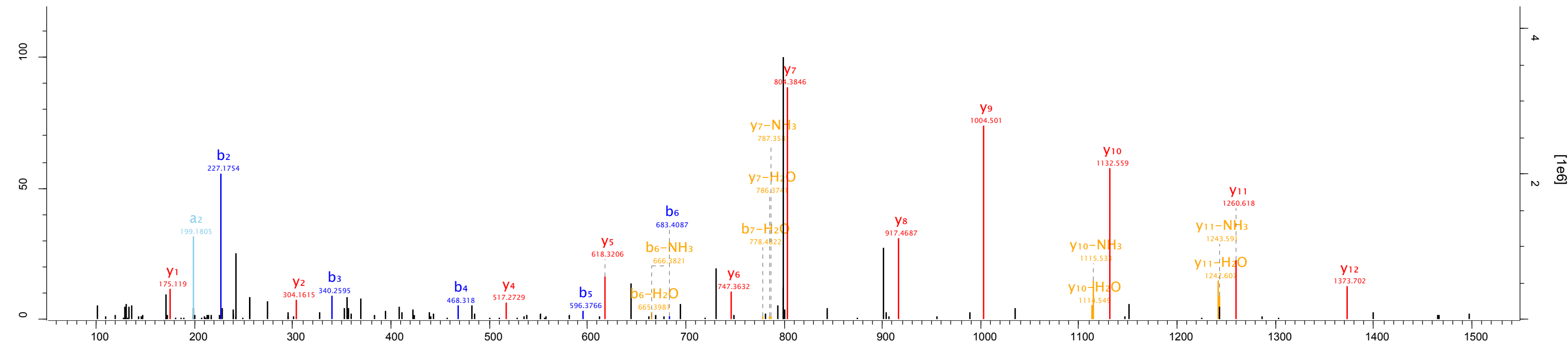


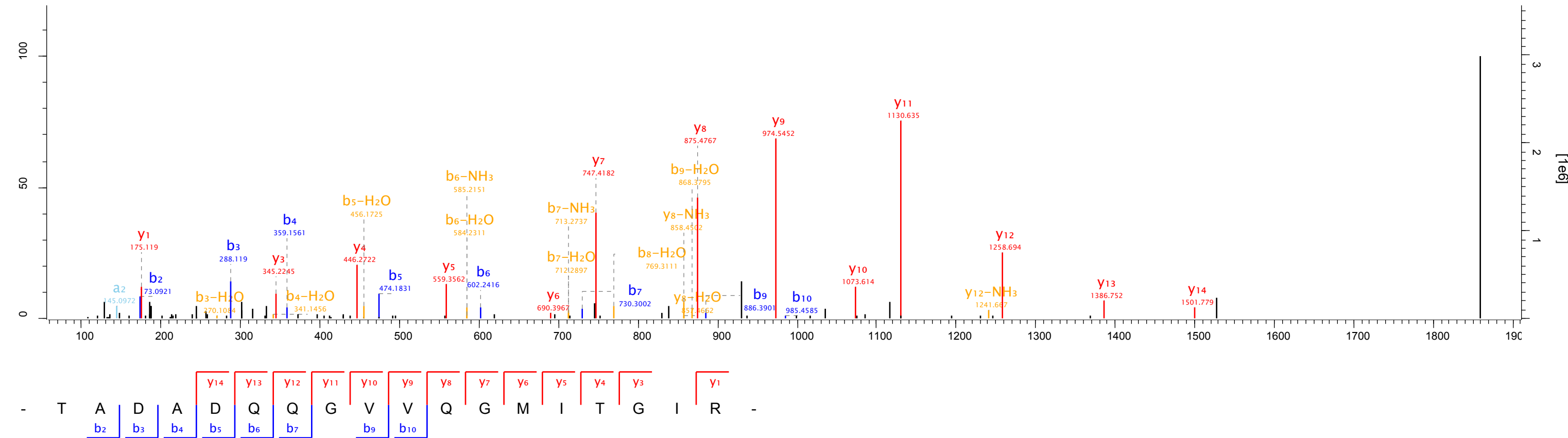
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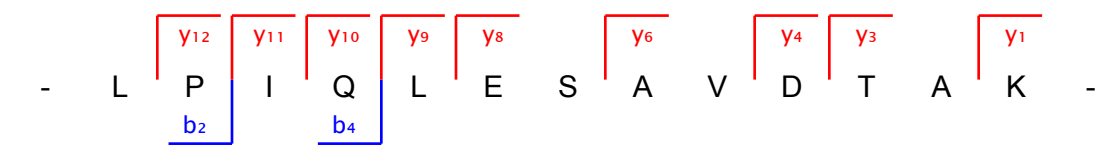
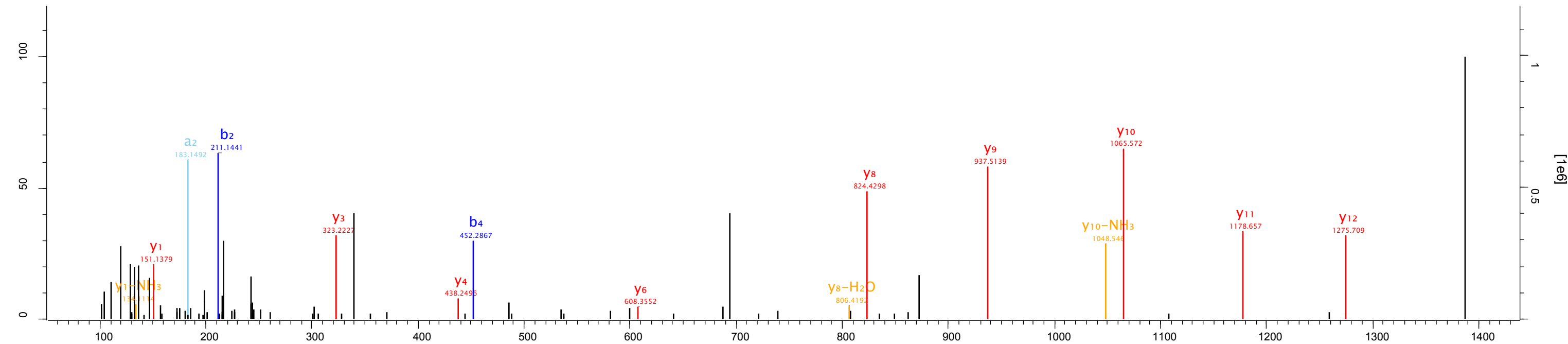
Raw file
20180707_MaS_A375SR_ML_proteome_2_29

Scan 19970 Method FTMS; HCD Score 119.87 m/z 800.44 Gene names ZCCHC10



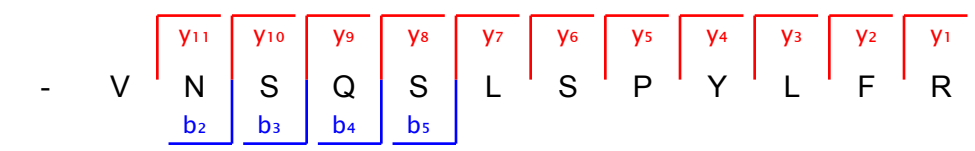
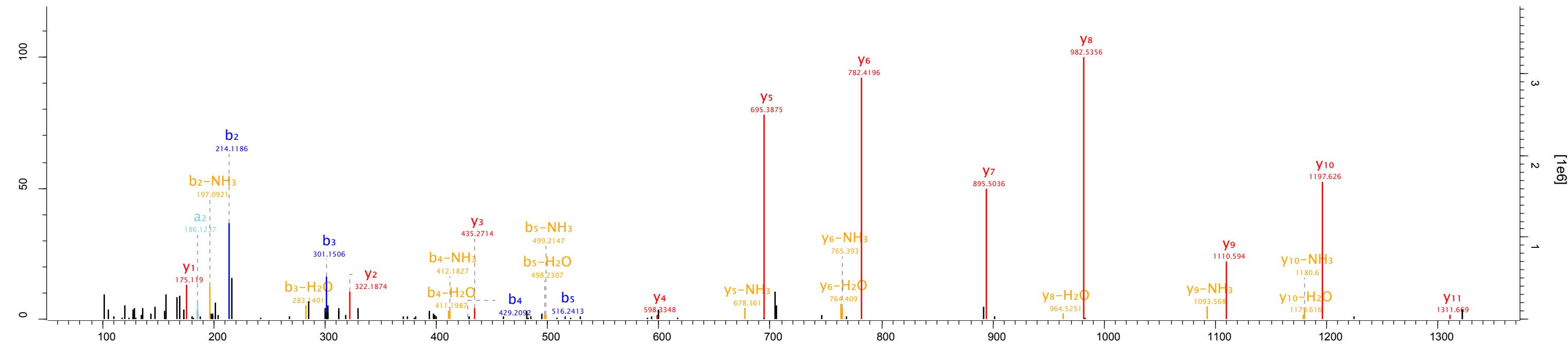


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 20180707_MaS_A375SR_ML_proteome_2_30
 Scan 23130 Method FTMS; HCD Score 74.99 m/z 694.9 Gene names CHRM3

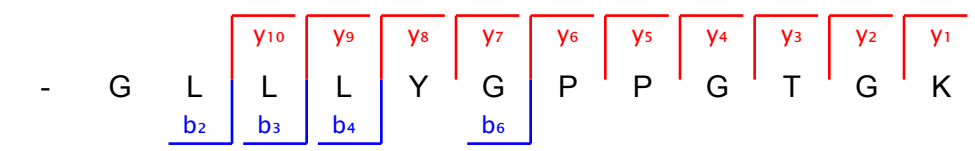
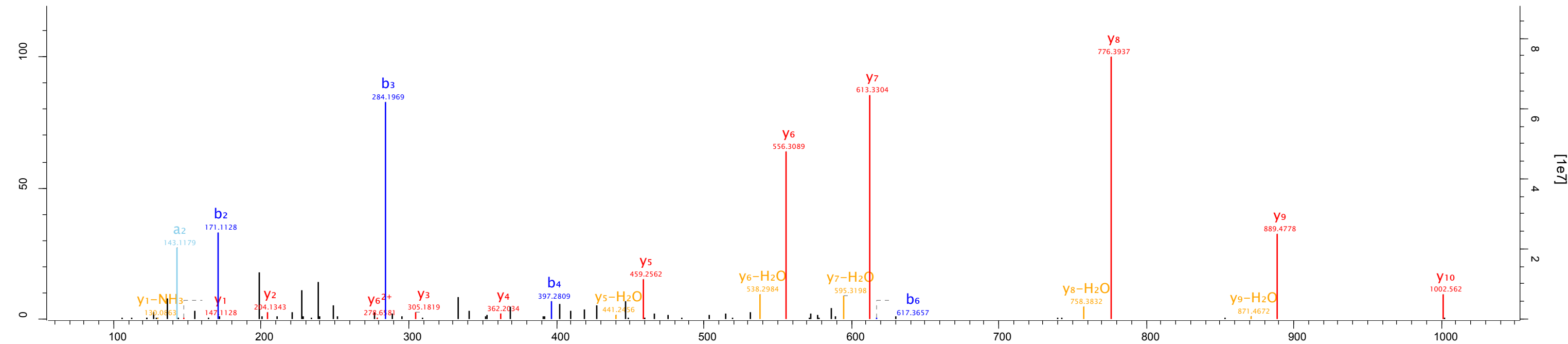


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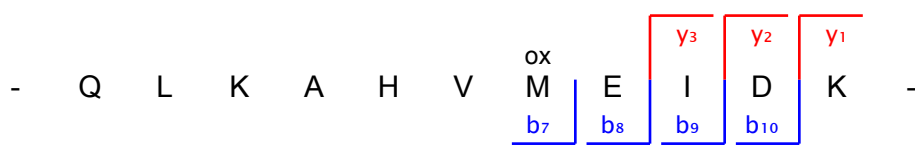
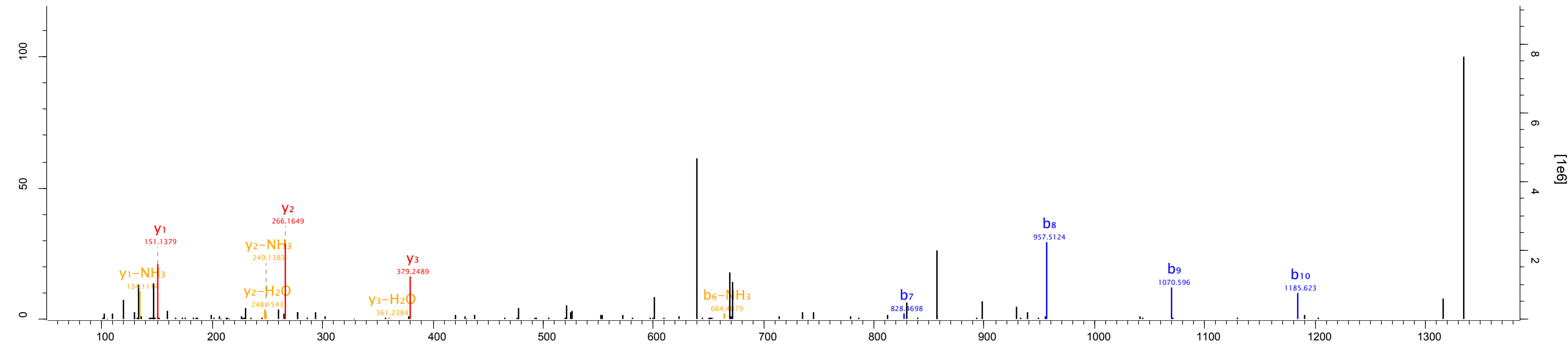
Scan 25530 Method FTMS; HCD Score 167.84 m/z 705.87 Gene names SPP2



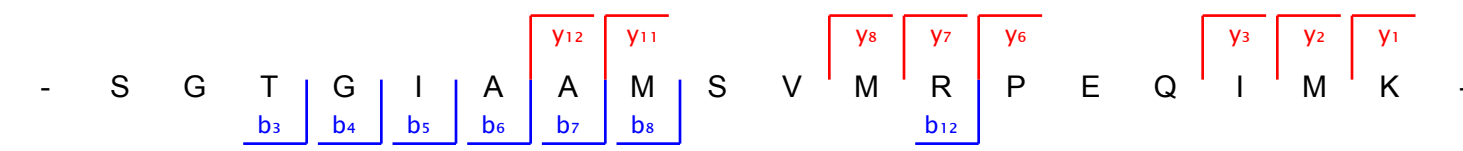
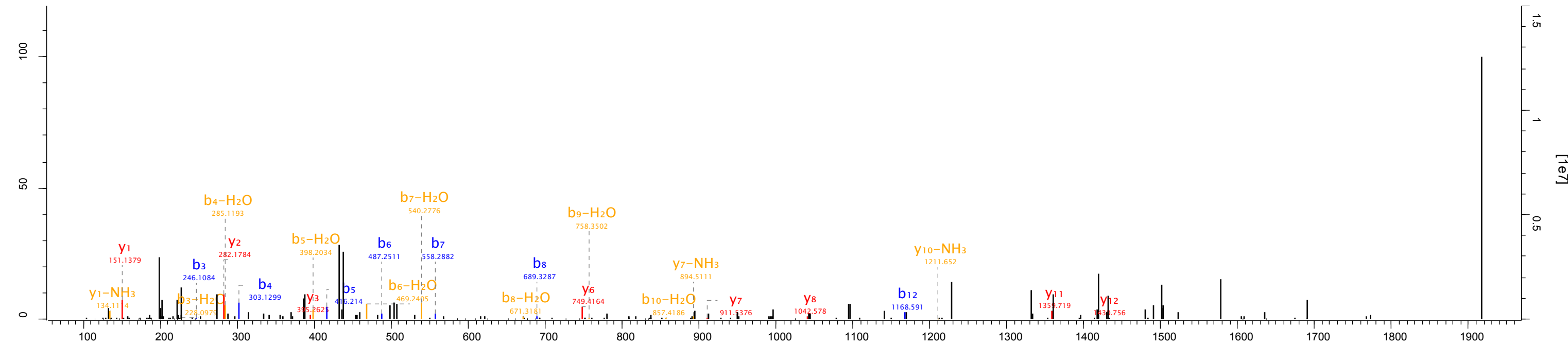
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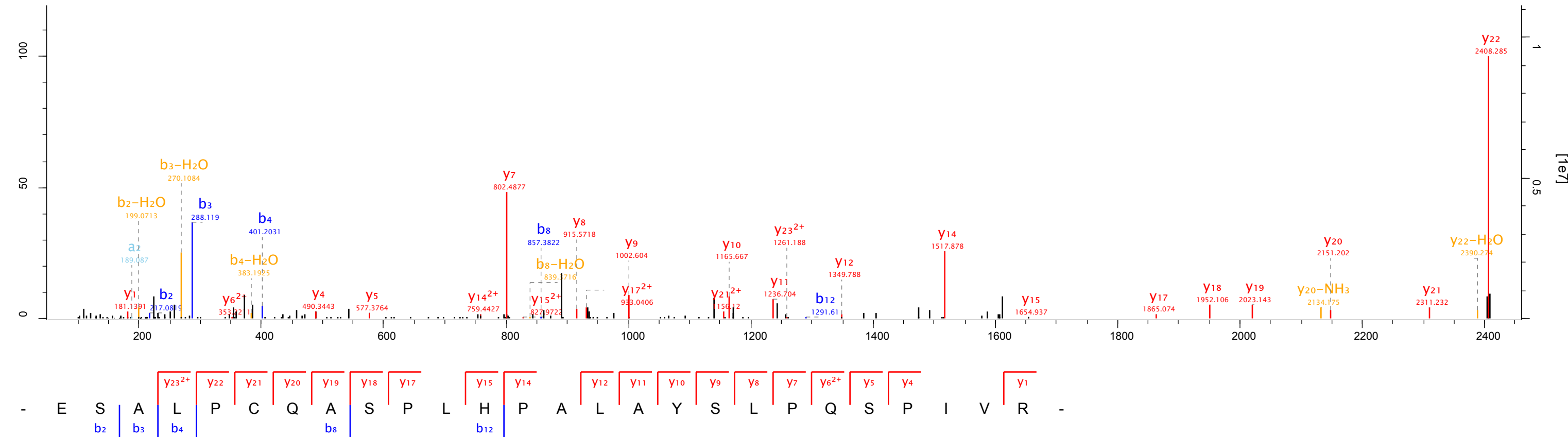


Raw file 20180707_MaS_A375SR_ML_proteome_20 Scan 23330 Method FTMS; HCD Score 44.54 m/z 668.38



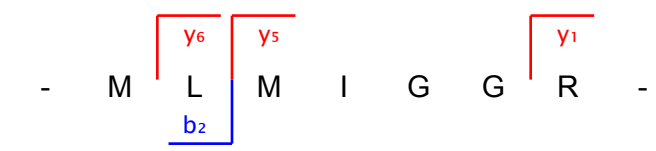
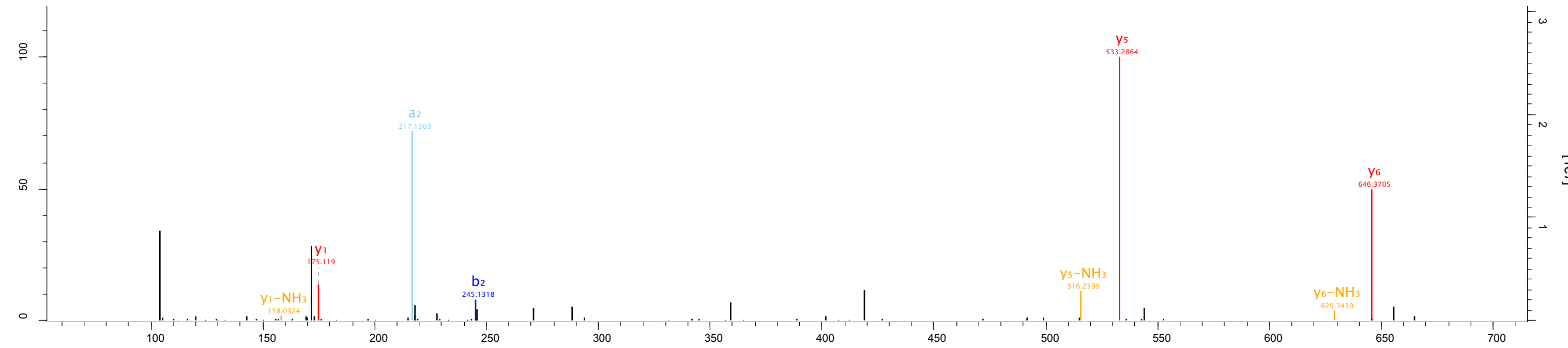
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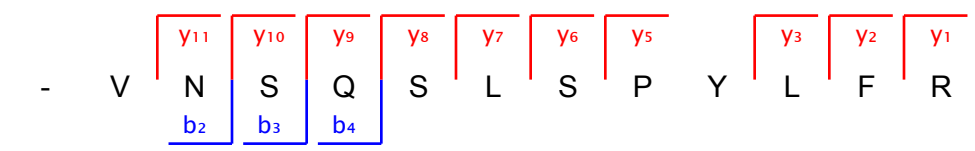
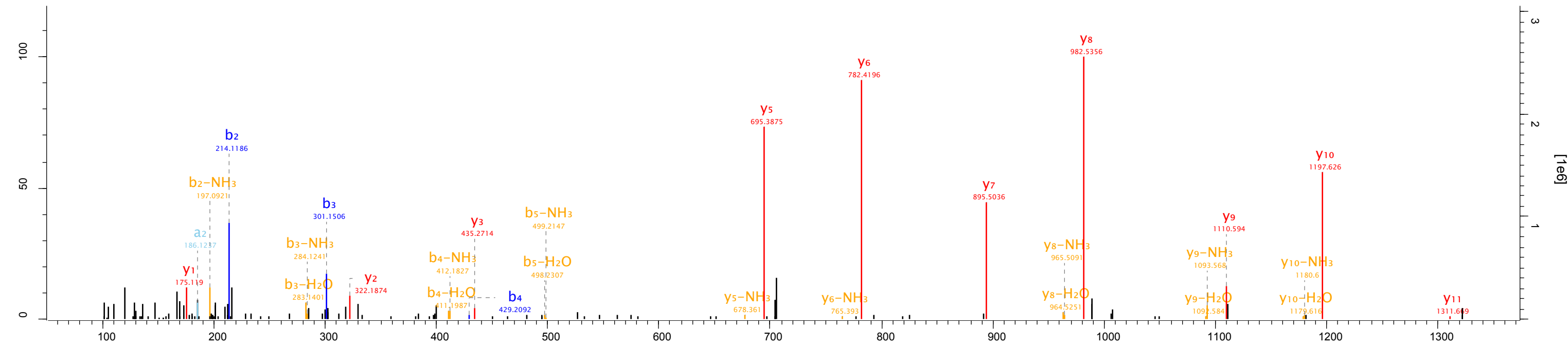


Raw file
20180707_MaS_A375SR_ML_proteome_21

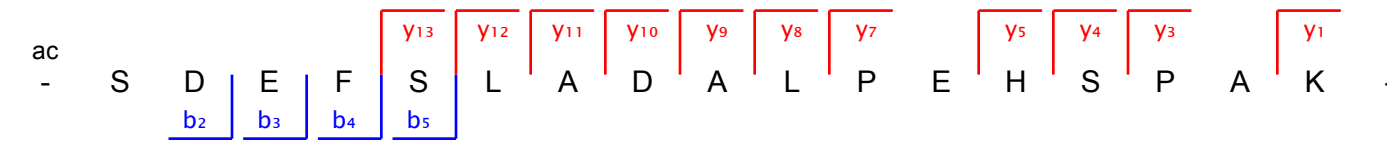
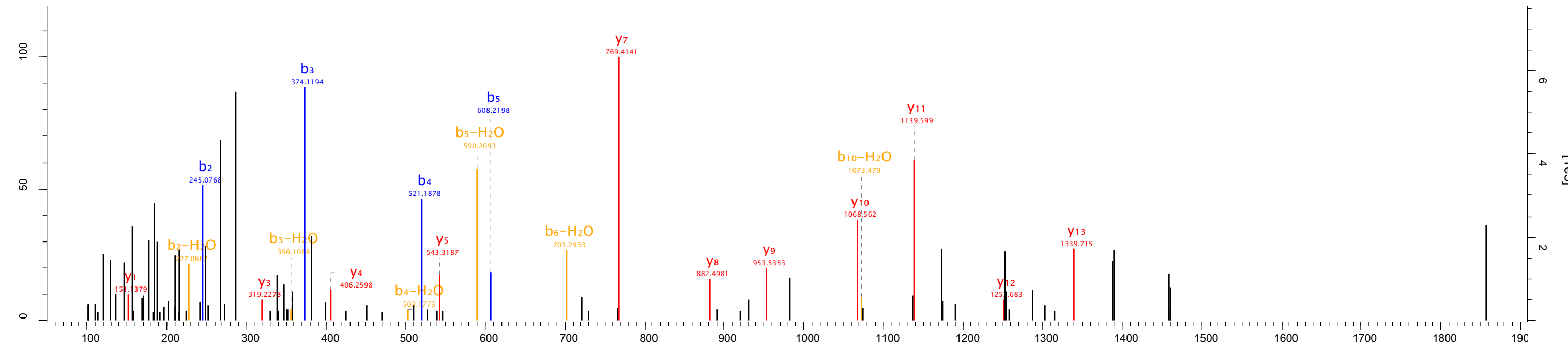
Scan	Method	Score	m/z
16240	FTMS; HCD	69.39	389.21



Raw file 20180707_MaS_A375SR_ML_proteome_22 Scan 23170 Method FTMS; HCD Score 153.54 m/z 705.87 Gene names SPP2

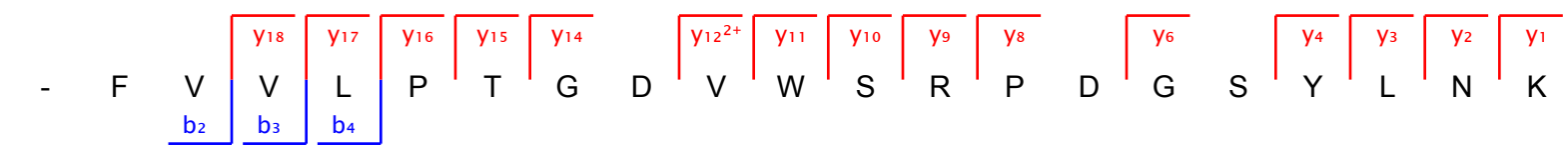
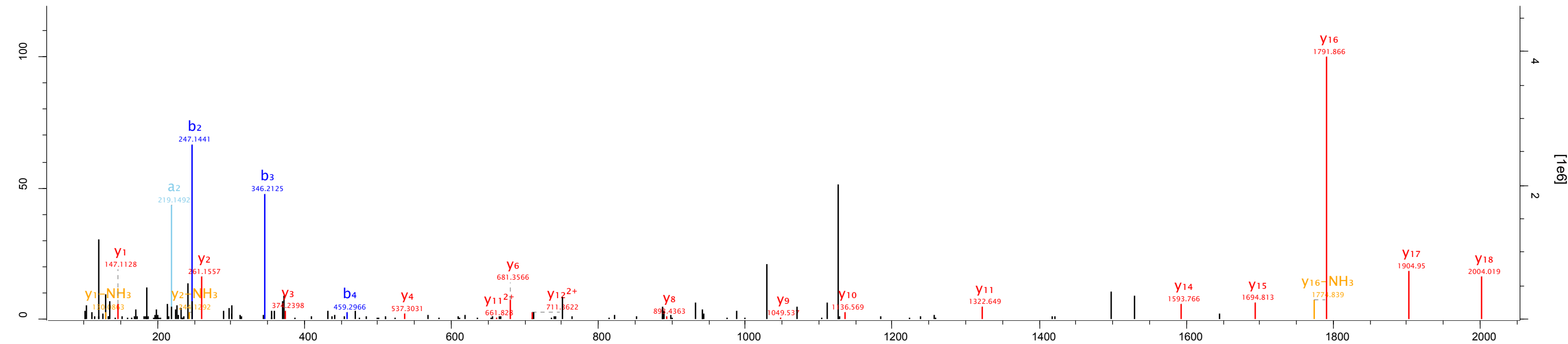


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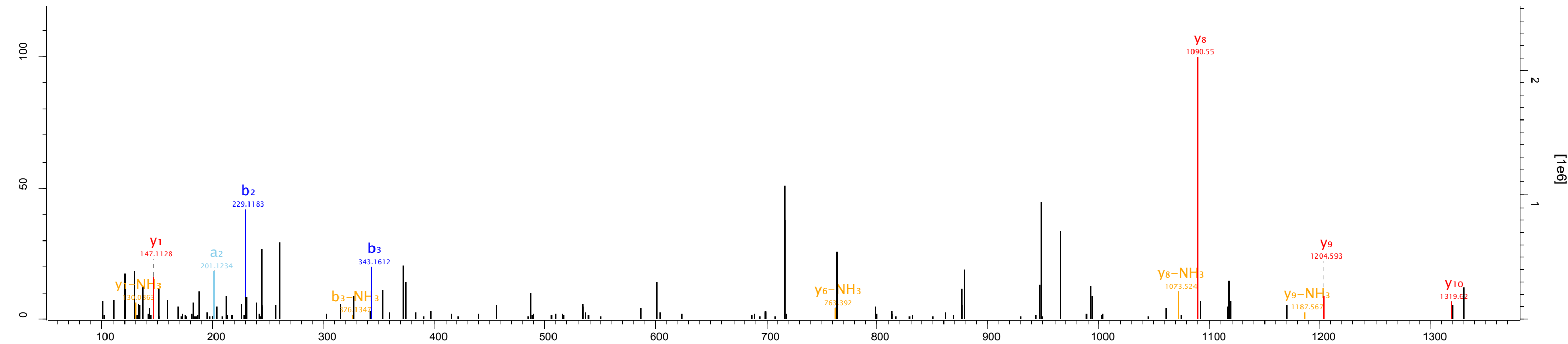


Raw file
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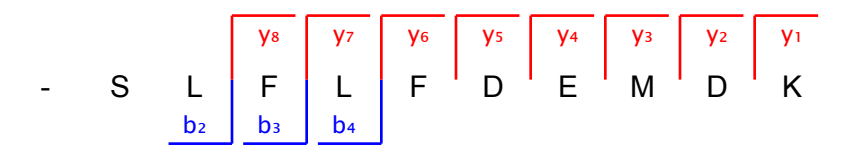
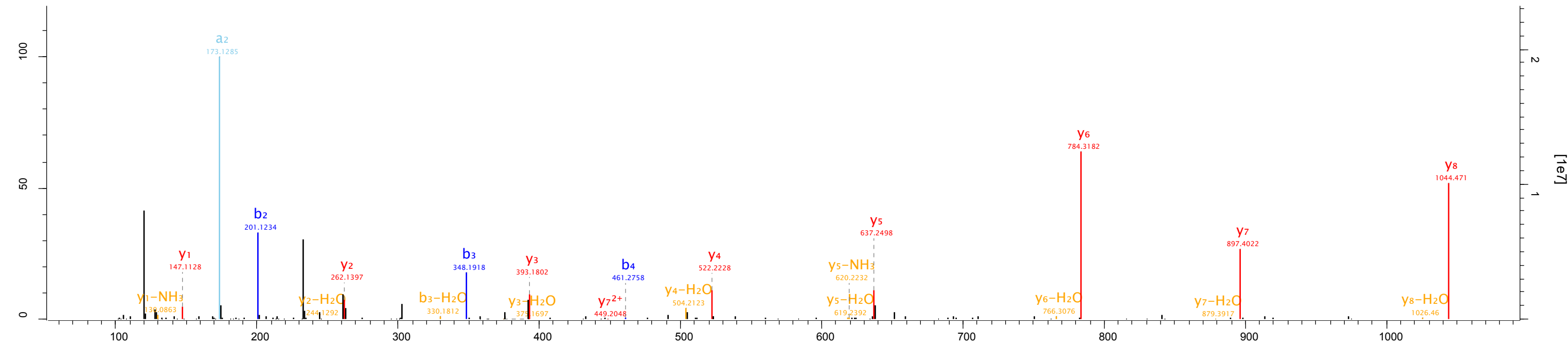
Scan 26280 Method FTMS; HCD Score 62.62 m/z 750.72 Gene names FGRL1



Raw file 20180707_MaS_A375SR_ML_proteome_24 Scan 17740 Method FTMS; HCD Score 48.28 m/z 717.36

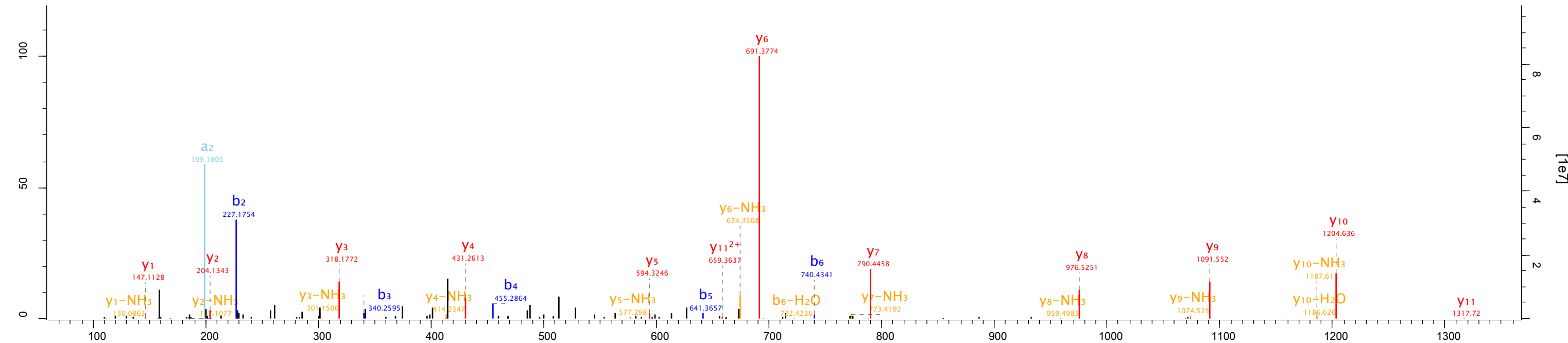


Raw file: 20180707_MaS_A375SR_ML_proteome_25
 Scan: 29480 Method: FTMS; HCD Score: 82.45 m/z: 622.8 Gene names: TOR2A



20180707_MaS_A375SR_ML_proteome_25

29850 FTMS; HCD 134.13 715.91 UQCR11

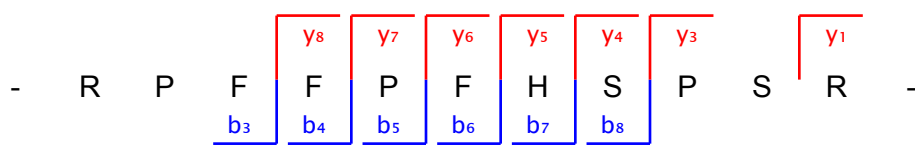
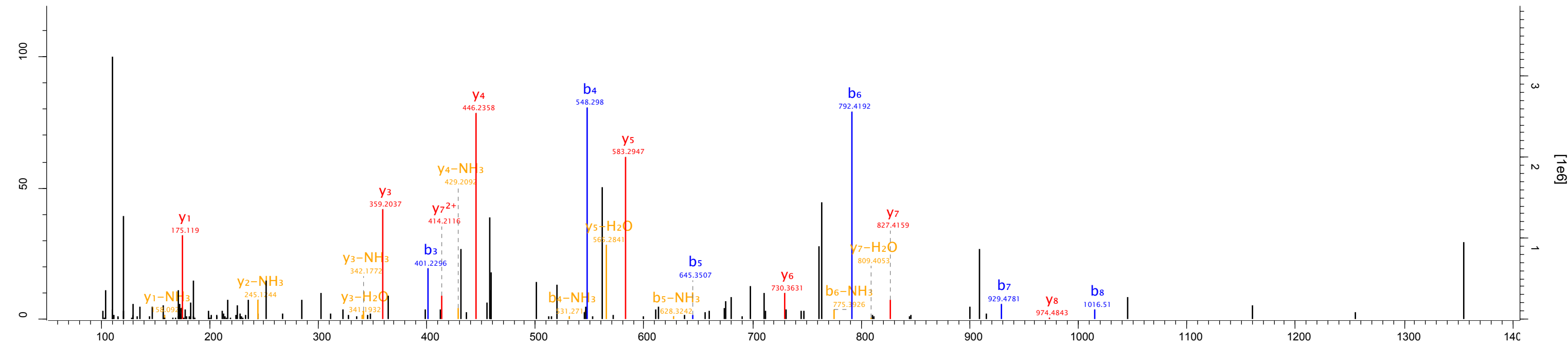


- L I L D W V P Y I N G K -

b₂ b₃ b₄ b₅ b₆

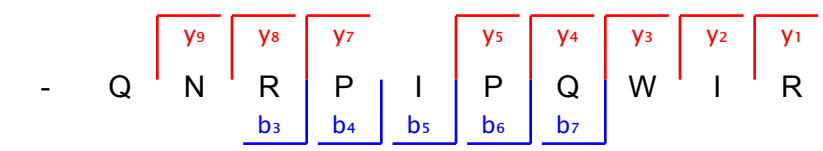
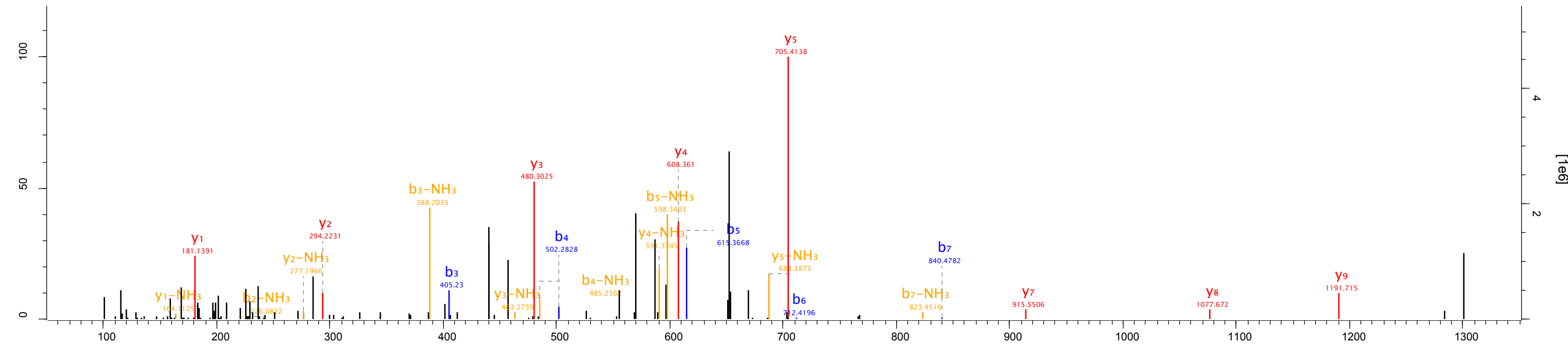
y₁ y₂ y₃ y₄ y₅ y₆ y₇ y₈ y₉ y₁₀ y₁₁

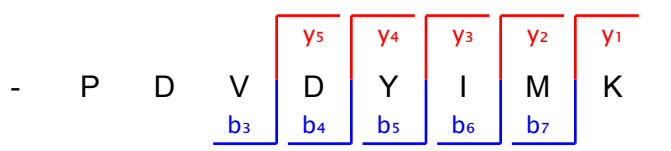
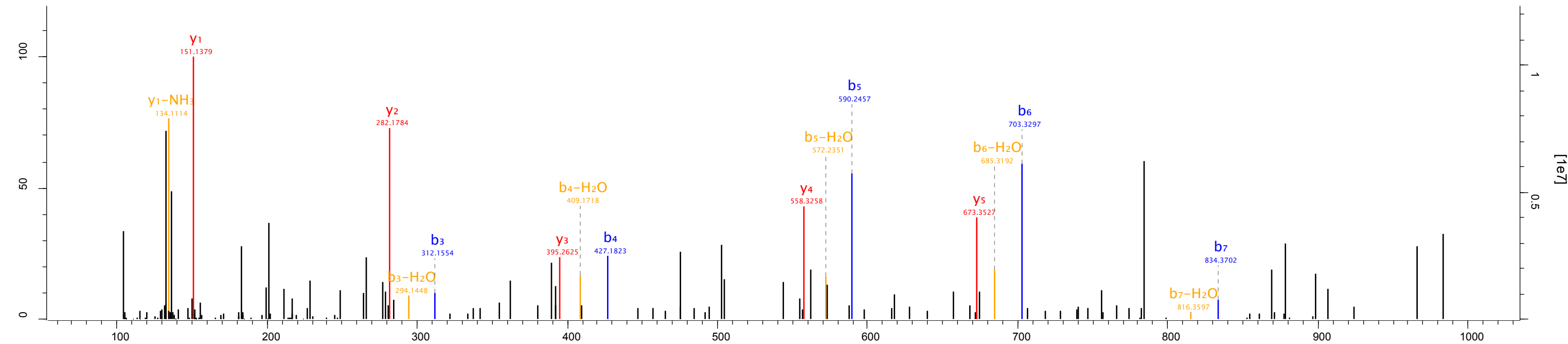
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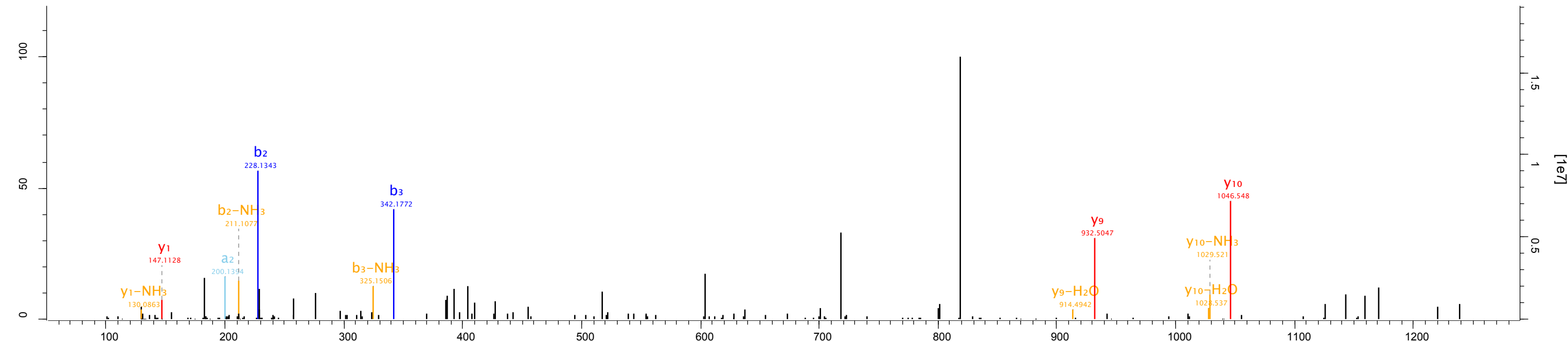


Raw file
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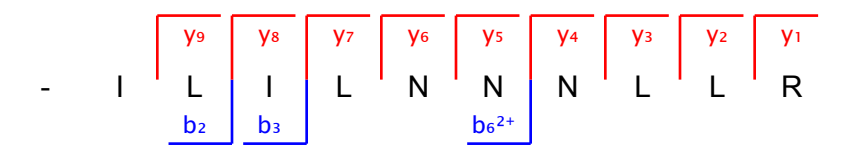
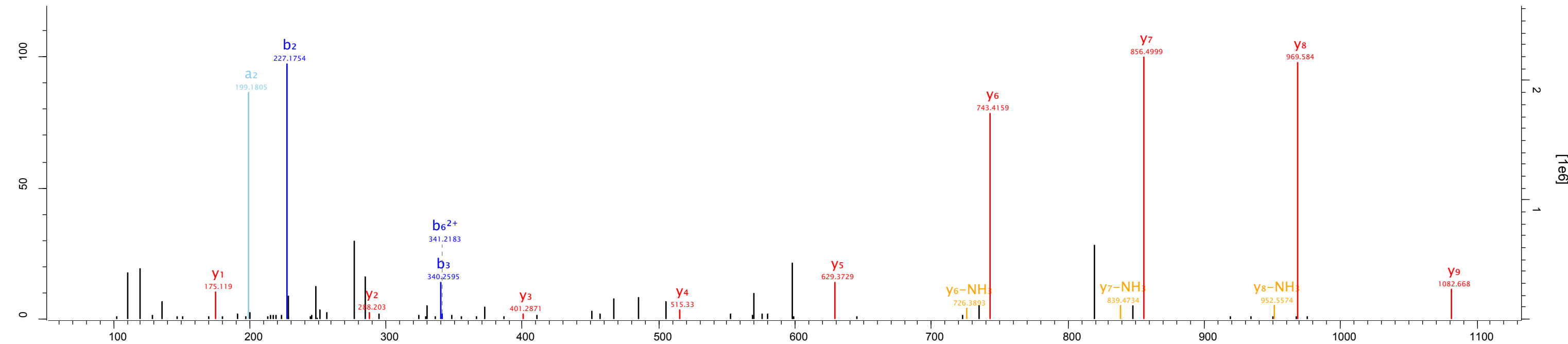
Scan 16060 Method FTMS; HCD Score 118.67 m/z 440.93 Gene names RPL39P5;RPL39





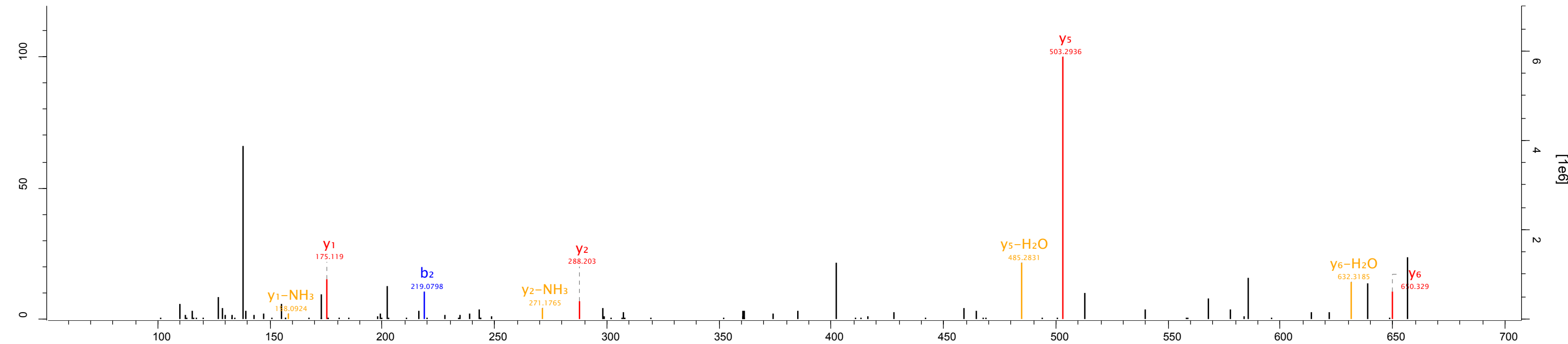


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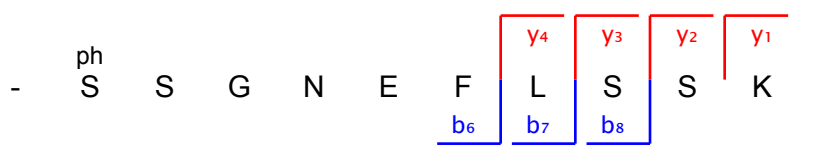
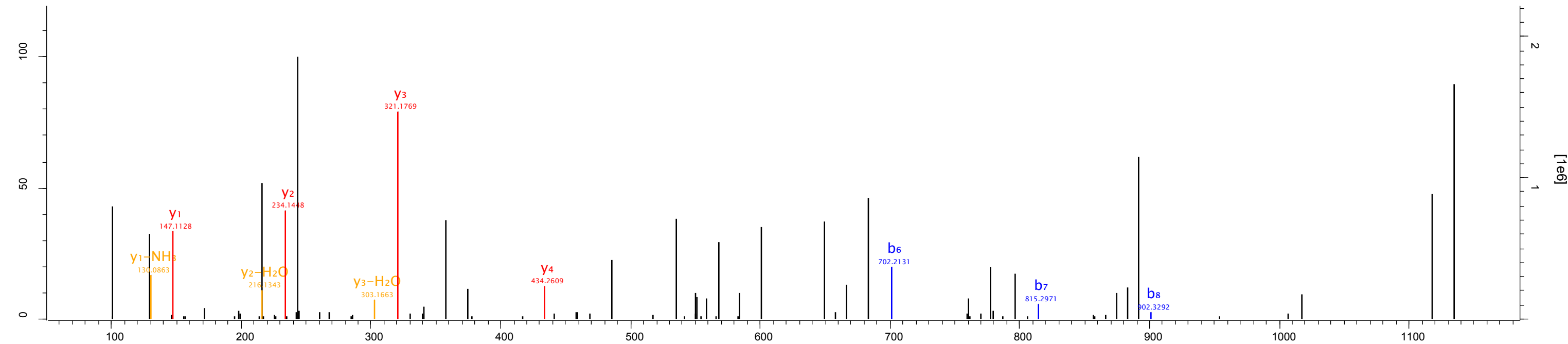
Raw file
20180707_MaS_A375SR_ML_proteome_30

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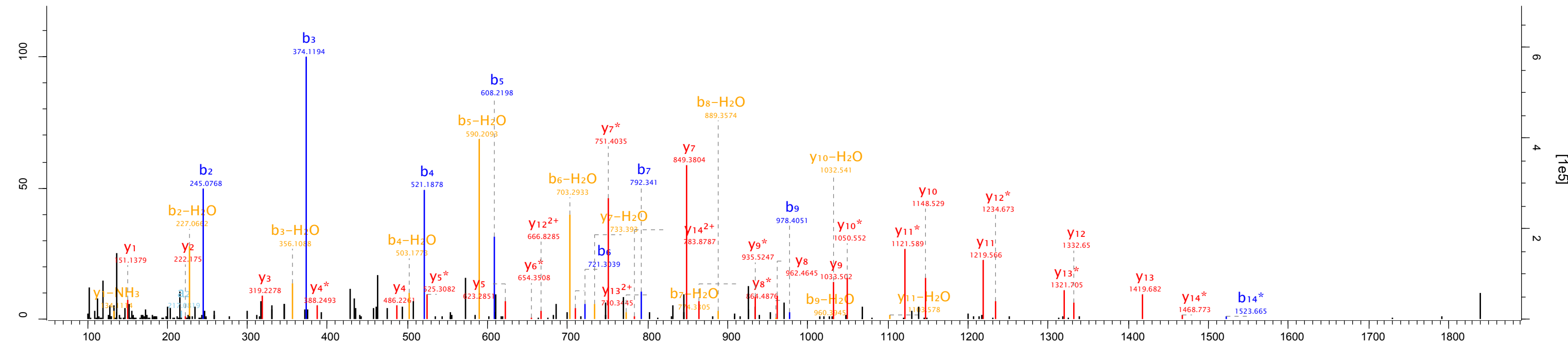


Raw file
20180707_MaS_A375SR_ML_proteome_30

Scan 3420 Method FTMS; HCD Score 66.19 m/z 568.24 Gene names MAP3K19

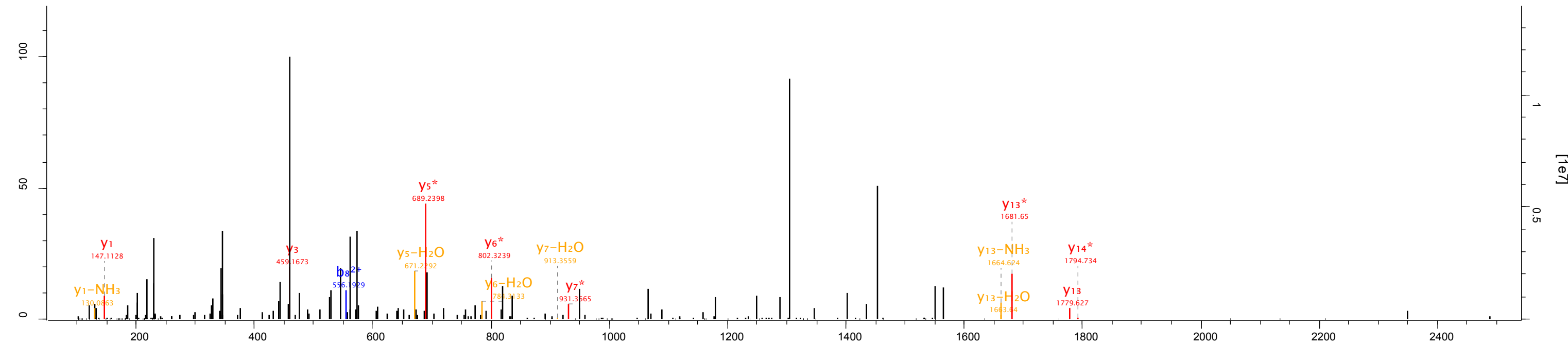


Raw file Scan Method Score m/z Gene names
 20150812_A375SR_Phospho_BR1_02 24311 FTMS; HCD 172.77 970.44 MAPK11P1L



ac
 - S D E F S L A D A L P E H S P A K -
 b2 b3 b4 b5 b6 b7 b9 b14*

Raw file 20150812_A375SR_Phospho_BR1_03 Scan 22141 Method FTMS; HCD Score 46.42 m/z 1177.43 Gene names PIH1D3

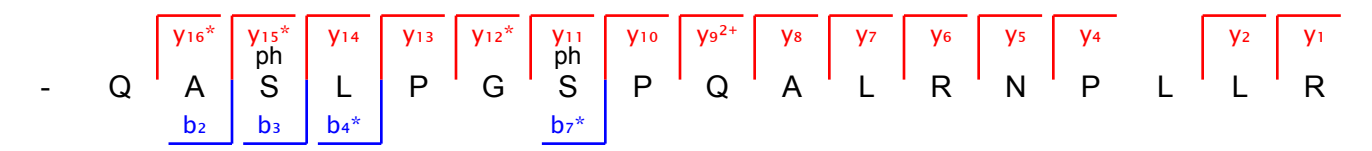
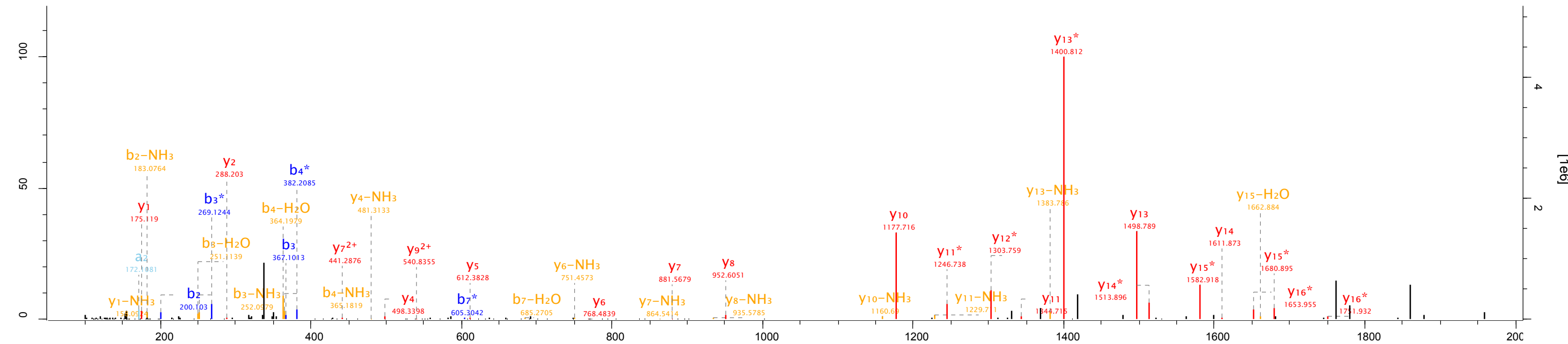


- A F Y ph I P E T E T L E I T M T M K -

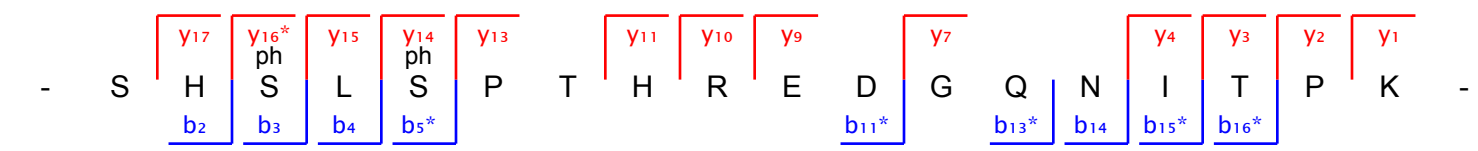
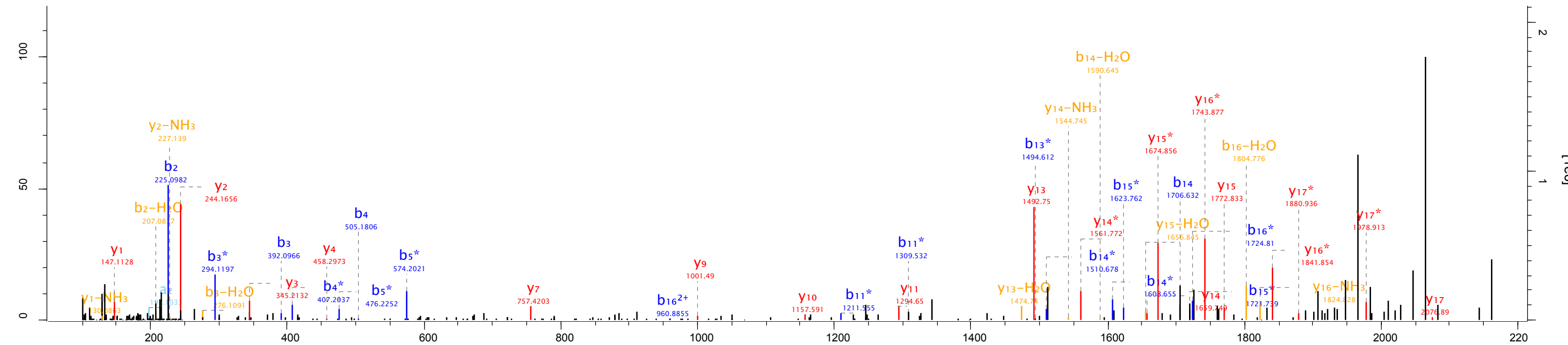
Fragmentation diagram showing peptide sequence and fragmentation sites:

- ph (phosphorylation) on Y
- y14* and y13 (backbone fragmentation) on I and P
- b8²⁺ (charge state) on E
- y7*, y6*, y5* (backbone fragmentation) on E, I, and T
- ph (phosphorylation) on T
- ox (oxidation) on M
- y3 (backbone fragmentation) on T
- y1 (backbone fragmentation) on K

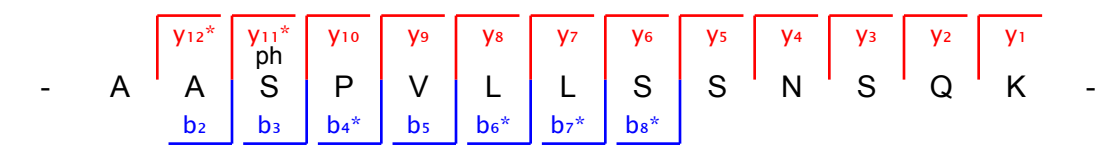
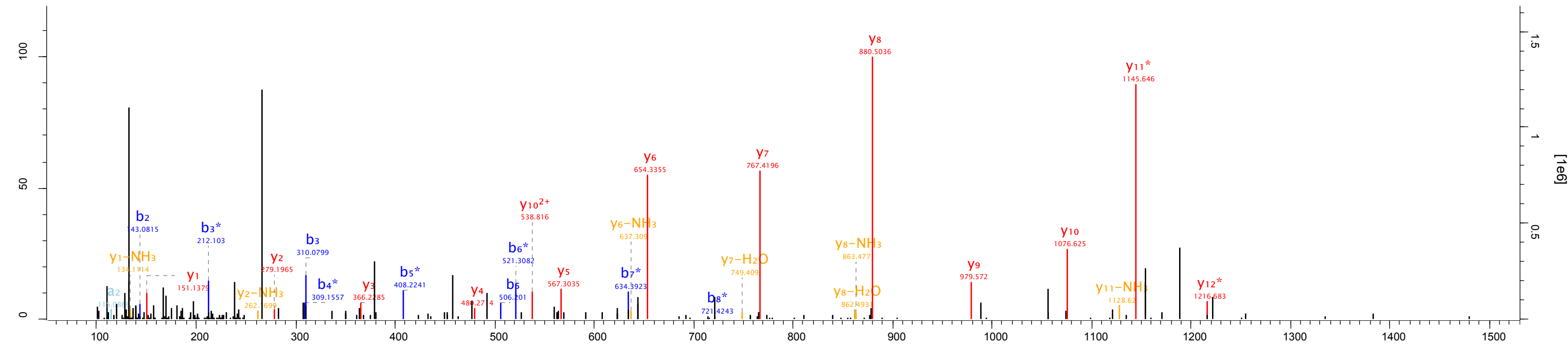
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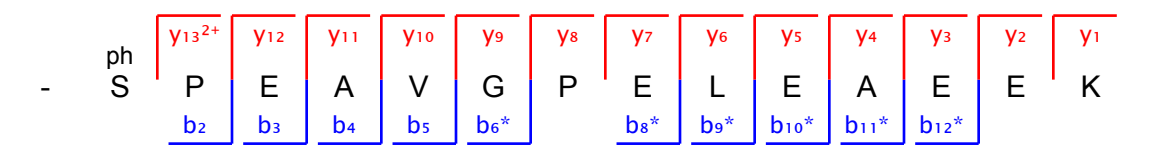
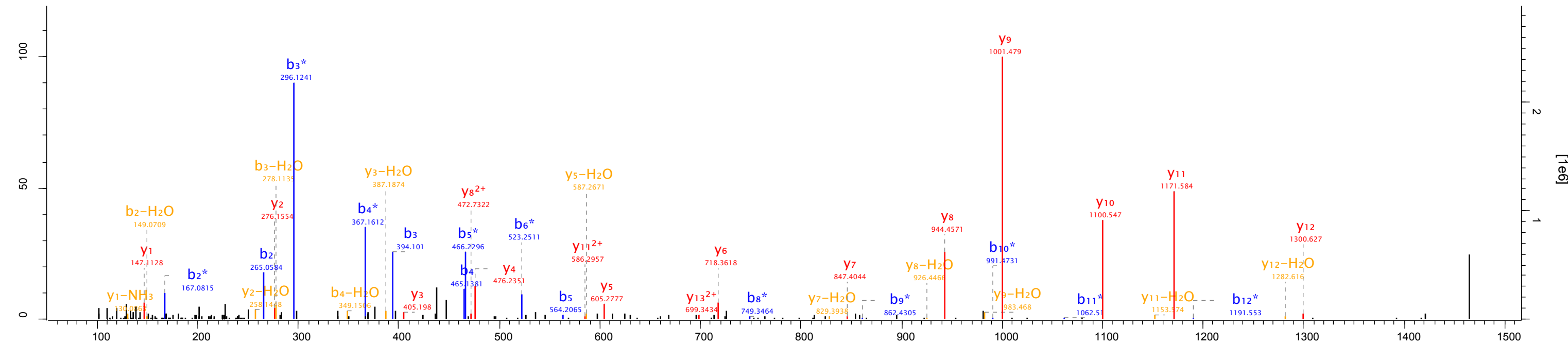
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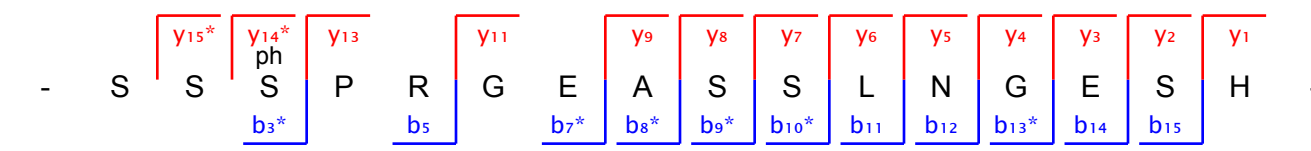
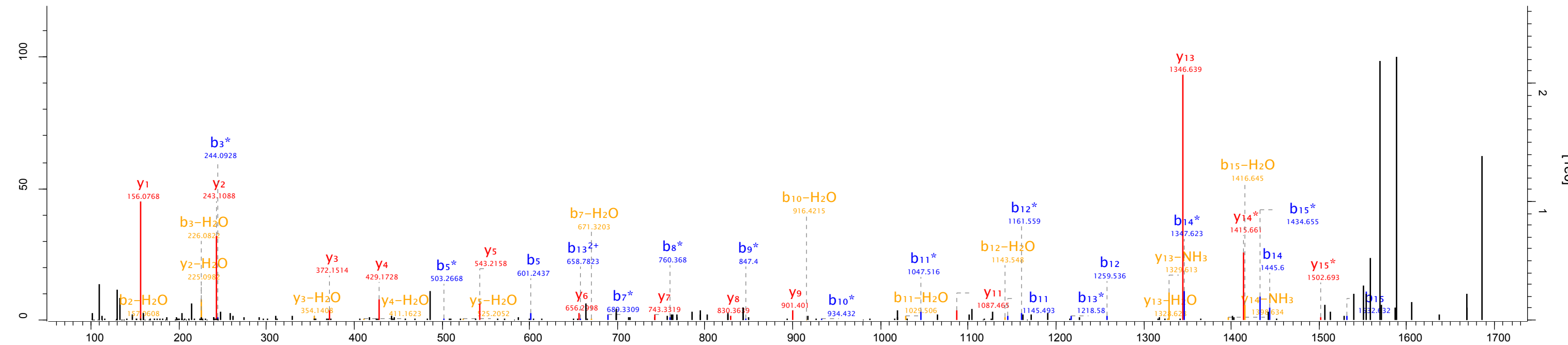
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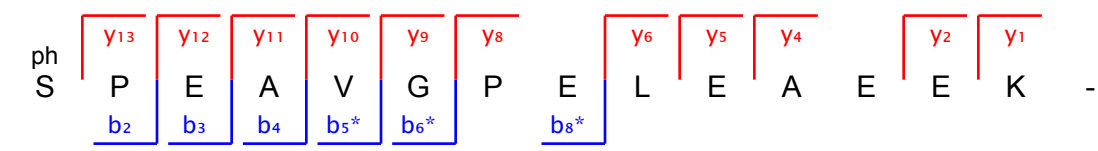
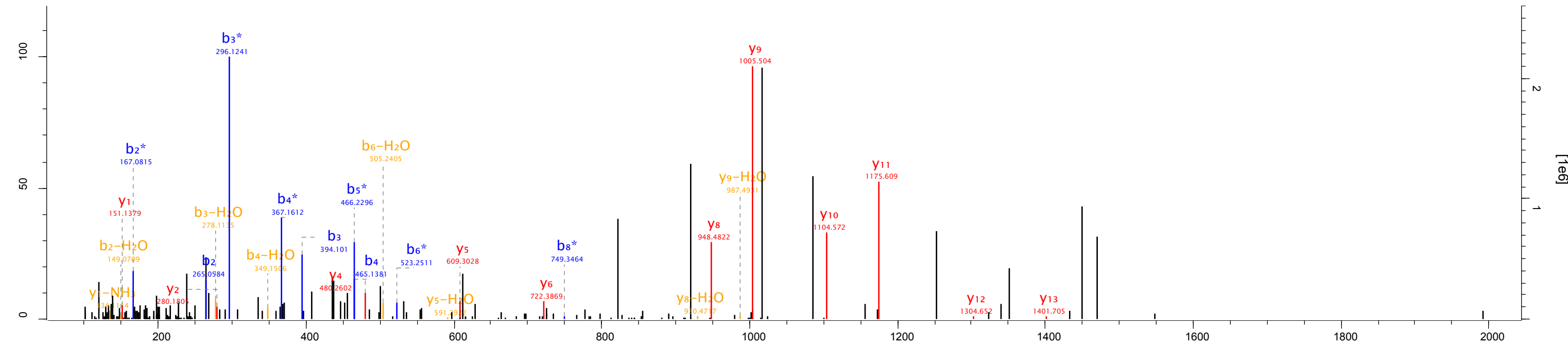
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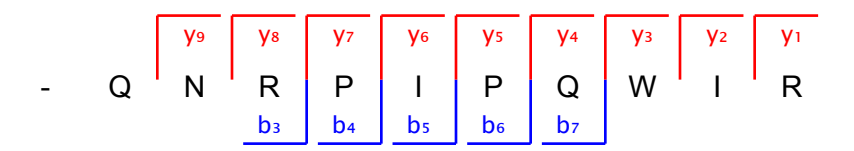
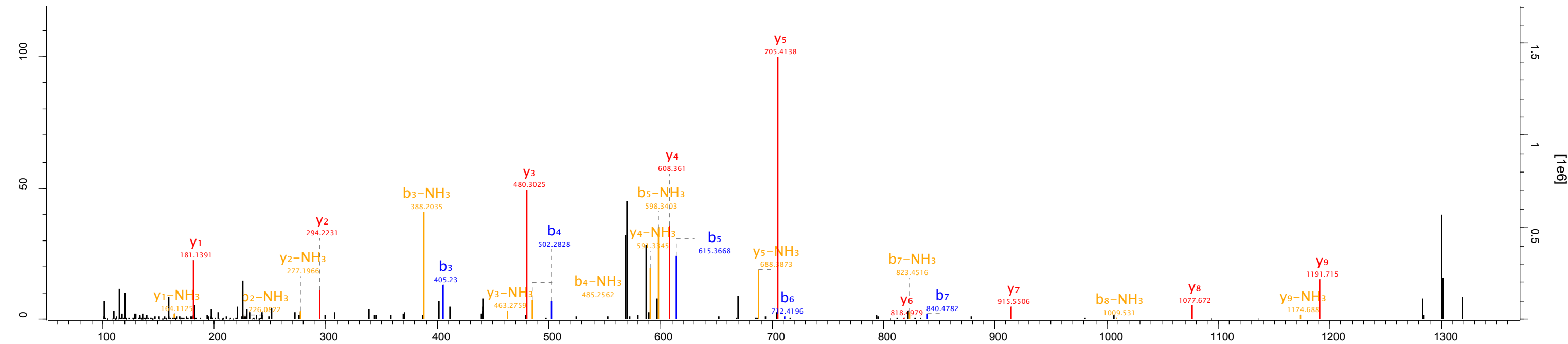
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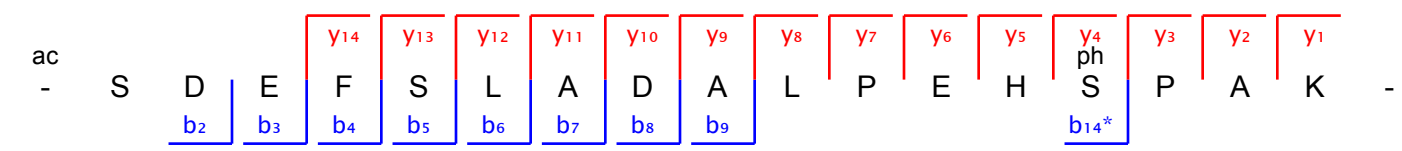
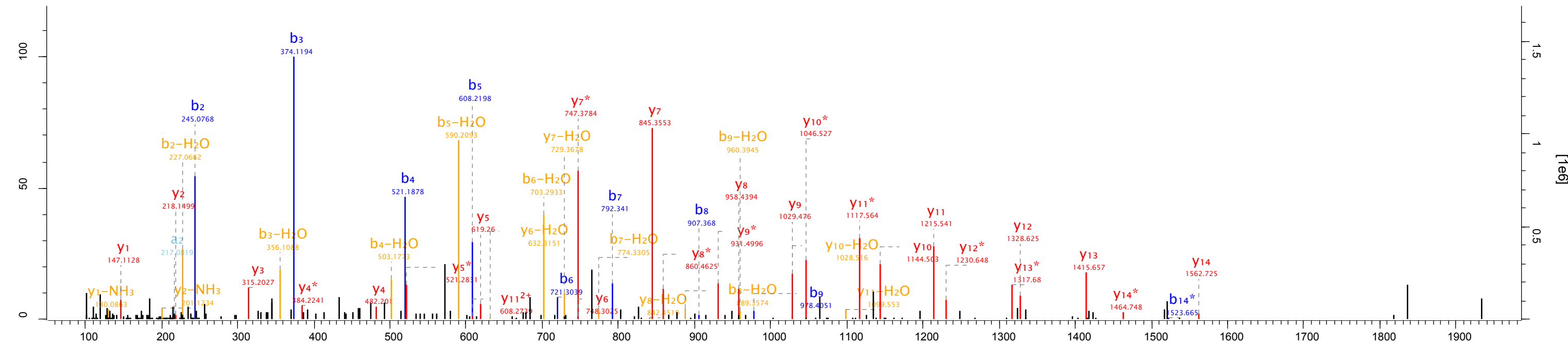
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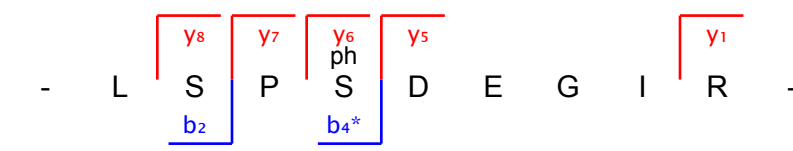
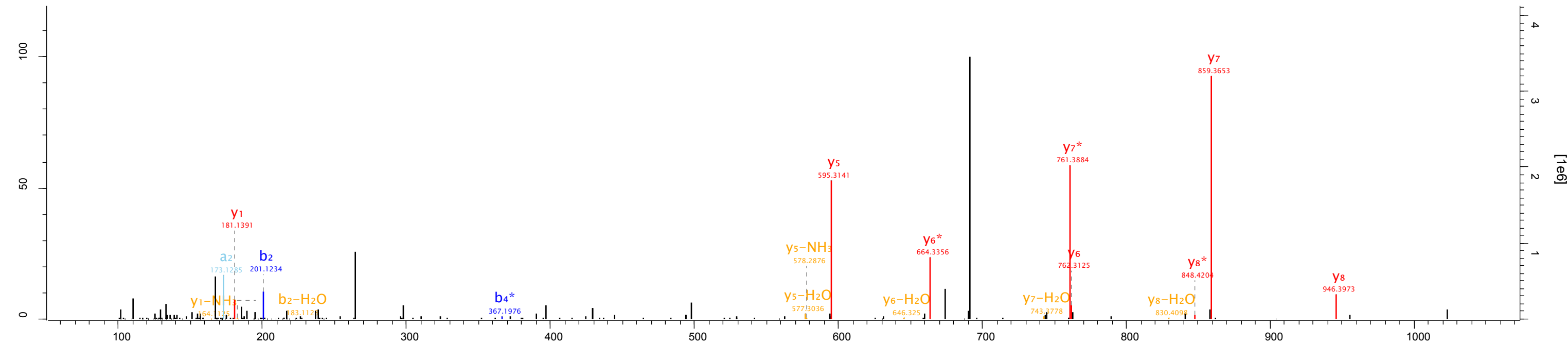
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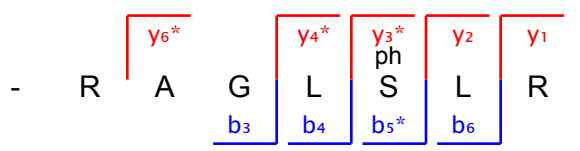
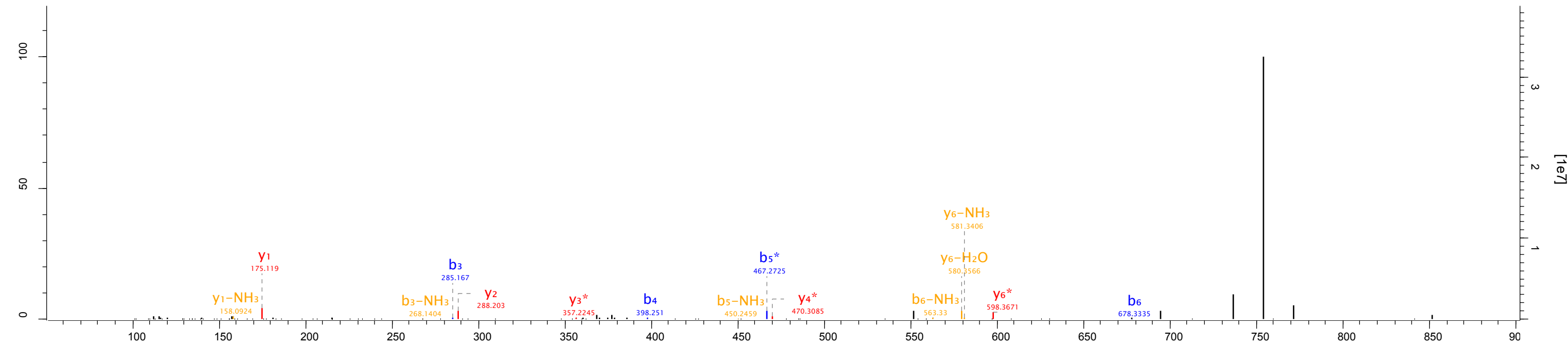
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 20150812_A375SR_Phospho_BR1_05
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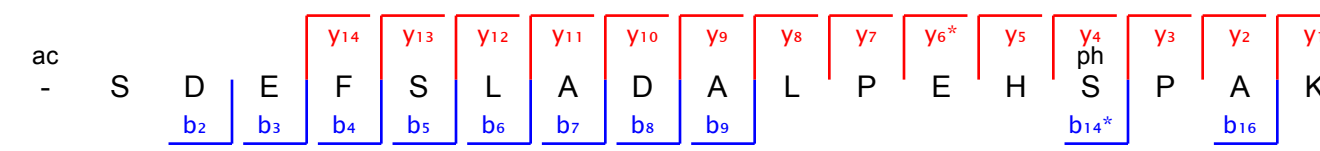
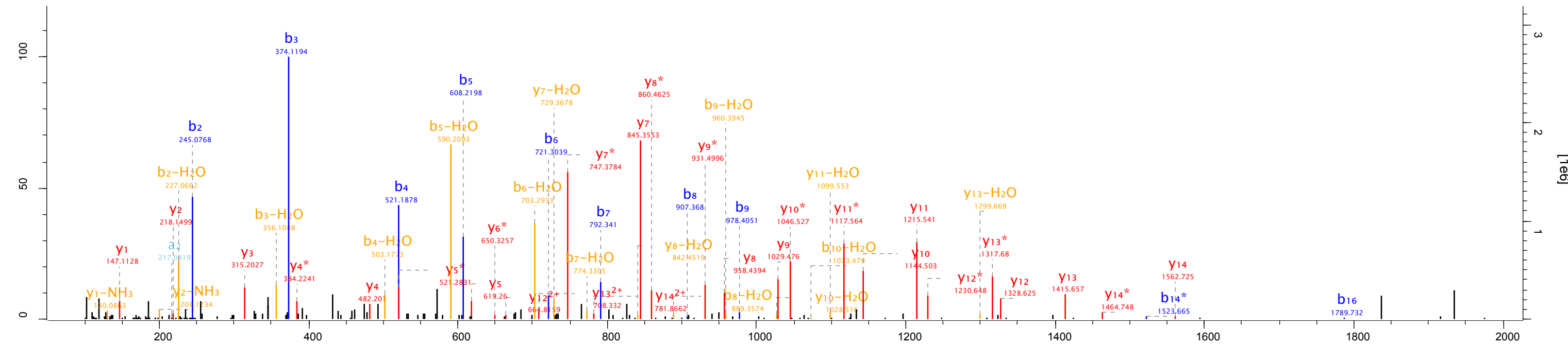
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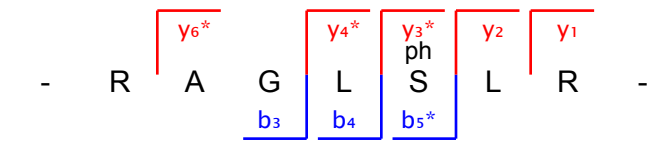
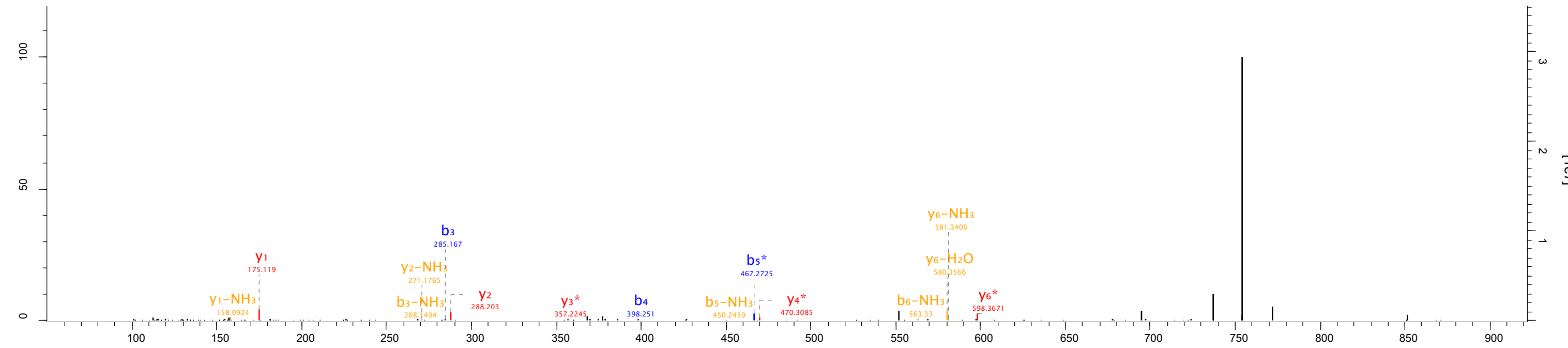
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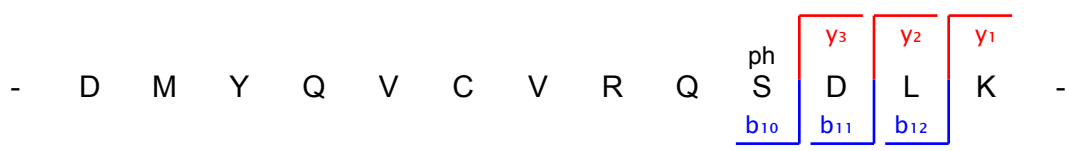
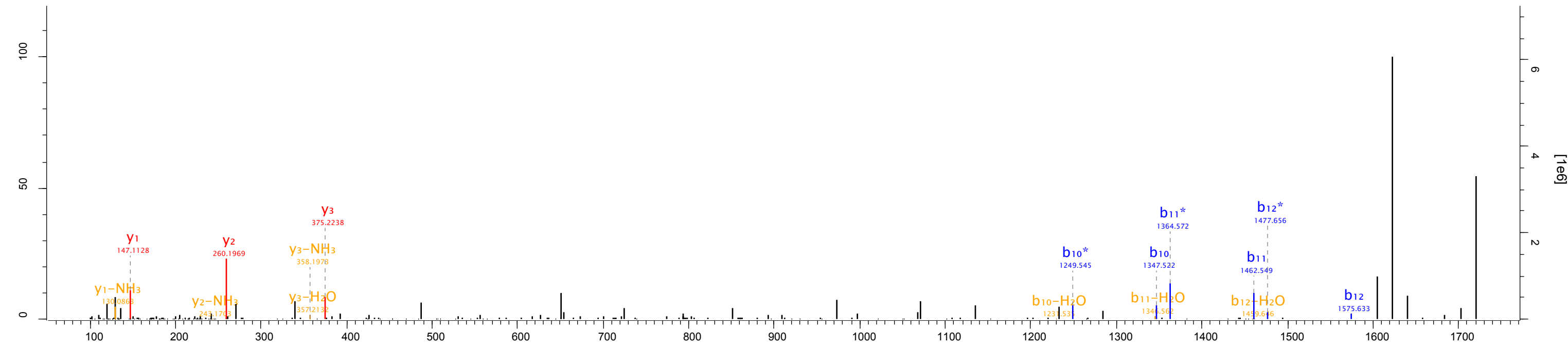
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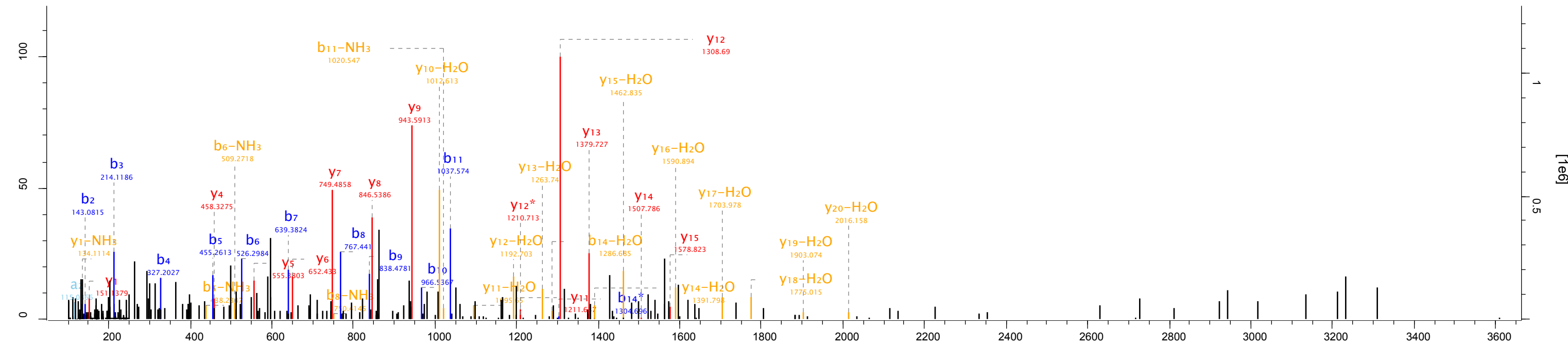
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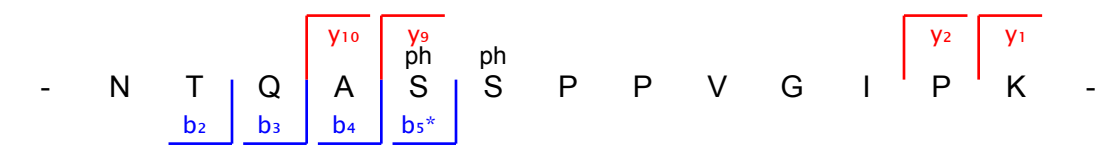
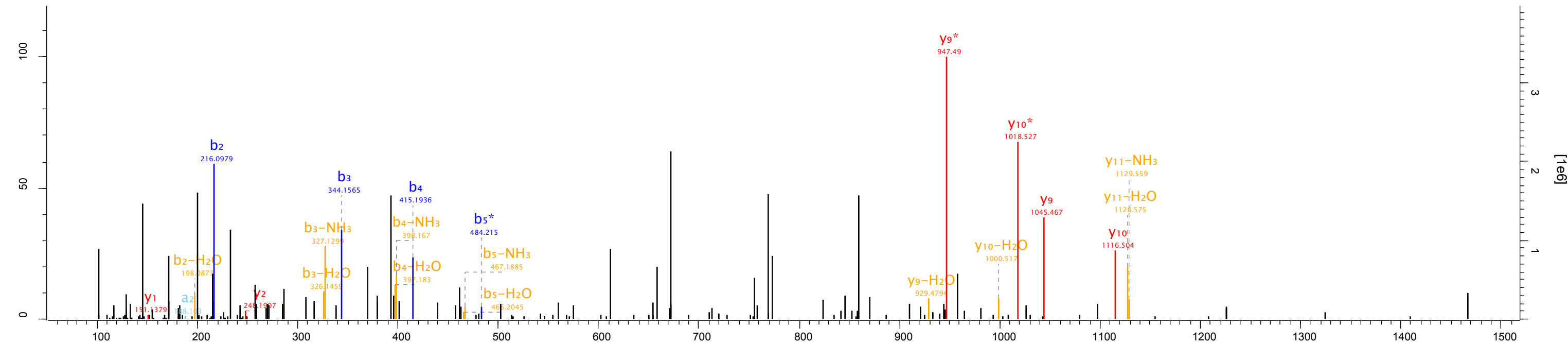
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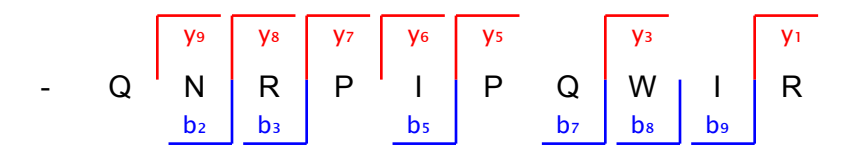
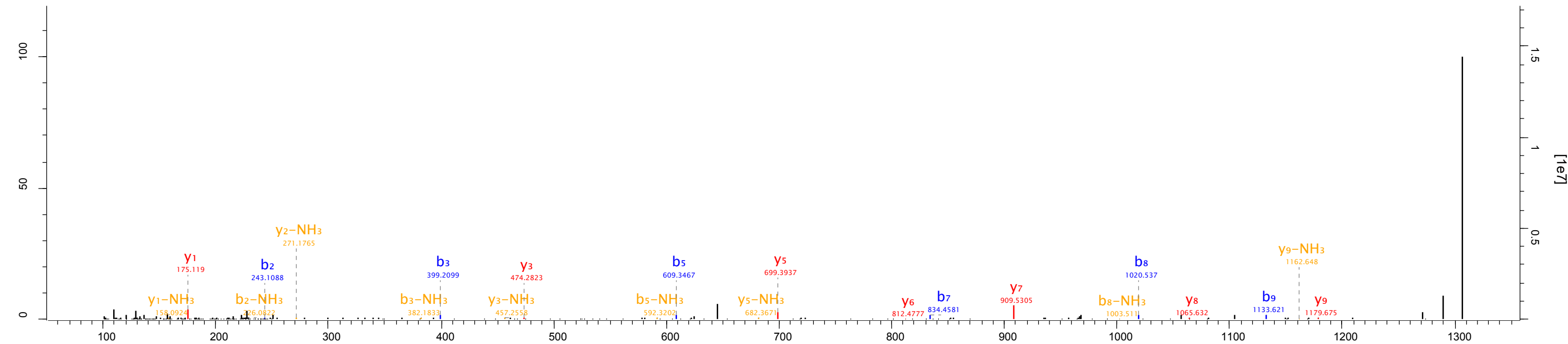
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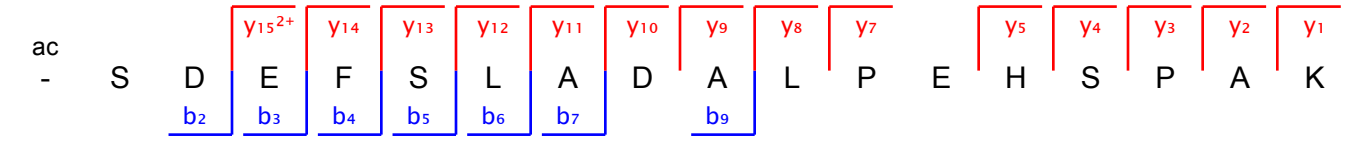
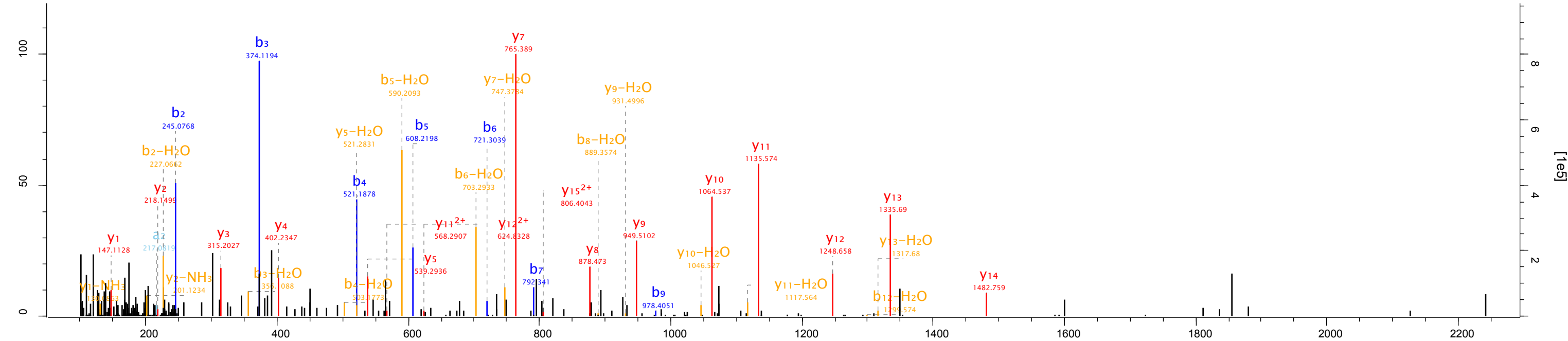


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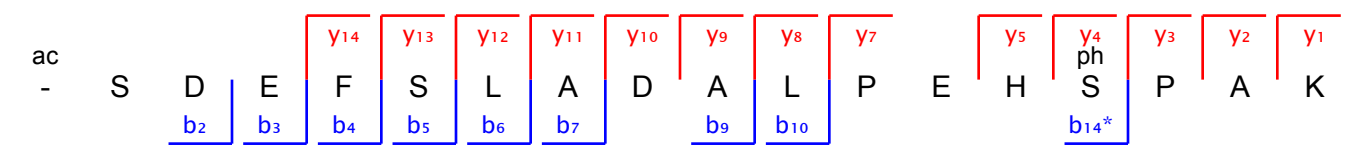
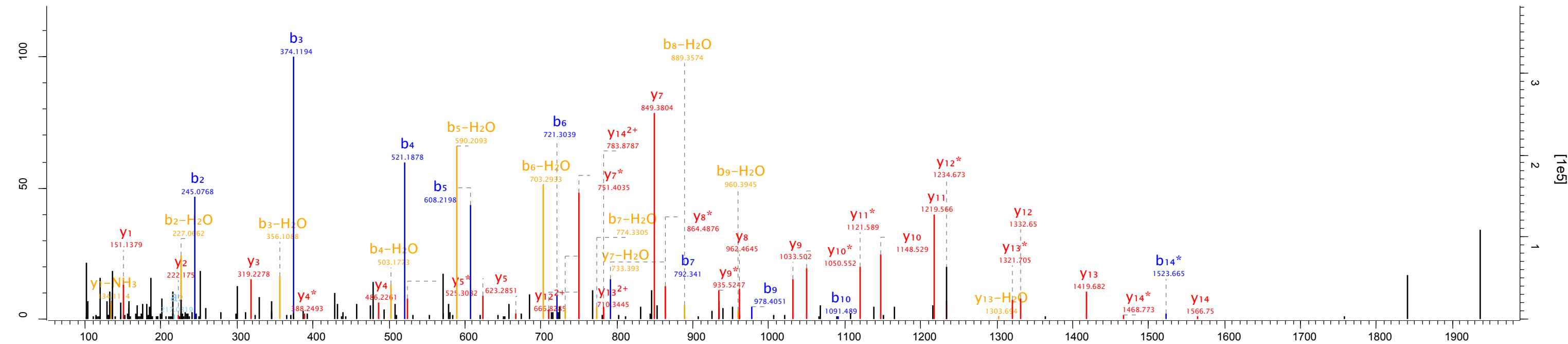


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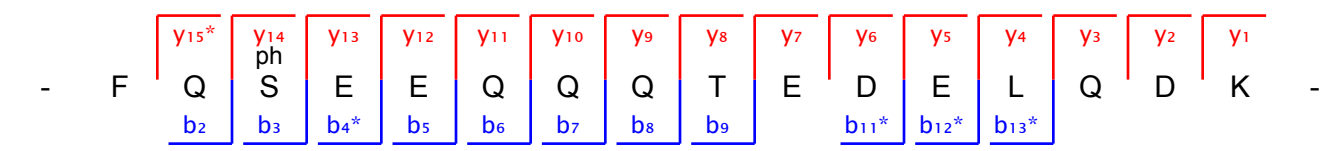
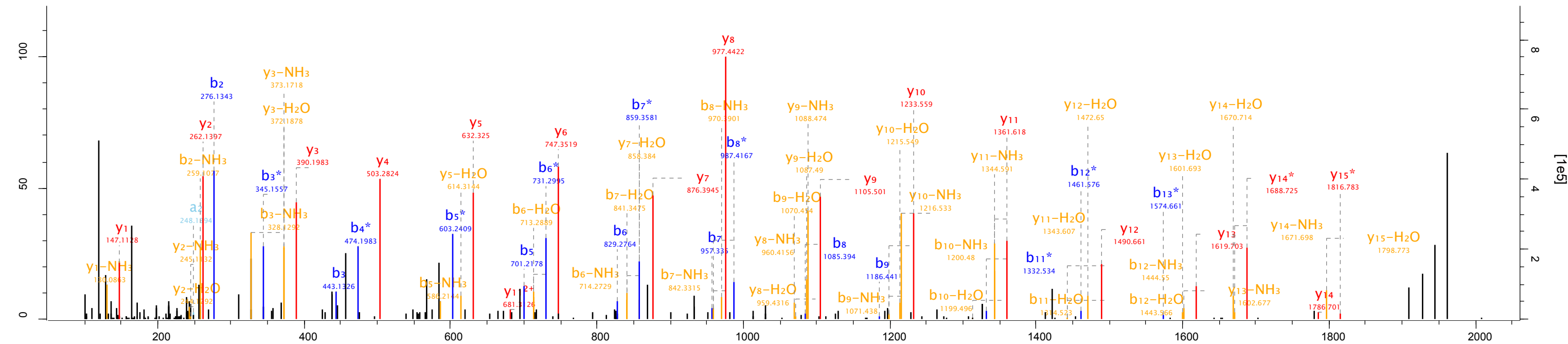
Scan 22201 Method FTMS; HCD Score 135.55 m/z 928.94 Gene names MAPK11P1L



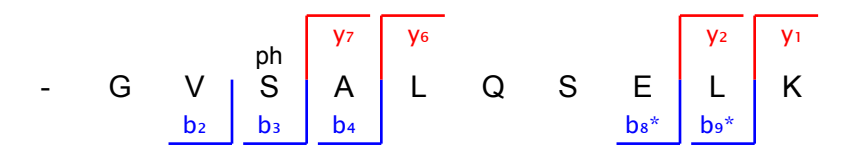
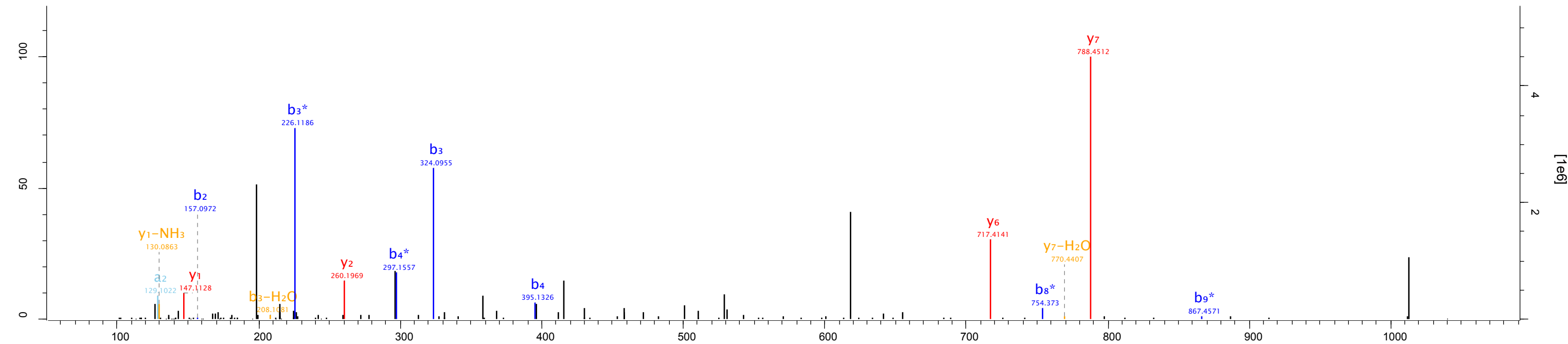
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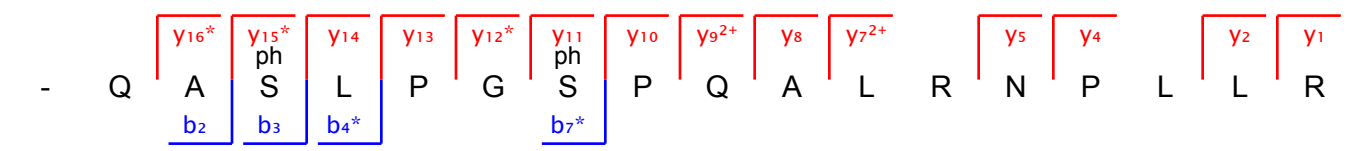
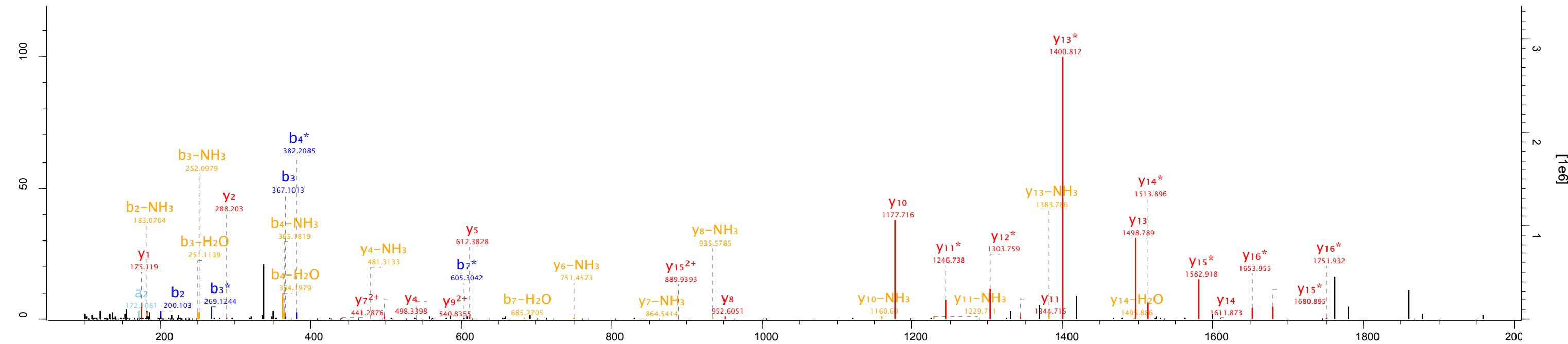
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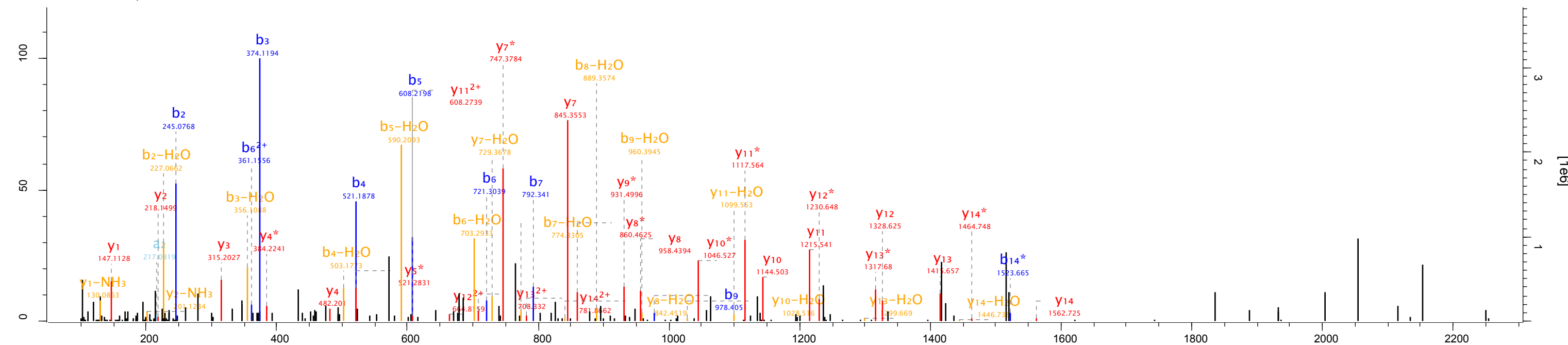


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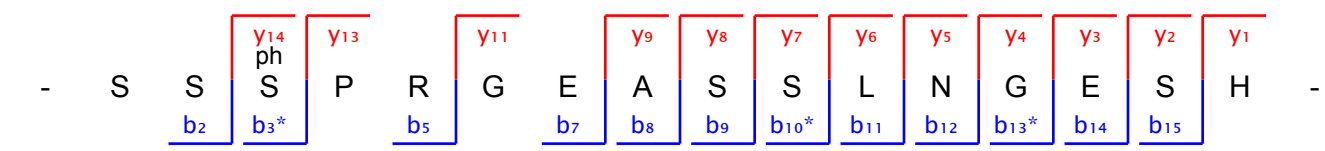
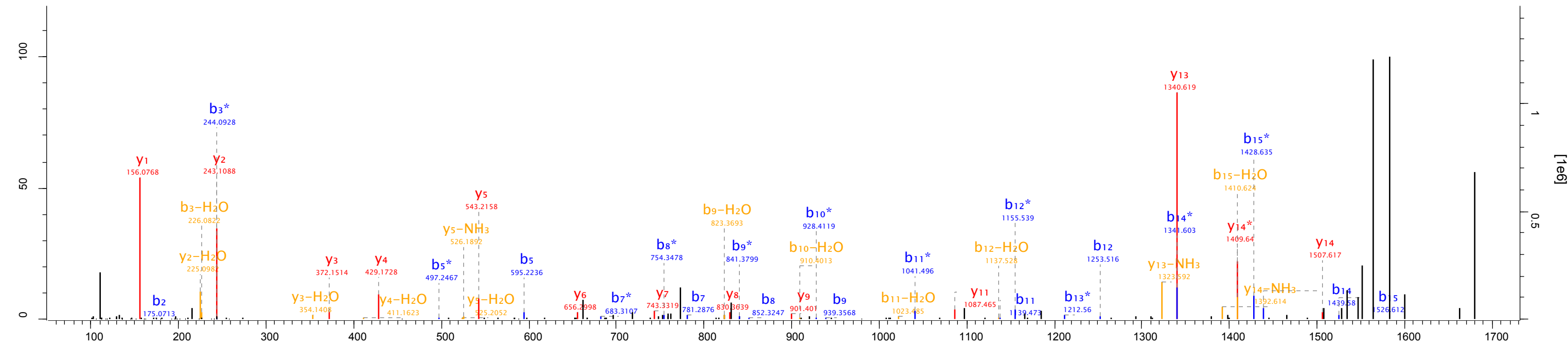
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Scan 23741 Method FTMS; HCD m/z 211.35 968.42 Gene names MAPK11P1L

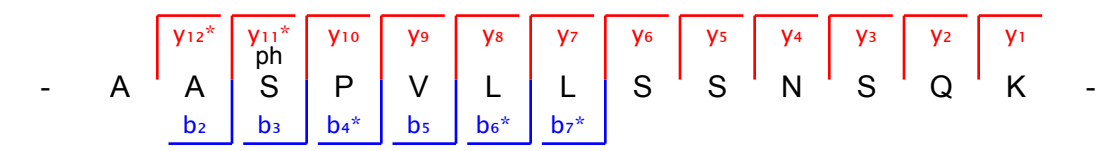
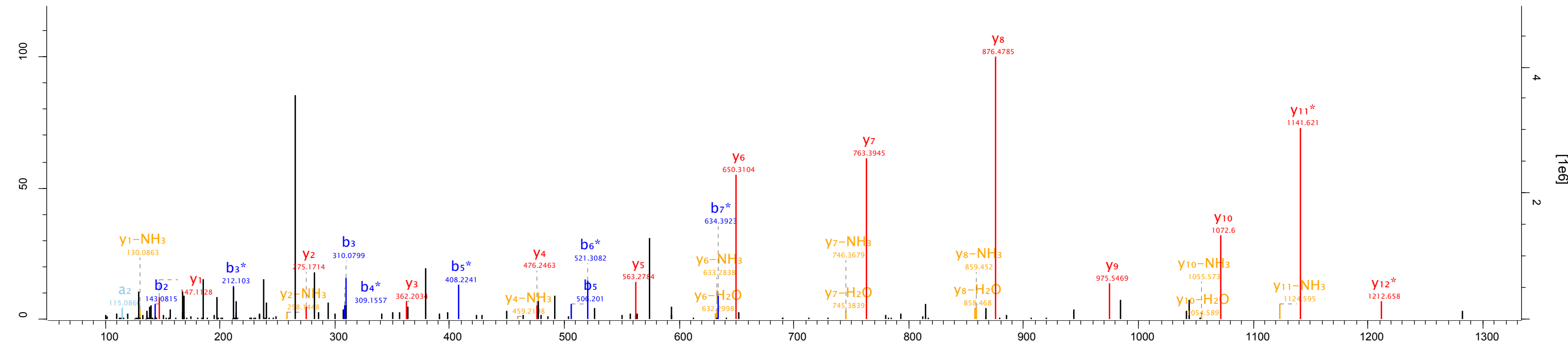


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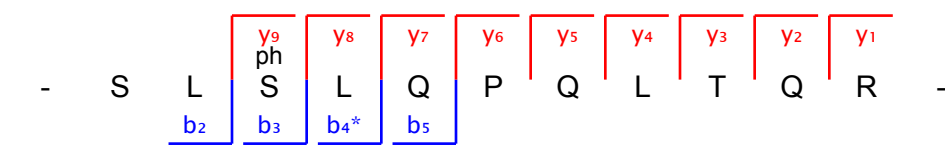
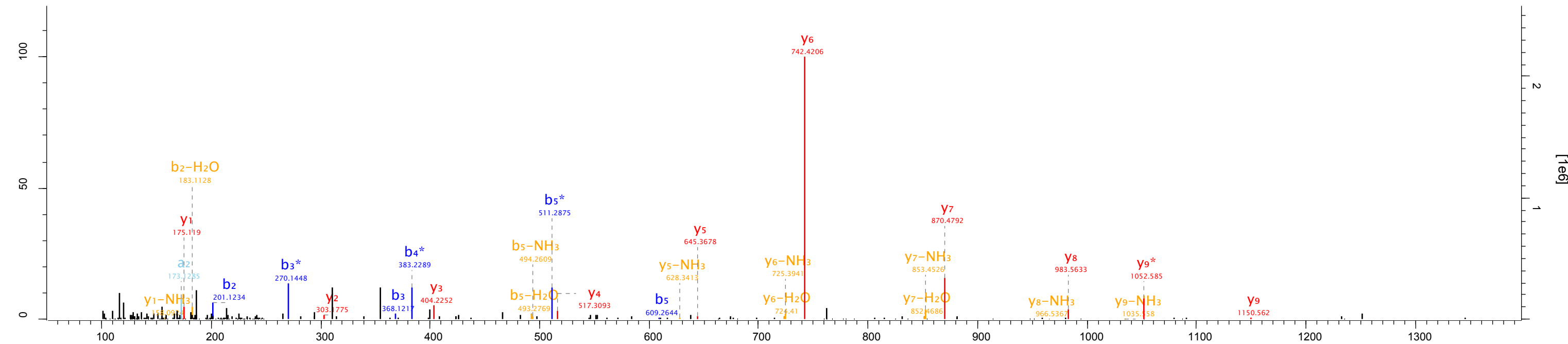
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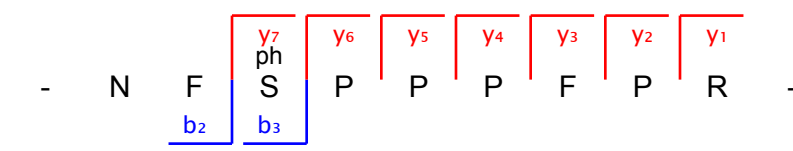
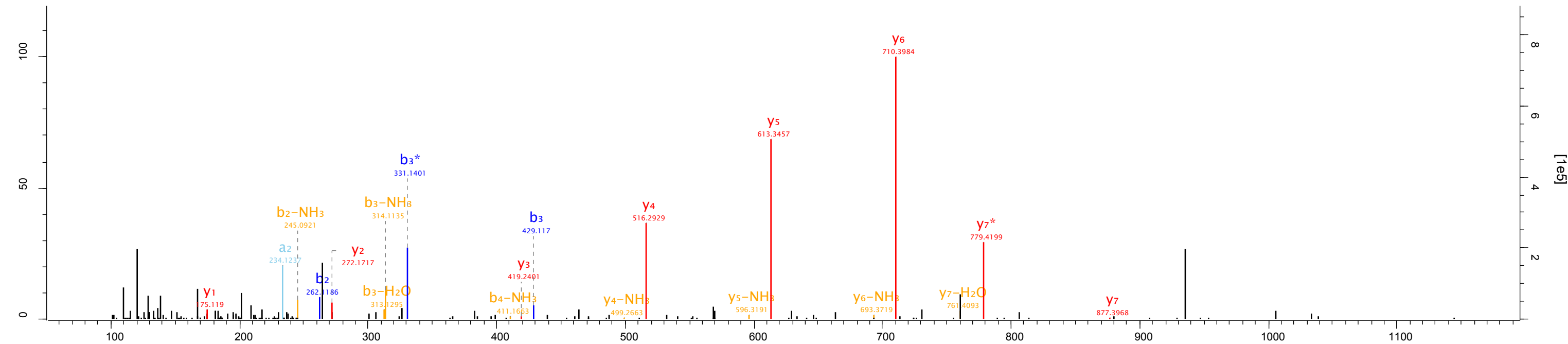
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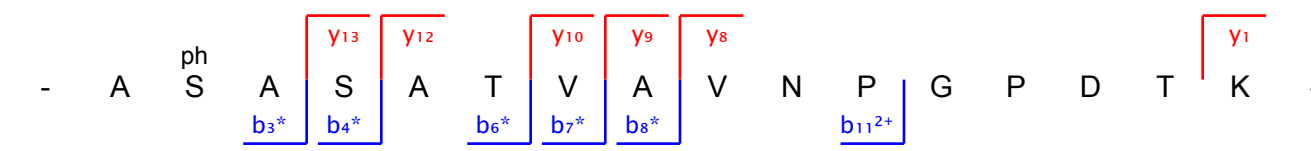
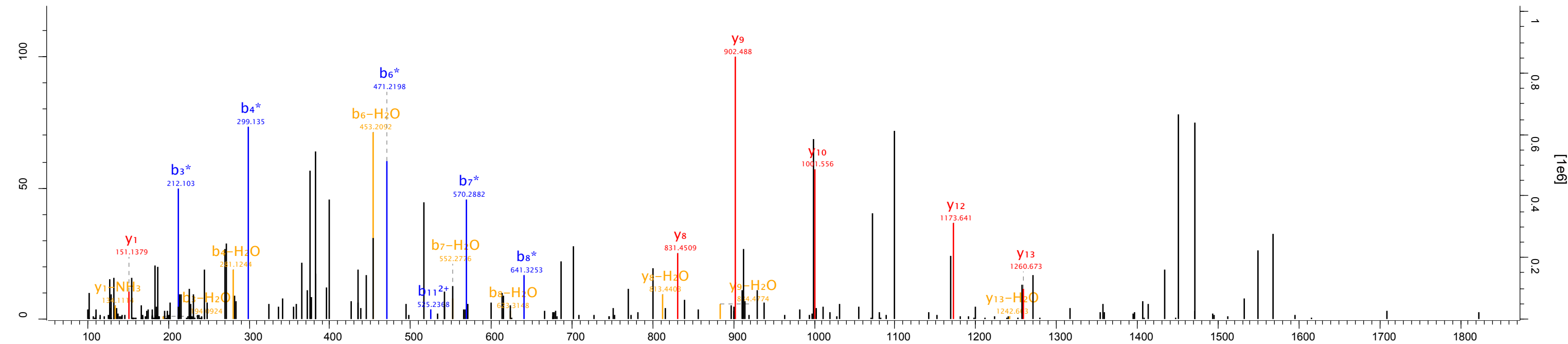
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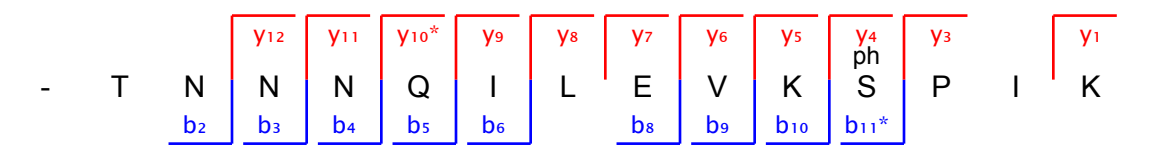
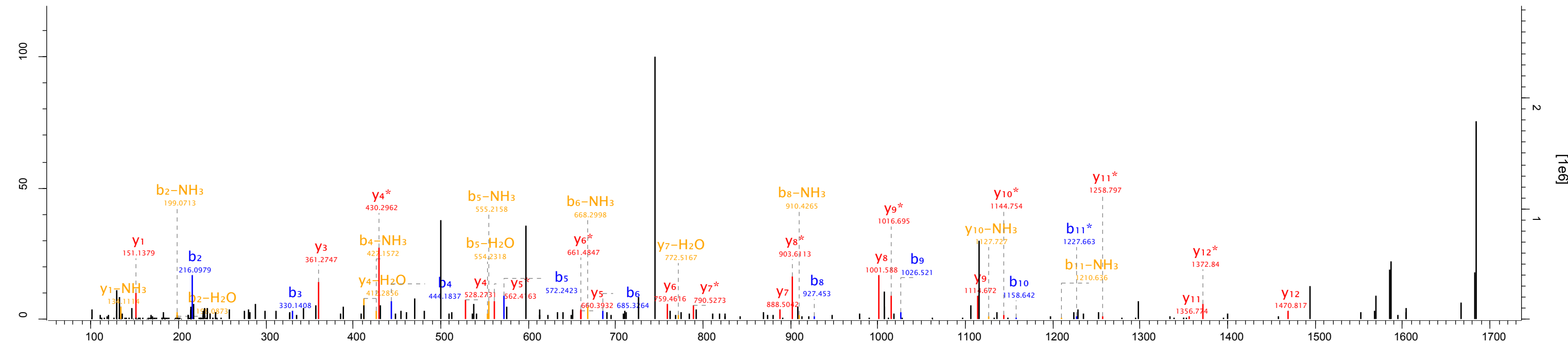
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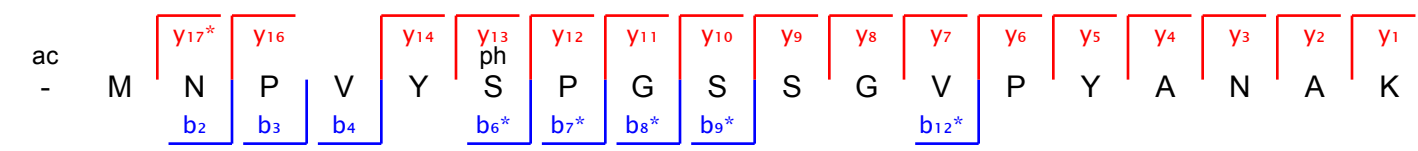
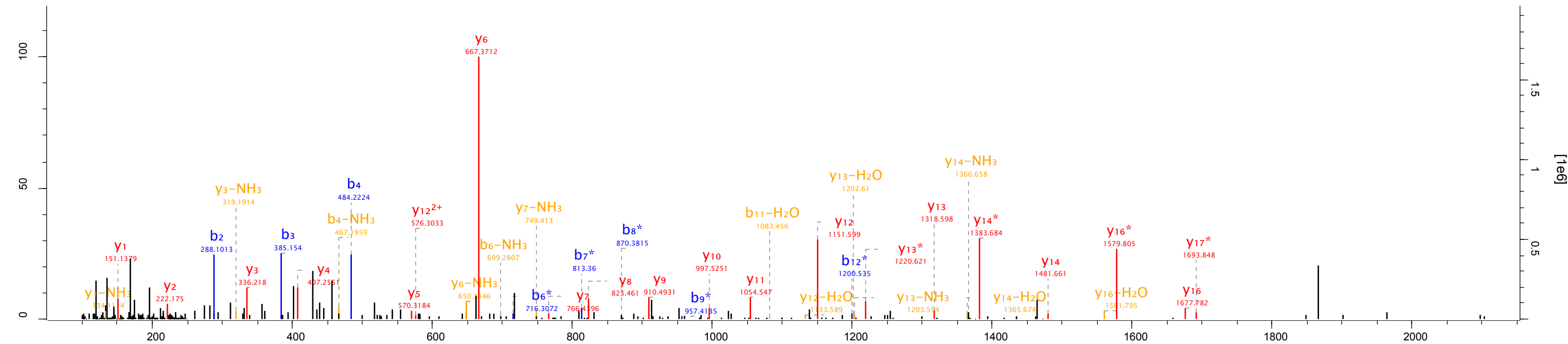
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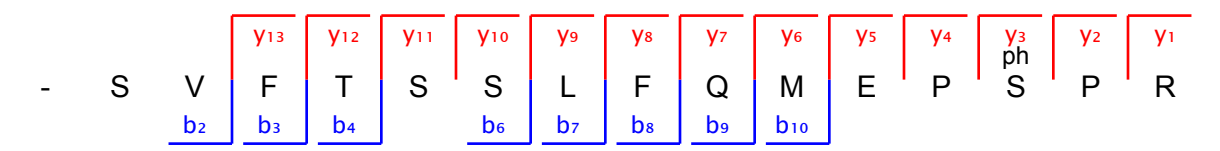
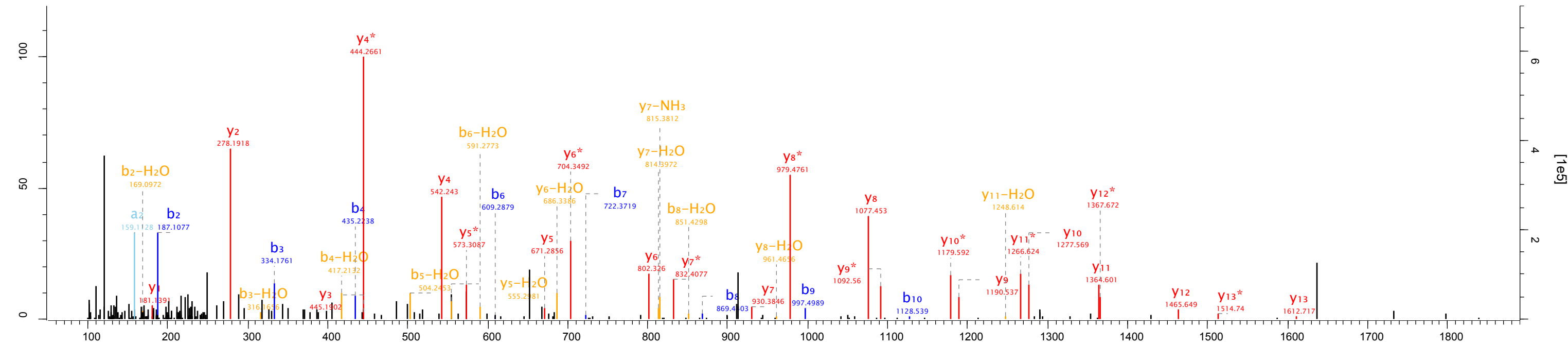
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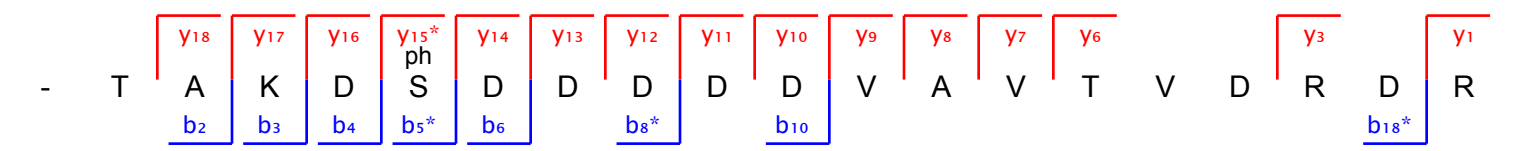
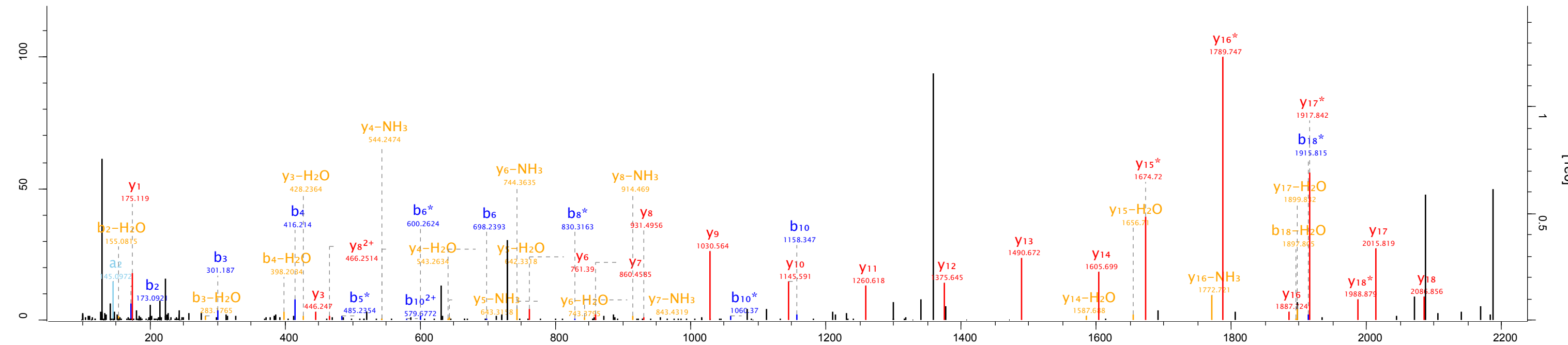
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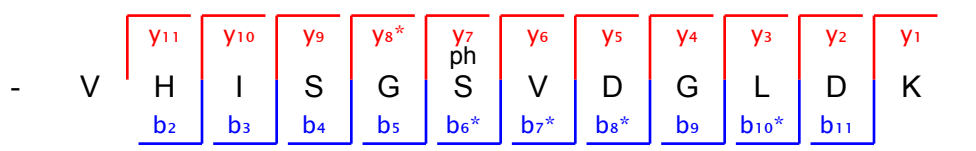
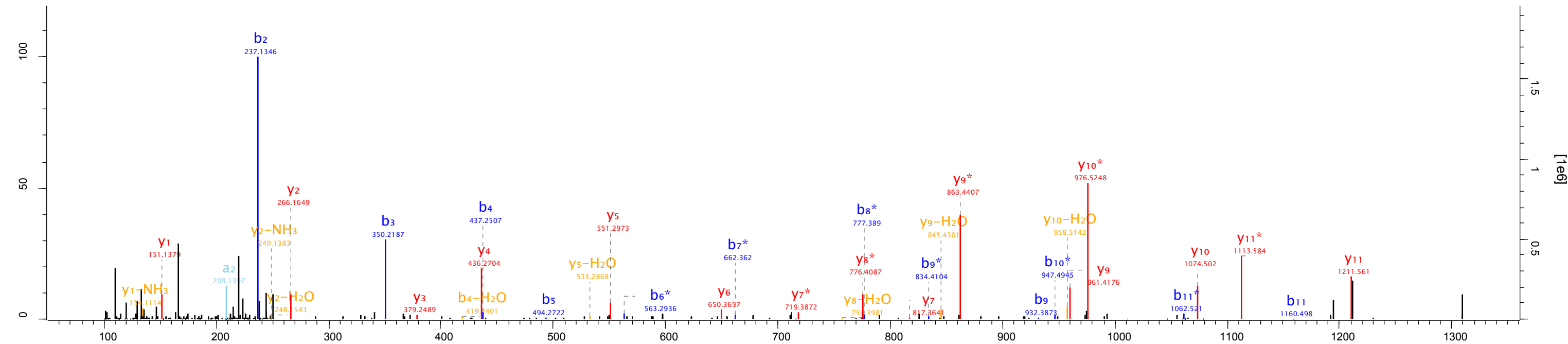
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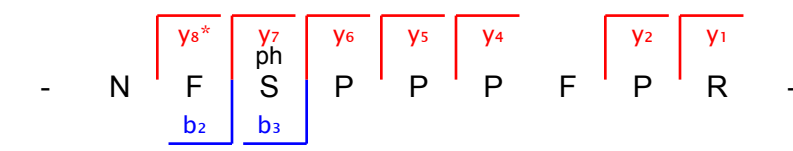
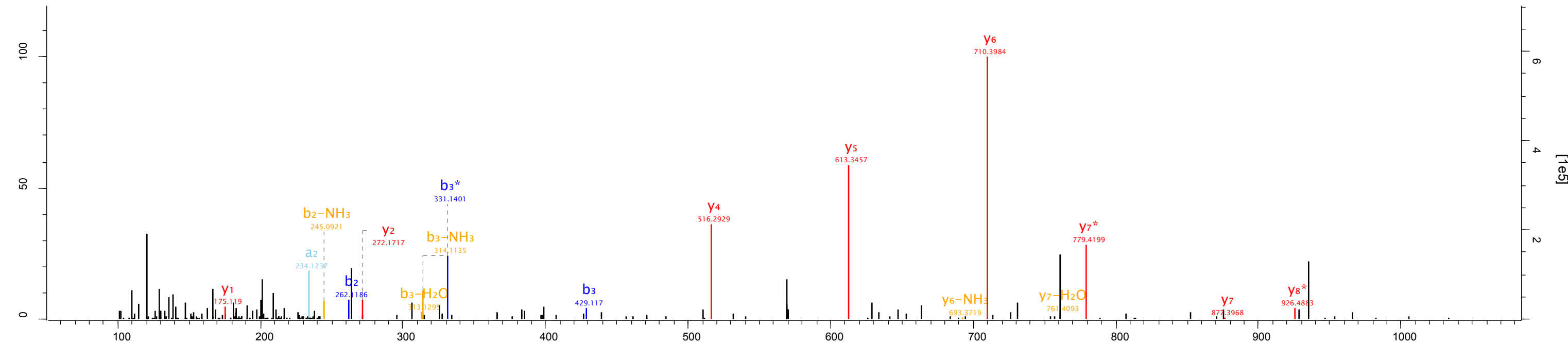
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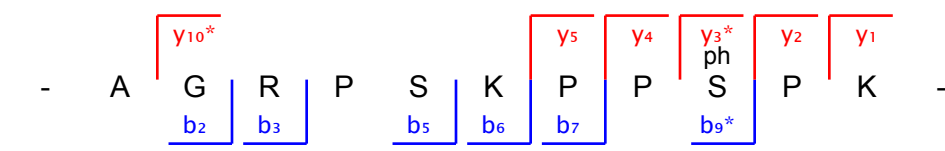
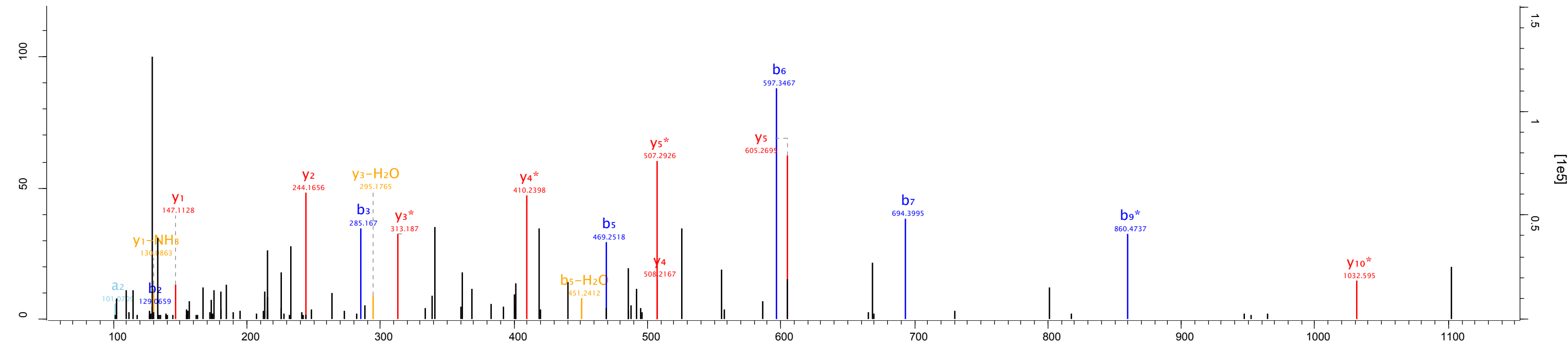
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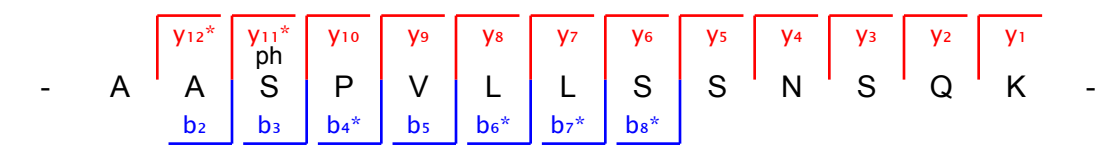
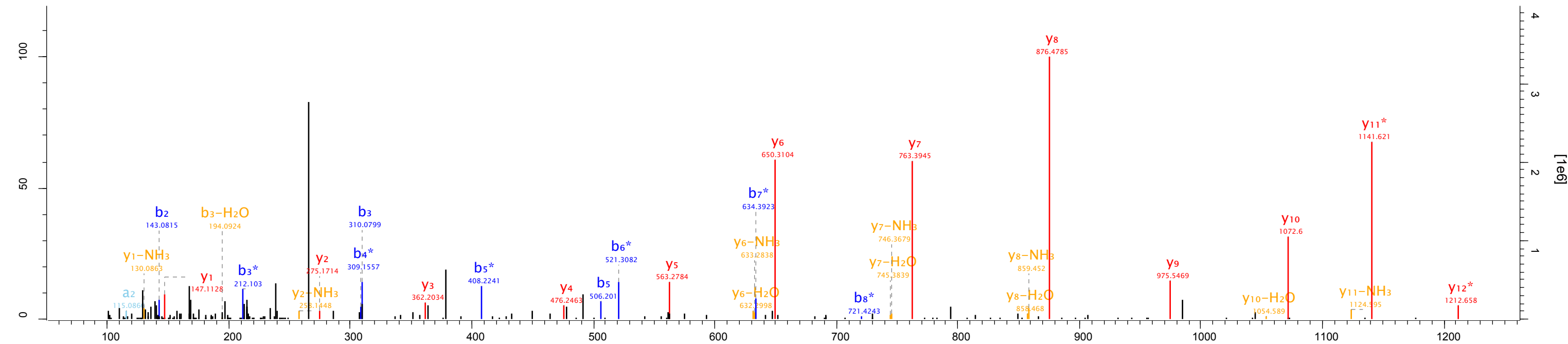
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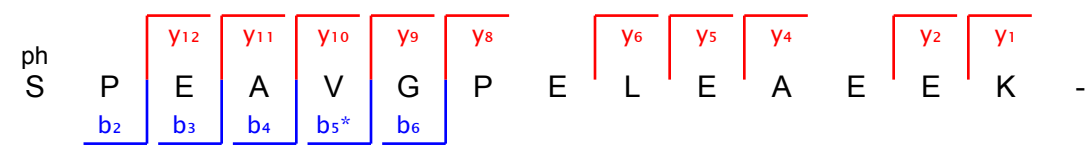
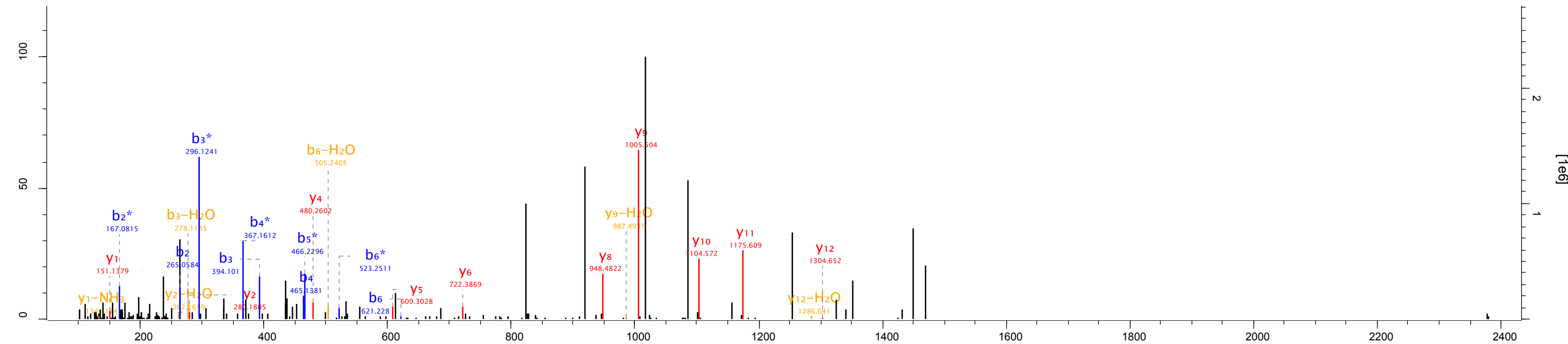
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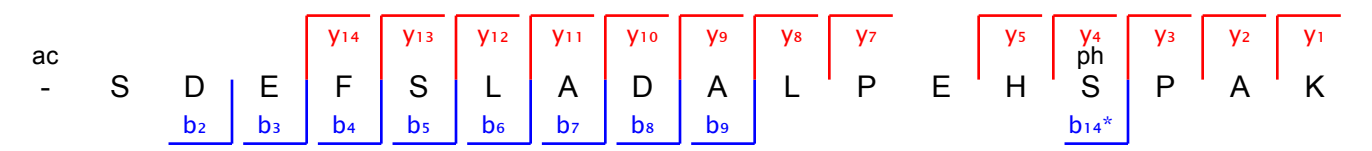
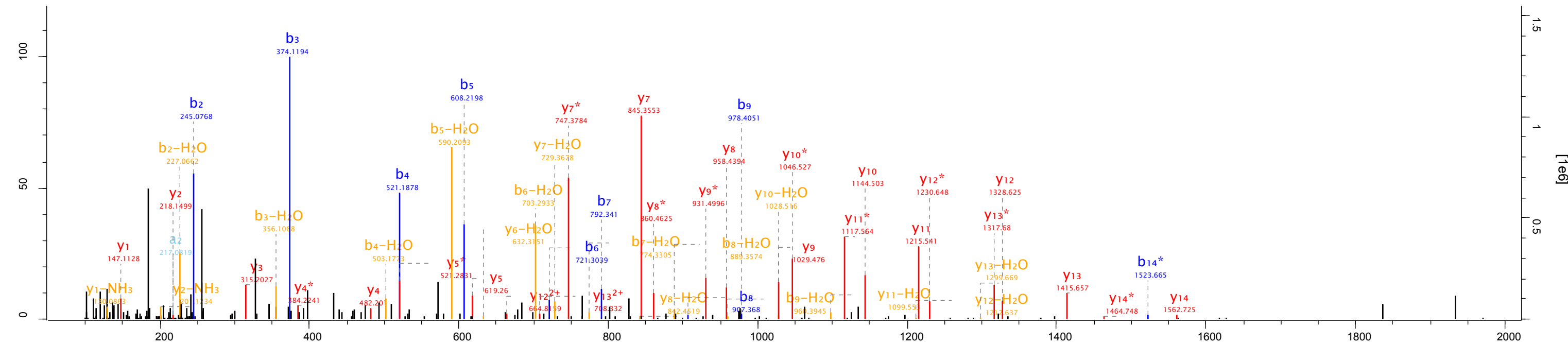
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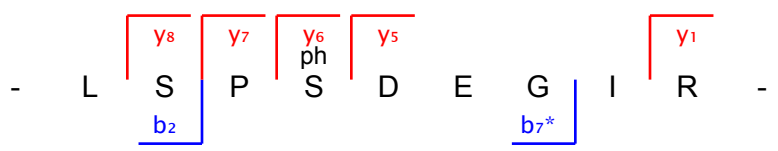
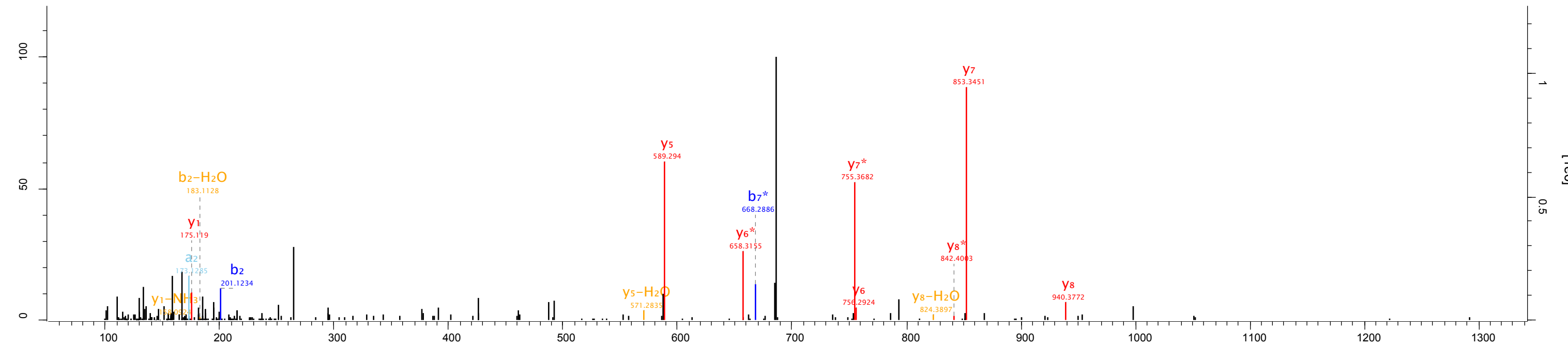
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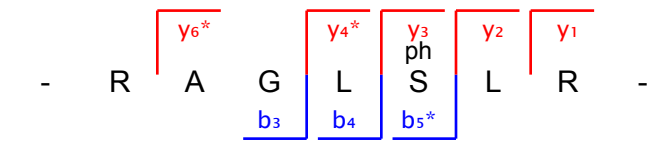
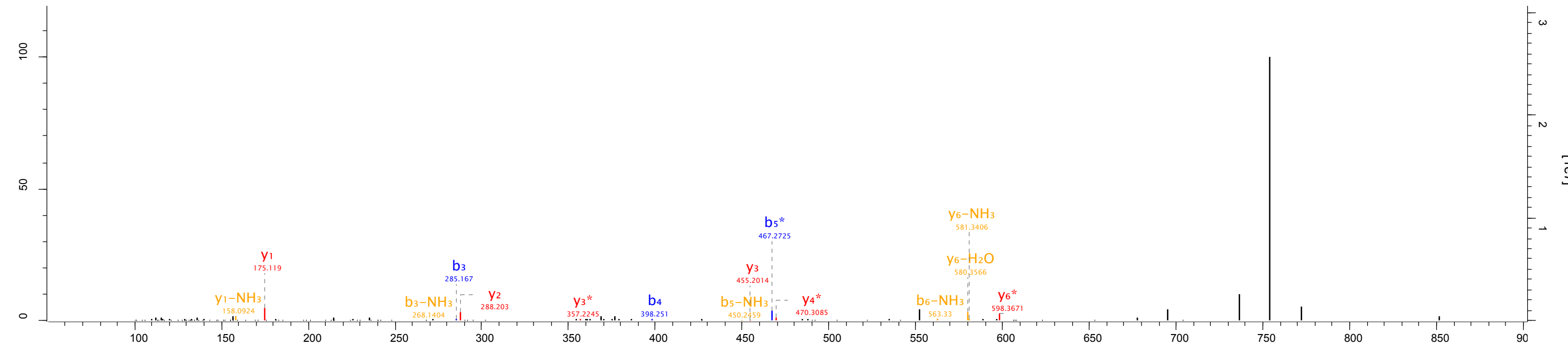
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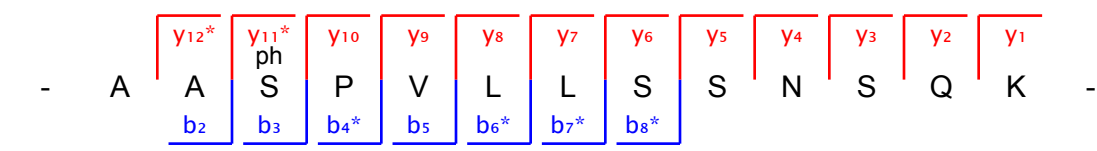
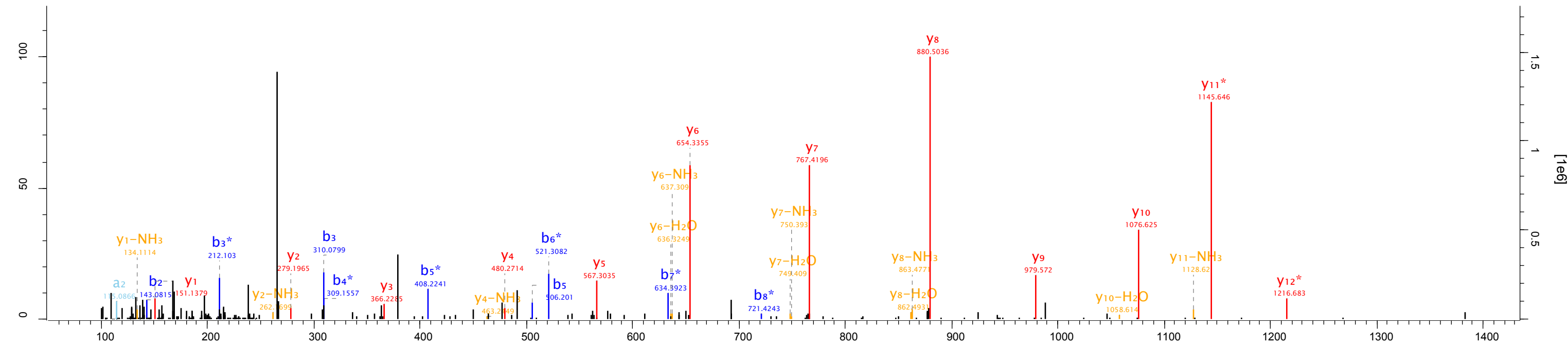
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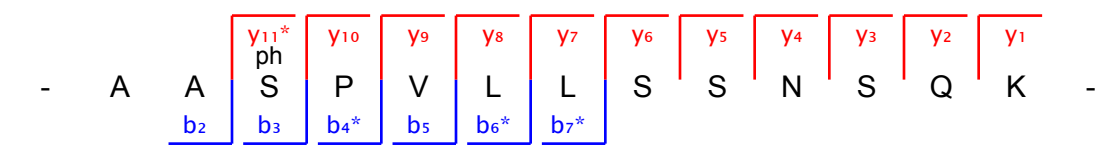
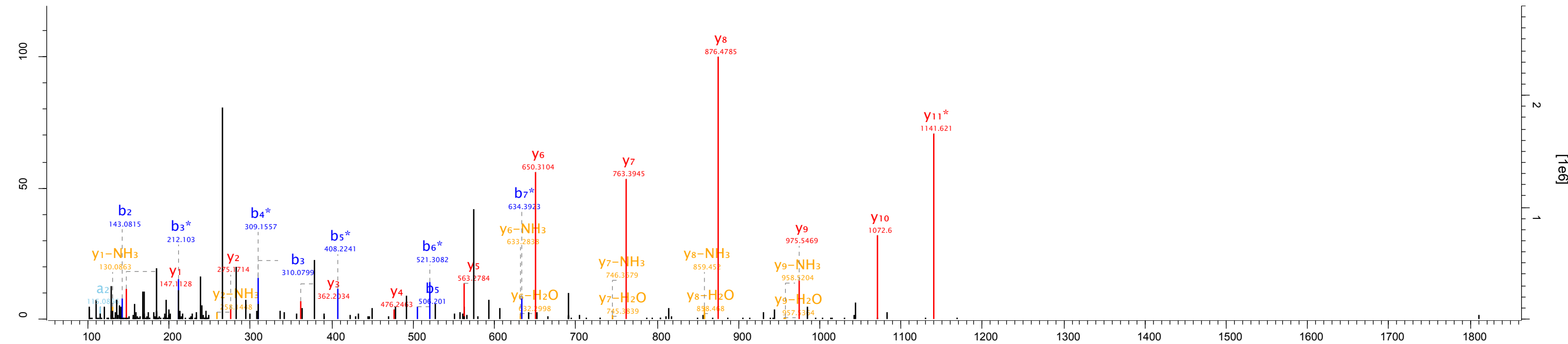
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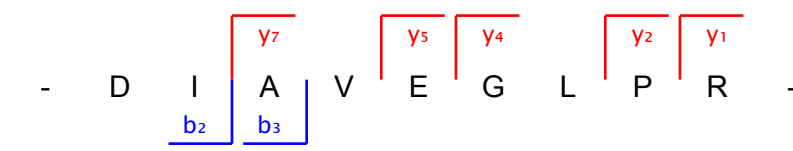
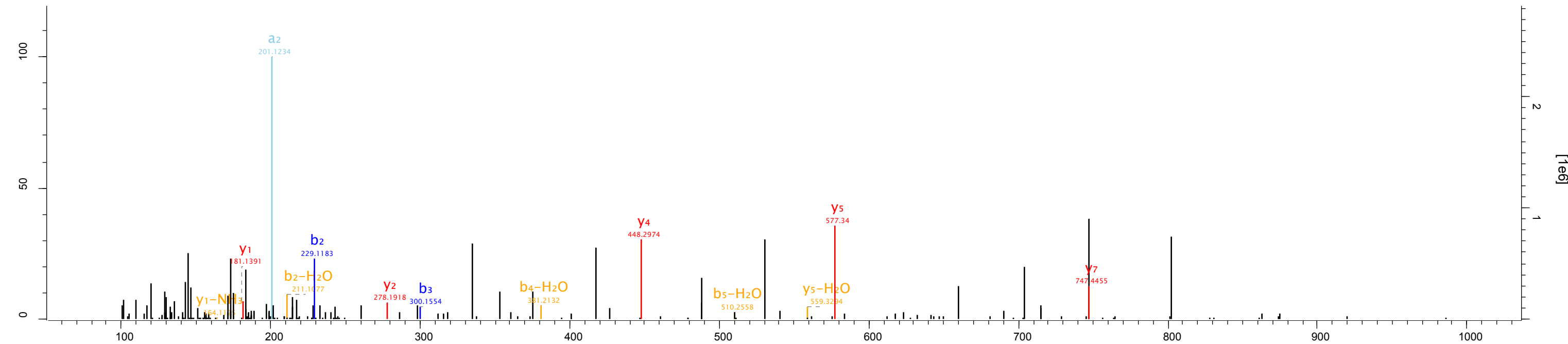
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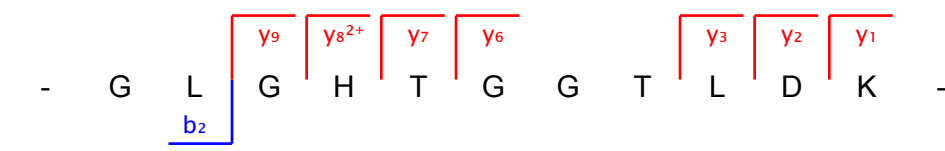
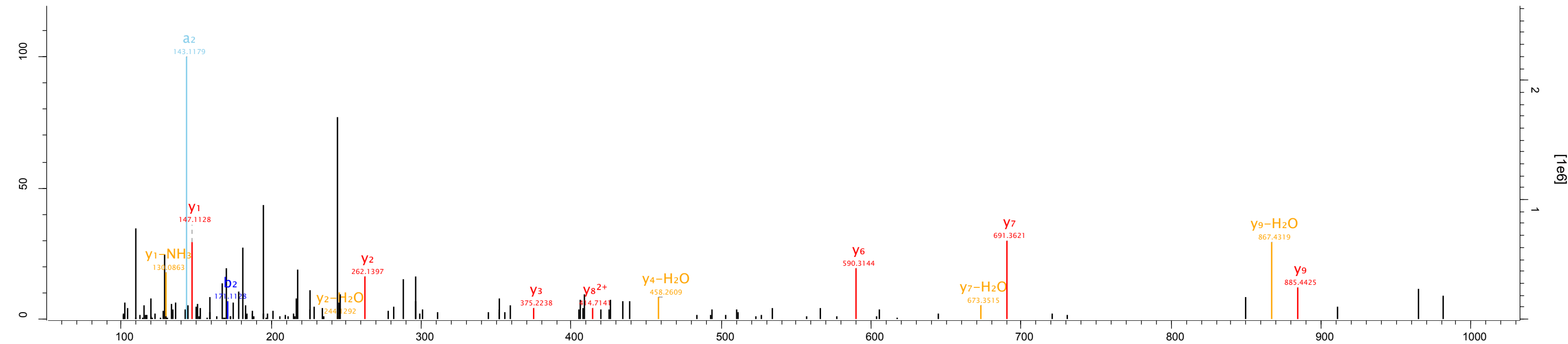
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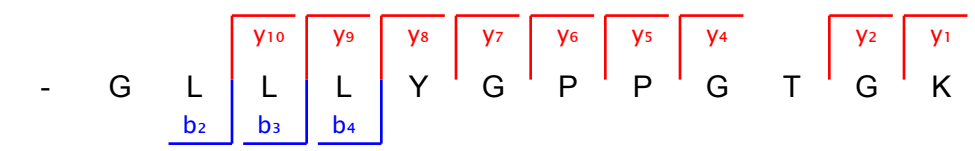
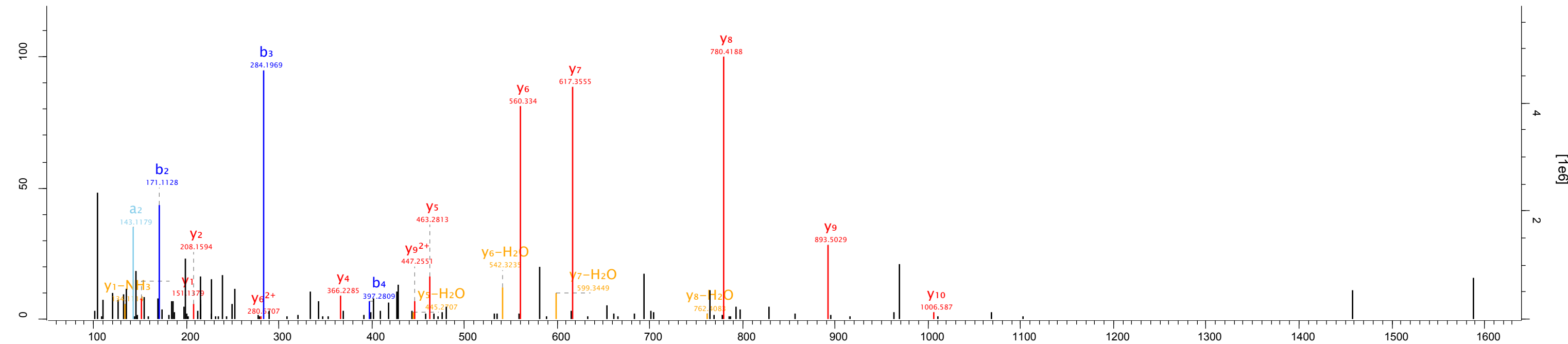
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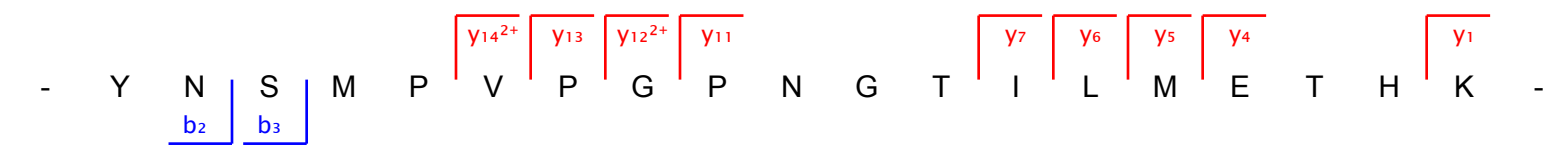
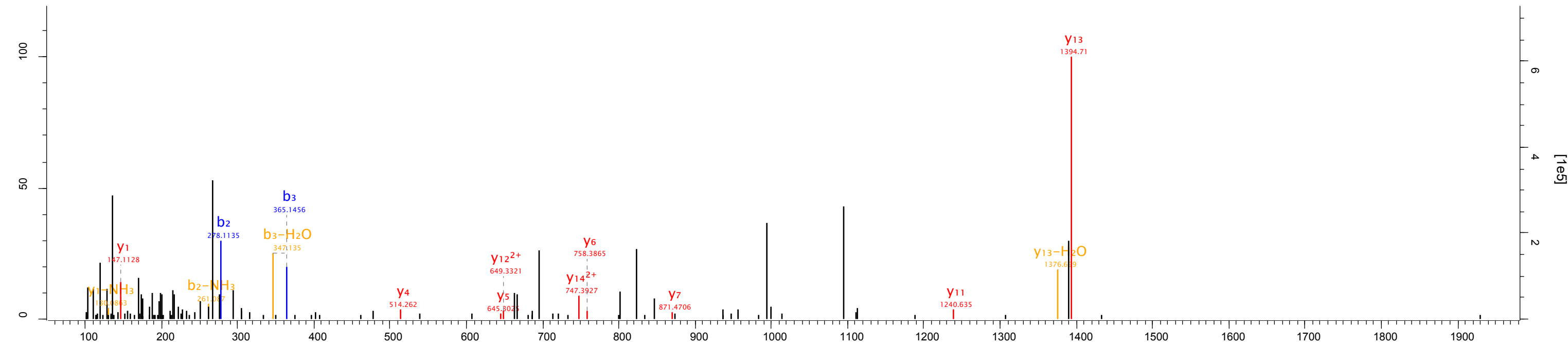
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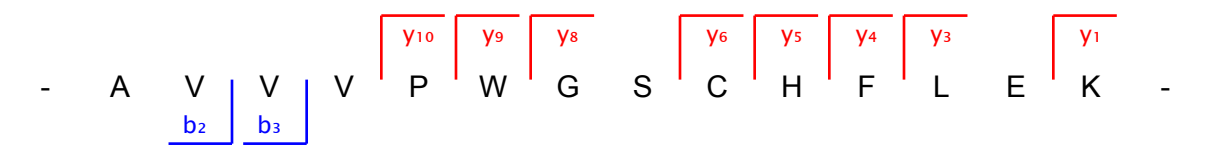
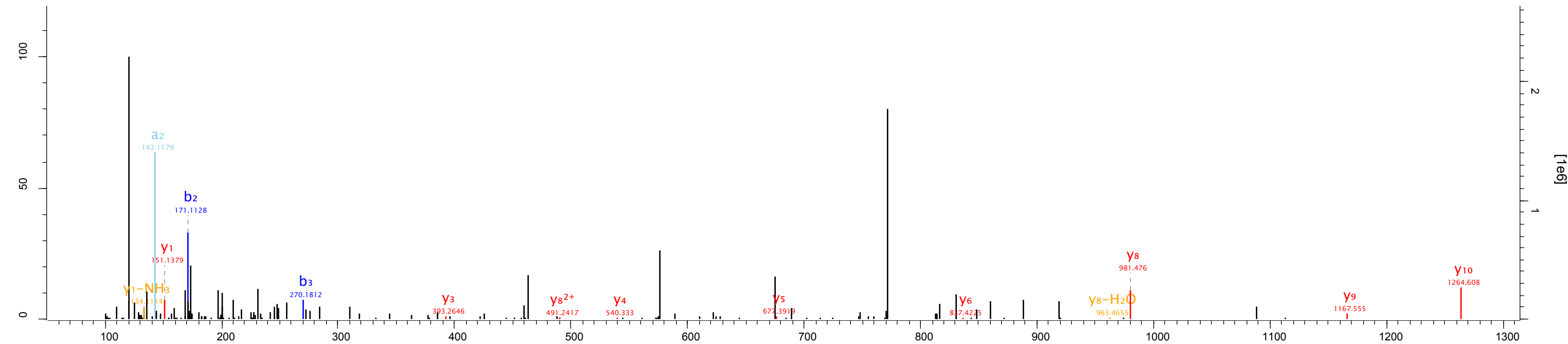
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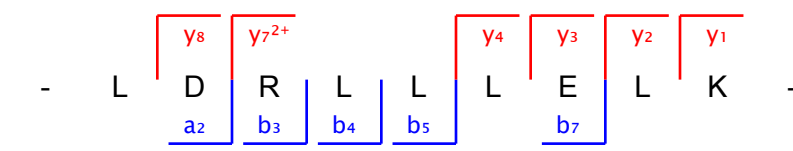
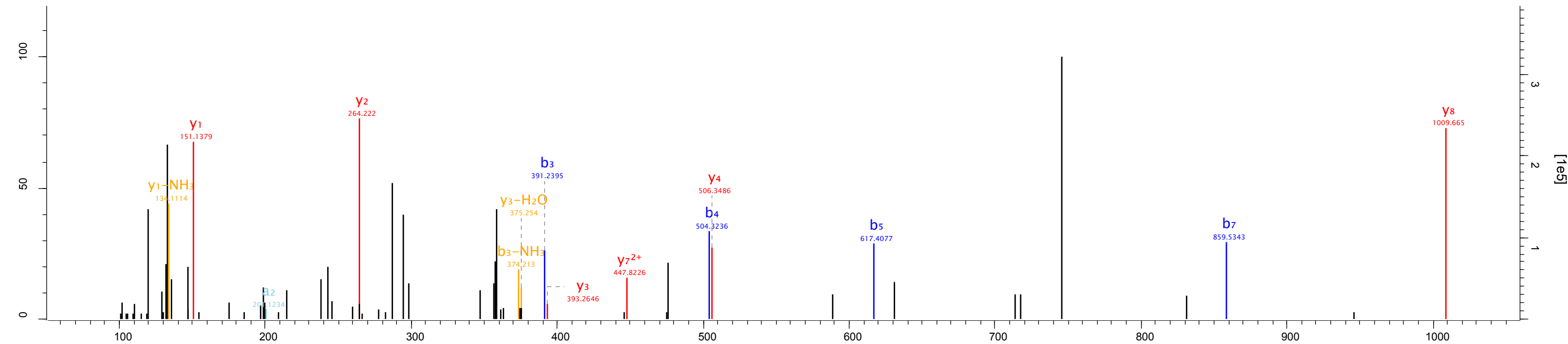
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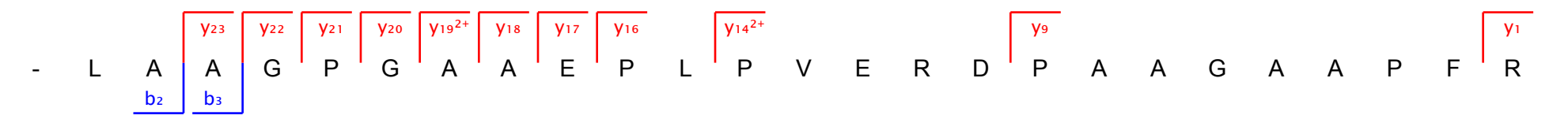
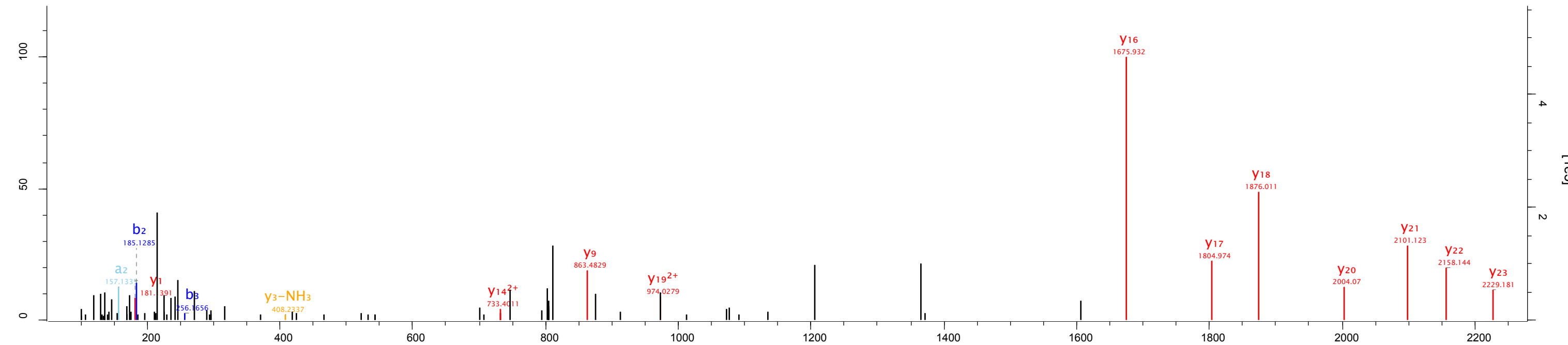
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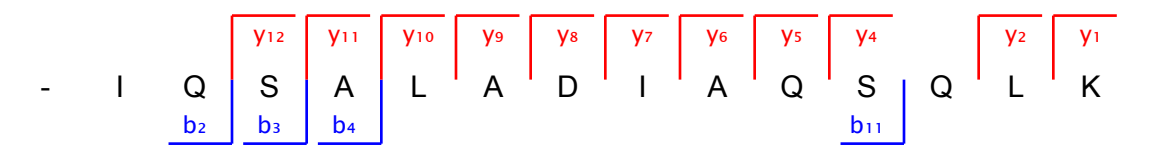
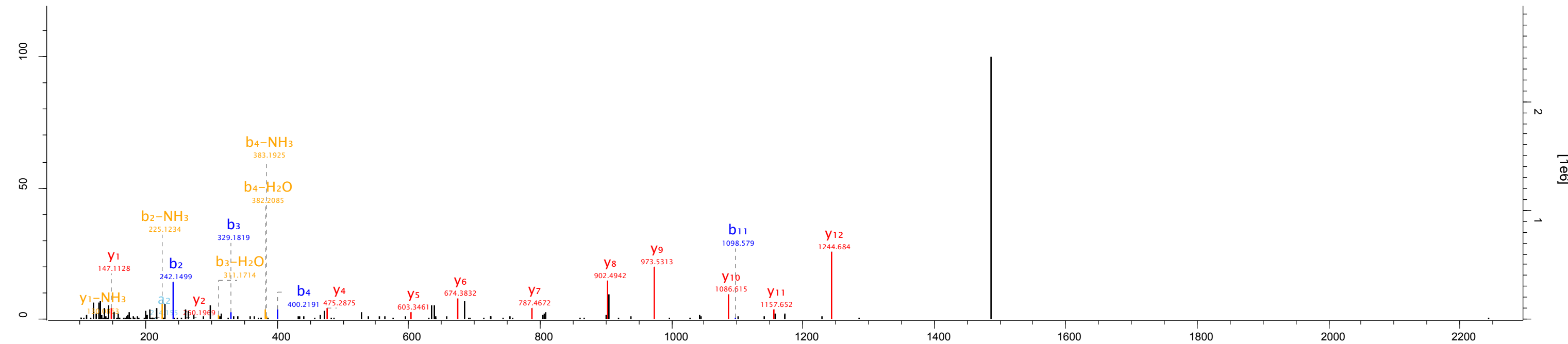
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 Scan: 54871 Method: FTMS; HCD Score: 57.79 m/z: 374.92 Gene names: BPI



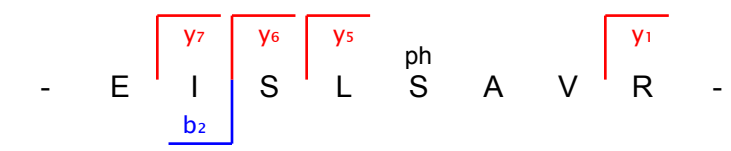
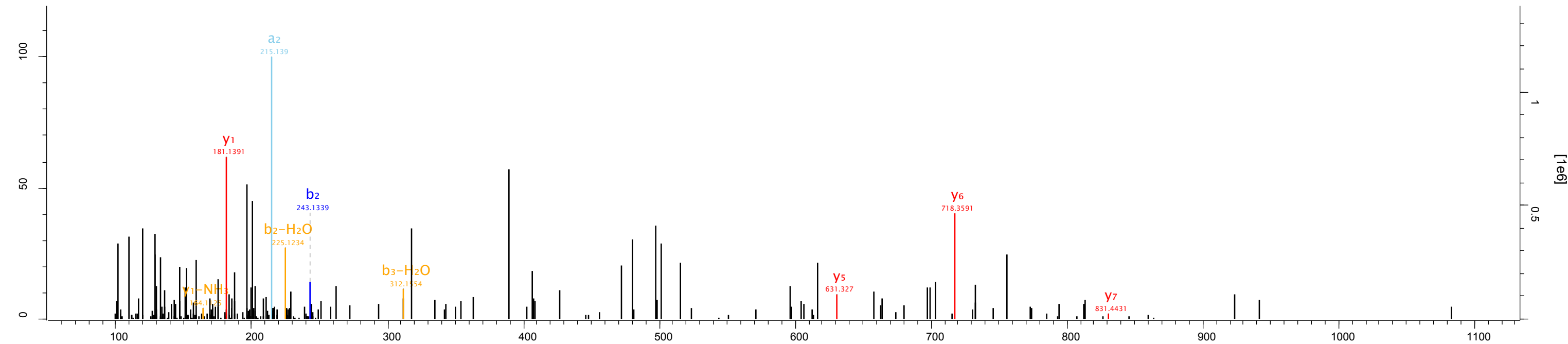
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 Scan: 63531 Method: FTMS; HCD Score: 25.82 m/z: 805.11 Gene names: ZNF511



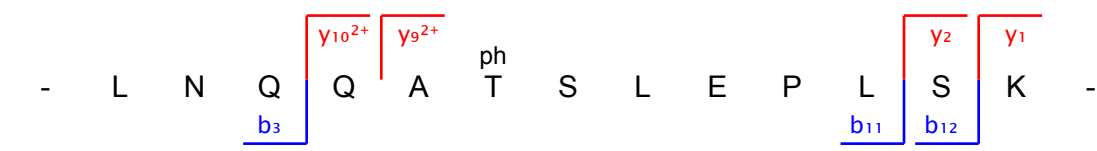
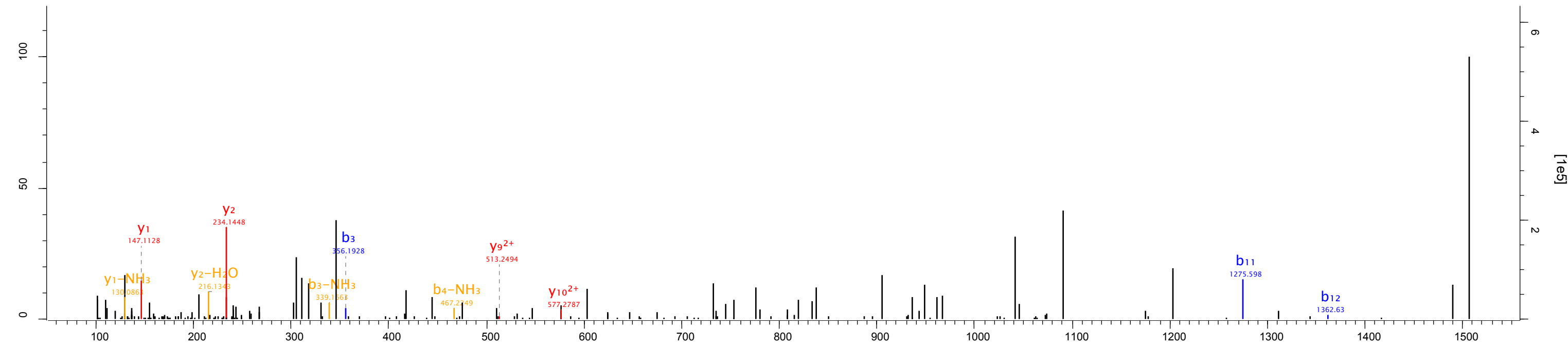
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 Method: FTMS; HCD
 Score: 62.86
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 Gene names: MED21



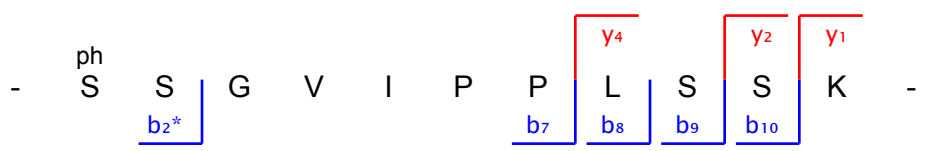
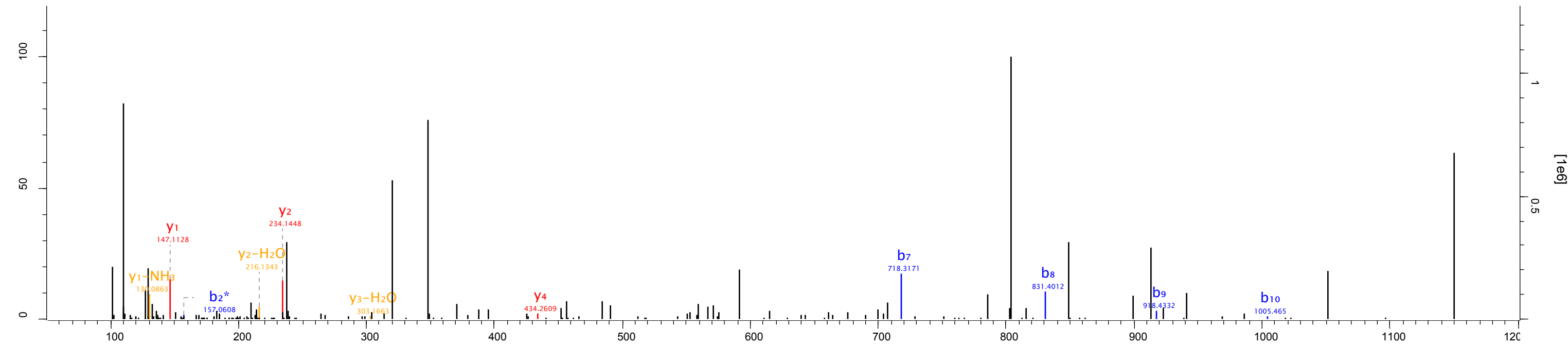
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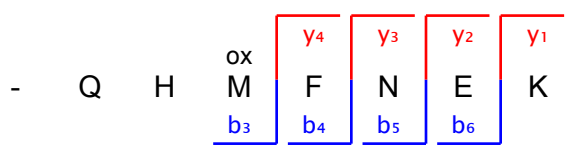
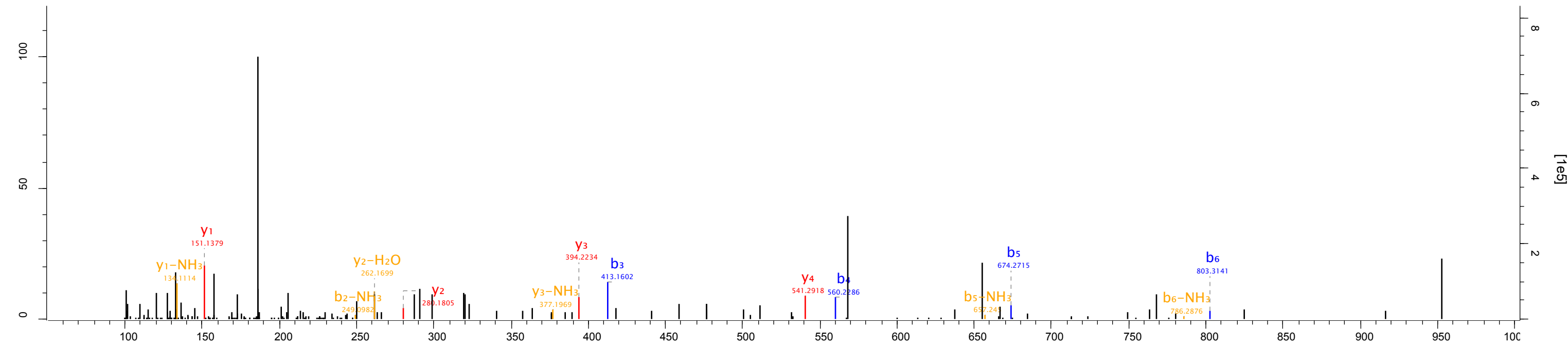
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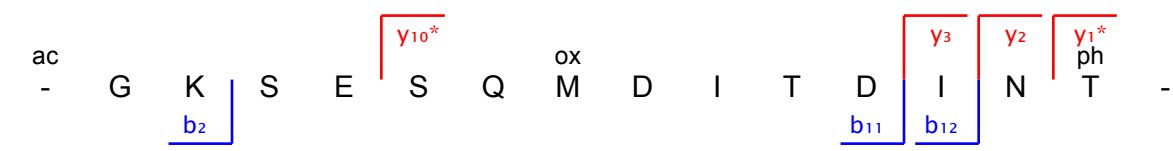
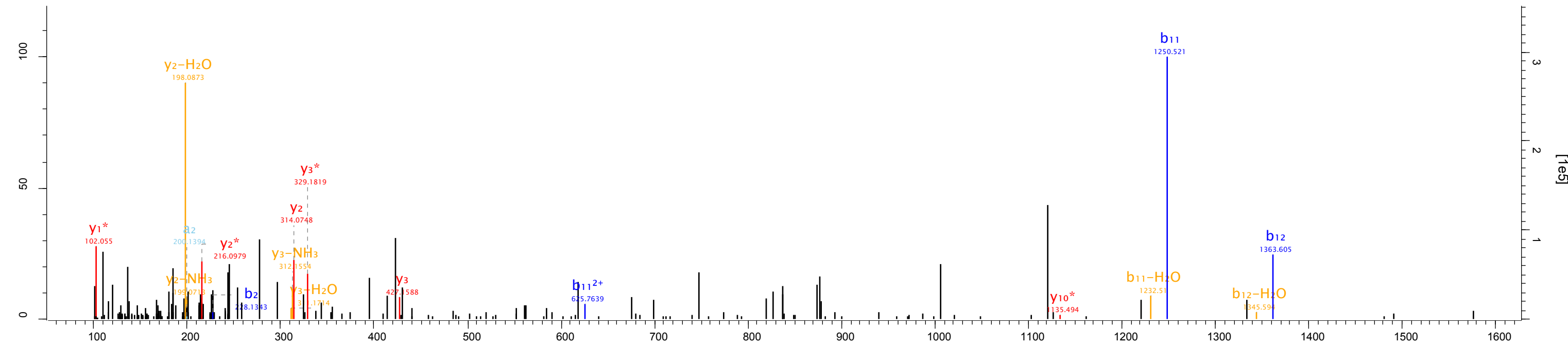
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 Scan: 6901 Method: FTMS; HCD Score: 52.17 m/z: 576.29



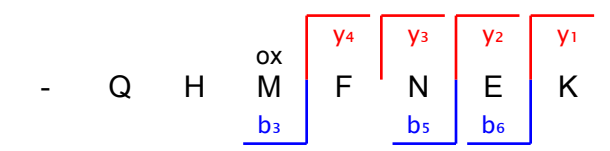
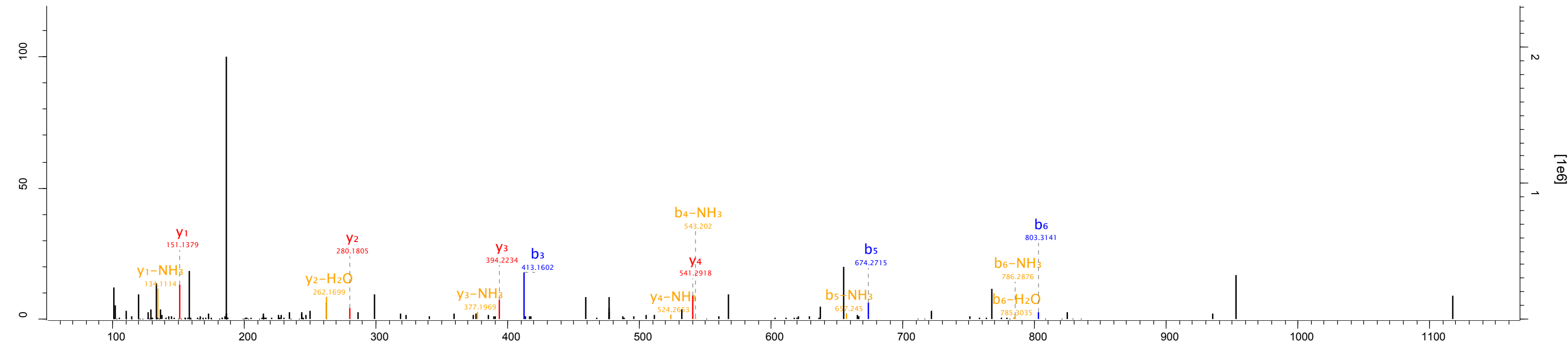
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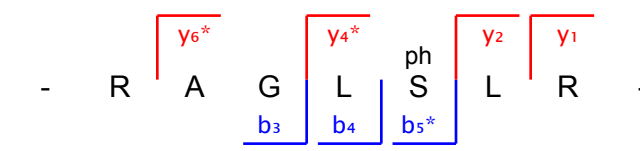
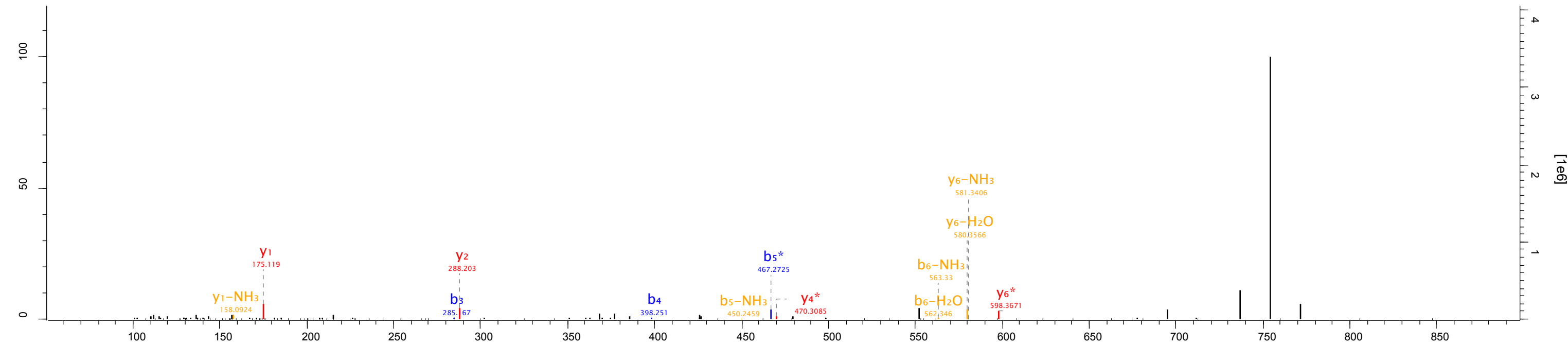
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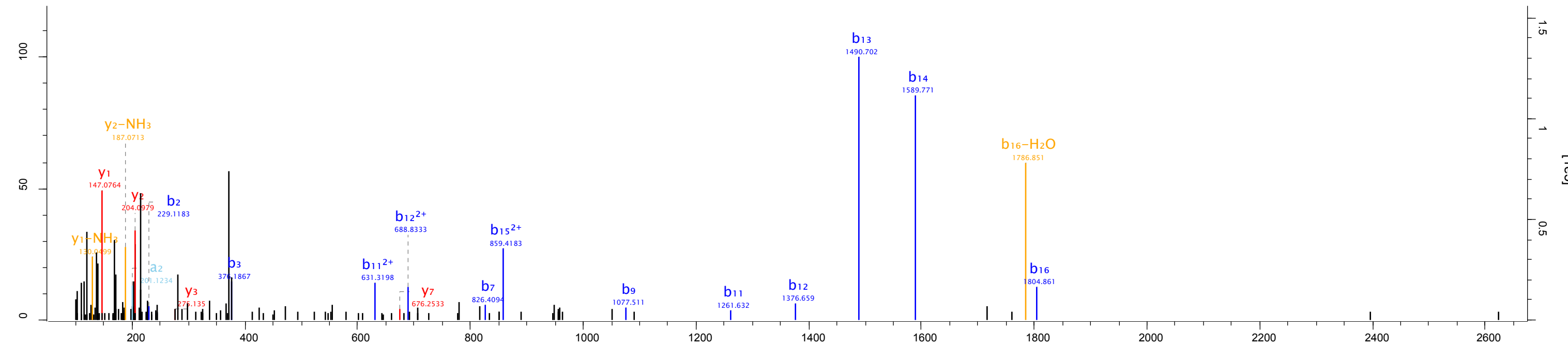
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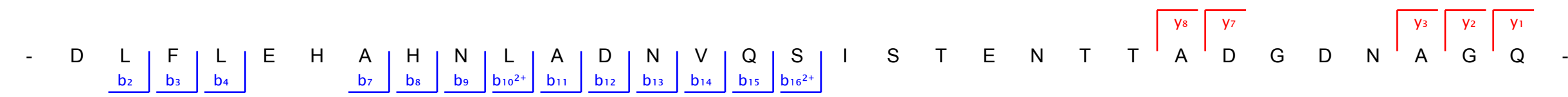
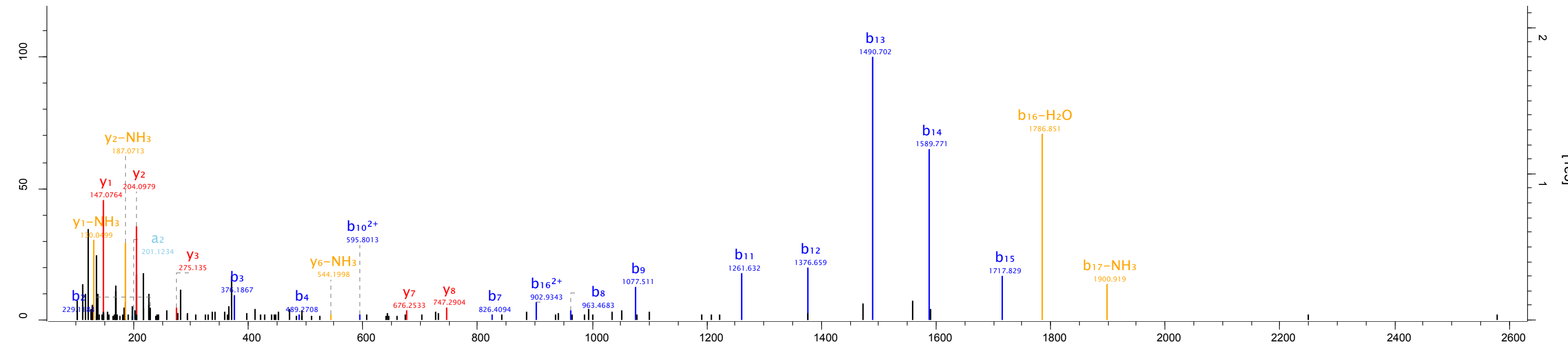
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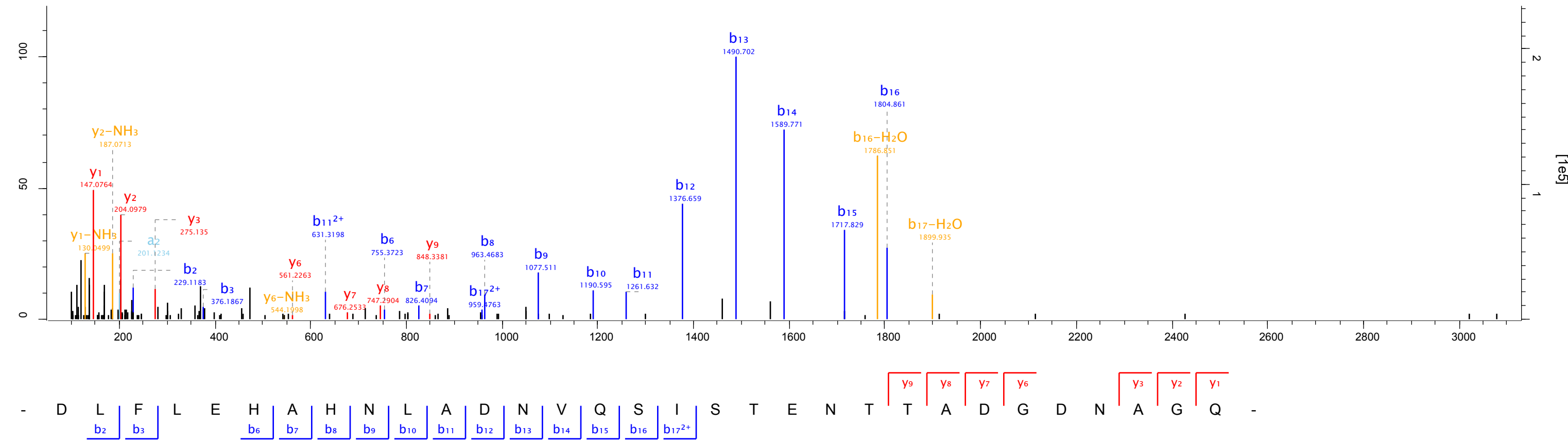
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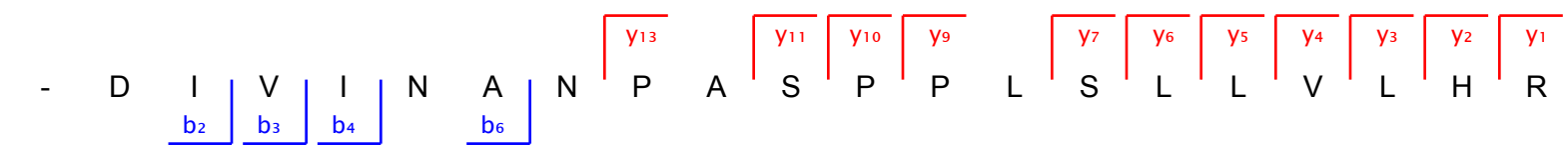
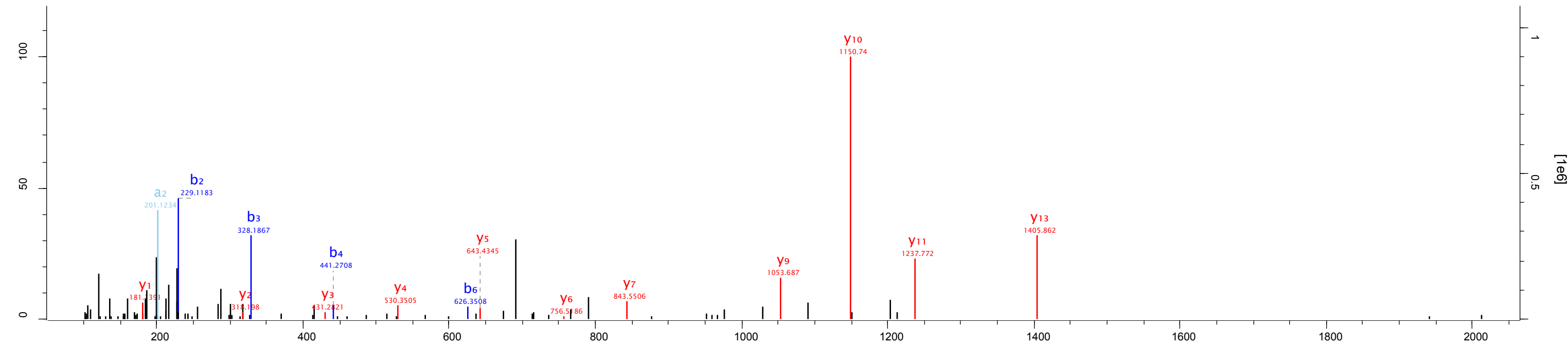
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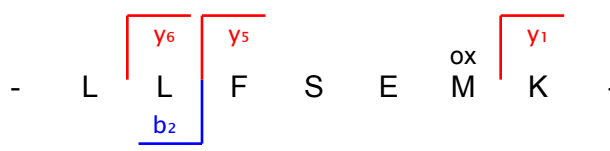
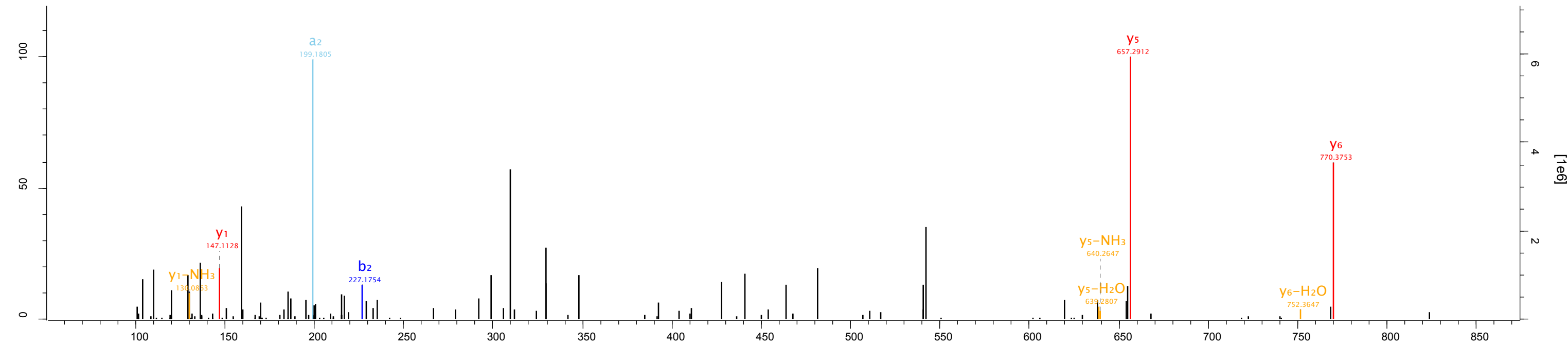
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 Scan: 22651 Method: FTMS; HCD Score: 78.91 m/z: 1100.5 Gene names: CEBPG



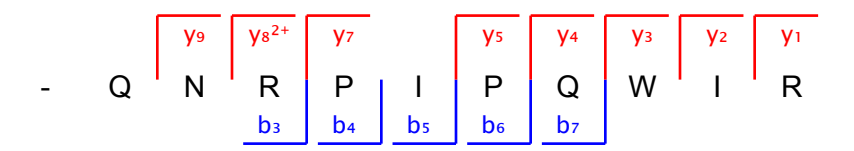
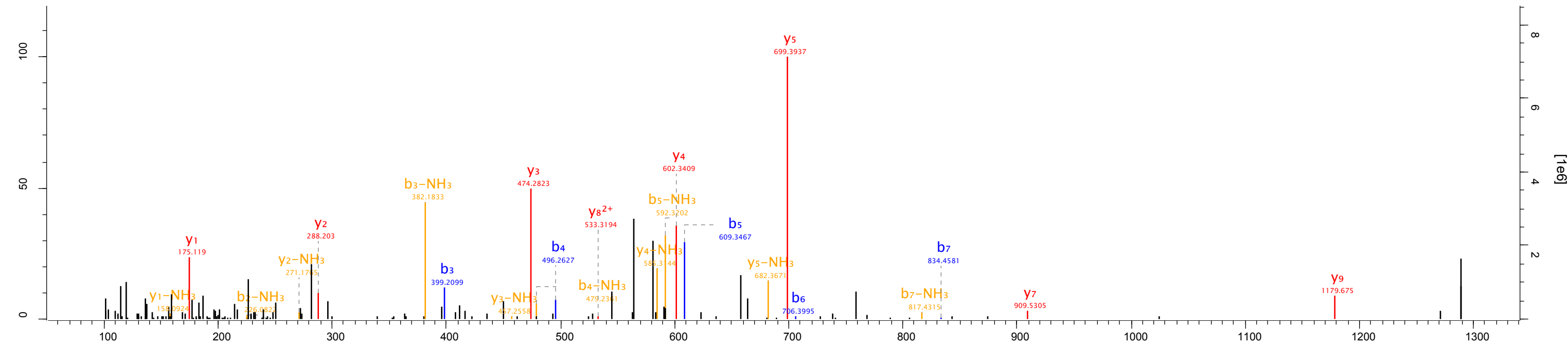
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 m/z: 715.75
 Gene names: AIMP2



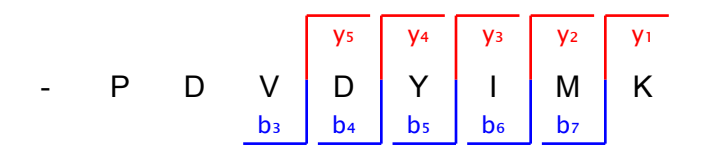
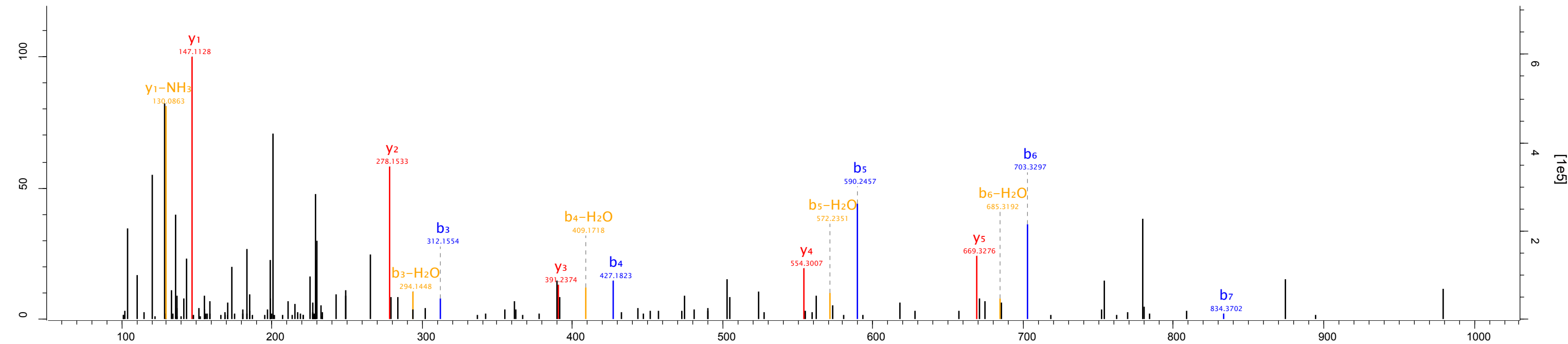
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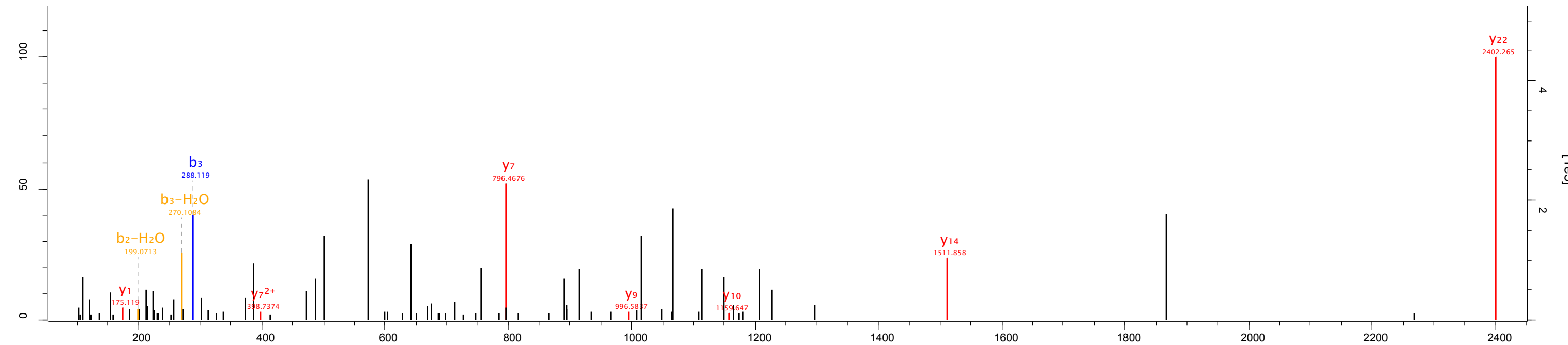
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 Scan: 44691 Method: FTMS; HCD Score: 119.75 m/z: 436.58 Gene names: RPL39P5;RPL39



Raw file Scan Method Score m/z
20150822_A375SR-Proteome_BR3 72411 FTMS; HCD 93.37 490.73



Raw file: 20150822_A375SR-Proteome_BR3
 Scan: 94111 Method: FTMS; HCD Score: 6.04 m/z: 935.16 Gene names: C1orf85



- E S A L P C Q A S P L H P A L A Y S L P Q S P I V R -

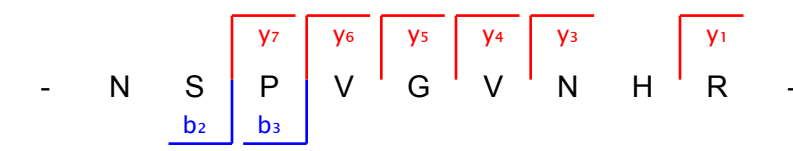
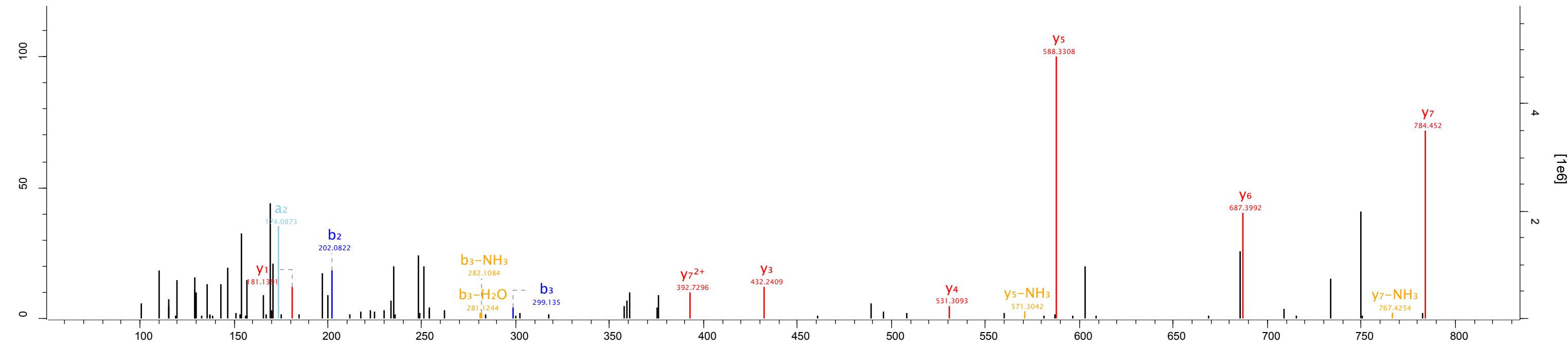
Fragmentation mapping (red brackets):

- y_{22} covers residues L, P, C, Q, A, S, P, L, H, P, A, L, A, Y, S, L, P, Q, S, P, I, V, R.
- y_{14} covers residues P, A, L, A, Y, S, L, P, Q, S, P, I, V, R.
- y_{10} covers residues Y, S, L, P, Q, S, P, I, V, R.
- y_9 covers residues S, L, P, Q, S, P, I, V, R.
- y_7 covers residues L, P, Q, S, P, I, V, R.
- y_1 covers residues R.

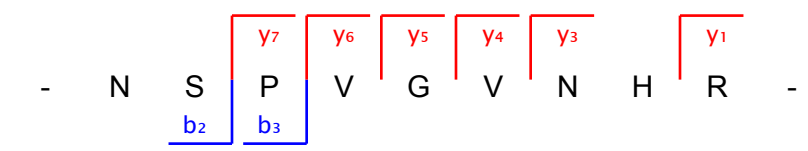
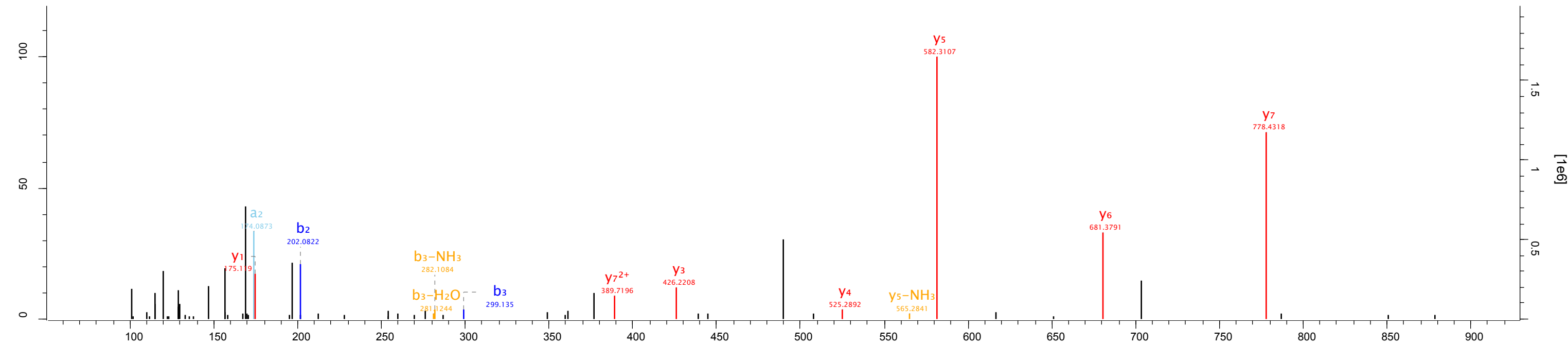
Fragmentation mapping (blue bracket):

- b_3 covers residues A, L, P, C, Q, A, S, P, L, H, P, A, L, A, Y, S, L, P, Q, S, P, I, V, R.

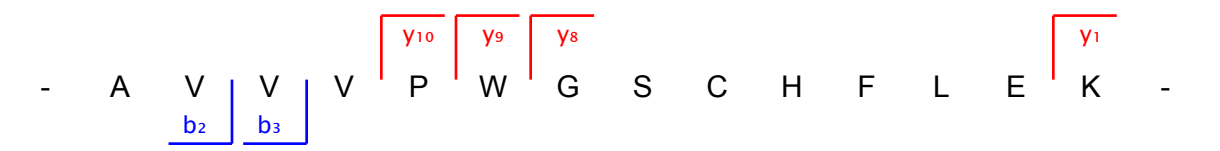
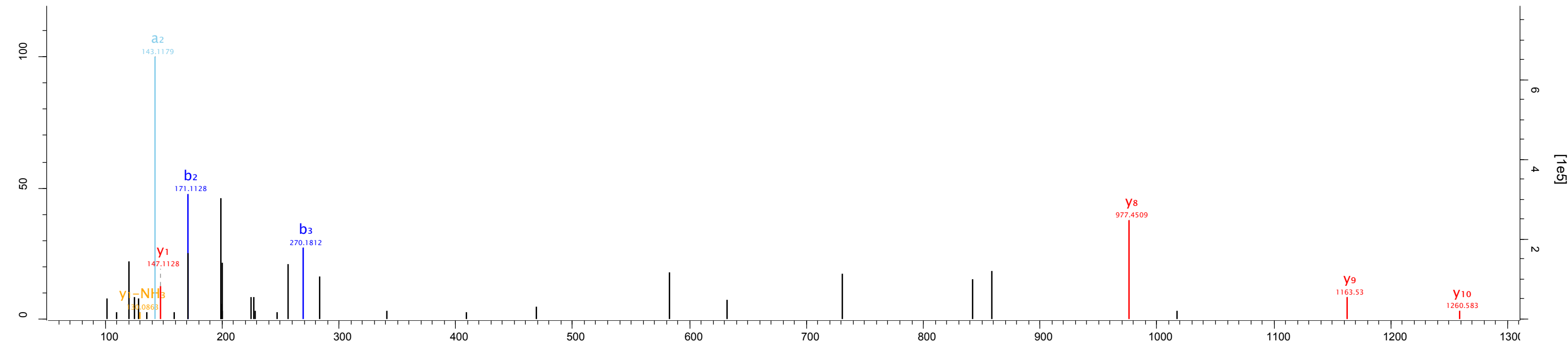
Raw file: 20180707_MaS_A375SR_LM_proteome_05
 Scan: 2931 Method: FTMS; HCD Score: 58.43 m/z: 493.27 Gene names: TIMM17A



Raw file 20180707_MaS_A375SR_LM_proteome_05 Scan 2951 Method FTMS; HCD Score 76.06 m/z 490.26 Gene names TIMM17A



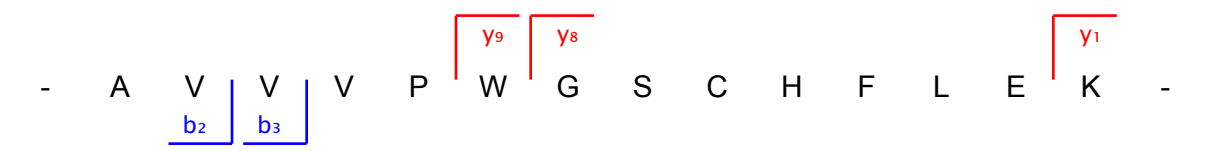
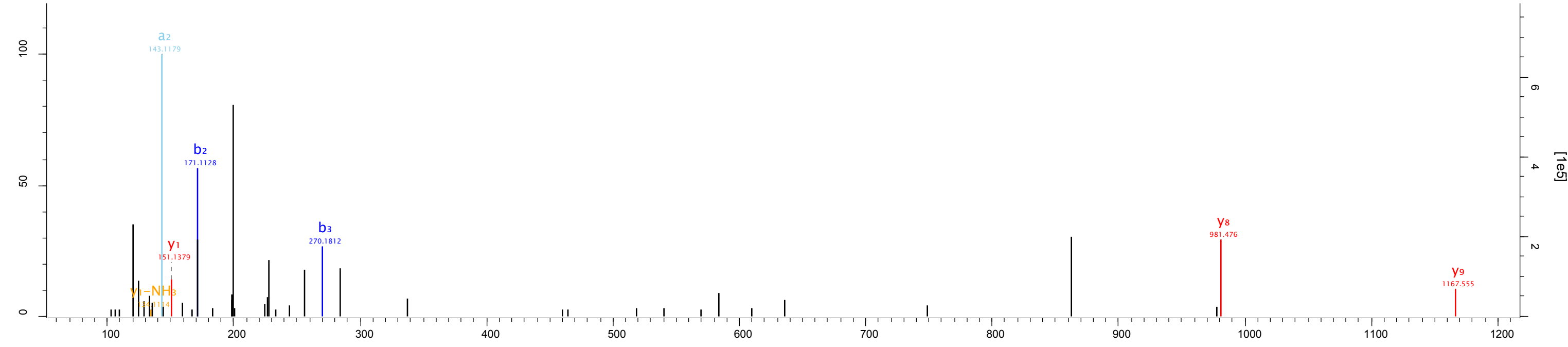
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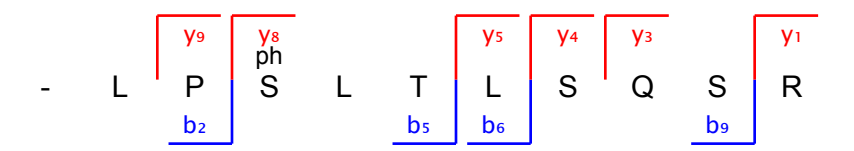
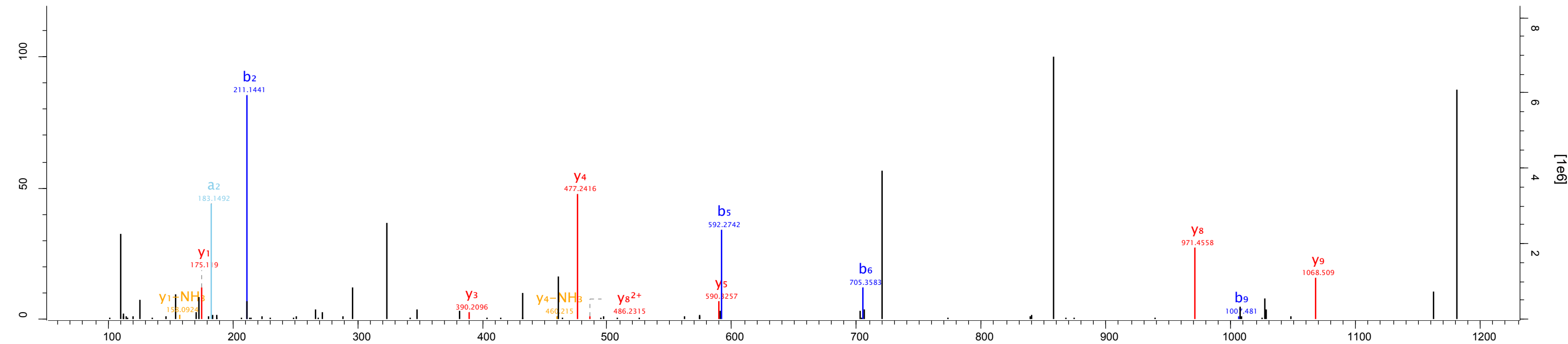
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20180707_MaS_A375SR_LM_proteome_07

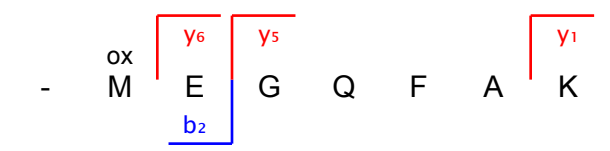
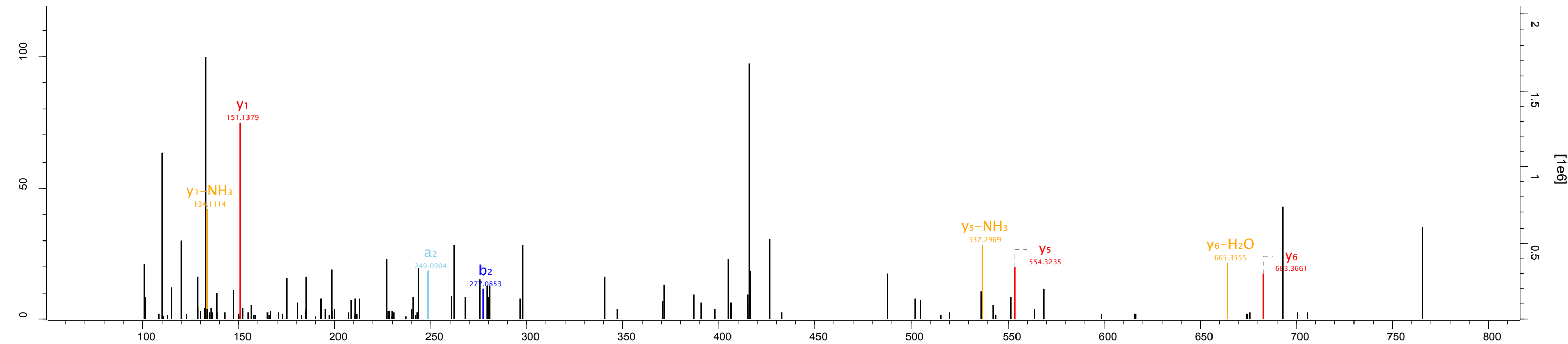
Scan	Method	Score	m/z	Gene names
24301	FTMS; HCD	14.08	545.29	SPPL2A



Raw file 20180707_MaS_A375SR_LM_proteome_08 Scan 8371 Method FTMS; HCD Score 72.43 m/z 591.3

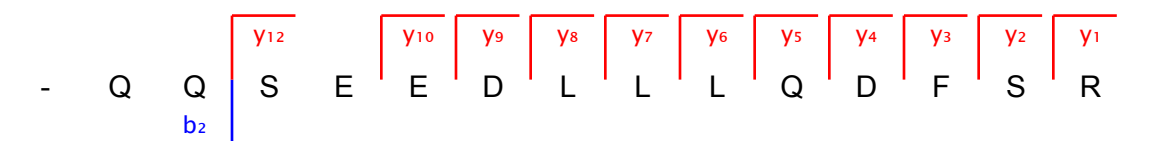
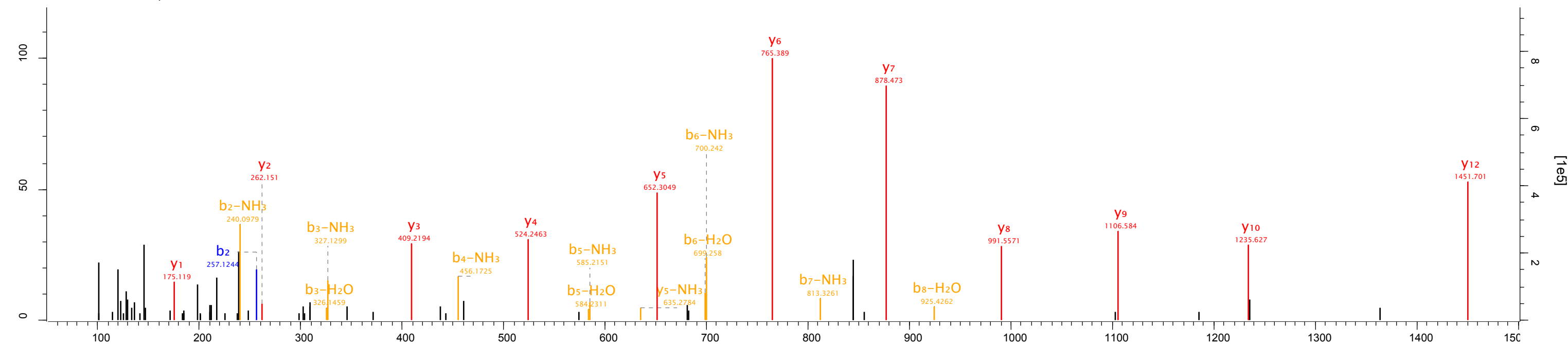


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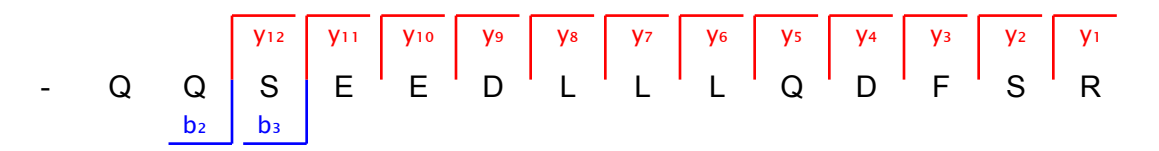
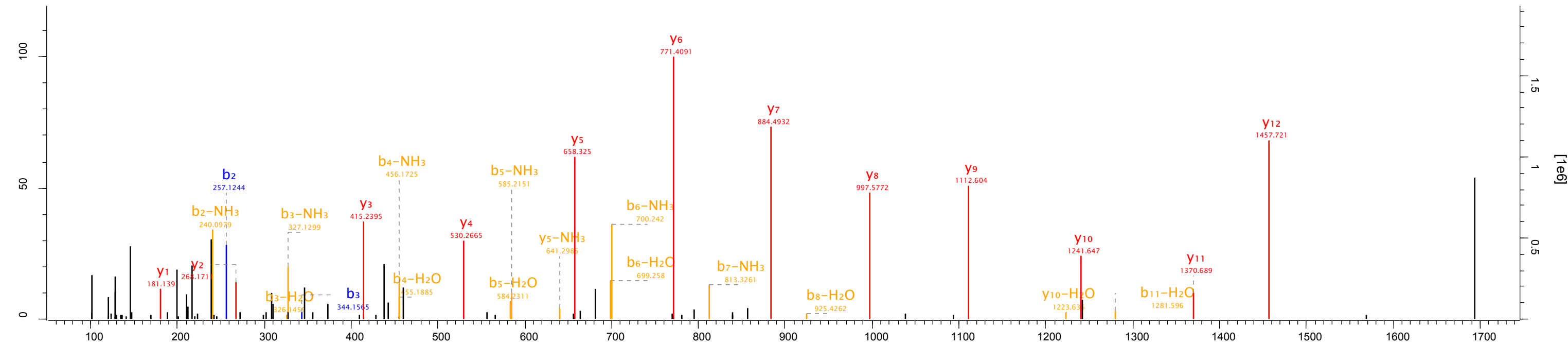
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20180707_MaS_A375SR_LM_proteome_21

Scan 27251 Method FTMS; HCD Score 55.66 m/z 854.41 Gene names SSR3



Raw file
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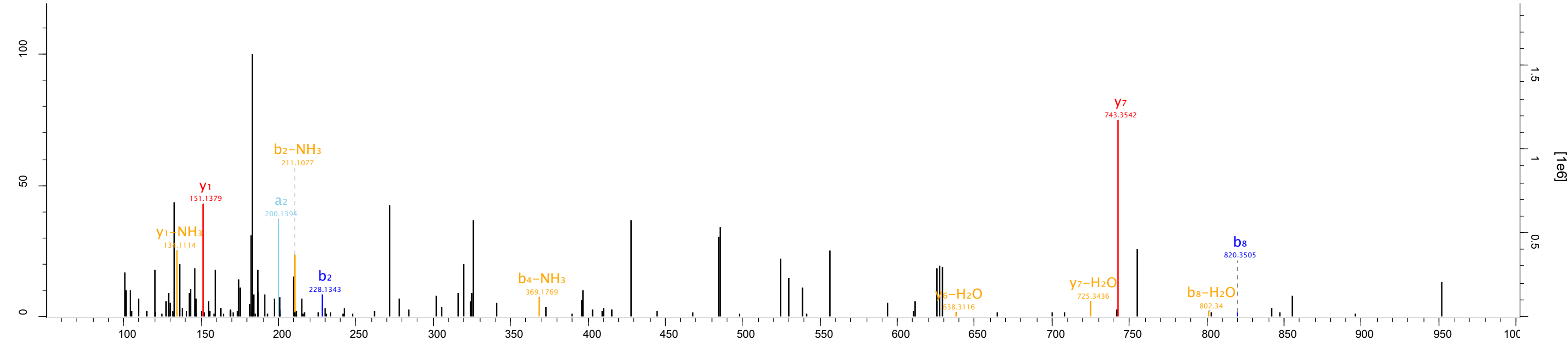
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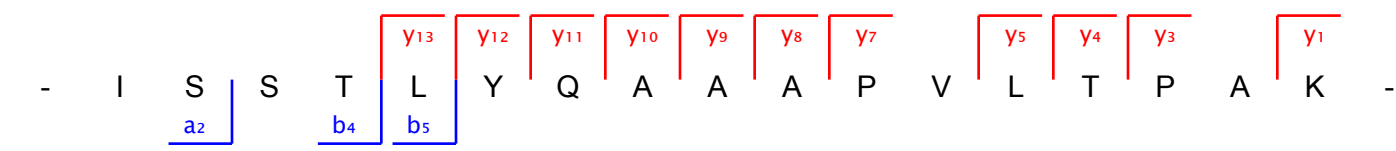
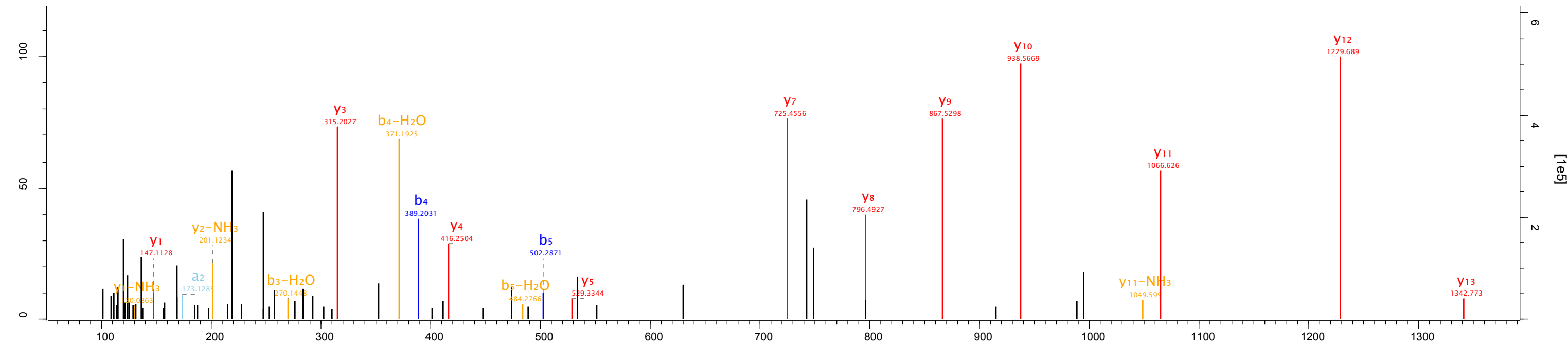
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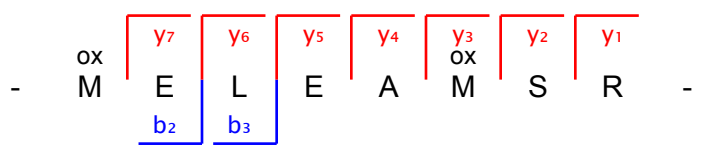
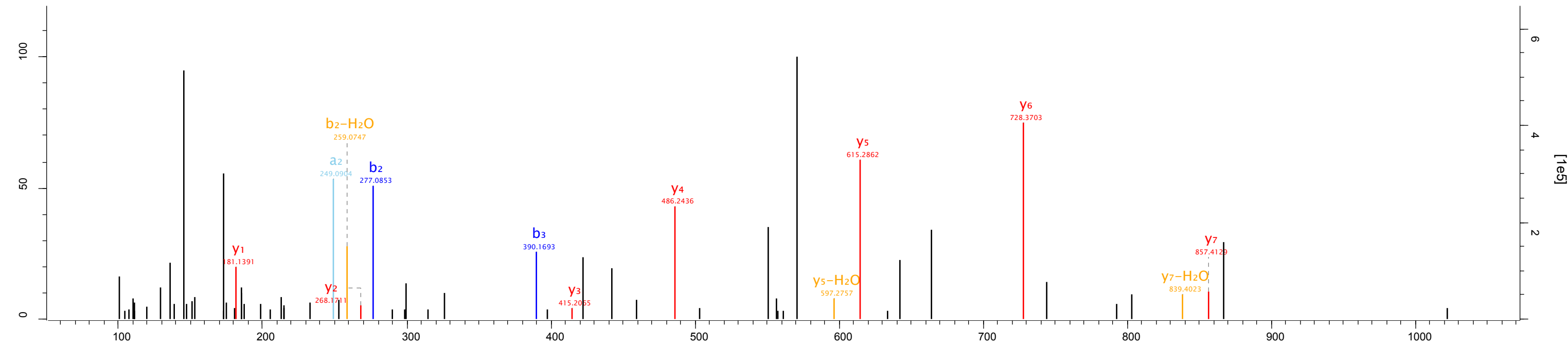
Scan 8711 Method FTMS; HCD Score 46.13 m/z 485.74 Gene names OR56B4



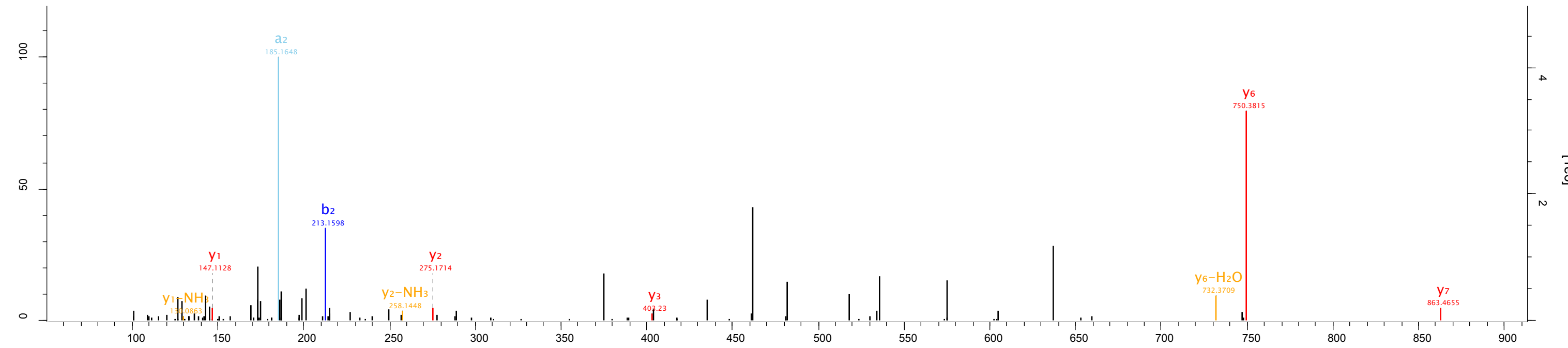
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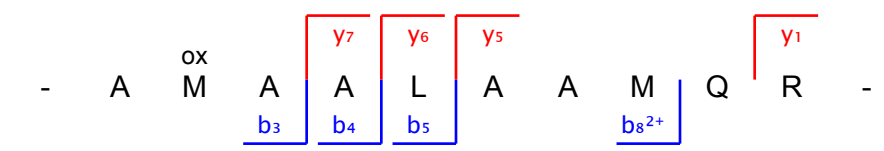
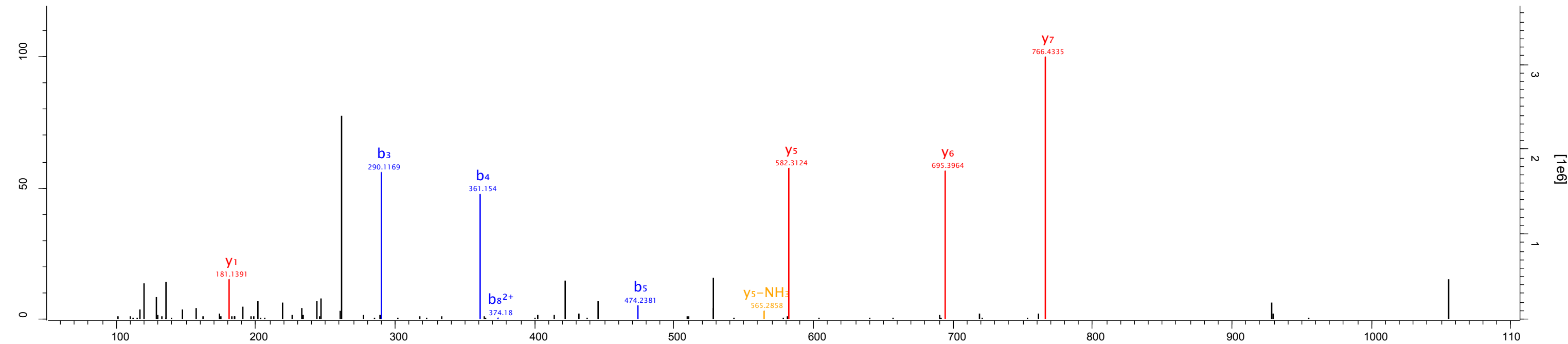
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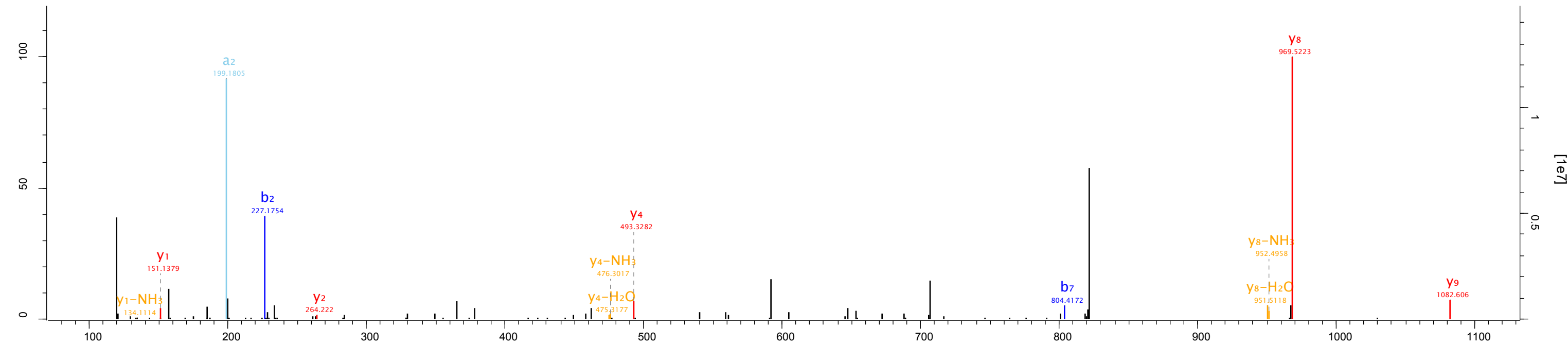


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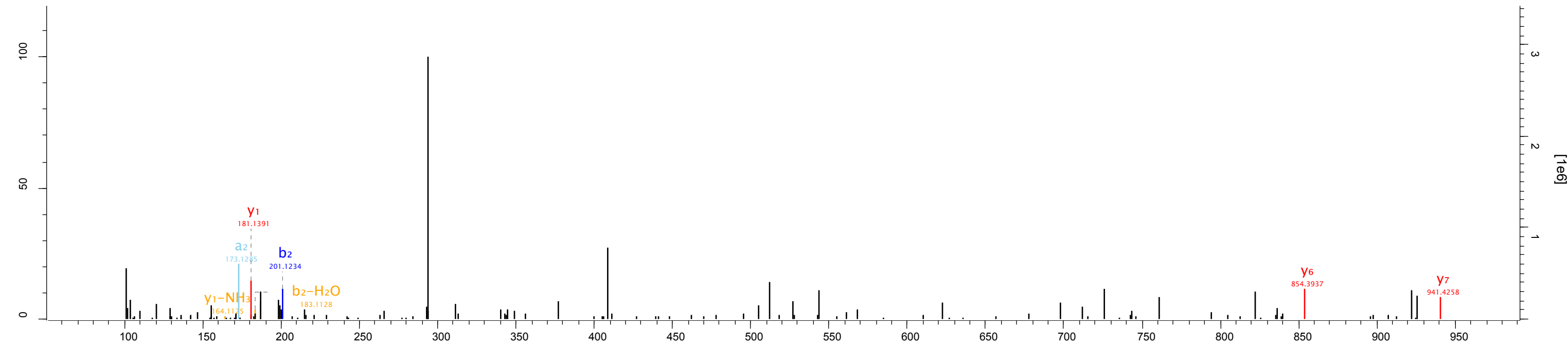


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 Scan 13561 Method FTMS; HCD Score 47.6 m/z 528.77



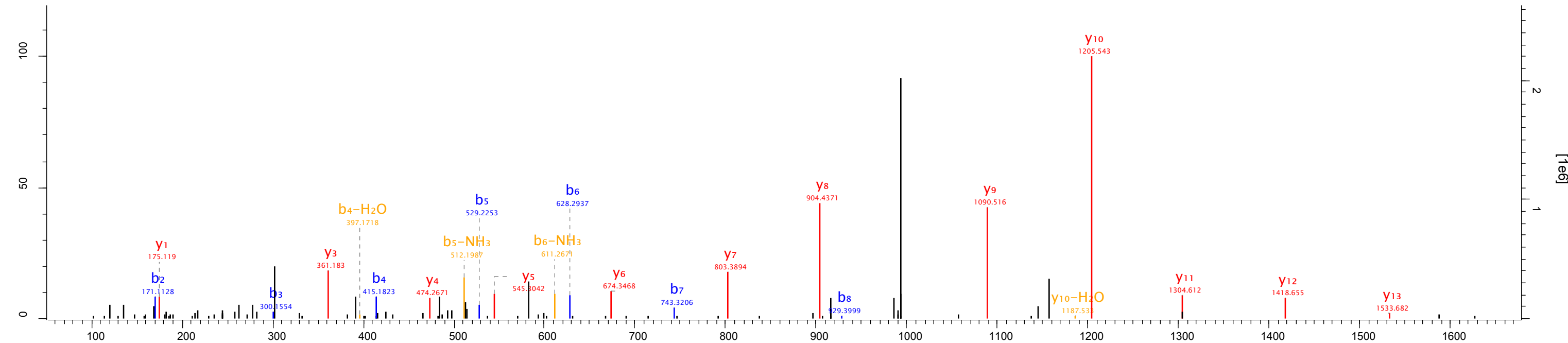


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 Scan: 18241 Method: FTMS; HCD Score: 45.08 m/z: 527.76 Gene names: BDKRB2



Raw file
20180707_MaS_A375SR_ML_proteome_04

Scan Method Score m/z Gene names
24791 FTMS; HCD 83.76 916.92 MIEF2



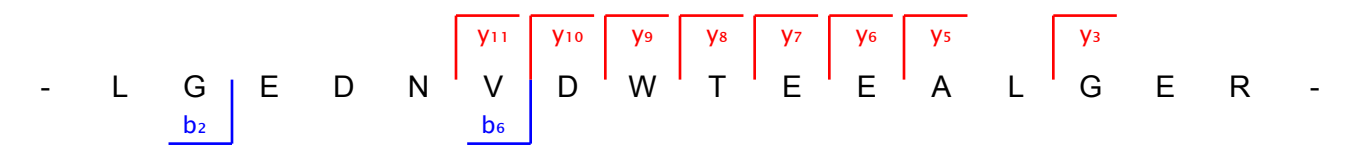
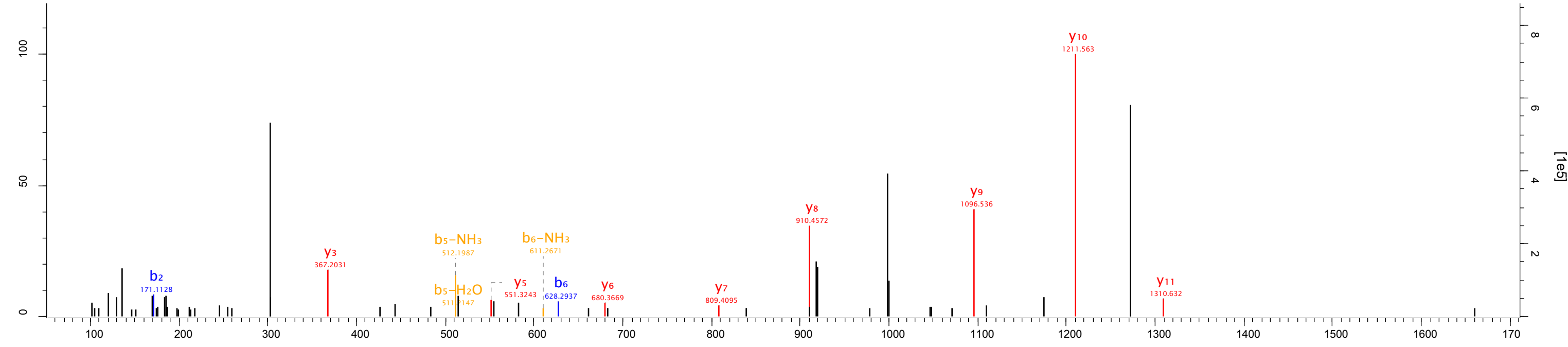
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b₂ b₃ b₄ b₅ b₆ b₇ b₈ y₁₃ y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₁

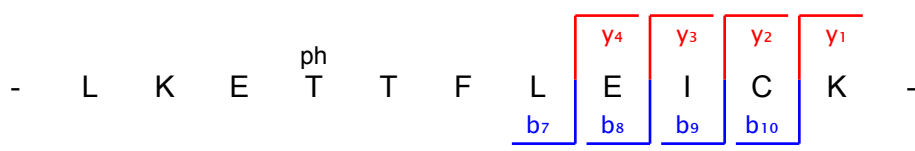
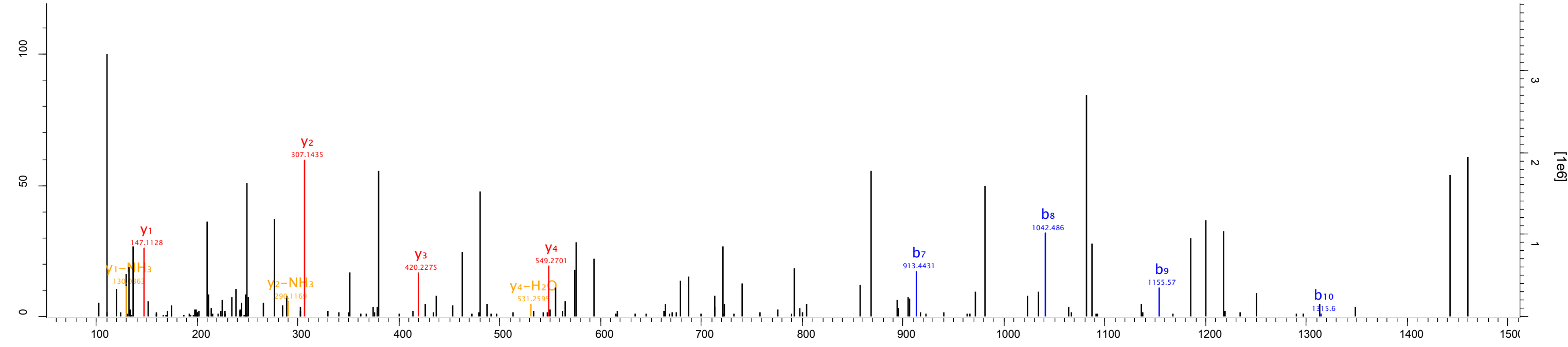
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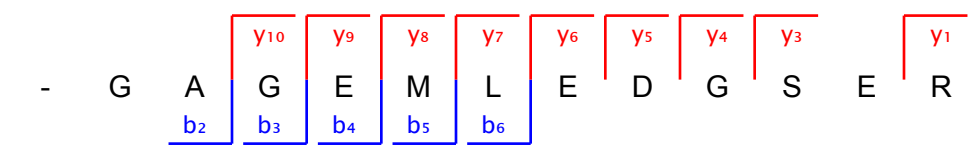
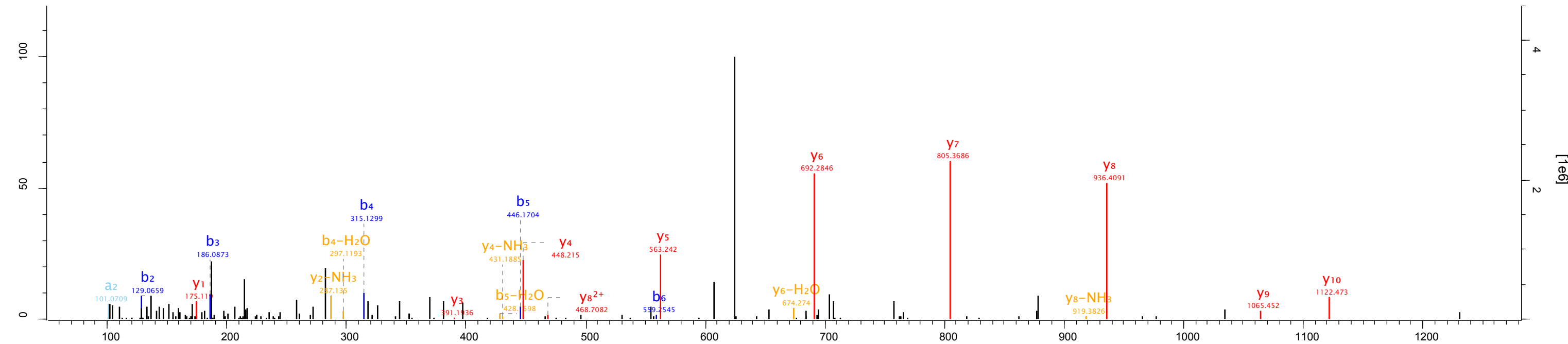
Scan	Method	Score	m/z	Gene names
24801	FTMS; HCD	34.39	919.93	MIEF2



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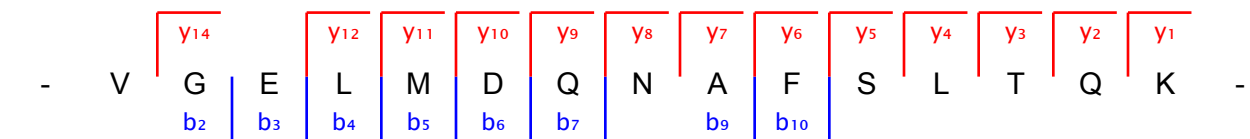
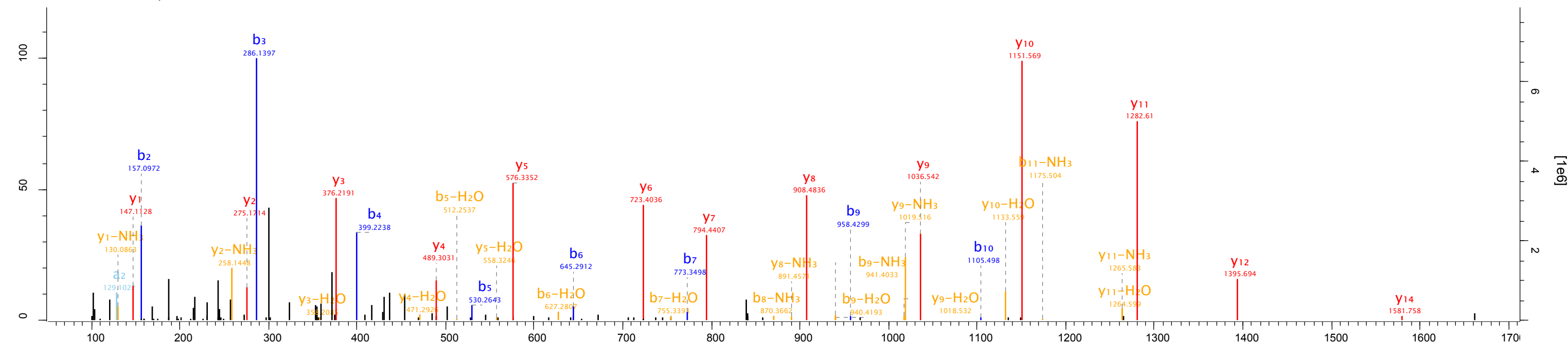


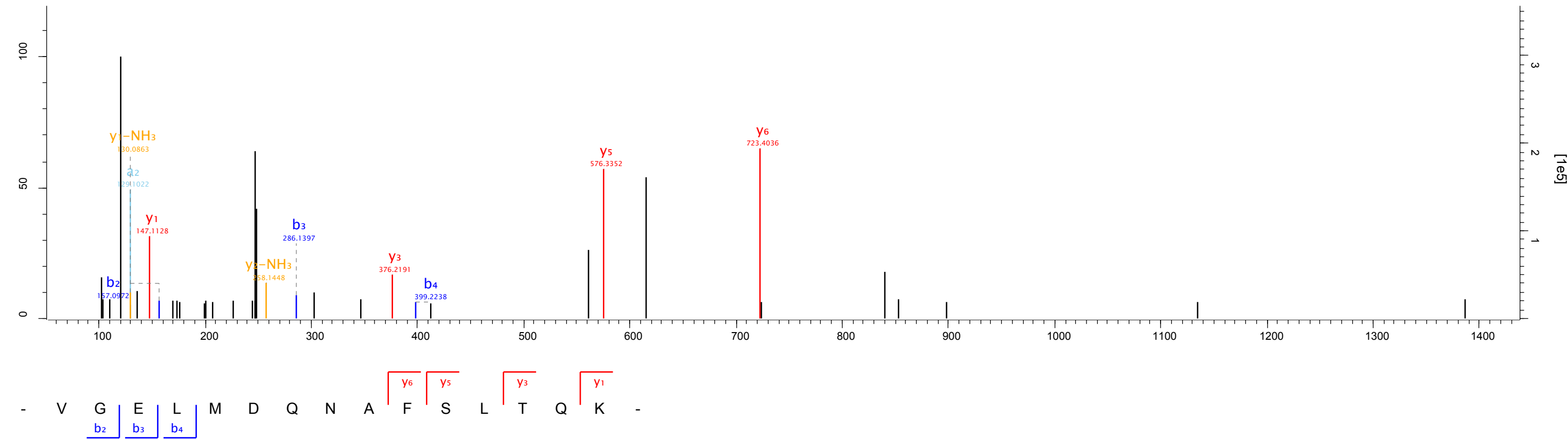
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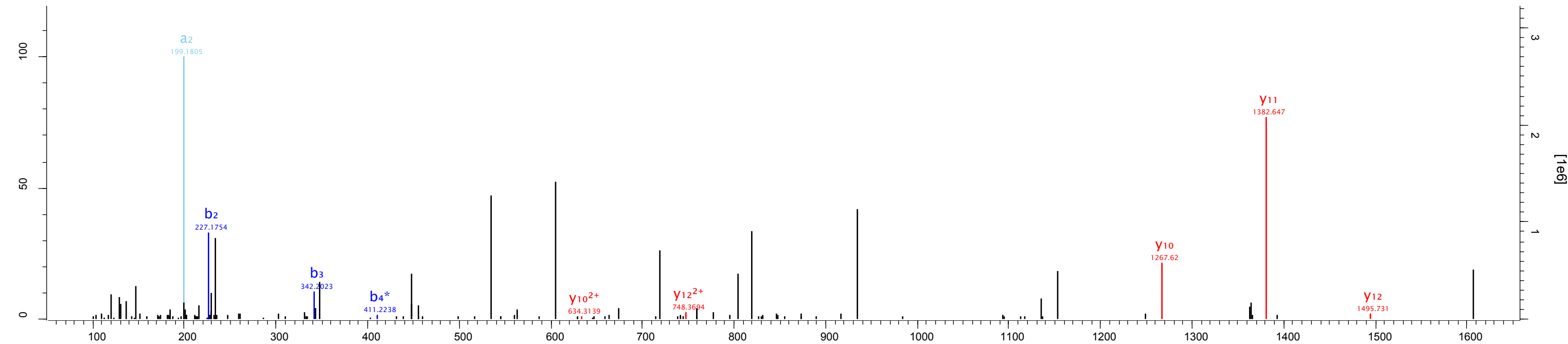
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20180707_MaS_A375SR_ML_proteome_05

Scan Method Score m/z Gene names
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Raw file 20180707_MaS_A375SR_ML_proteome_06 Scan 27421 Method FTMS; HCD Score 50.35 m/z 804.91 Gene names IQCK

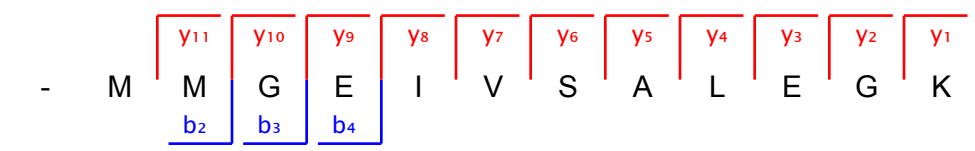
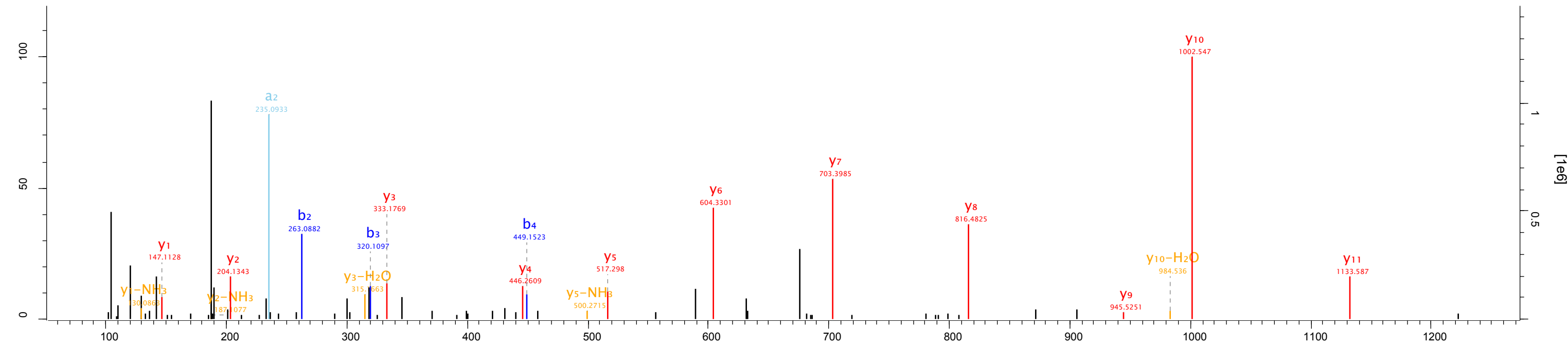


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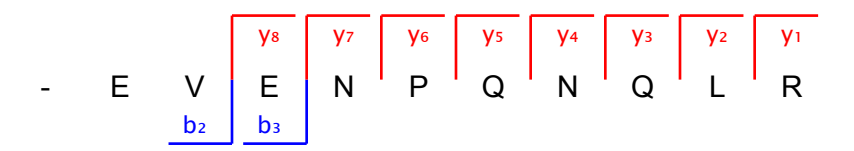
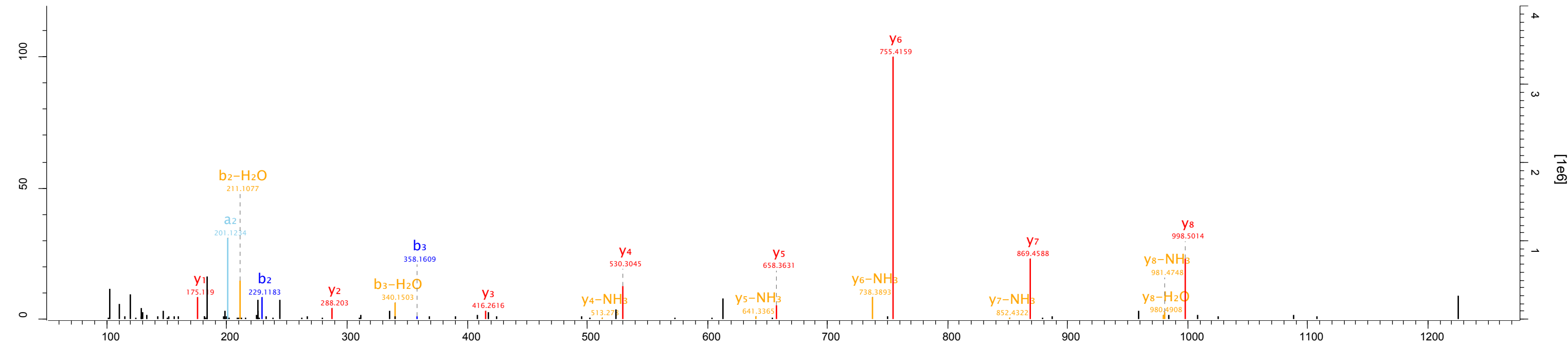
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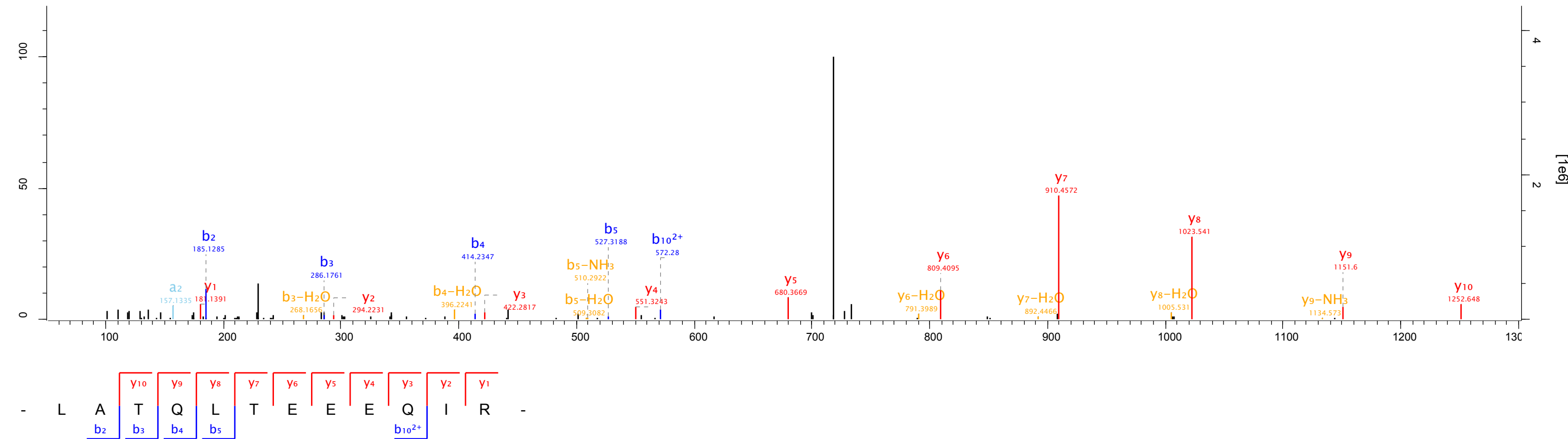
b₂
b₃
b₄*
y₁₂
y₁₁
y₁₀

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 Scan: 27101 Method: FTMS; HCD Score: 85.55 m/z: 632.82 Gene names: CCNF



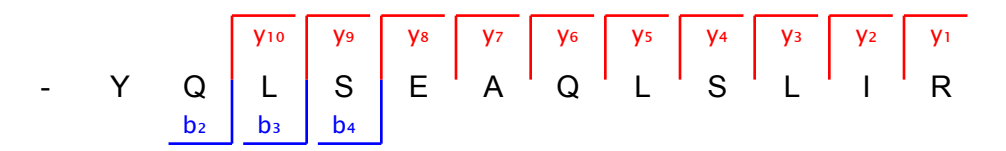
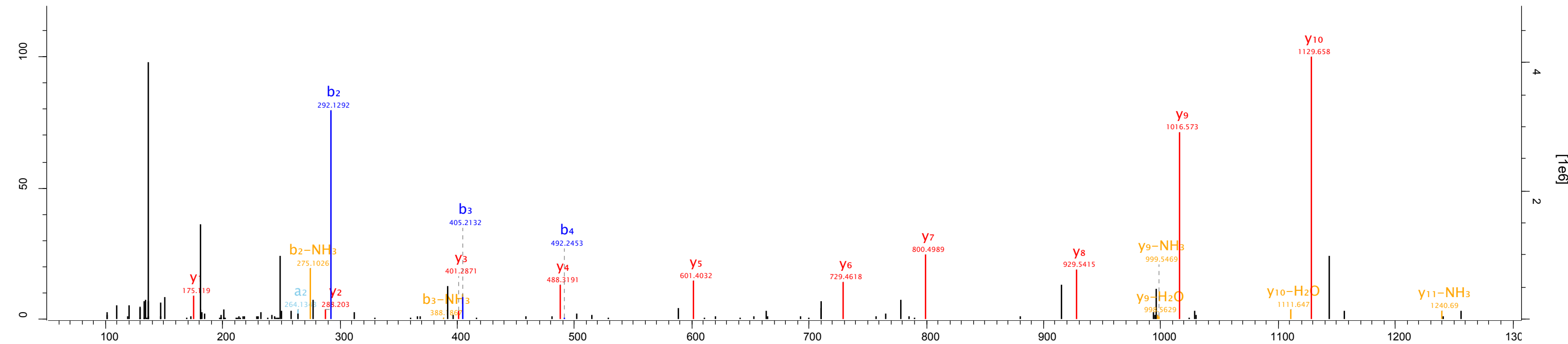
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 Scan: 8491 Method: FTMS; HCD Score: 134.26 m/z: 613.81 Gene names: SGCE



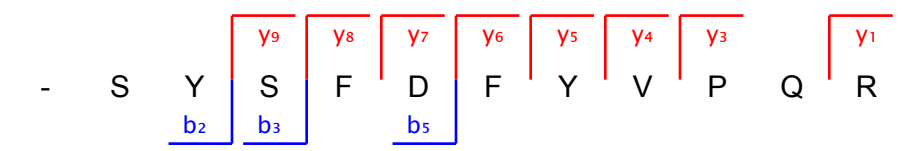
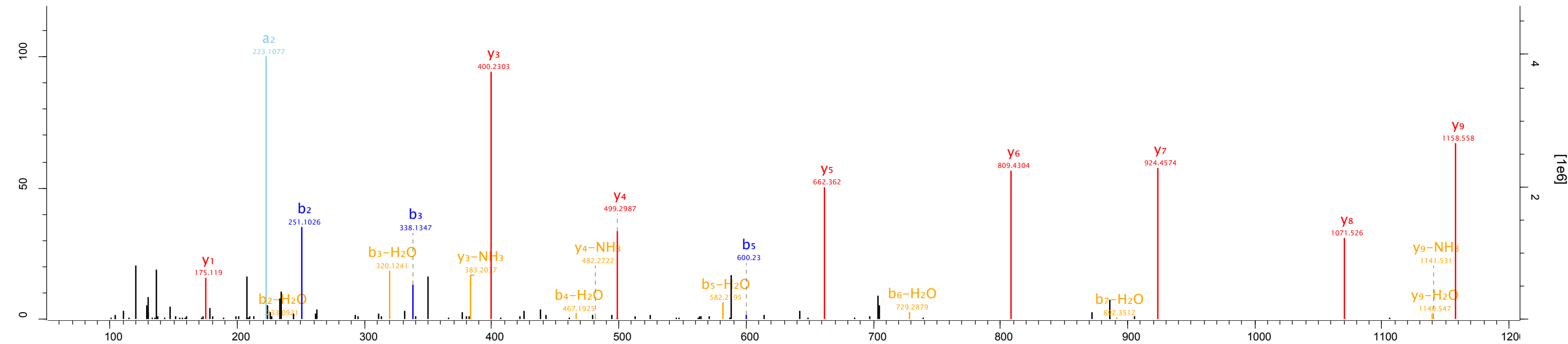


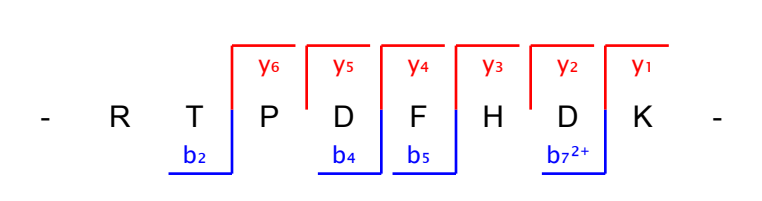
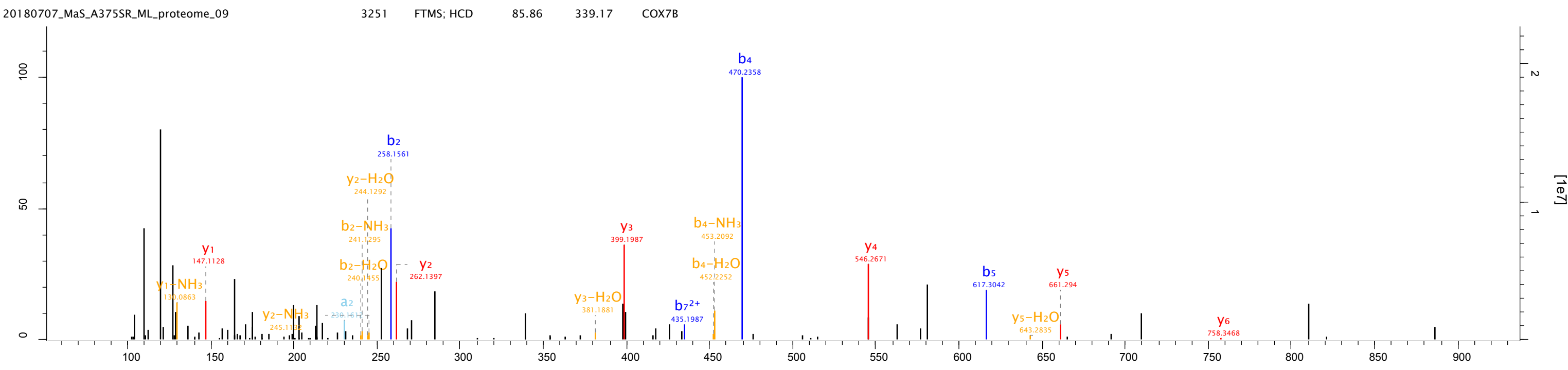
Raw file
20180707_MaS_A375SR_ML_proteome_09

Scan: 24121
Method: FTMS; HCD
Score: 69.23
m/z: 711.4
Gene names: NFE2L1



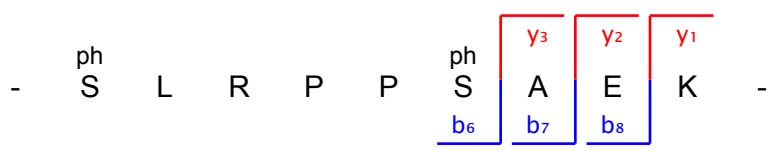
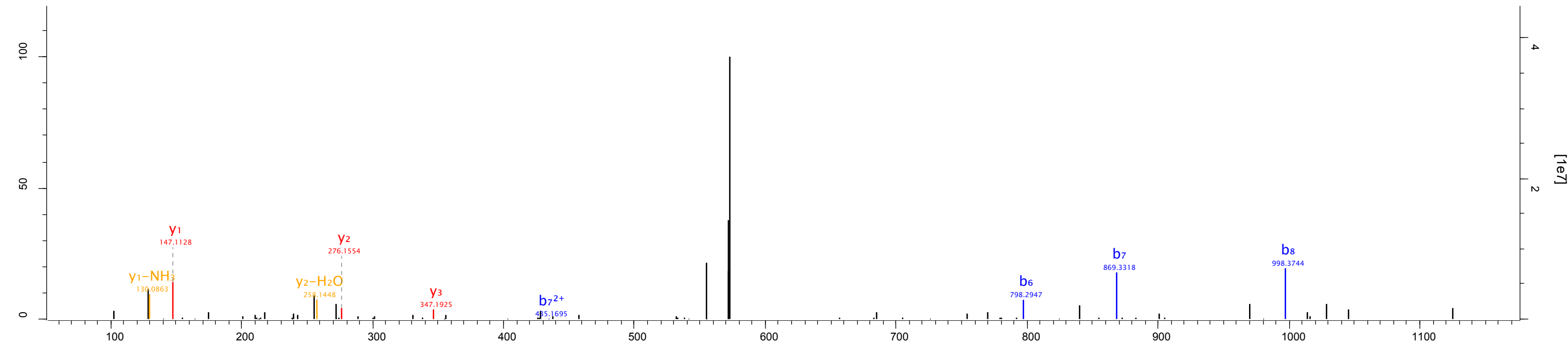
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 Scan: 25421 Method: FTMS; HCD Score: 108.47 m/z: 704.83 Gene names: OAF





Raw file
20180707_MaS_A375SR_ML_proteome_09

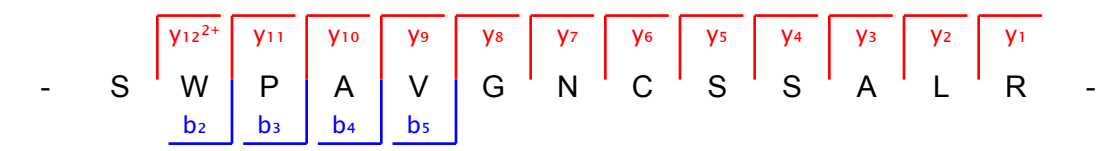
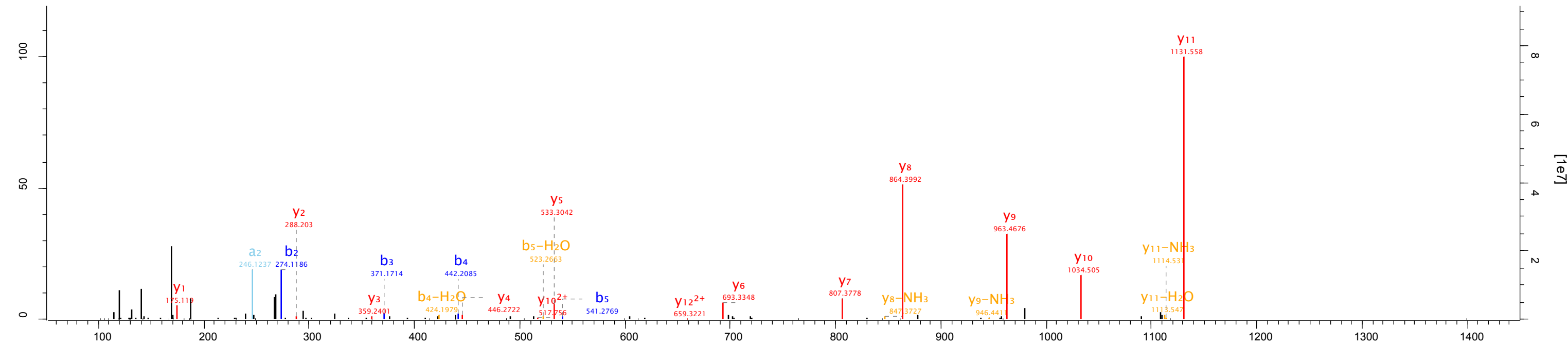
Scan 5301 Method FTMS; HCD Score 50.47 m/z 572.74



[1e7]

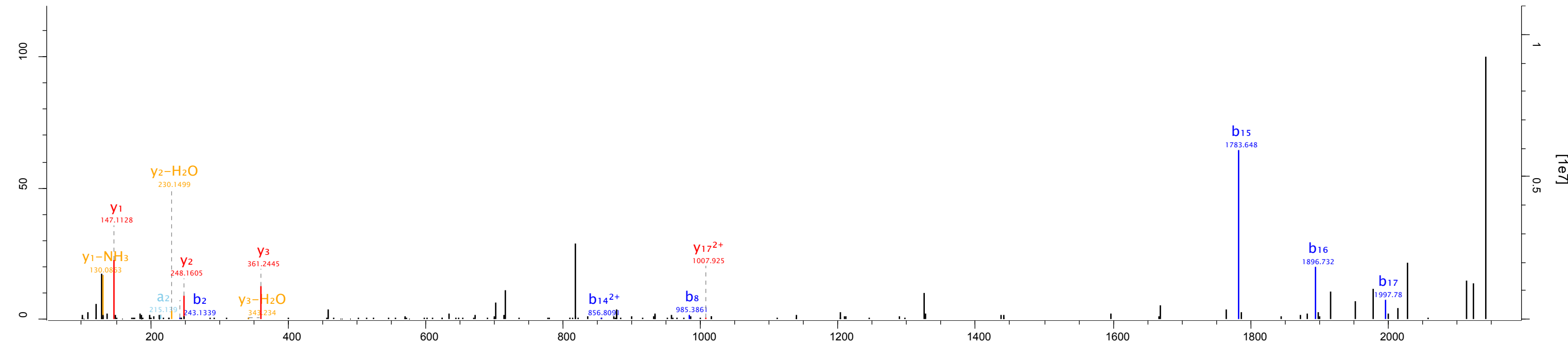
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Scan 17451 Method FTMS; HCD Score 110.92 m/z 702.84 Gene names HPX



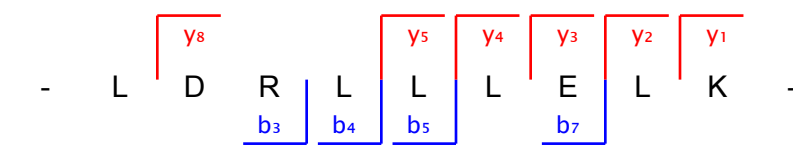
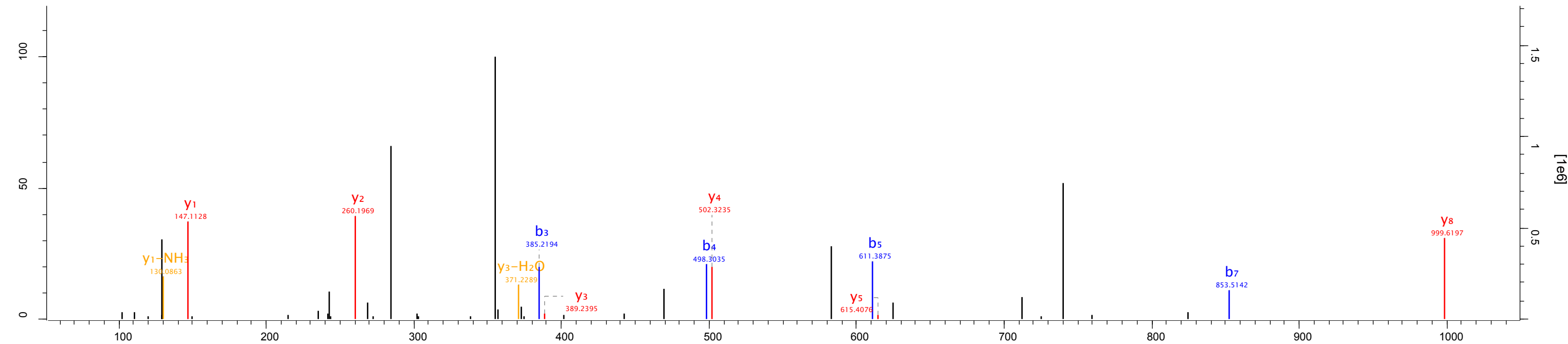
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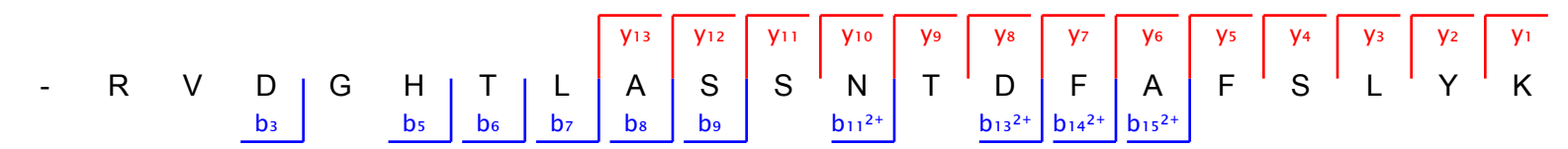
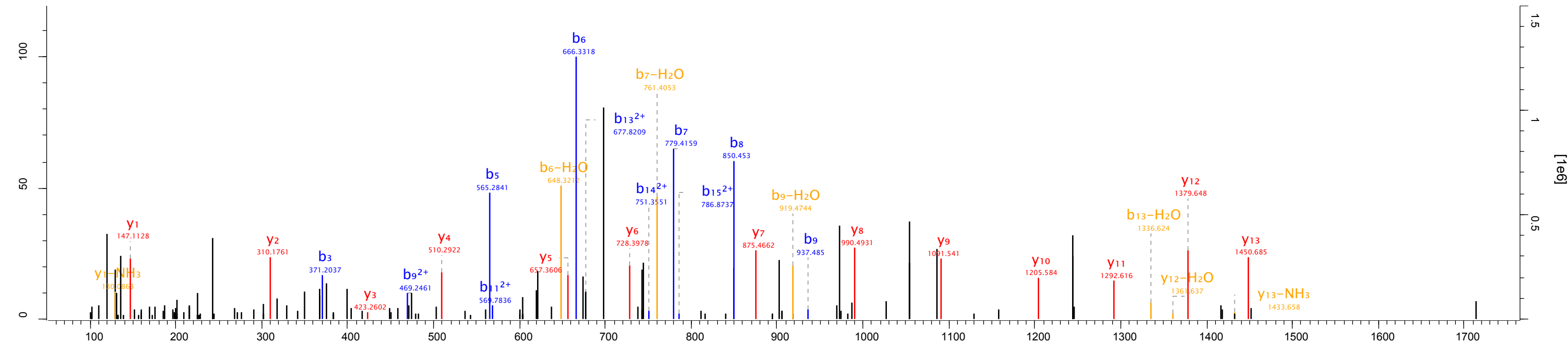
Scan Method Score m/z Gene names
21461 FTMS; HCD 63.68 715.63 PDE6B;PDE6A



- E I V ox M A ox M M M ph T A C D L S A I T K -
b₂ b₈ b₁₄²⁺ b₁₅ b₁₆ b₁₇ y₁₇²⁺ y₃ y₂ y₁

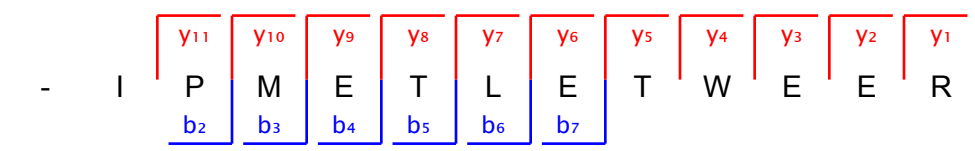
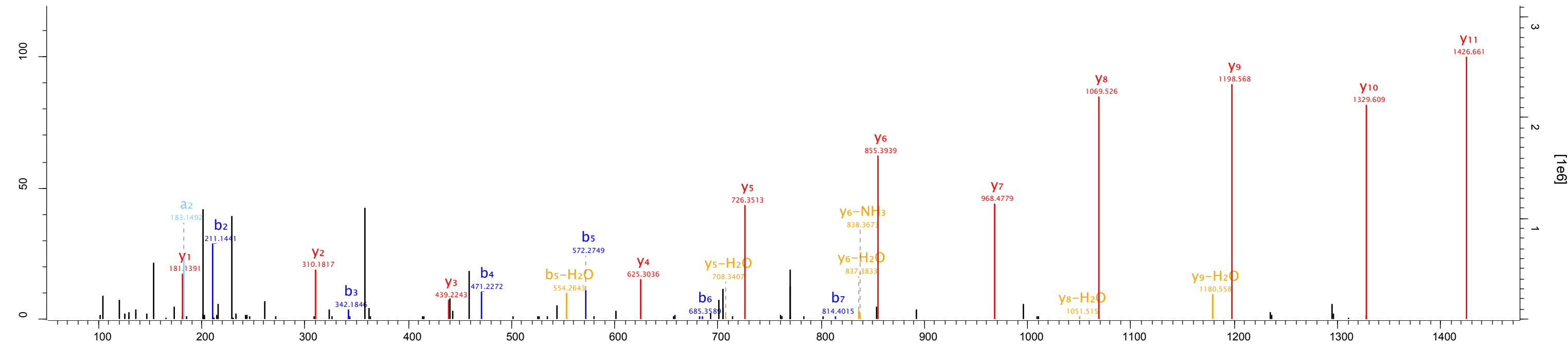
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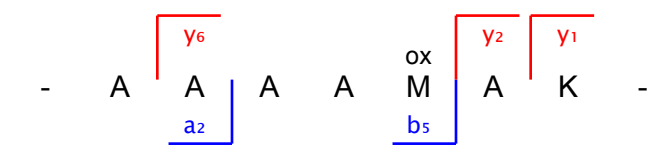
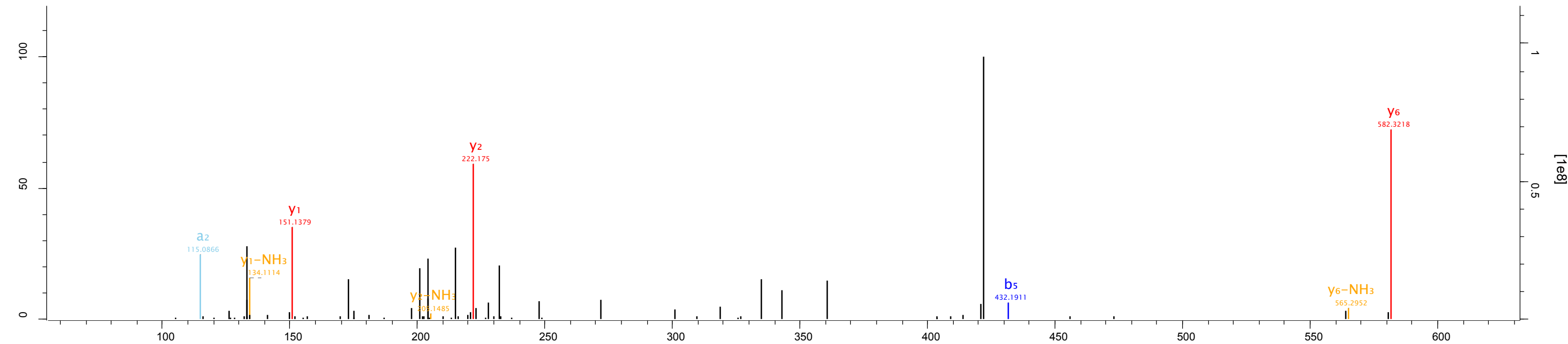


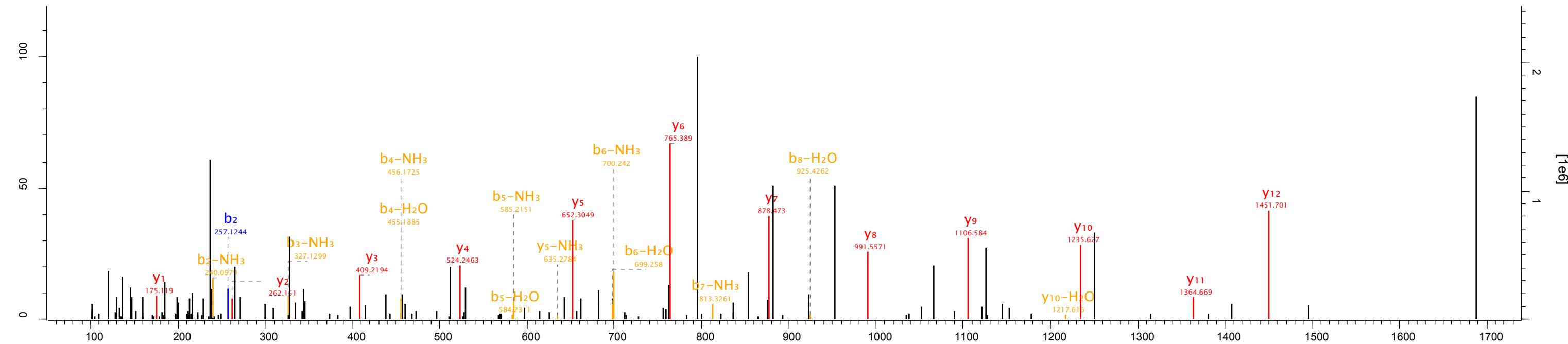
Raw file
20180707_MaS_A375SR_ML_proteome_11

Scan 26141 Method FTMS; HCD Score 110.38 m/z 770.38 Gene names R3HDM4



Raw file 20180707_MaS_A375SR_ML_proteome_11 Scan 2751 Method FTMS; HCD Score 44.97 m/z 327.18





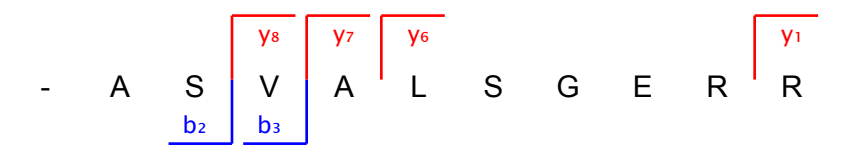
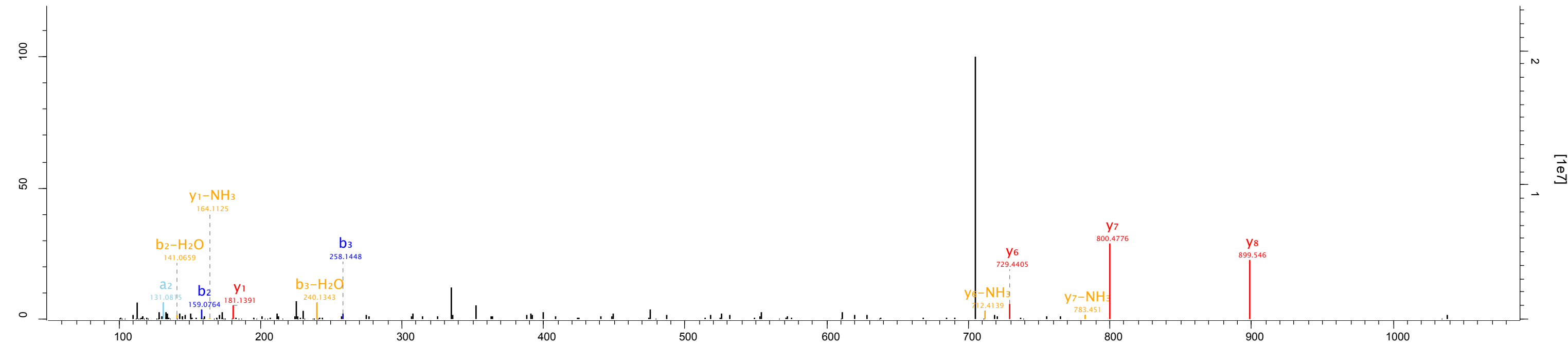
- Q Q S E E D L L L Q D F S R -

b₂ is indicated by a blue bracket under the second Q.

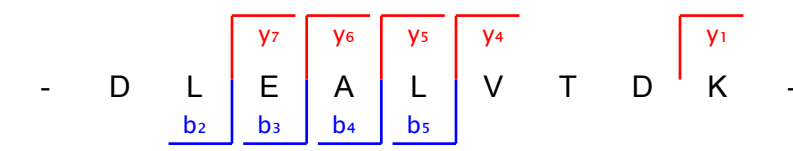
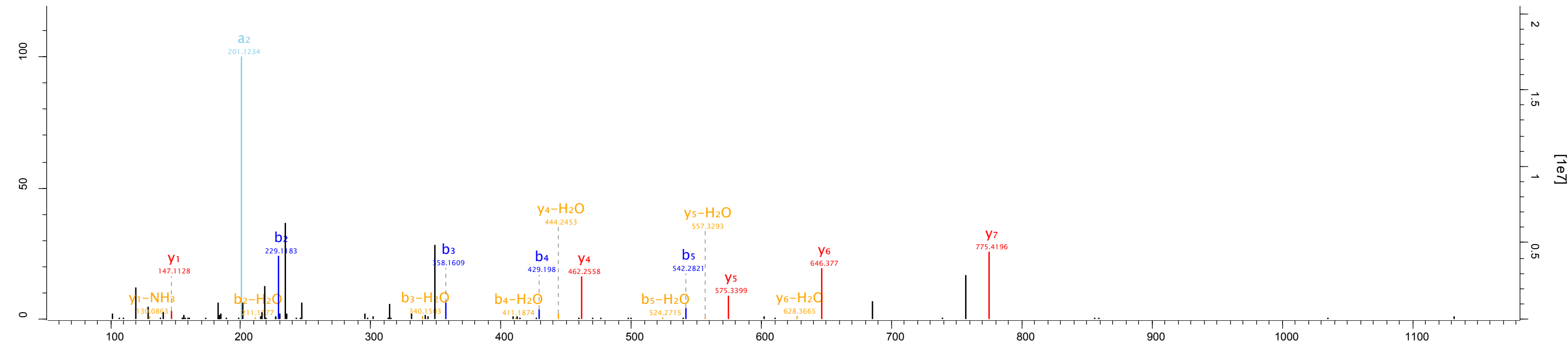
Fragmentation scheme showing b and y ions for the peptide sequence: - Q Q S E E D L L L Q D F S R -

Red brackets above the sequence indicate y ions (y₁ to y₁₂) and blue brackets below indicate b ions (b₂).

Raw file 20180707_MaS_A375SR_ML_proteome_11 Scan 3011 Method FTMS; HCD Score 61.16 m/z 353.21

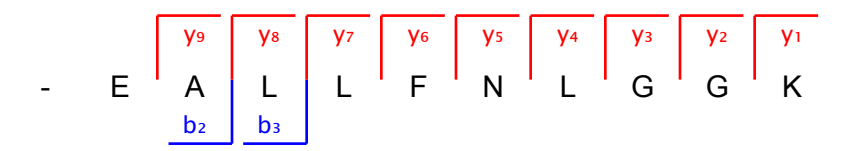
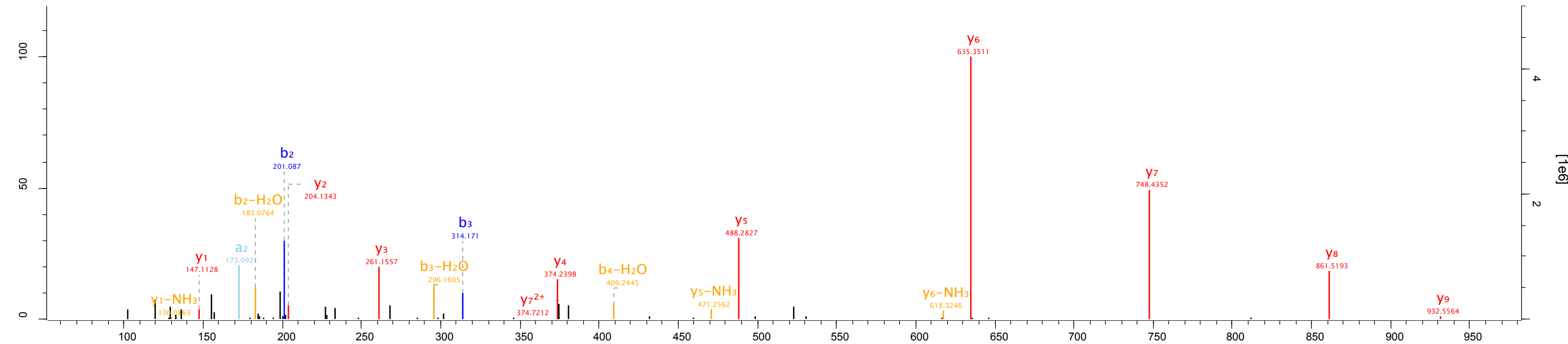


Raw file 20180707_MaS_A375SR_ML_proteome_12 Scan 23831 Method FTMS; HCD Score 72.61 m/z 502.27 Gene names PGM5



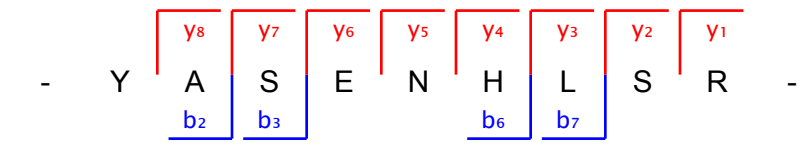
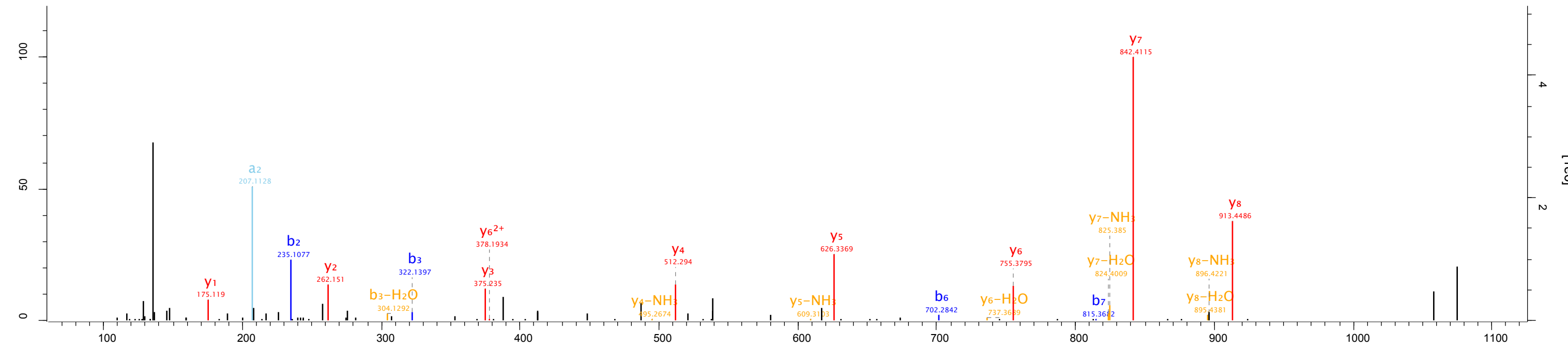
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20180707_MaS_A375SR_ML_proteome_12

Scan 27461 Method FTMS; HCD Score 101.65 m/z 531.3 Gene names CYB561



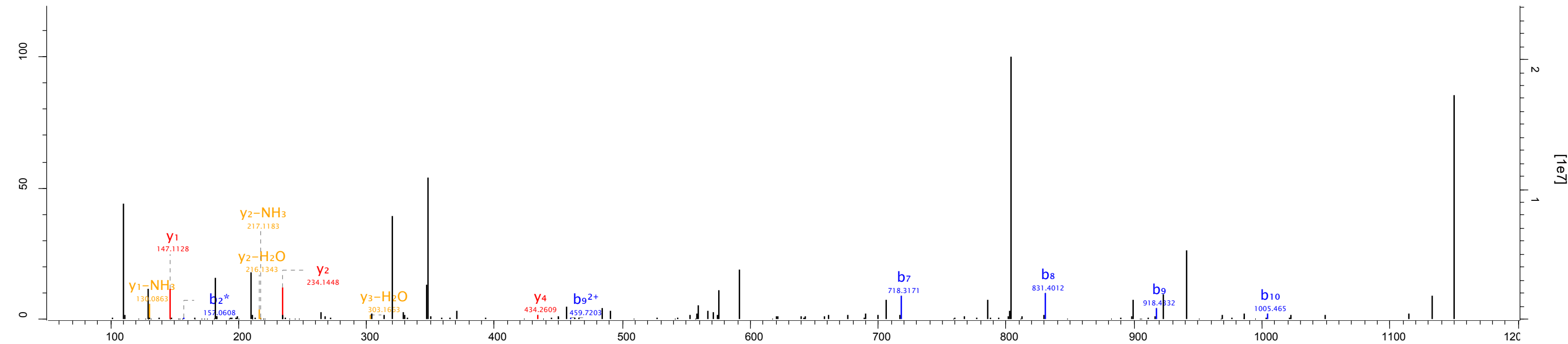
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20180707_MaS_A375SR_ML_proteome_12

Scan 3041 Method FTMS; HCD Score 123.75 m/z 538.76 Gene names TM4SF1



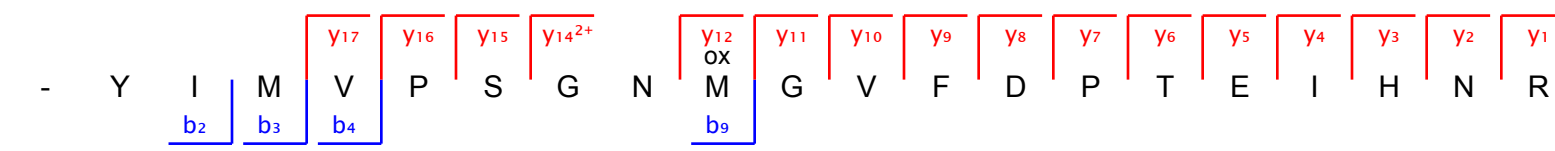
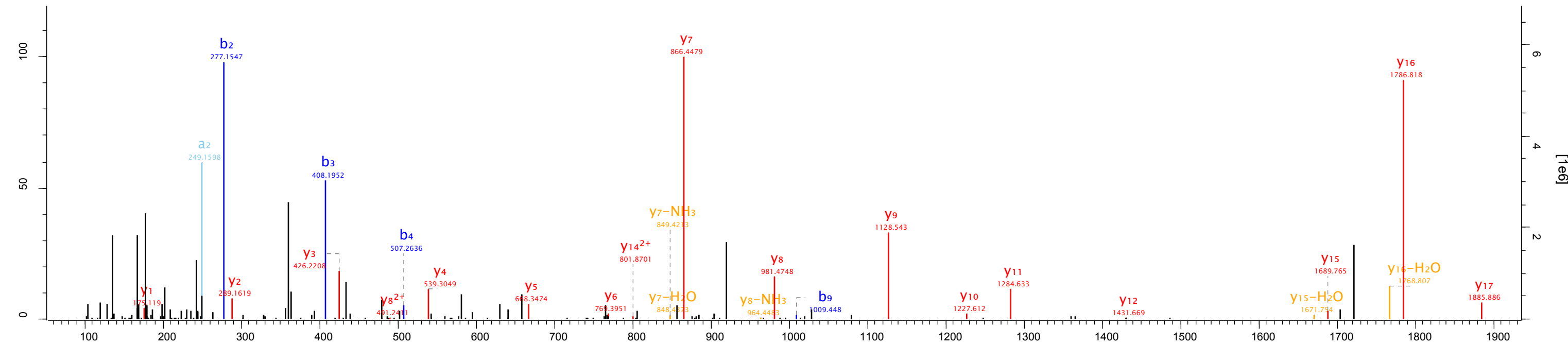
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20180707_MaS_A375SR_ML_proteome_12

Scan 4171 Method FTMS; HCD Score 58.59 m/z 576.29



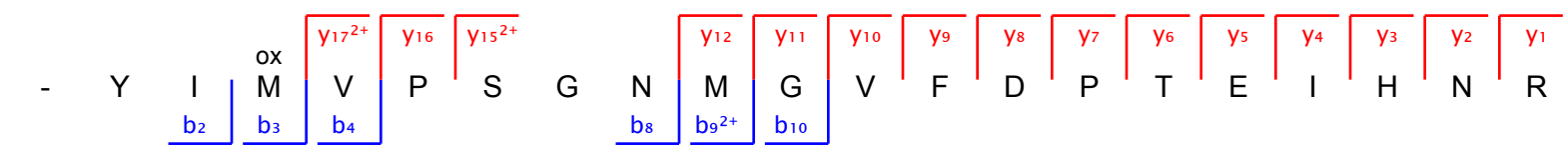
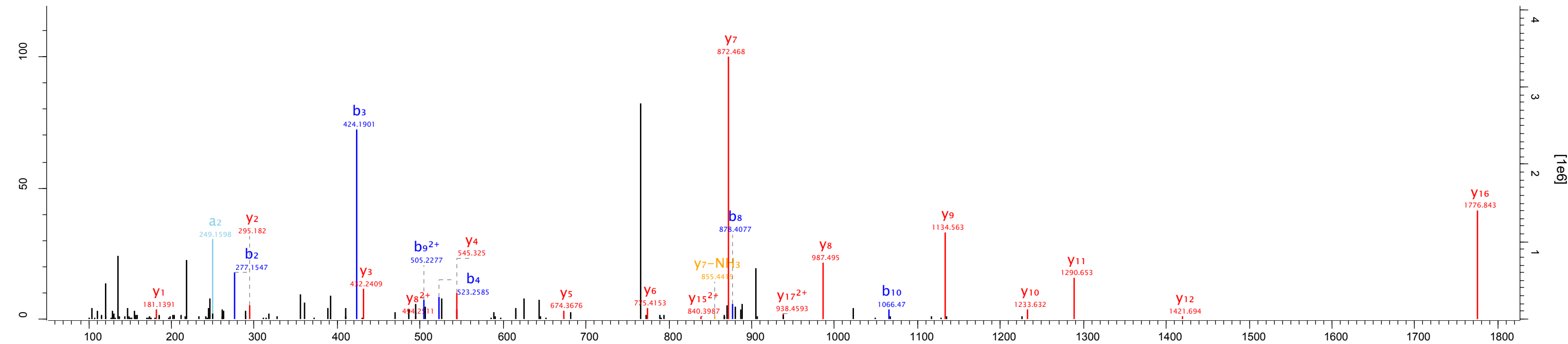
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20180707_MaS_A375SR_ML_proteome_13

Scan 23731 Method FTMS; HCD Score 75.21 m/z 765.36 Gene names CNIH4

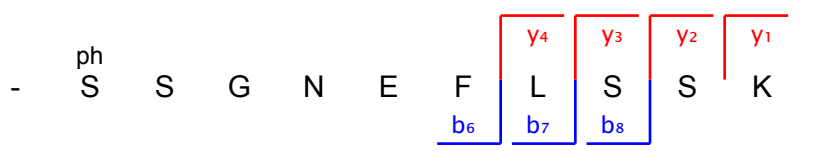
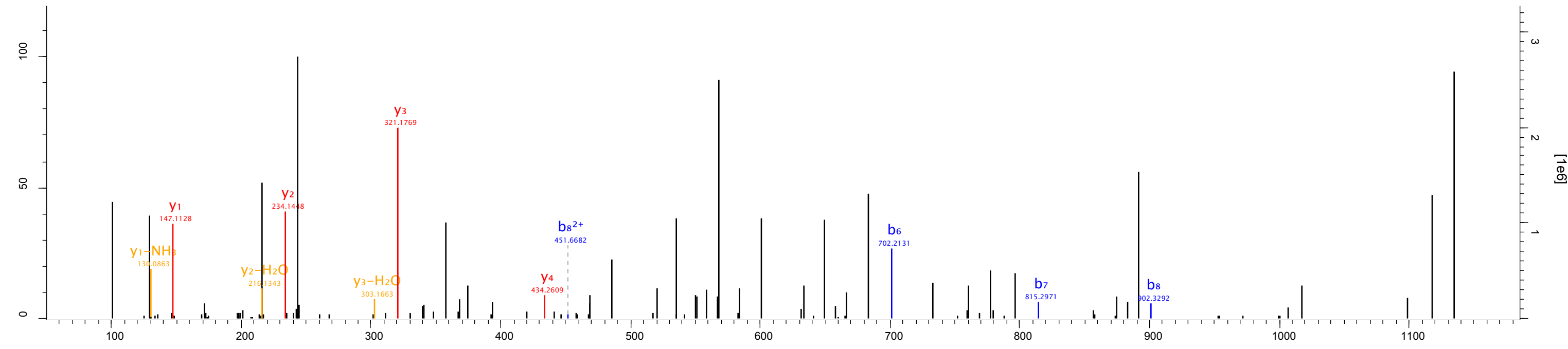


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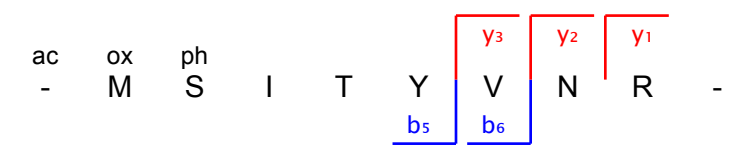
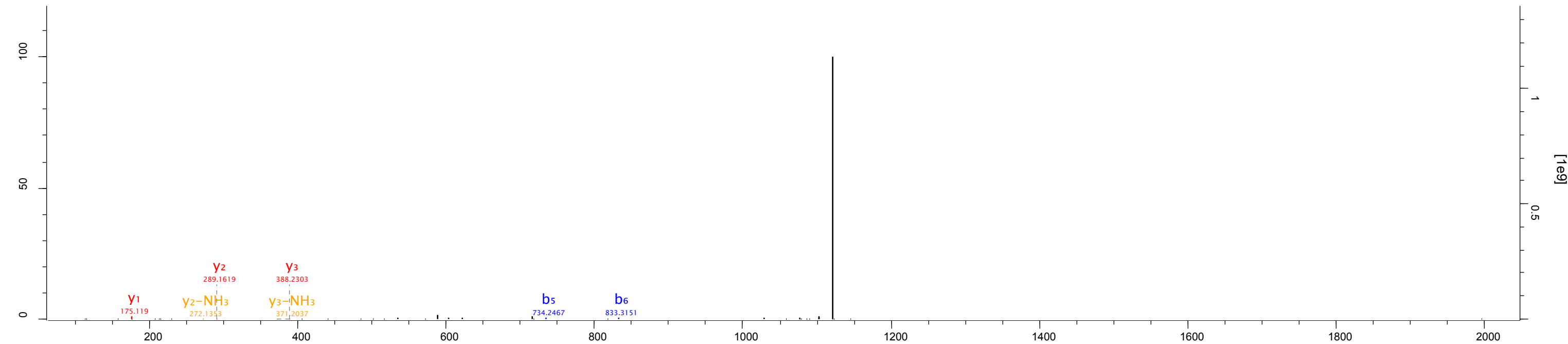
Scan 25331 Method FTMS; HCD Score 76.3 m/z 767.04 Gene names CNIH4



Raw file 20180707_MaS_A375SR_ML_proteome_13 Scan 3411 Method FTMS; HCD Score 76.23 m/z 568.24 Gene names MAP3K19

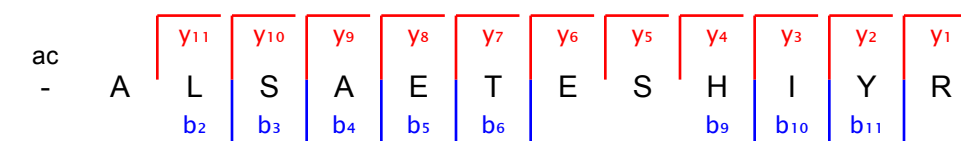
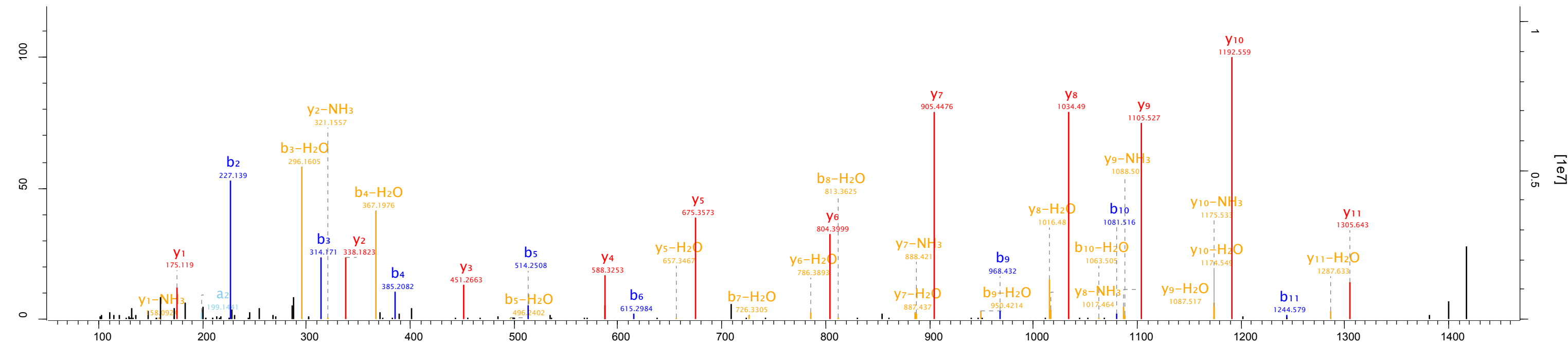


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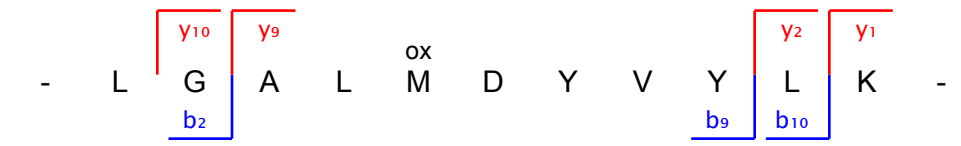
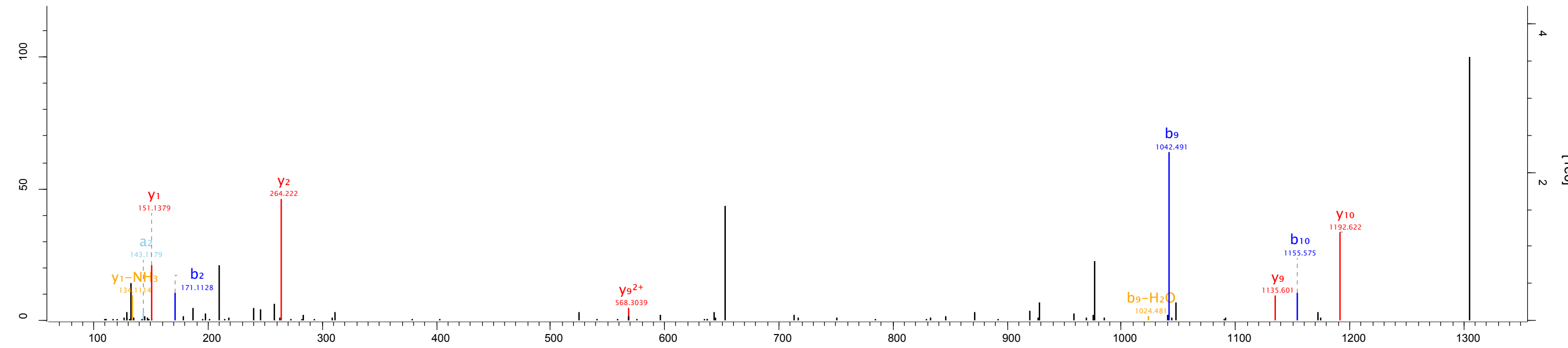
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Scan Method Score m/z Gene names
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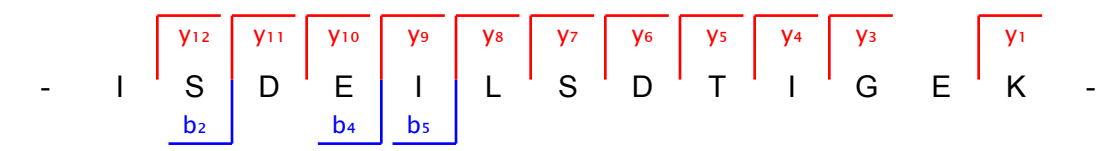
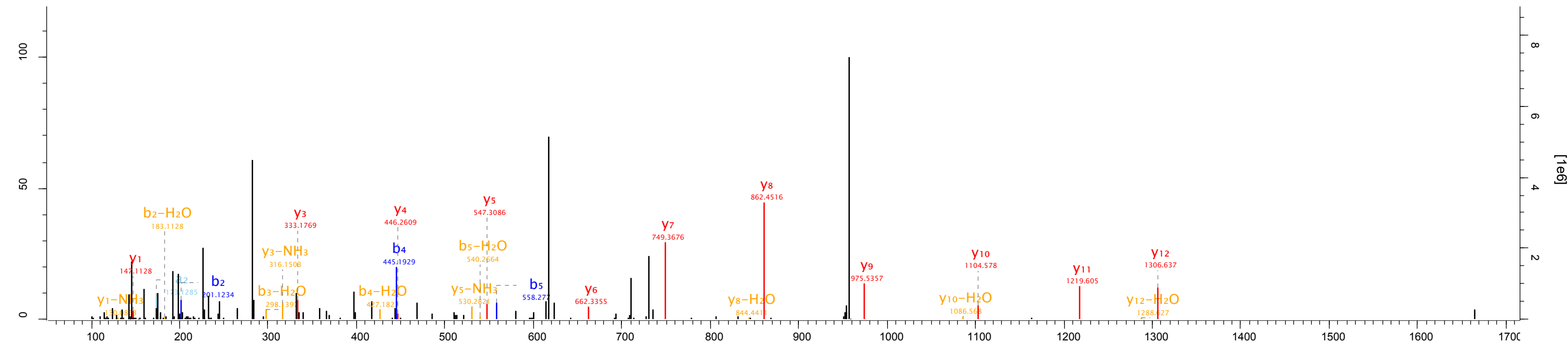
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Scan 8031 Method FTMS; HCD Score 42.21 m/z 653.35



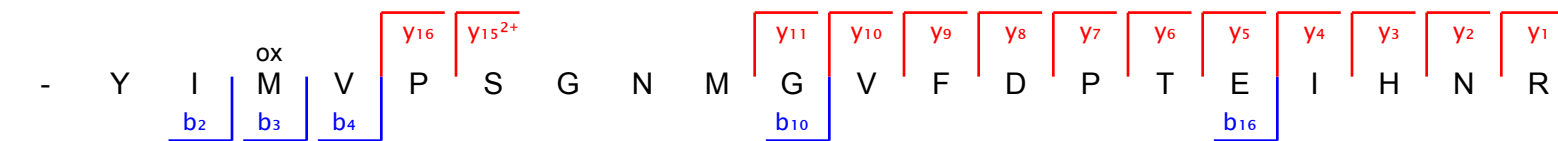
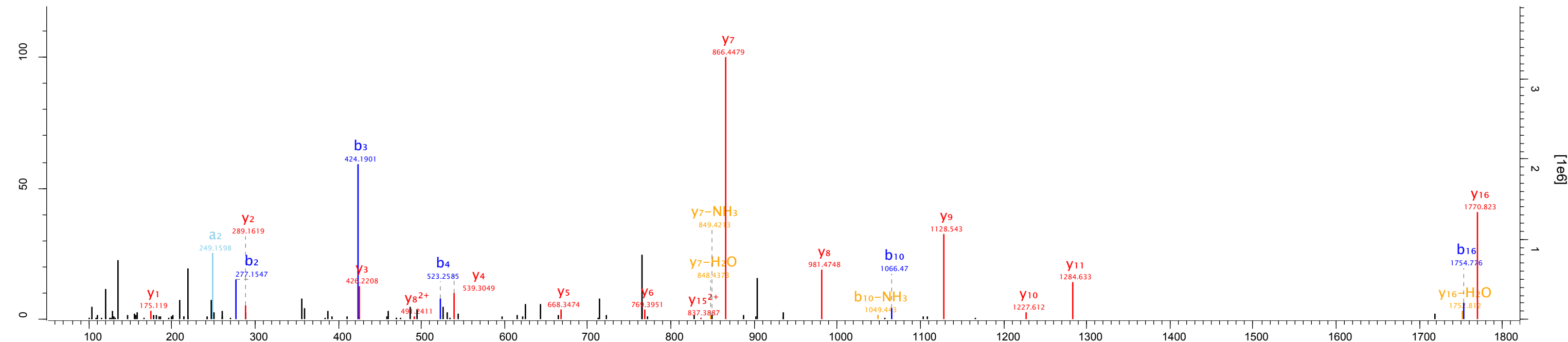
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20180707_MaS_A375SR_ML_proteome_15

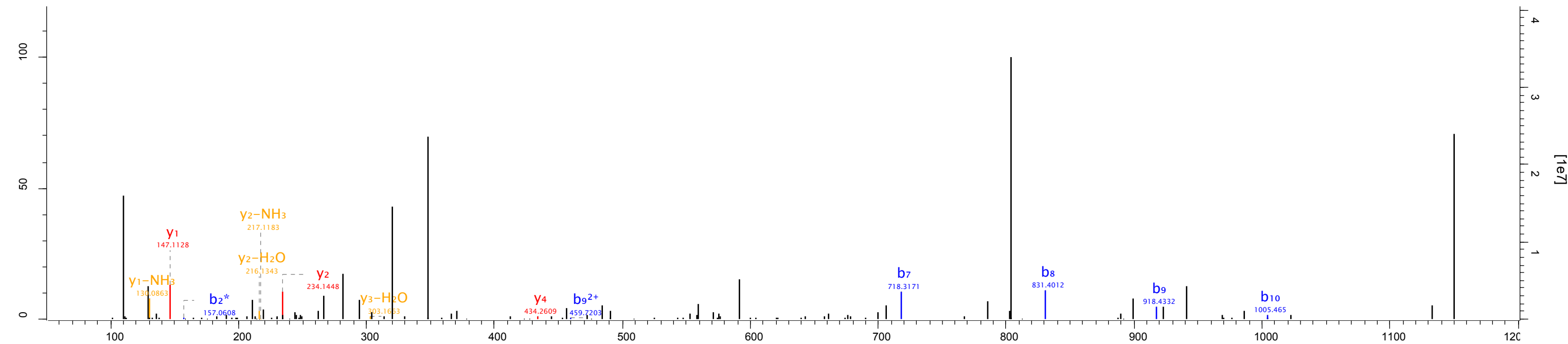
Scan 22141 Method FTMS; HCD Score 72.82 m/z 710.36 Gene names TMEM184C



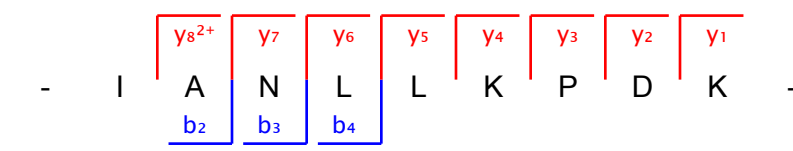
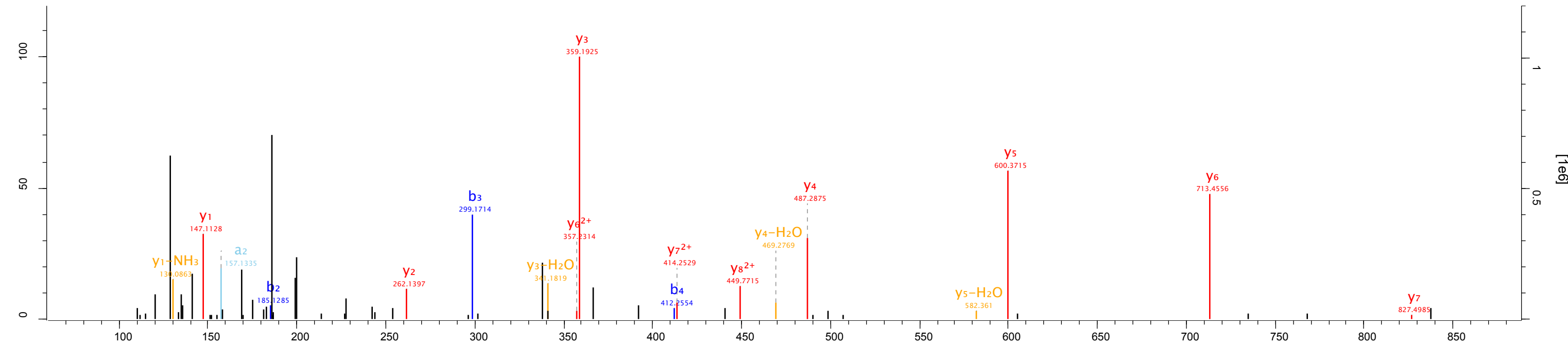
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Scan 25401 Method FTMS; HCD Score 77.87 m/z 765.36 Gene names CNIH4

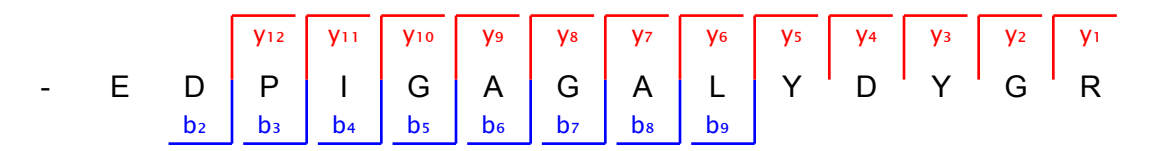
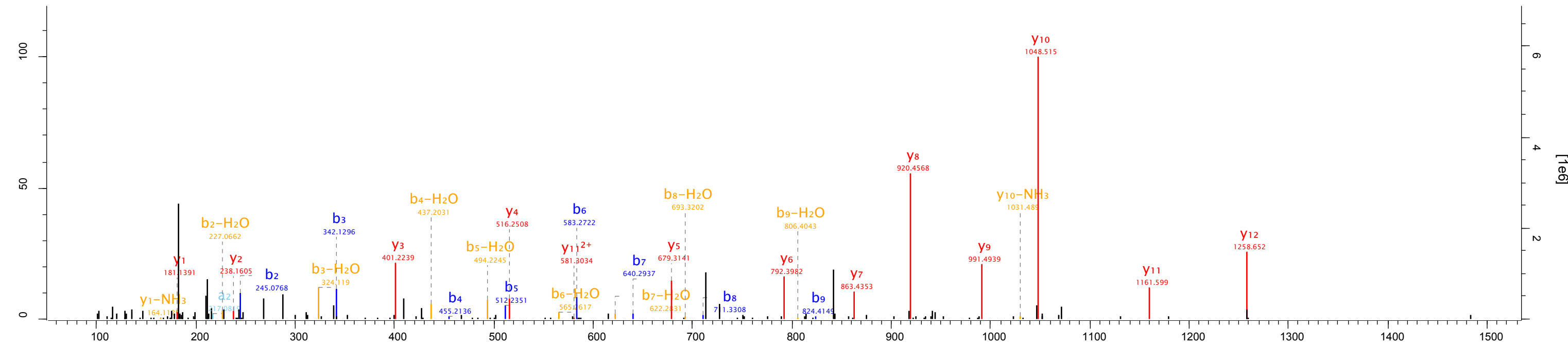




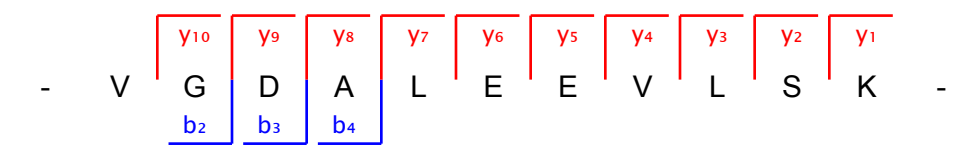
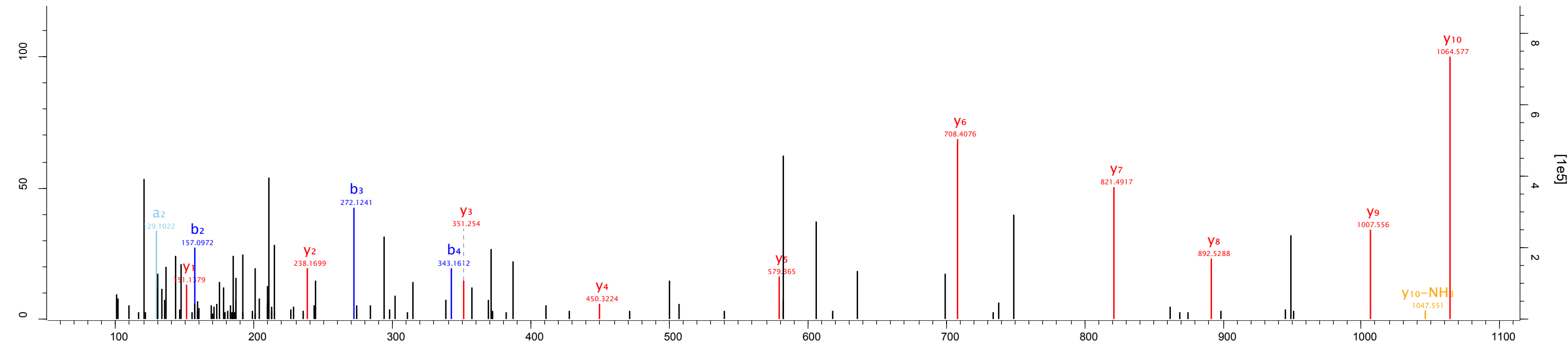
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Raw file 20180707_MaS_A375SR_ML_proteome_16 Scan 22471 Method FTMS; HCD Score 109.1 m/z 751.87 Gene names MT-ND6

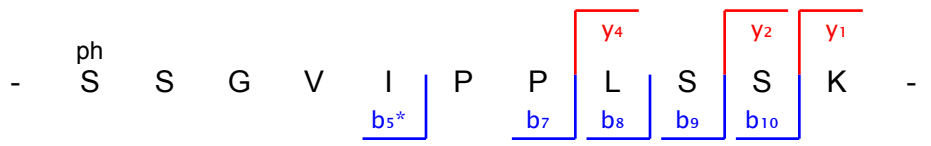
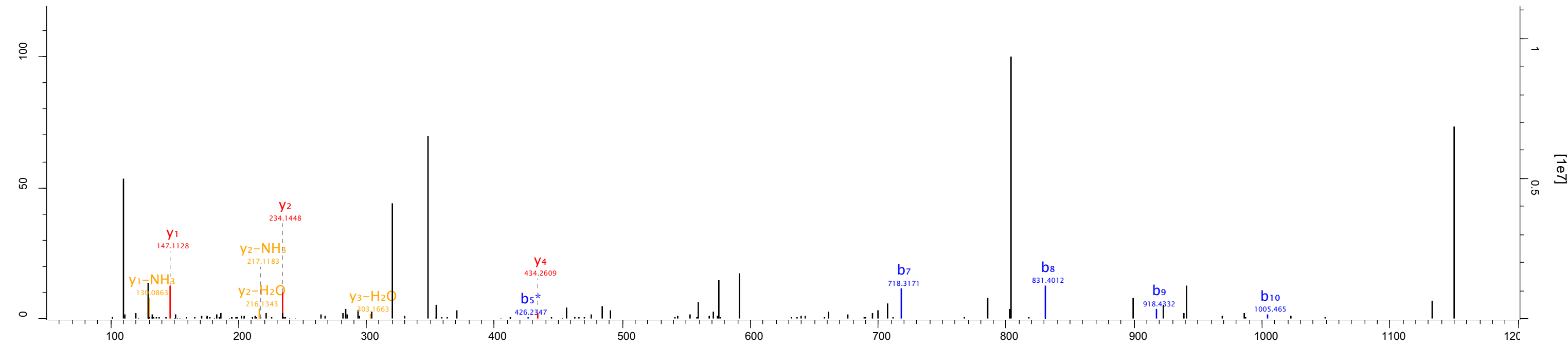


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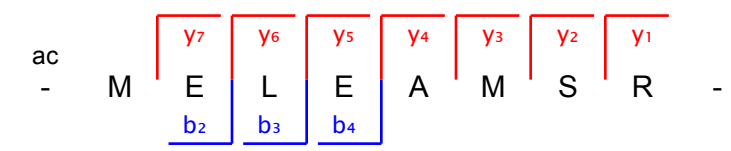
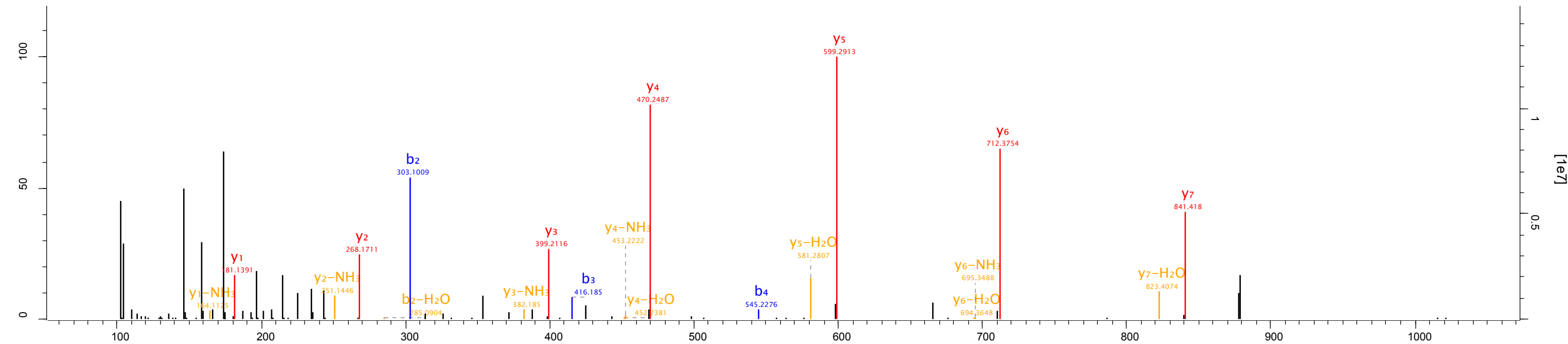
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20180707_MaS_A375SR_ML_proteome_18

Scan 8031 Method FTMS; HCD Score 57.35 m/z 576.29

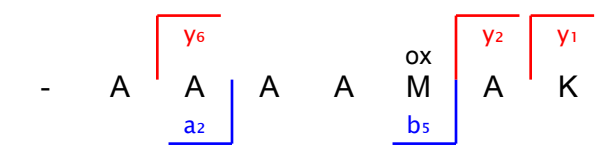
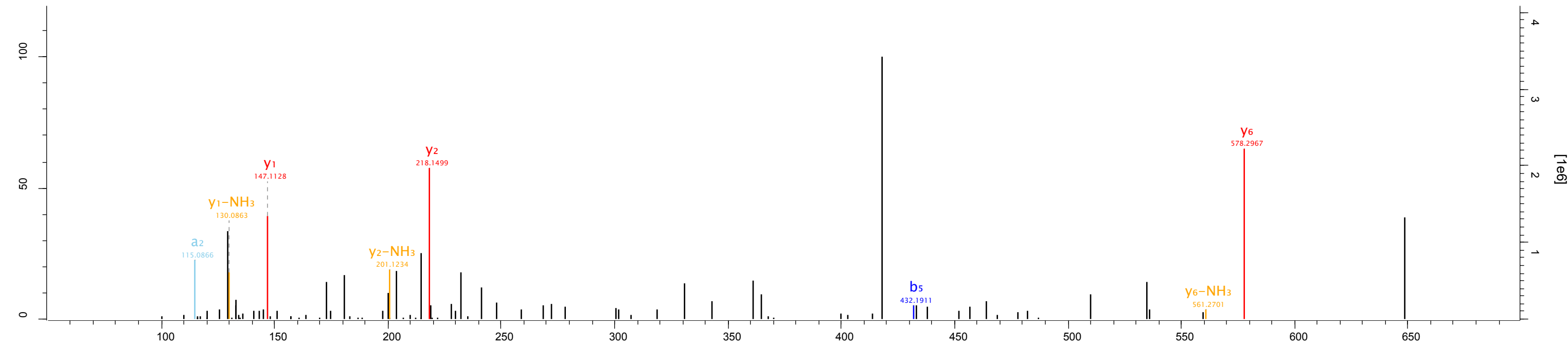


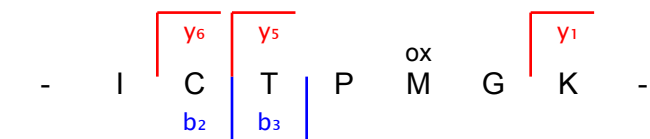
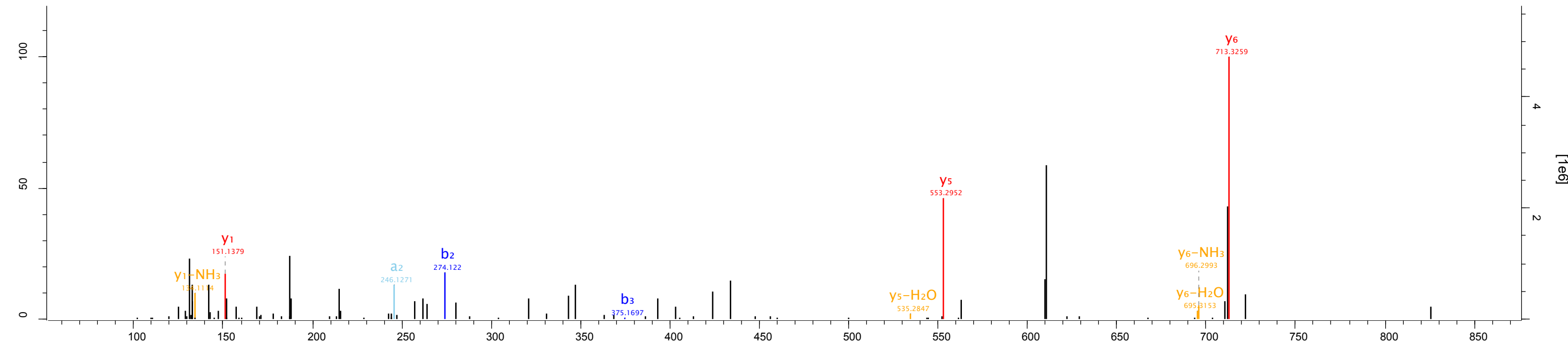
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20180707_MaS_A375SR_ML_proteome_2_01

Scan 24511 Method FTMS; HCD Score 109.48 m/z 507.74 Gene names TMEM258



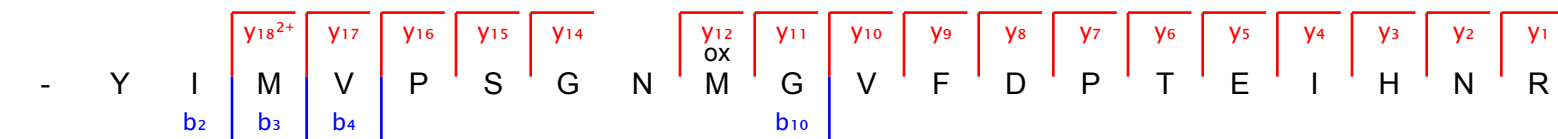
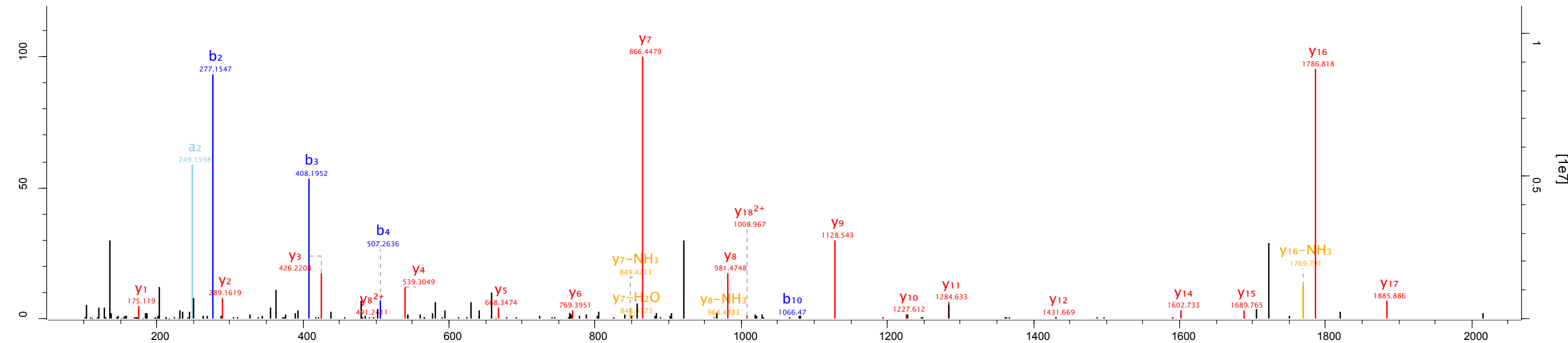
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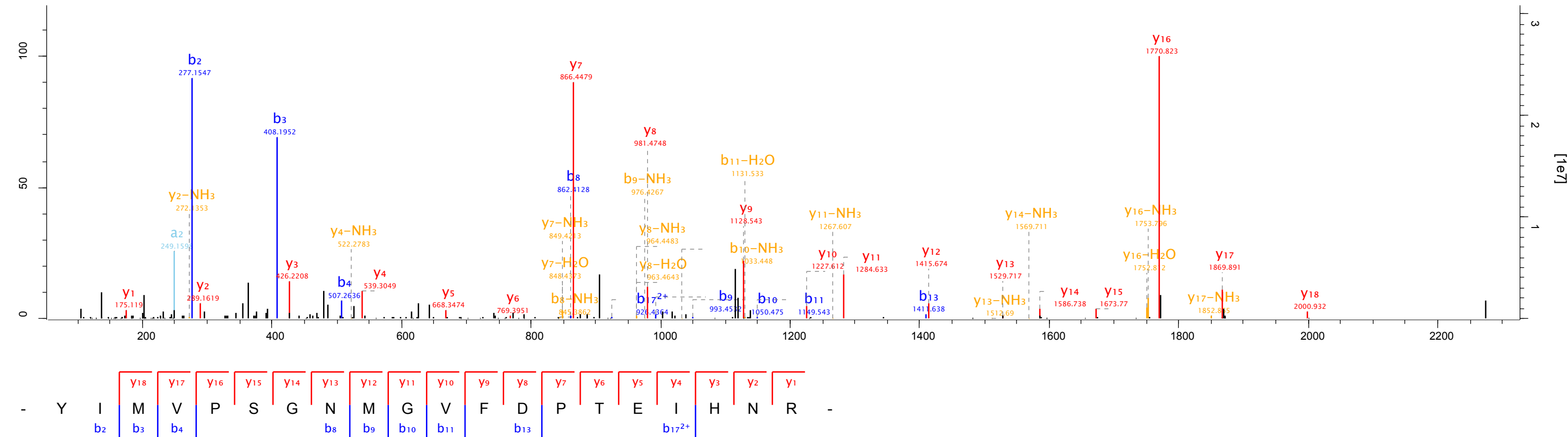




20180707_MaS_A375SR_ML_proteome_2_02

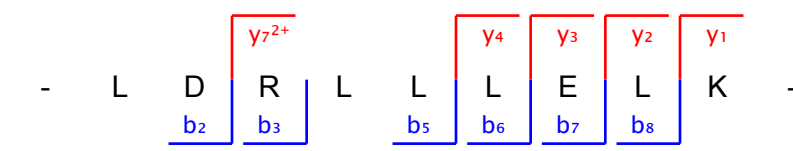
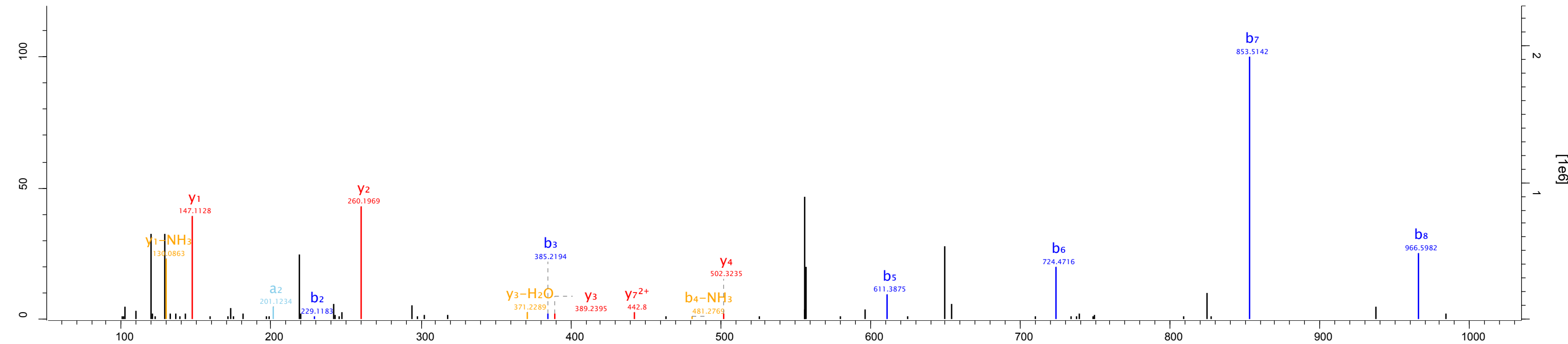
23611 FTMS; HCD 87.65 765.36 CNIH4





Raw file
20180707_MaS_A375SR_ML_proteome_2_03

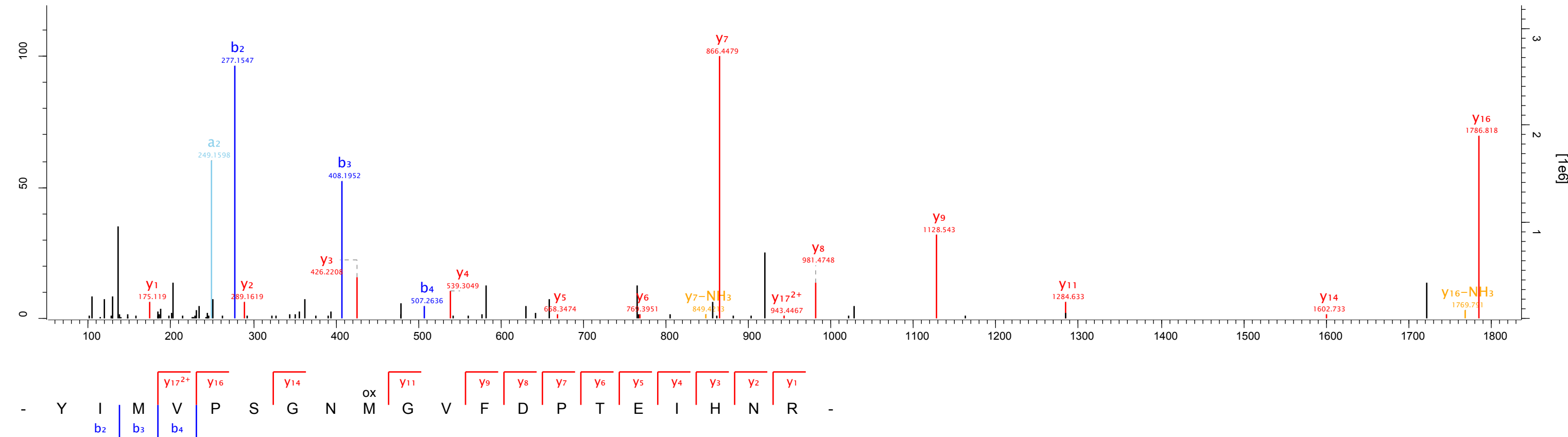
Scan 22071 Method FTMS; HCD Score 66.19 m/z 556.86 Gene names BPI



Raw file

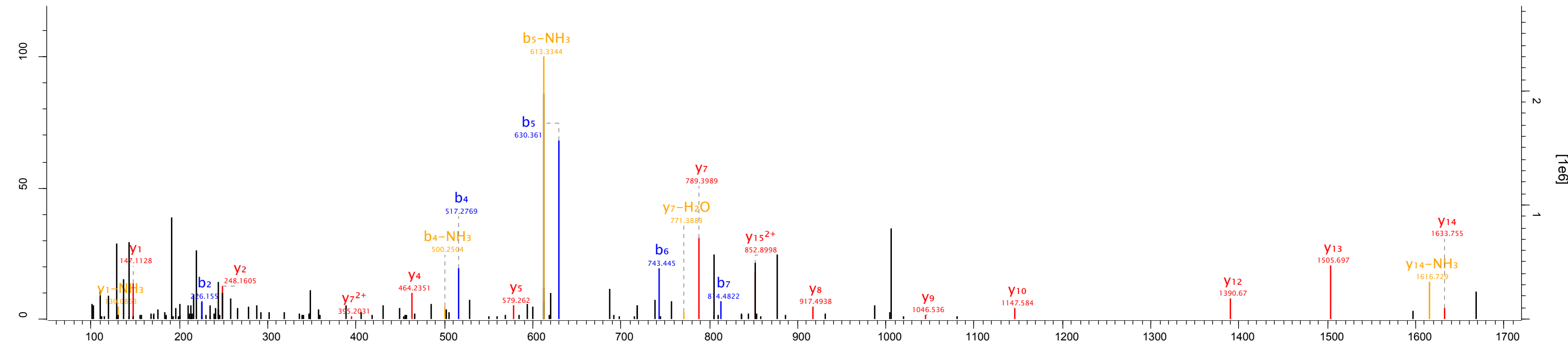
20180707_MaS_A375SR_ML_proteome_2_03

Scan	Method	Score	m/z	Gene names
24001	FTMS; HCD	73.92	765.36	CNIH4



Raw file
20180707_MaS_A375SR_ML_proteome_2_04

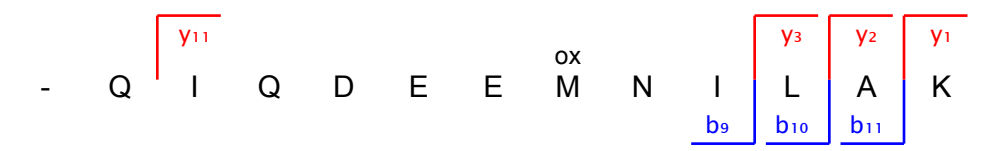
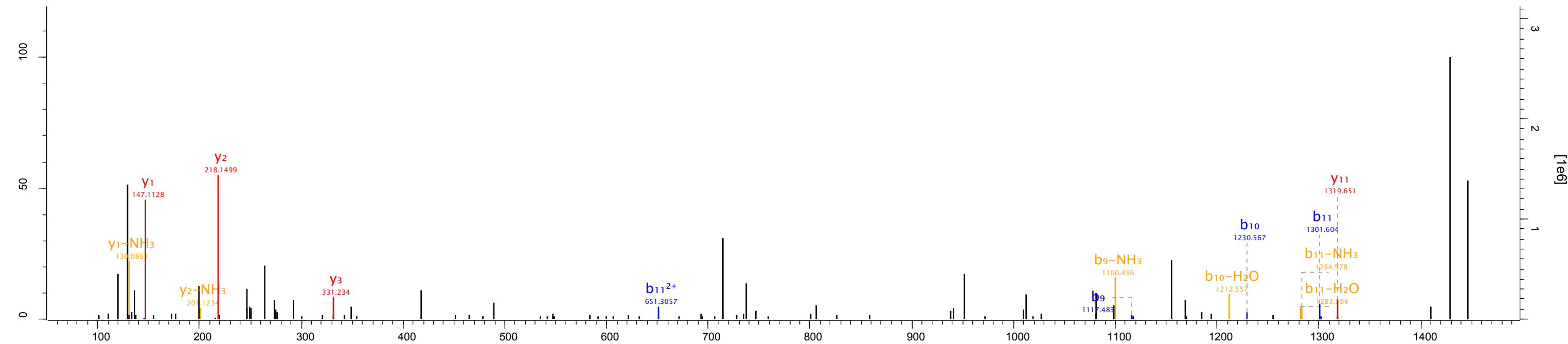
Scan 12251 Method FTMS; HCD Score 52.72 m/z 612.81 Gene names SLC1A3



- K P Y Q L I A Q D N E T E K P I D S E T K -
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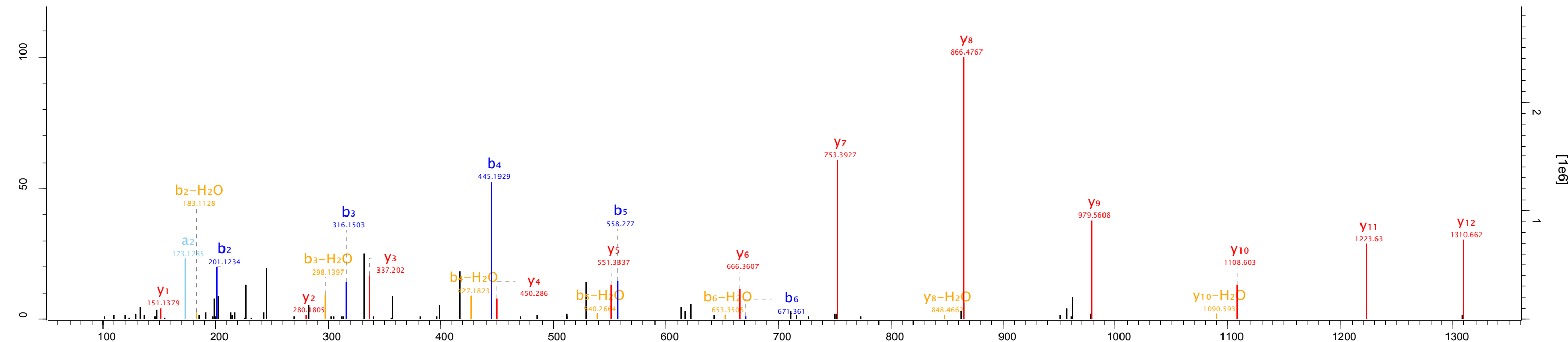
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20180707_MaS_A375SR_ML_proteome_2_05

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Raw file
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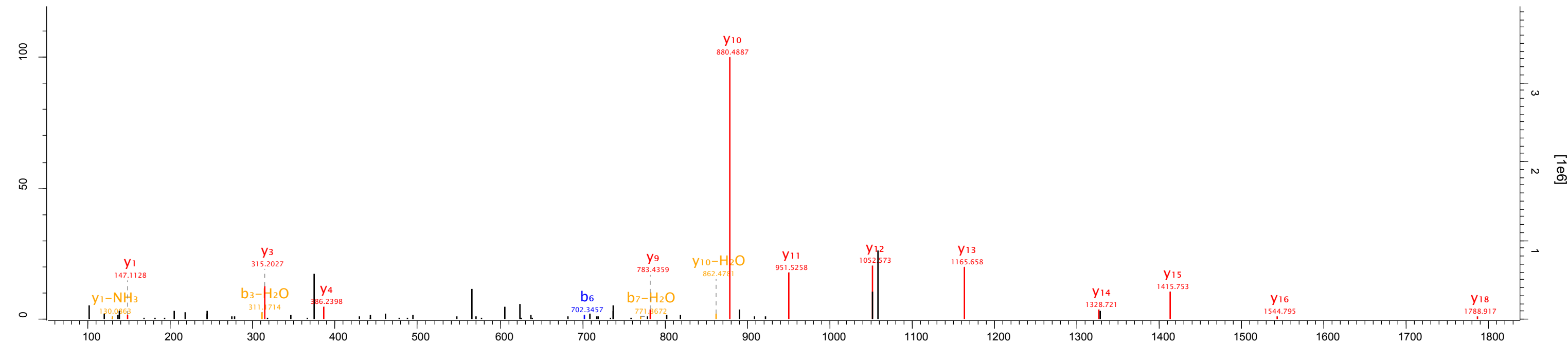
Scan 22111 Method FTMS; HCD Score 103.83 m/z 712.38 Gene names TMEM184C



- I S D E I L S D T I G E K -
b₂ b₃ b₄ b₅ b₆ y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

Raw file
20180707_MaS_A375SR_ML_proteome_2_05

Scan Method Score m/z Gene names
24911 FTMS; HCD 40.62 1059.55 TMEM261



- L S Q P F E S Y I T A P P G T A A A P A K -

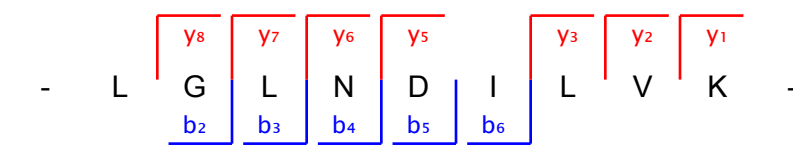
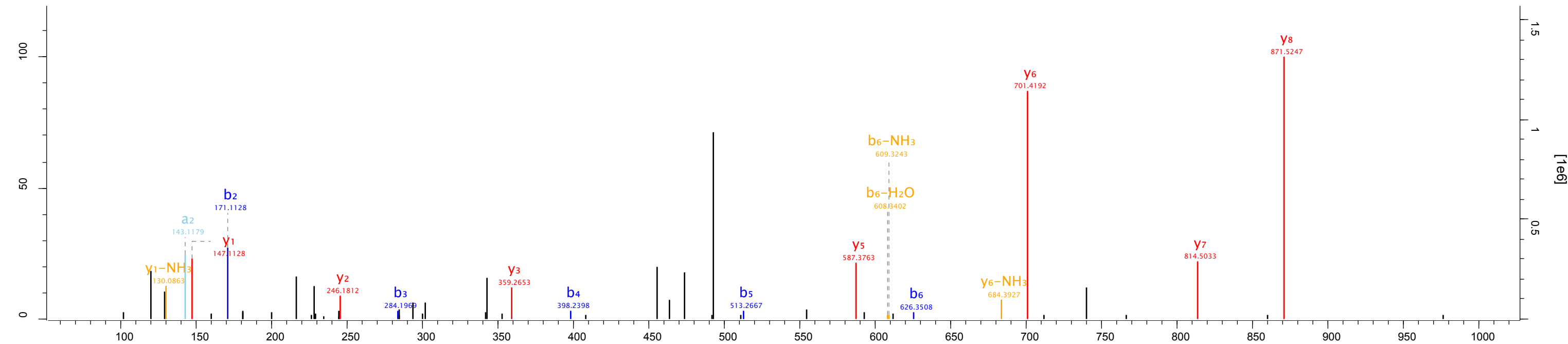
Fragmentation mapping (red brackets):

- y18: P
- y16: E
- y15: ES
- y14: SY
- y13: IY
- y12: IT
- y11: IA
- y10: AP
- y9: PP
- y4: AA
- y3: AP
- y1: AK

Fragmentation mapping (blue bracket):

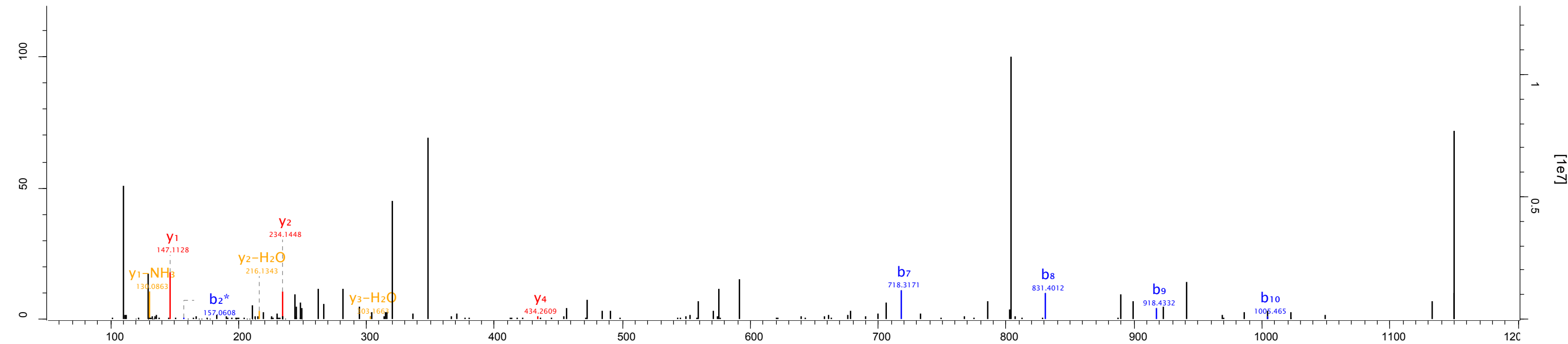
- b6: E

Raw file 20180707_MaS_A375SR_ML_proteome_2_05 Scan 26181 Method FTMS; HCD Score 97.97 m/z 492.81 Gene names STON2

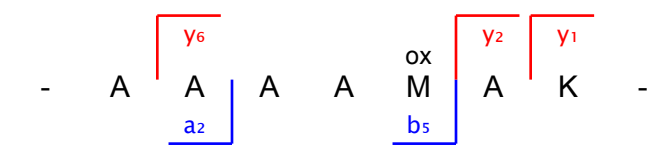
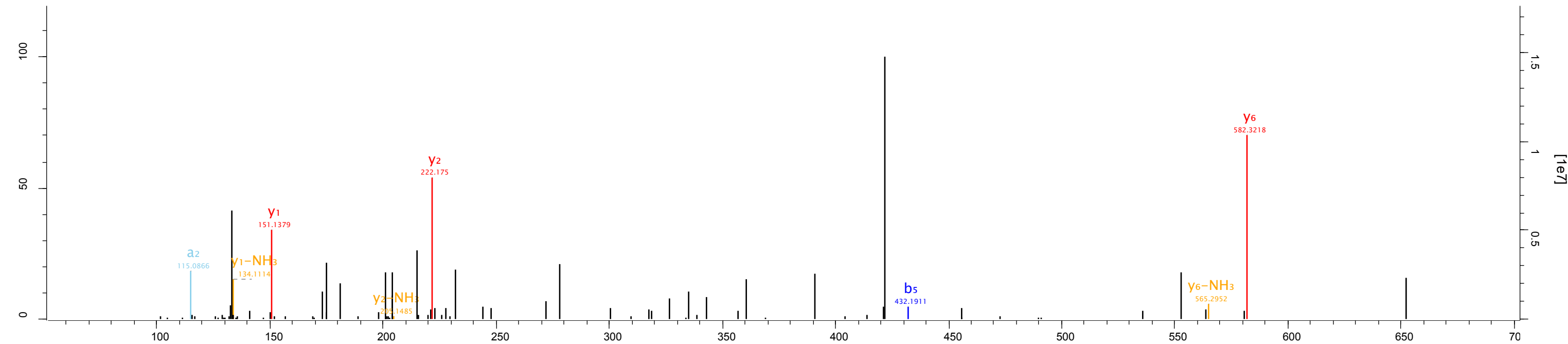


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20180707_MaS_A375SR_ML_proteome_2_05

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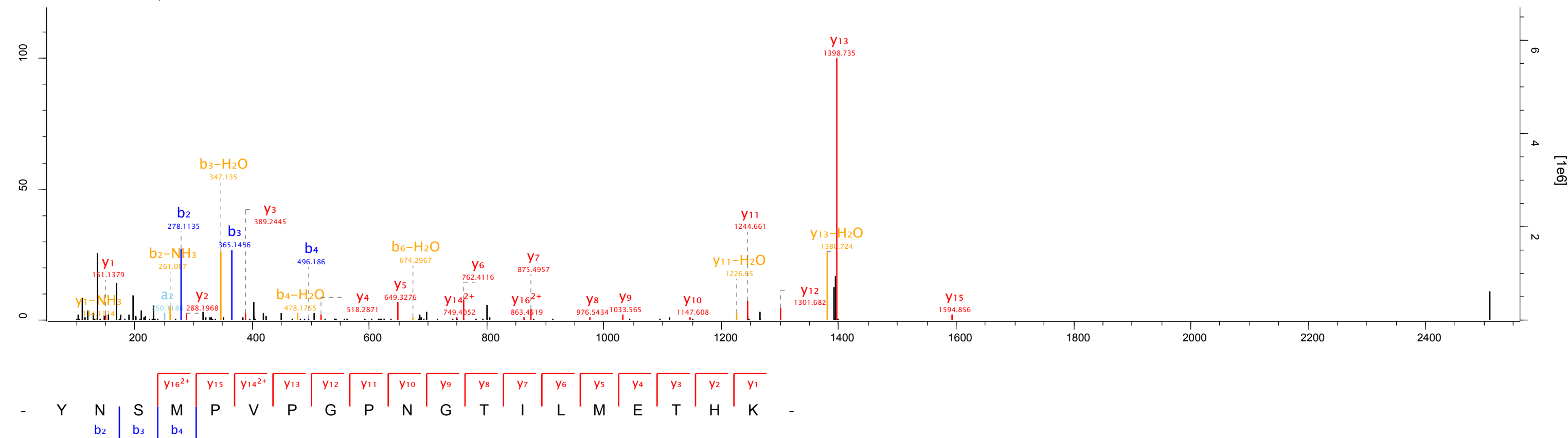


Raw file 20180707_MaS_A375SR_ML_proteome_2_06 Scan 2721 Method FTMS; HCD Score 44.97 m/z 327.18



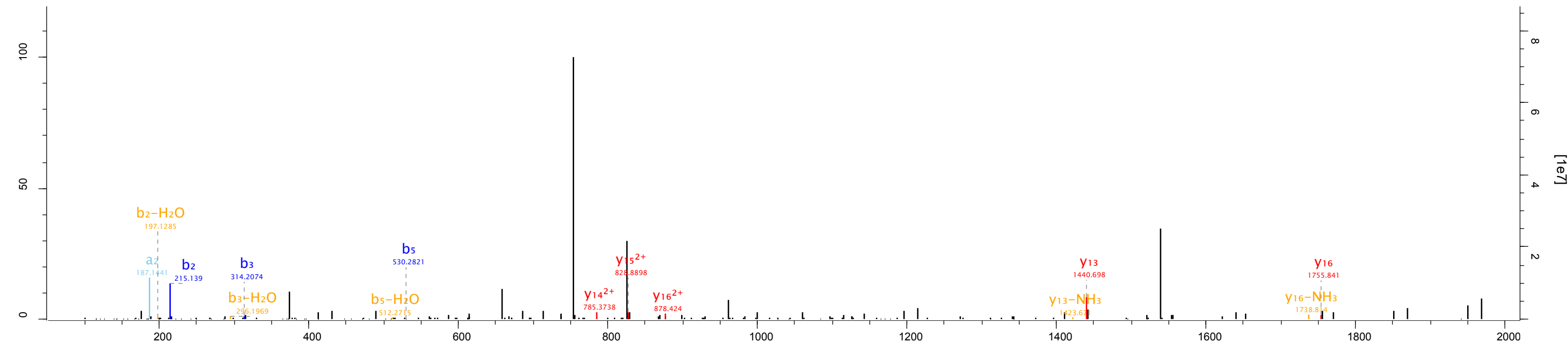
Raw file
20180707_MaS_A375SR_ML_proteome_2_07

Scan 20811 Method FTMS; HCD Score 91.59 m/z 697.35 Gene names SLC31A1



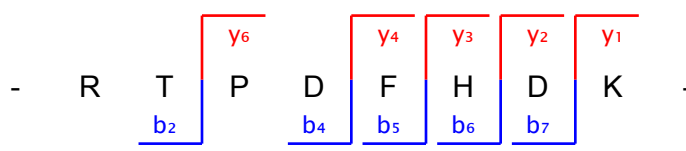
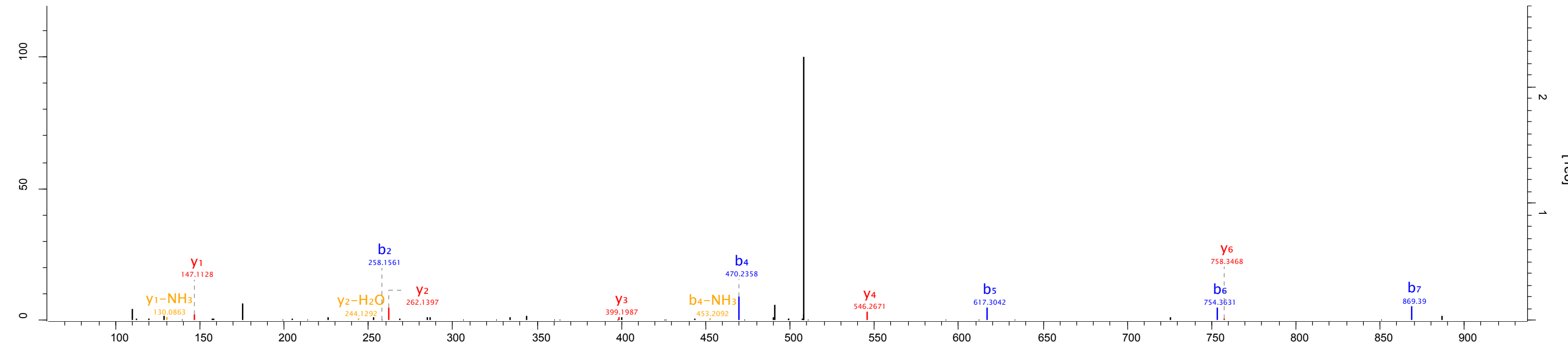
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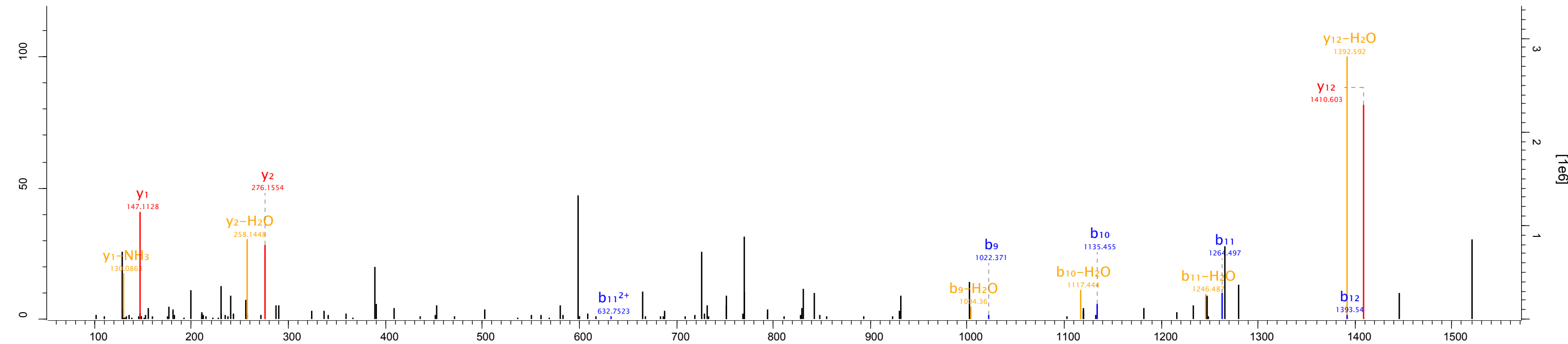
Scan 28201 Method FTMS; HCD Score 47.64 m/z 985.99 Gene names FAM35A



Raw file
20180707_MaS_A375SR_ML_proteome_2_07

Scan 3271 Method FTMS; HCD Score 50.11 m/z 508.25 Gene names COX7B





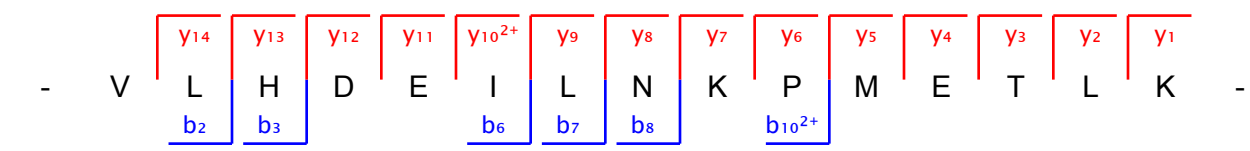
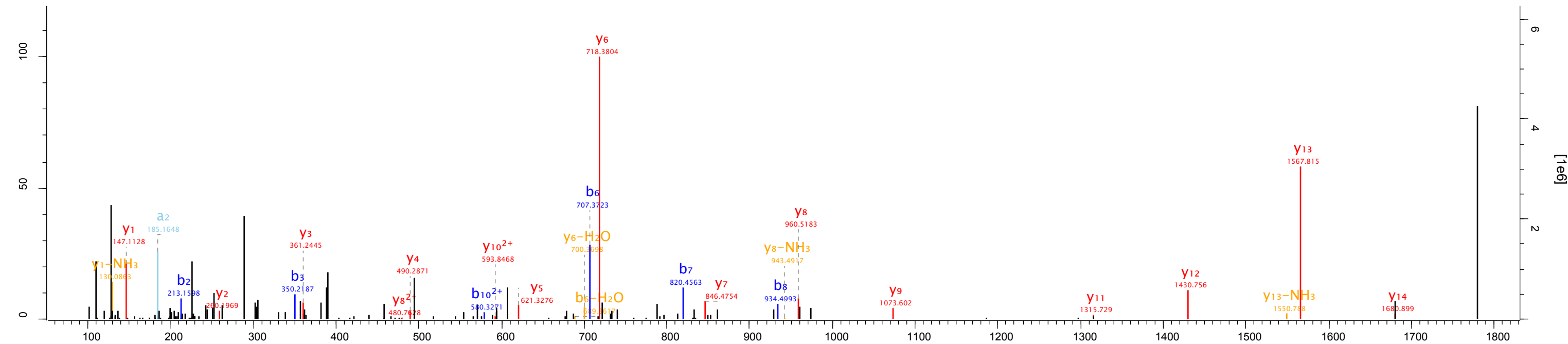
- E A M S G F M D H L E E K -

ox

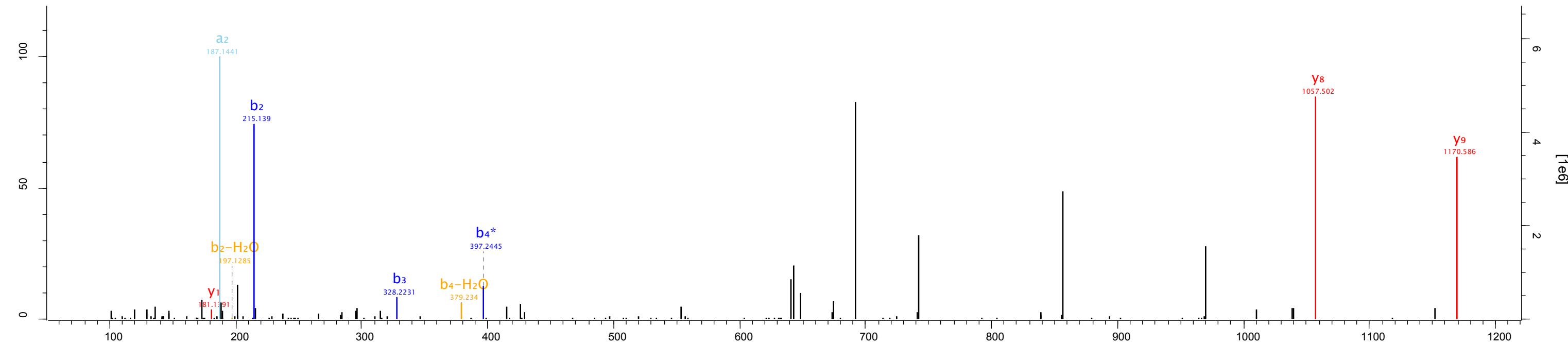
b₉ b₁₀ b₁₁ b₁₂ y₁₂ y₂ y₁

Raw file
20180707_MaS_A375SR_ML_proteome_2_10

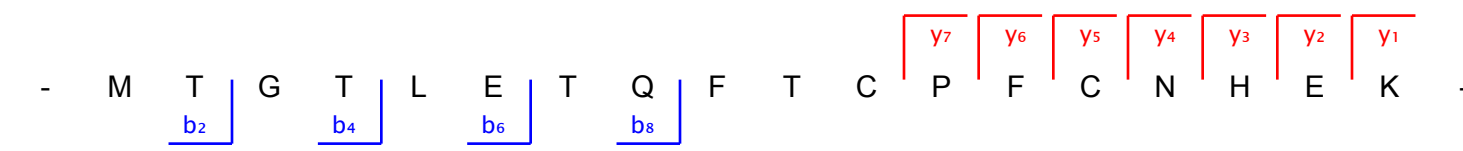
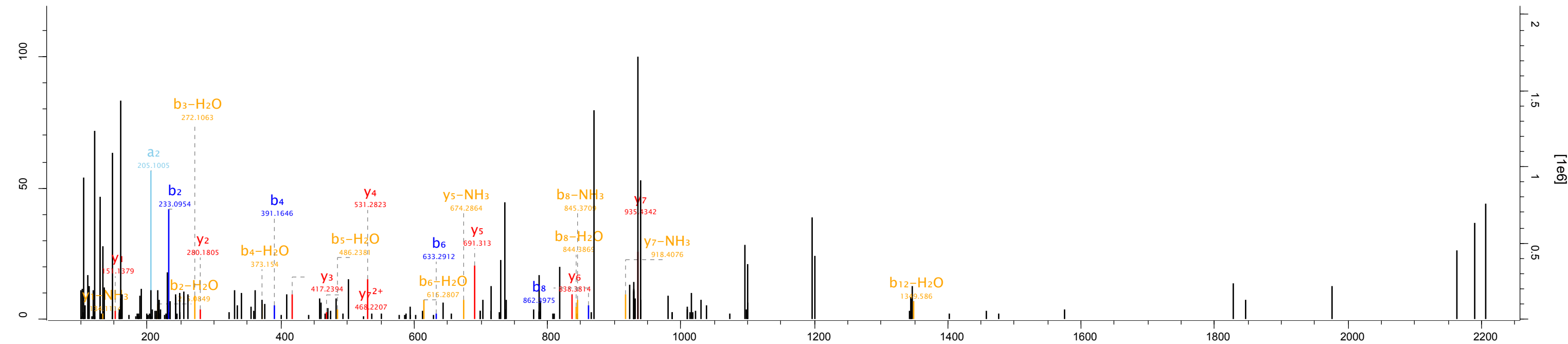
Scan Method Score m/z Gene names
17741 FTMS; HCD 96.49 594.33 SLC35A3



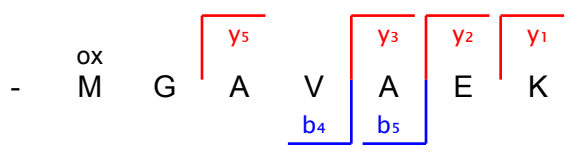
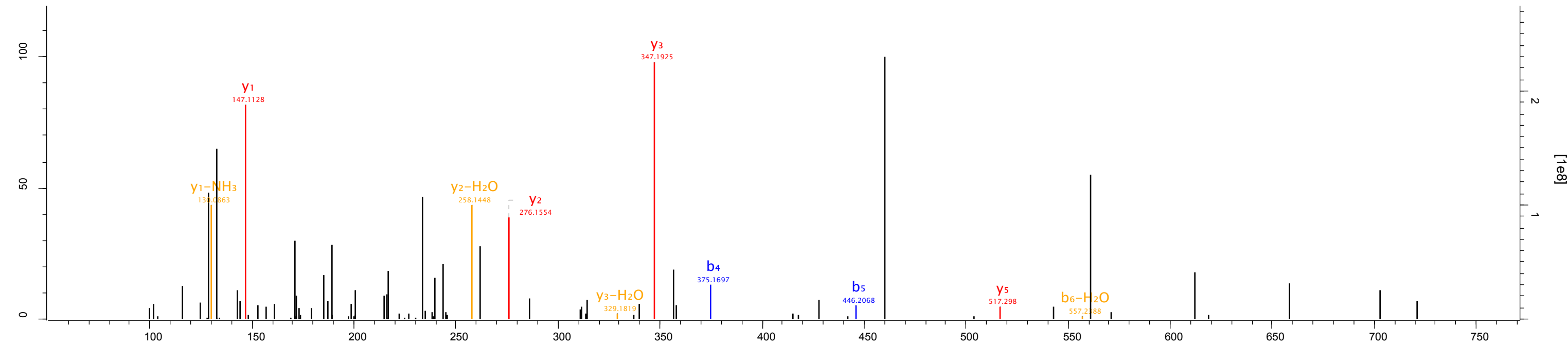
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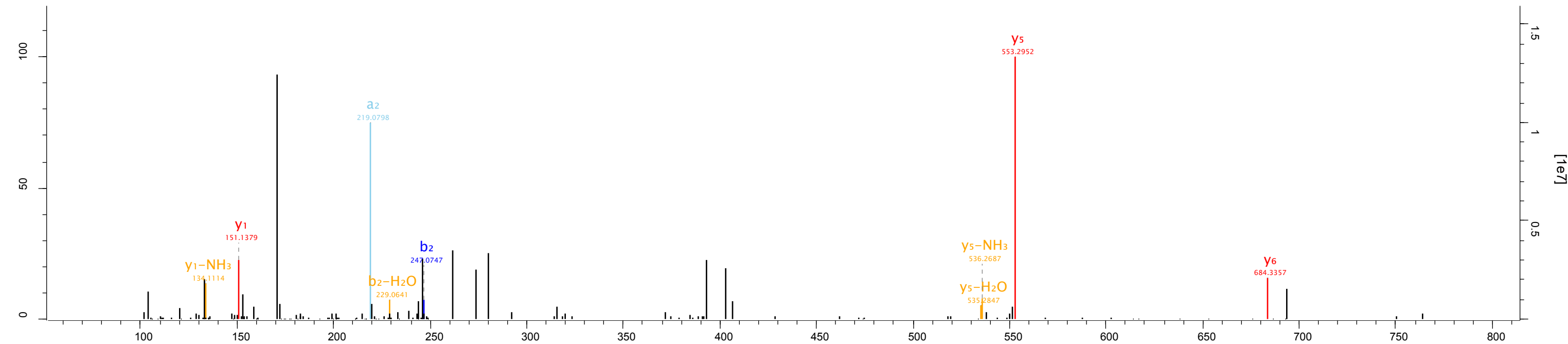
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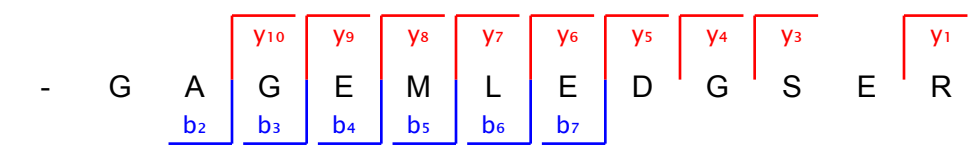
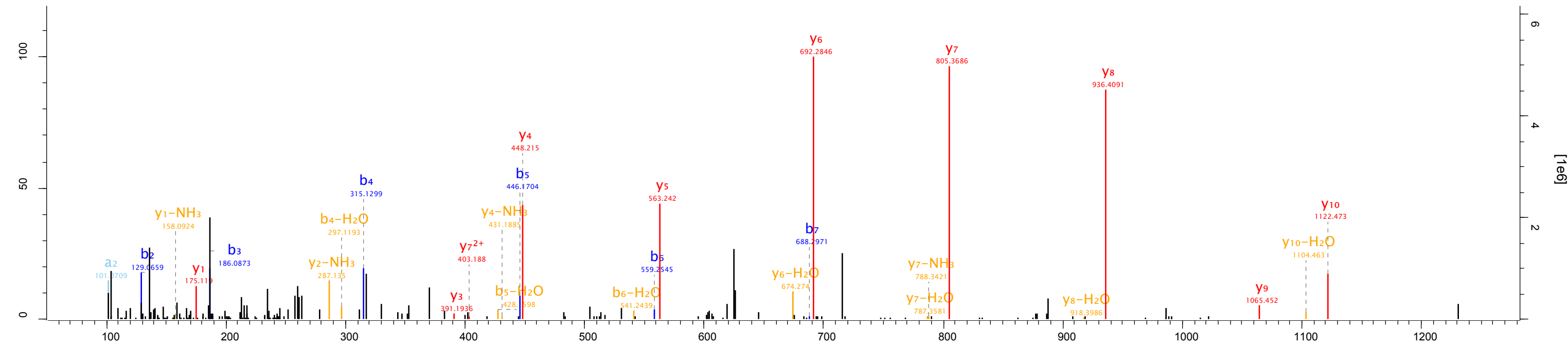
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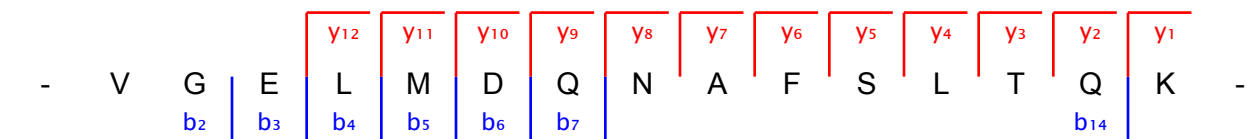
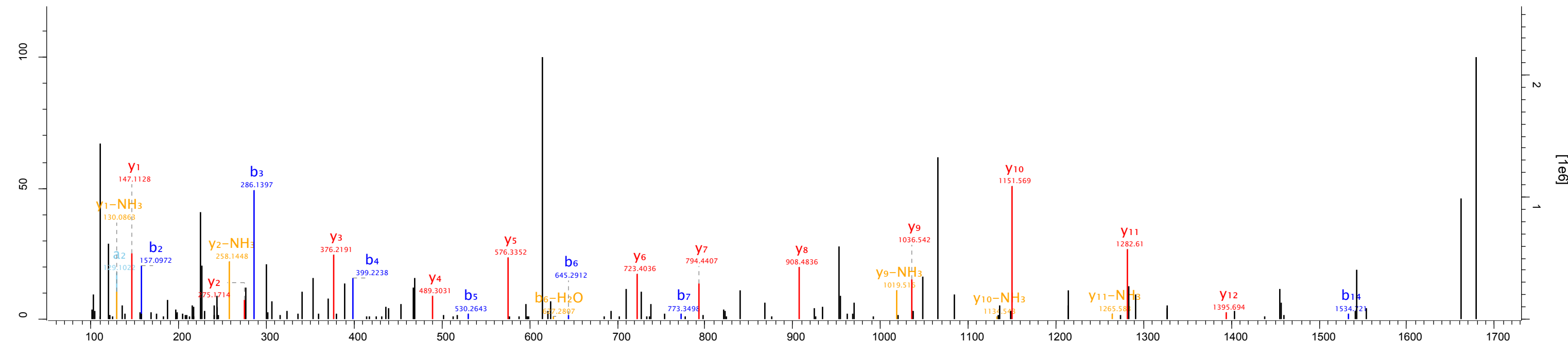


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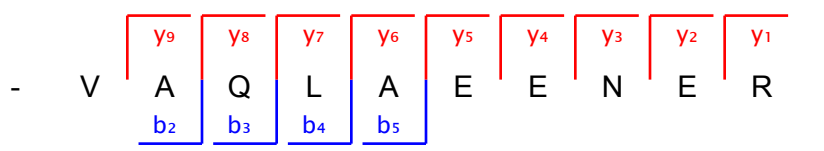
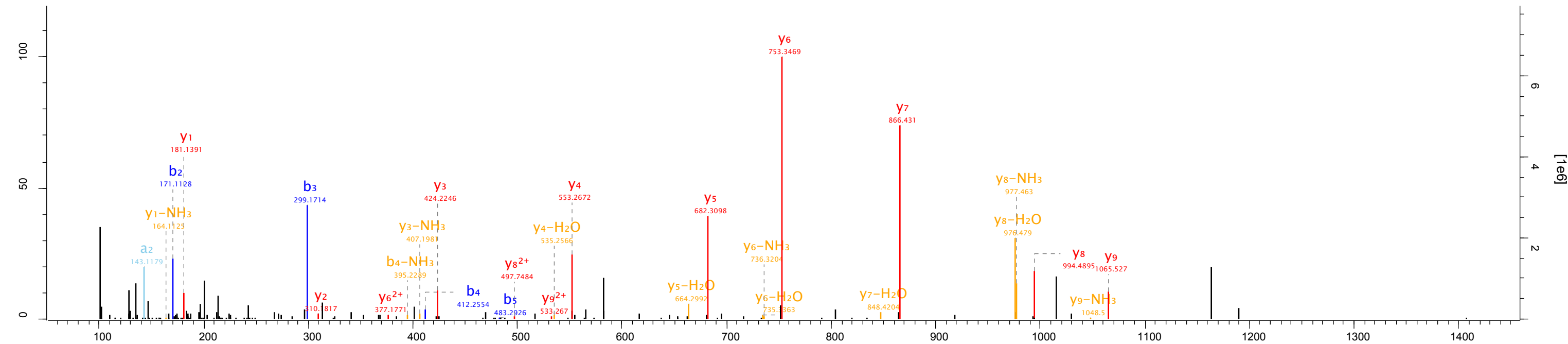
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 Scan: 12871 Method: FTMS; HCD Score: 99.59 m/z: 625.77 Gene names: ANAPC16



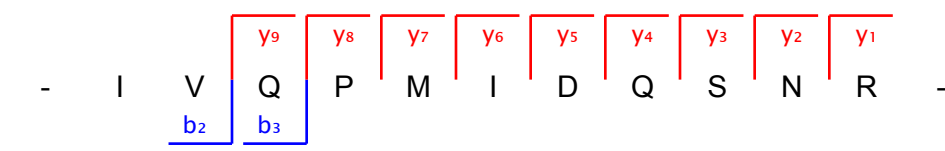
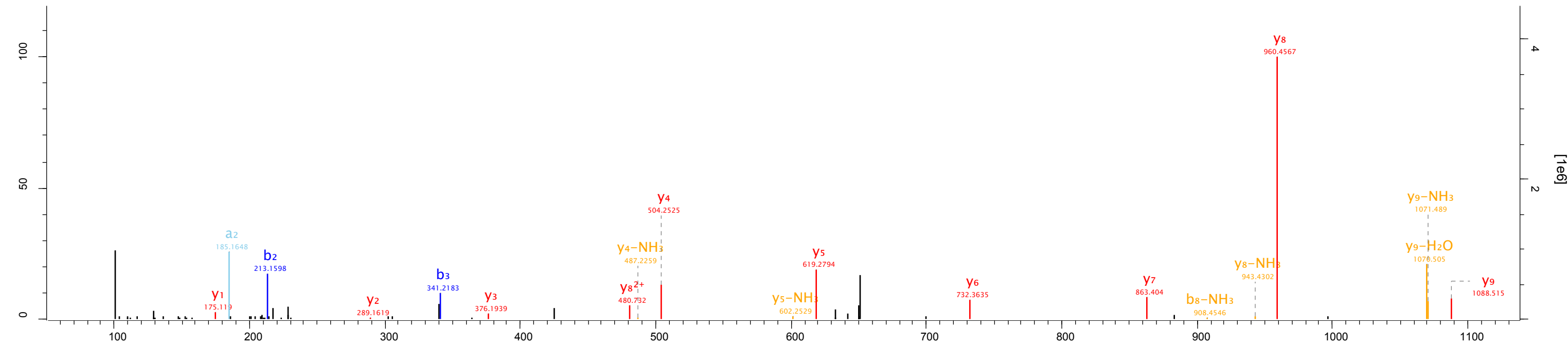


Raw file
20180707_MaS_A375SR_ML_proteome_2_12

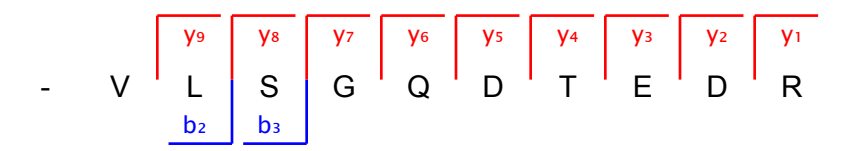
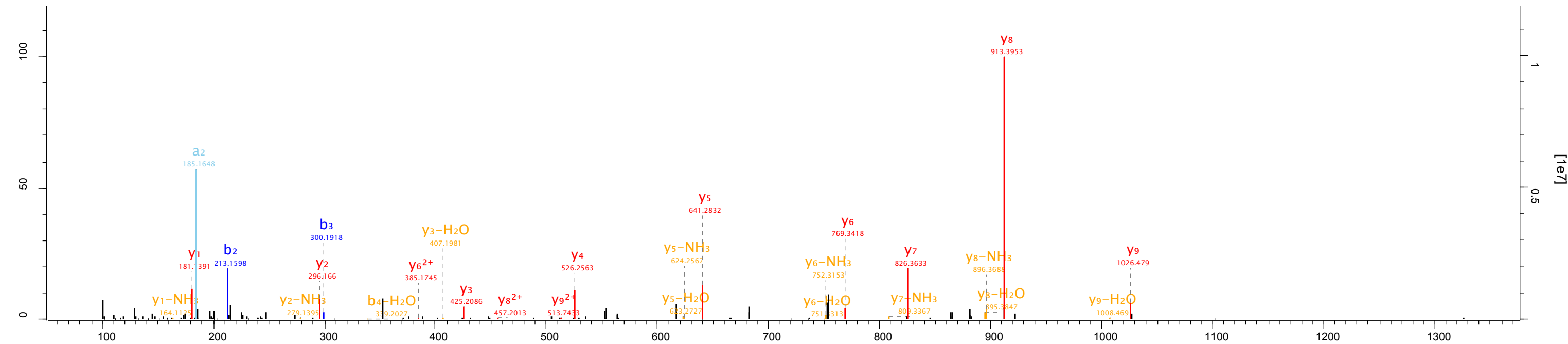
Scan: 9201
Method: FTMS; HCD
Score: 154.84
m/z: 582.8
Gene names: DDIT3



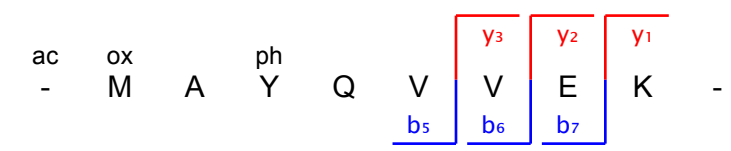
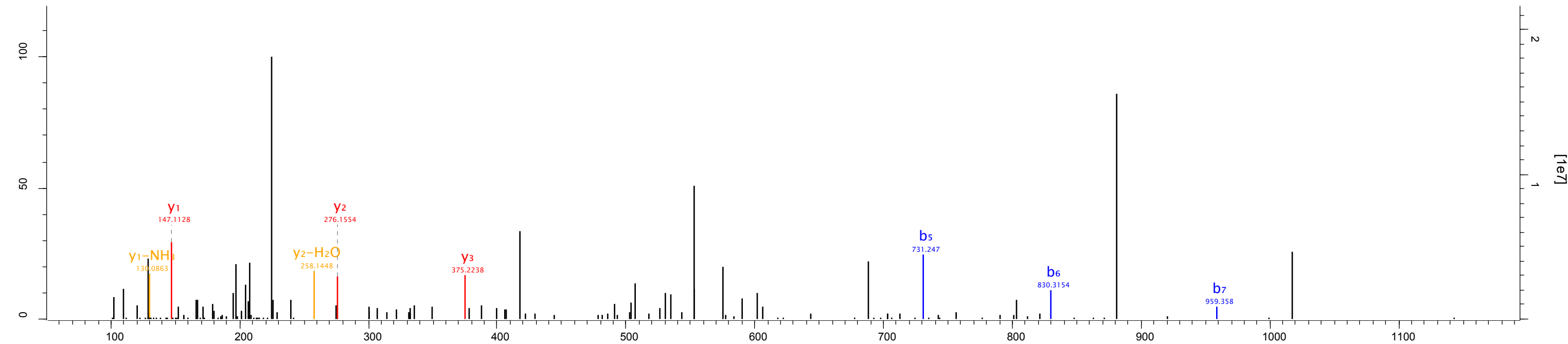
Raw file: 20180707_MaS_A375SR_ML_proteome_2_13
 Scan: 13411 Method: FTMS; HCD Score: 103.08 m/z: 650.84 Gene names: MEIS2;MEIS3;MEIS1;MEIS3P1



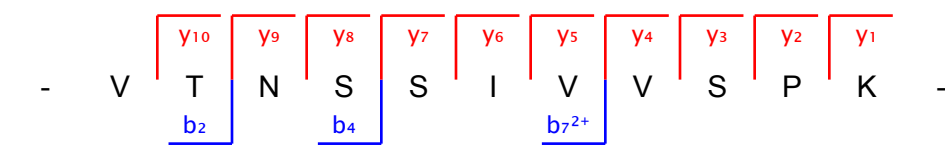
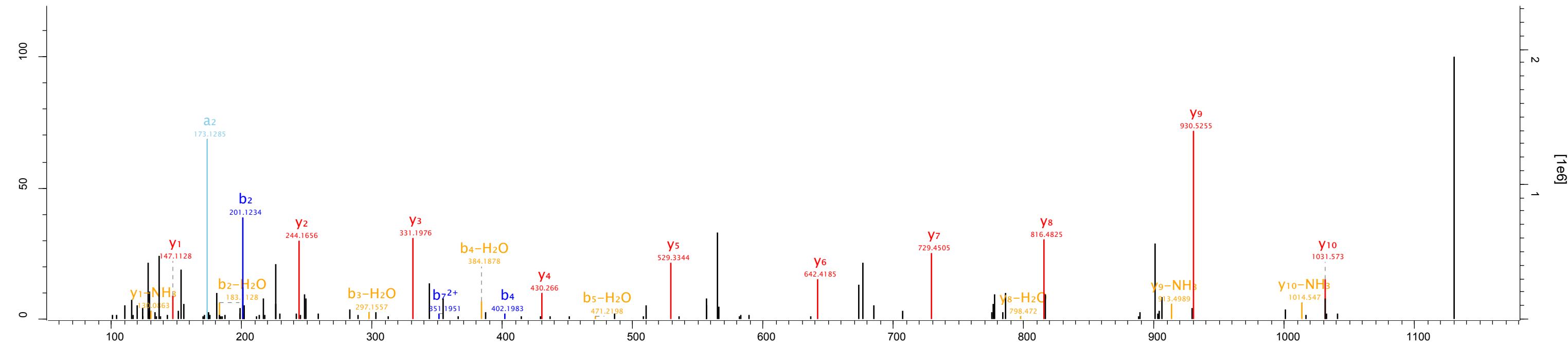
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 Scan: 4911 Method: FTMS; HCD Score: 116.13 m/z: 563.28 Gene names: SFT2D2



Raw file
 20180707_MaS_A375SR_ML_proteome_2_13
 Scan 7921 Method FTMS; HCD Score 50.04 m/z 553.24

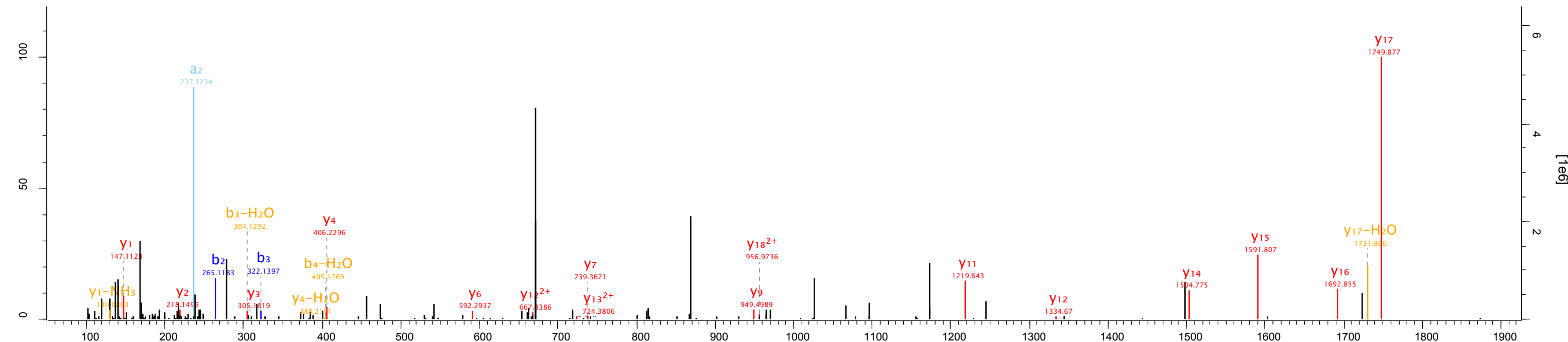


Raw file 20180707_MaS_A375SR_ML_proteome_2_14 Scan 10191 Method FTMS; HCD Score 80.69 m/z 565.83 Gene names FBXO6



Raw file
20180707_MaS_A375SR_ML_proteome_2_14

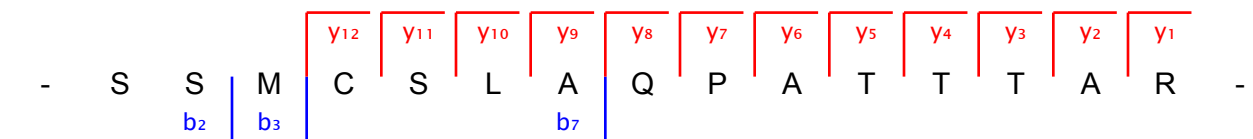
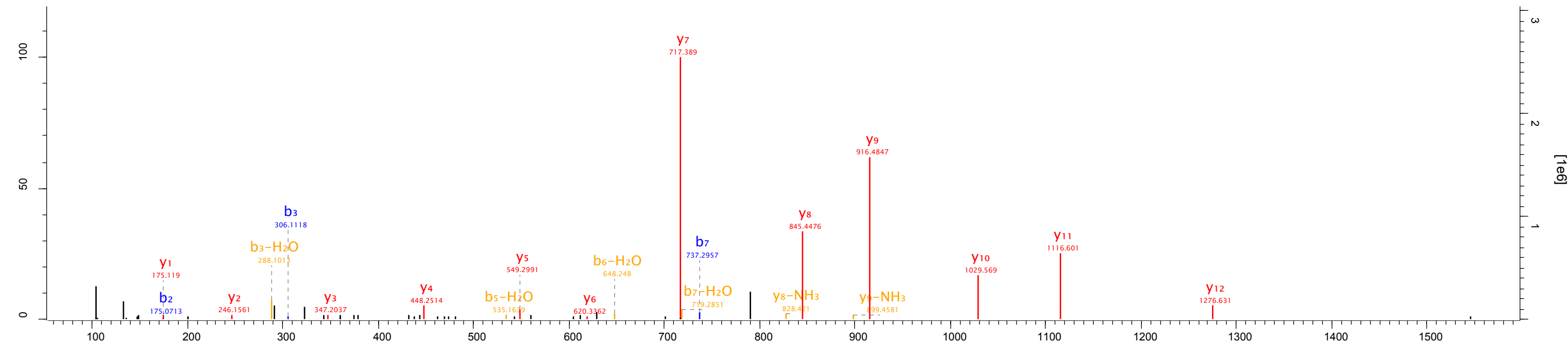
Scan 17711 Method FTMS; HCD Score 45.56 m/z 672 Gene names TMEM243



- T Y G T S G L D N R P L F G E T S A K -
b2 b3

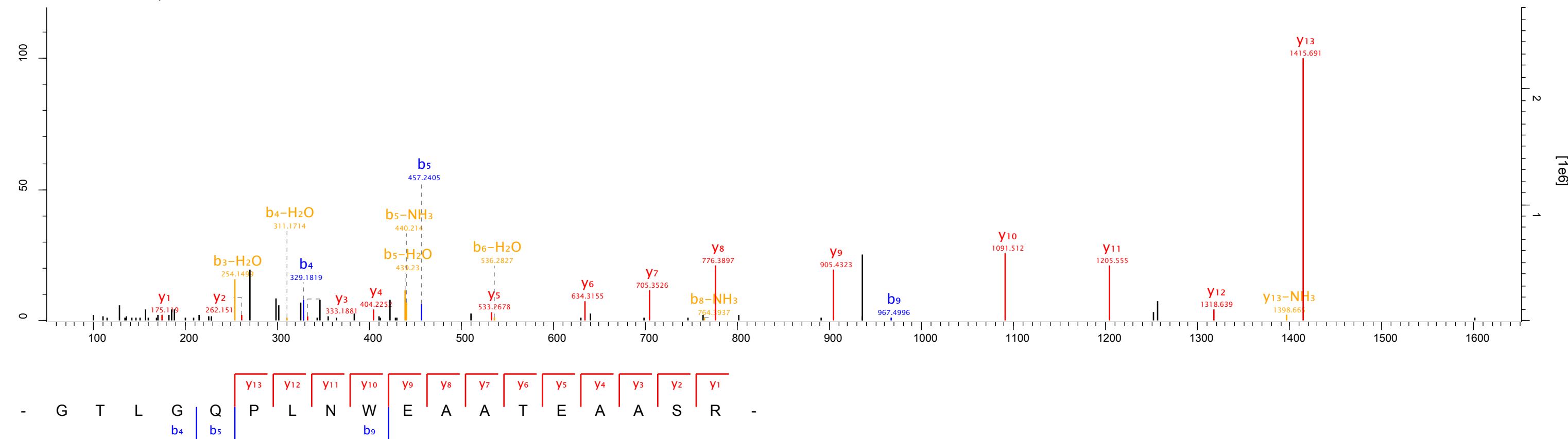
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20180707_MaS_A375SR_ML_proteome_2_15

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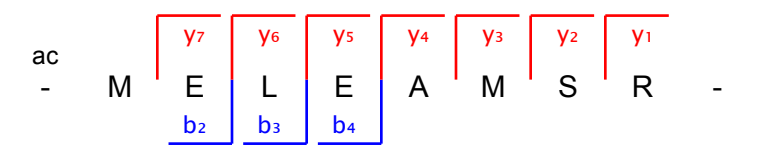
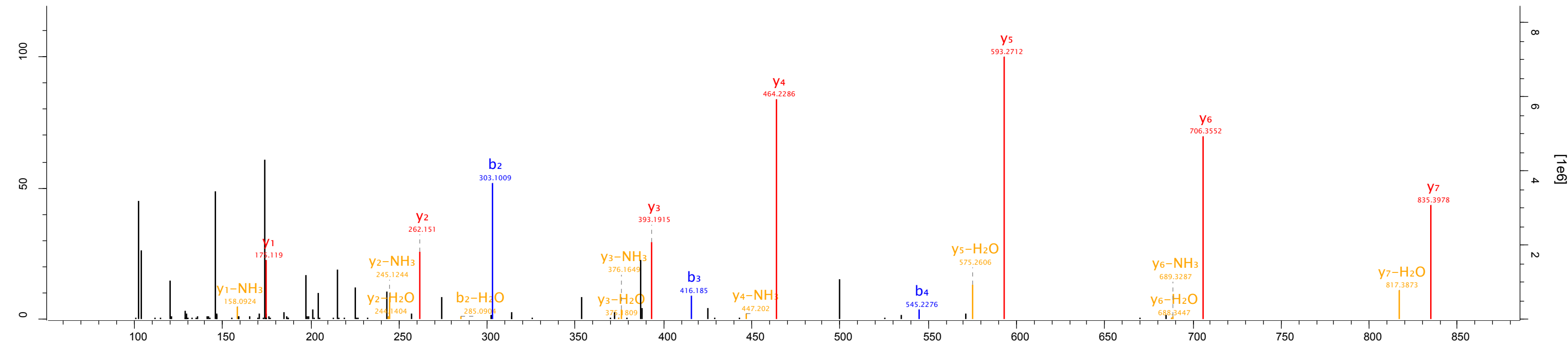


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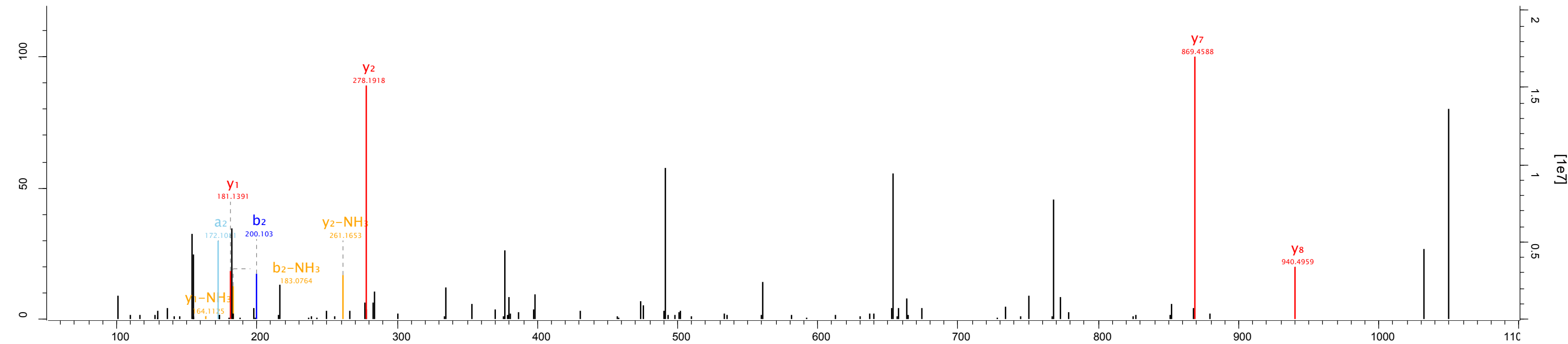
Scan 25391 Method FTMS; HCD Score 56.72 m/z 936.46 Gene names SIRT7



Raw file: 20180707_MaS_A375SR_ML_proteome_2_16
 Scan: 25681 Method: FTMS; HCD Score: 109.48 m/z: 504.73 Gene names: TMEM258

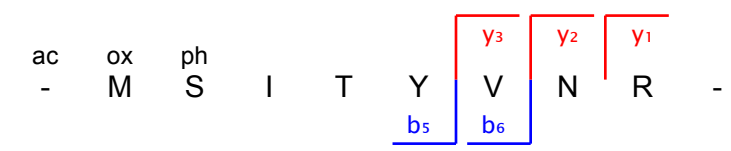
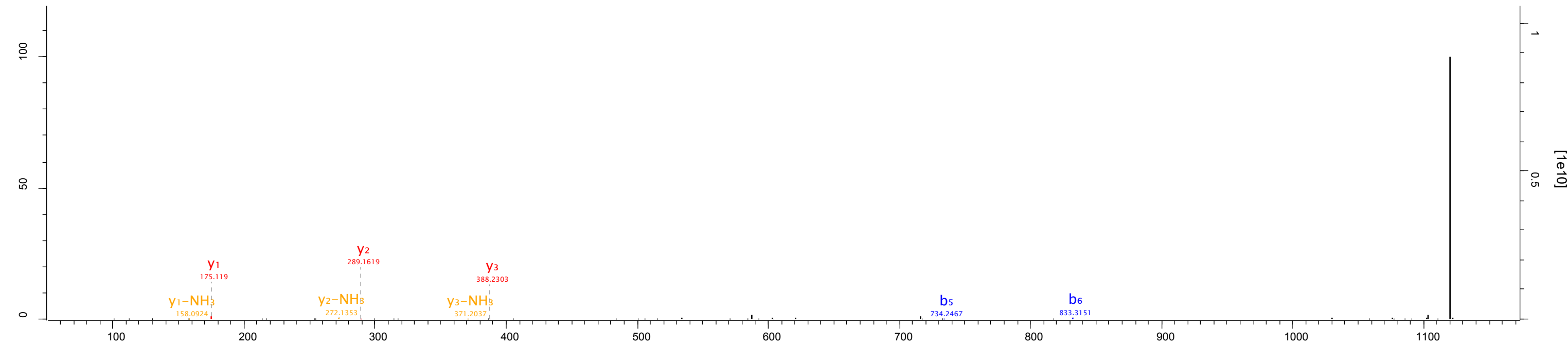


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 Scan: 7711 Method: FTMS; HCD Score: 47.87 m/z: 534.78 Gene names: HOOK2



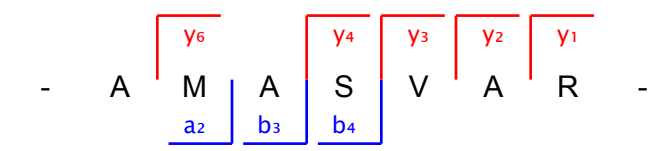
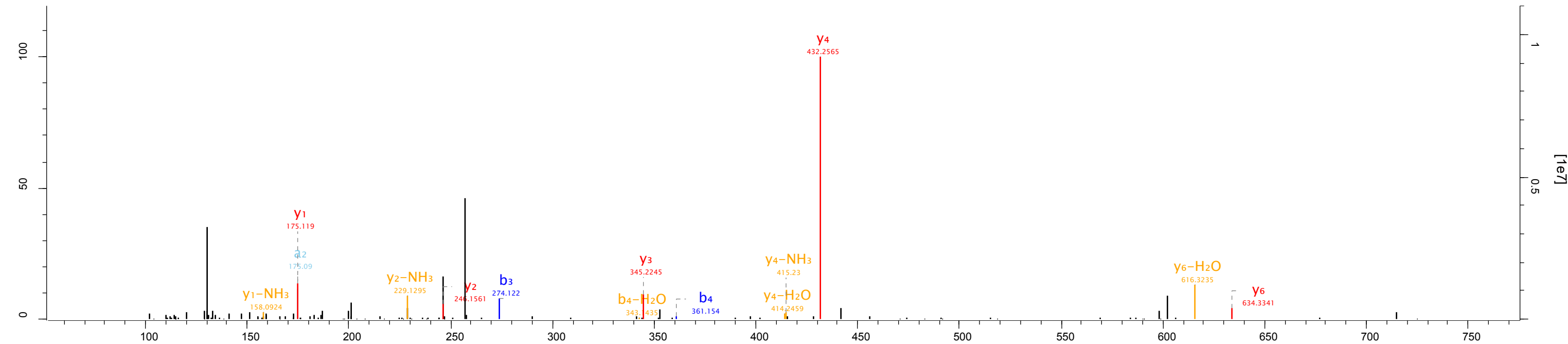
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20180707_MaS_A375SR_ML_proteome_2_17

Scan 15531 Method FTMS; HCD Score 77.75 m/z 1121.47

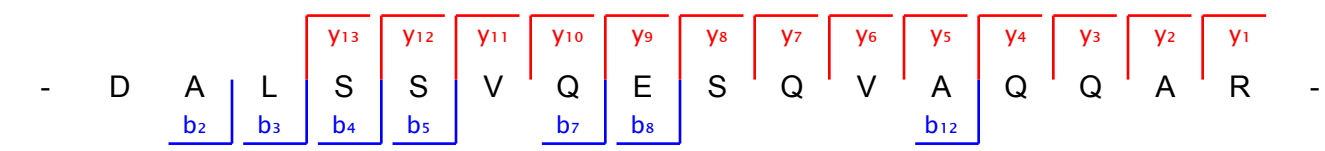
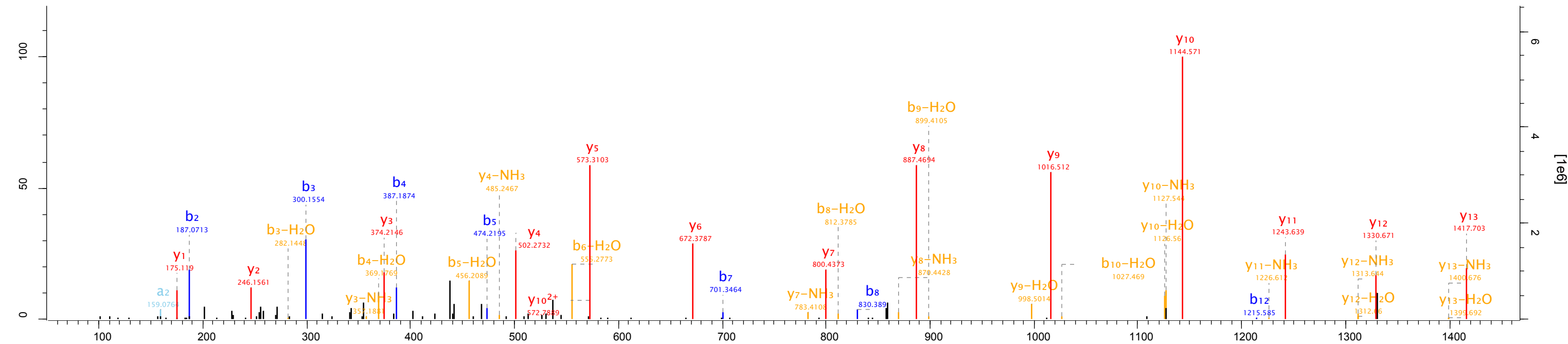


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20180707_MaS_A375SR_ML_proteome_2_17

Scan	Method	Score	m/z	Gene names
8301	FTMS; HCD	78.62	353.19	ART4

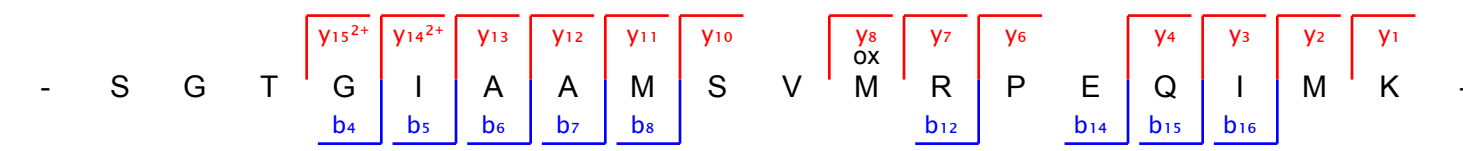
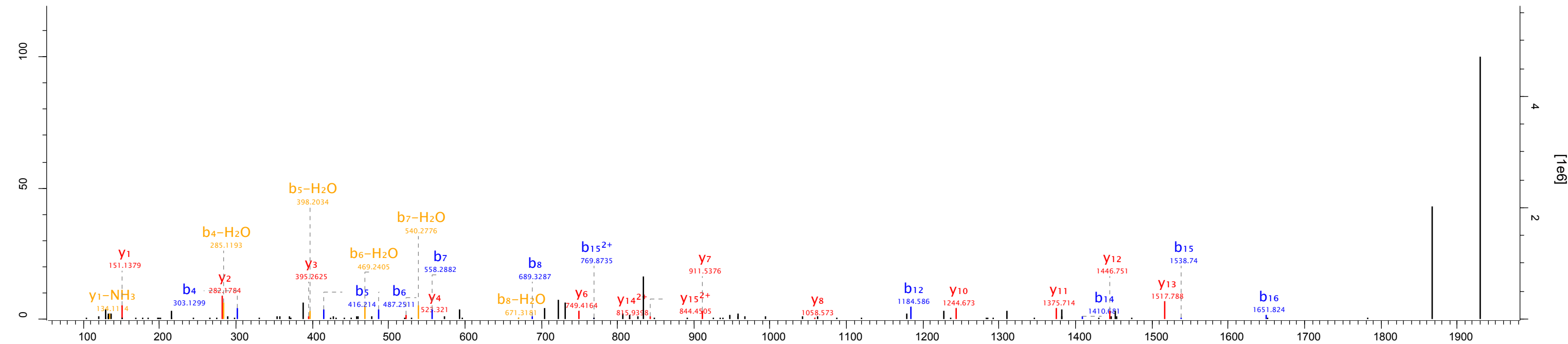


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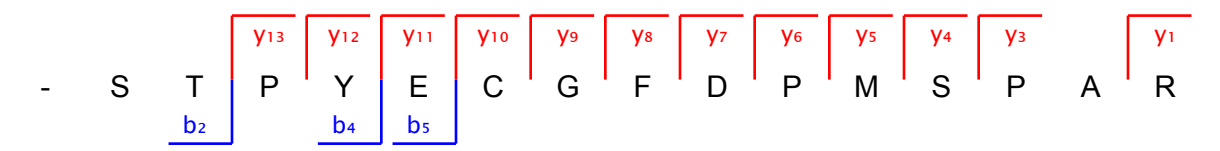
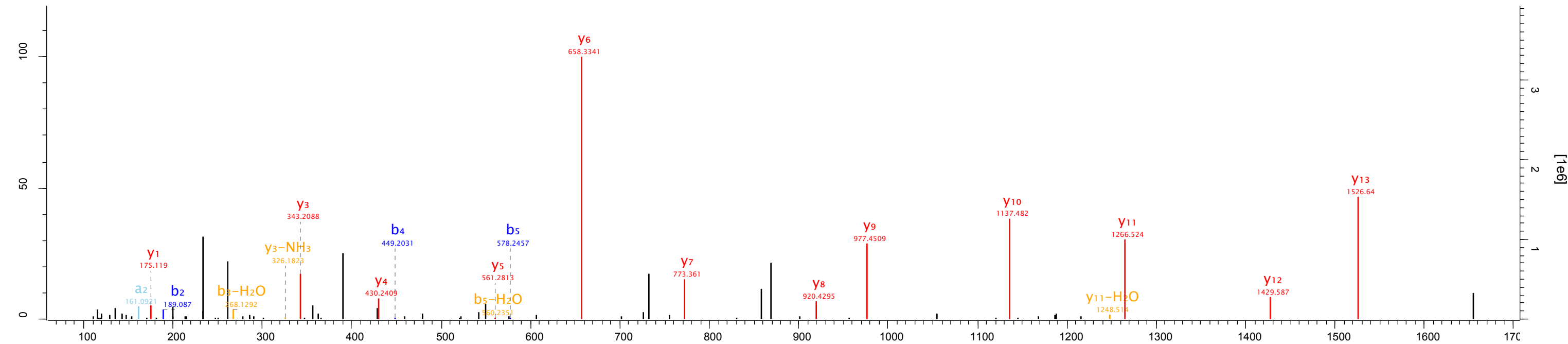


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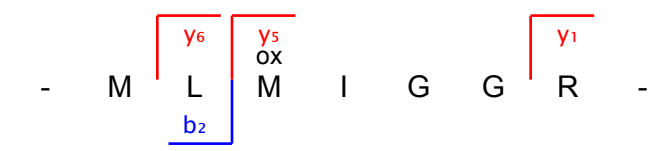
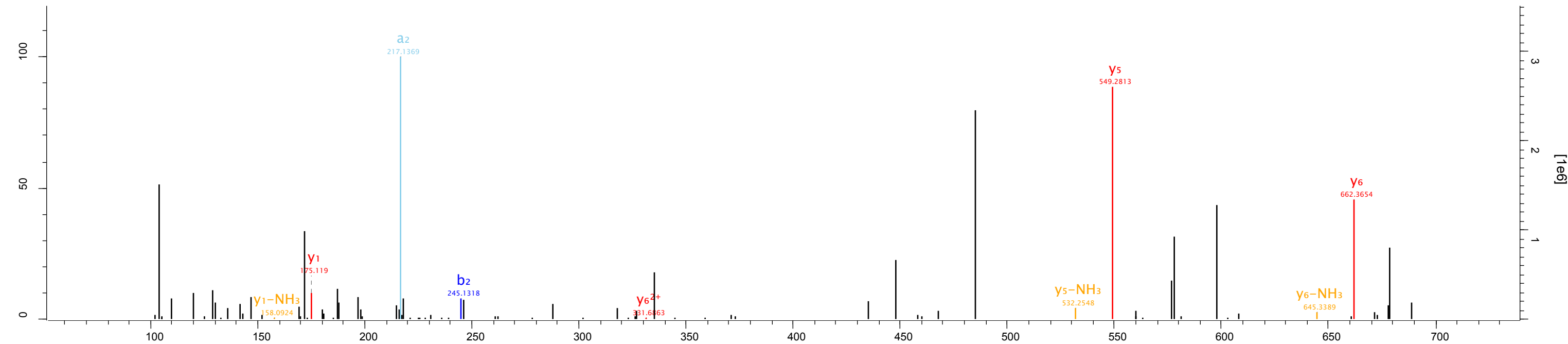
Scan 18581 Method FTMS; HCD Score 131.45 m/z 967 Gene names ATP6V0C



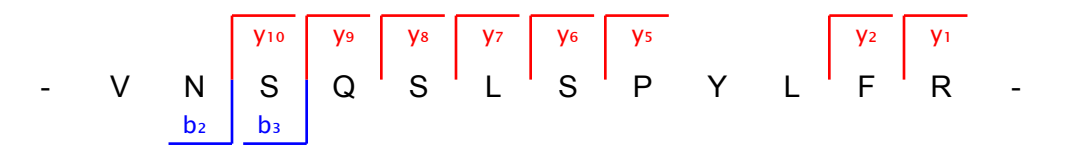
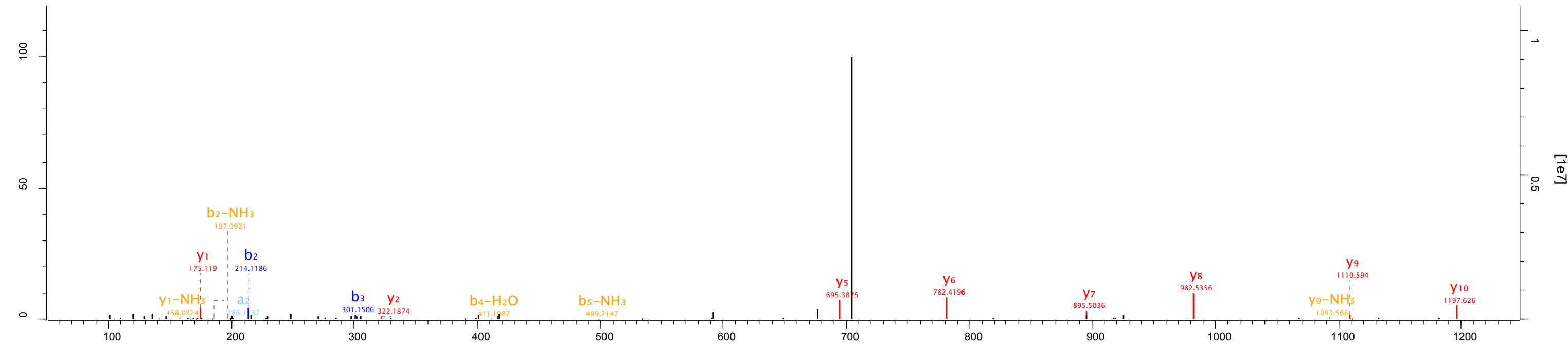
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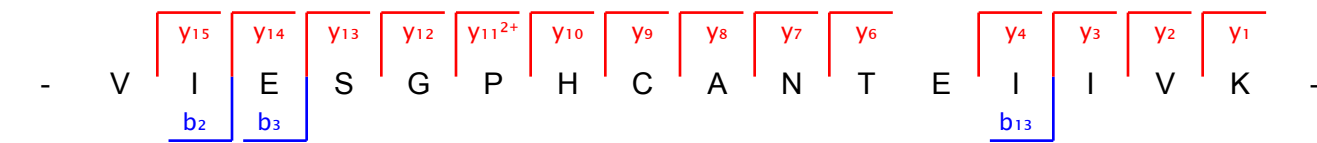
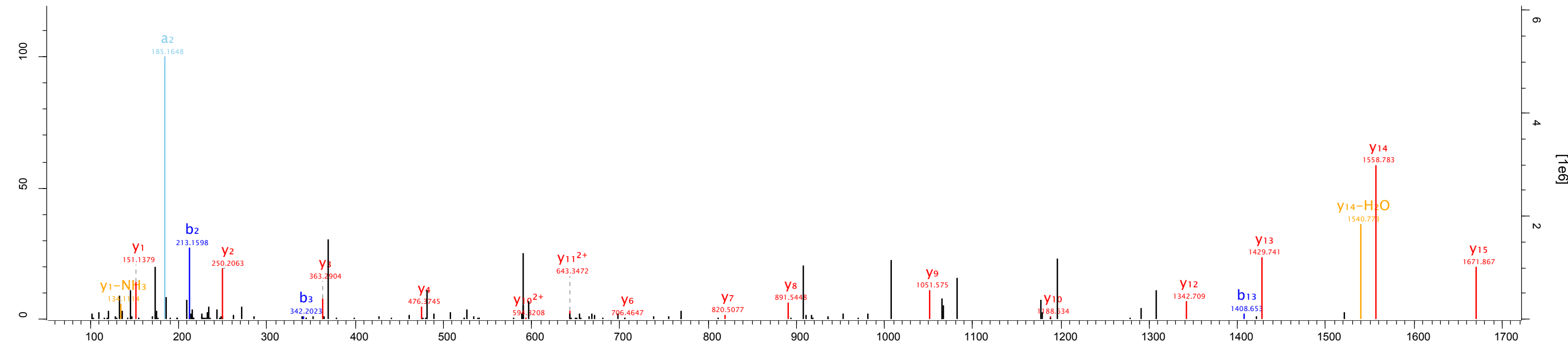


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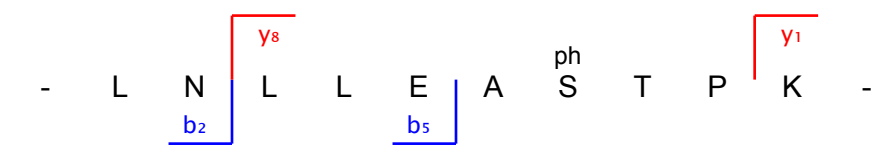
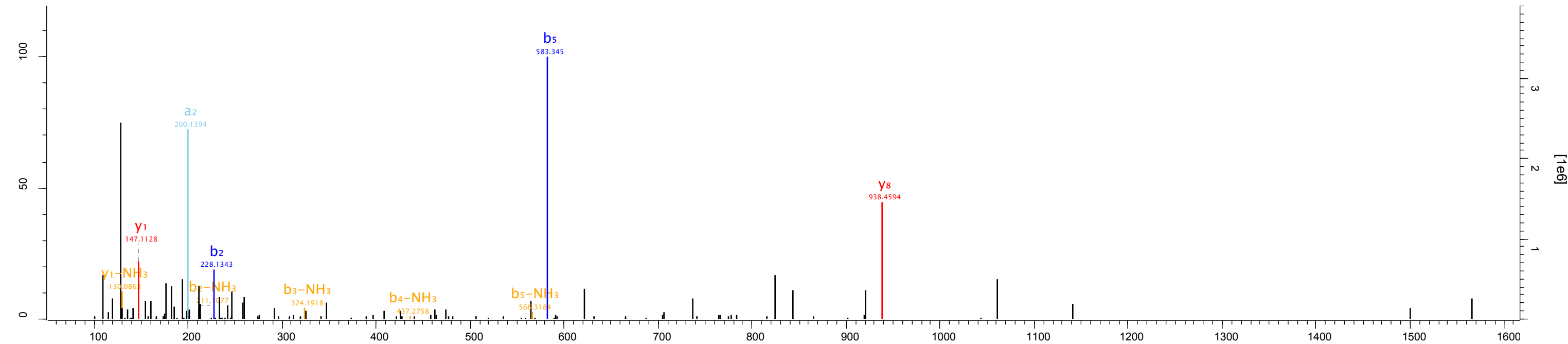


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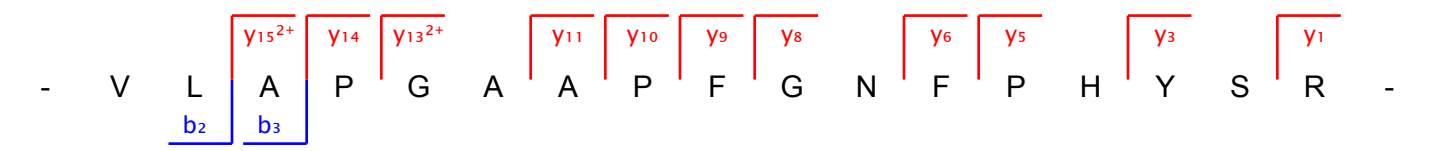
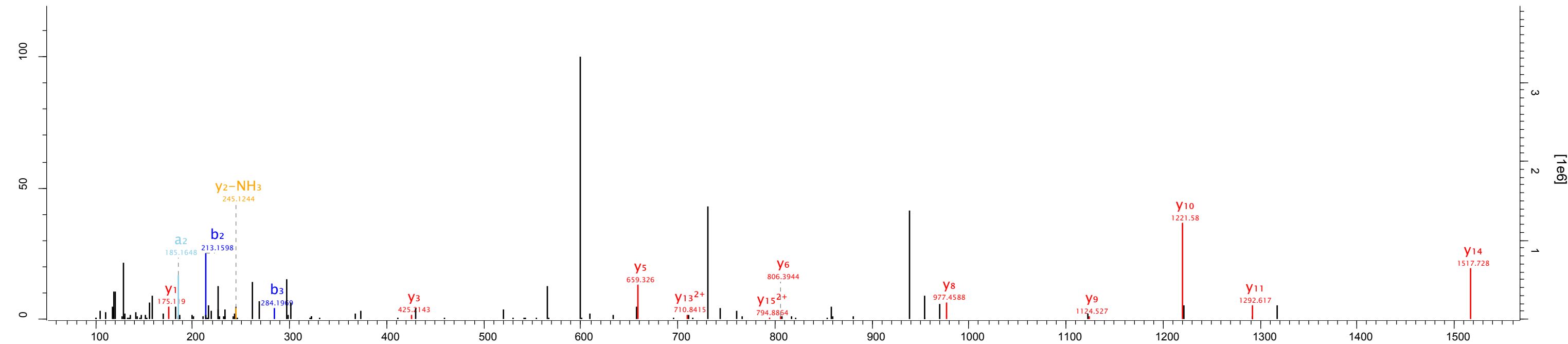
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Raw file

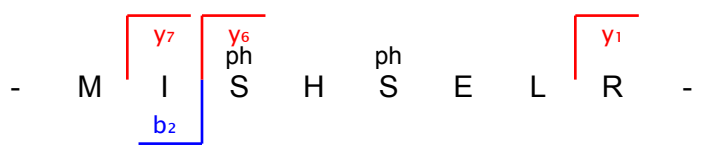
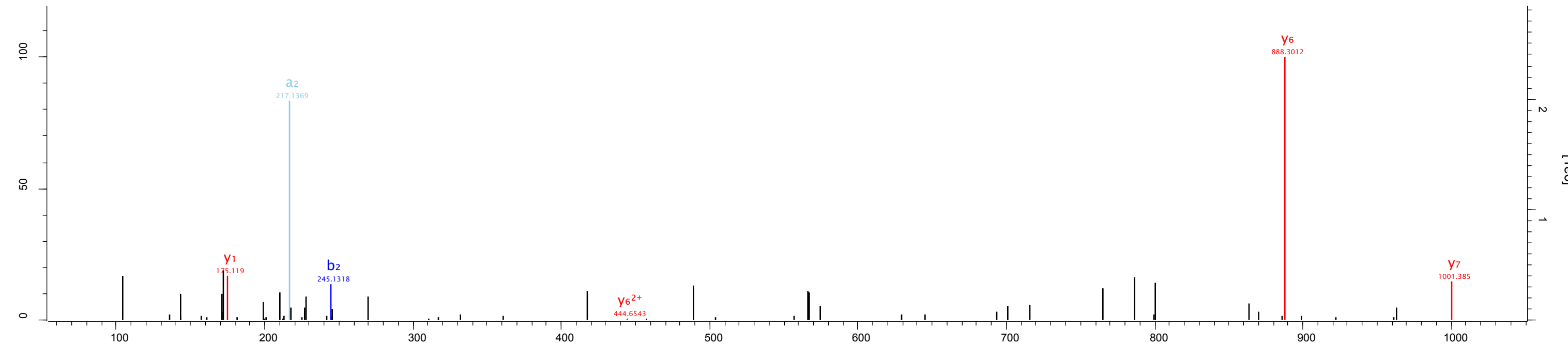
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Scan 23251 Method FTMS; HCD Score 32.86 m/z 601.05 Gene names BCDIN3D

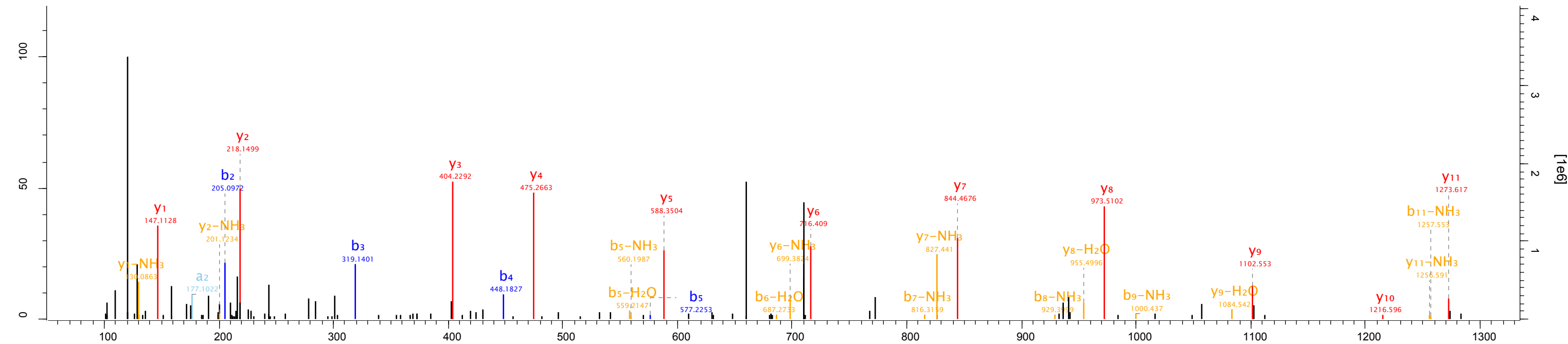


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20180707_MaS_A375SR_ML_proteome_2_23

Scan 9371 Method FTMS; HCD Score 46.43 m/z 566.72 Gene names PSPHP1



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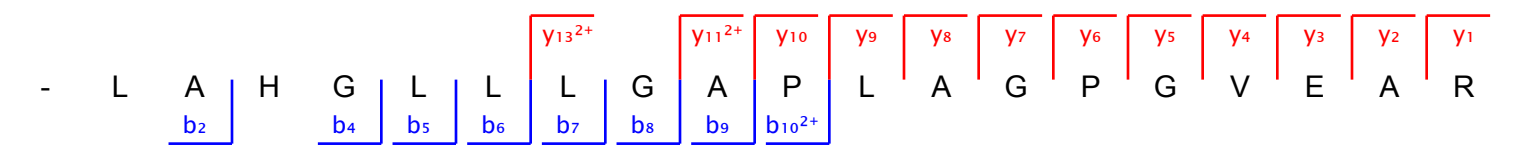
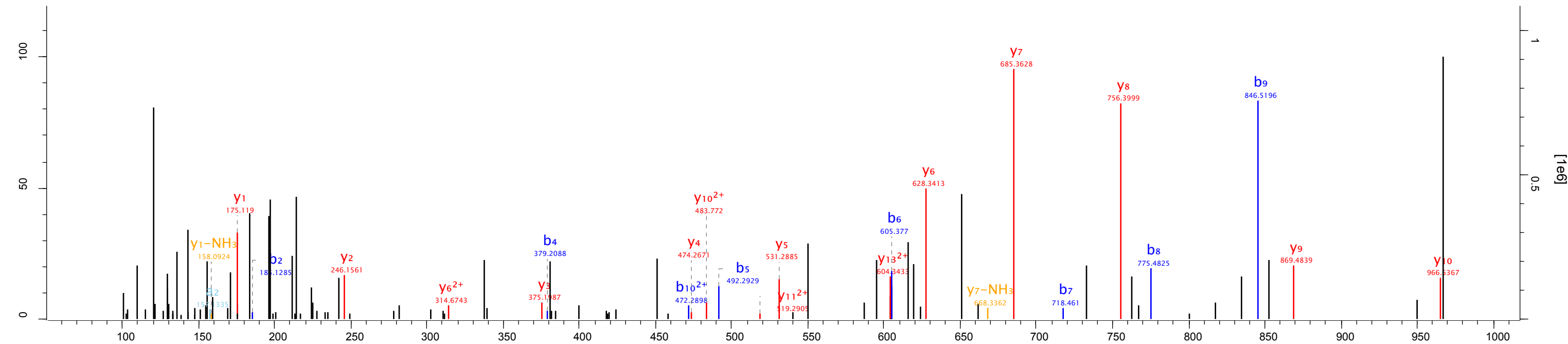
Peptide sequence: F G N E E Q Q L A W A K

Fragmentation sites (b and y ions):

- b₂ (G)
- b₃ (GN)
- b₄ (GNE)
- b₅ (GNEE)

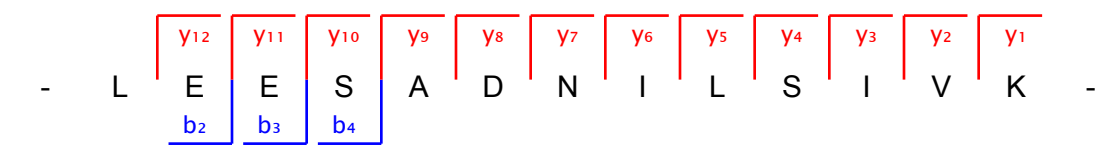
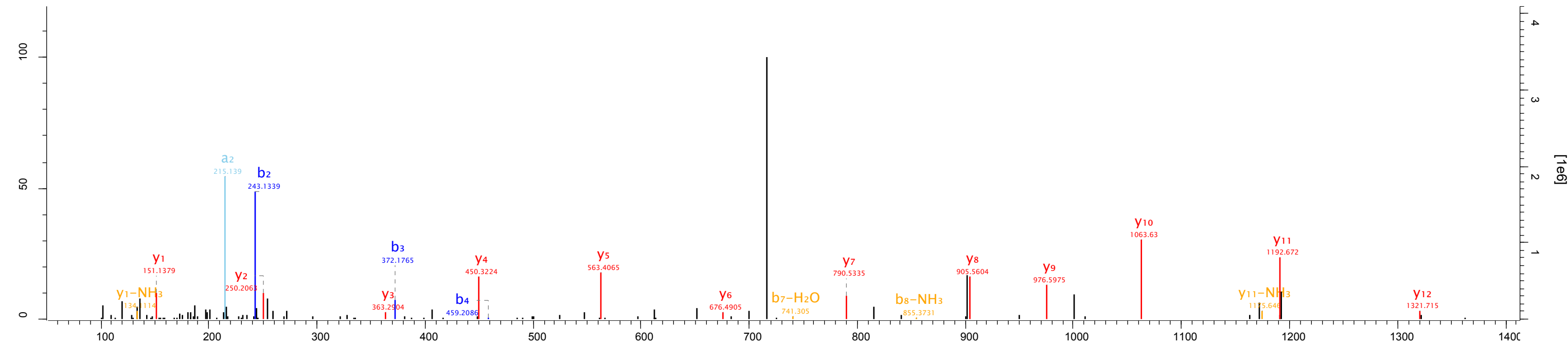
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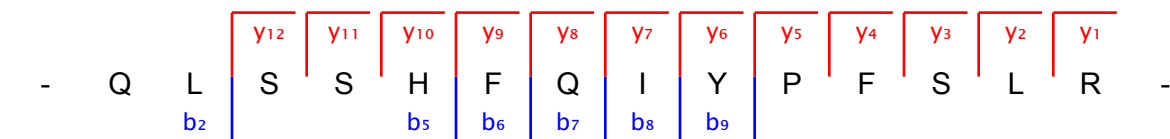
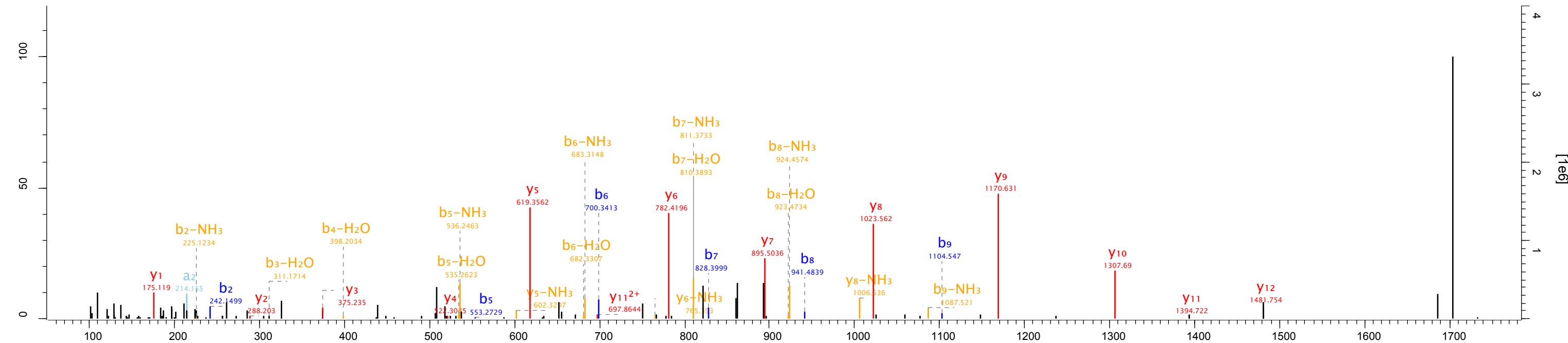
Scan Method Score m/z Gene names
24271 FTMS; HCD 60.54 604.83 ZFPM1



Raw file
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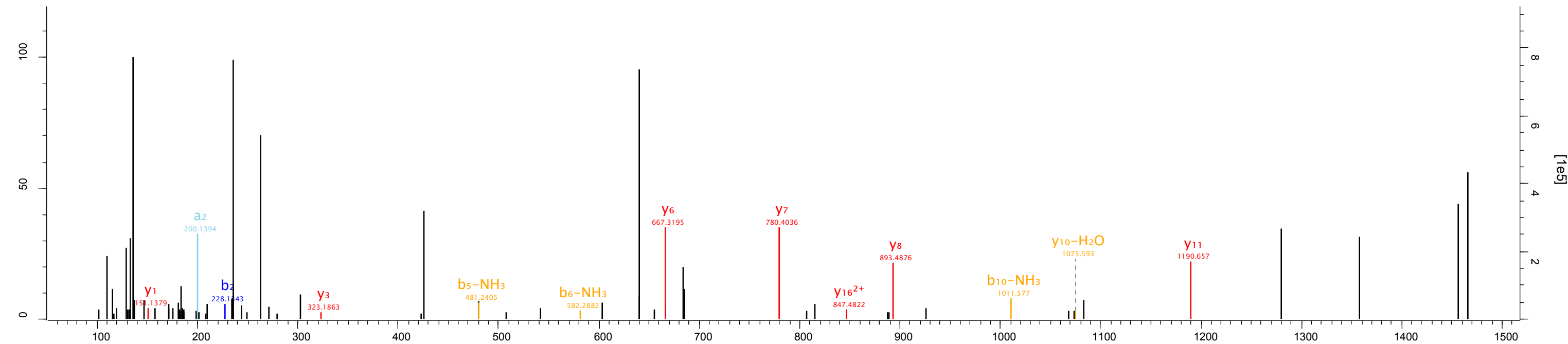
Scan 27551 Method FTMS; HCD Score 77.78 m/z 717.91 Gene names RFXAP





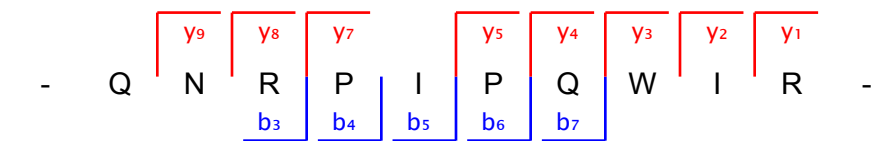
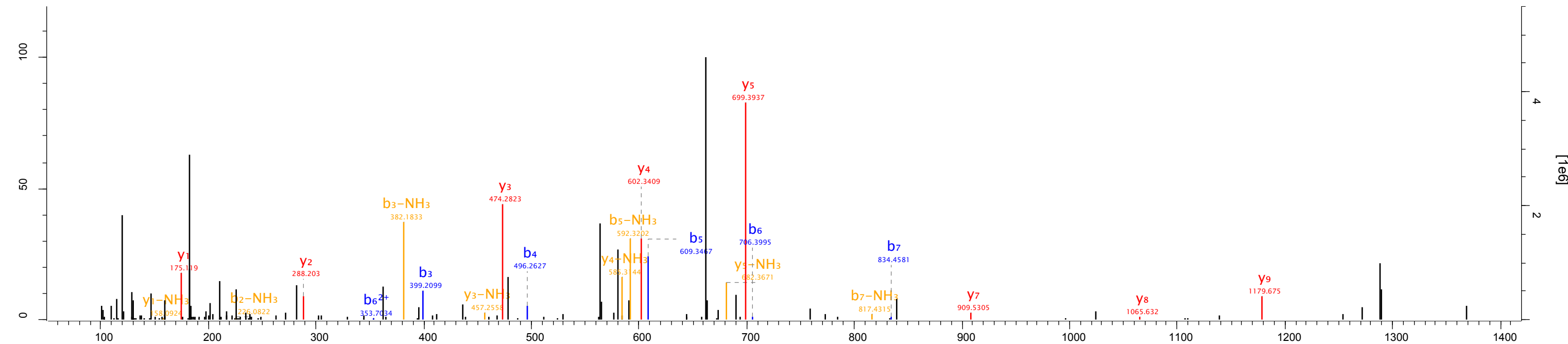
Raw file
20180707_MaS_A375SR_ML_proteome_2_26

Scan 13041 Method FTMS; HCD Score 12.13 m/z 641.03 Gene names FABP7

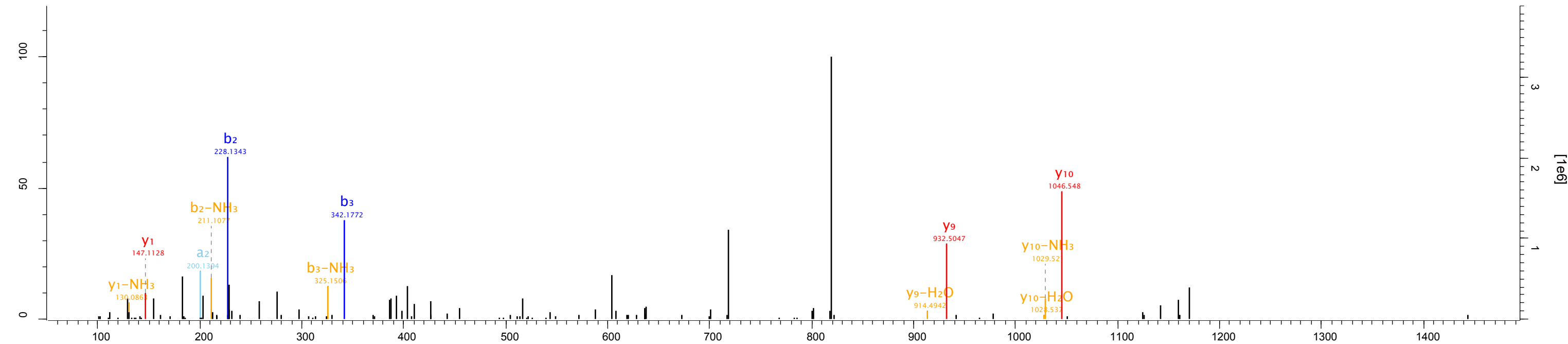


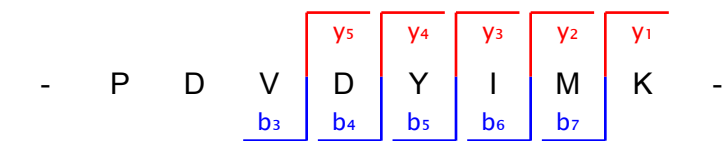
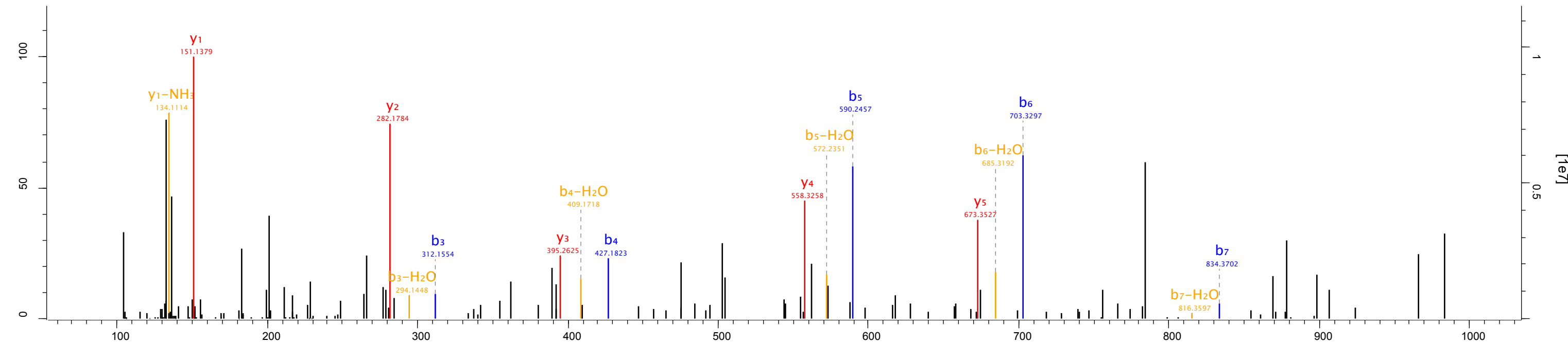
- Q V G N V T K P T V I I S Q E G D K -

Fragmentation labels: b₂ (under V), y₁₆²⁺ (over G), y₁₁ (over P), y₈ (over I), y₇ (over I), y₆ (over S), y₃ (over G), y₁ (over K).

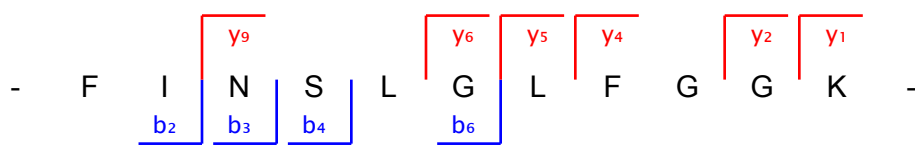
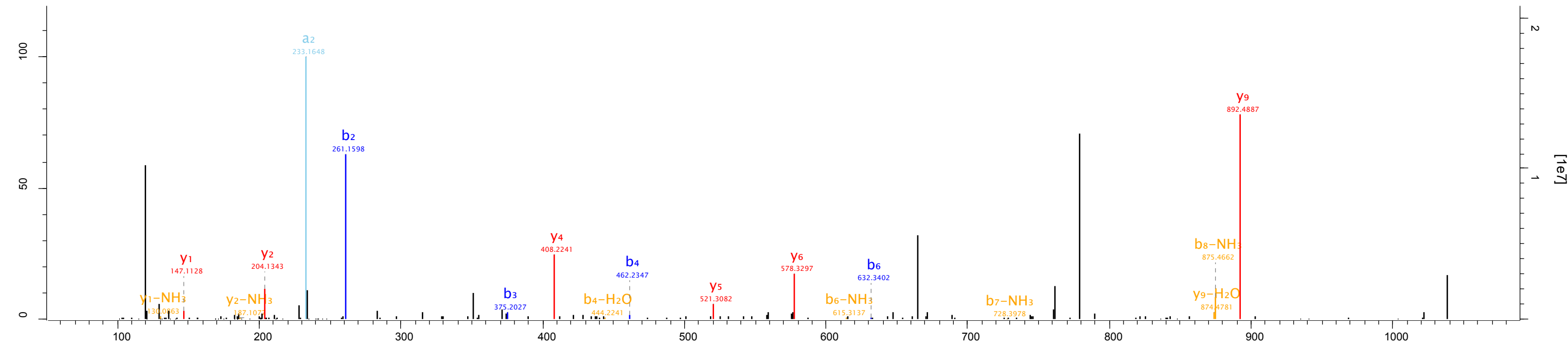


Raw file 20180707_MaS_A375SR_ML_proteome_2_27 Scan 12751 Method FTMS; HCD Score 54.78 m/z 637.34

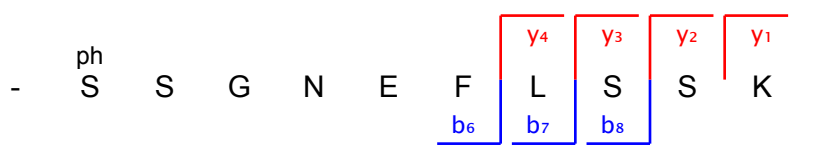
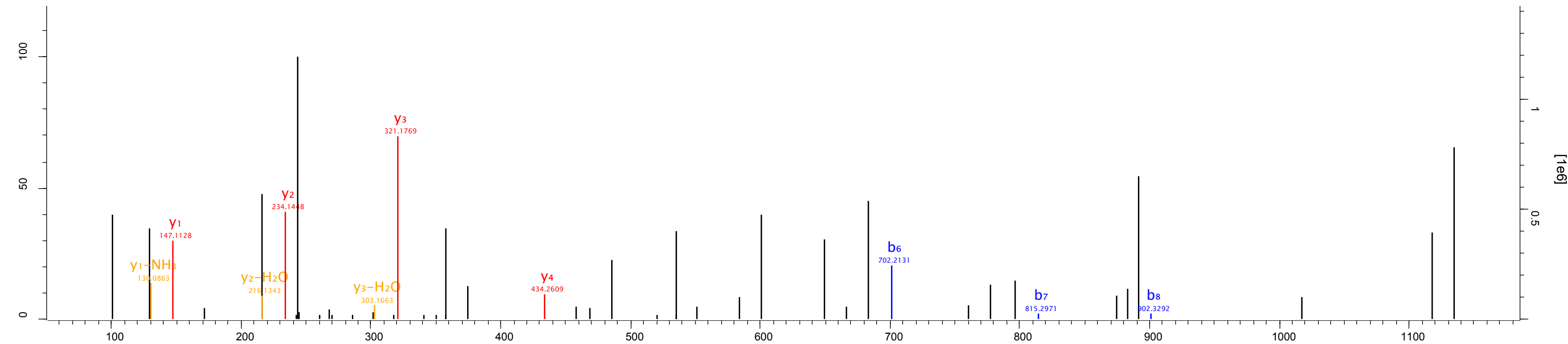


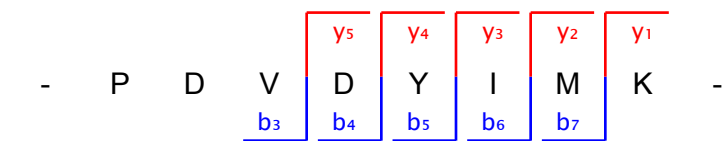
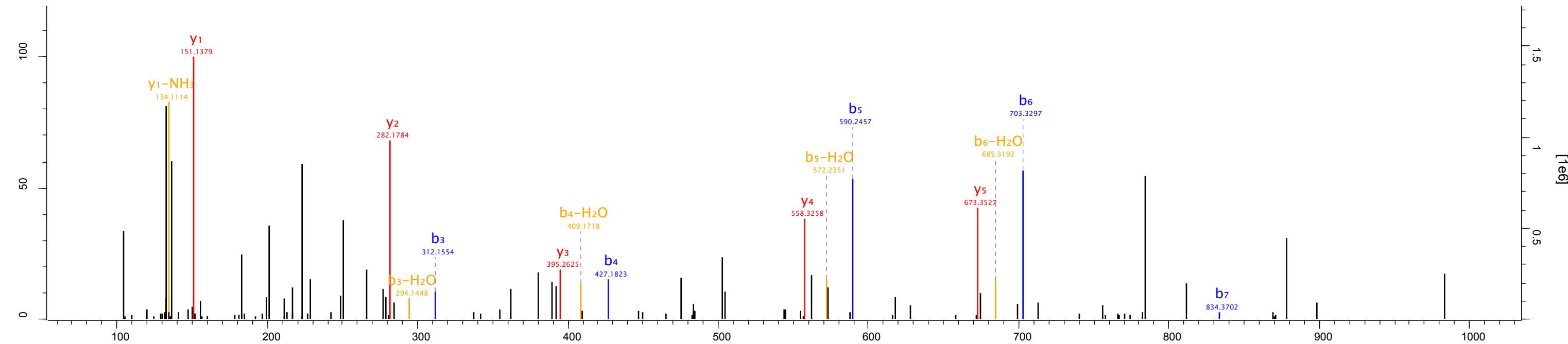


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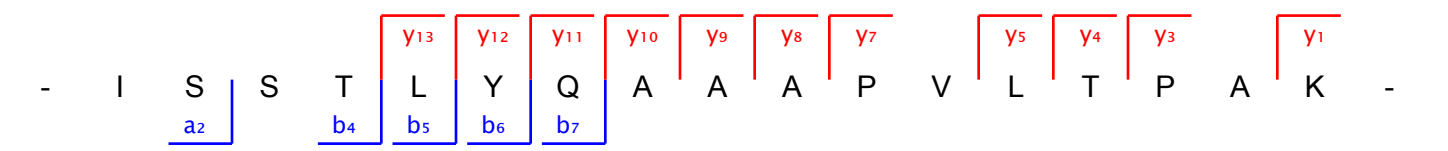
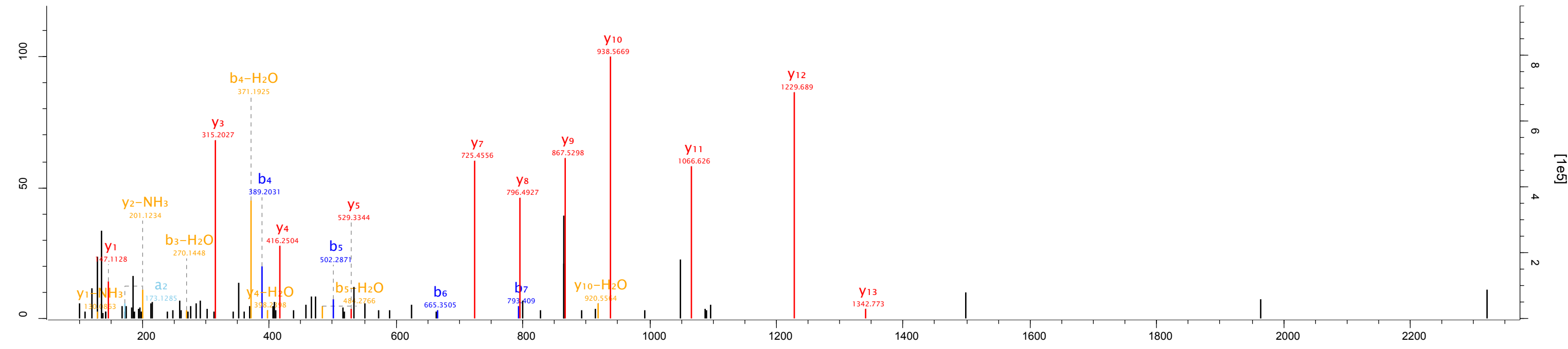


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 Scan: 3041 Method: FTMS; HCD Score: 75.39 m/z: 568.24 Gene names: MAP3K19

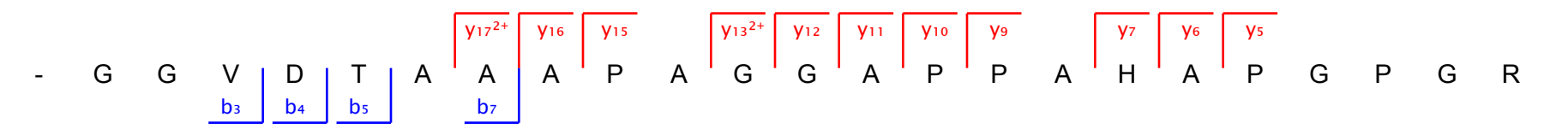
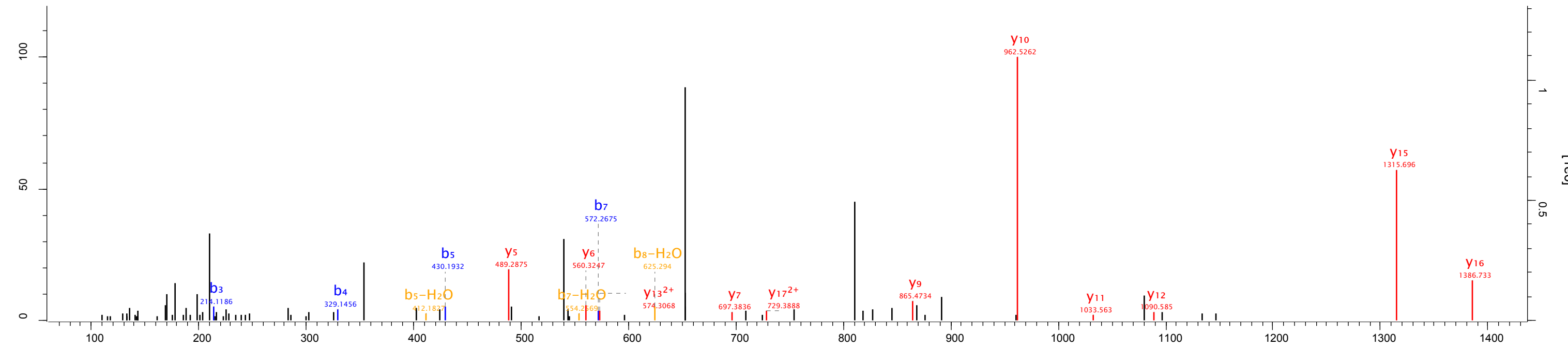




Raw file: 20180707_MaS_A375SR_ML_proteome_2_29
 Scan: 23641 Method: FTMS; HCD Score: 62.2 m/z: 865.99 Gene names: KRTCAP2

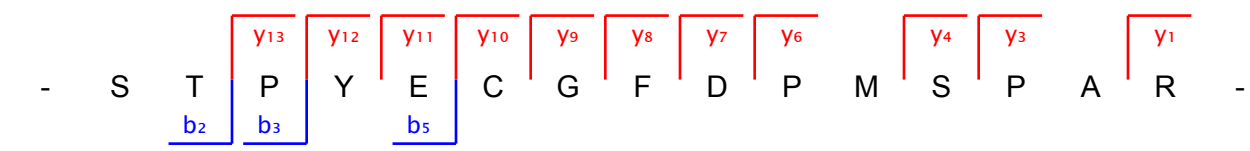
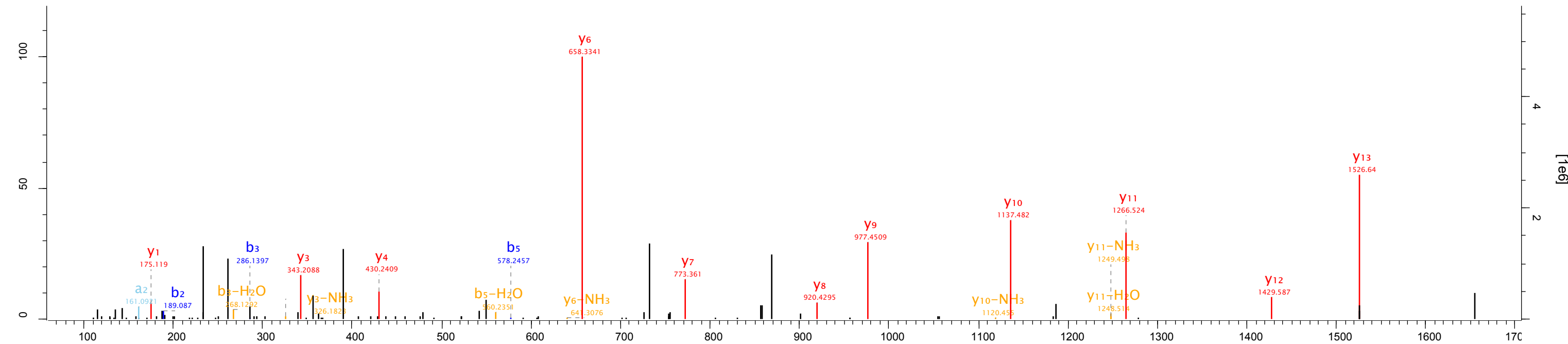


20180707_MaS_A375SR_ML_proteome_20 9001 FTMS; HCD 33.13 653.34 LAGE3

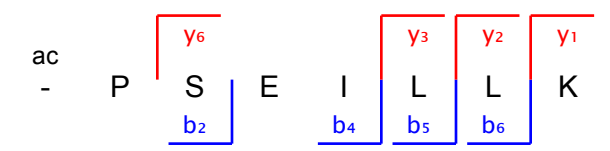
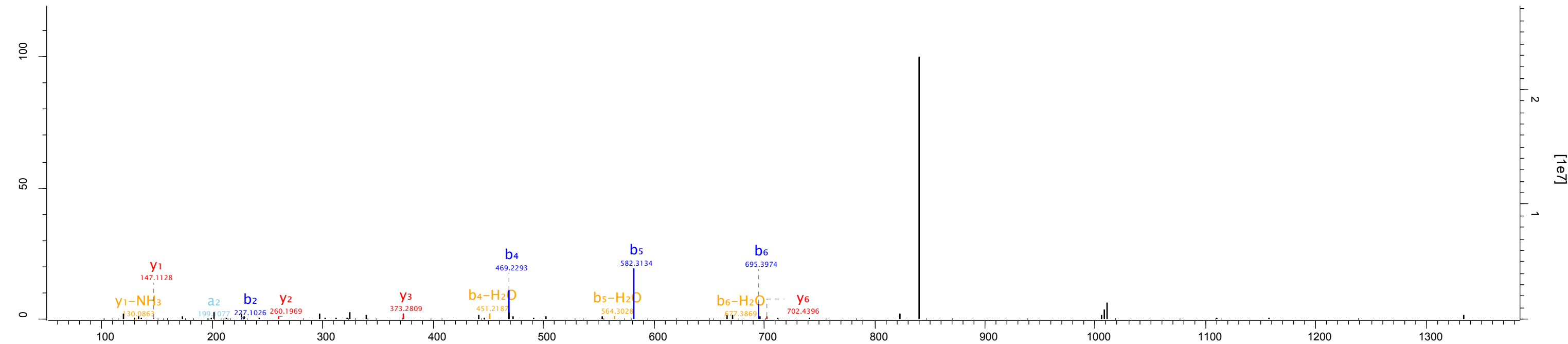


Raw file
20180707_MaS_A375SR_ML_proteome_22

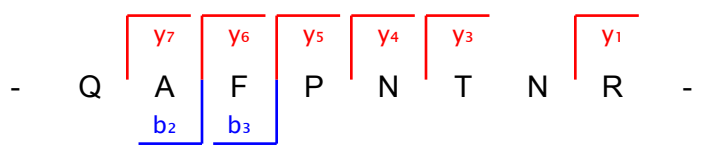
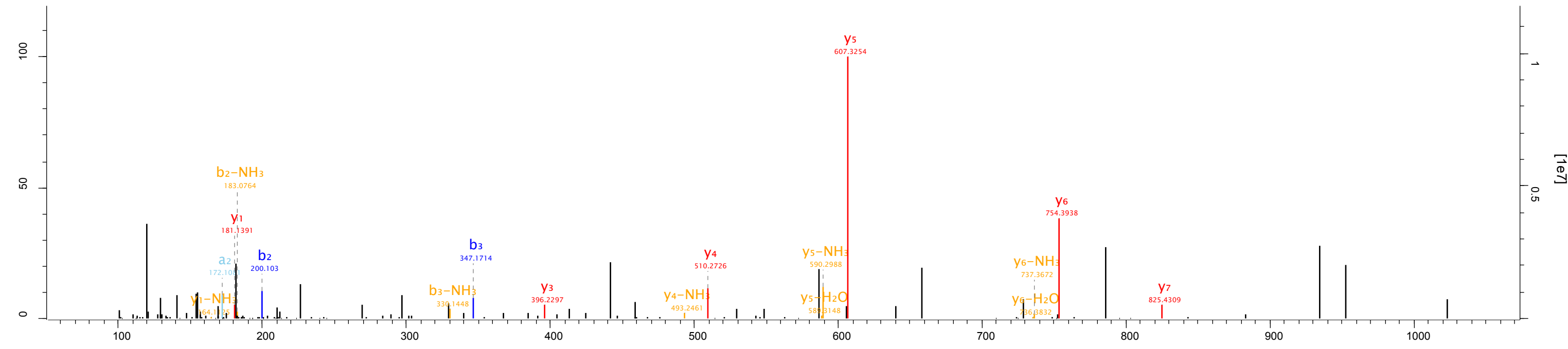
Scan 19251 Method FTMS; HCD Score 88.56 m/z 857.87 Gene names MT-ND3



Raw file 20180707_MaS_A375SR_ML_proteome_22 Scan 25351 Method FTMS; HCD Score 76.85 m/z 841.5

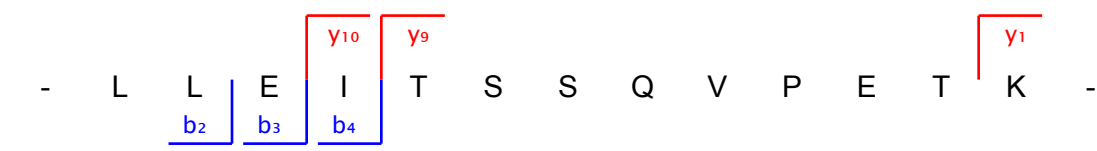
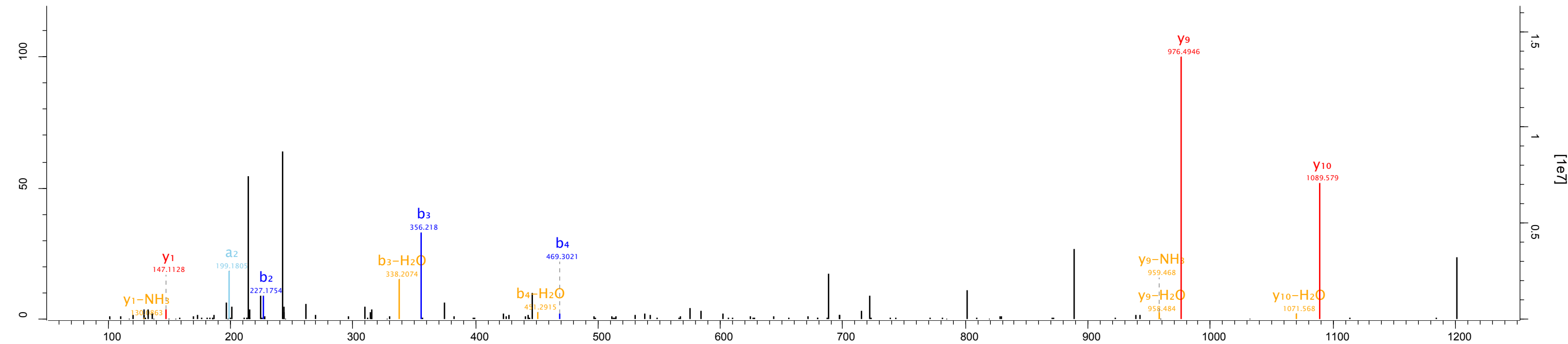


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 Scan: 6221 Method: FTMS; HCD Score: 78.19 m/z: 477.25 Gene names: EEF1G

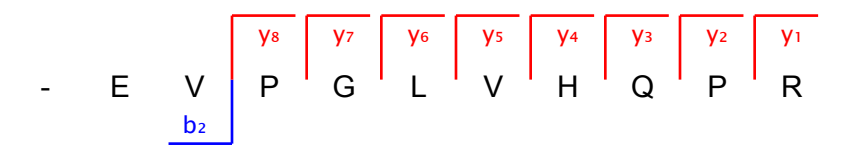
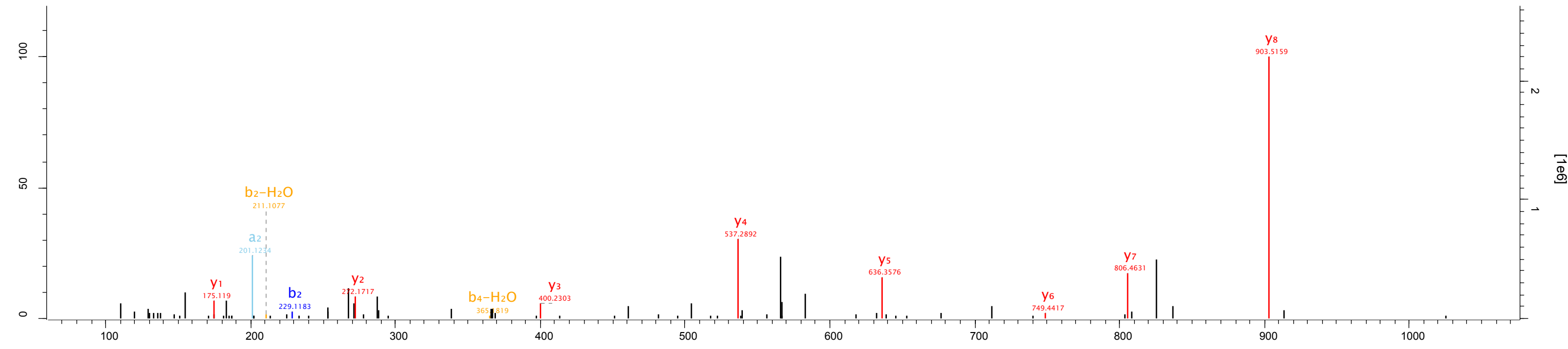


Raw file
20180707_MaS_A375SR_ML_proteome_24

Scan 27041 Method FTMS; HCD Score 68.54 m/z 722.9

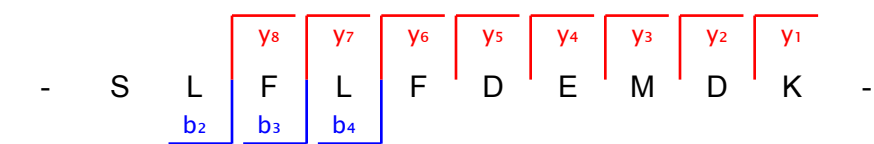
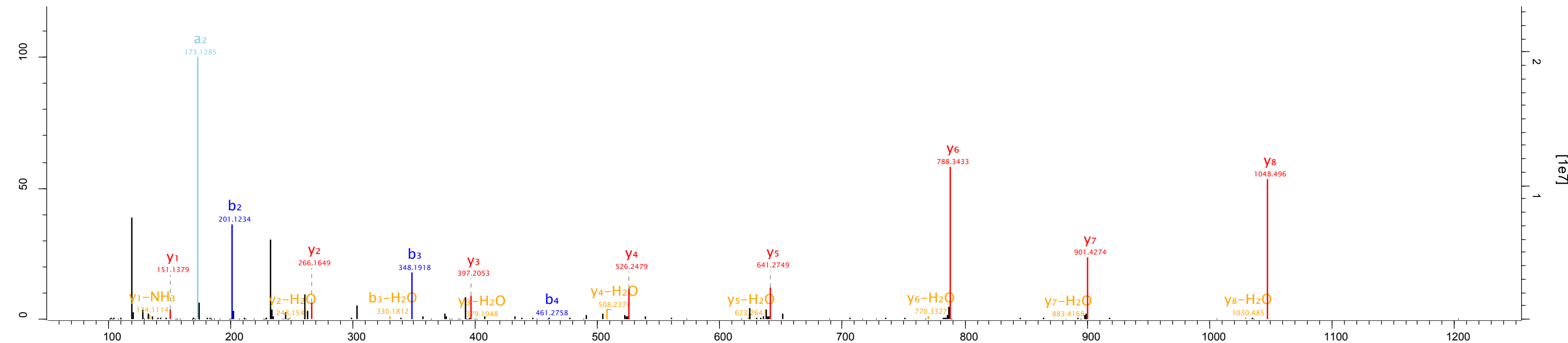


Raw file: 20180707_MaS_A375SR_ML_proteome_24
 Scan: 9691 Method: FTMS; HCD Score: 42.34 m/z: 566.82 Gene names: C1orf21

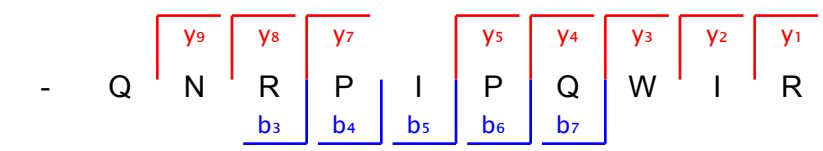
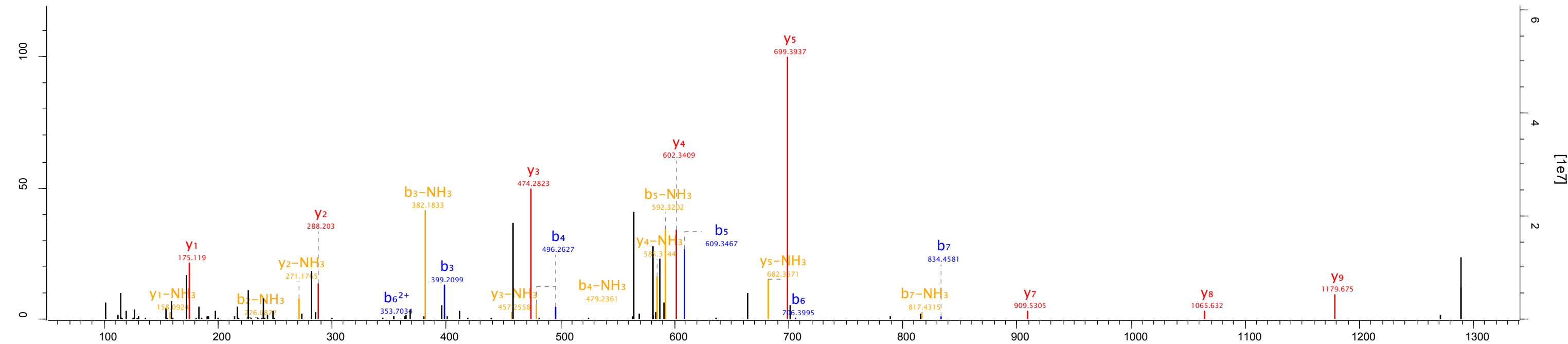


Raw file
20180707_MaS_A375SR_ML_proteome_25

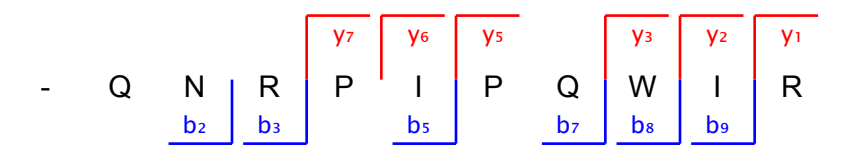
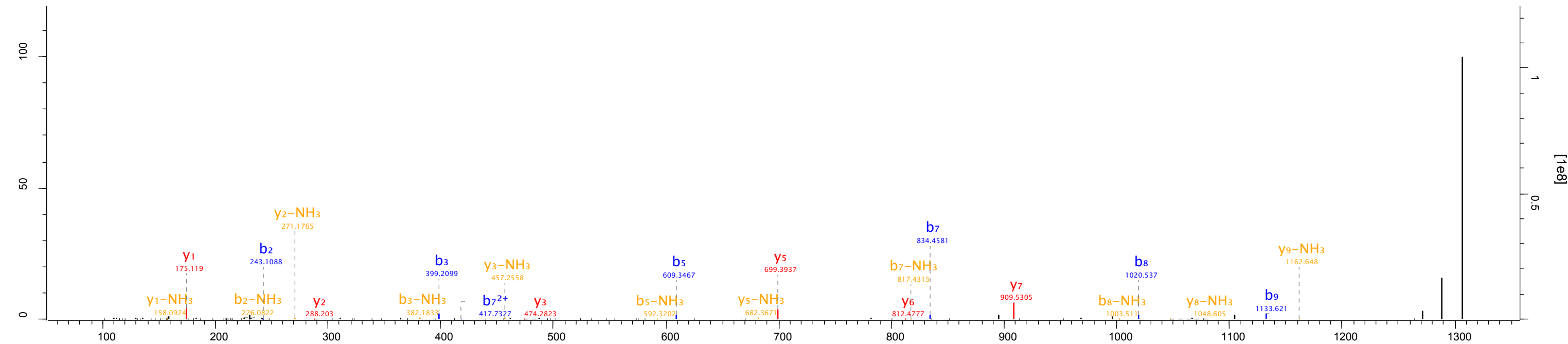
Scan: 29481
Method: FTMS; HCD
Score: 87.57
m/z: 624.81
Gene names: TOR2A



Raw file 20180707_MaS_A375SR_ML_proteome_26 Scan 15931 Method FTMS; HCD Score 143.03 m/z 436.58 Gene names RPL39P5;RPL39



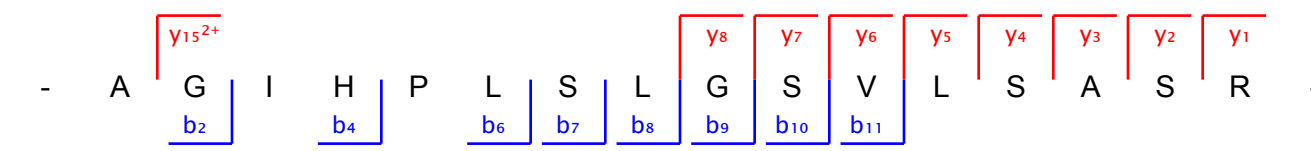
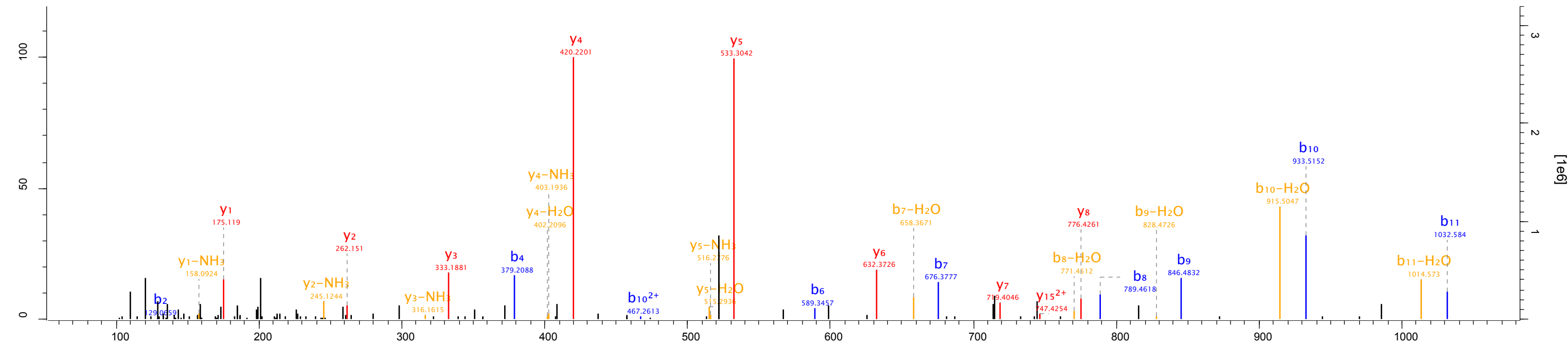
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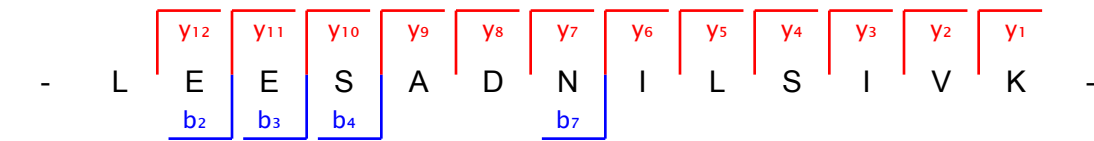
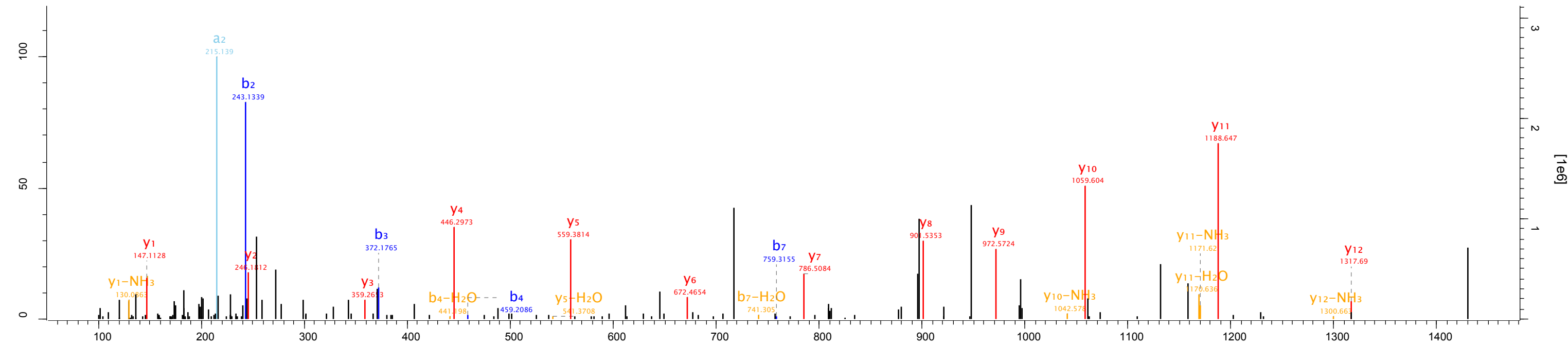


[1e8]

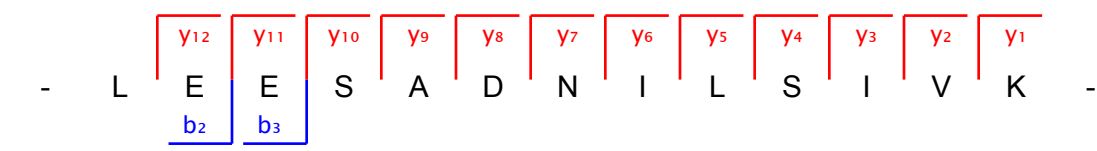
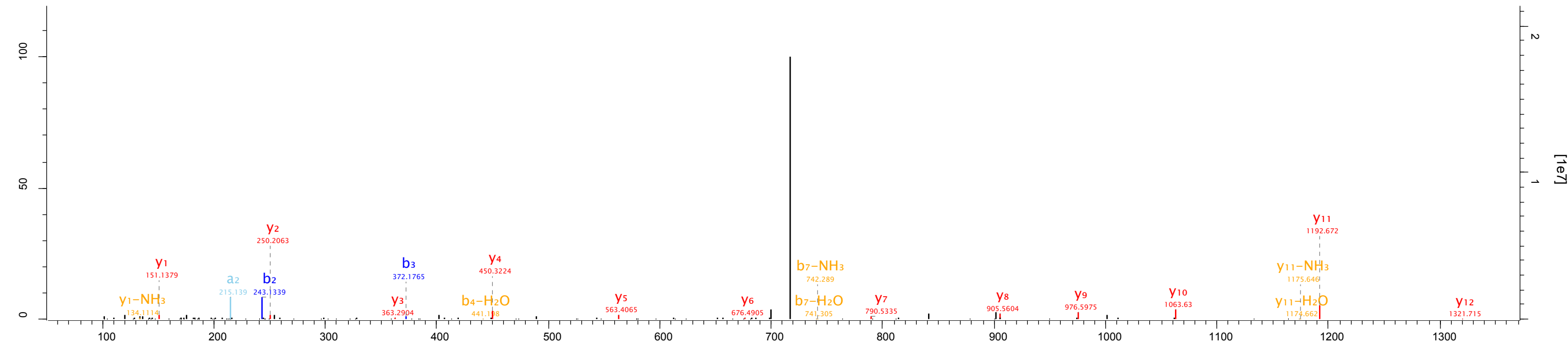
Raw file
20180707_MaS_A375SR_ML_proteome_26

Scan: 24791
Method: FTMS; HCD
Score: 106.14
m/z: 522.3
Gene names: NEIL2

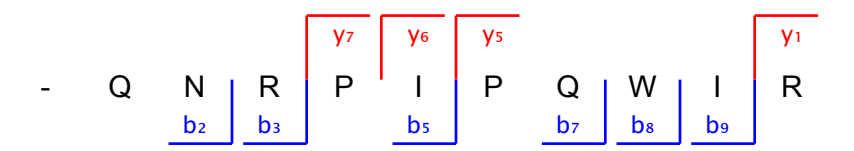
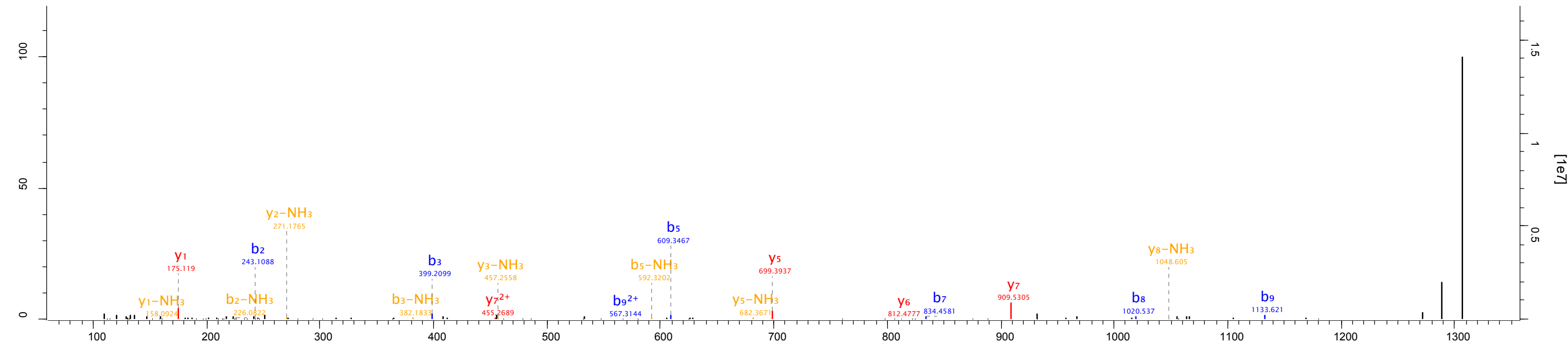


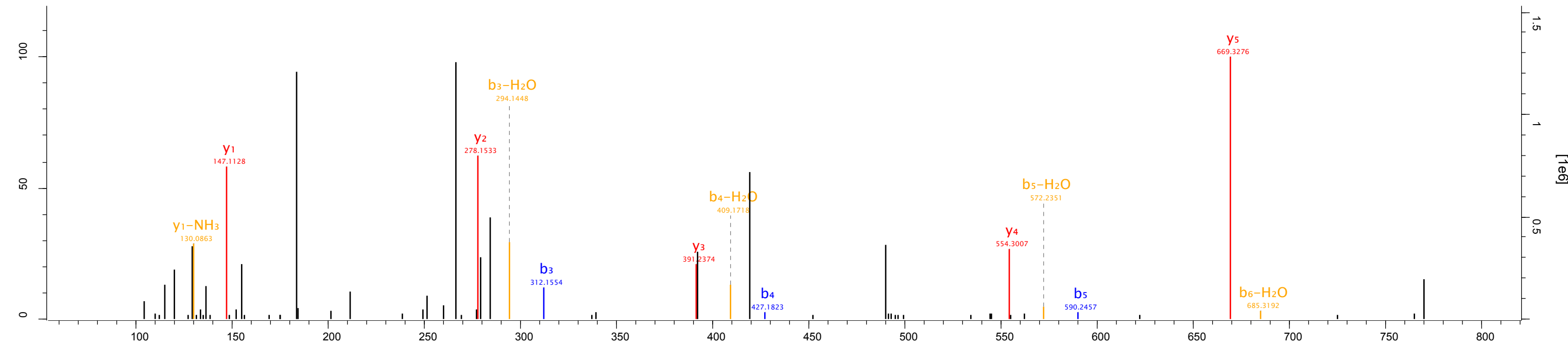


Raw file: 20180707_MaS_A375SR_ML_proteome_26
 Scan: 27201 Method: FTMS; HCD Score: 88.08 m/z: 717.9 Gene names: RFXAP



Raw file 20180707_MaS_A375SR_ML_proteome_27
 Scan 16141 Method FTMS; HCD Score 81.95 m/z 654.37 Gene names RPL39P5;RPL39



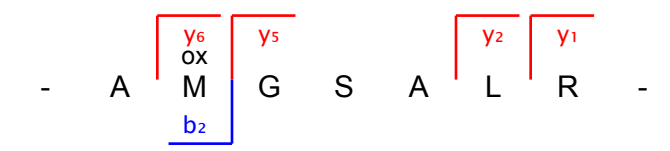
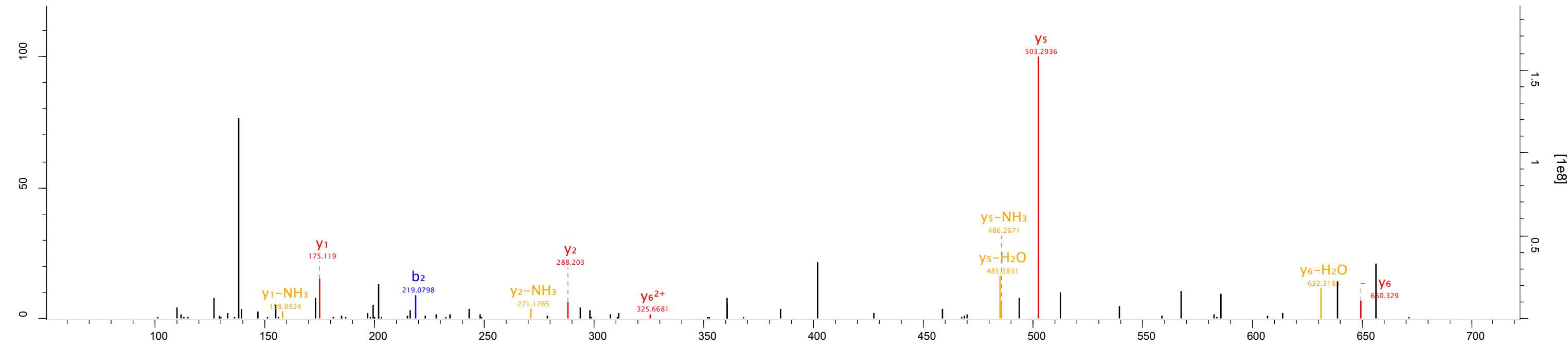


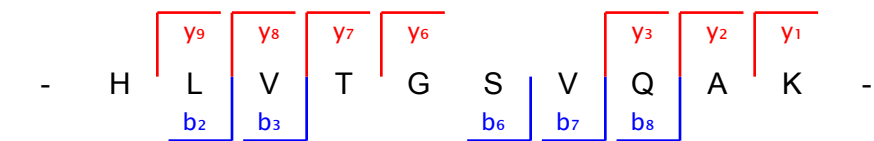
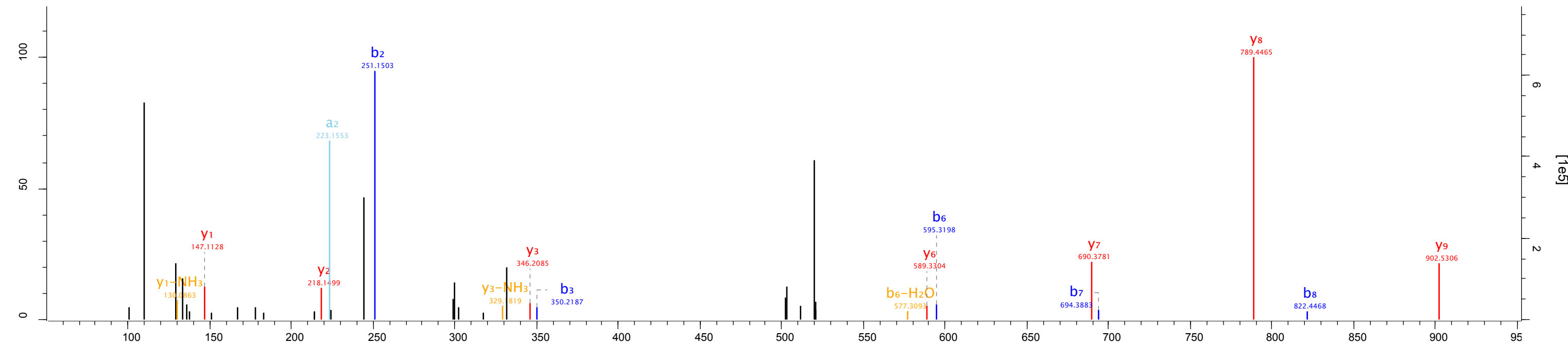
- P D V D Y I M K -

b3 b4 b5 y5 y4 y3 y2 y1

Raw file
20180707_MaS_A375SR_ML_proteome_27

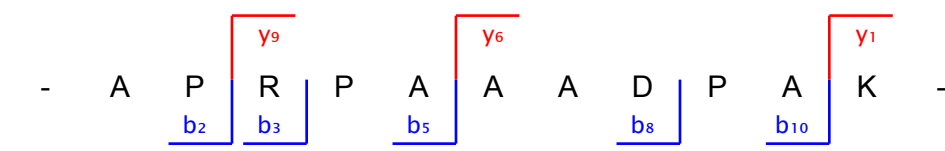
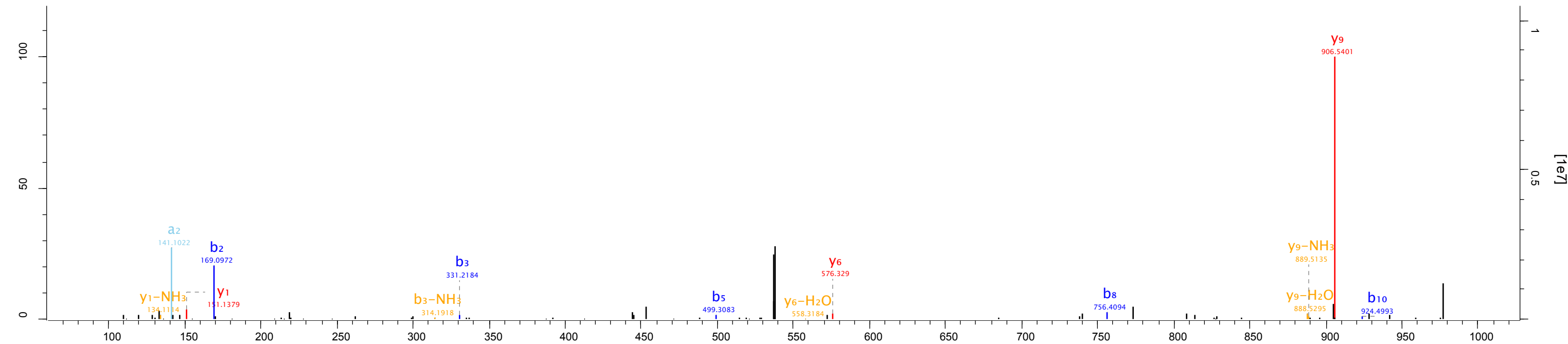
Scan	Method	Score	m/z
2681	FTMS; HCD	65.67	361.19



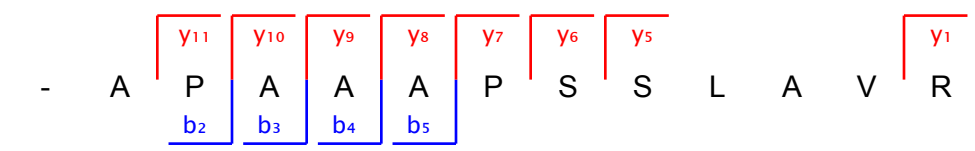
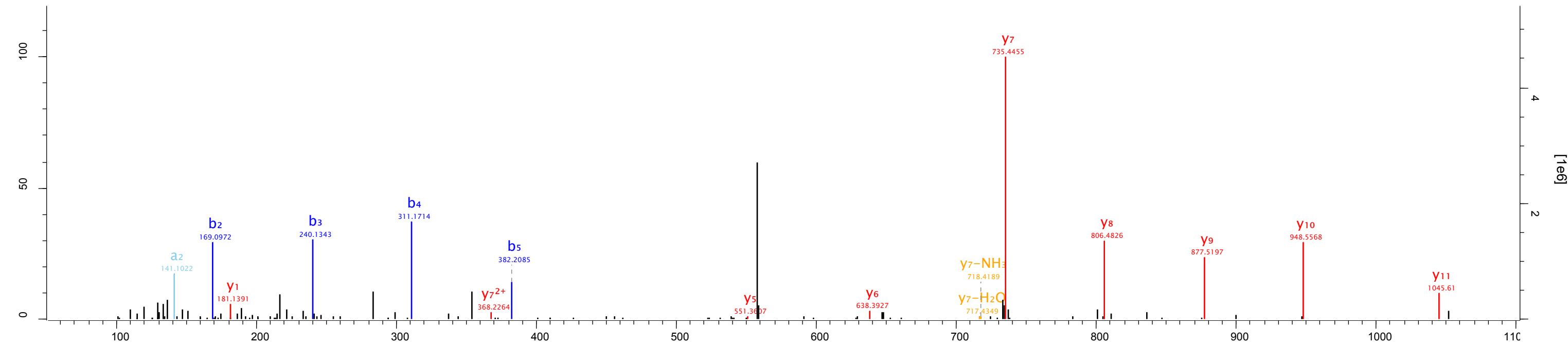


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20180707_MaS_A375SR_ML_proteome_29

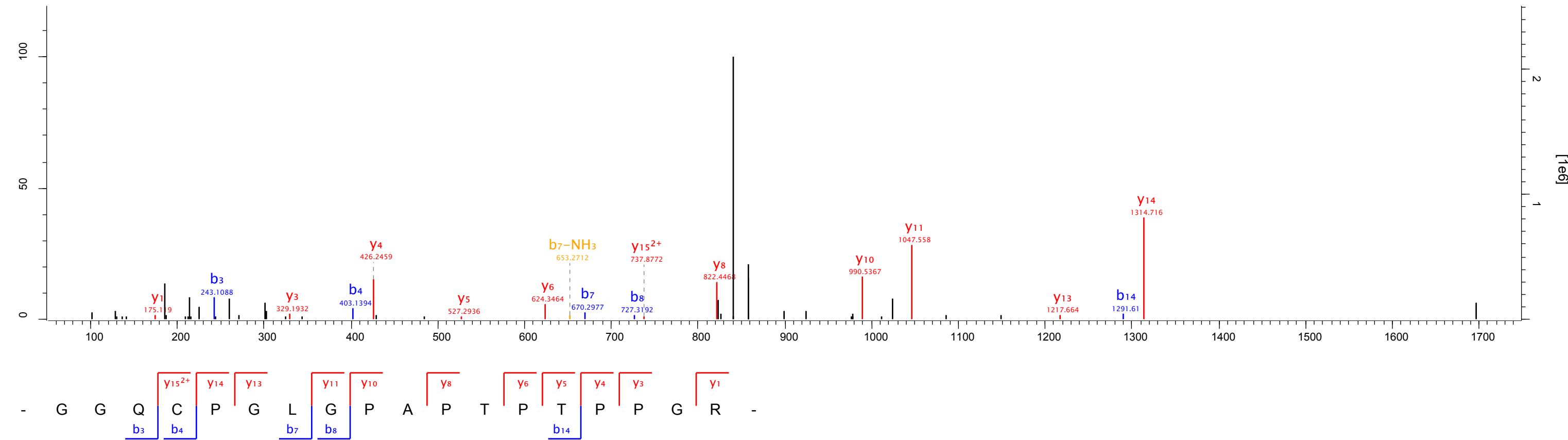
Scan 3941 Method FTMS; HCD Score 49.47 m/z 537.82



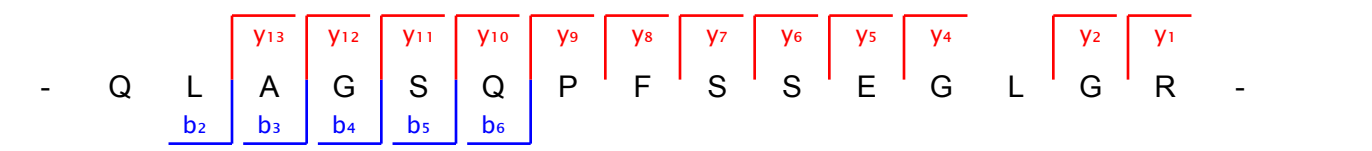
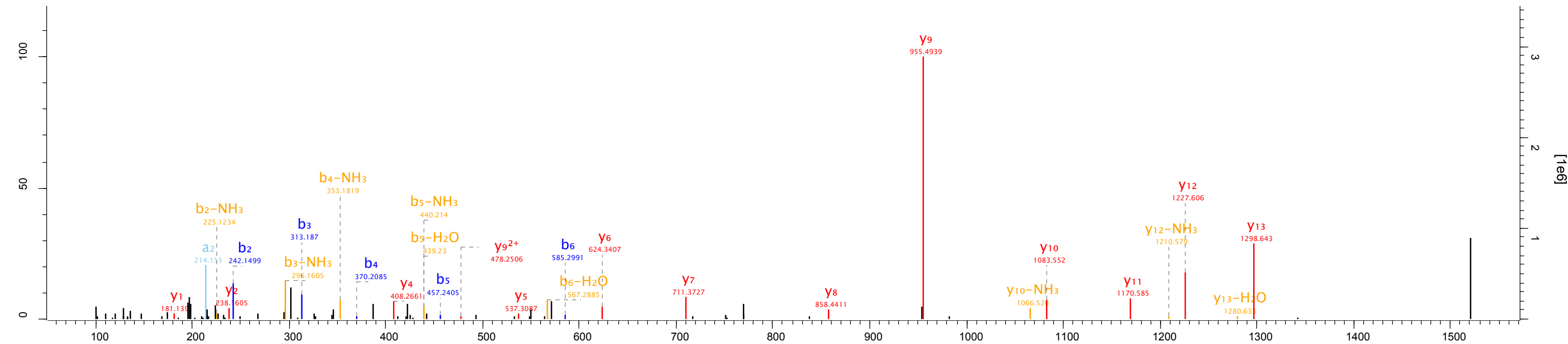
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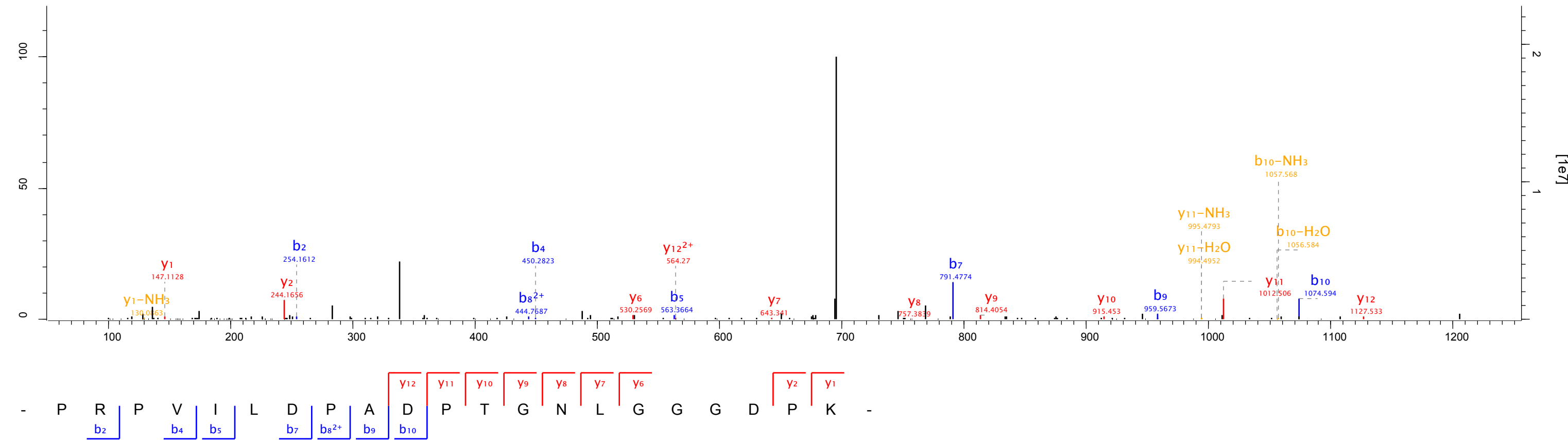


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 Scan 13101 Method FTMS; HCD Score 69.19 m/z 858.93 Gene names ZBED3

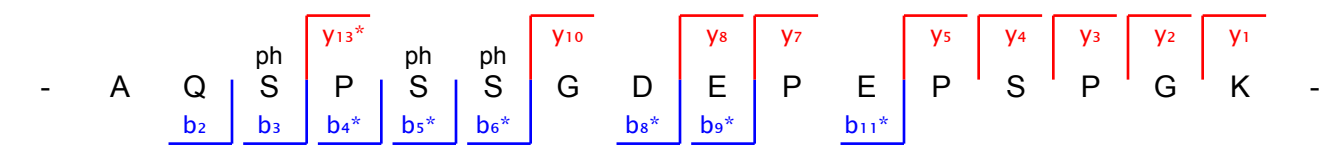
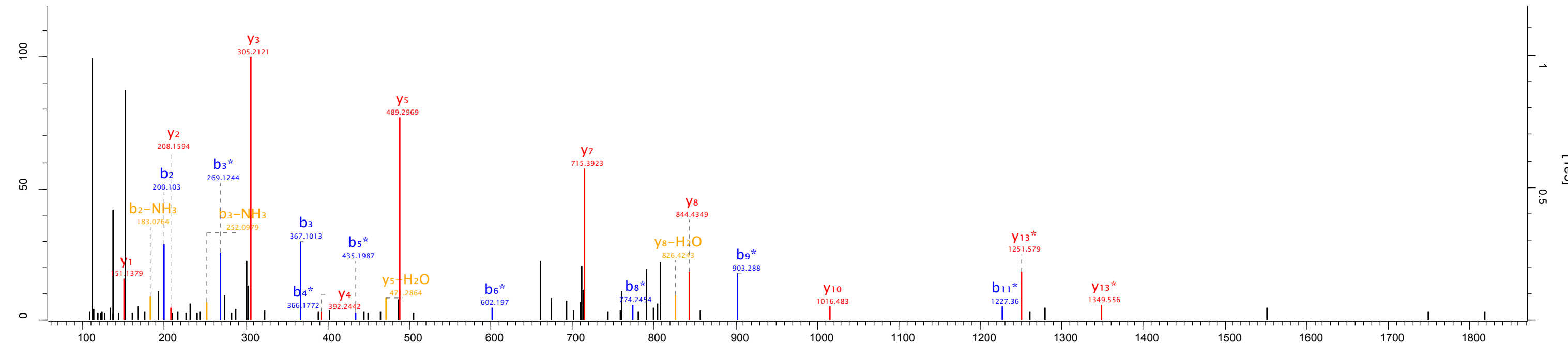


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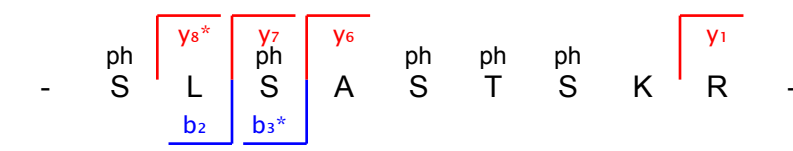
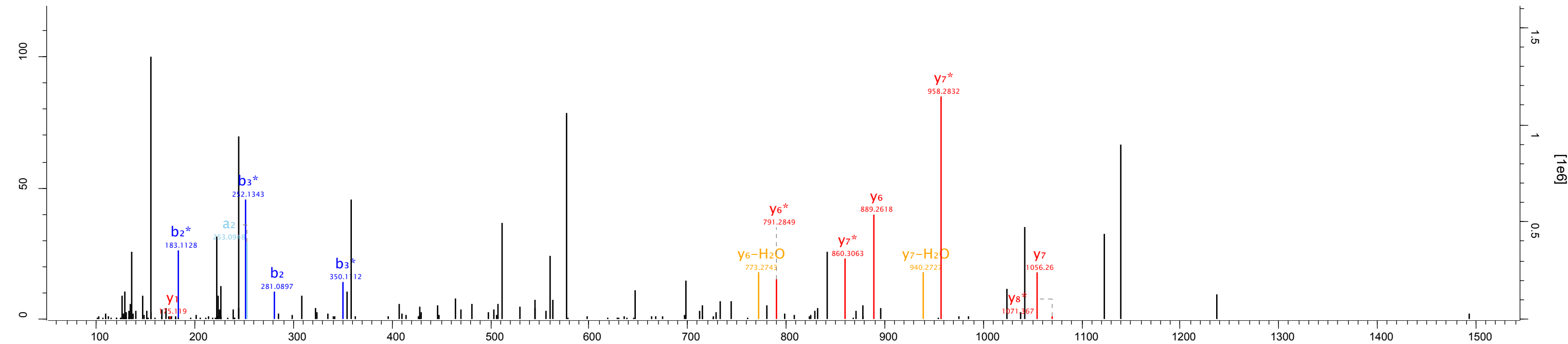




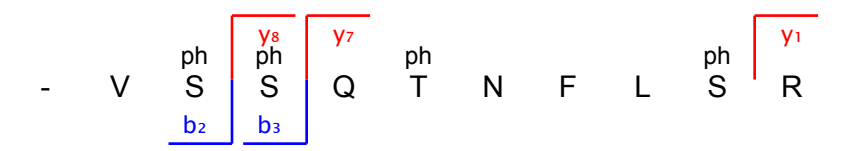
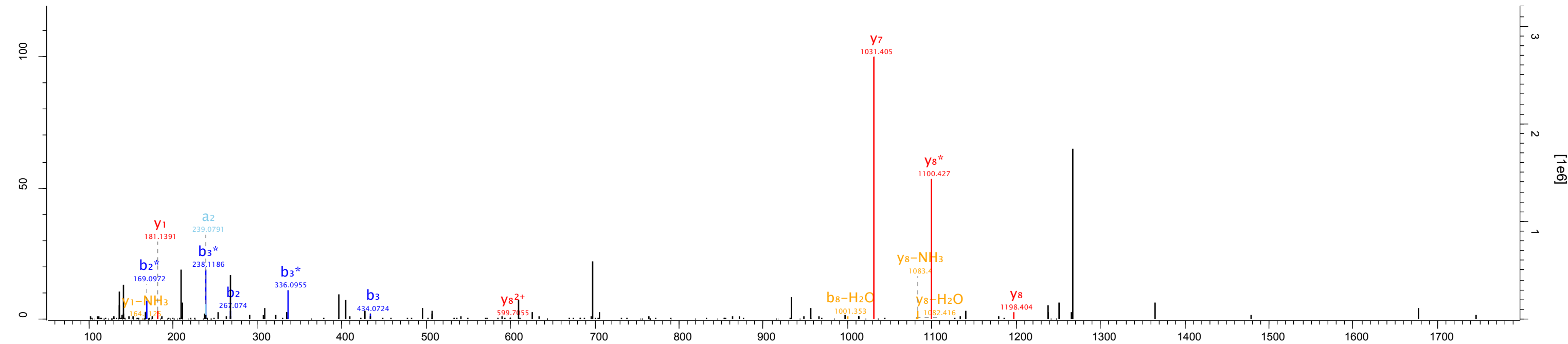
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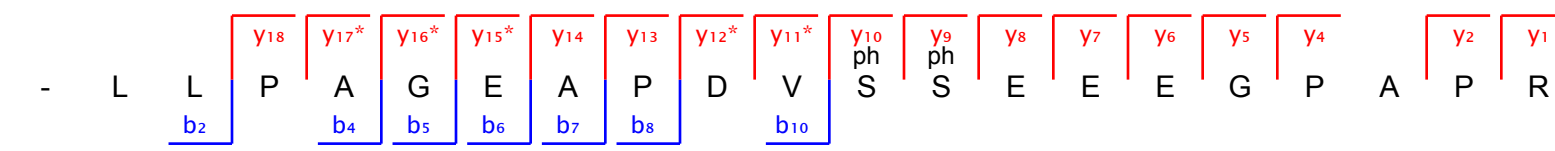
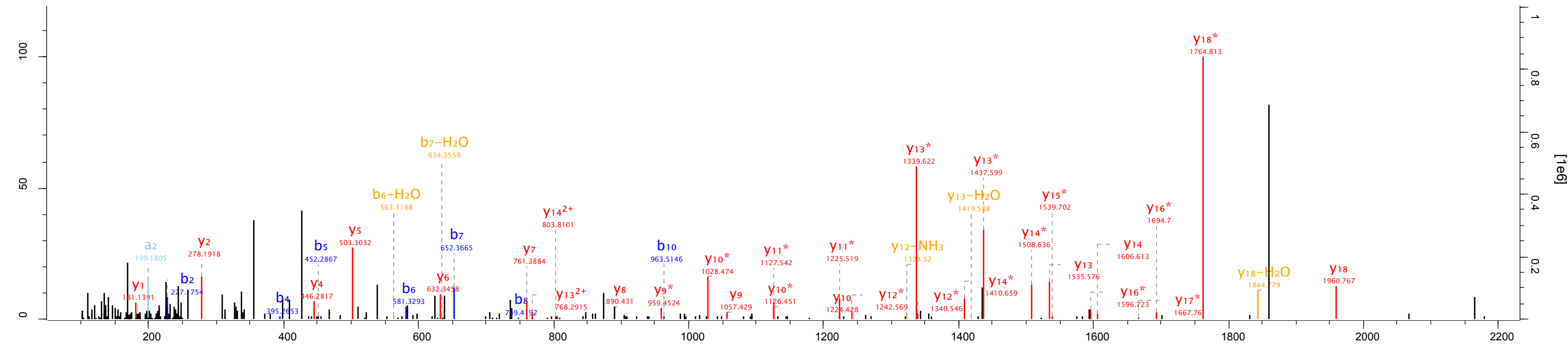
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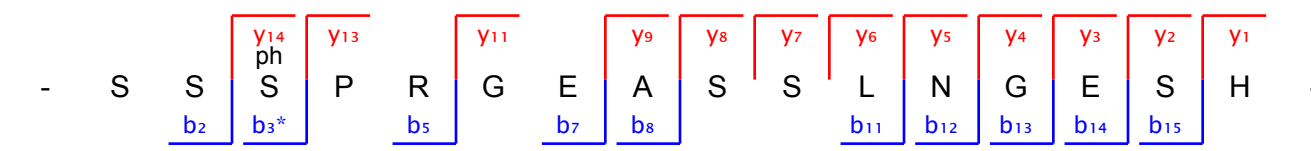
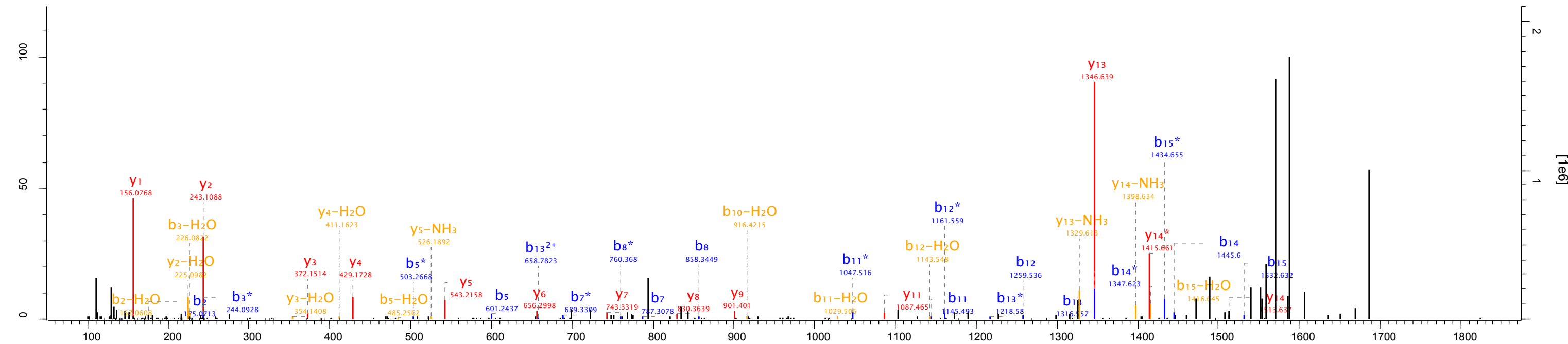
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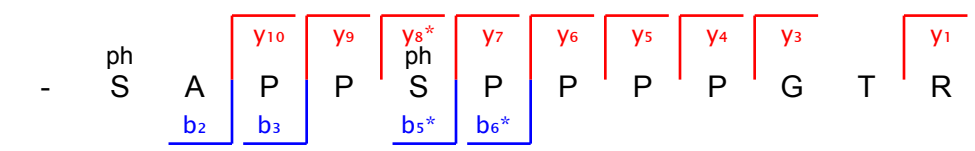
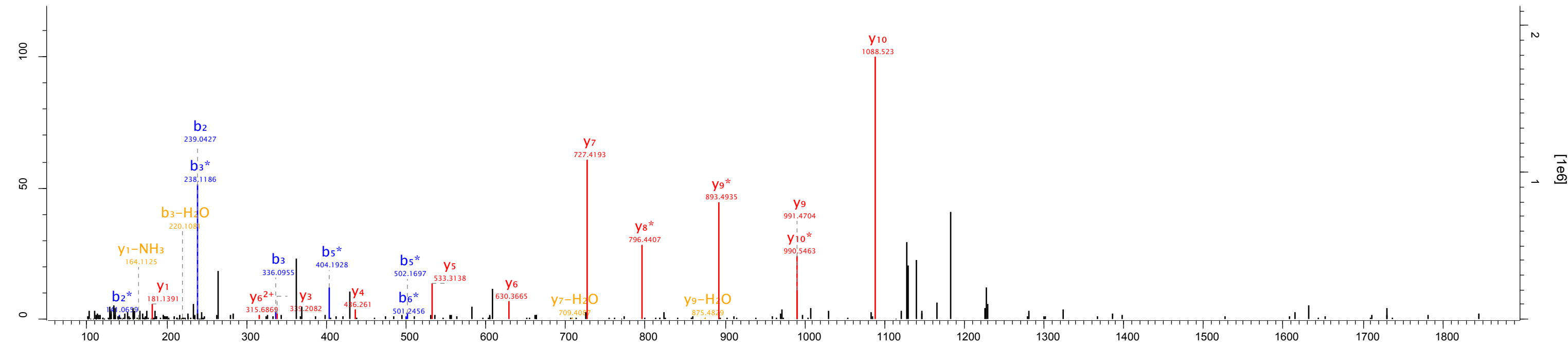
Raw file: 20150812_A375SR_Phospho_BR1_03
 Scan: 17922 Method: FTMS; HCD Score: 106.28 m/z: 1093.97 Gene names: FAM214B



Raw file 20150812_A375SR_Phospho_BR1_03 Scan 7242 Method FTMS; HCD Score 124.1 m/z 844.36 Gene names YAF2

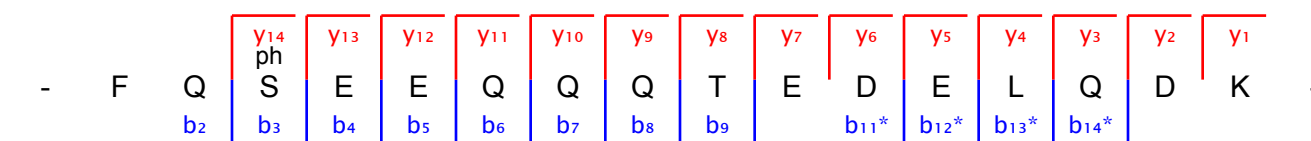
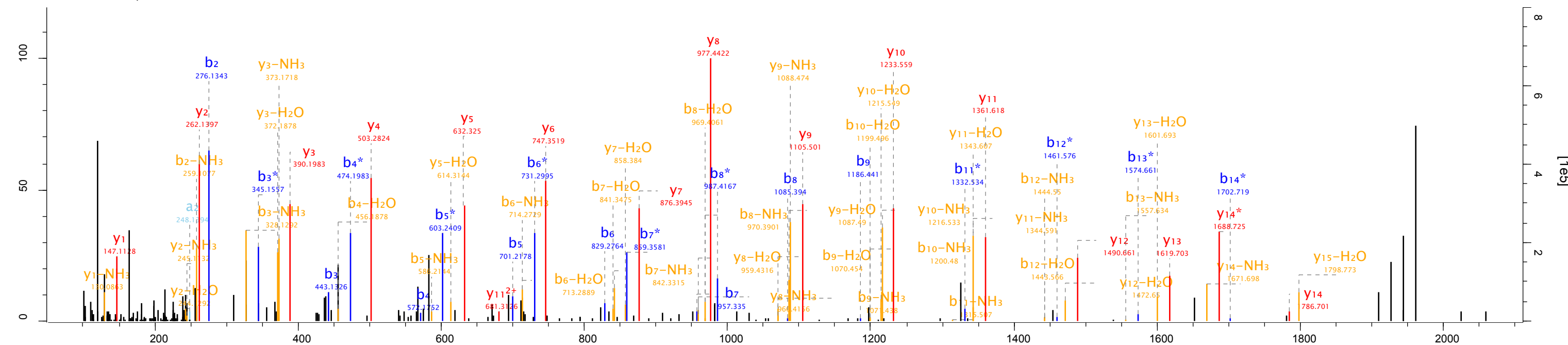


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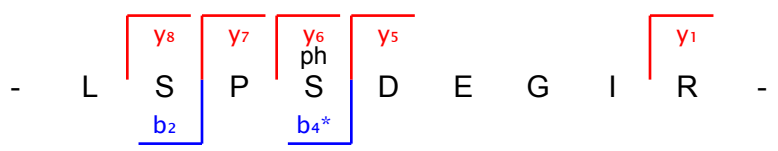
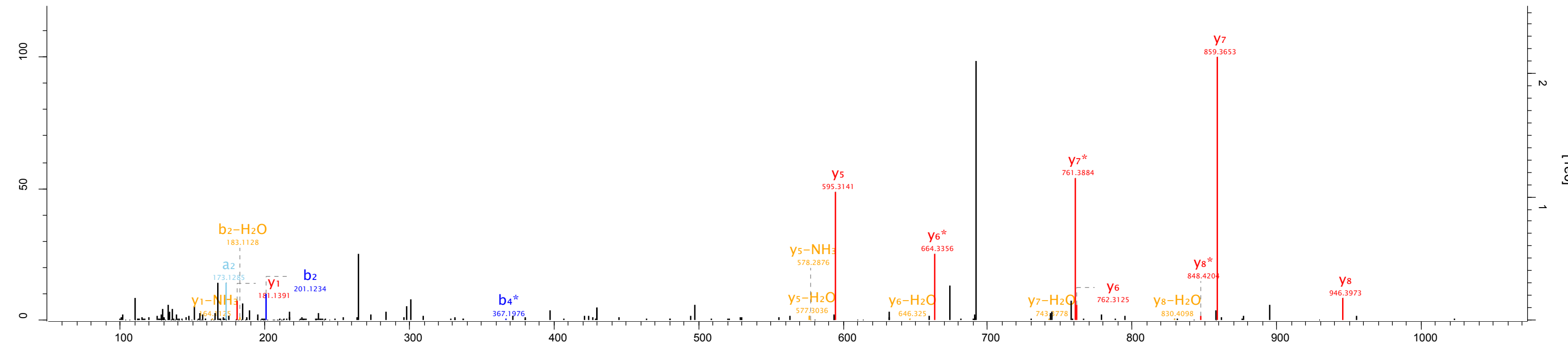


Raw file
20150812_A375SR_Phospho_BR1_04

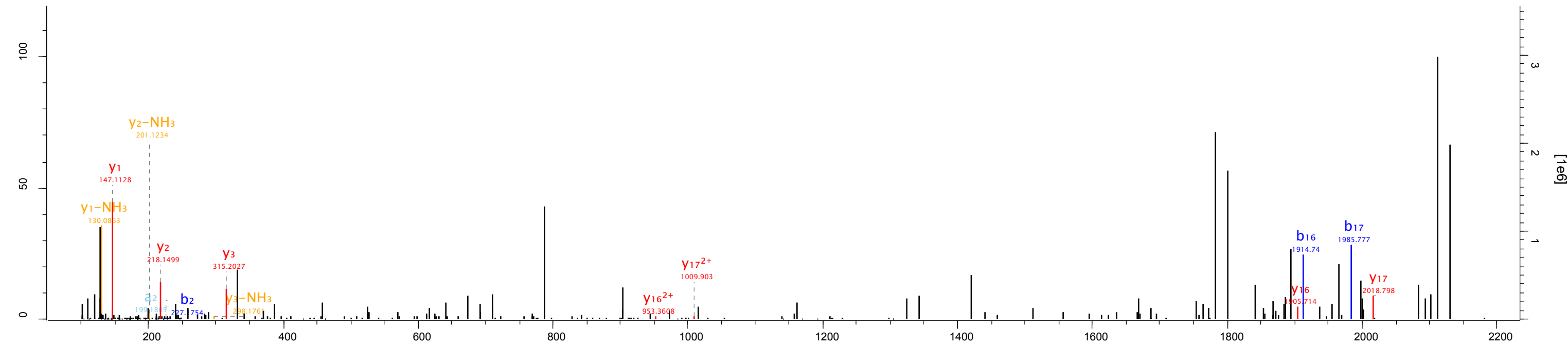
Scan 12212 Method FTMS; HCD Score 319.18 m/z 1031.92



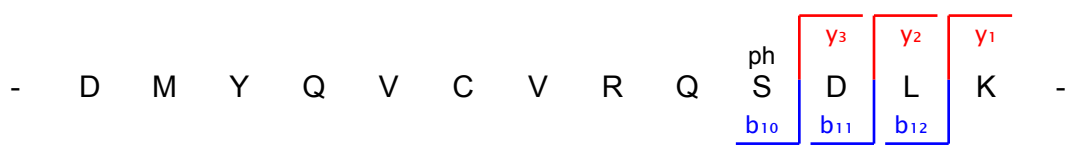
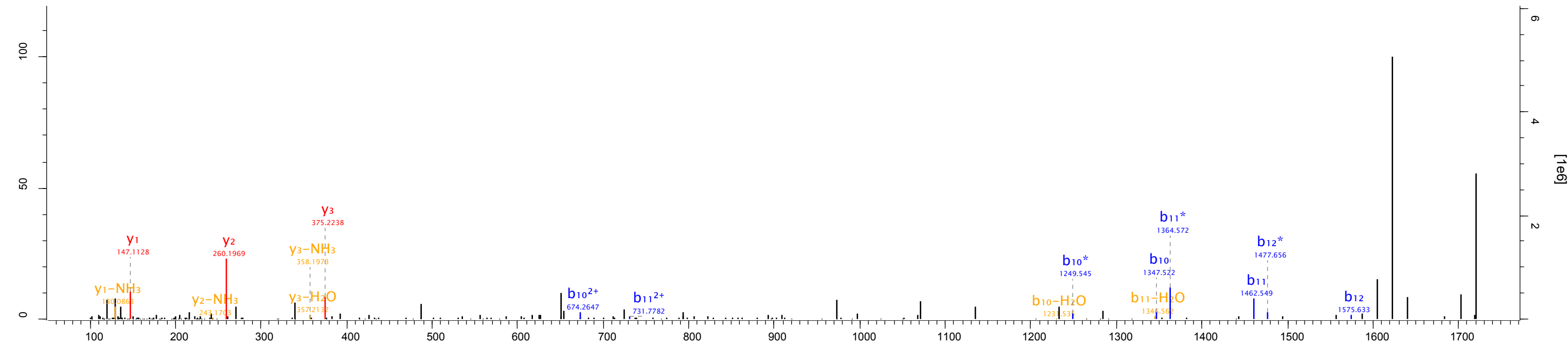
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 Scan: 5242 Method: FTMS; HCD Score: 48.57 m/z: 530.24



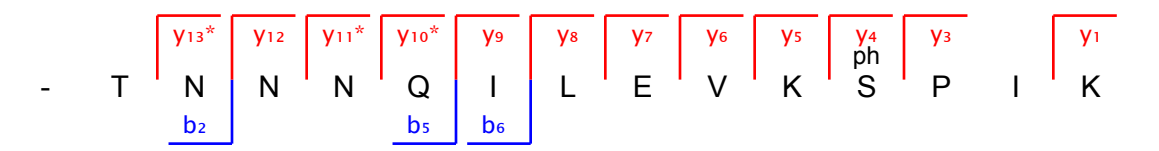
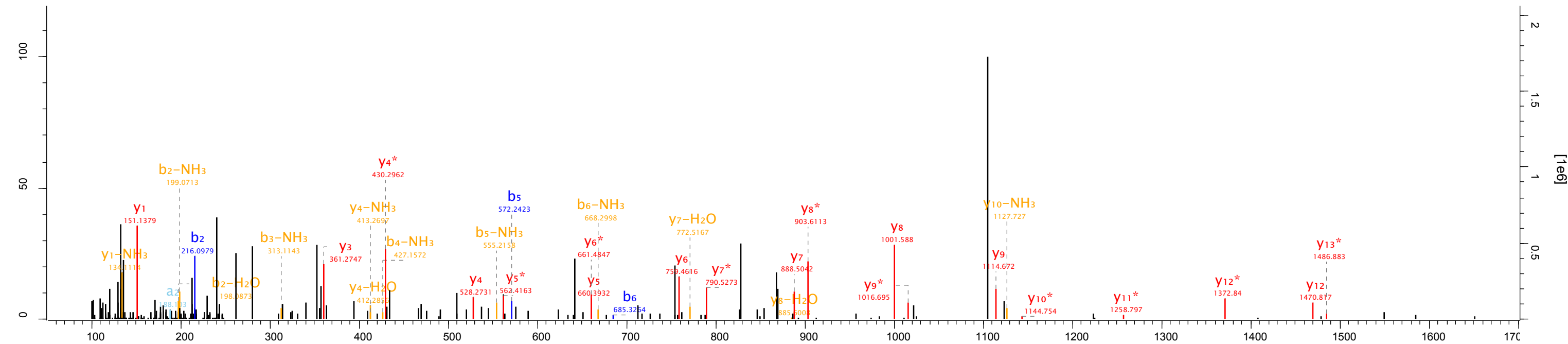
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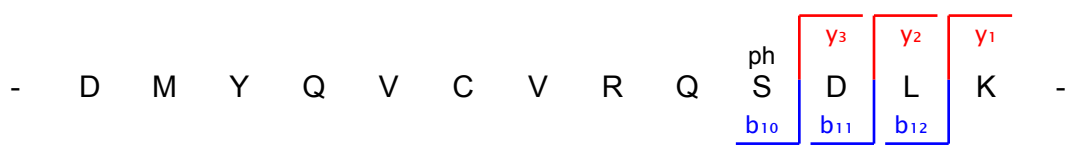
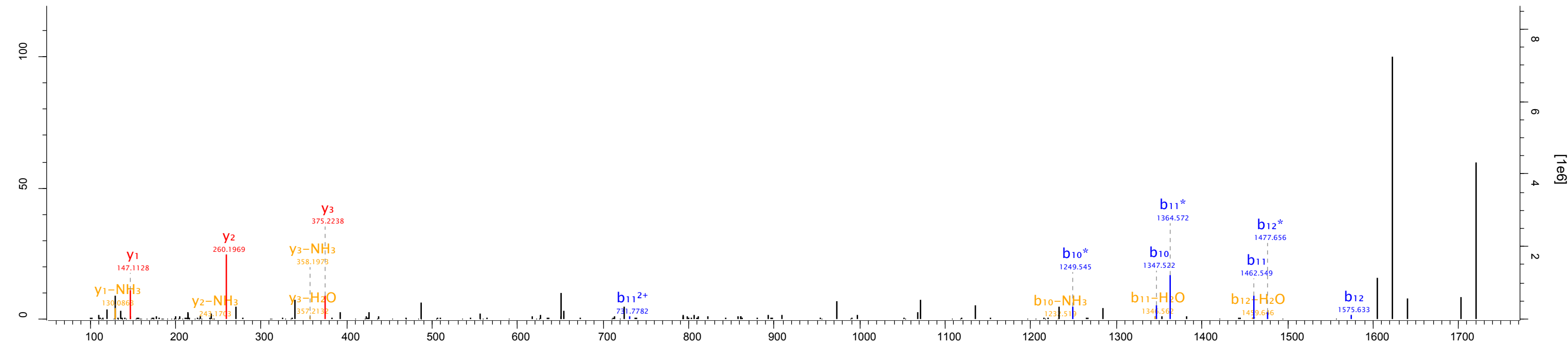
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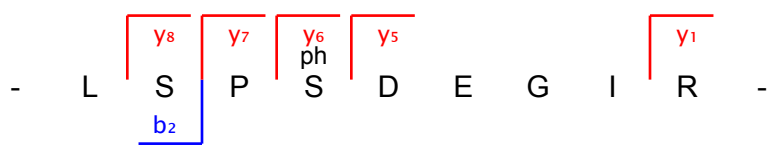
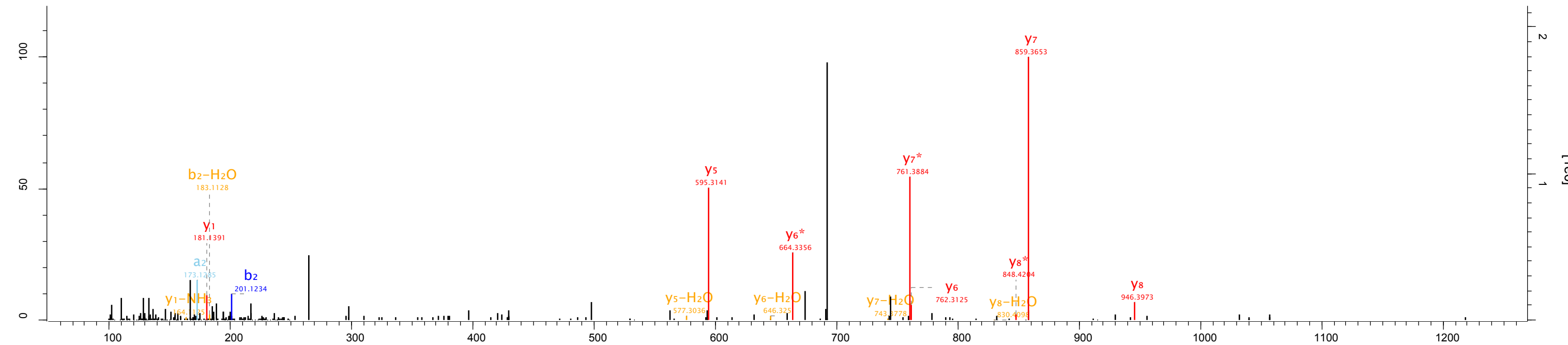
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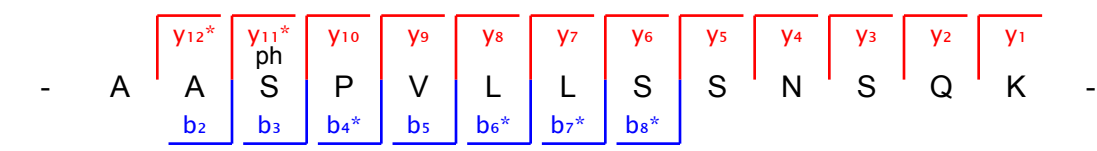
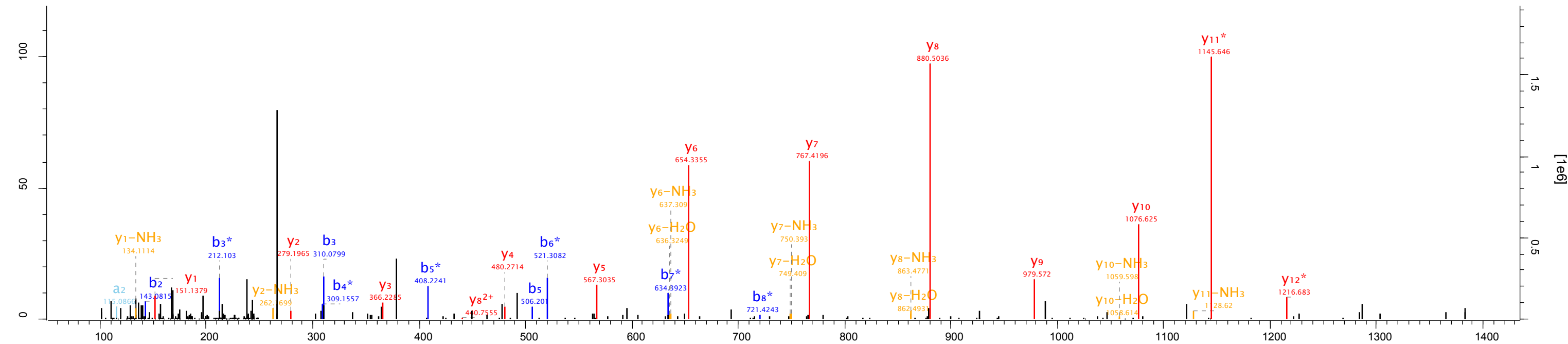
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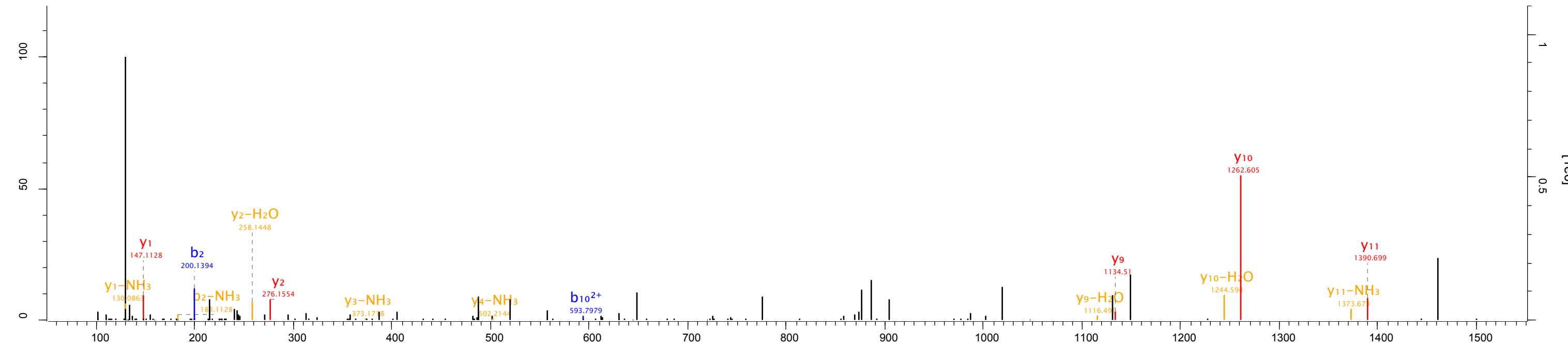
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Raw file: 20150812_A375SR_Phospho_BR1_07
 Scan: 12112 Method: FTMS; HCD Score: 131.4 m/z: 693.35 Gene names: ELK3

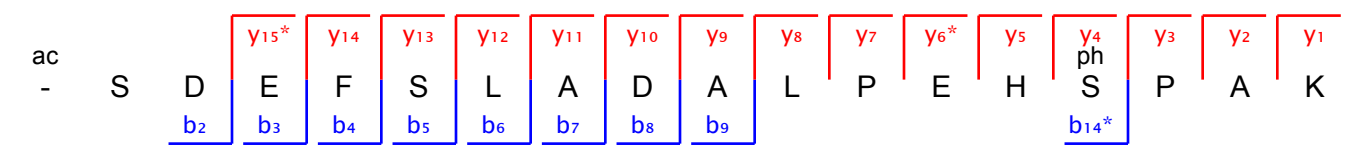
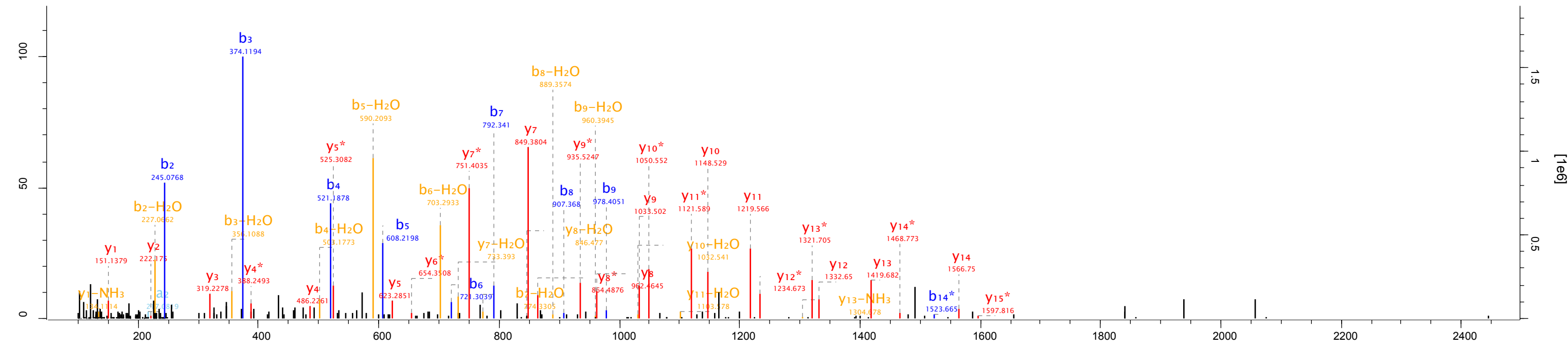


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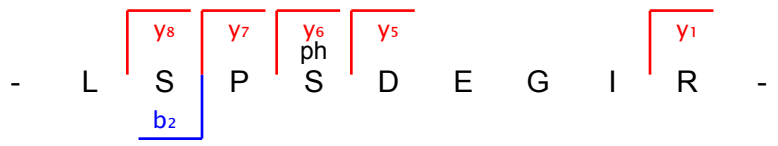
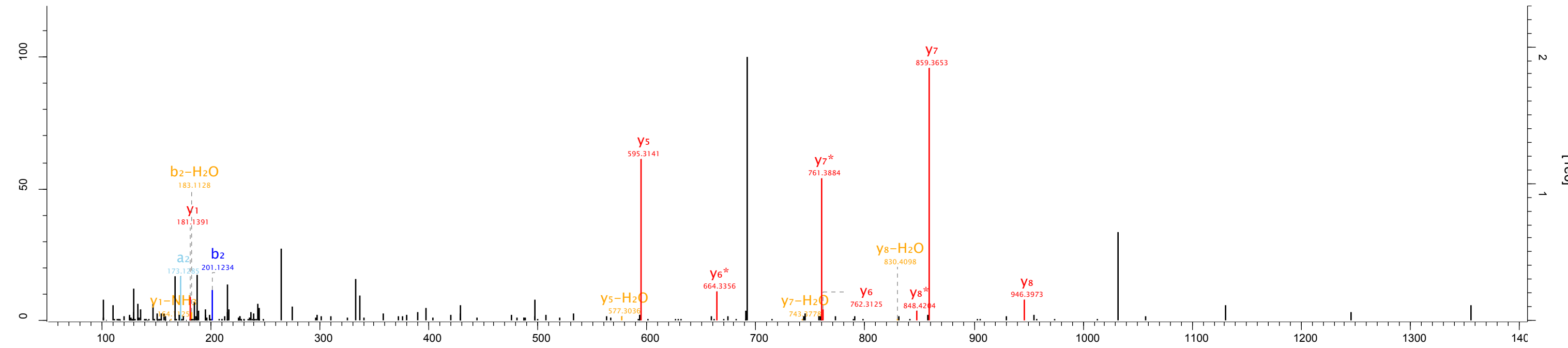


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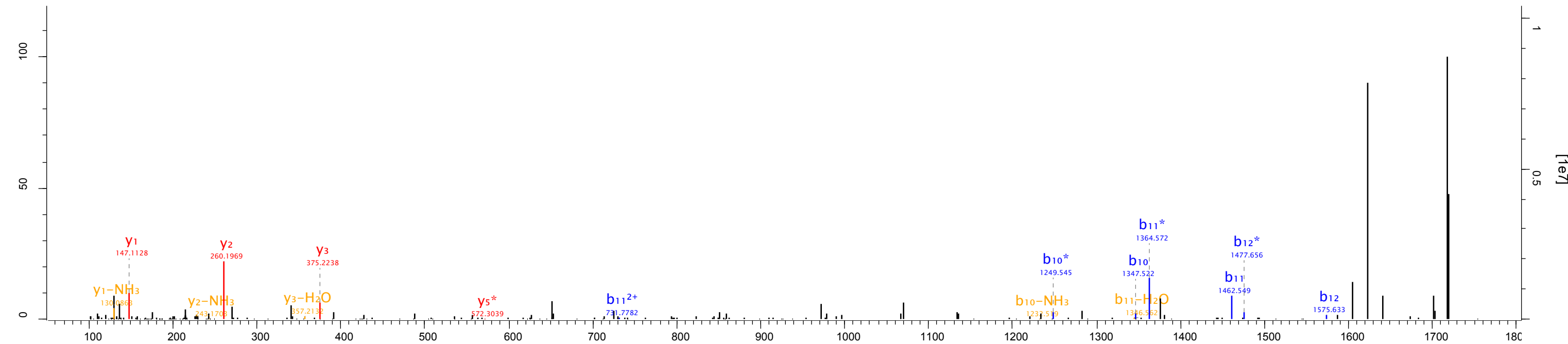
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24572 FTMS; HCD 254.71 970.94 MAPK11P1L



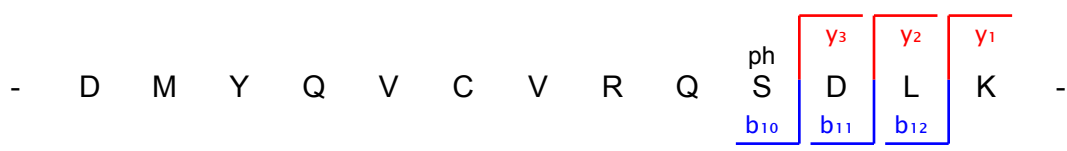
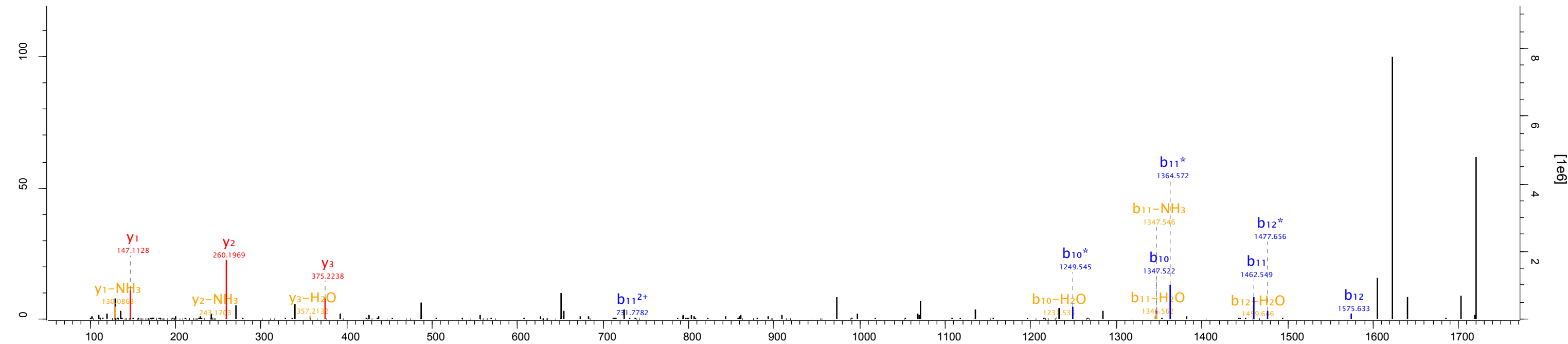
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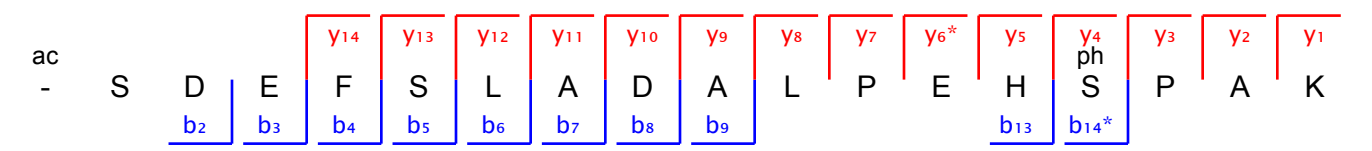
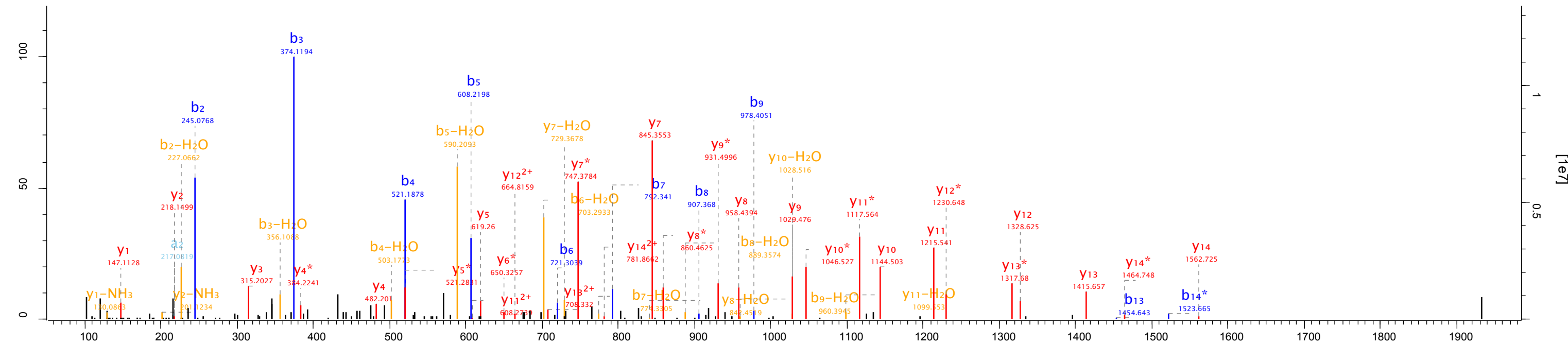
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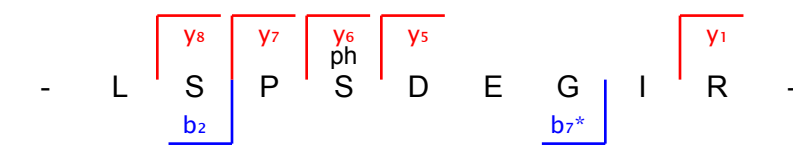
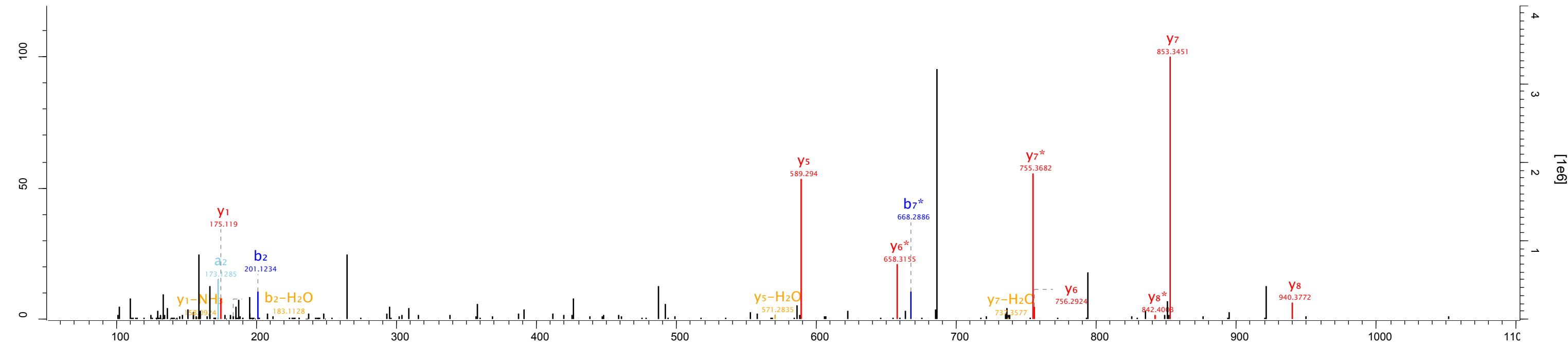
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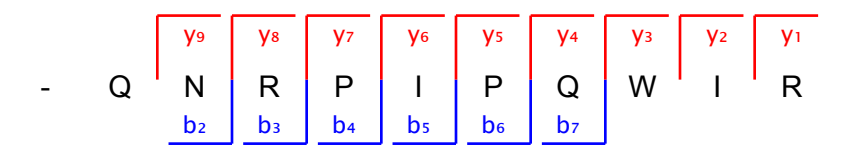
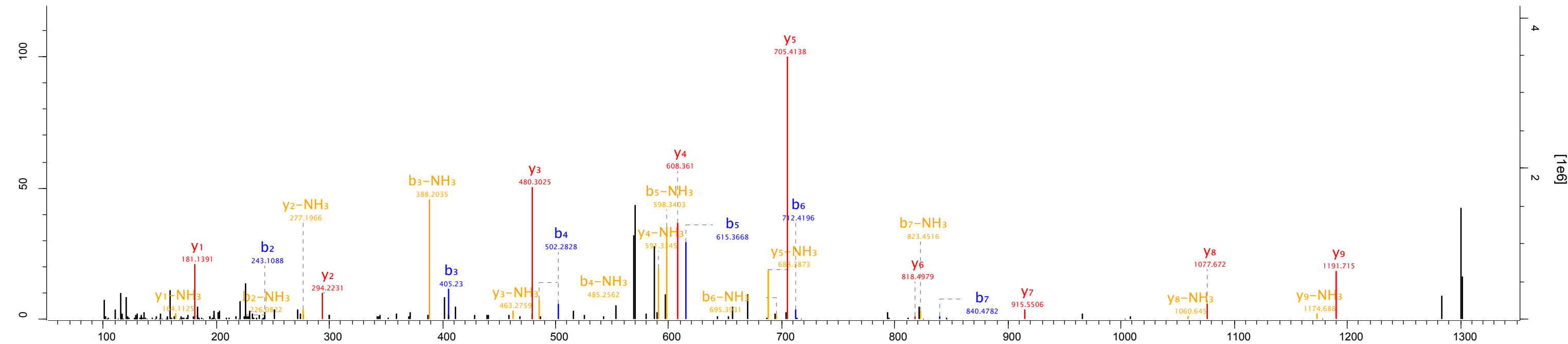
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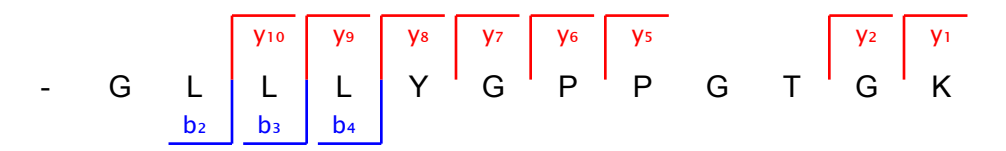
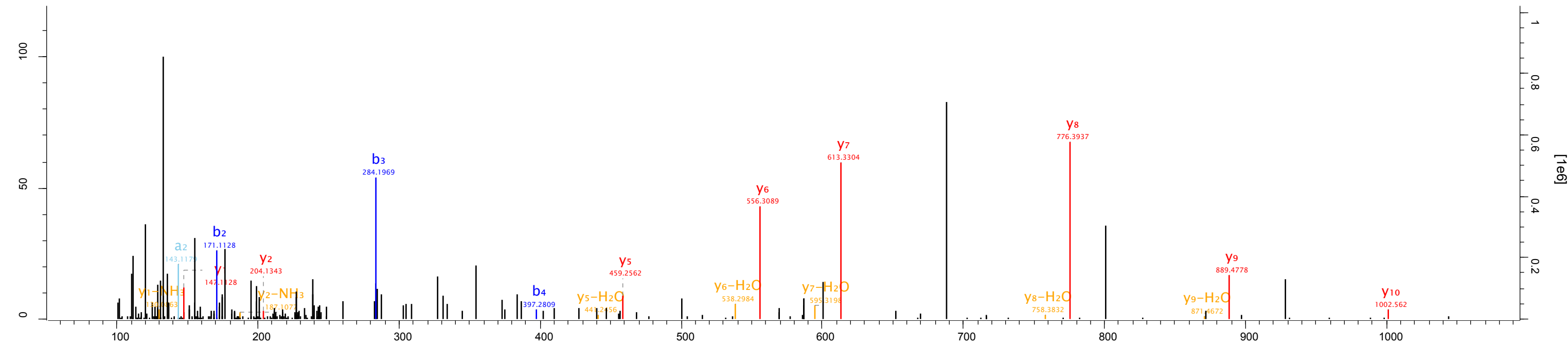
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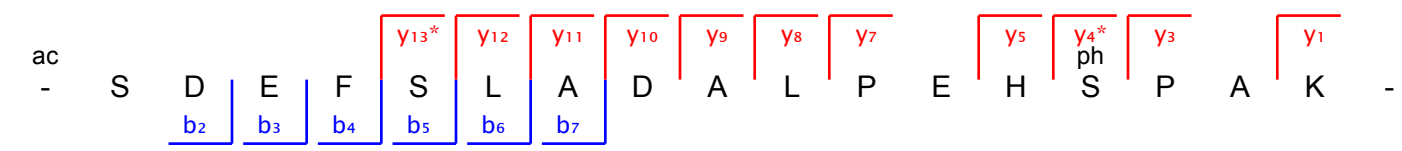
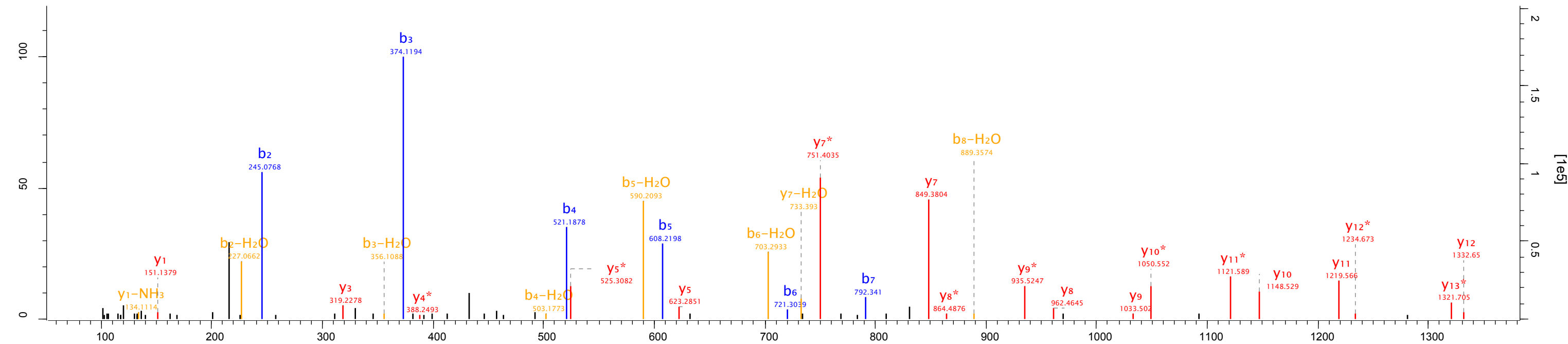
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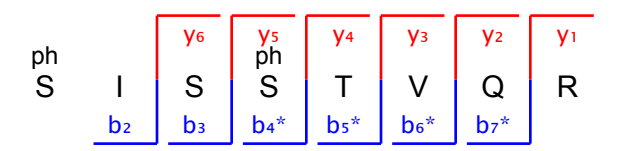
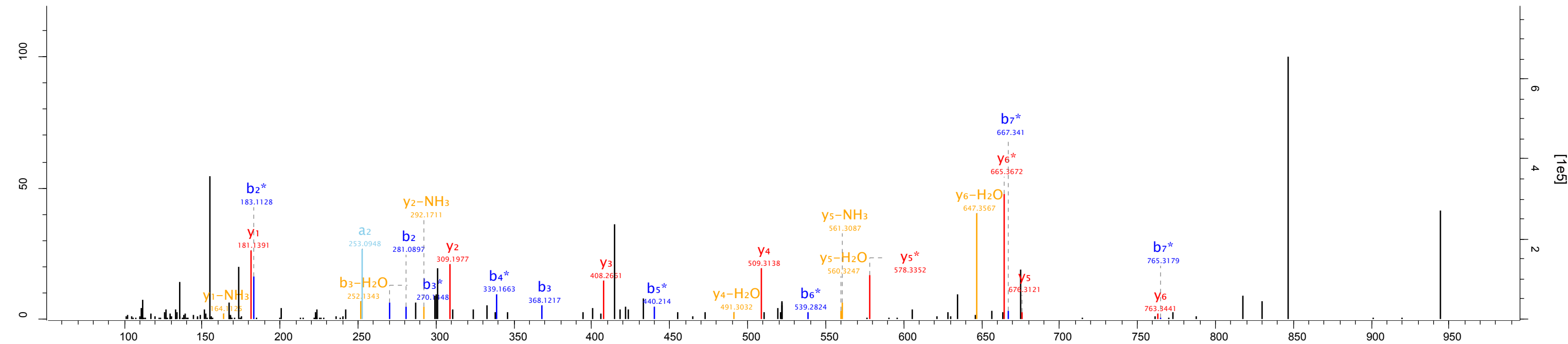
Raw file Scan Method Score m/z Gene names
 20150812_A375SR_Phospho_BR1_10 17292 FTMS; HCD 41.38 587.33 KATNAL2



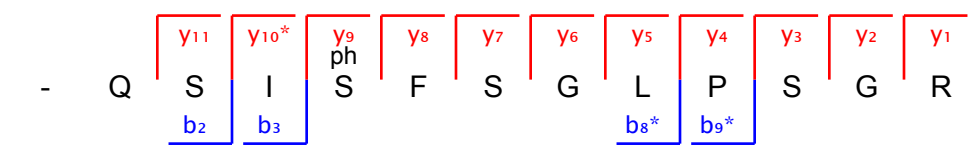
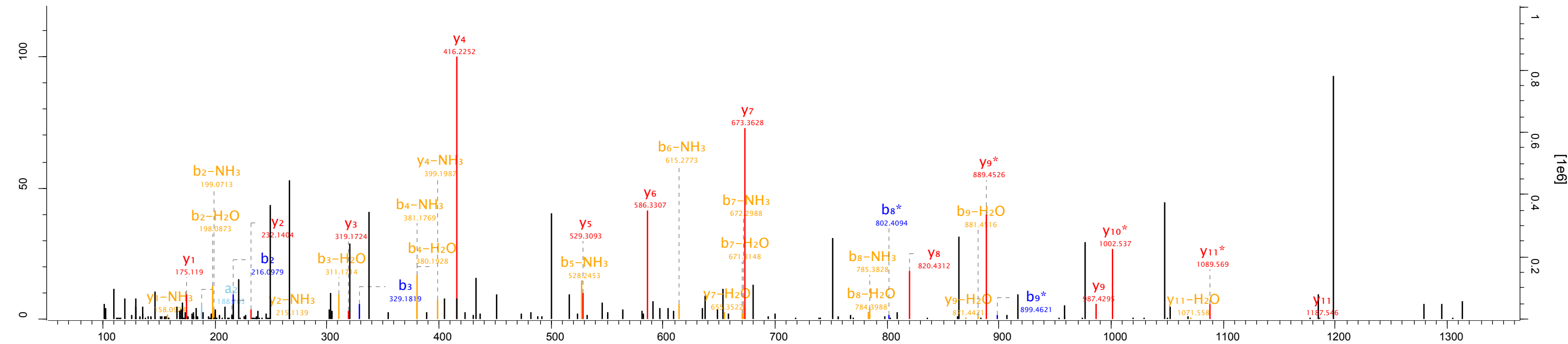
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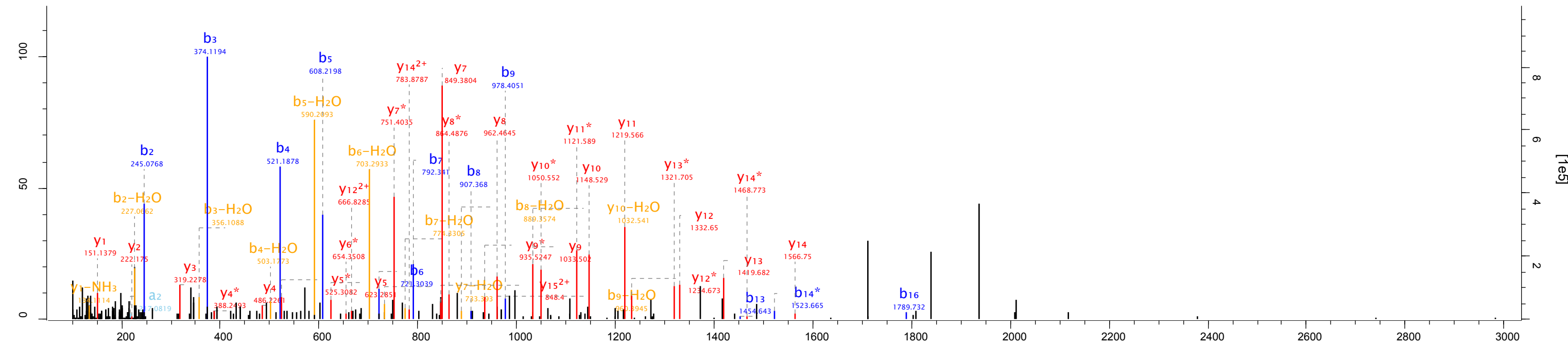
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 Scan: 8082 Method: FTMS; HCD Score: 92.11 m/z: 522.22 Gene names: RHBDF2



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 Scan: 17762 Method: FTMS; HCD Score: 85.51 m/z: 658.3 Gene names: ZFP36

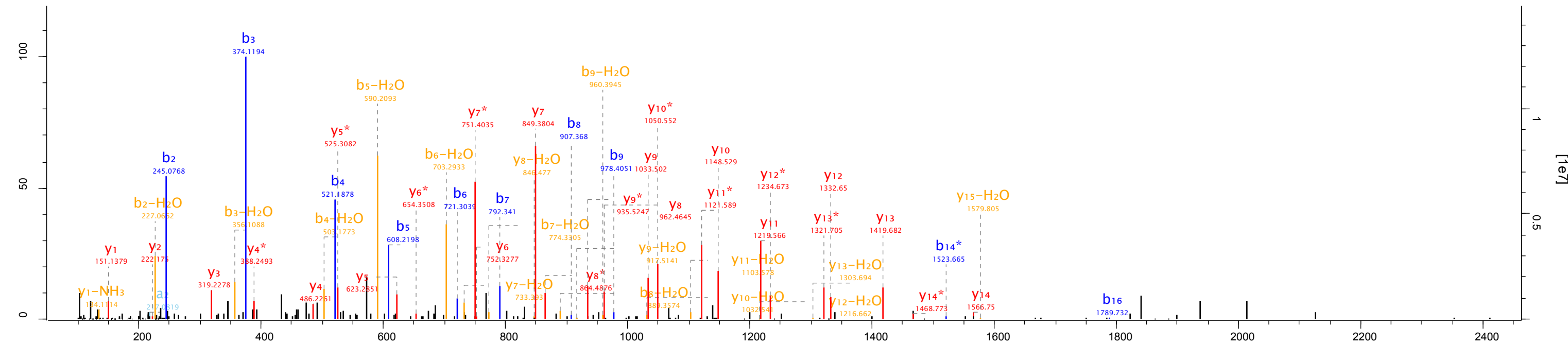


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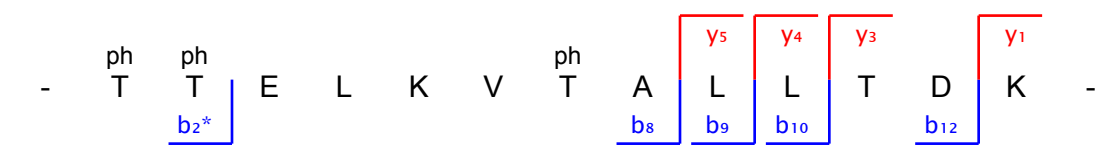
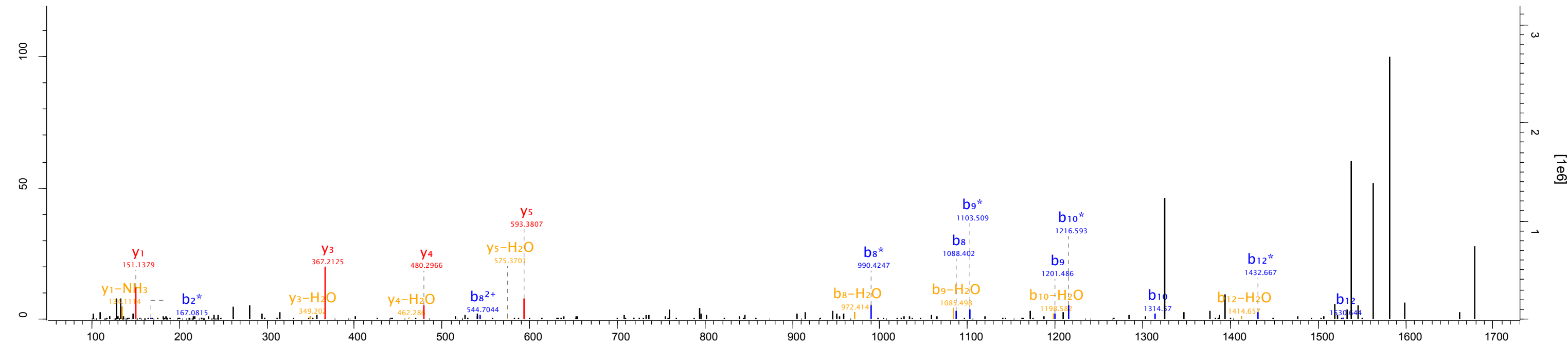
ac - S D E F S L A D A L P E H S P A K -
 b2 b3 b4 b5 b6 b7 b8 b9 b13 b14* b16

Raw file 20150814_A375SR_Phospho_BR2_03 Scan 23702 Method FTMS; HCD Score 271.66 m/z 970.94 Gene names MAPK11P1L

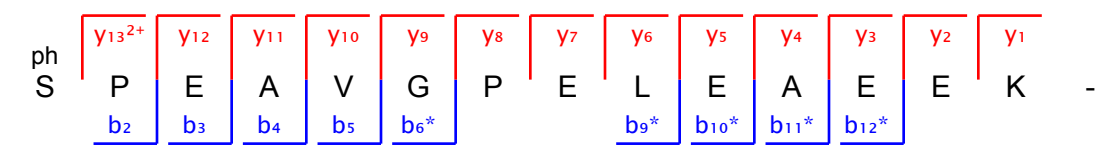
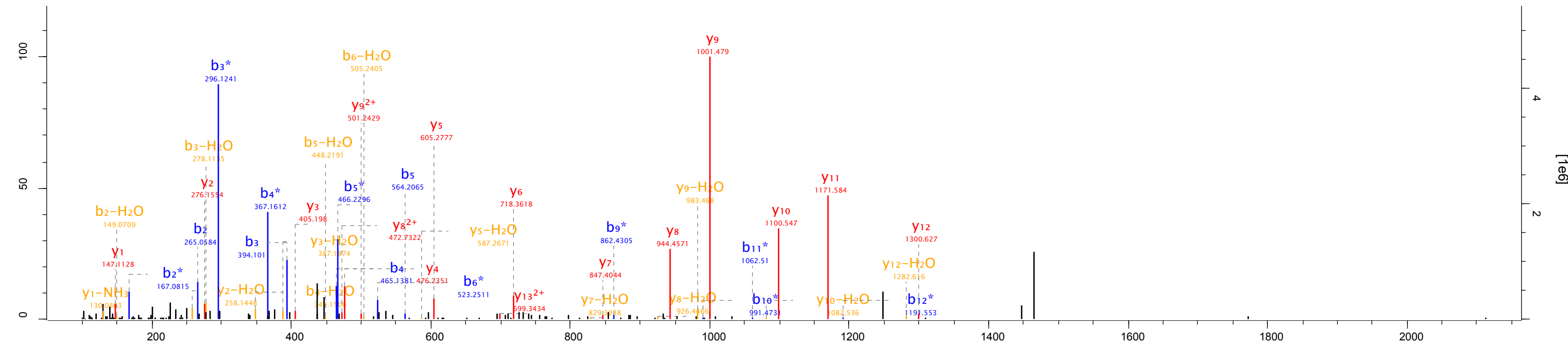


ac
 - S D E F S L A D A L P E H S P A K -
 b₂ b₃ b₄ b₅ b₆ b₇ b₈ b₉ b₁₄* b₁₆

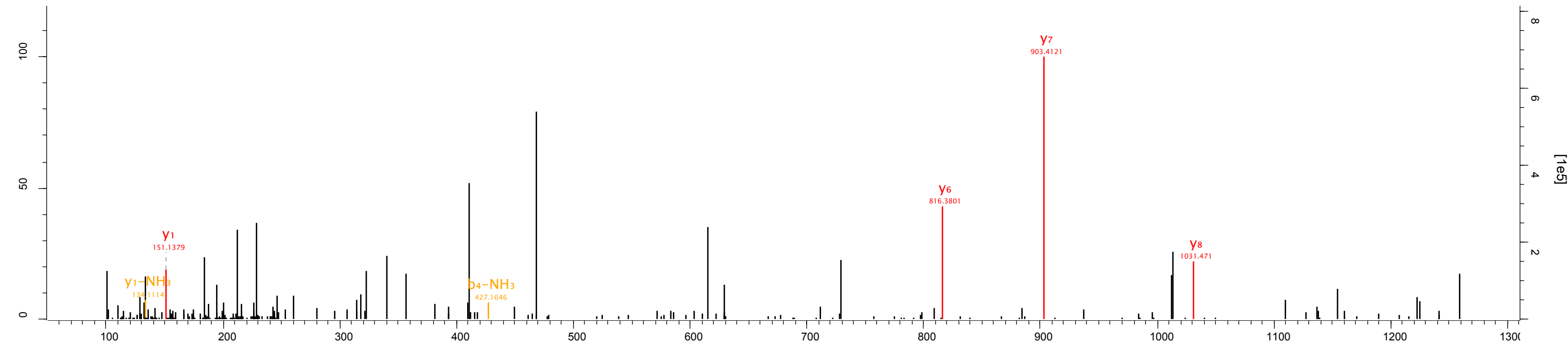
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 Scan: 13672 Method: FTMS; HCD Score: 178.02 m/z: 782.84 Gene names: PWWP2A



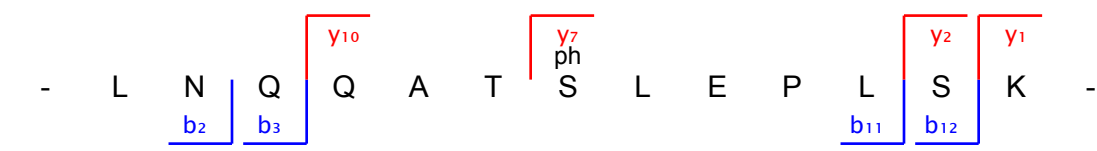
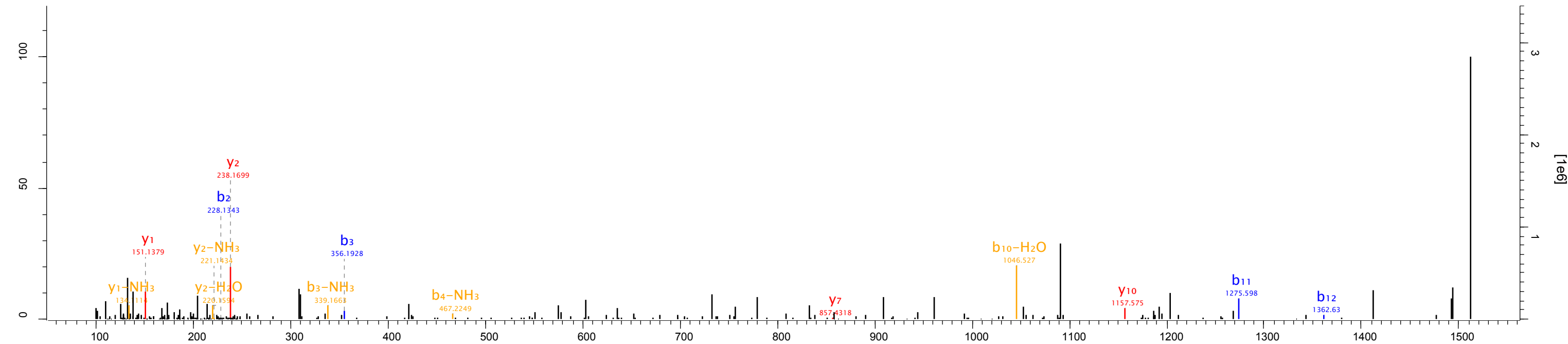
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Scan 4732 Method FTMS; HCD Score 53.76 m/z 630.79



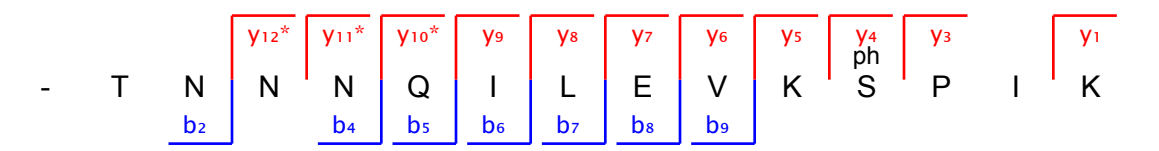
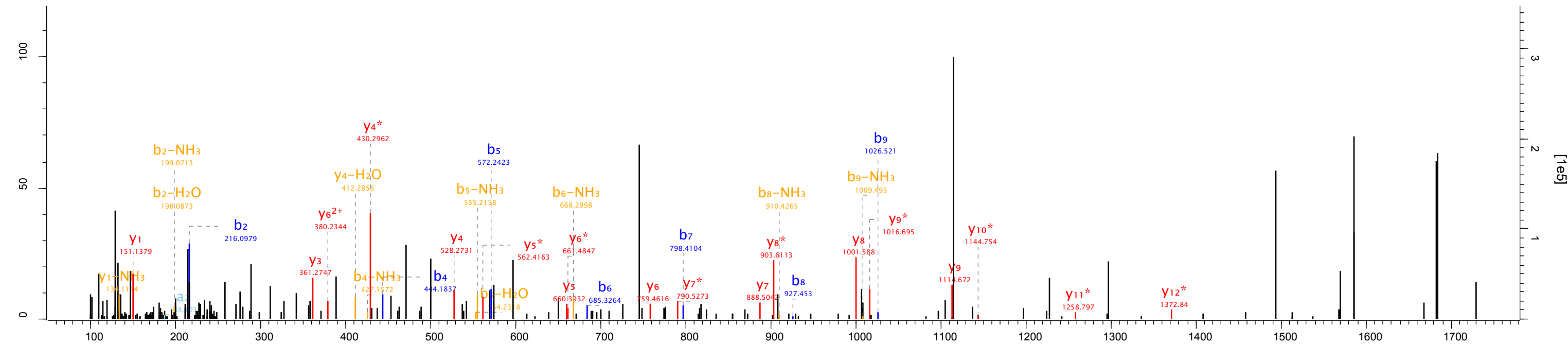
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Annotations above the sequence: y8 (above Q), y7 (above S), y6 (above Q), ph (above S), y1 (above K)

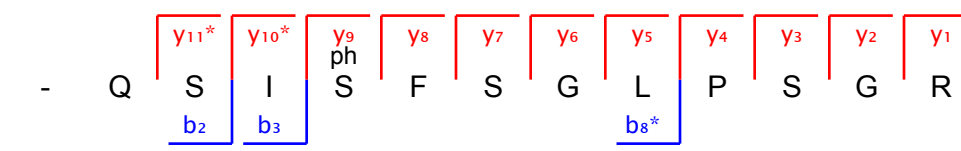
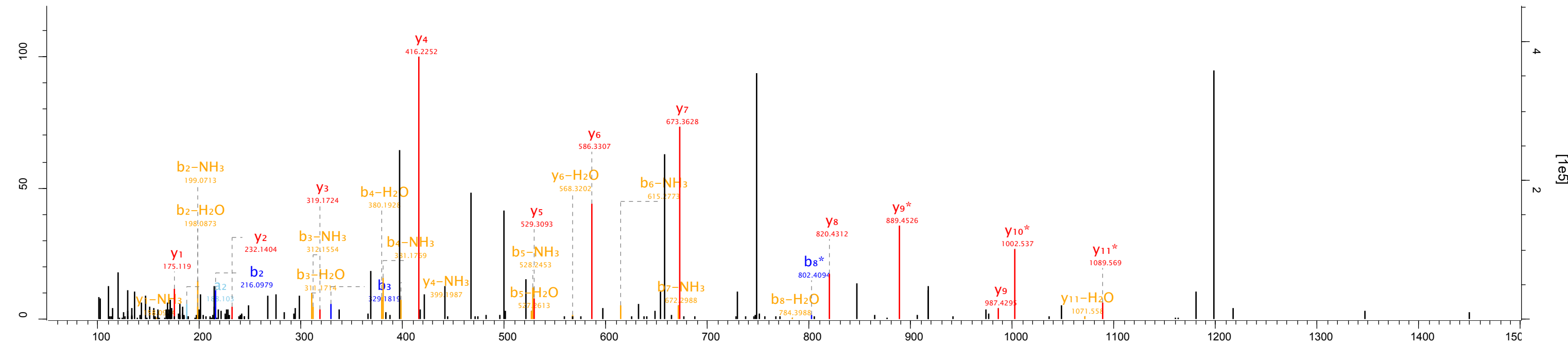
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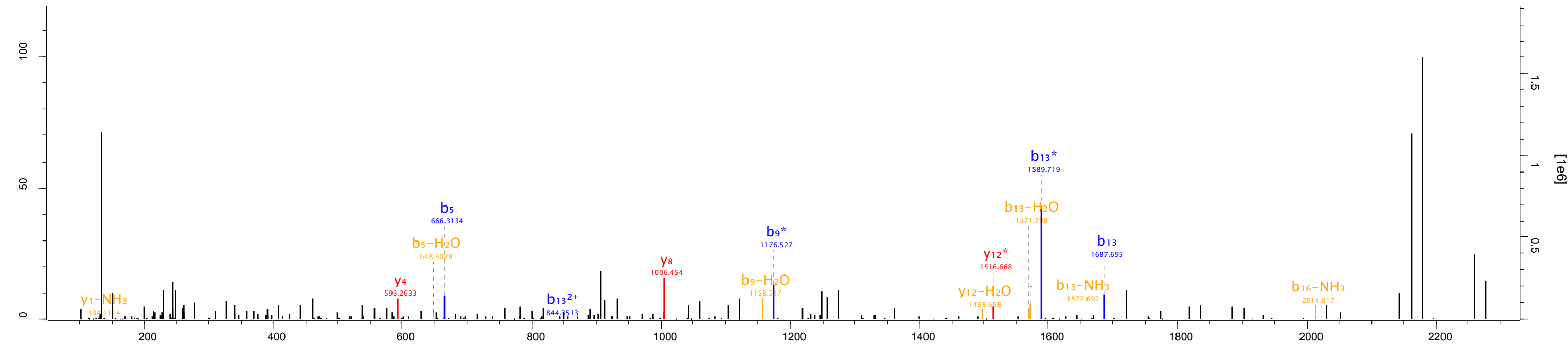
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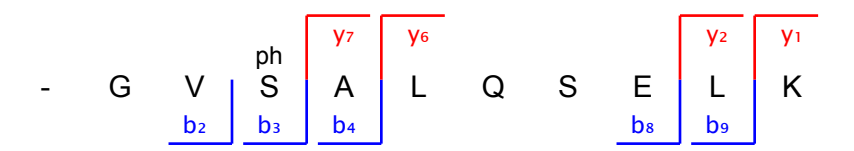
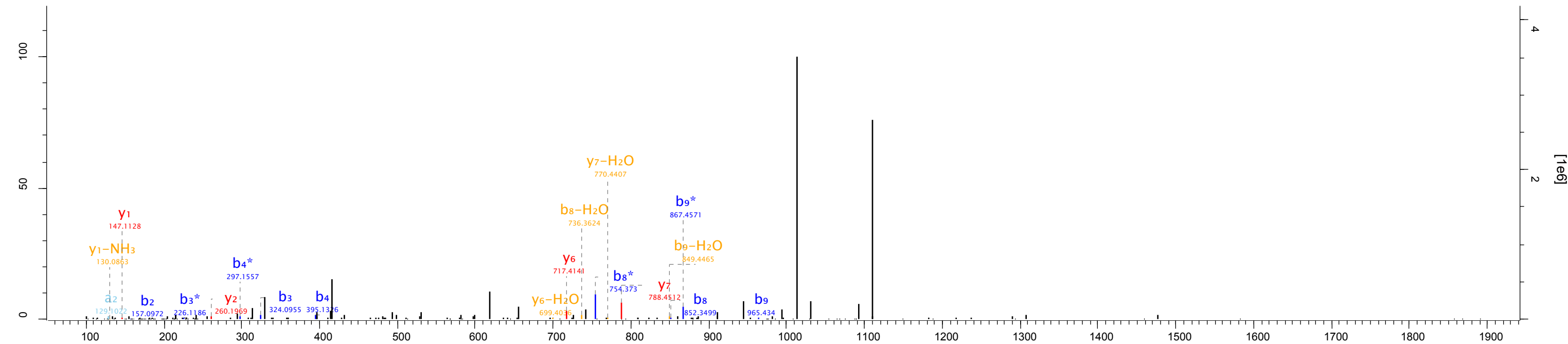
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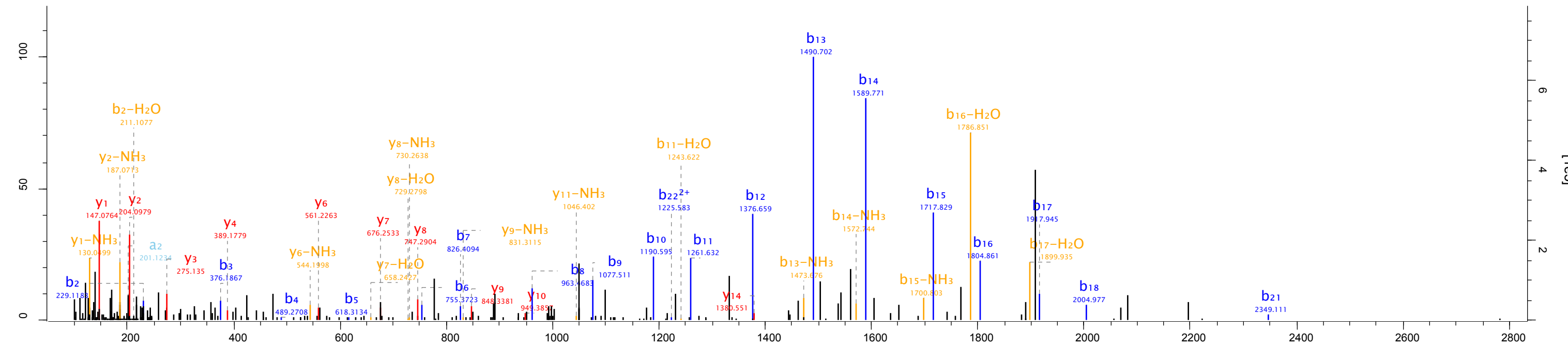
- Y P E L Y K T S Q N A L D F N T K -

Fragmentation mapping:
 - b₅ (blue line) connects Y and K.
 - y₁₂* (red line) connects K and N.
 - b₉* (blue line) connects Q and N.
 - y₈ (red line) connects N and A.
 - b₁₃ (blue line) connects D and F.
 - y₄ (red line) connects F and N.

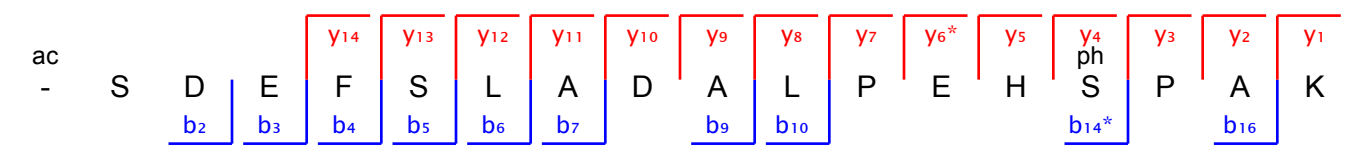
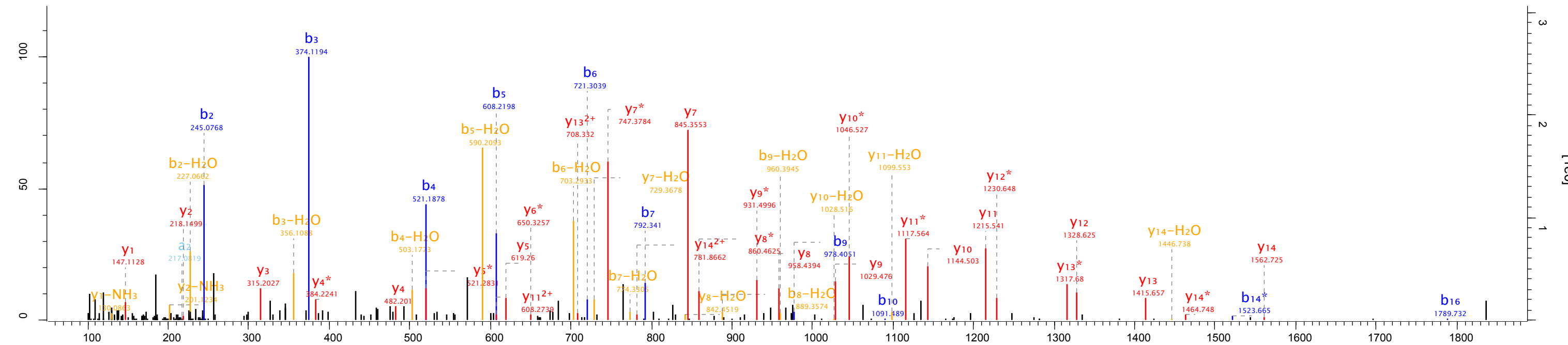
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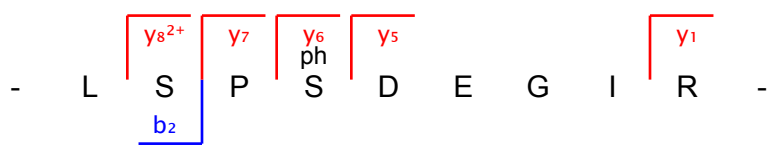
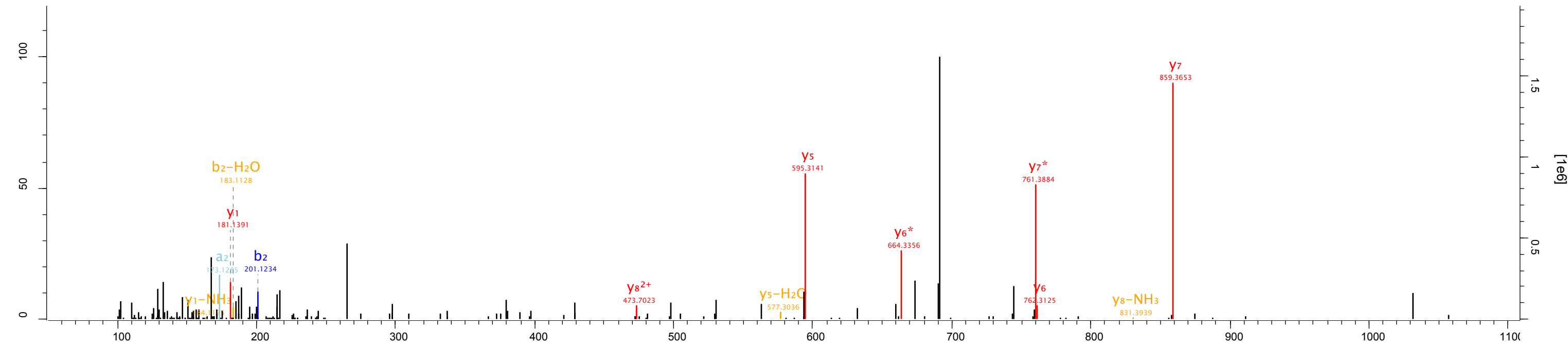
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 Score: 104.09
 m/z: 1100.17
 Gene names: CEBPG



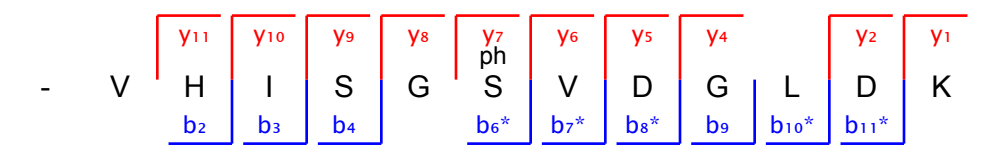
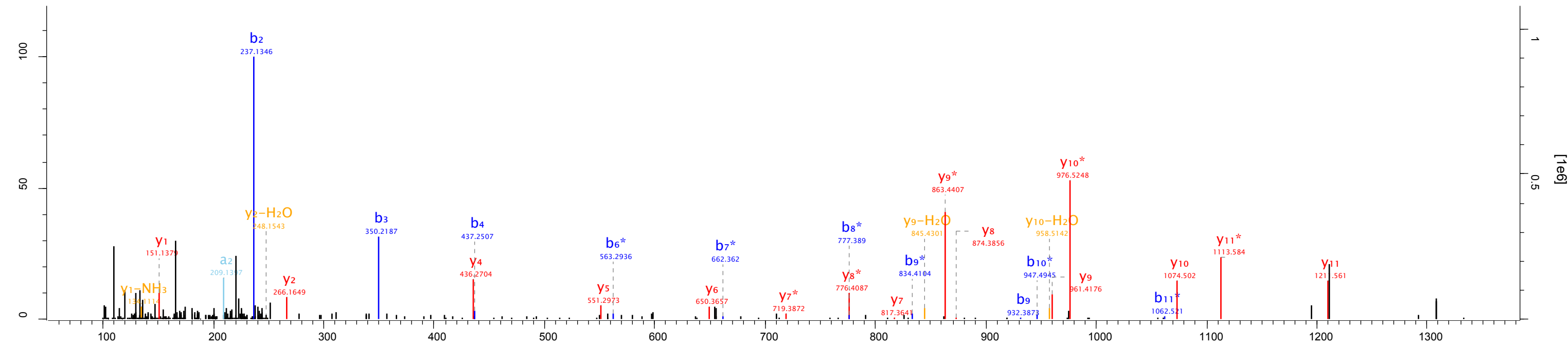
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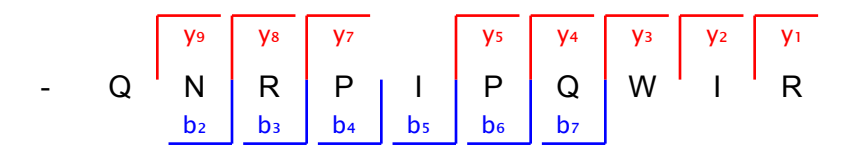
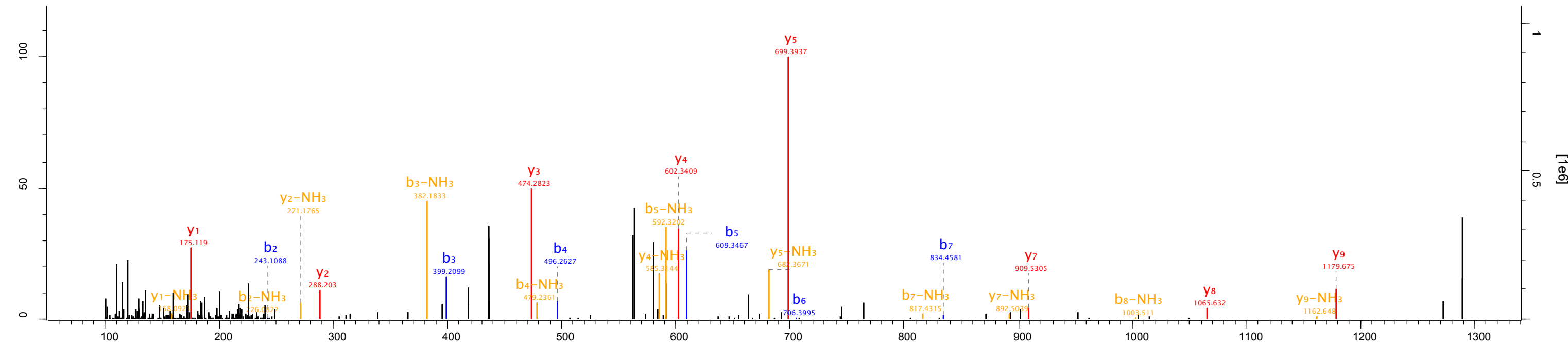
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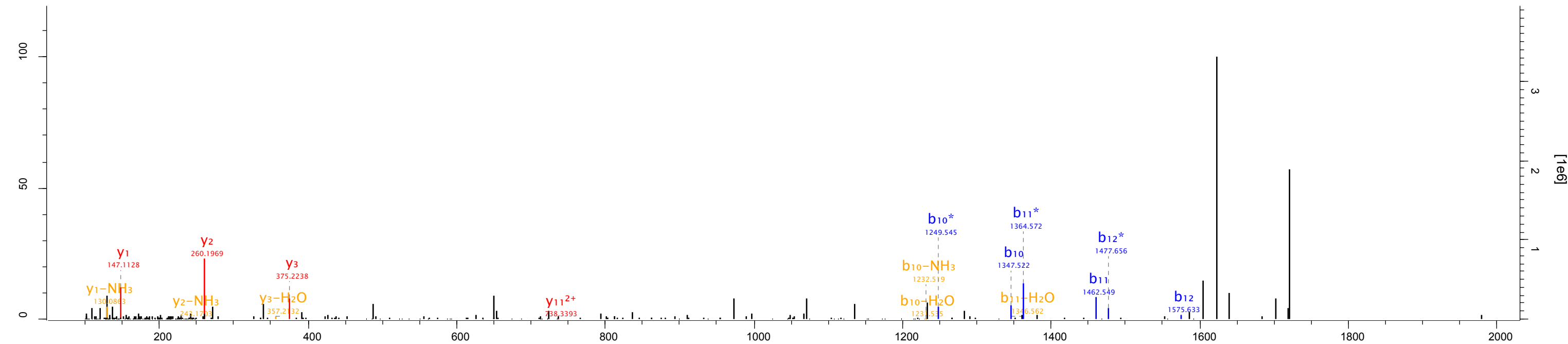
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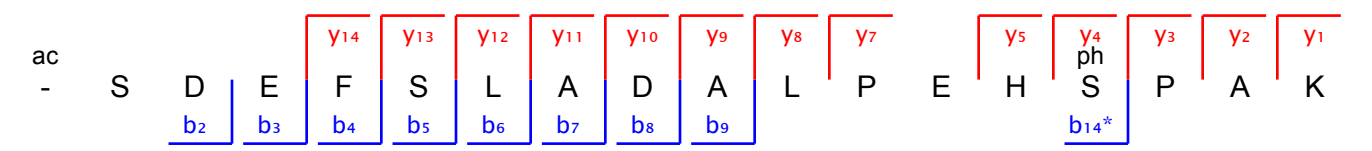
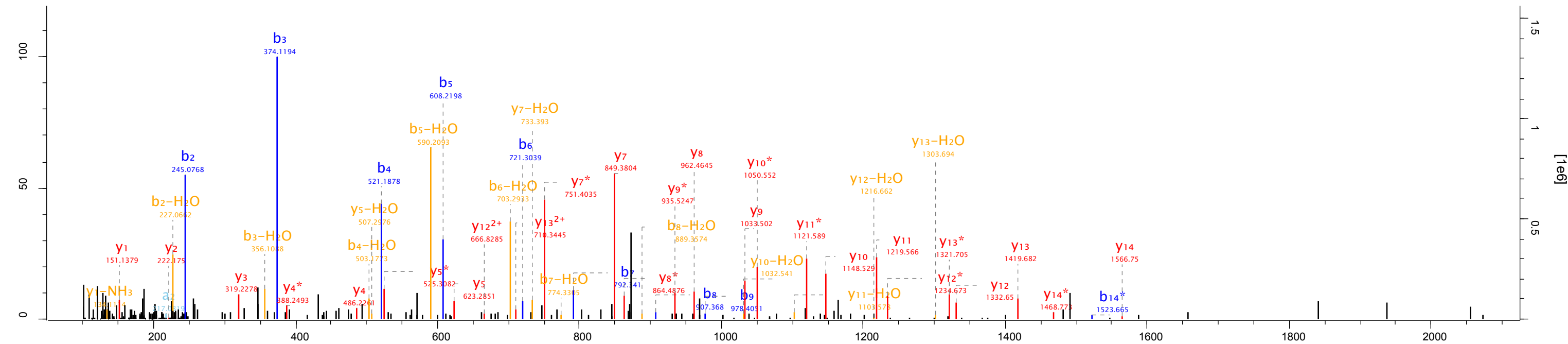


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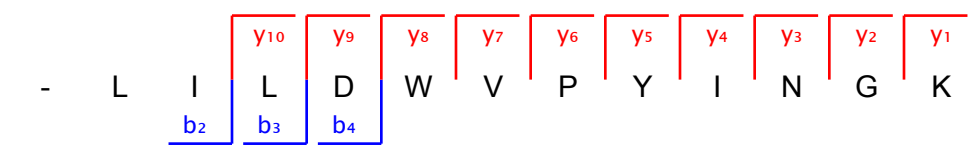
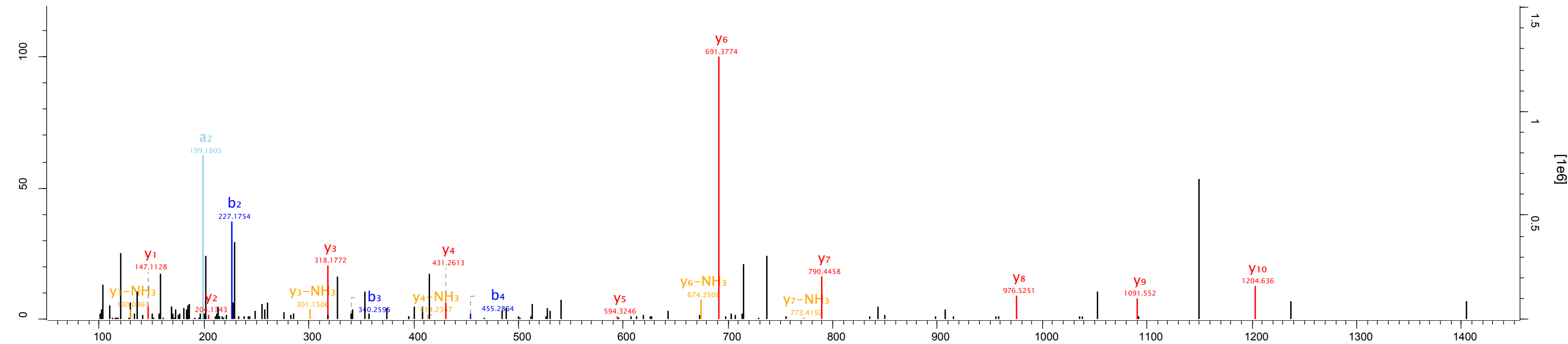


- D M Y^{y11²⁺} Q V C V R Q S^{b10} D^{y3} L^{y2} K^{y1} -

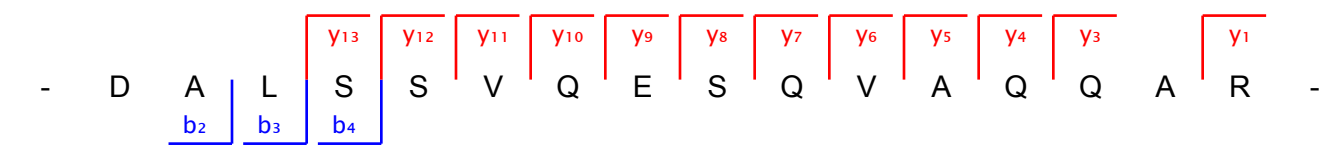
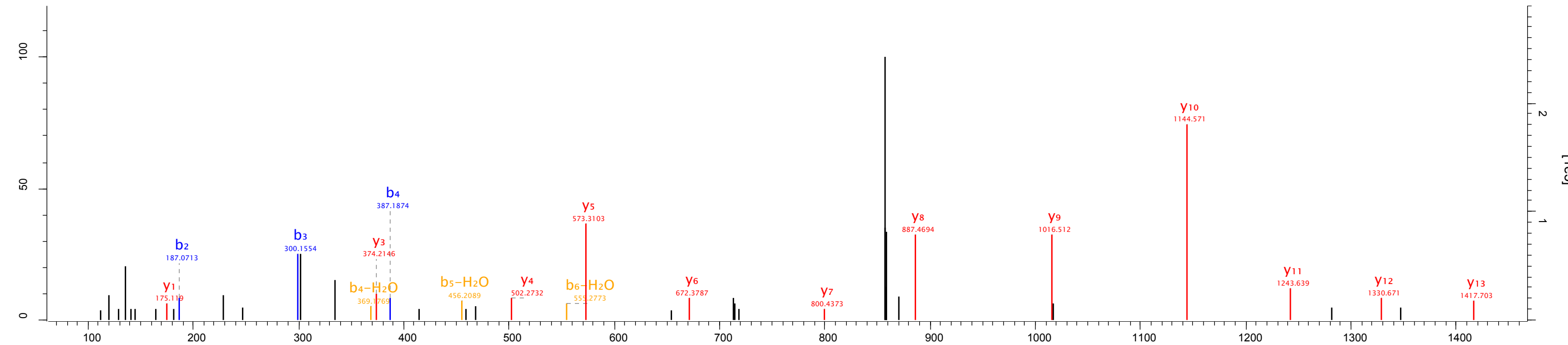
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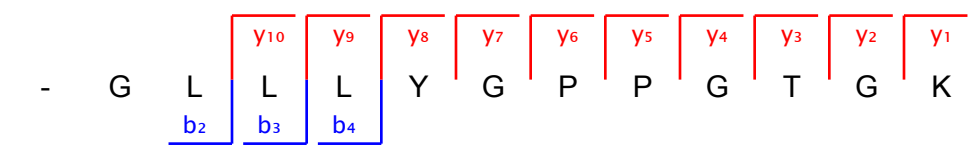
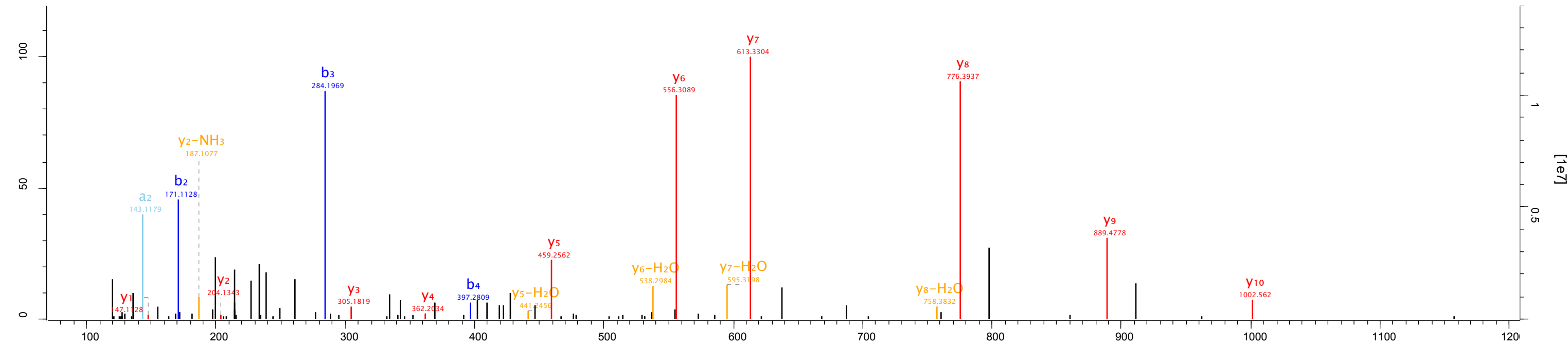
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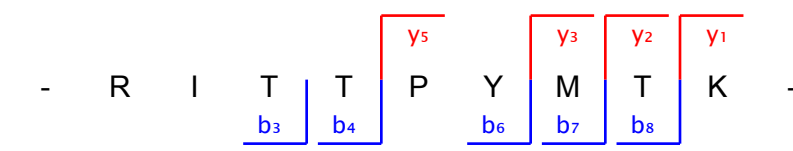
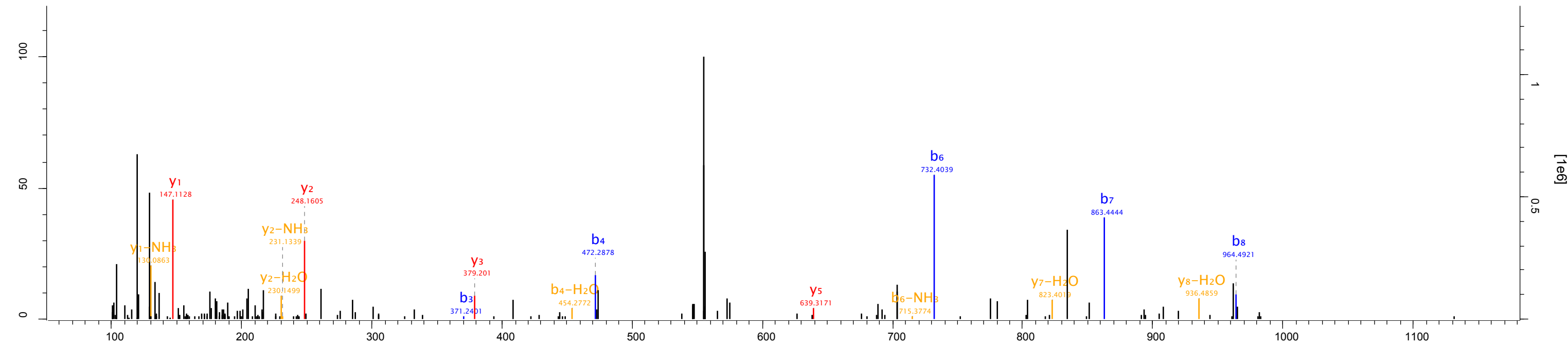
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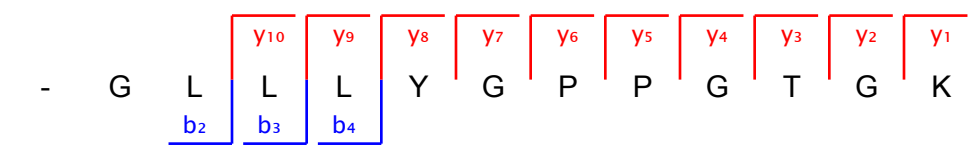
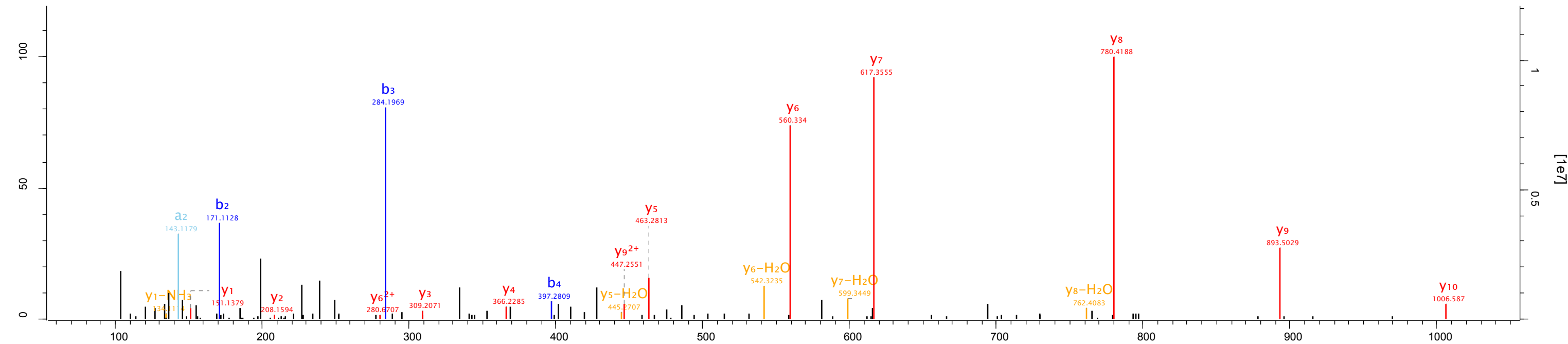
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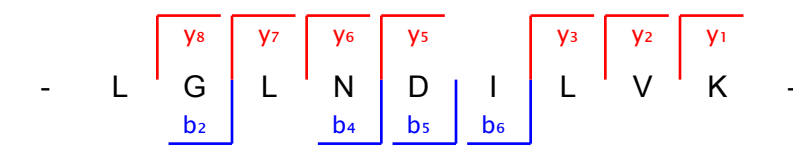
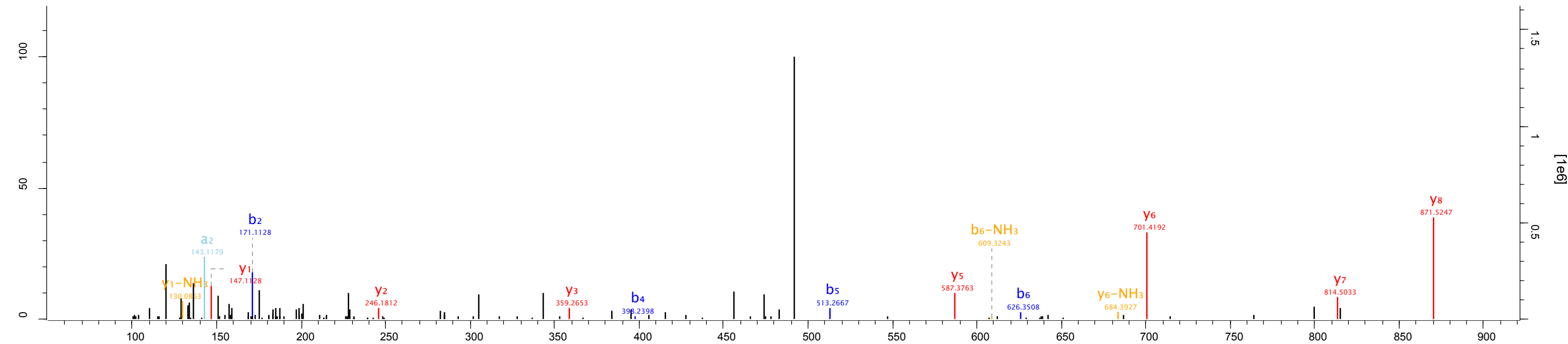
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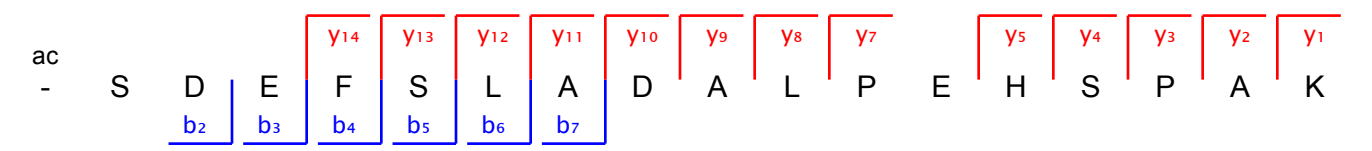
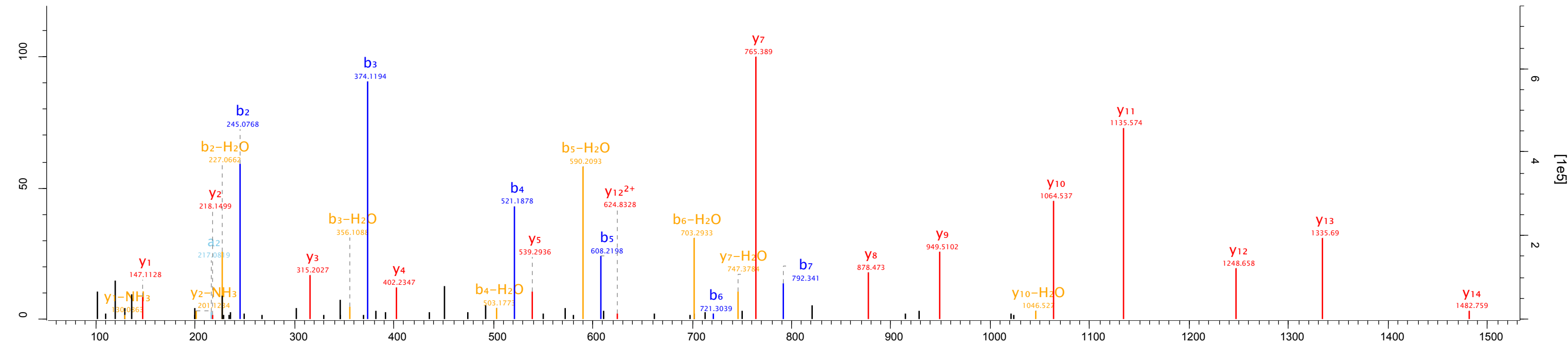
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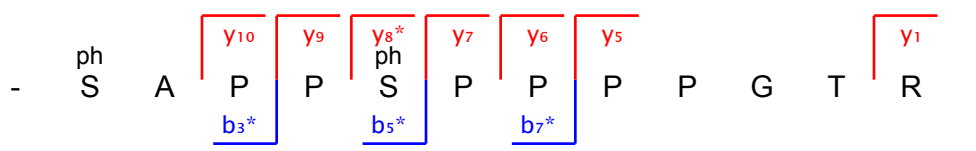
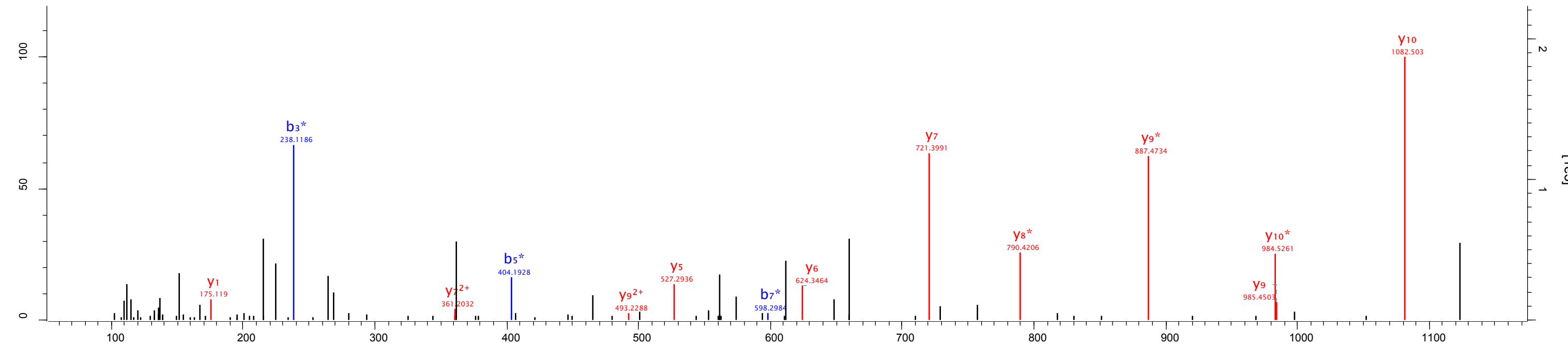
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 Scan: 70432 Method: FTMS; HCD Score: 67.33 m/z: 492.81 Gene names: STON2



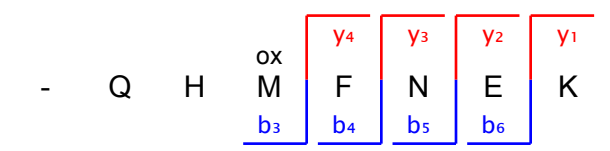
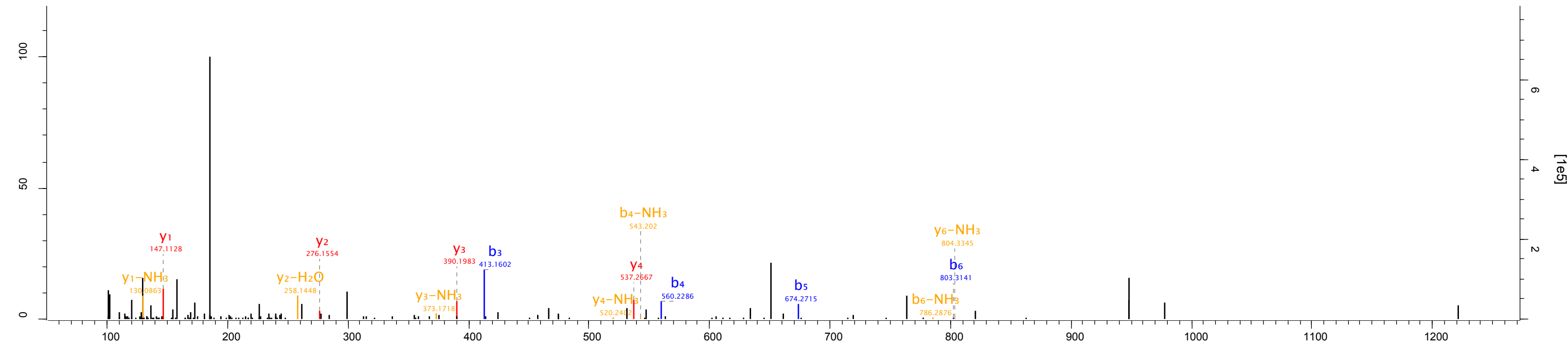
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 Scan: 78362 Method: FTMS; HCD Score: 138.91 m/z: 928.44 Gene names: MAPK11P1L



Raw file: 20150822_A375SR_Phospho_BR3_02
 Scan: 5442 Method: FTMS; HCD Score: 44.39 m/z: 660.77 Gene names: GPSM3

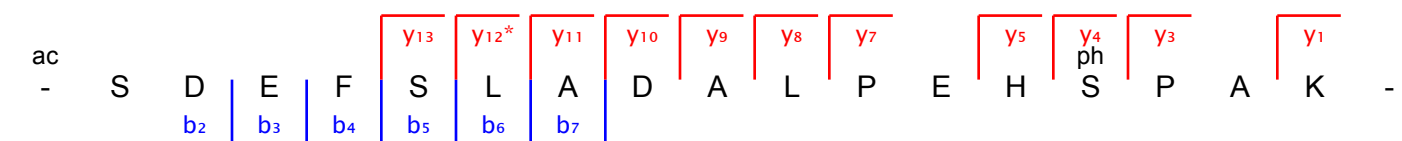
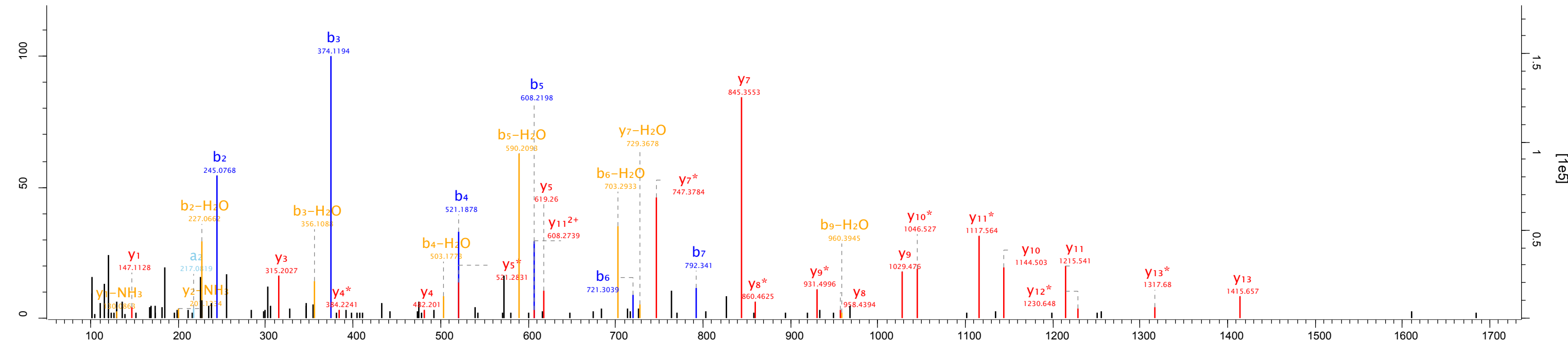


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 Scan: 8992 Method: FTMS; HCD Score: 77.28 m/z: 475.21 Gene names: GPR64

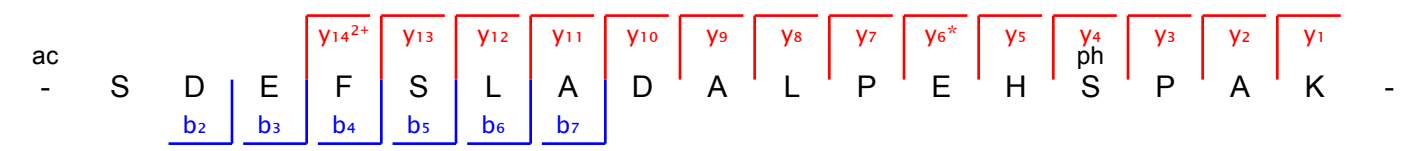
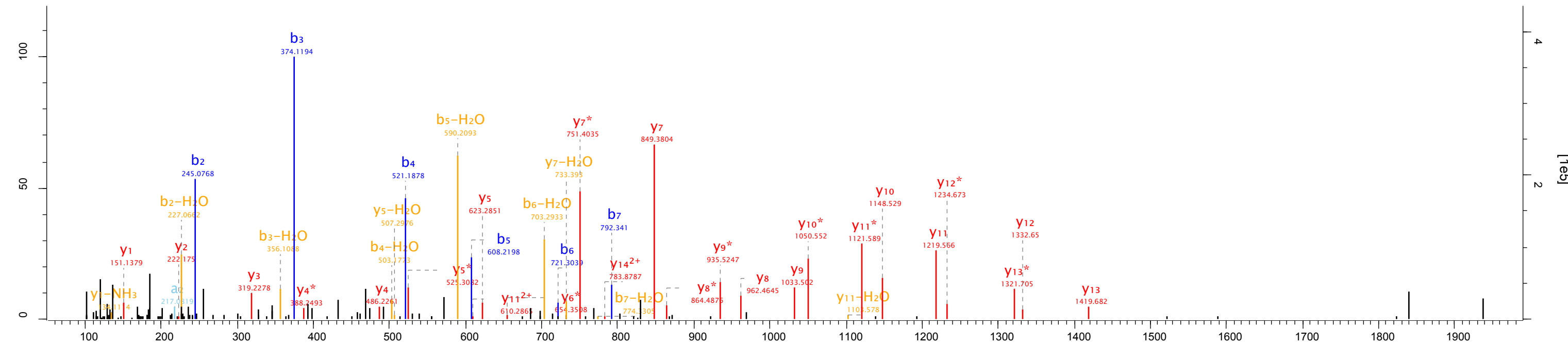


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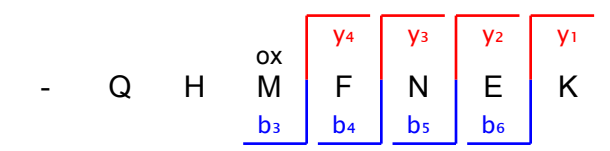
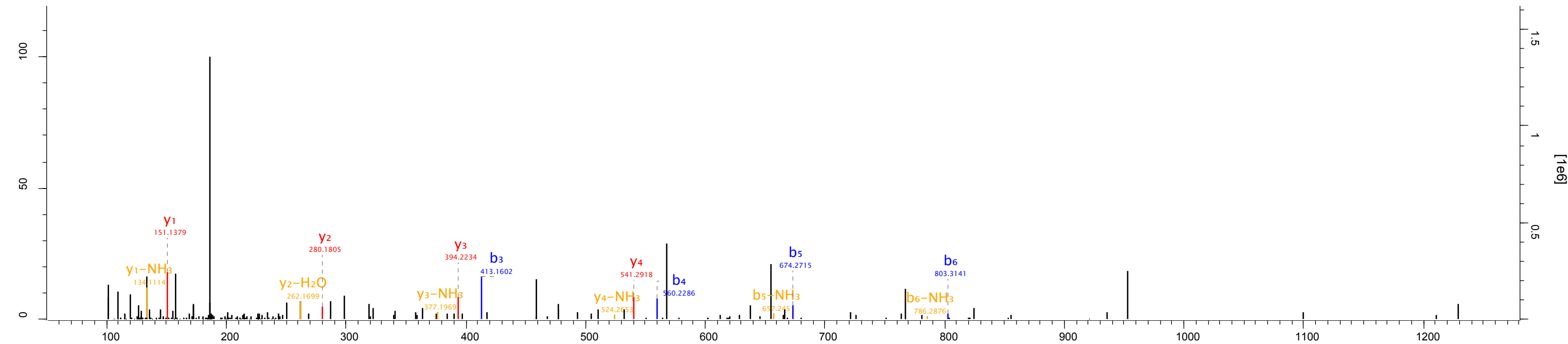
Scan 23872 Method FTMS; HCD Score 127.58 m/z 968.42 Gene names MAPK11P1L



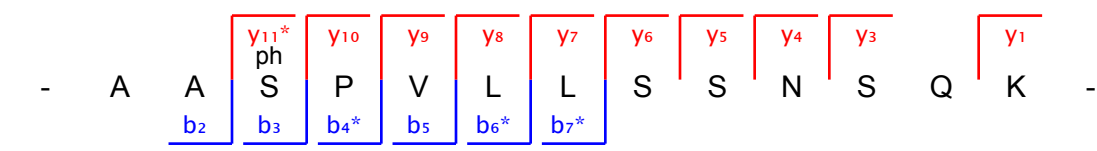
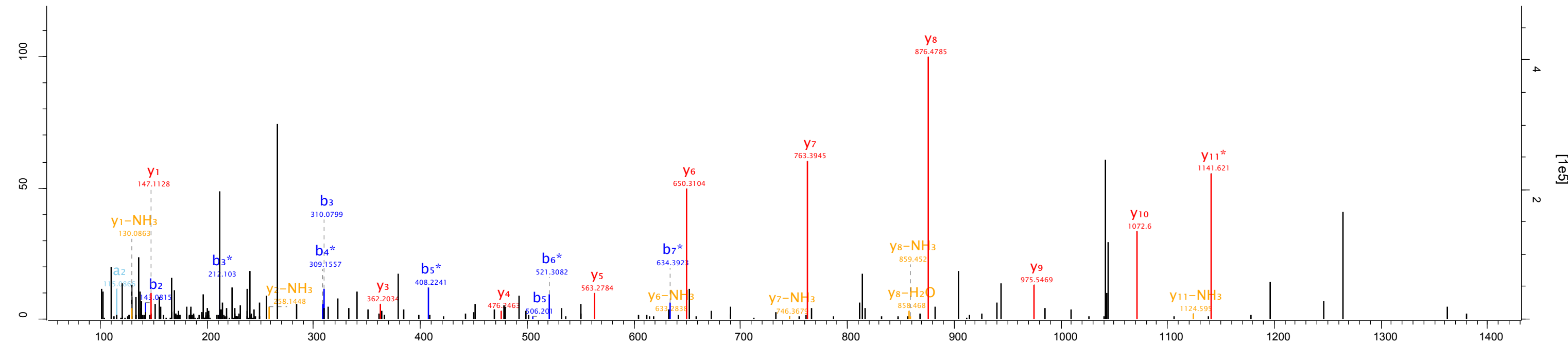
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 Scan: 23952 Method: FTMS; HCD Score: 164.94 m/z: 970.94 Gene names: MAPK11P1L



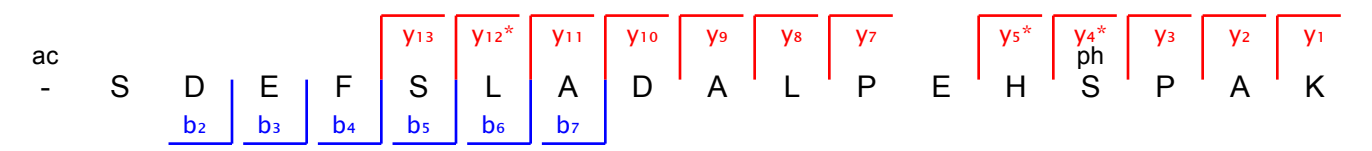
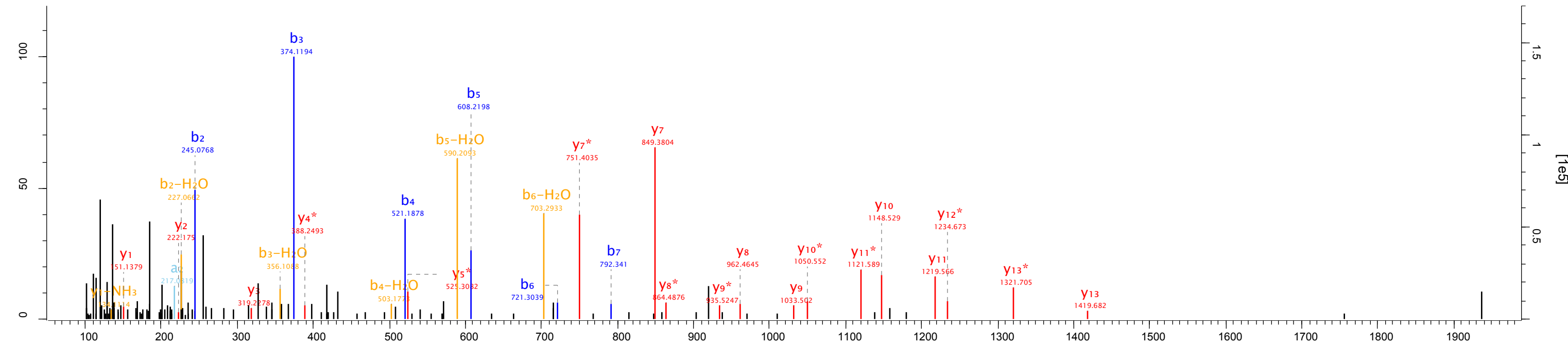
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 Scan: 10152 Method: FTMS; HCD Score: 83.75 m/z: 477.23 Gene names: GPR64



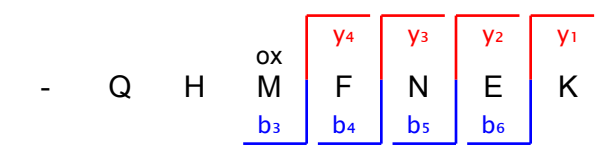
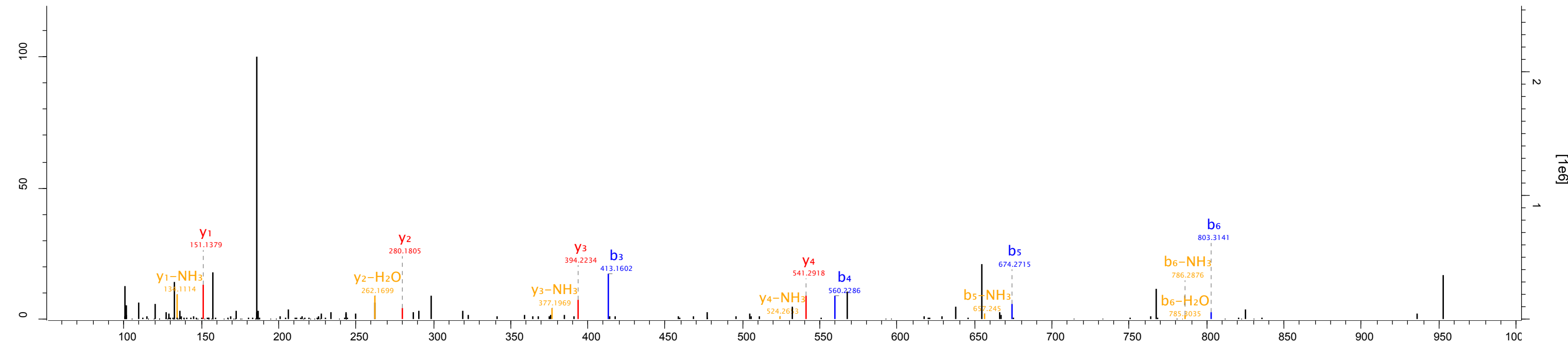
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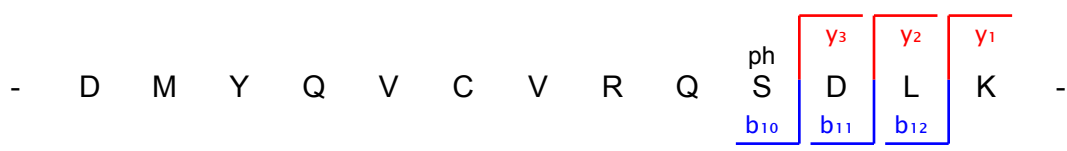
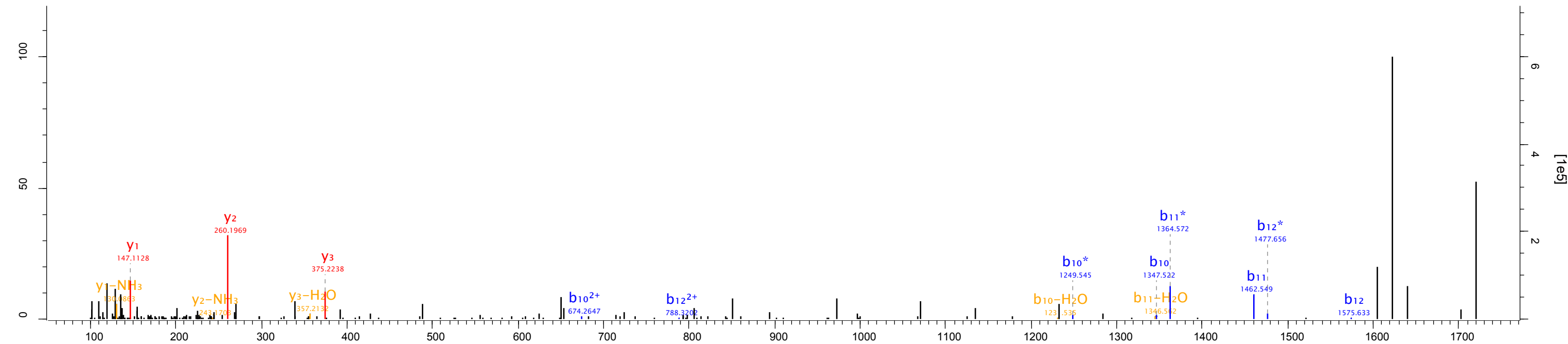
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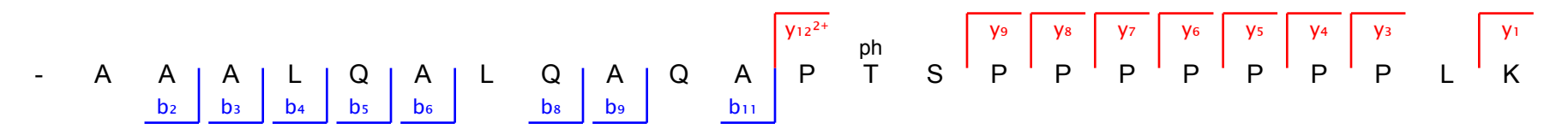
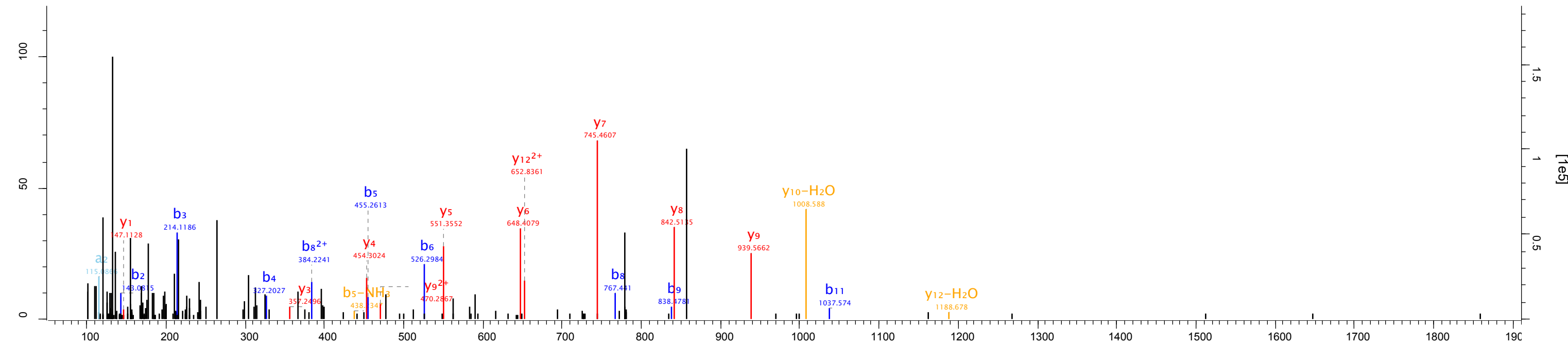
Raw file Scan Method Score m/z Gene names
 20150822_A375SR_Phospho_BR3_08 10572 FTMS; HCD 107.59 477.23 GPR64



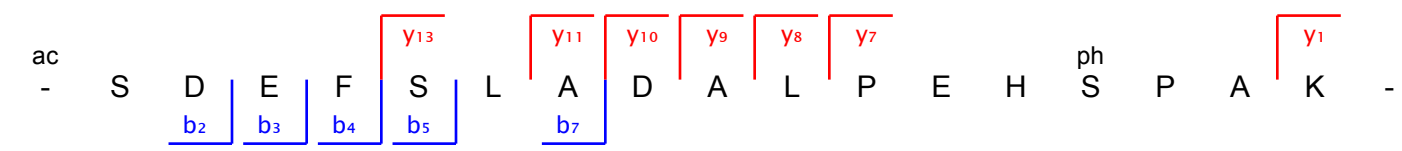
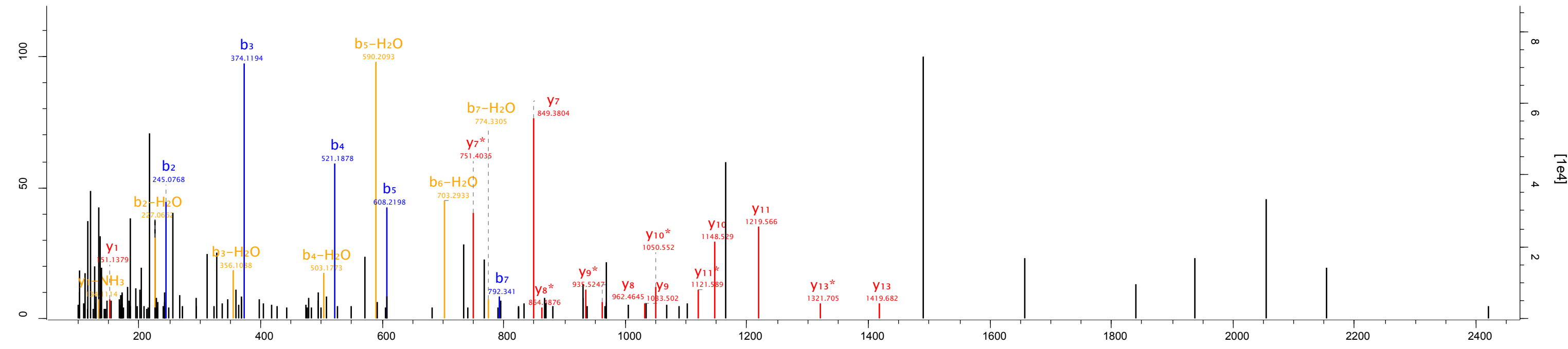
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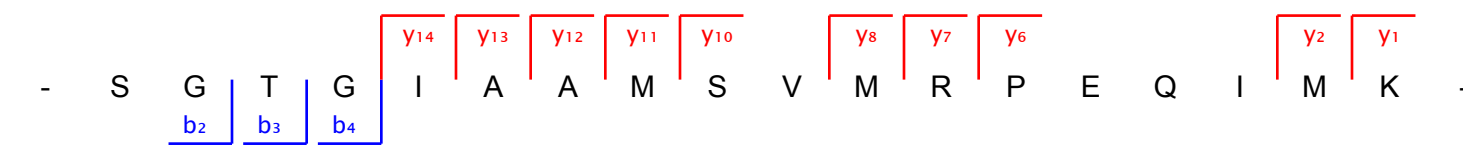
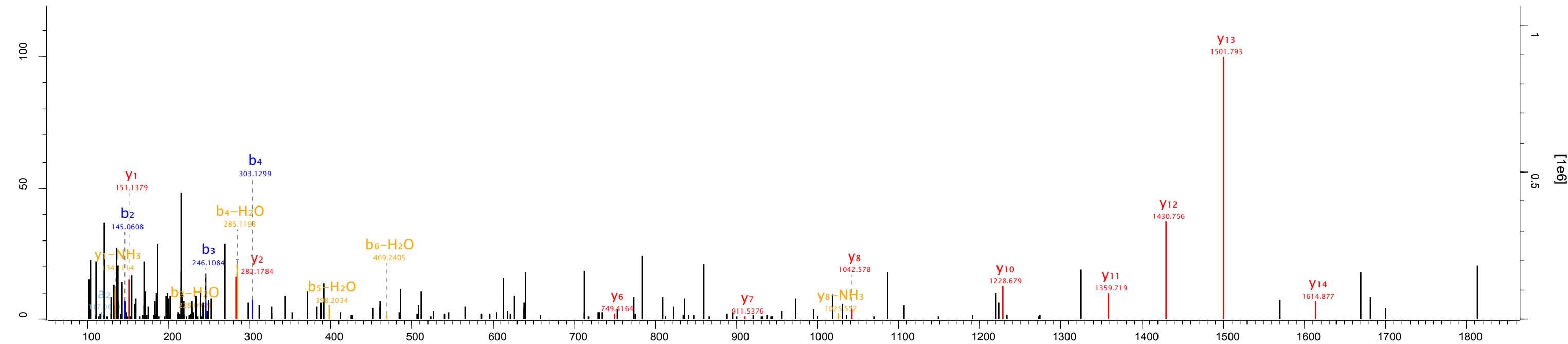
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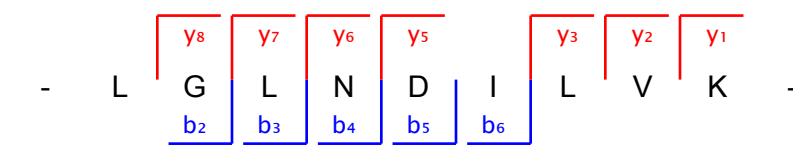
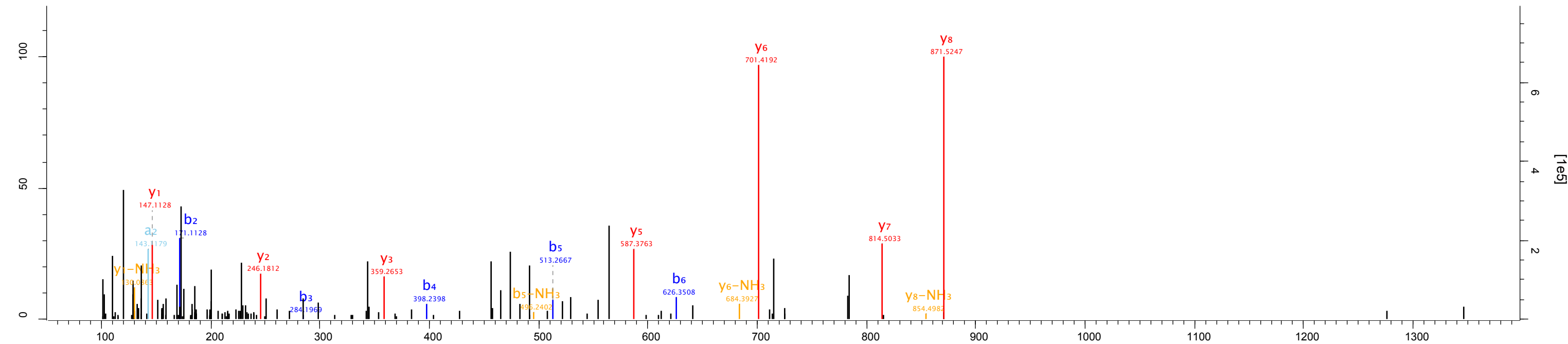
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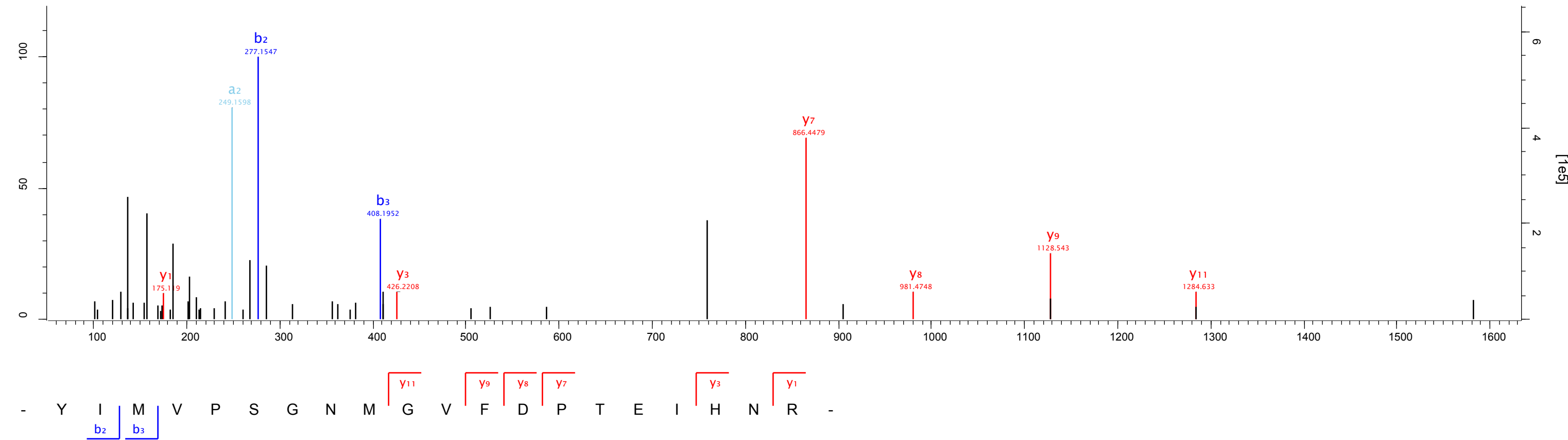


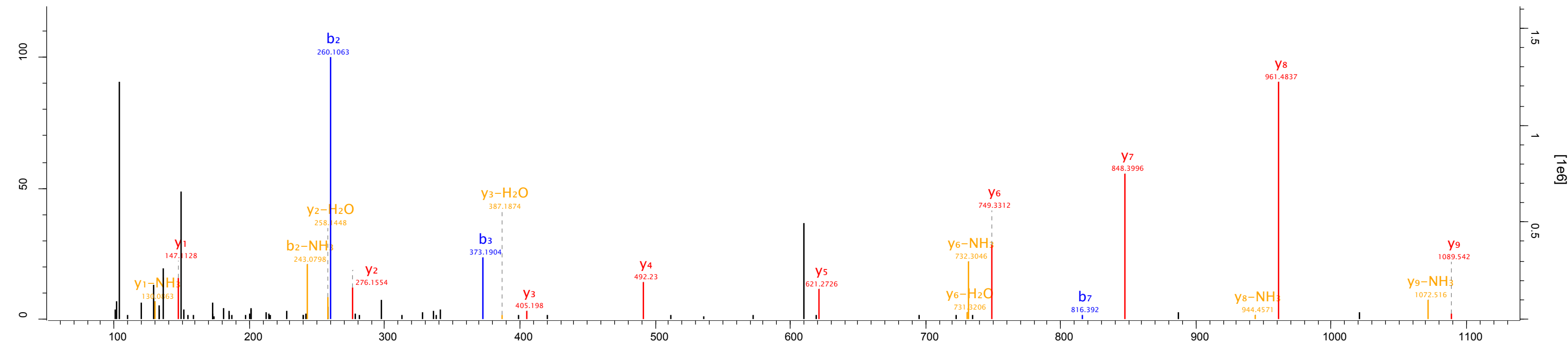
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 Scan: 71612 Method: FTMS; HCD Score: 14.11 m/z: 639.67 Gene names: ATP6V0C



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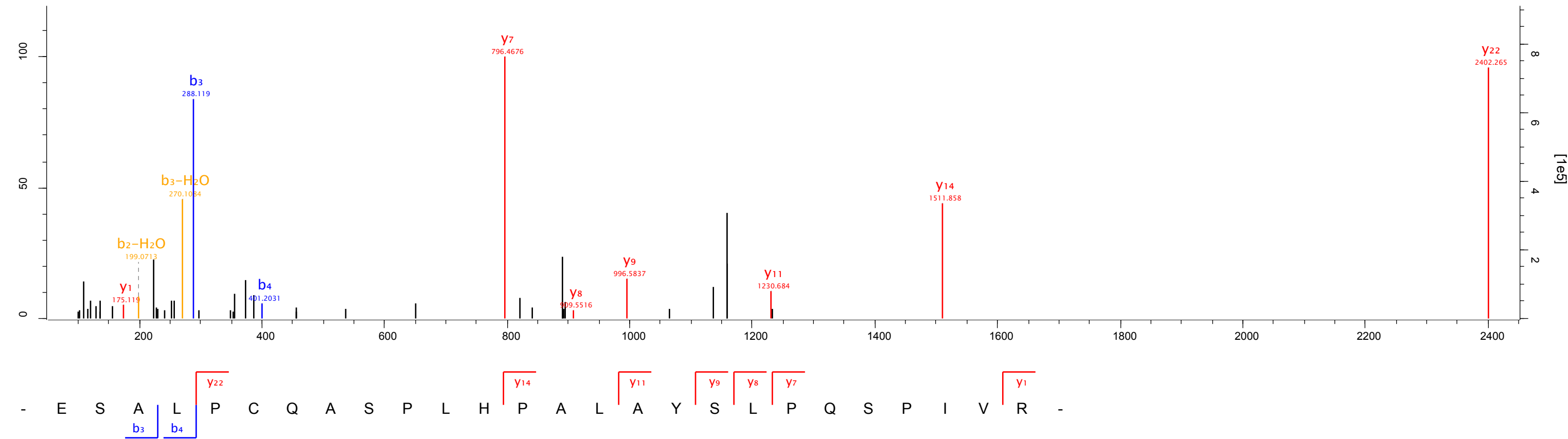


- M Q L V Q E S E E K -

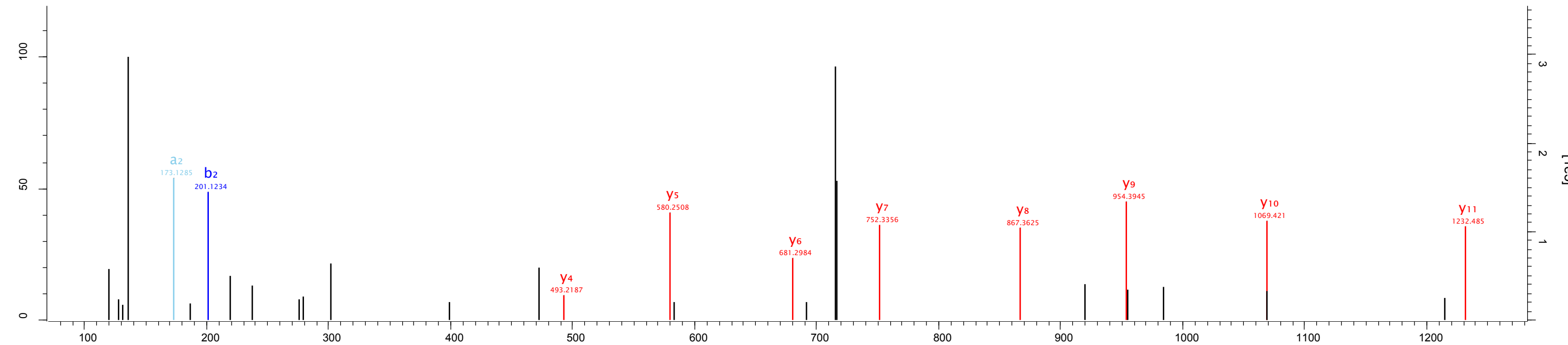
b2 b3 b7

Raw file
20180707_MaS_A375SR_LM_proteome_06

Scan 26402 Method FTMS; HCD Score 12.22 m/z 935.5 Gene names C1orf85



Raw file 20180707_MaS_A375SR_LM_proteome_06 Scan 6822 Method FTMS; HCD Score 42.32 m/z 716.8 Gene names LEPROT

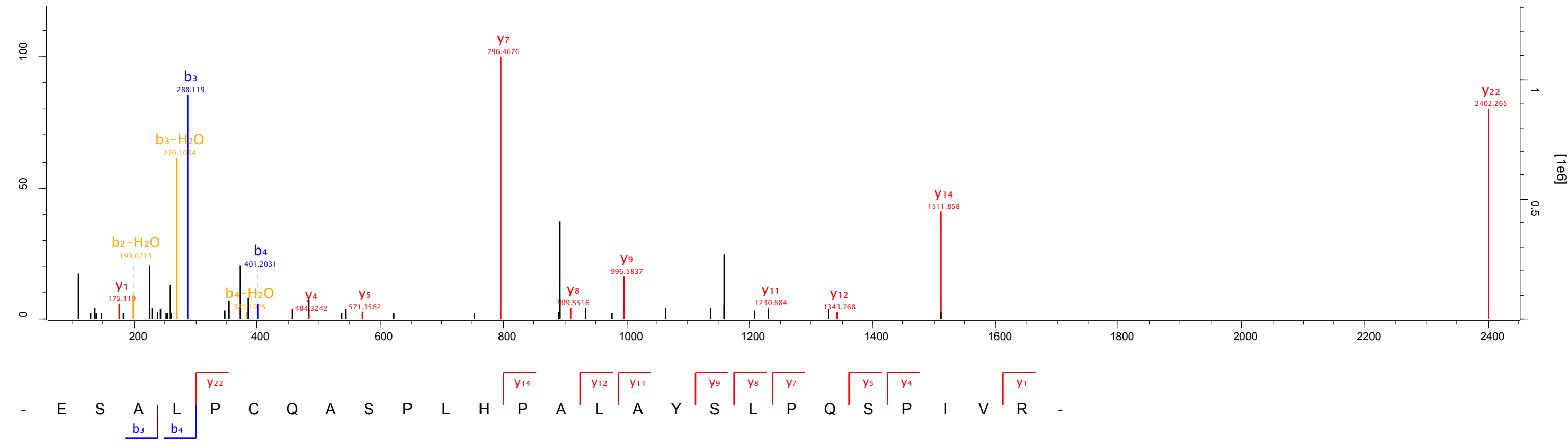


- V T Y D S D A T S S A C R -

Fragmentation diagram showing b₂ (blue) and y₄-y₁₁ (red) ions. The b₂ ion is formed from the first two residues (V, T). The y₄-y₁₁ ions are formed from the last eight residues (Y, D, S, D, A, T, S, S).

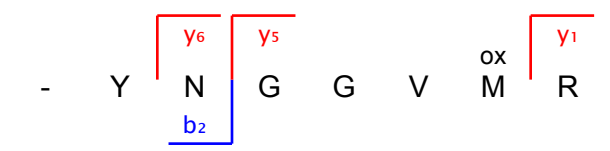
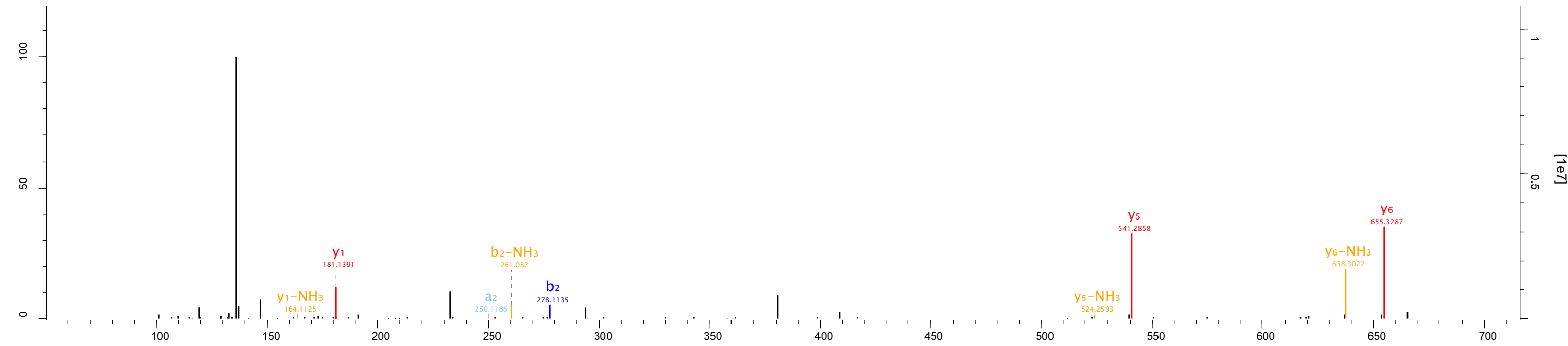
Raw file
20180707_MaS_A375SR_LM_proteome_07

Scan Method Score m/z Gene names
26382 FTMS; HCD 28.09 935.16 C1orf85

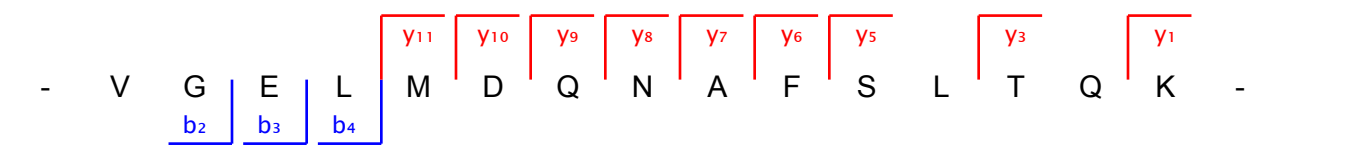
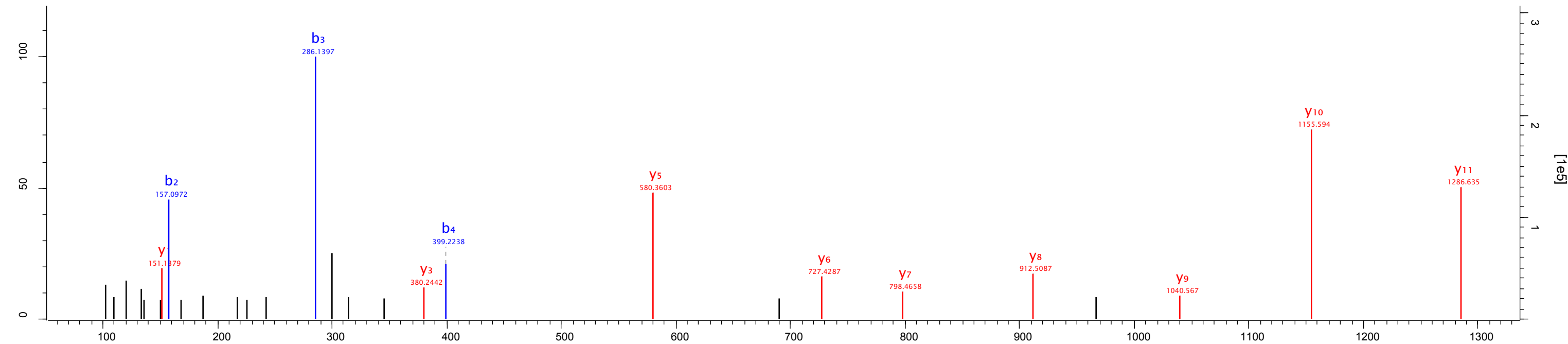


Raw file
20180707_MaS_A375SR_LM_proteome_16

Scan Method Score m/z Gene names
5072 FTMS; HCD 59.64 409.7 KCNN2



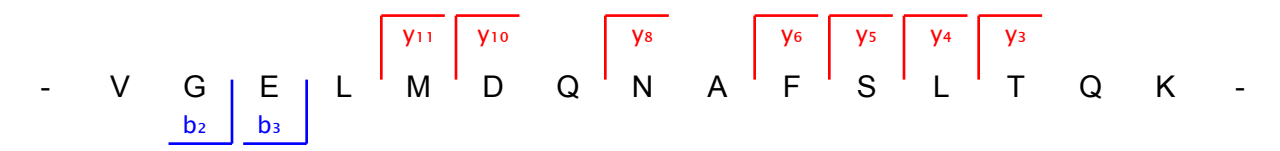
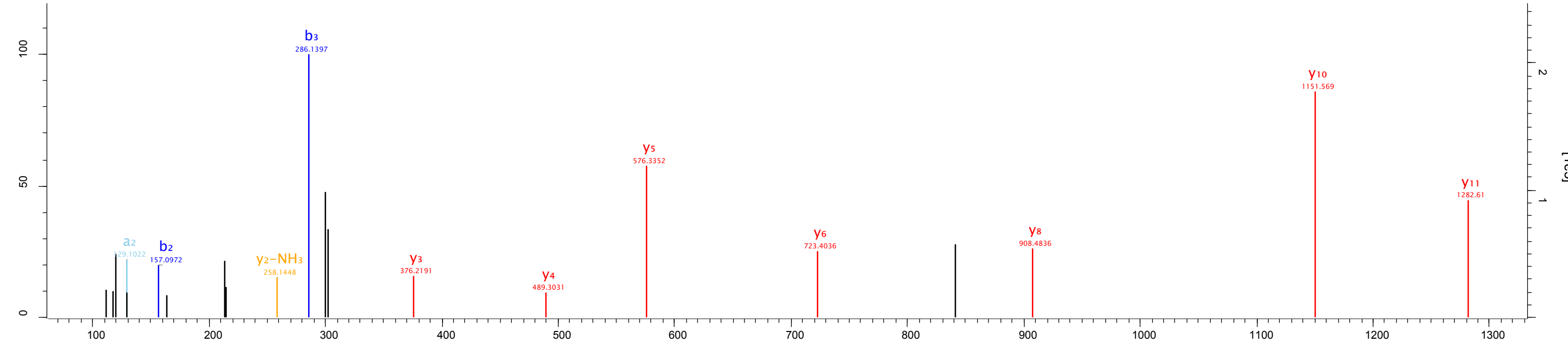
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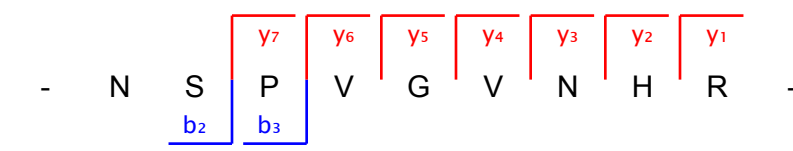
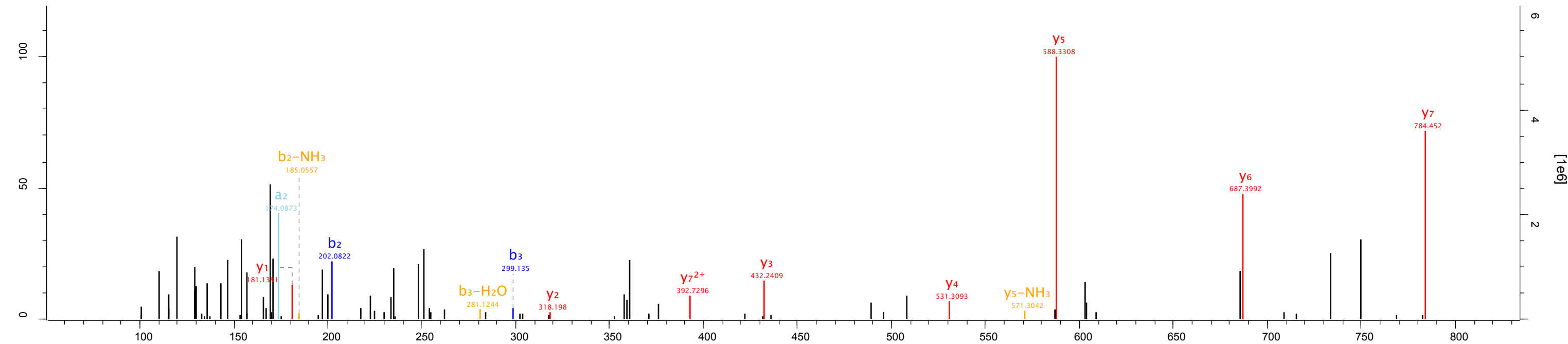
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20180707_MaS_A375SR_LM_proteome_19

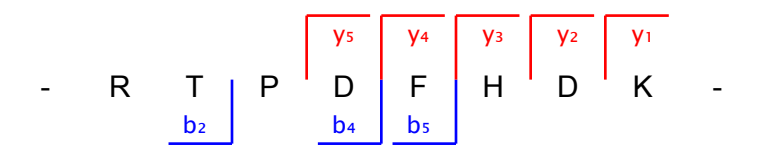
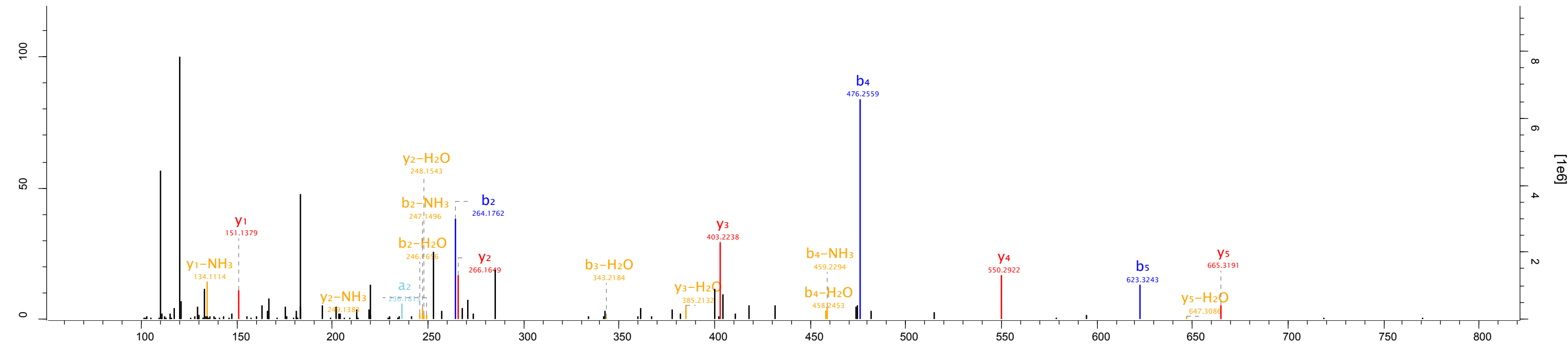
Scan	Method	Score	m/z	Gene names
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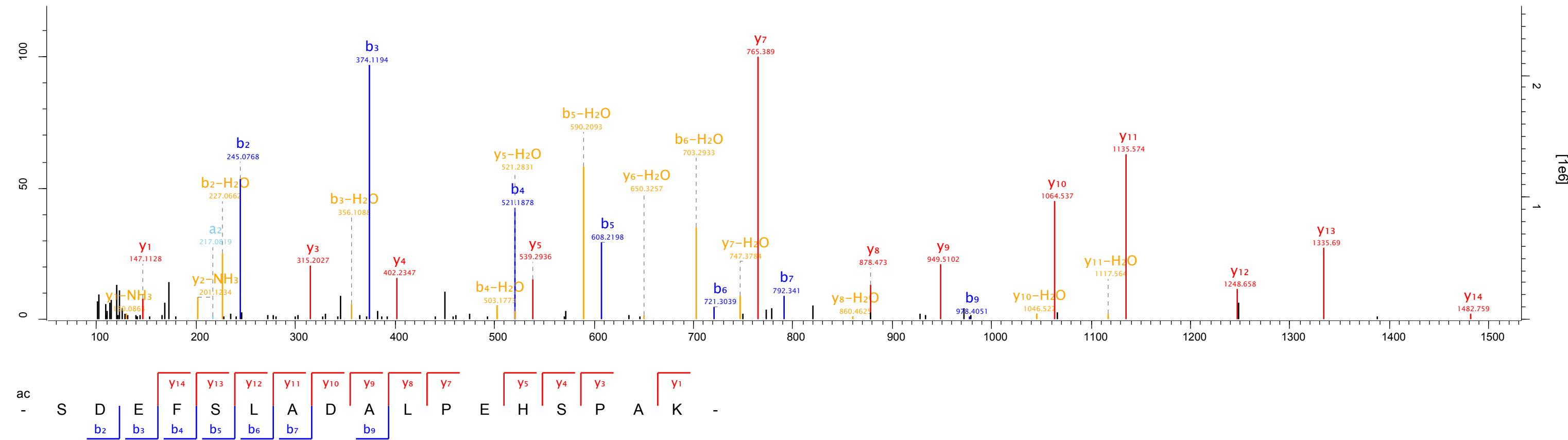


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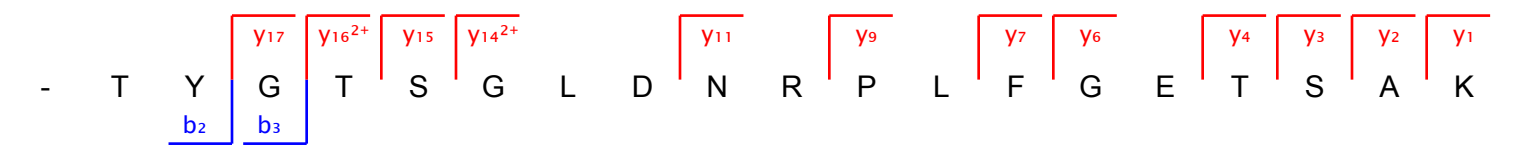
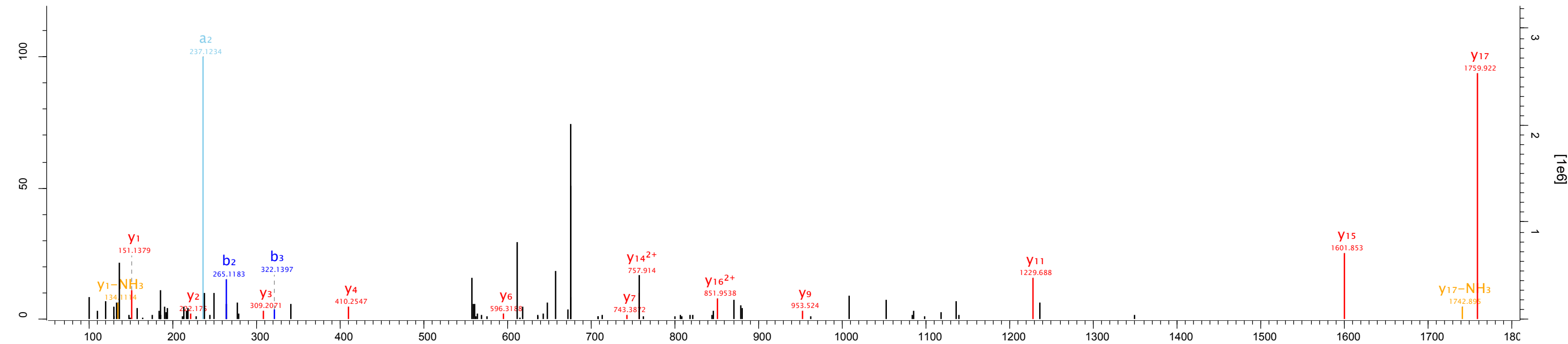
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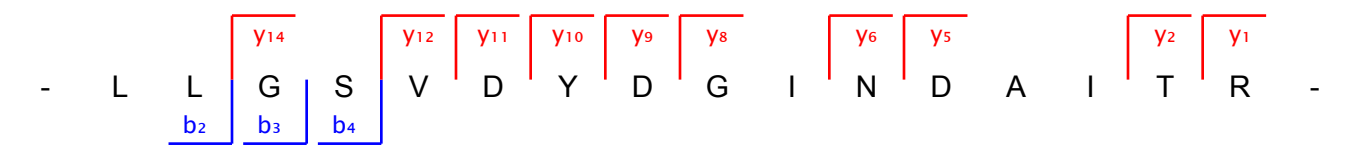
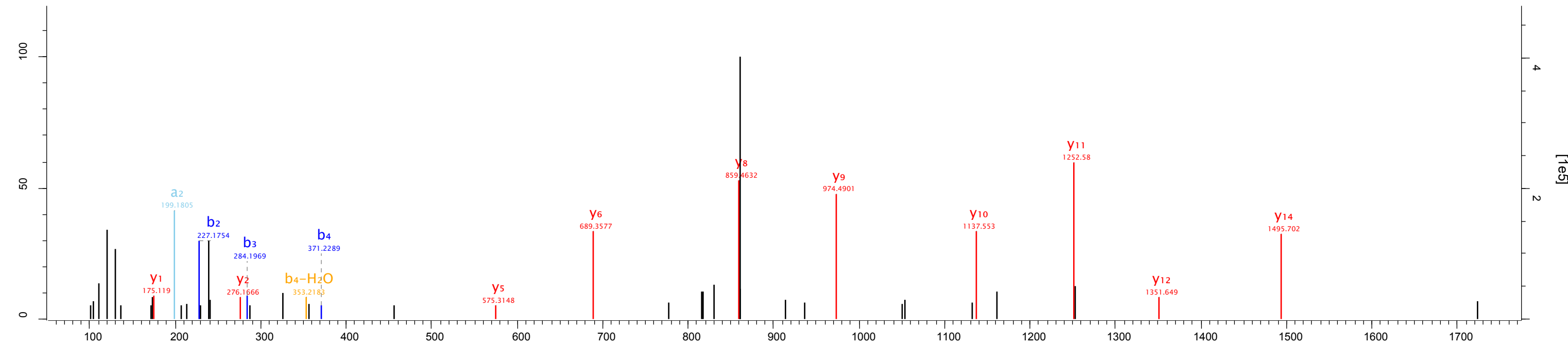


Raw file
20180707_MaS_A375SR_ML_proteome_01

Scan 16542 Method FTMS; HCD Score 27.92 m/z 675.69 Gene names TMEM243

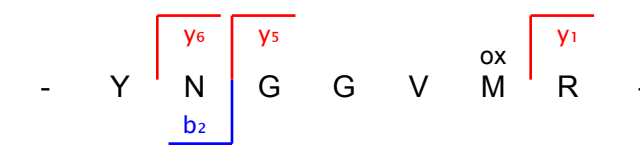
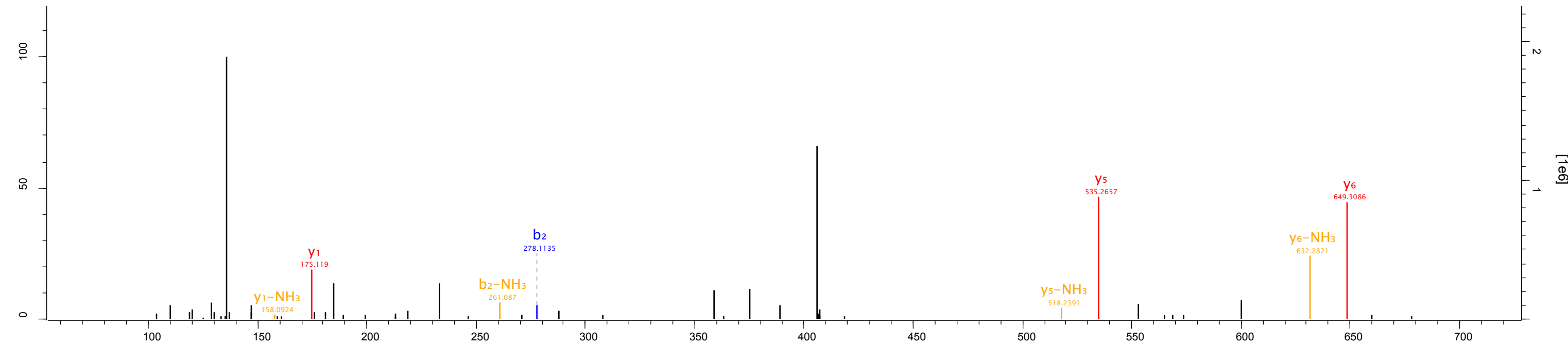


Raw file 20180707_MaS_A375SR_ML_proteome_01 Scan 23142 Method FTMS; HCD Score 57.97 m/z 861.43 Gene names PIK3C2B



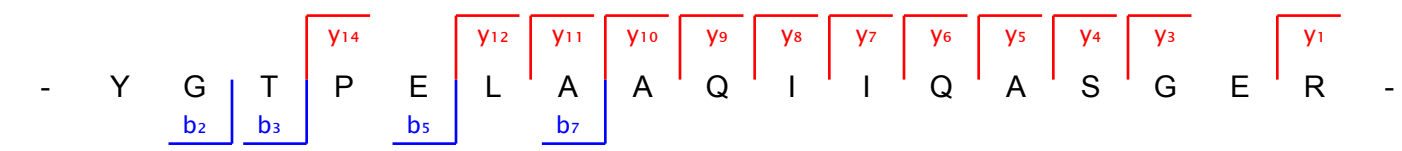
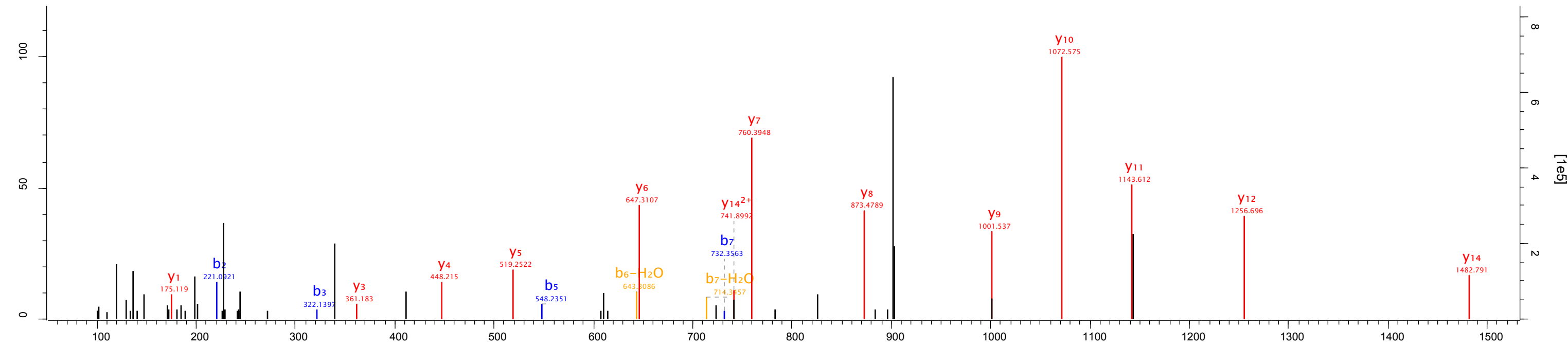
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20180707_MaS_A375SR_ML_proteome_02

Scan Method Score m/z Gene names
4812 FTMS; HCD 54.53 406.69 KCNN2

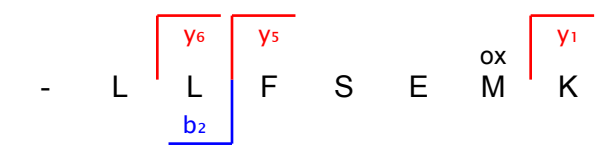
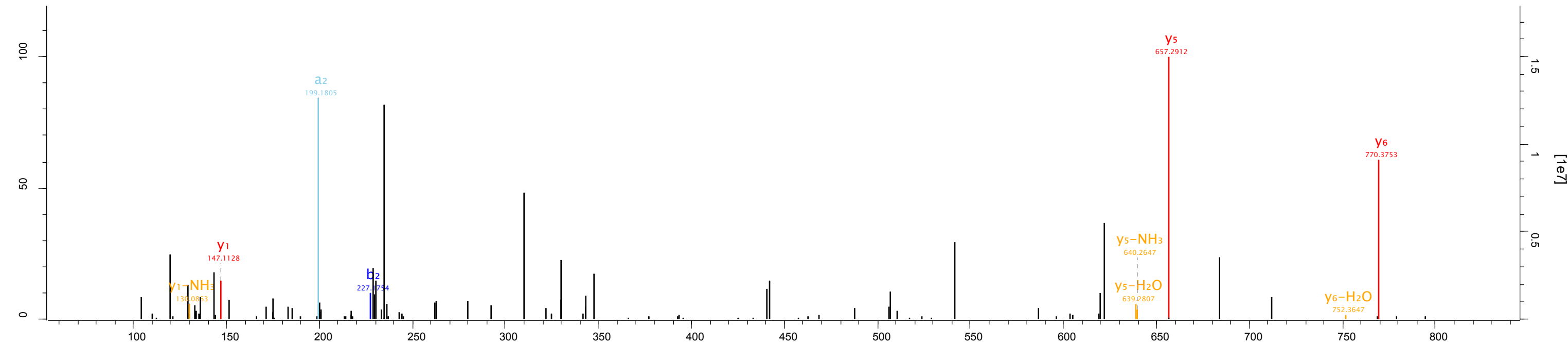


Raw file
20180707_MaS_A375SR_ML_proteome_04

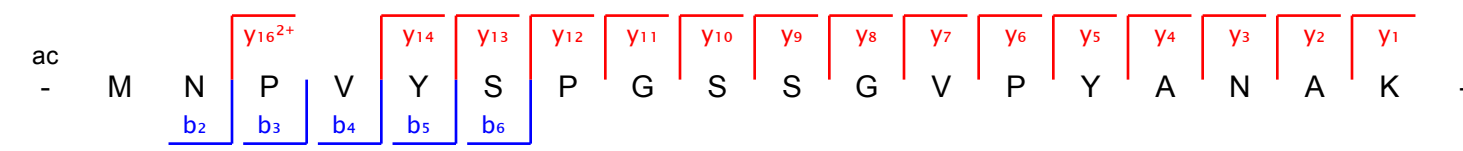
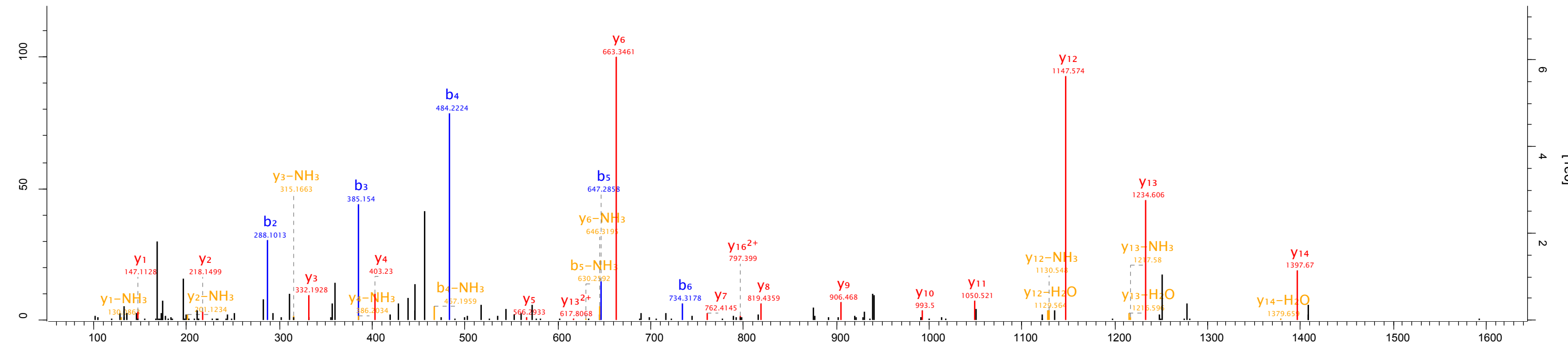
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Method: FTMS; HCD
Score: 62.2
m/z: 902.97
Gene names: LNX2



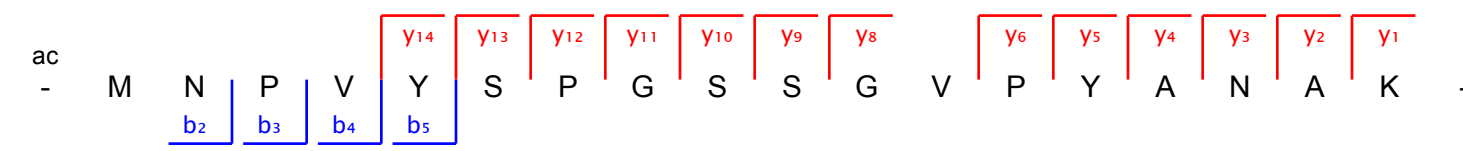
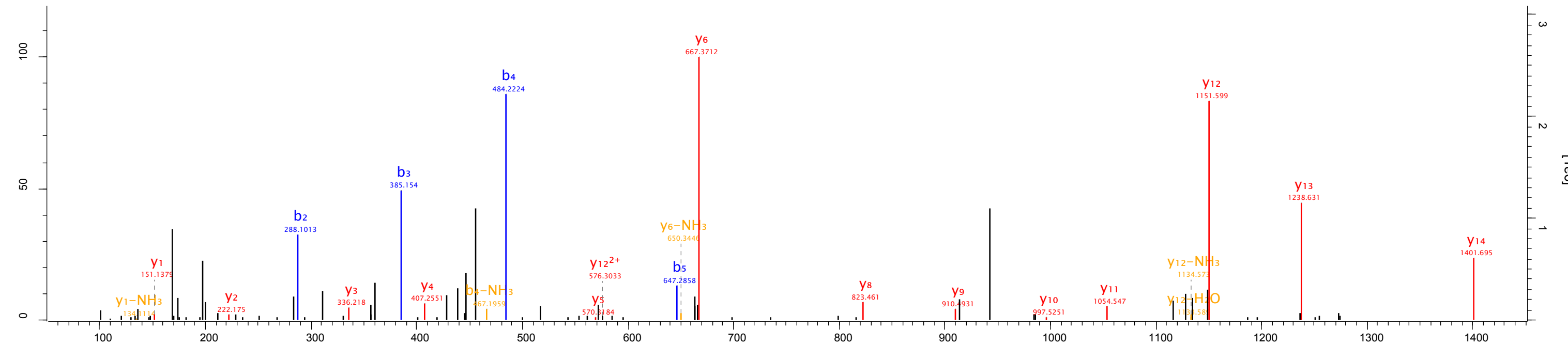
Raw file 20180707_MaS_A375SR_ML_proteome_05 Scan 13202 Method FTMS; HCD Score 42.47 m/z 442.23 Gene names C1orf234

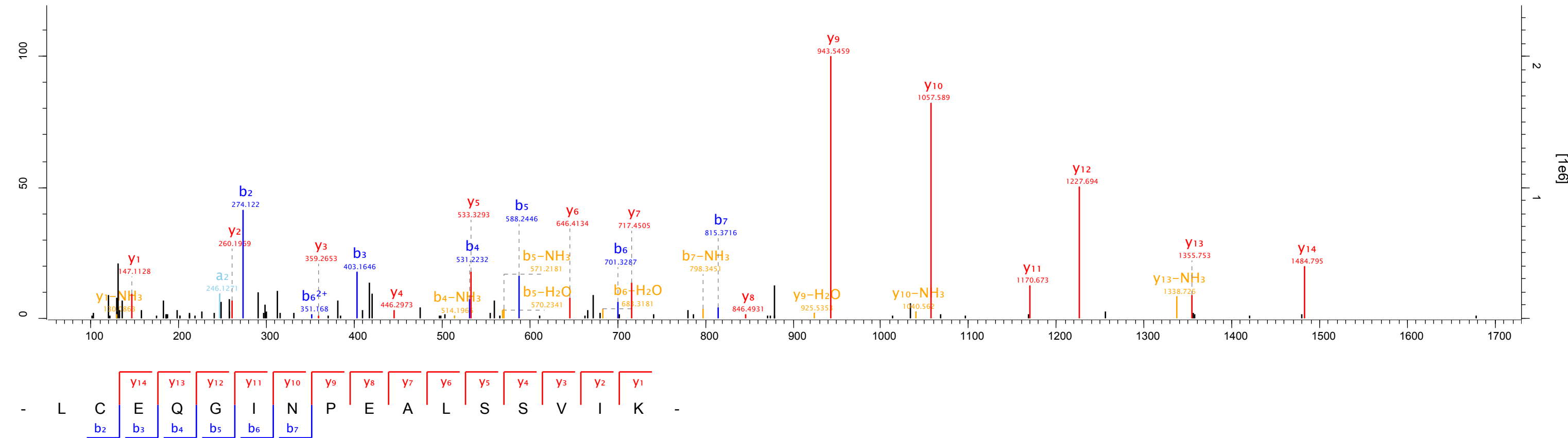


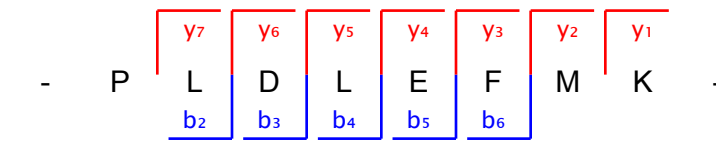
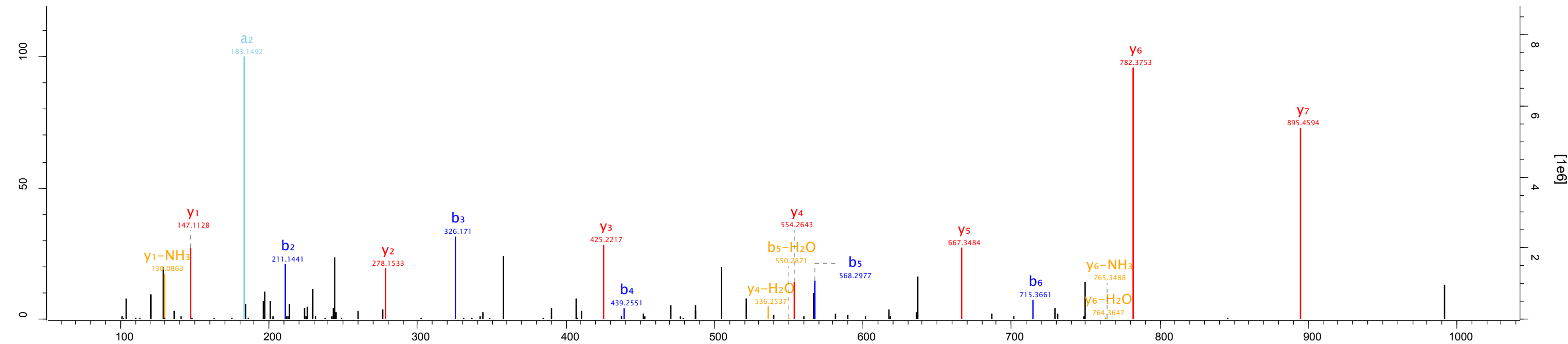
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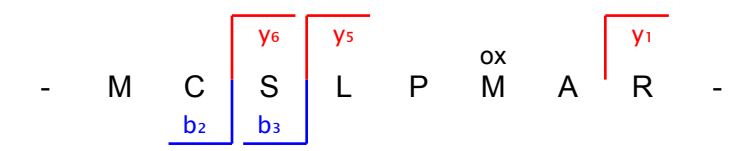
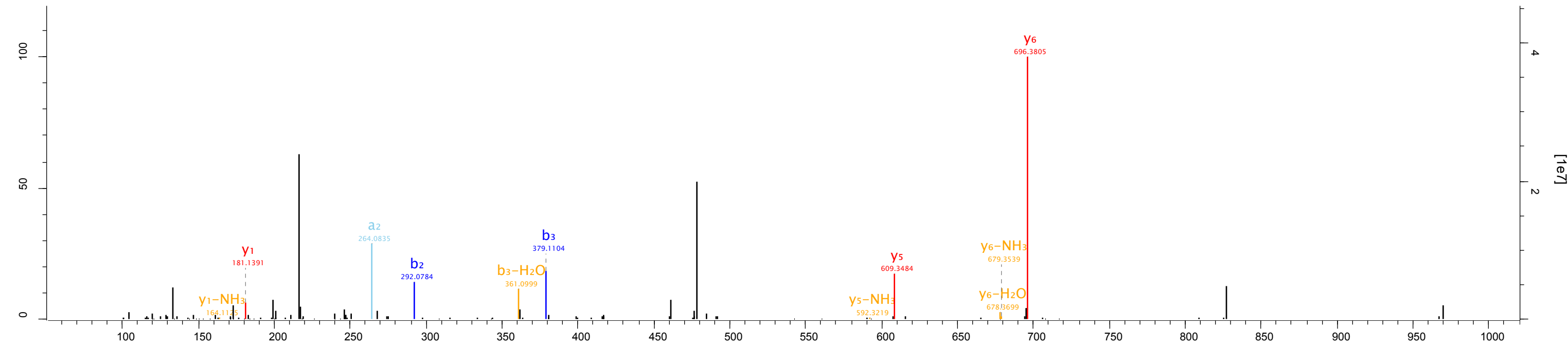
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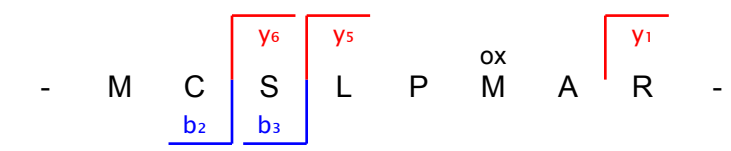
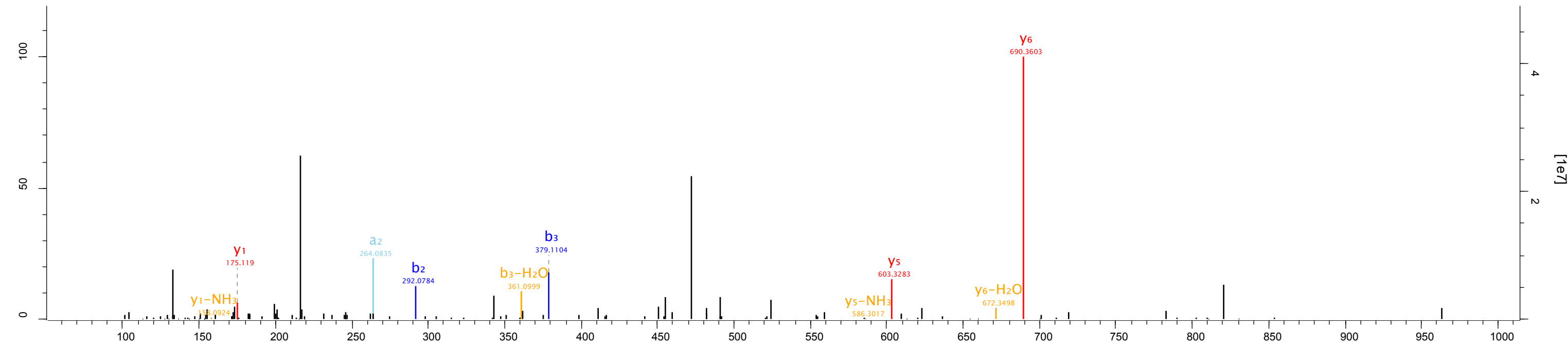


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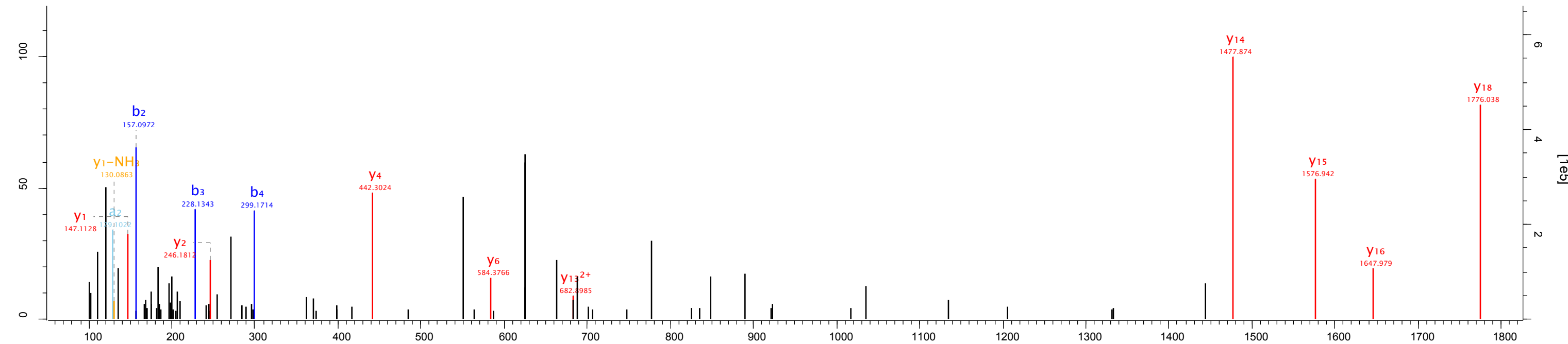
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20180707_MaS_A375SR_ML_proteome_08

Scan Method Score m/z Gene names
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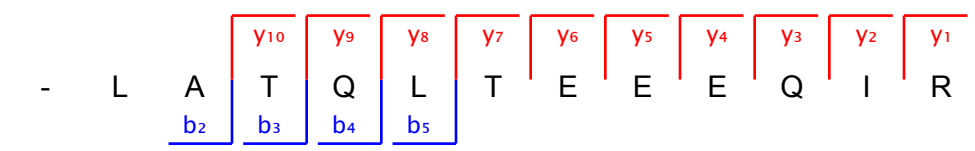
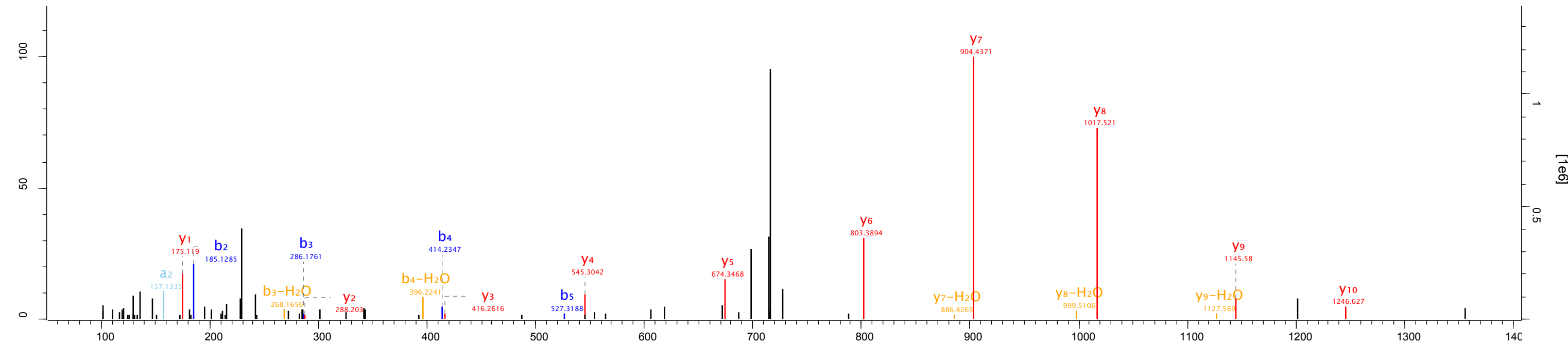


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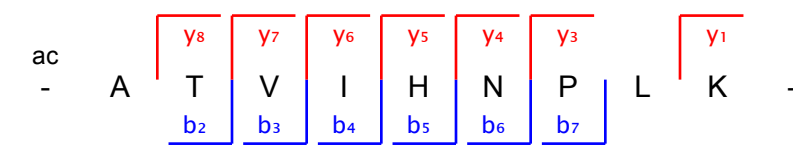
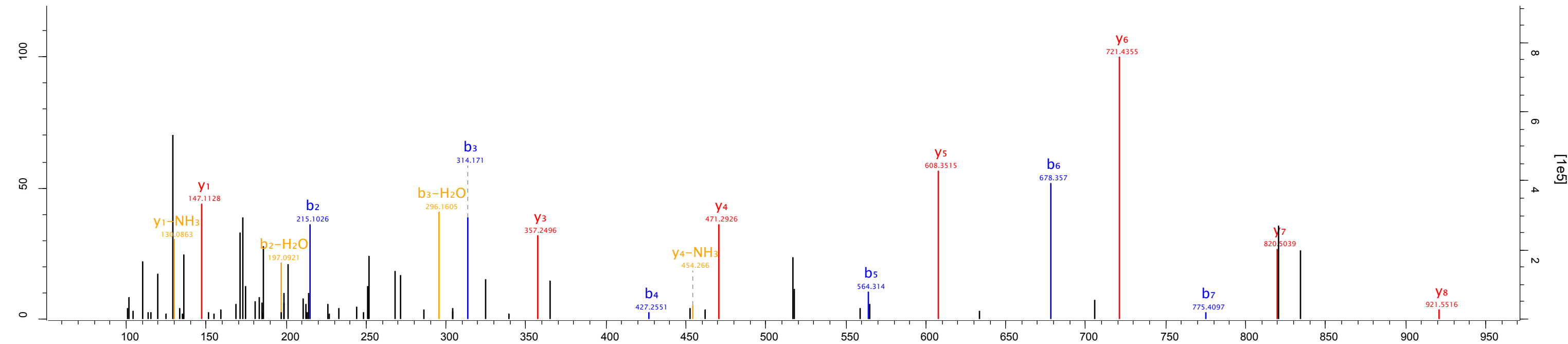
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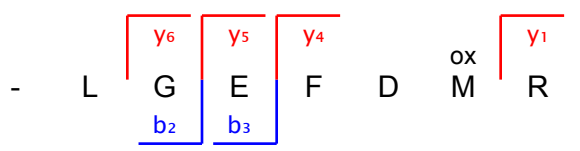
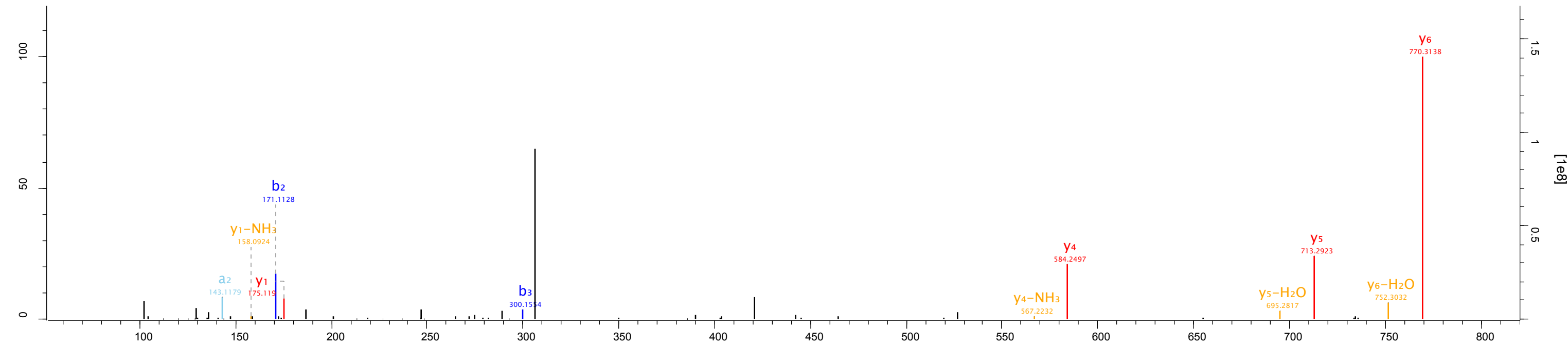
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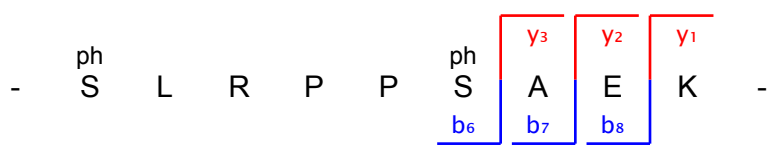
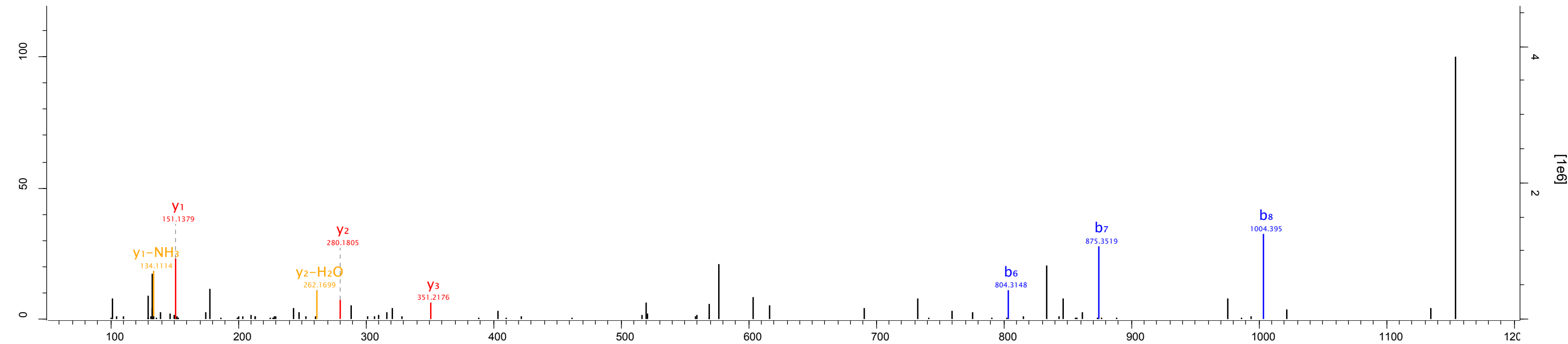


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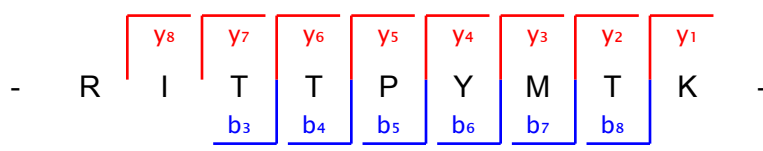
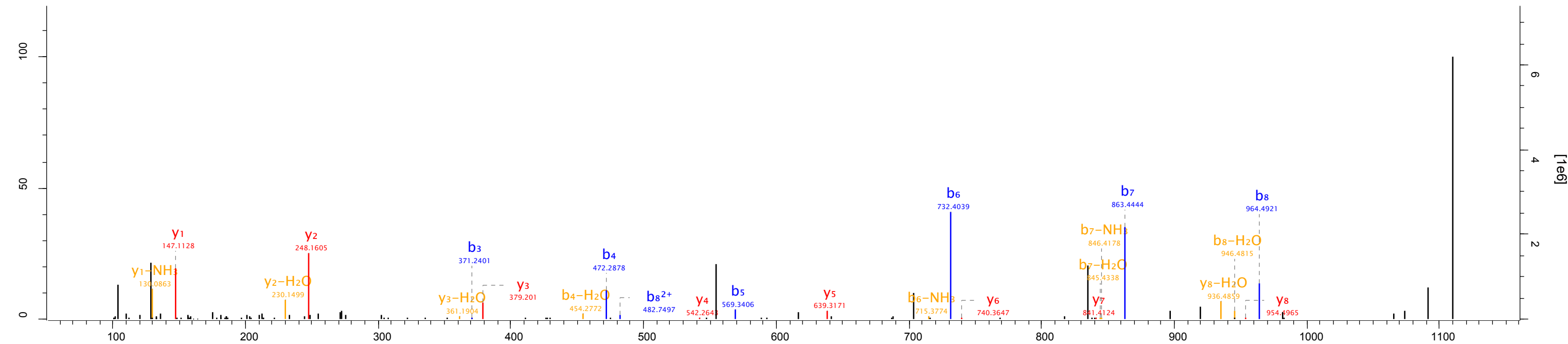
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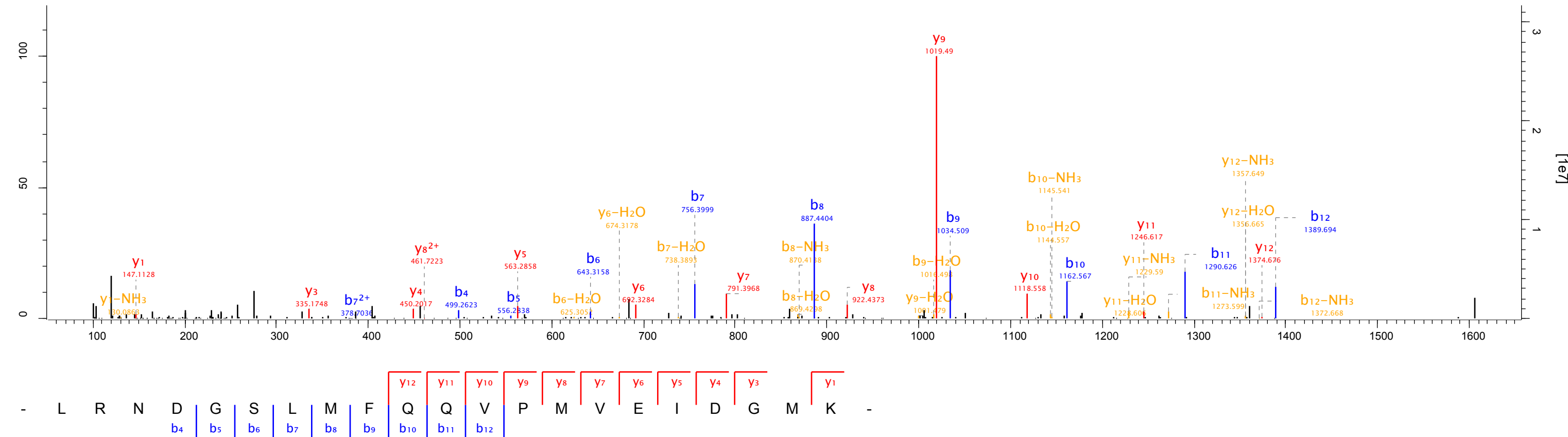
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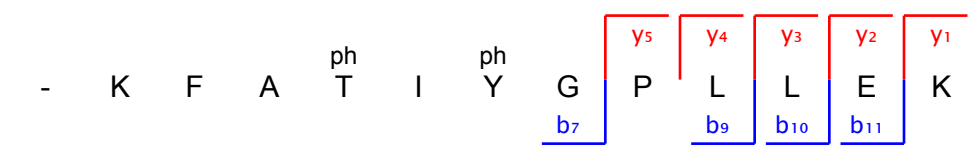
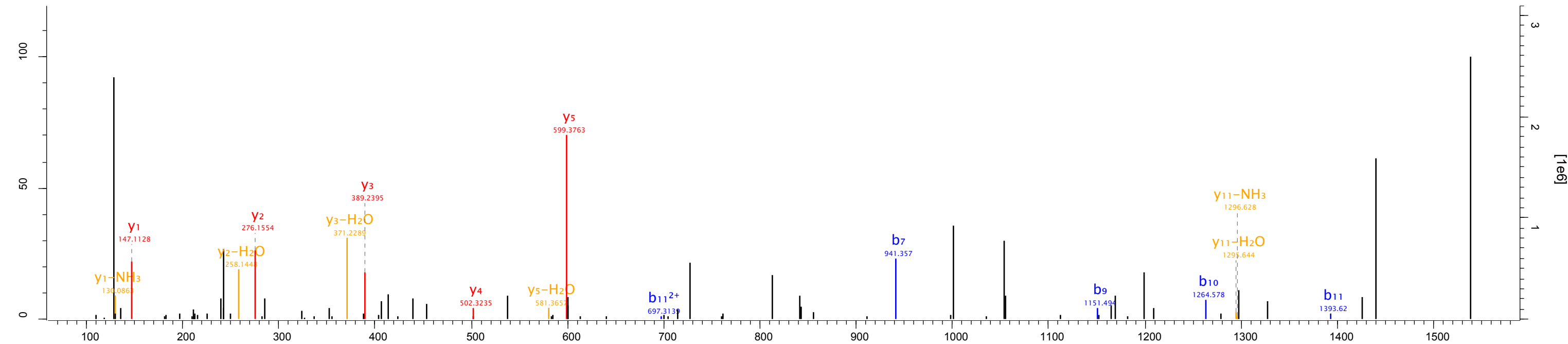
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20180707_MaS_A375SR_ML_proteome_10

Scan Method Score m/z Gene names
9432 FTMS; HCD 127.83 555.8 POLR2F



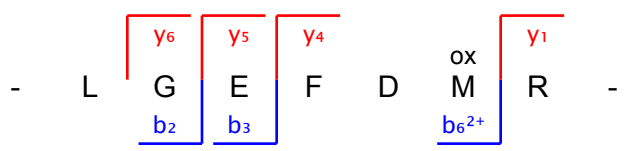
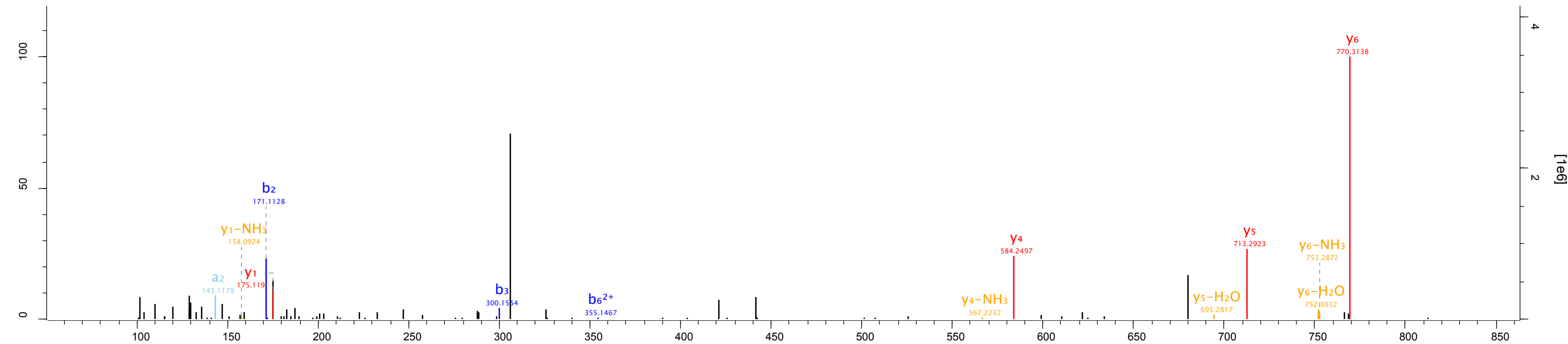


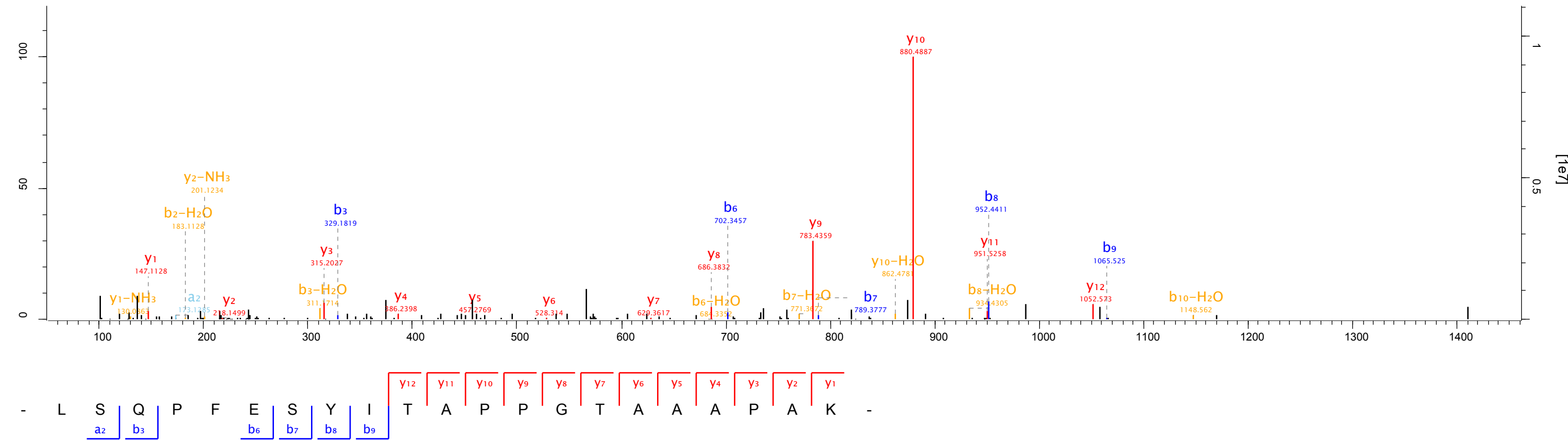
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 Scan: 10352 Method: FTMS; HCD Score: 57.11 m/z: 770.37 Gene names: NAP1L6



Raw file
20180707_MaS_A375SR_ML_proteome_12

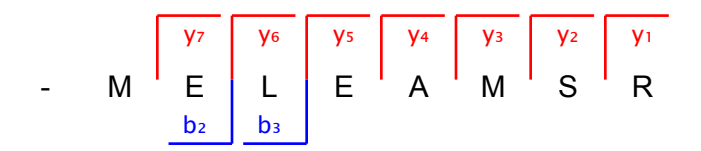
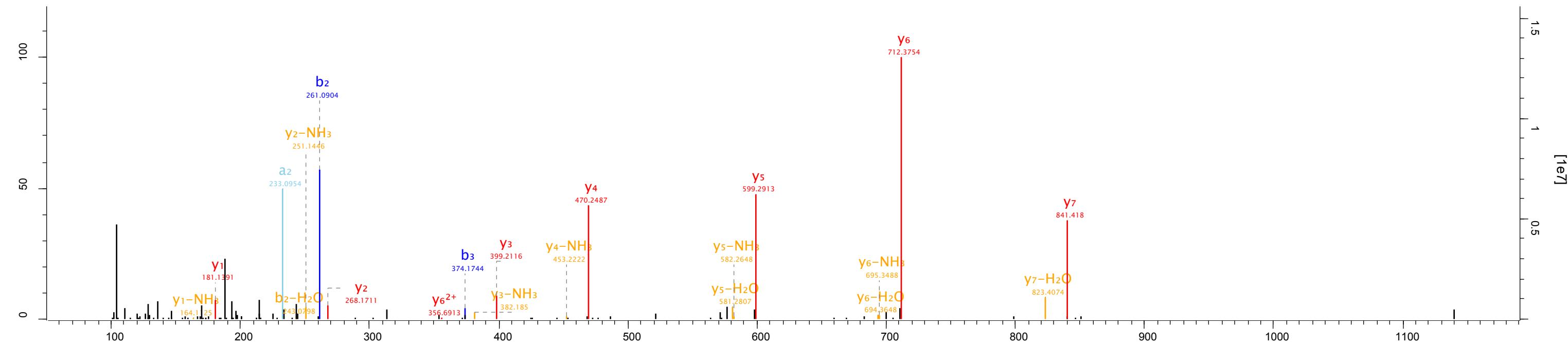
Scan 10732 Method FTMS; HCD Score 97.07 m/z 442.2



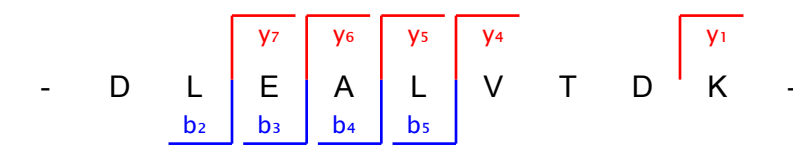
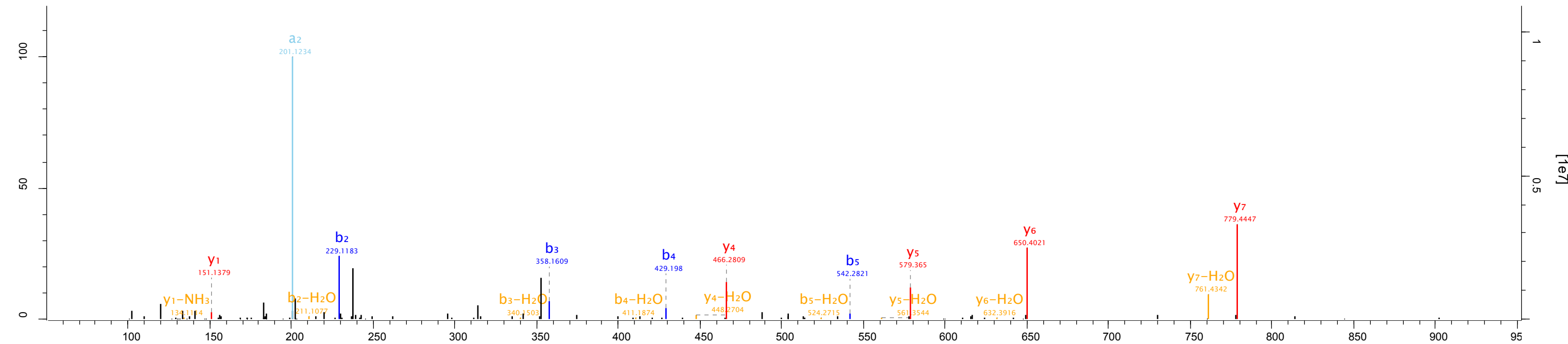


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20180707_MaS_A375SR_ML_proteome_13

Scan 14102 Method FTMS; HCD Score 133.58 m/z 486.73 Gene names TMEM258

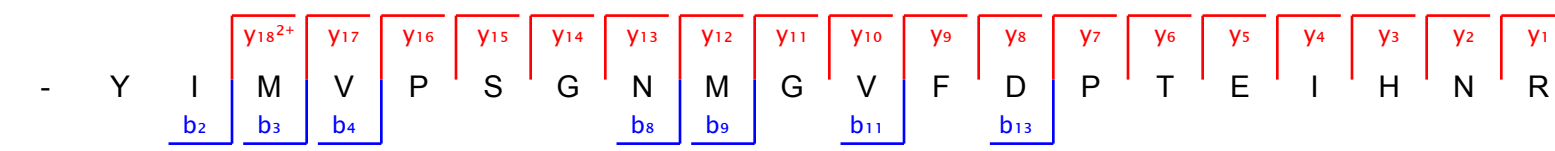
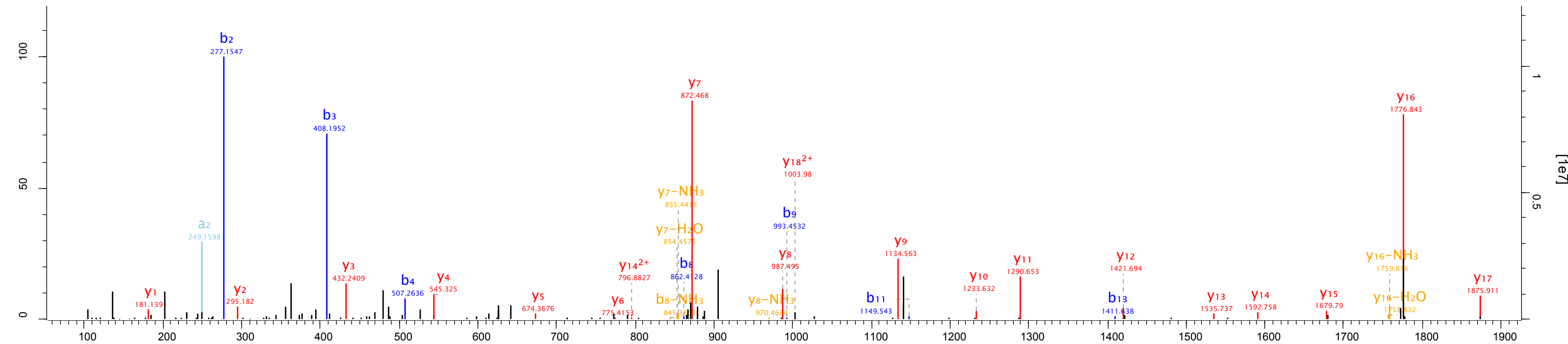


Raw file 20180707_MaS_A375SR_ML_proteome_13 Scan 26102 Method FTMS; HCD Score 66.27 m/z 504.28 Gene names PGM5

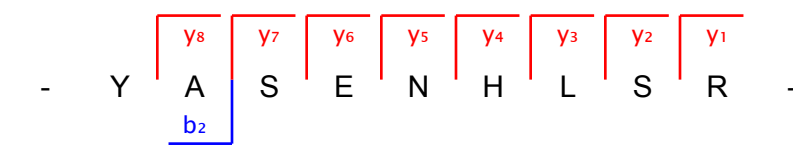
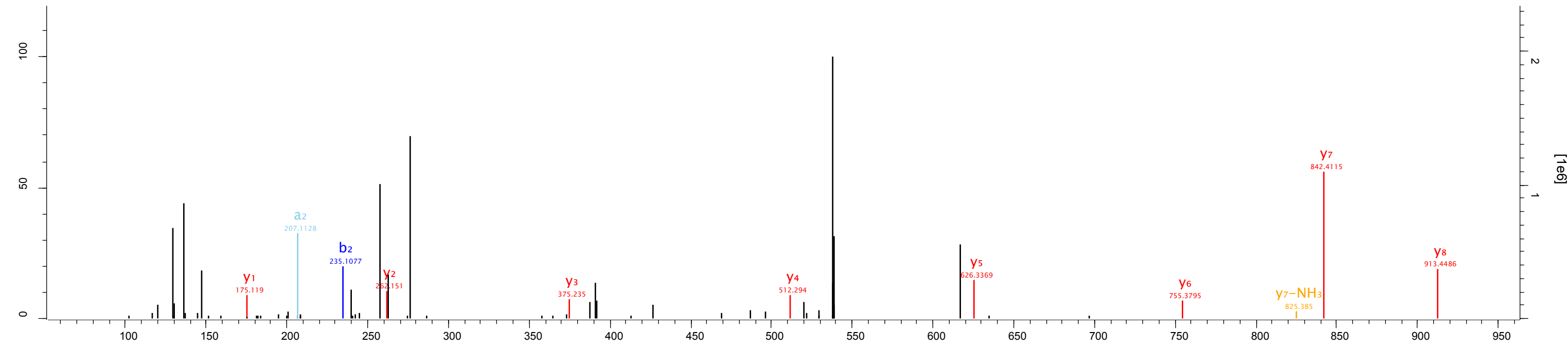


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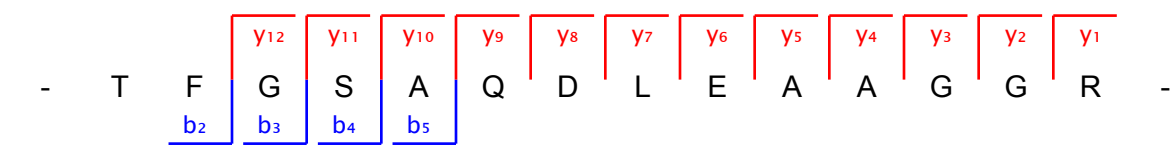
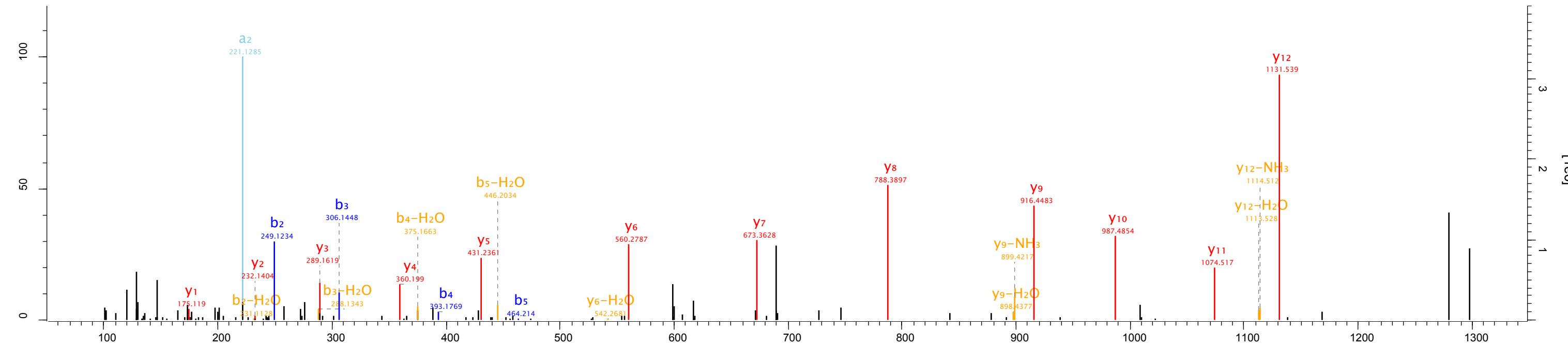
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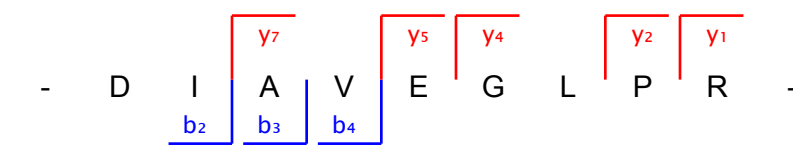
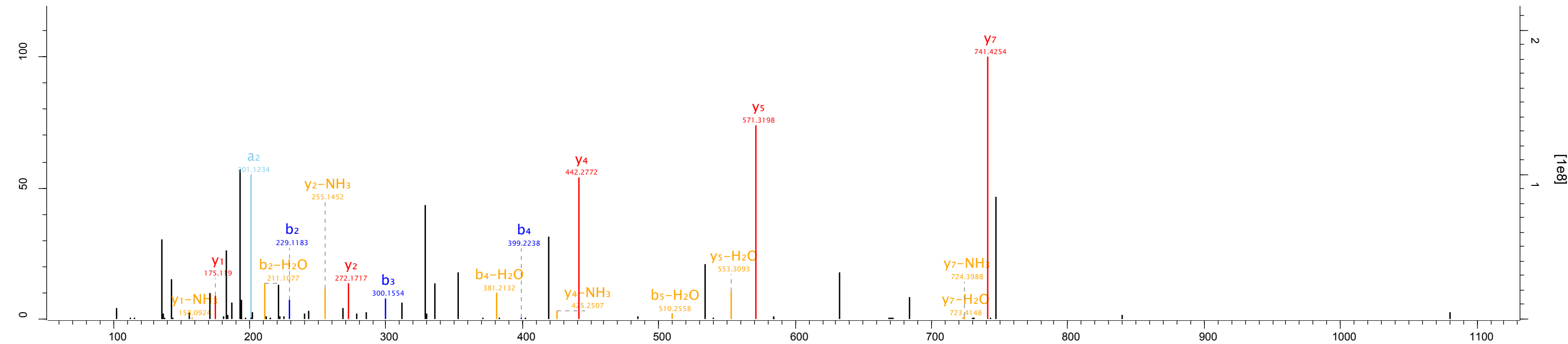
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Raw file 20180707_MaS_A375SR_ML_proteome_14 Scan 13882 Method FTMS; HCD Score 112.42 m/z 690.33 Gene names ZNF324

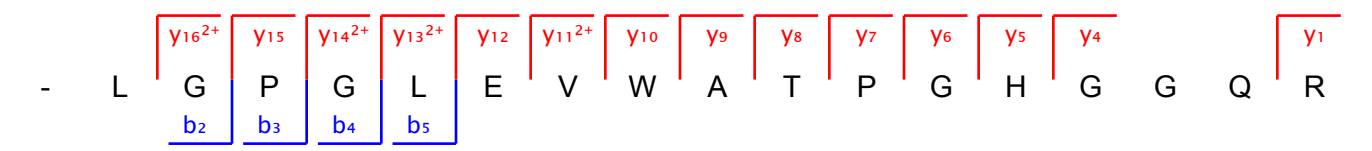
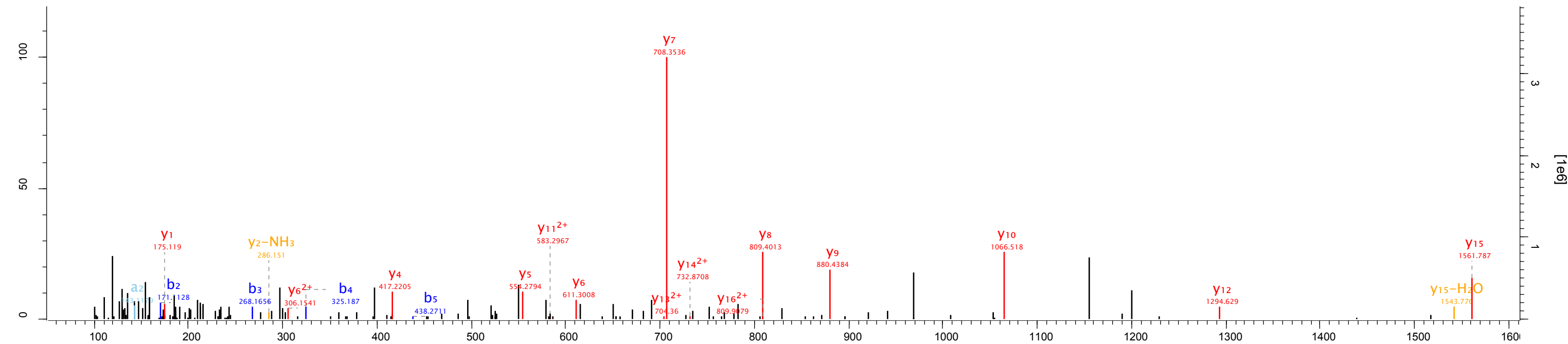


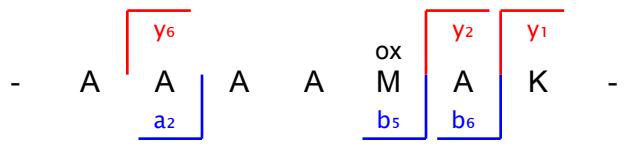
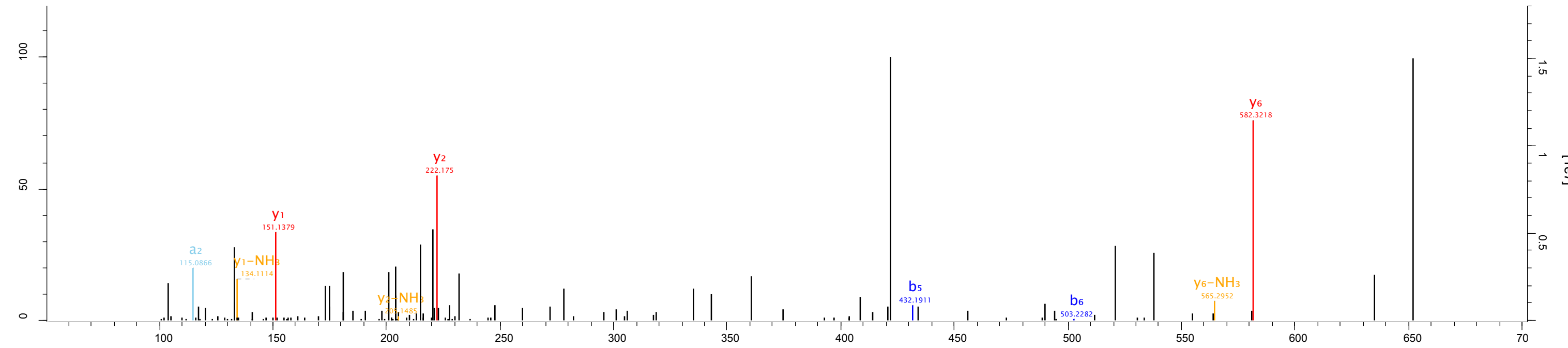
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 Scan: 17112 Method: FTMS; HCD Score: 90.71 m/z: 485.27



Raw file
20180707_MaS_A375SR_ML_proteome_14

Scan 20462 Method FTMS; HCD Score 40.49 m/z 578.31 Gene names MBLAC1

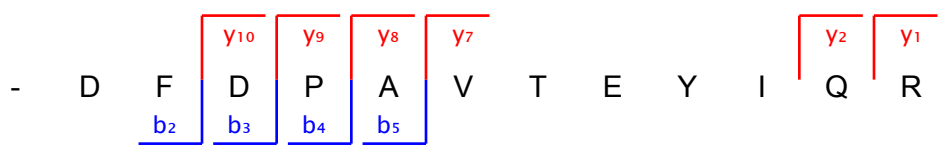
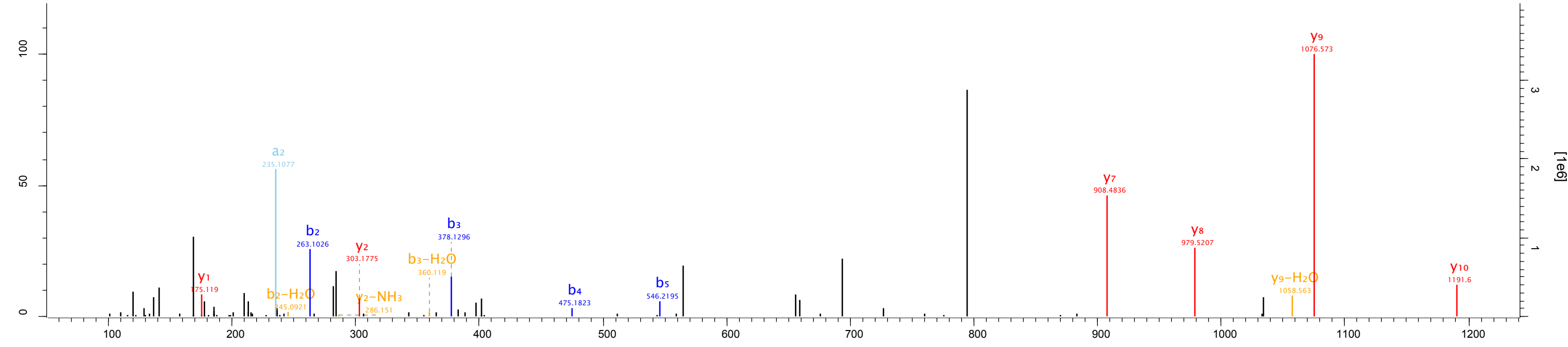




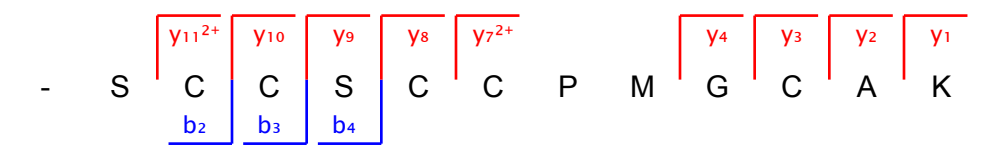
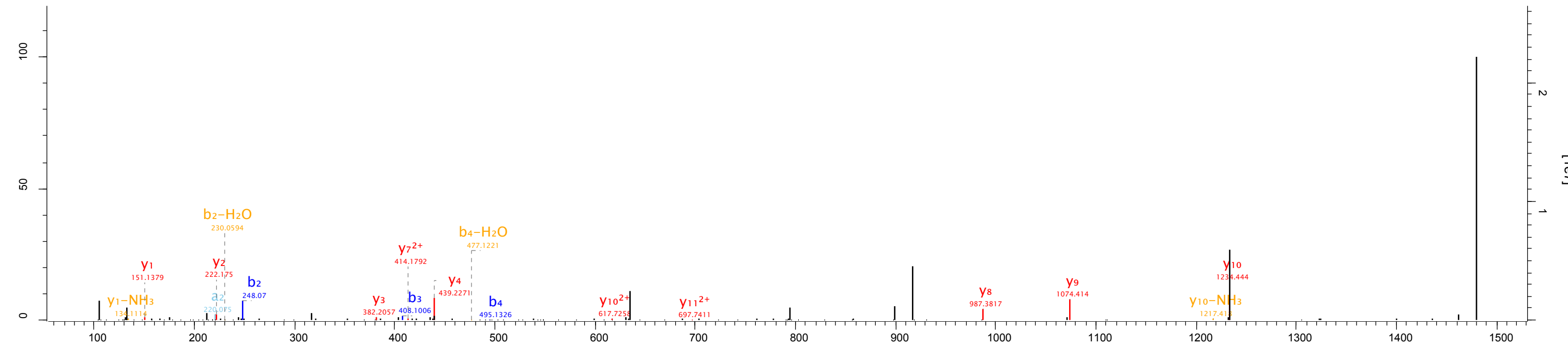
Raw file

20180707_MaS_A375SR_ML_proteome_16

Scan	Method	Score	m/z	Gene names
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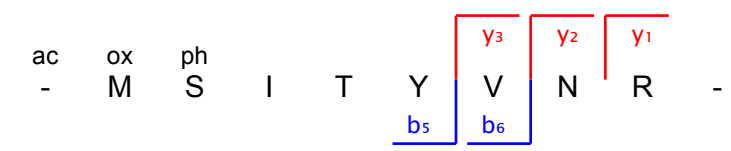
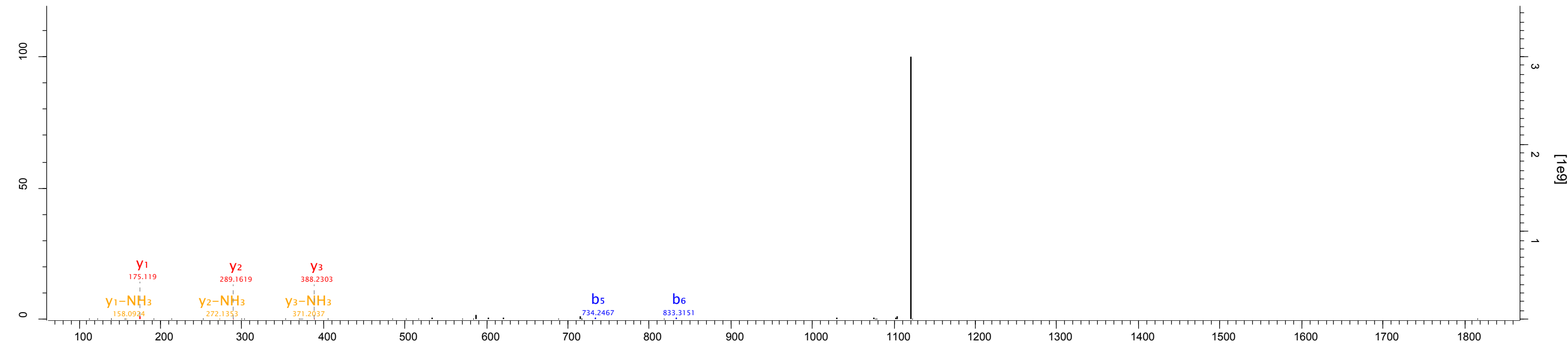


Raw file: 20180707_MaS_A375SR_ML_proteome_17
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Raw file
20180707_MaS_A375SR_ML_proteome_18

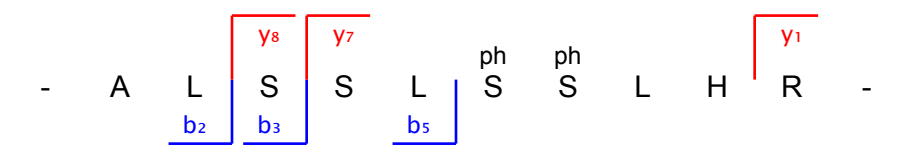
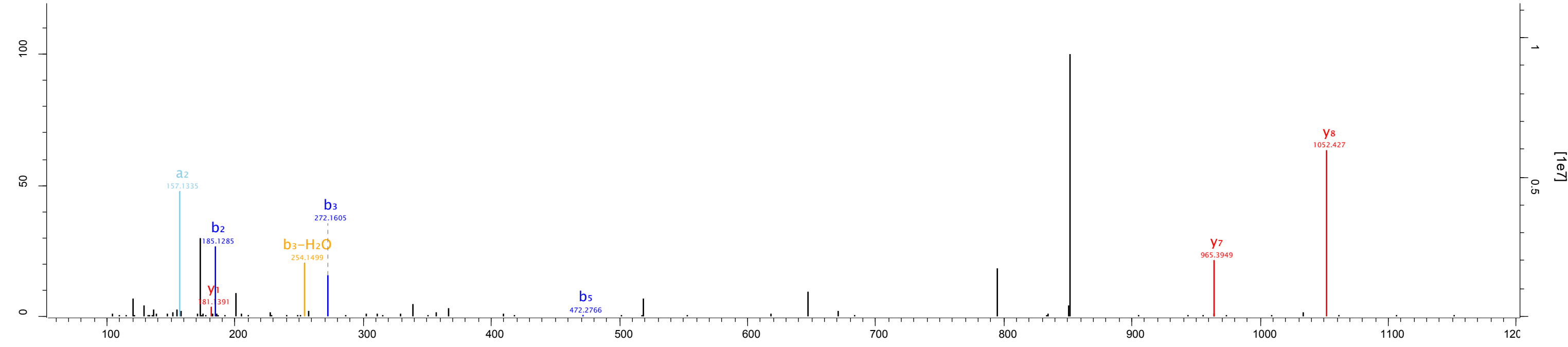
Scan 15292 Method FTMS; HCD Score 69.43 m/z 1121.47



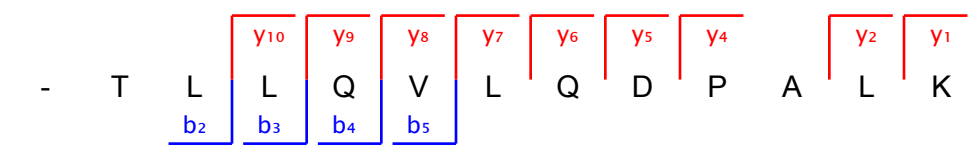
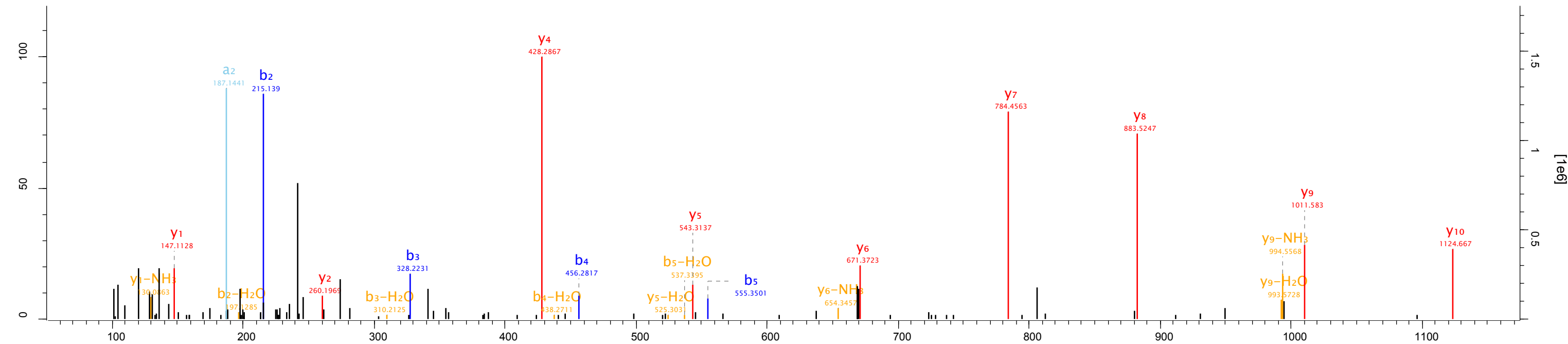
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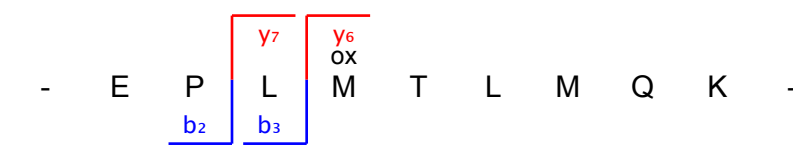
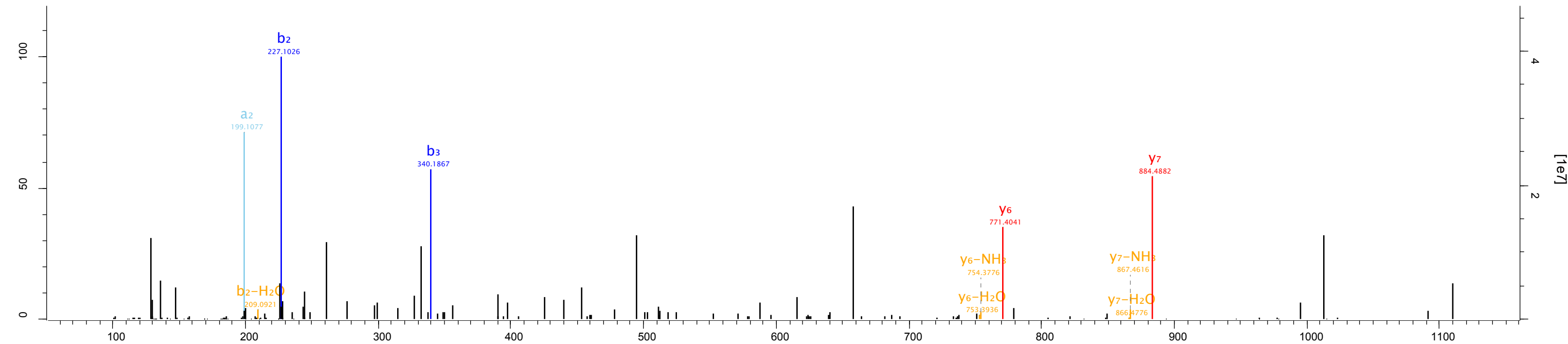
20180707_MaS_A375SR_ML_proteome_18

Scan	Method	Score	m/z	Gene names
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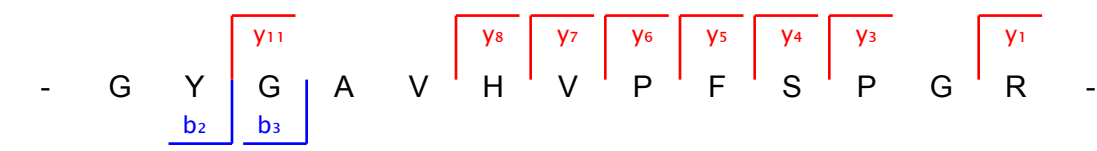
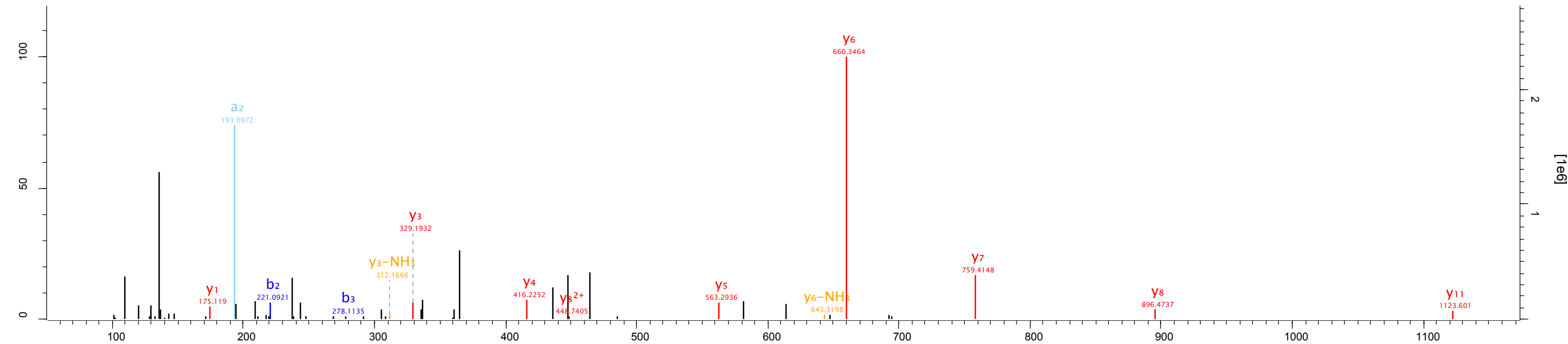


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 Scan: 28522 Method: FTMS; HCD Score: 105.65 m/z: 669.9 Gene names: THEMIS2



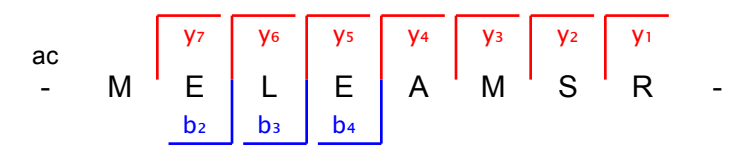
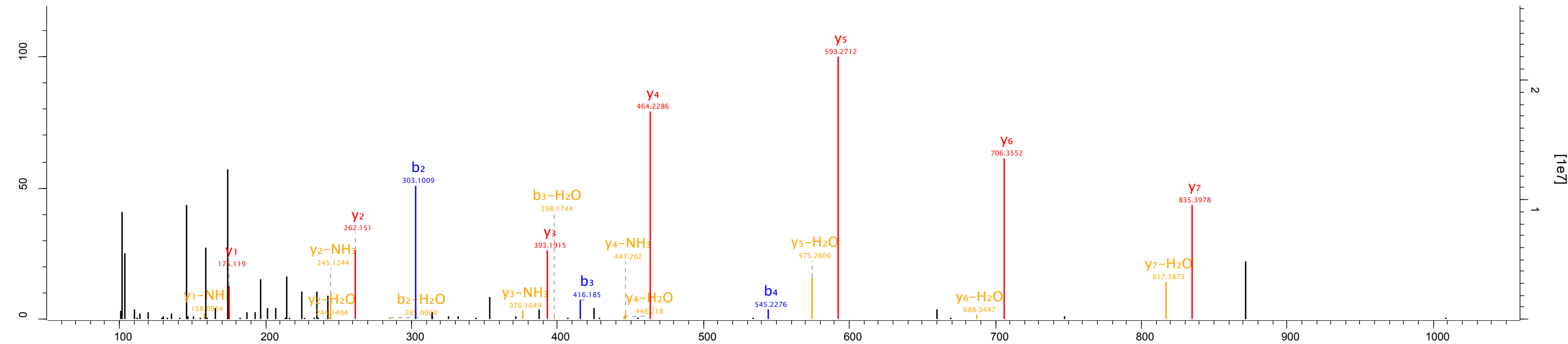


Raw file 20180707_MaS_A375SR_ML_proteome_2_01
 Scan 17112 Method FTMS; HCD Score 43.59 m/z 448.57 Gene names B9D1



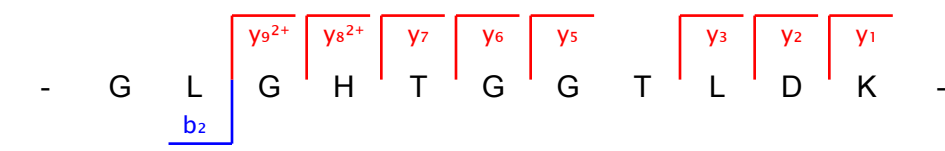
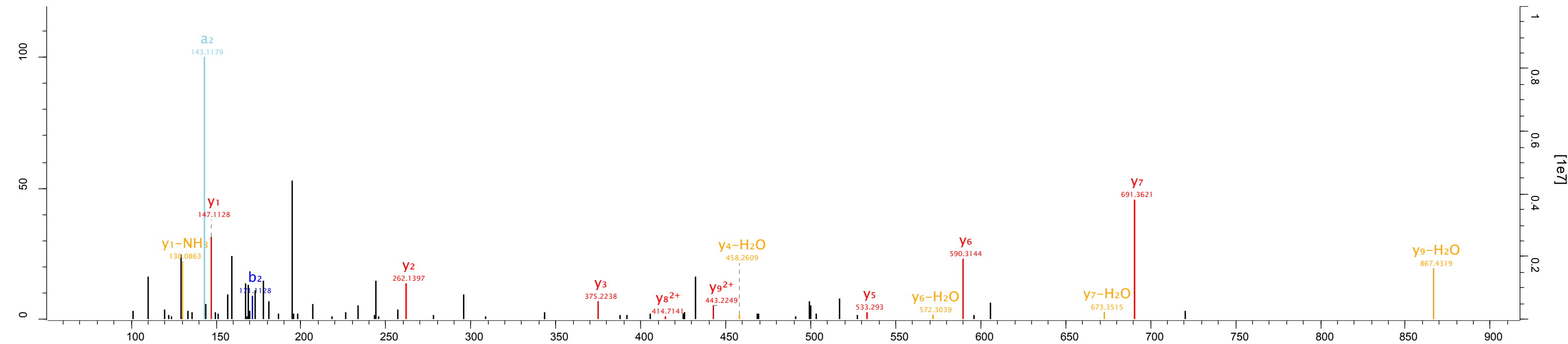
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20180707_MaS_A375SR_ML_proteome_2_01

Scan 24532 Method FTMS; HCD Score 107.69 m/z 504.73 Gene names TMEM258

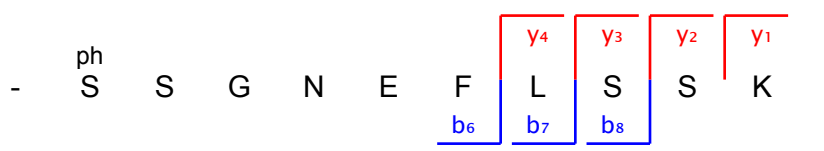
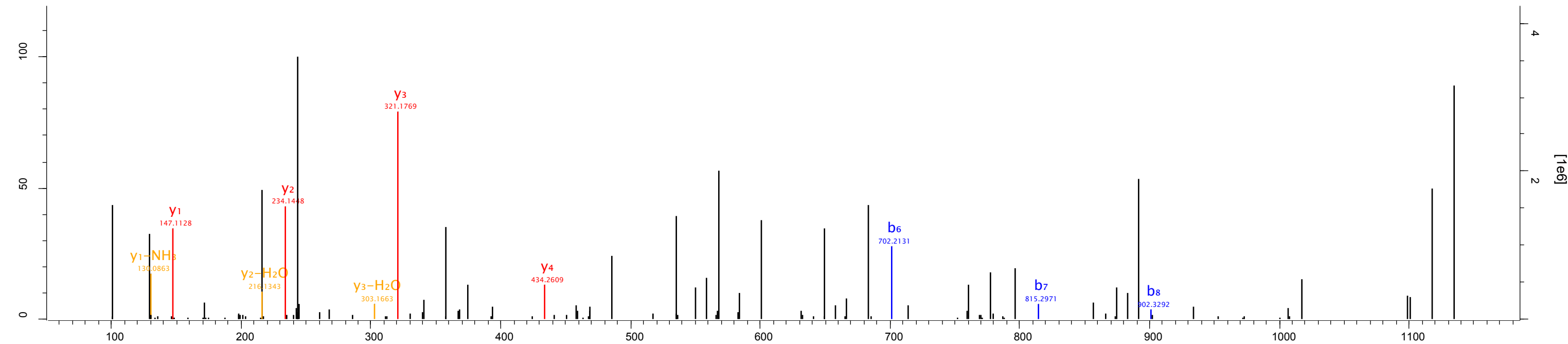


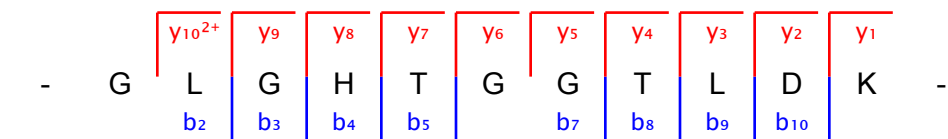
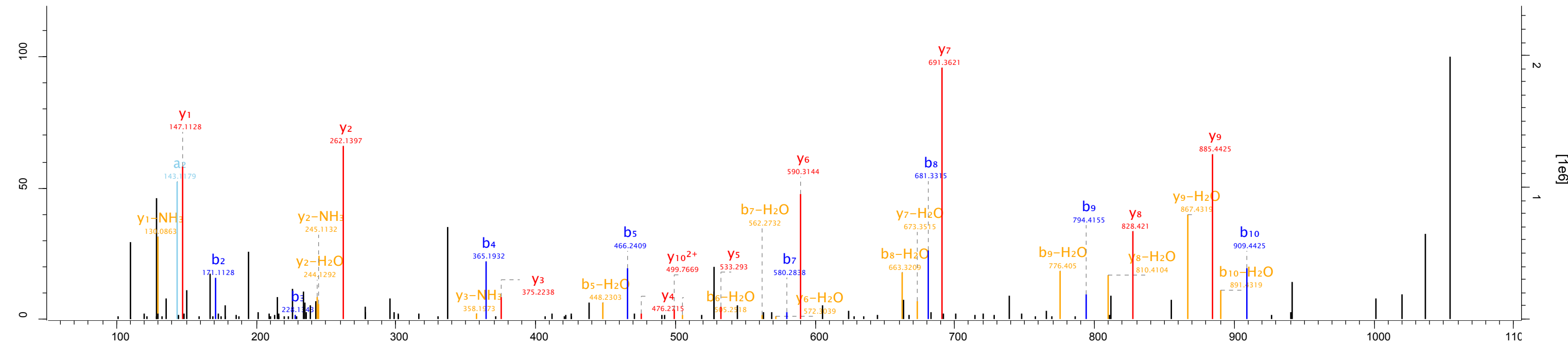
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20180707_MaS_A375SR_ML_proteome_2_01

Scan 4542 Method FTMS; HCD Score 45.43 m/z 352.52 Gene names TYMP

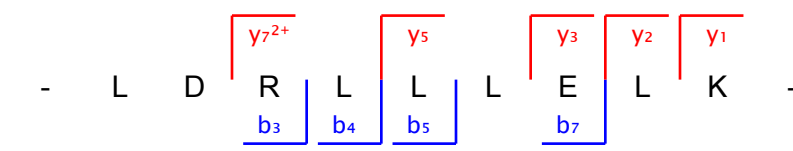
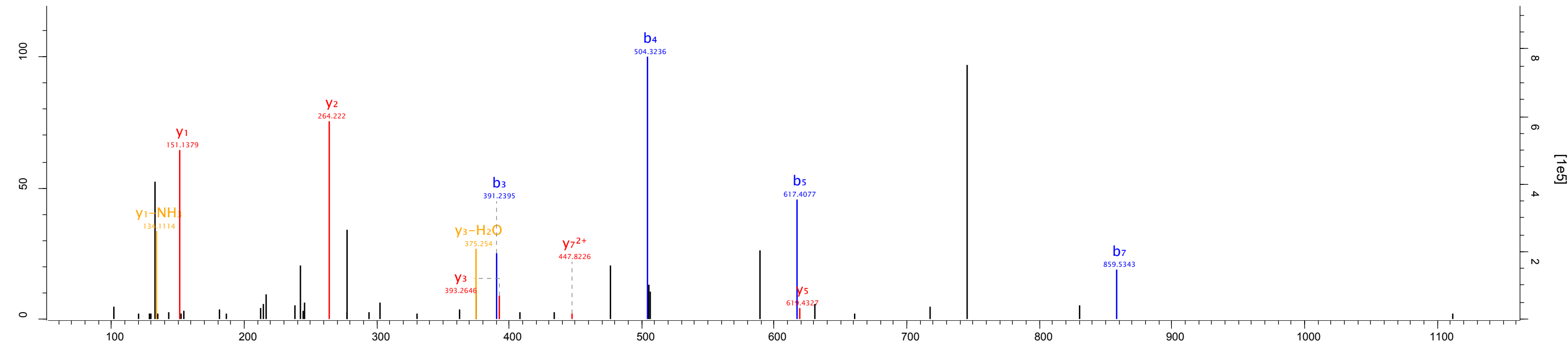


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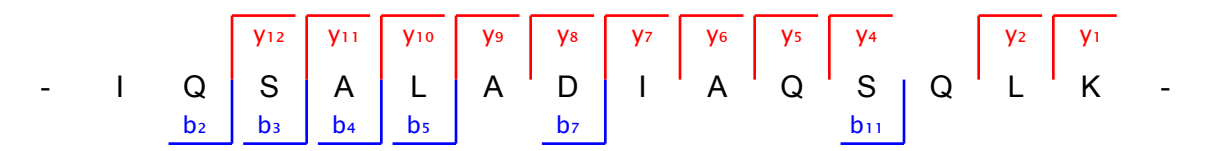
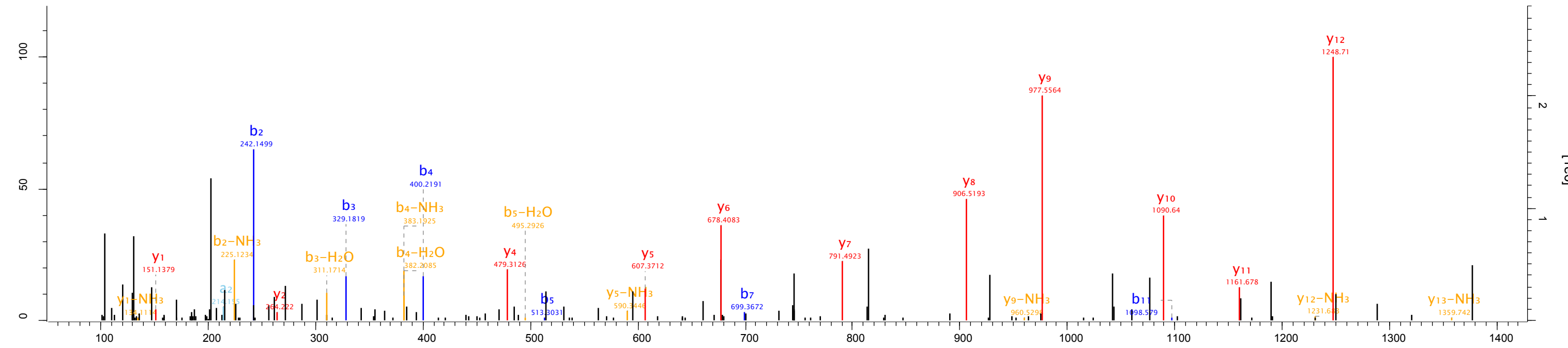




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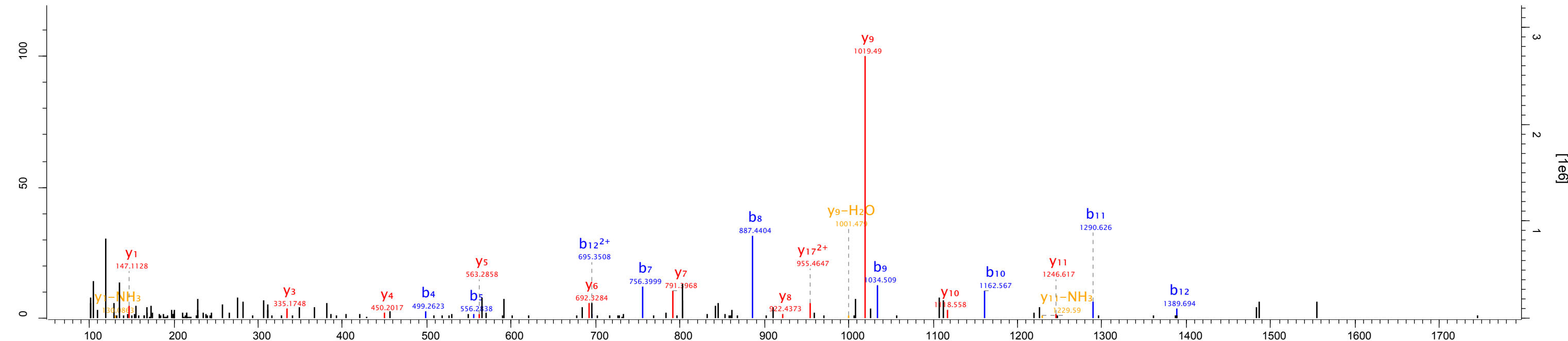


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20180707_MaS_A375SR_ML_proteome_2_03

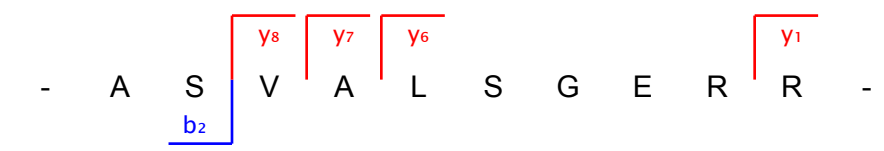
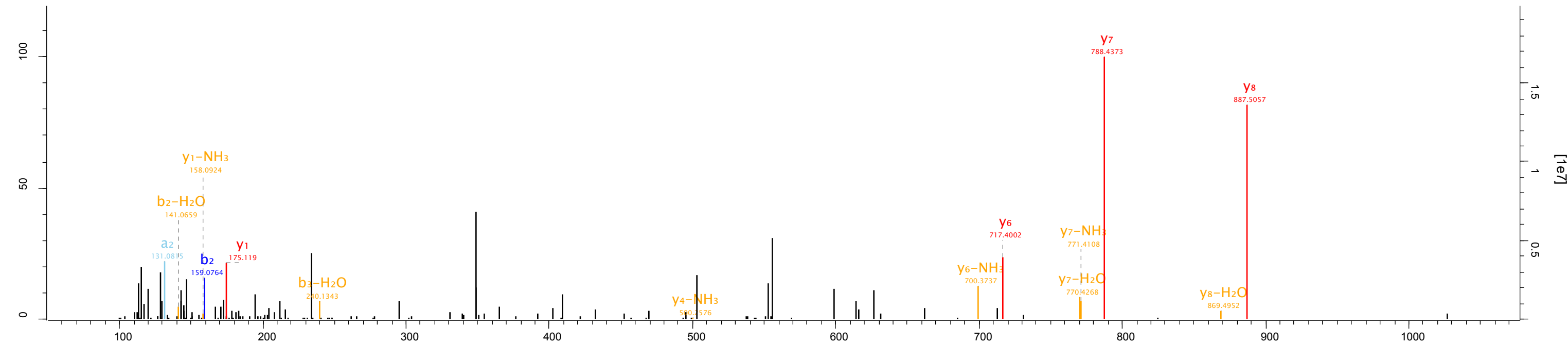
29172 FTMS; HCD 50.19 803.73 GSTA3



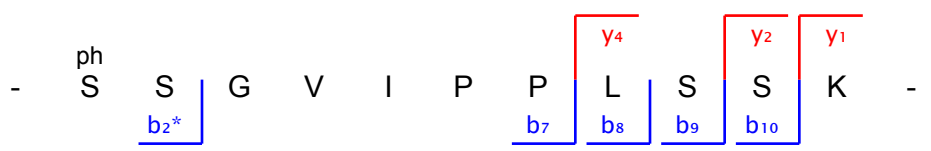
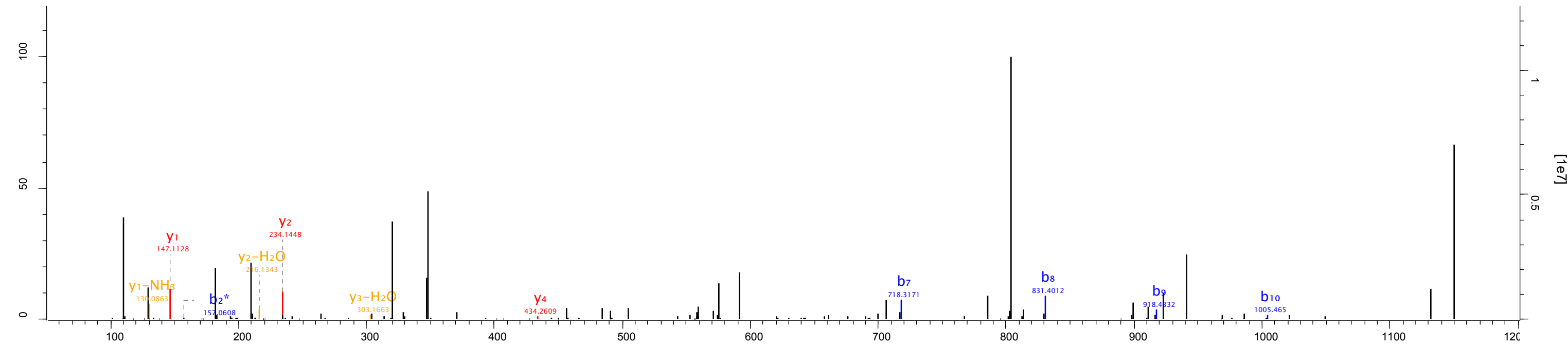
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b₄ b₅ b₇ b₈ b₉ b₁₀ b₁₁ b₁₂ y₁₇²⁺ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₁

Raw file 20180707_MaS_A375SR_ML_proteome_2_03 Scan 2982 Method FTMS; HCD Score 53.75 m/z 349.53

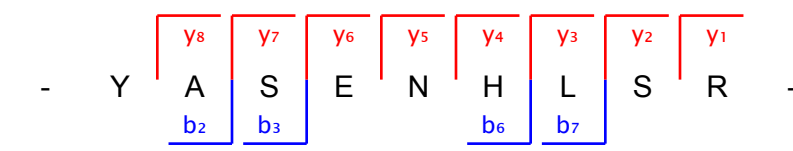
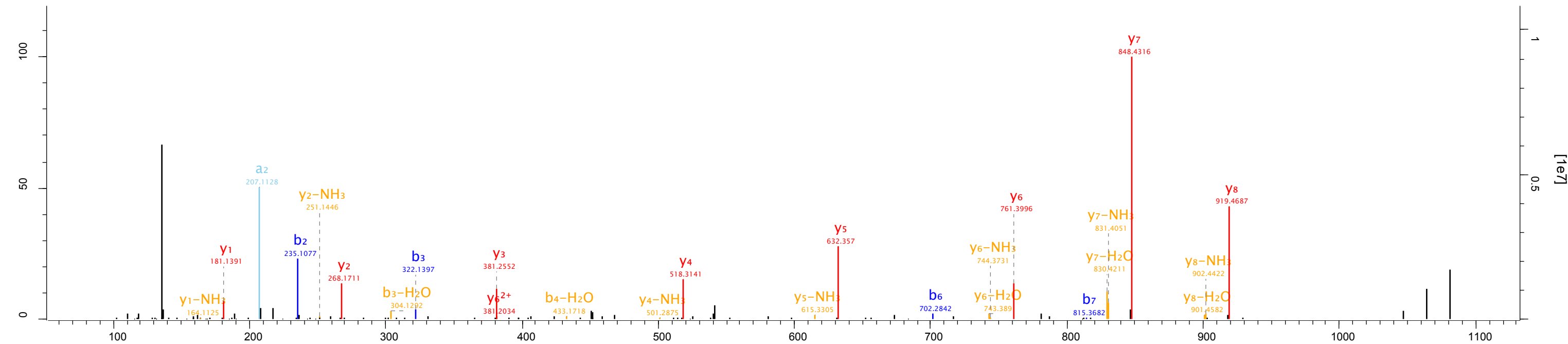


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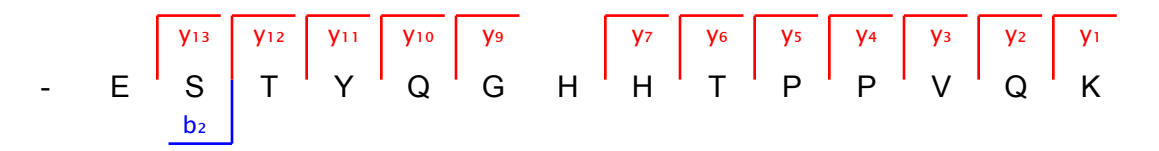
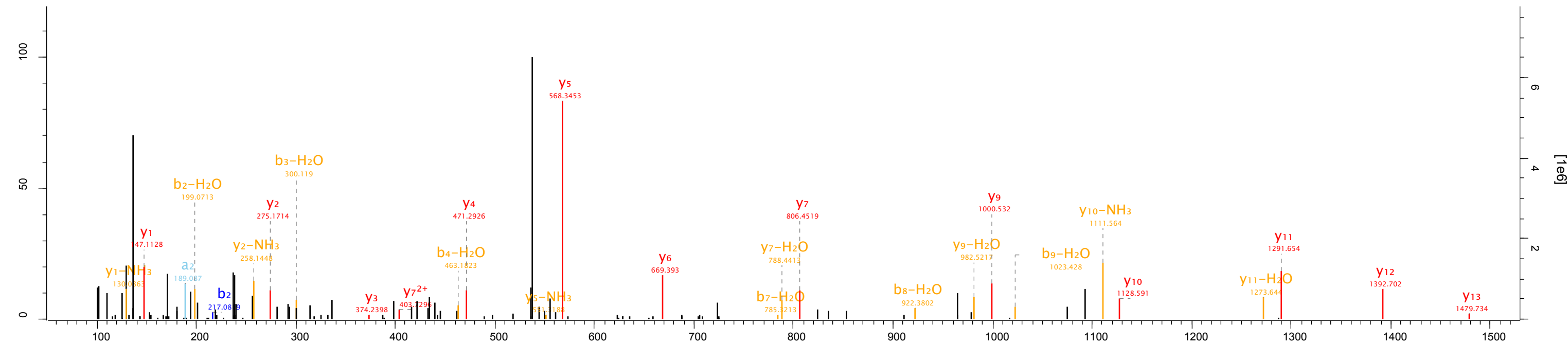
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20180707_MaS_A375SR_ML_proteome_2_04

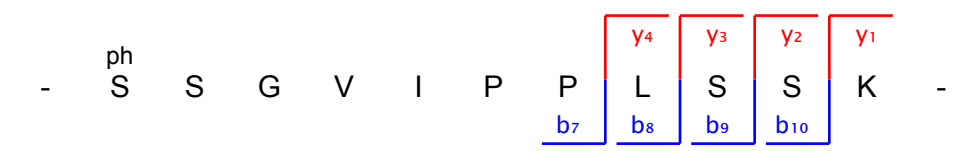
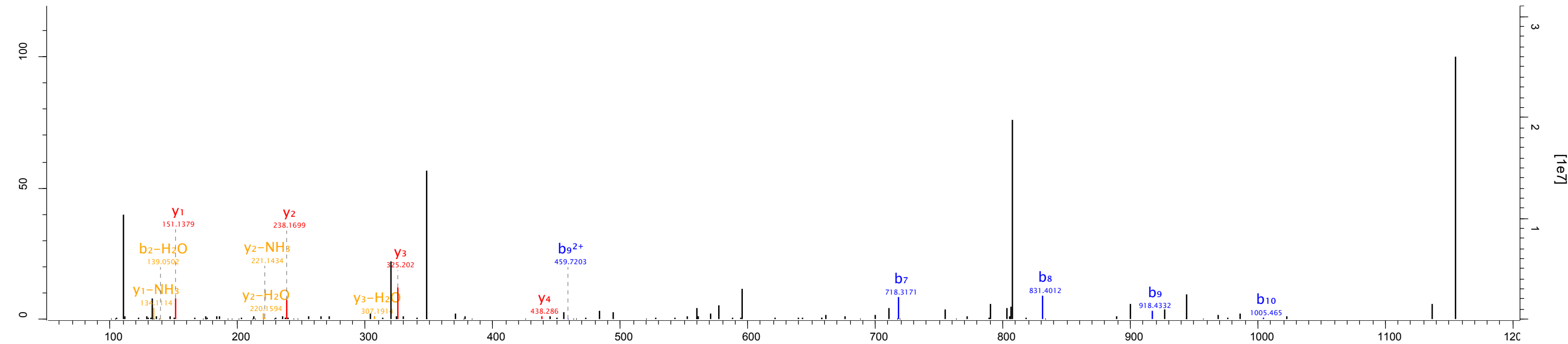
Scan 2892 Method FTMS; HCD Score 144.65 m/z 541.77 Gene names TM4SF1



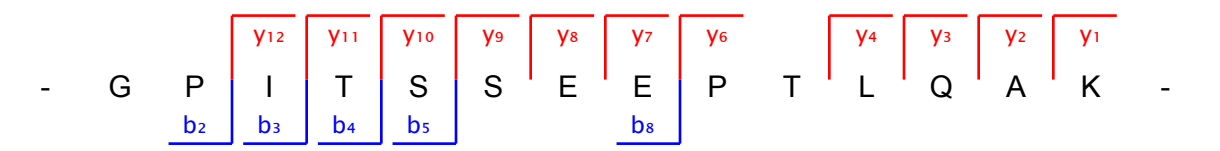
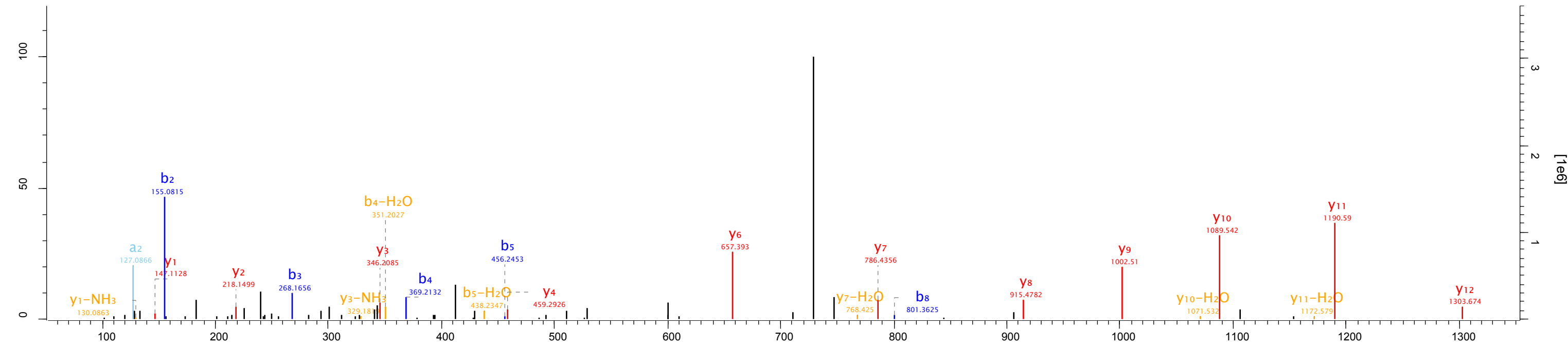
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Scan 3012 Method FTMS; HCD Score 90.76 m/z 536.93 Gene names MT-CO3

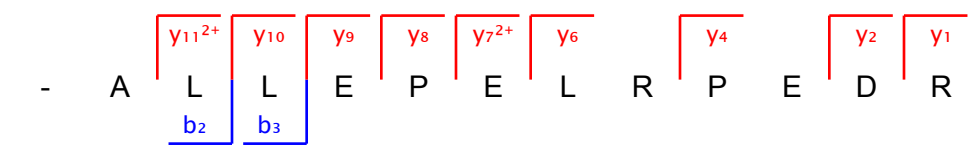
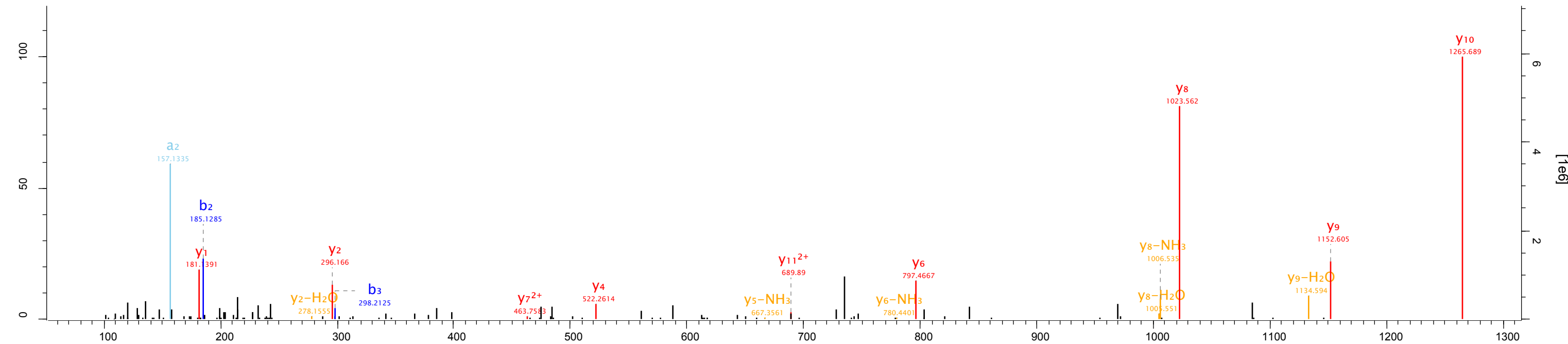




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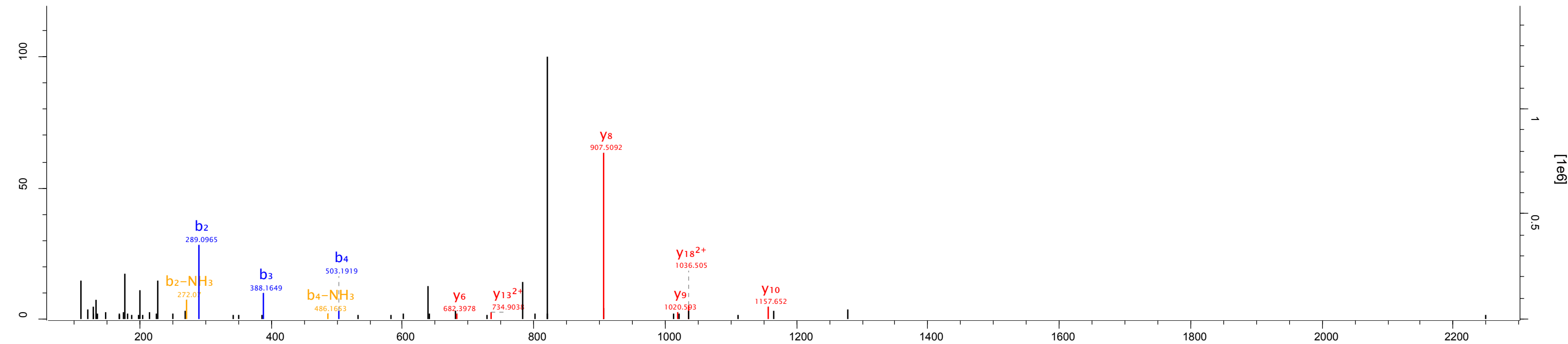


Raw file
 20180707_MaS_A375SR_ML_proteome_2_05
 Scan 16962 Method FTMS; HCD Score 73.63 m/z 483.94 Gene names ECE2



Raw file
20180707_MaS_A375SR_ML_proteome_2_05

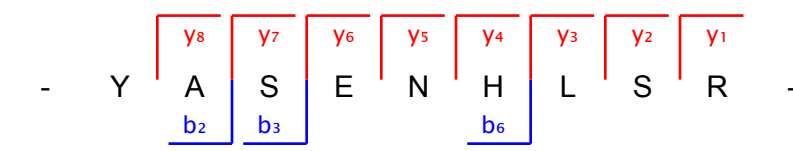
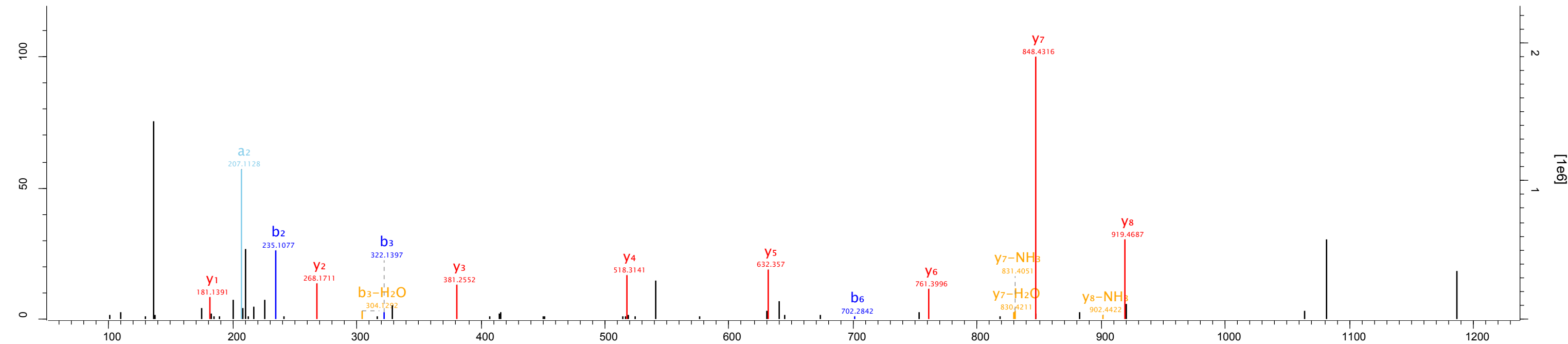
Scan 20622 Method FTMS; HCD Score 35.63 m/z 820.73 Gene names TPRA1



- C Q V D E T E P D V H L P Q P Y A V A R -

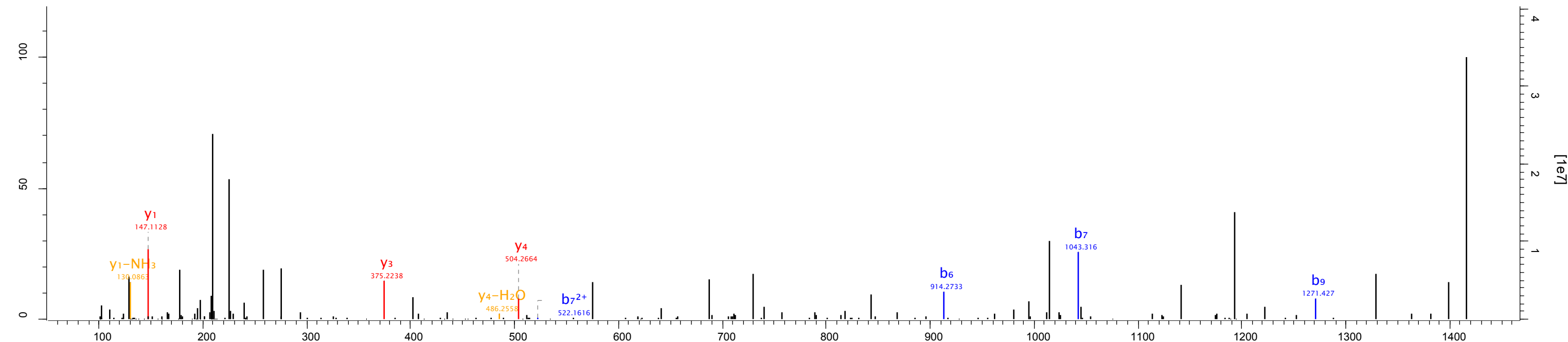
Fragmentation mapping:
b₂ (C-Q), b₃ (Q-V), b₄ (V-D)
y₁₈²⁺ (V-D), y₁₃²⁺ (E-P), y₁₀ (H-L), y₉ (L-P), y₈ (P-Q), y₆ (Q-P)

Raw file 20180707_MaS_A375SR_ML_proteome_2_05 Scan 3362 Method FTMS; HCD Score 96.34 m/z 541.77 Gene names TM4SF1



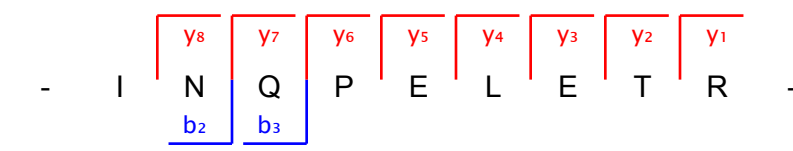
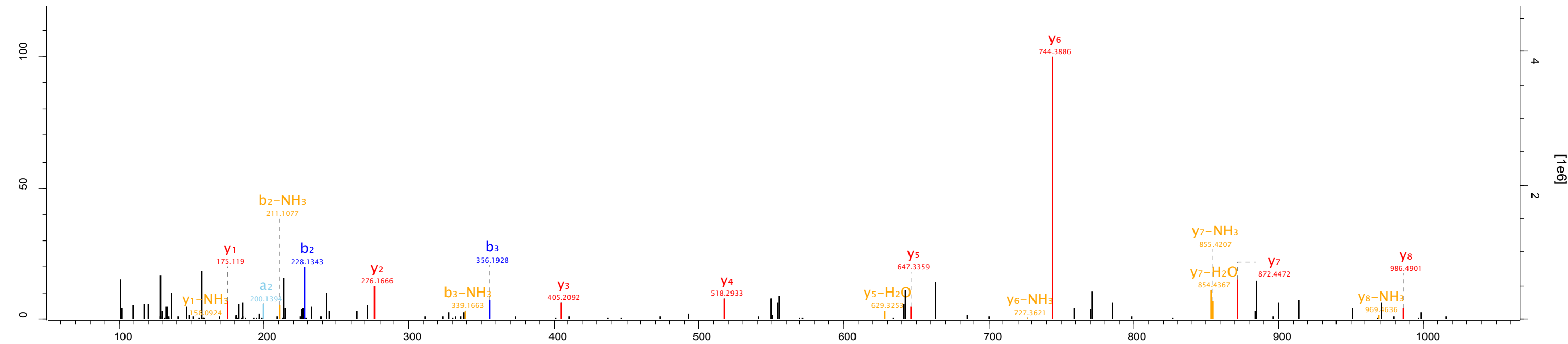
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20180707_MaS_A375SR_ML_proteome_2_05

Scan 8072 Method FTMS; HCD Score 61.59 m/z 709.27 Gene names ZNF704

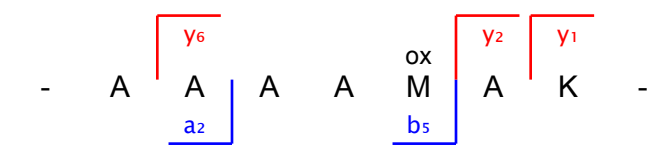
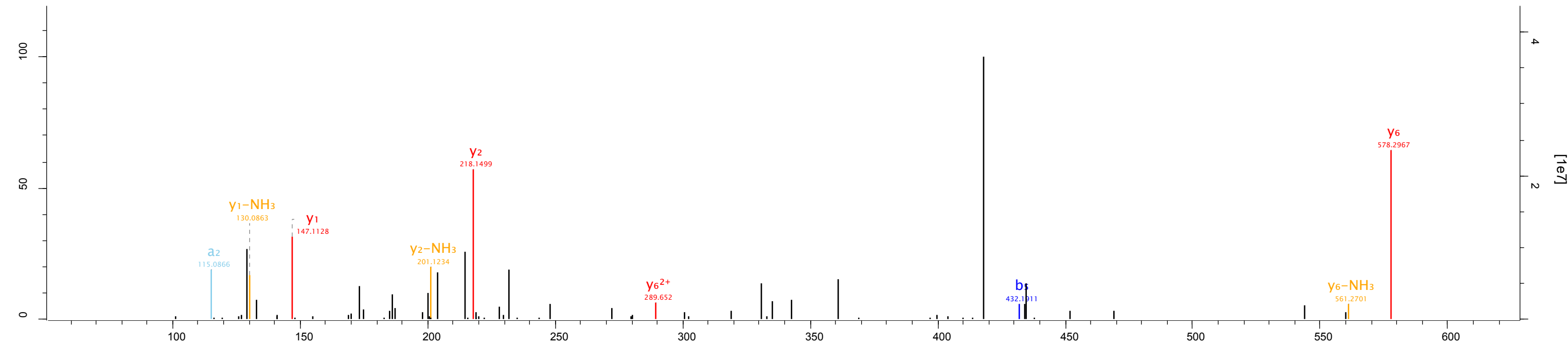


ac
- T F ph T F Q ph S E D L K -
b6 b7 b9 y4 y3 y1

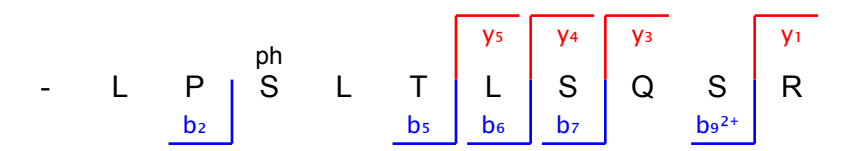
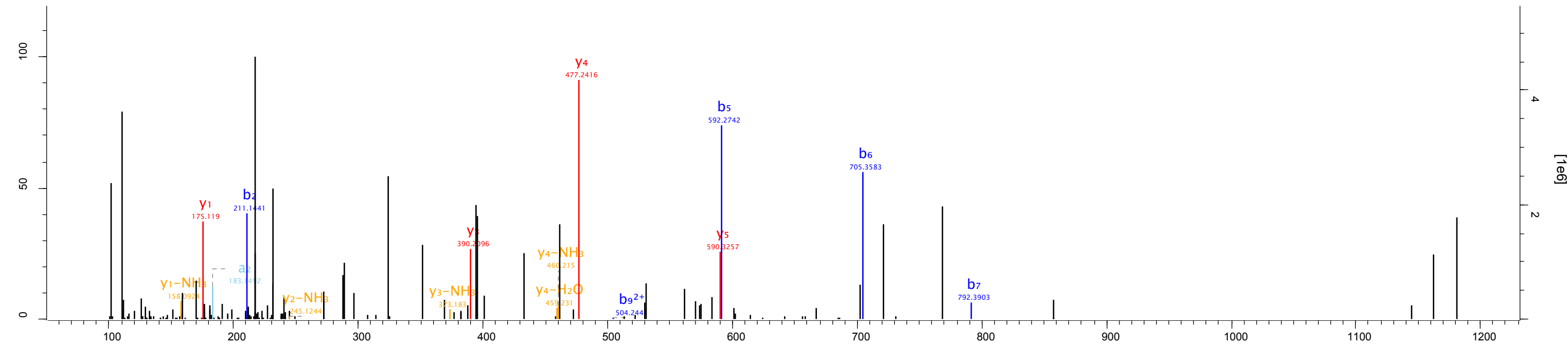
Raw file 20180707_MaS_A375SR_ML_proteome_2_06 Scan 10352 Method FTMS; HCD Score 86.88 m/z 550.29 Gene names ESCO1

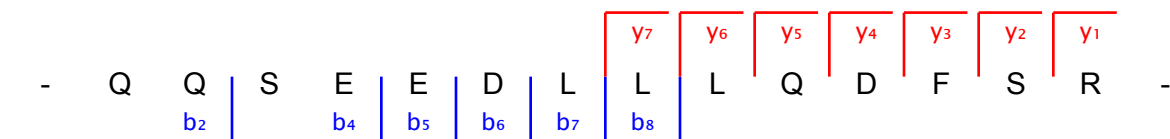
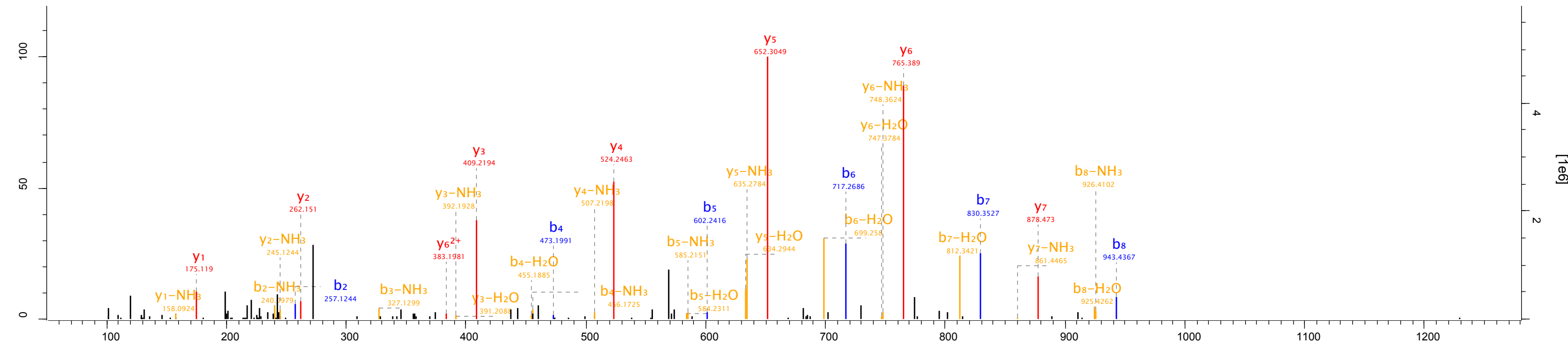


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20180707_MaS_A375SR_ML_proteome_2_06
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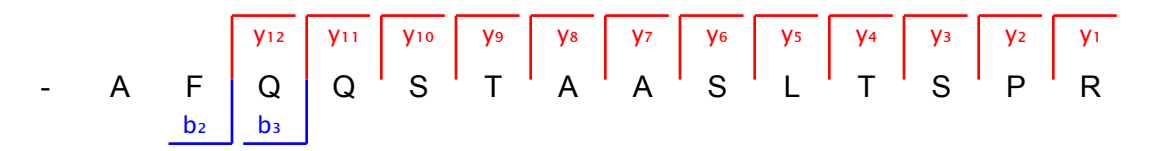
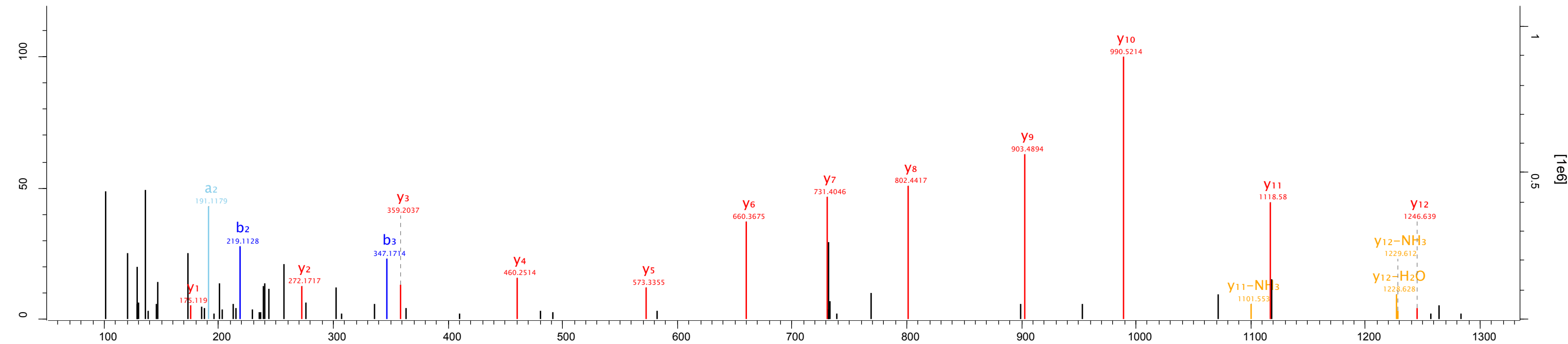


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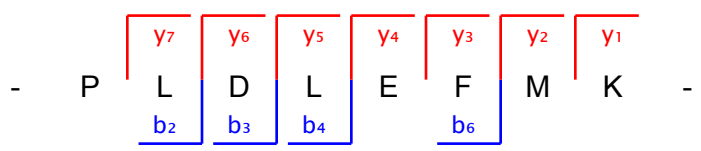
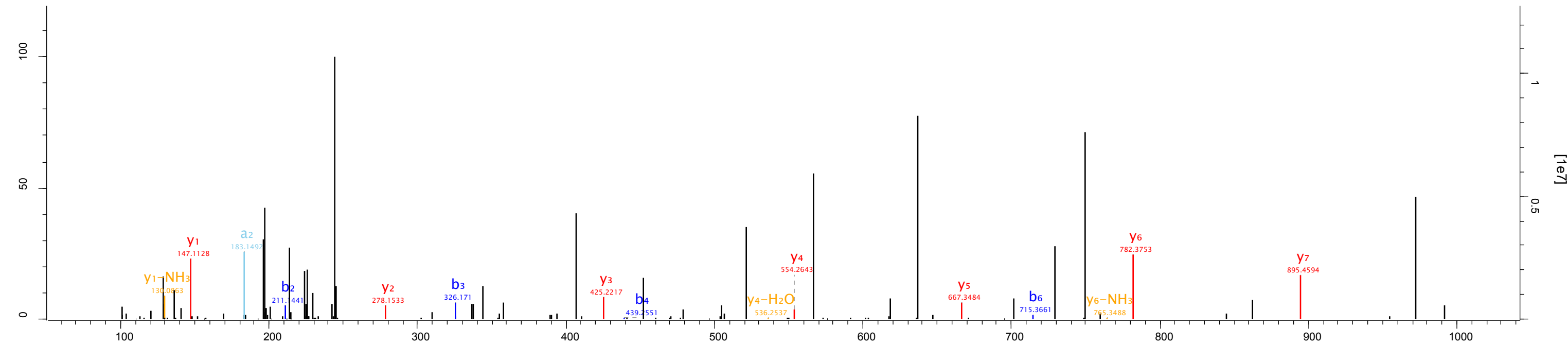


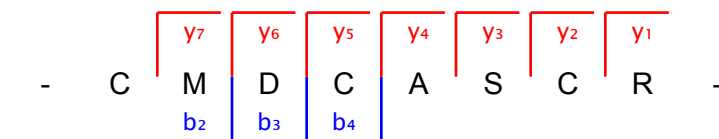
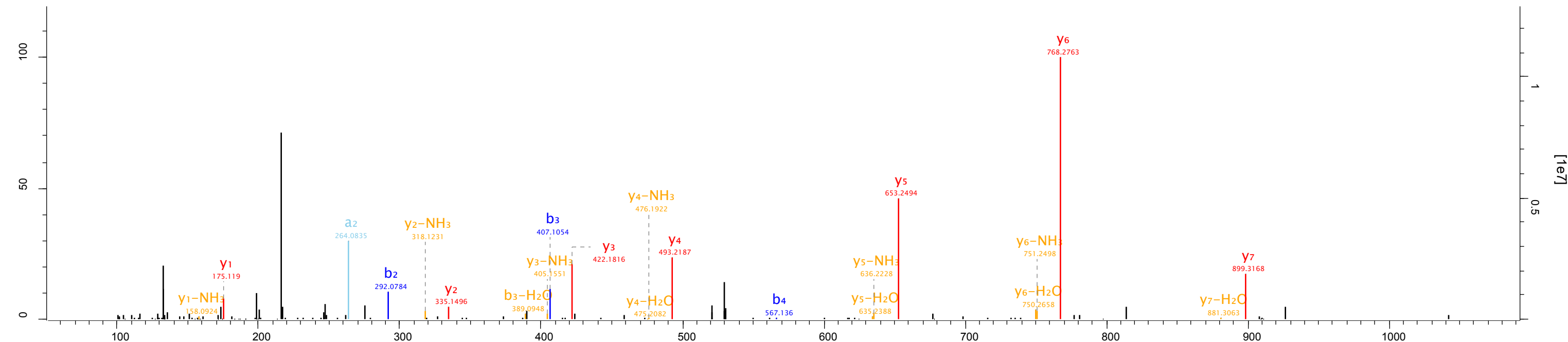


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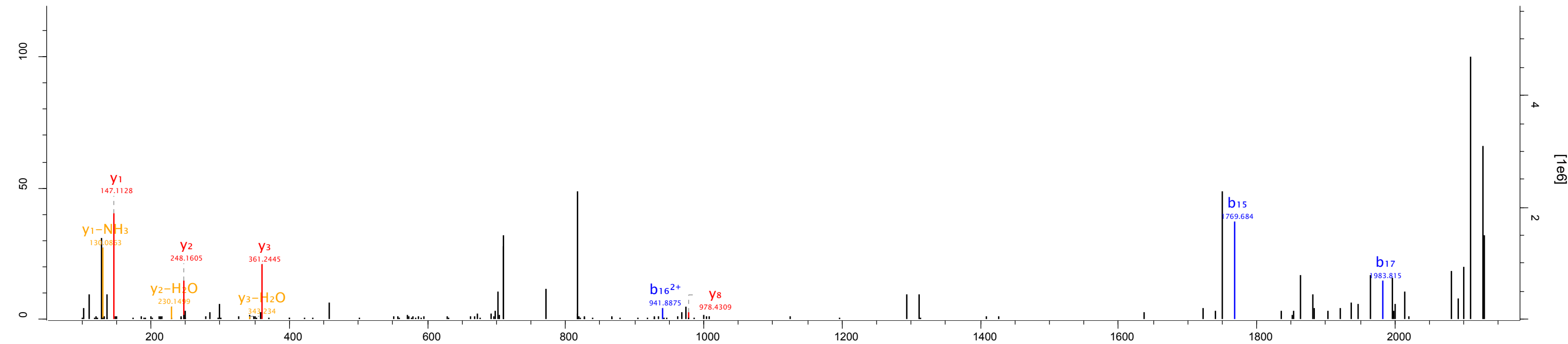


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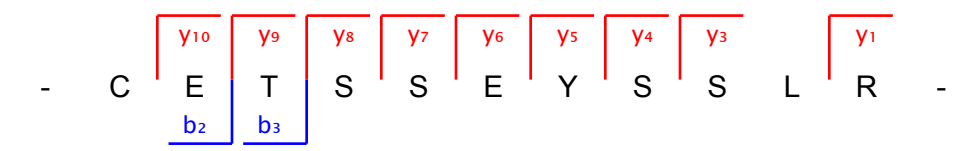
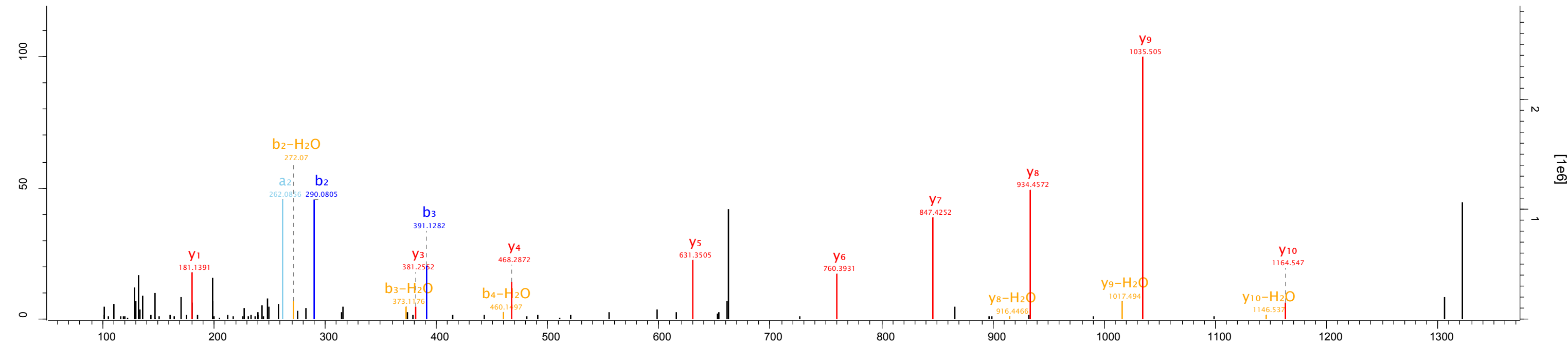
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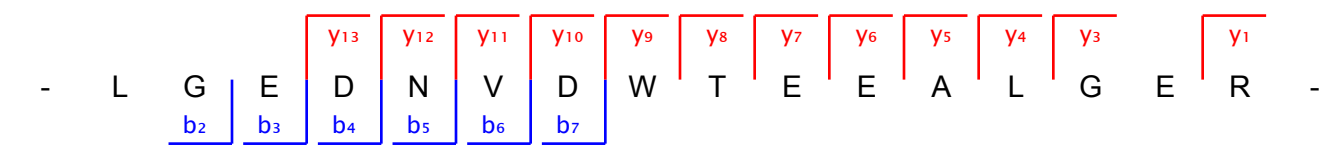
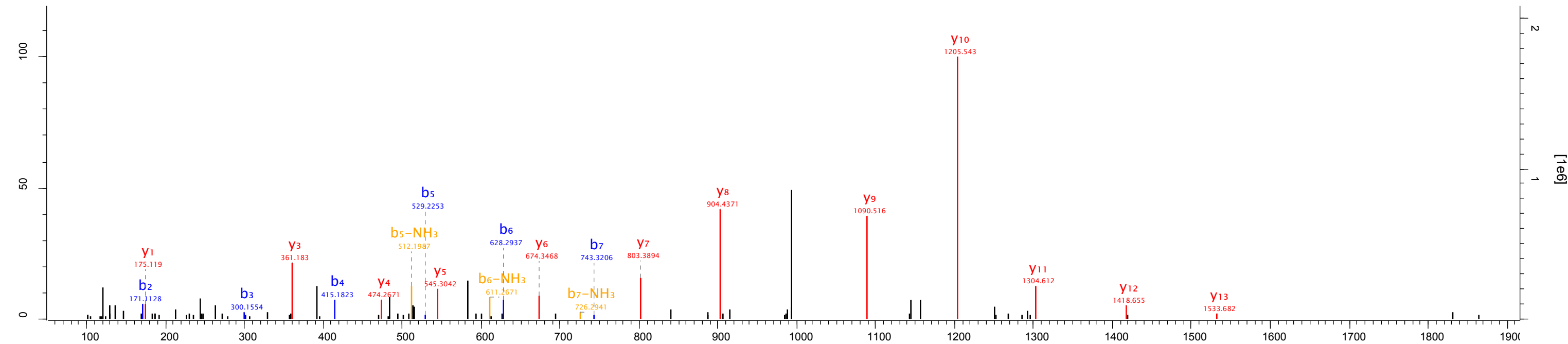
ac - L Y Q L P A A D S ph A ^{y8} T A S V b15 b16²⁺ b17 ^{y3} I ^{y2} T ^{y1} K -

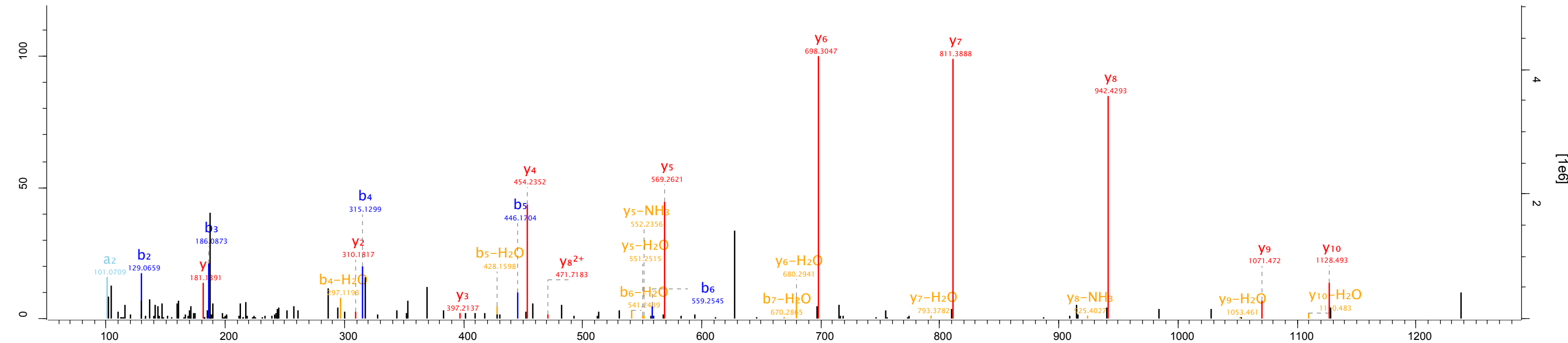
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20180707_MaS_A375SR_ML_proteome_2_10

Scan 9242 Method FTMS; HCD Score 103.91 m/z 662.79 Gene names NRG1



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 Scan 25182 Method FTMS; HCD Score 94.2 m/z 916.91 Gene names MIEF2



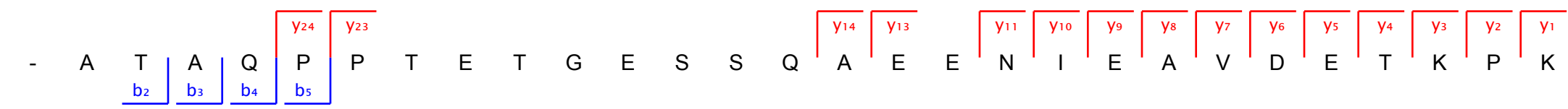
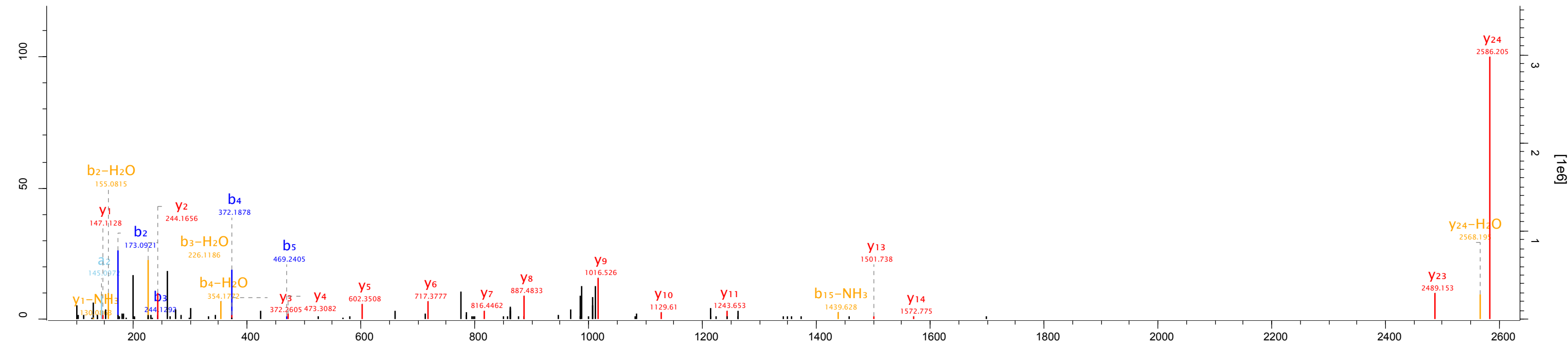


- G A G E M L E D G S E R -

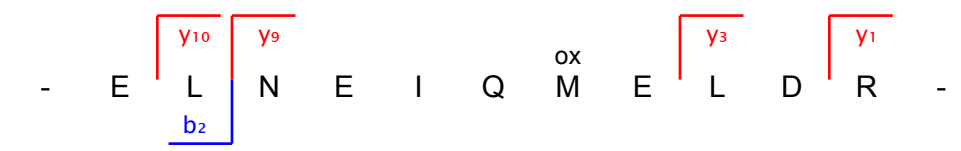
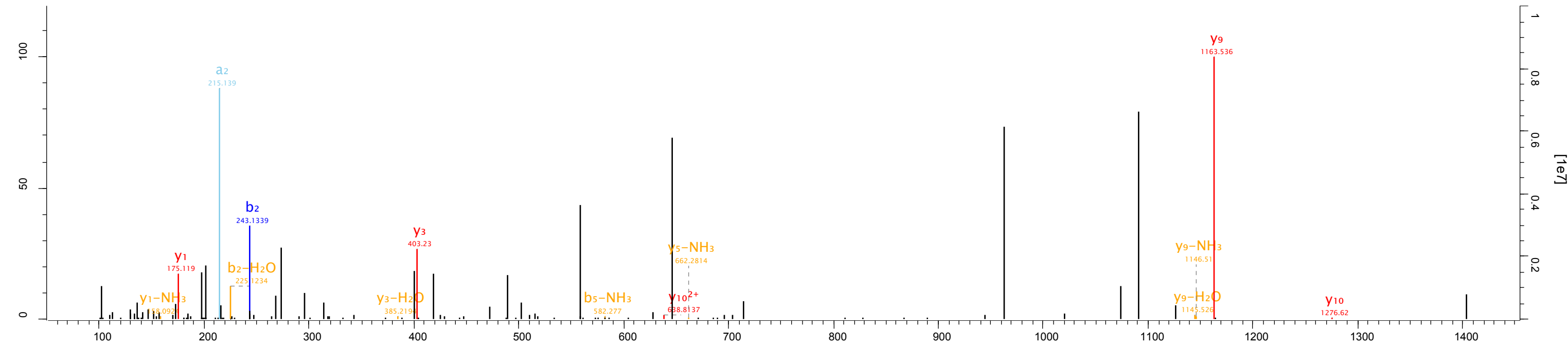
b₂
b₃
b₄
b₅
b₆
y₁₀
y₉
y₈
y₇
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y₅
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y₃
y₂
y₁

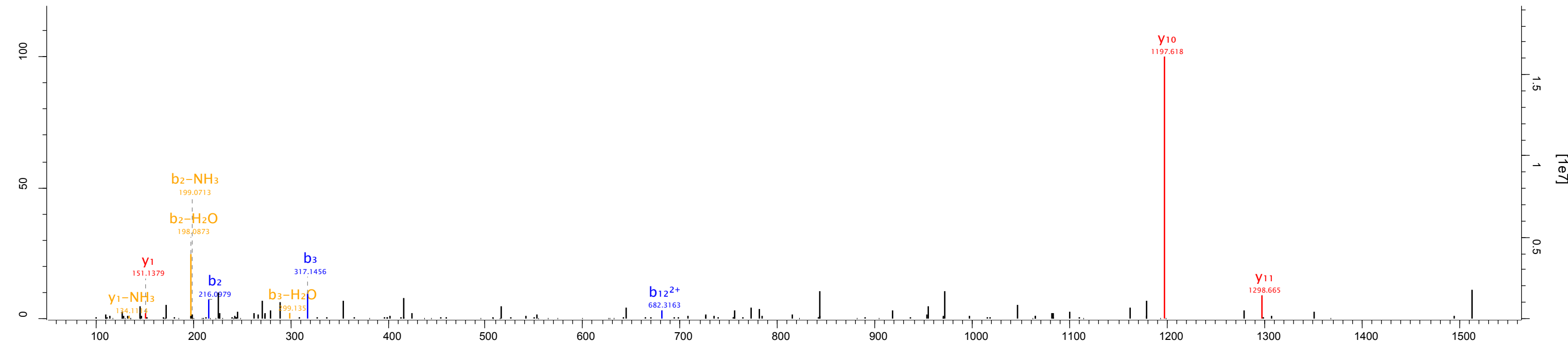
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20180707_MaS_A375SR_ML_proteome_2_12

Scan 17902 Method FTMS; HCD Score 58.86 m/z 986.8 Gene names GAP43



Raw file 20180707_MaS_A375SR_ML_proteome_2_12 Scan 19342 Method FTMS; HCD Score 51.76 m/z 703.34

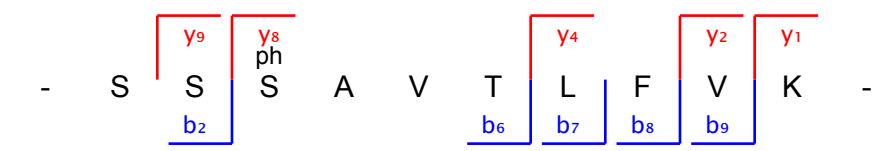
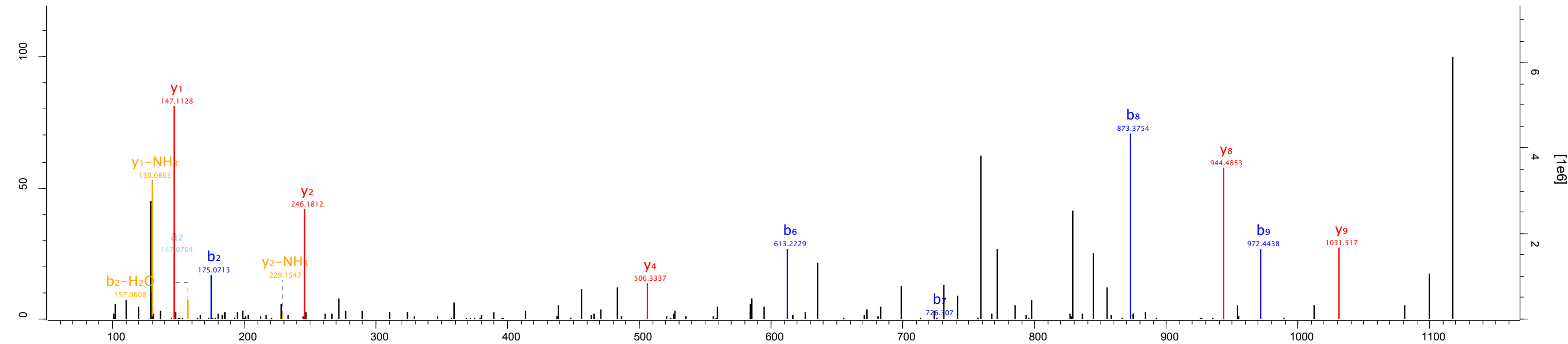




- Q S T V I Q S N Q S P I K -

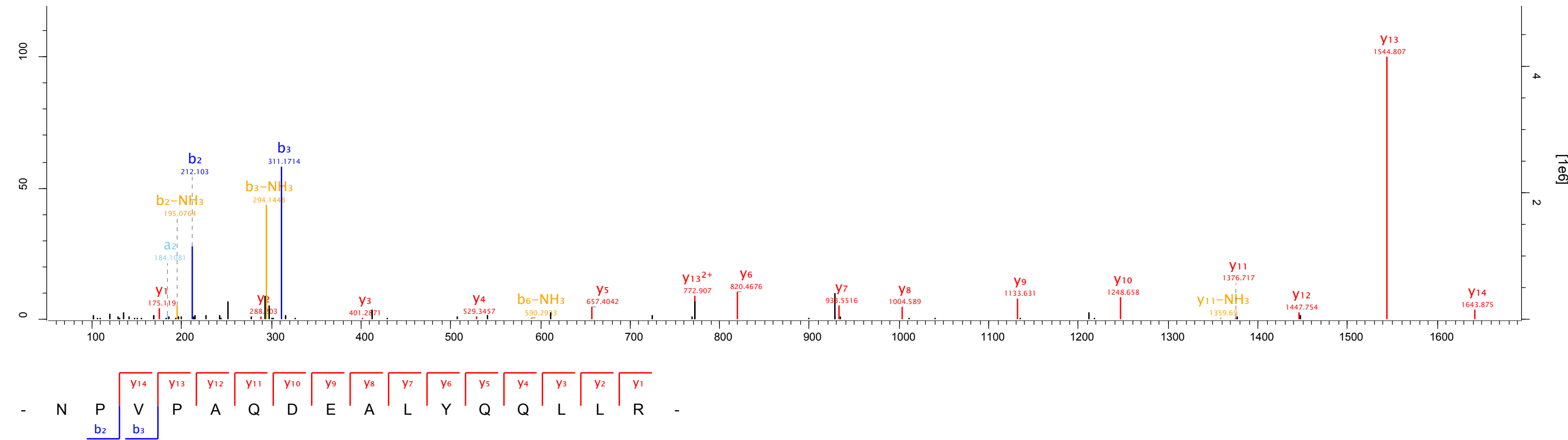
Fragmentation labels: b₂, b₃, y₁₁, y₁₀, b_{12²⁺}, y₁

Raw file 20180707_MaS_A375SR_ML_proteome_2_15 Scan 16492 Method FTMS; HCD Score 97.97 m/z 559.78



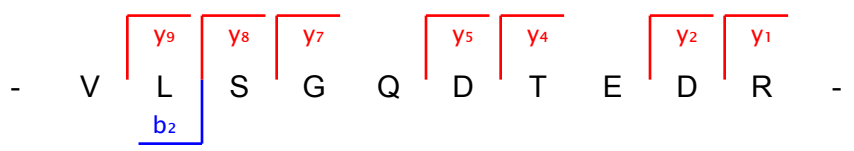
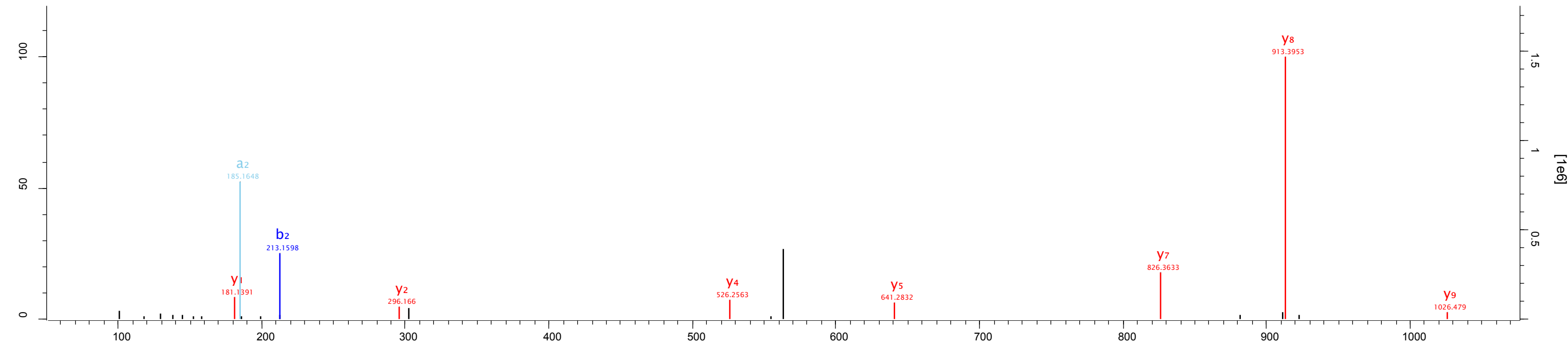
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20180707_MaS_A375SR_ML_proteome_2_15

Scan: 27912
Method: FTMS; HCD
Score: 85.49
m/z: 928.5
Gene names: CLIC3



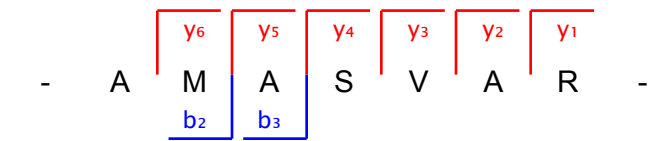
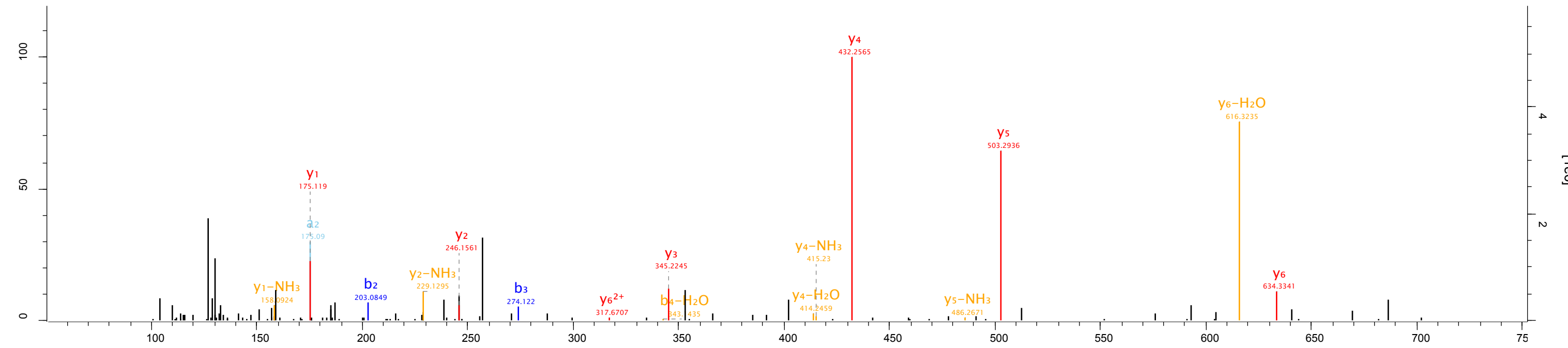
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20180707_MaS_A375SR_ML_proteome_2_15

Scan 4772 Method FTMS; HCD Score 47.3 m/z 563.28 Gene names SFT2D2



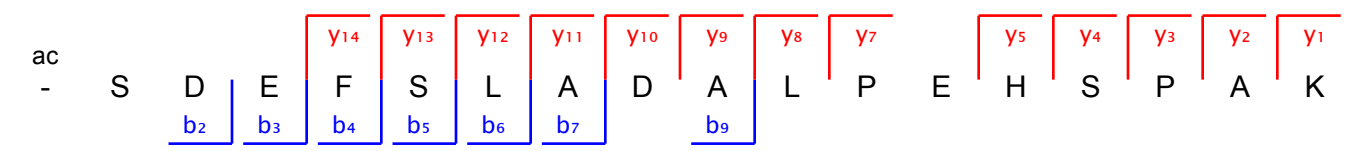
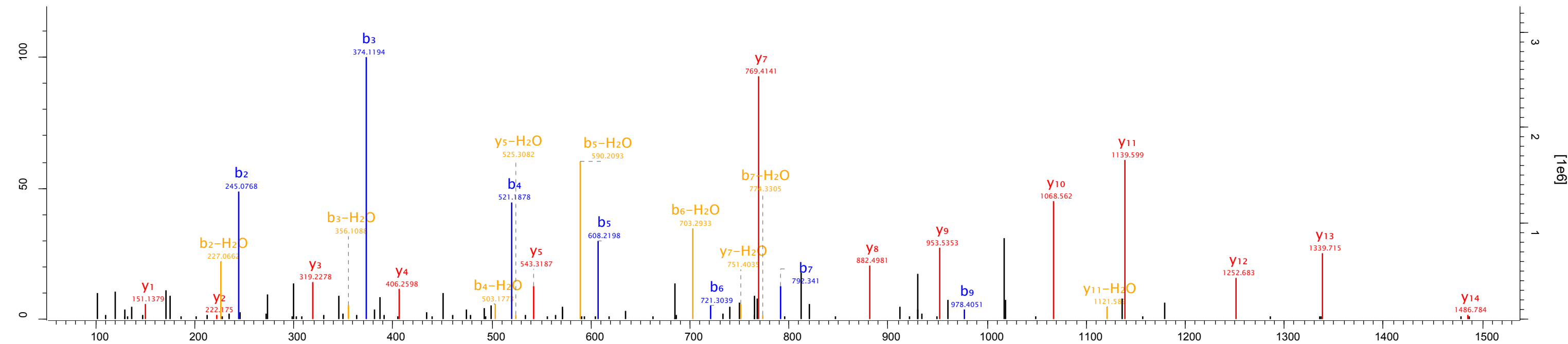
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20180707_MaS_A375SR_ML_proteome_2_15

Scan 6612 Method FTMS; HCD Score 96.51 m/z 353.19 Gene names ART4

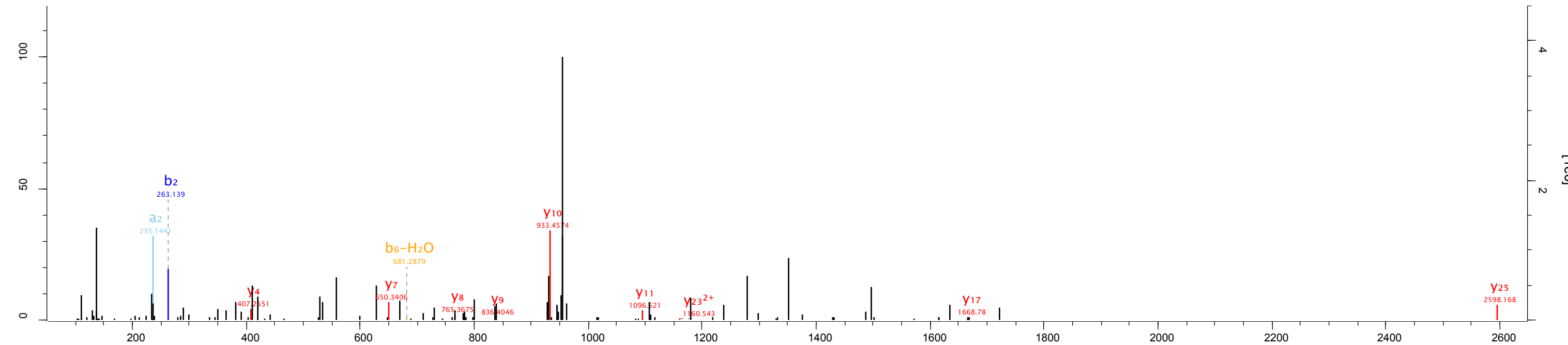


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Scan 26442 Method FTMS; HCD Score 100.04 m/z 930.45 Gene names MAPK1IP1L



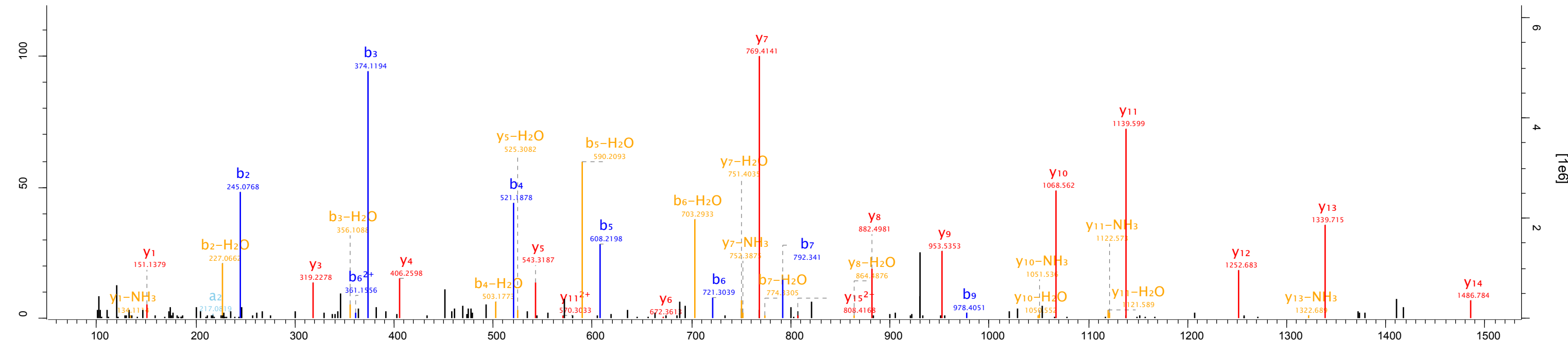
Raw file 20180707_MaS_A375SR_ML_proteome_2_17
 Scan 19082 Method FTMS; HCD Score 8.32 m/z 954.45 Gene names C6orf120



- V Y Y D G T V E Q H P F G E A A Y P A D G A D A G Q K -

Fragmentation sites are indicated by brackets above the sequence:

- b₂** (blue bracket) under Y (position 3)
- y₂₅** (red bracket) above Y (position 3)
- y₂₃²⁺** (red bracket) above G (position 5)
- y₁₇** (red bracket) above H (position 9)
- y₁₁** (red bracket) above Y (position 14)
- y₁₀** (red bracket) above P (position 15)
- y₉** (red bracket) above A (position 16)
- y₈** (red bracket) above D (position 17)
- y₇** (red bracket) above G (position 18)
- y₄** (red bracket) above A (position 21)



ac

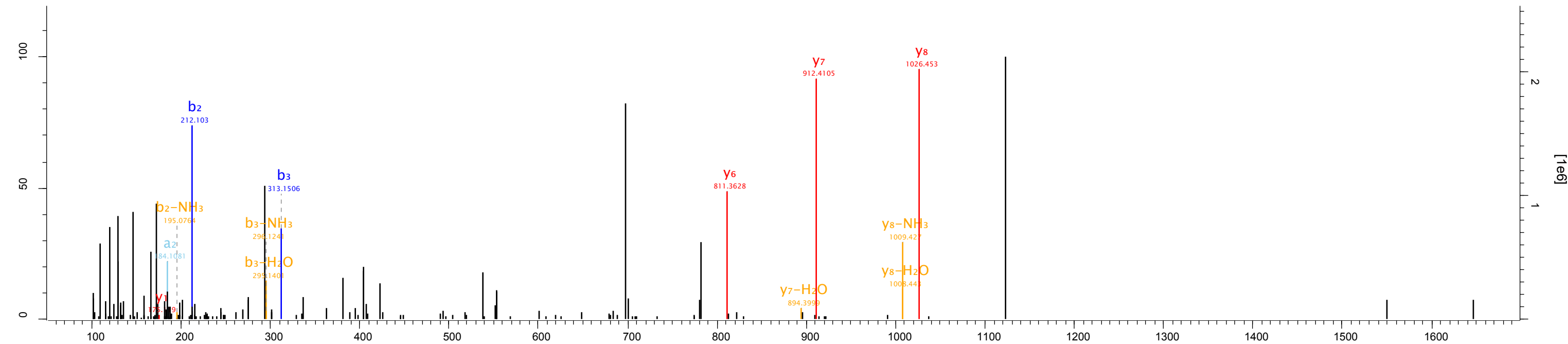
- S D E F S L A D A L P E H S P A K -

b₂ b₃ b₄ b₅ b₆ b₇ b₉

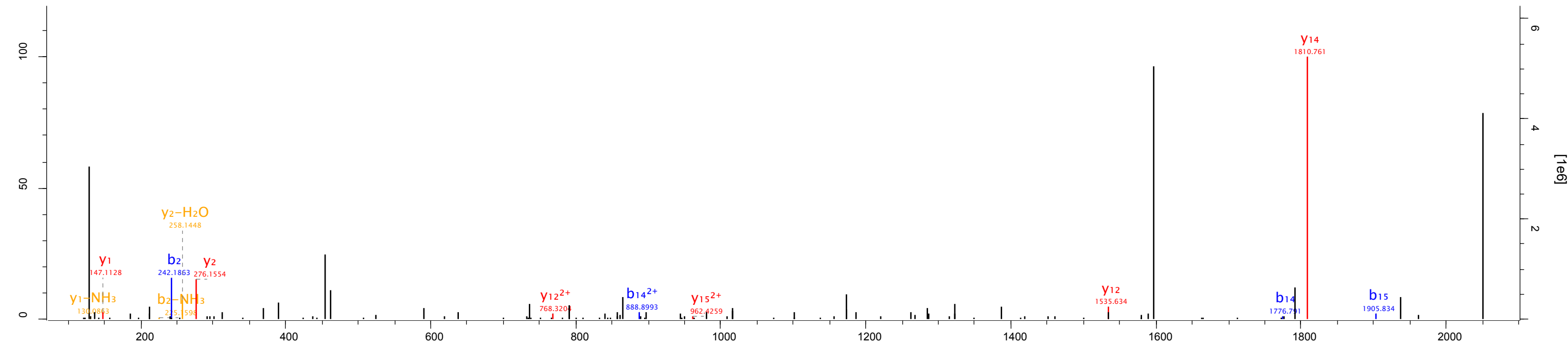
y₁₅²⁺ y₁₄ y₁₃ y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₁

Raw file
20180707_MaS_A375SR_ML_proteome_2_18

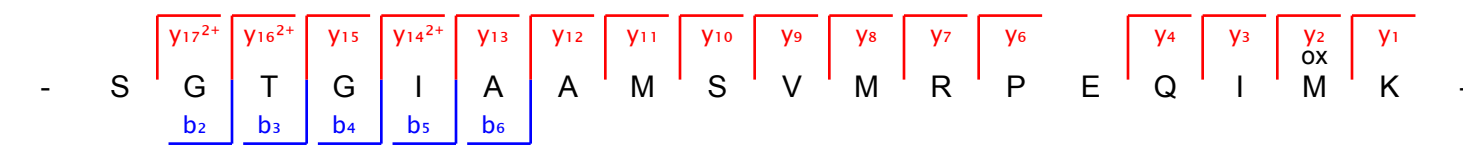
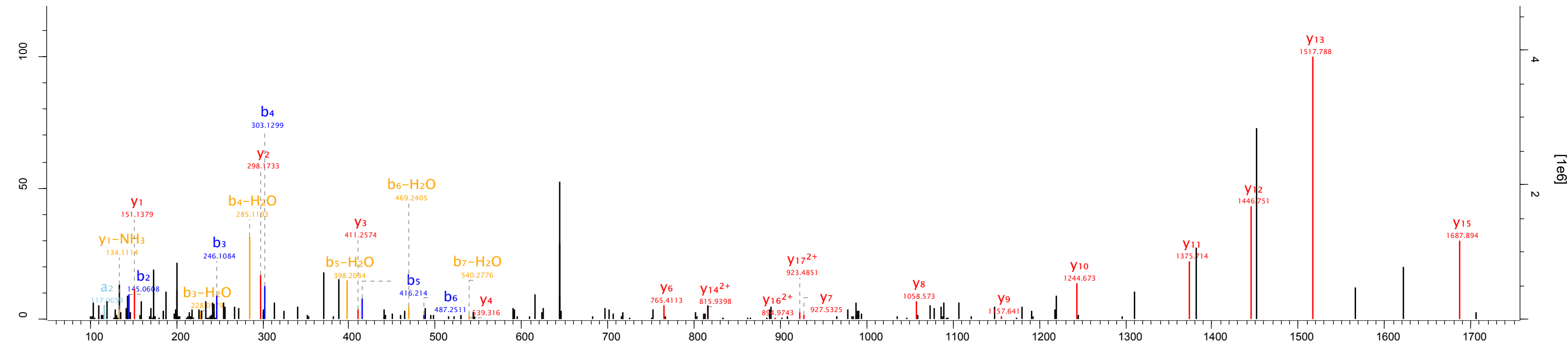
Scan 15192 Method FTMS; HCD Score 54.98 m/z 562.26



Raw file 20180707_MaS_A375SR_ML_proteome_2_18 Scan 18722 Method FTMS; HCD Score 44.93 m/z 1026.47

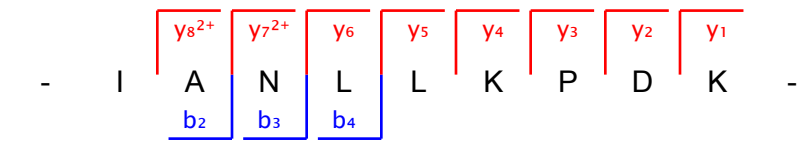
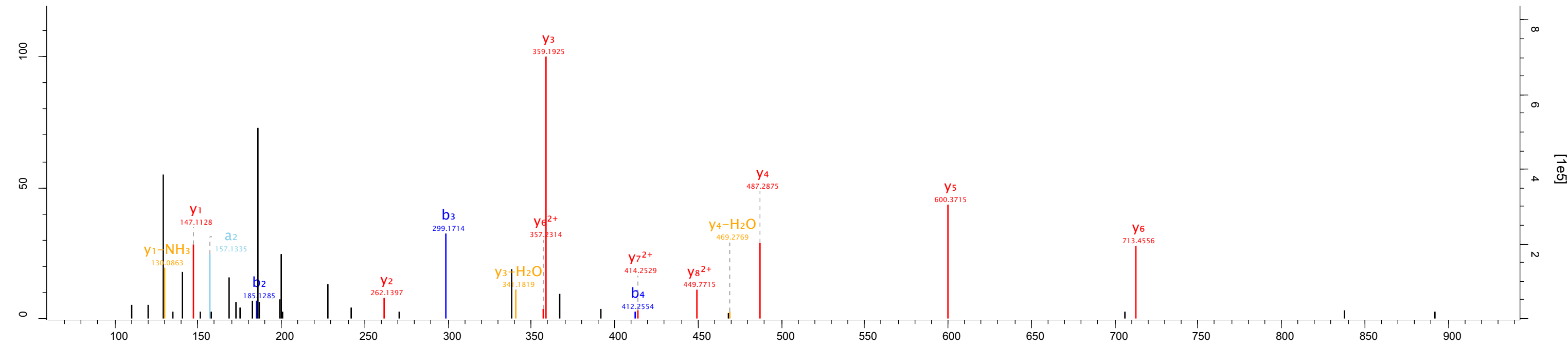


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 Scan: 19472 Method: FTMS; HCD Score: 73.93 m/z: 645 Gene names: ATP6V0C

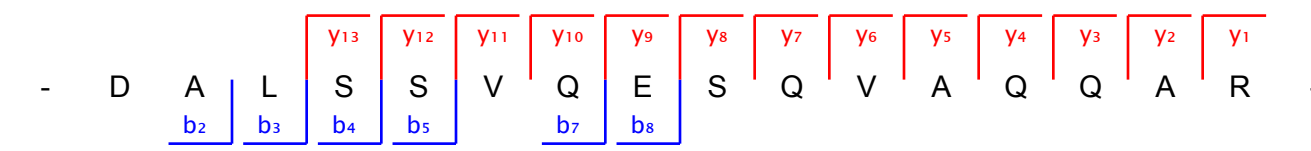
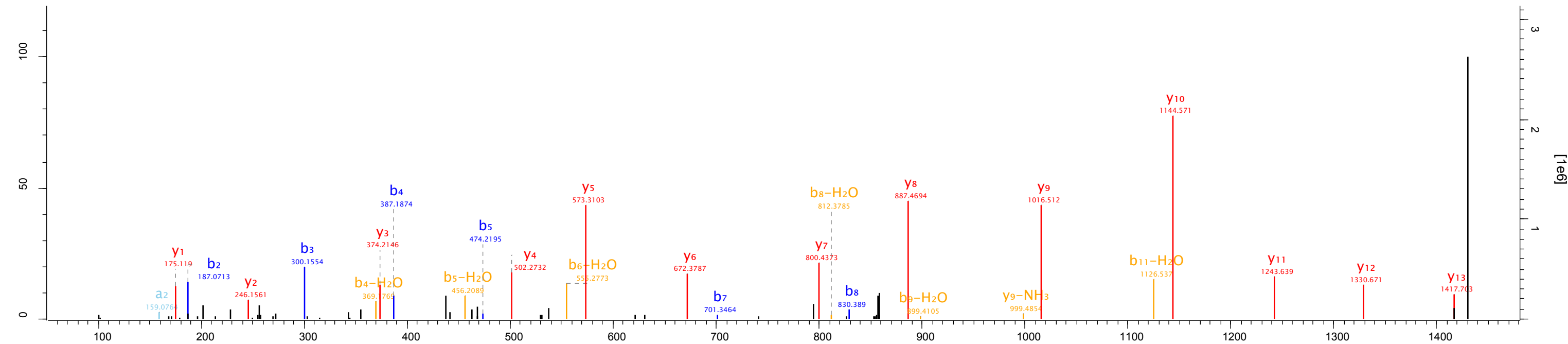


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20180707_MaS_A375SR_ML_proteome_2_19

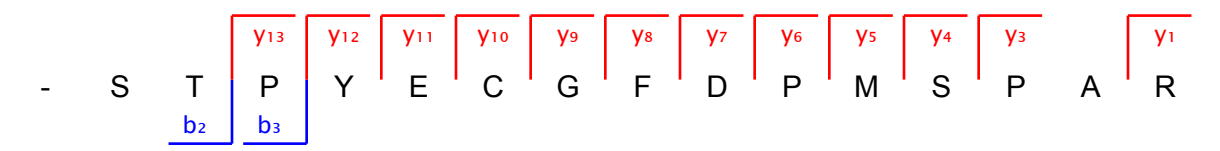
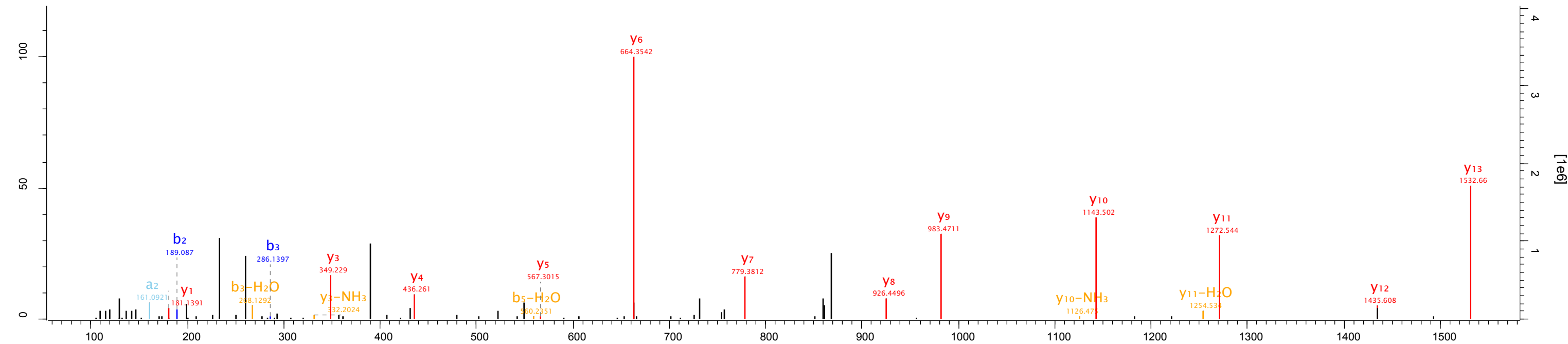
Scan 11692 Method FTMS; HCD Score 93.18 m/z 337.88 Gene names RBP1



Raw file 20180707_MaS_A375SR_ML_proteome_2_19 Scan 14762 Method FTMS; HCD Score 117 m/z 858.93 Gene names APOC3

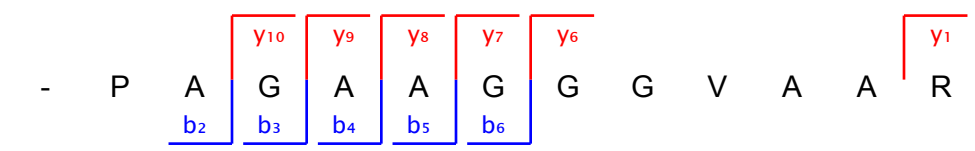
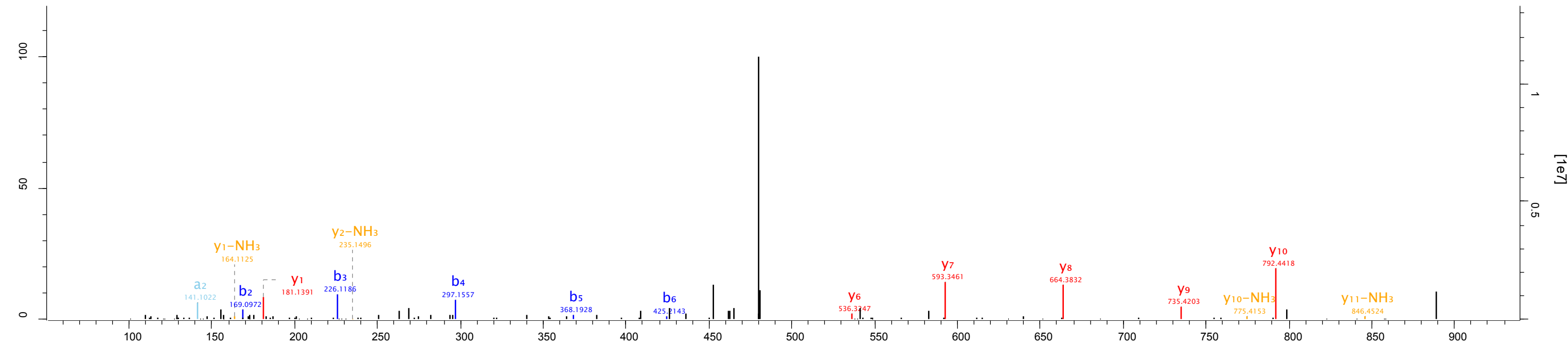


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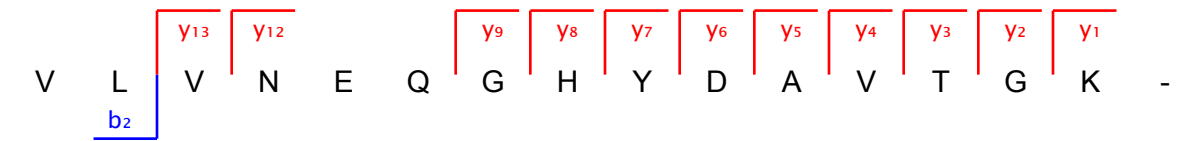
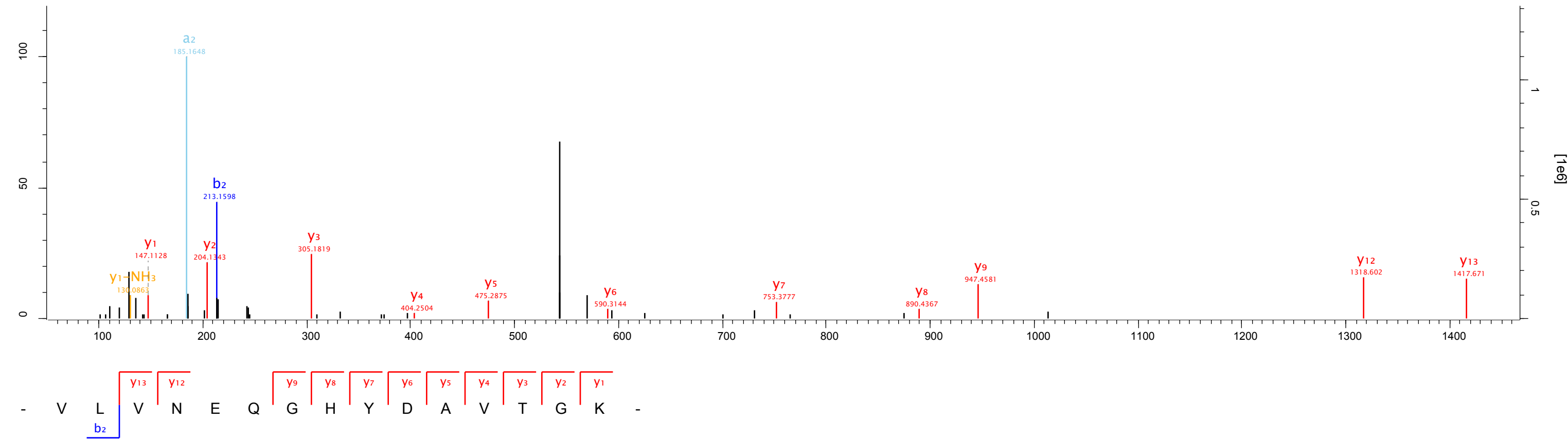
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Scan 6472 Method FTMS; HCD Score 64.82 m/z 480.77 Gene names EPM2A



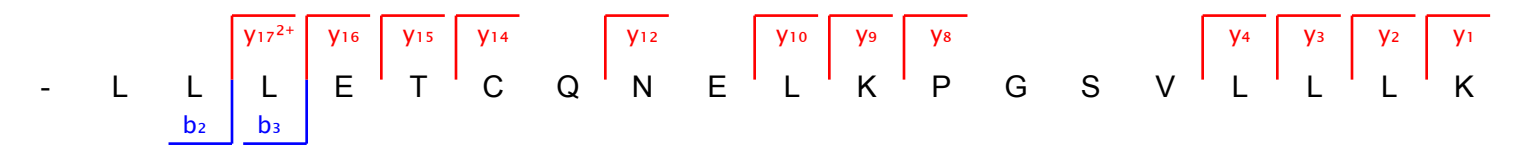
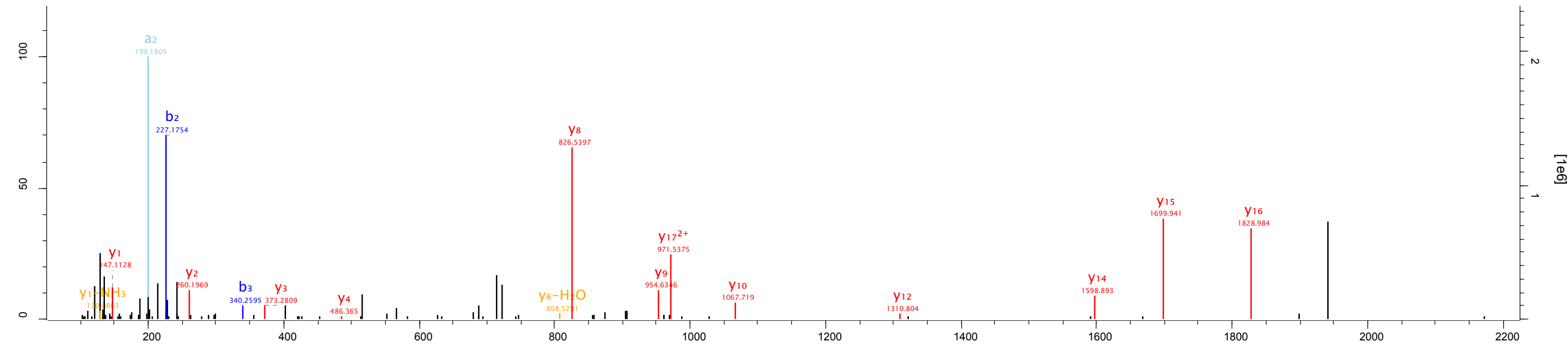
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Scan 11502 Method FTMS; HCD Score 53.98 m/z 543.95 Gene names C1QTNF5

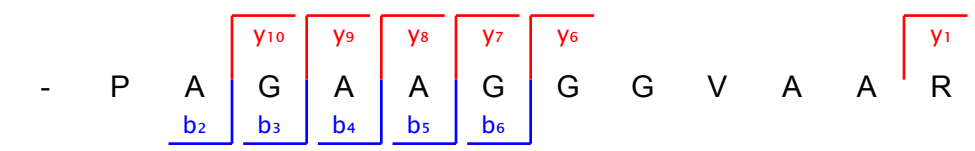
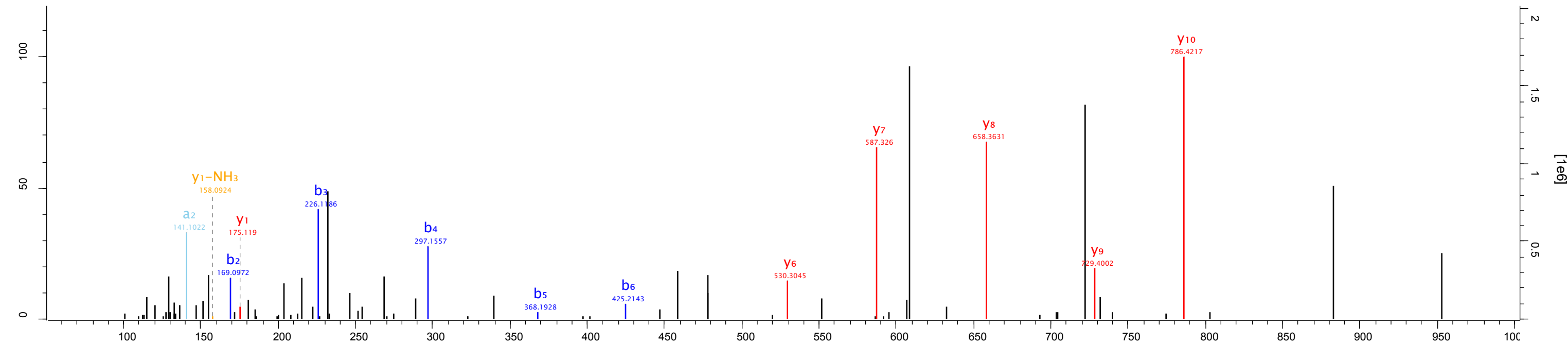


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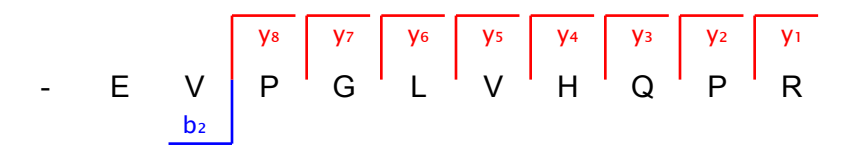
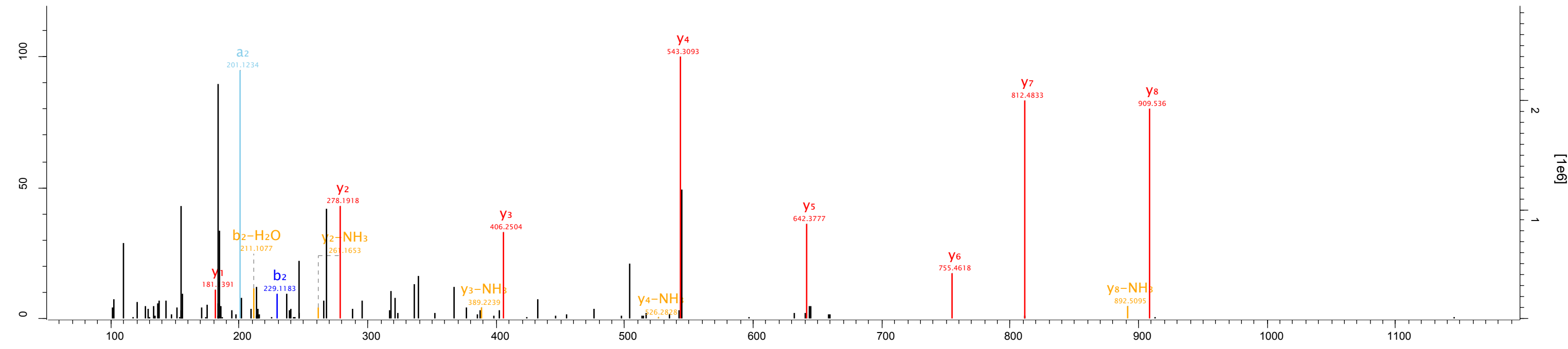
Scan 28652 Method FTMS; HCD Score 54.76 m/z 723.75 Gene names C17orf53



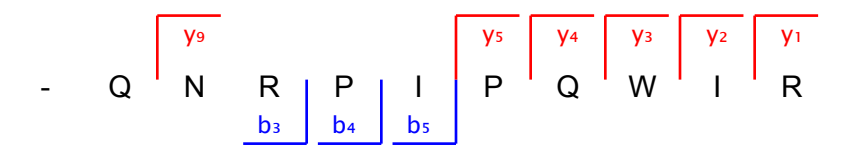
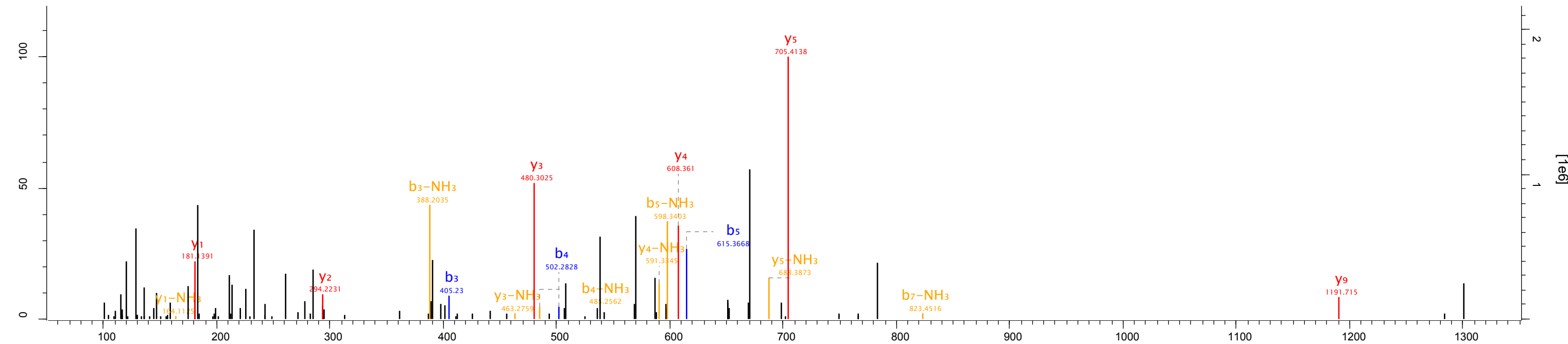
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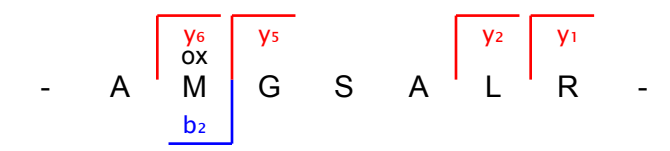
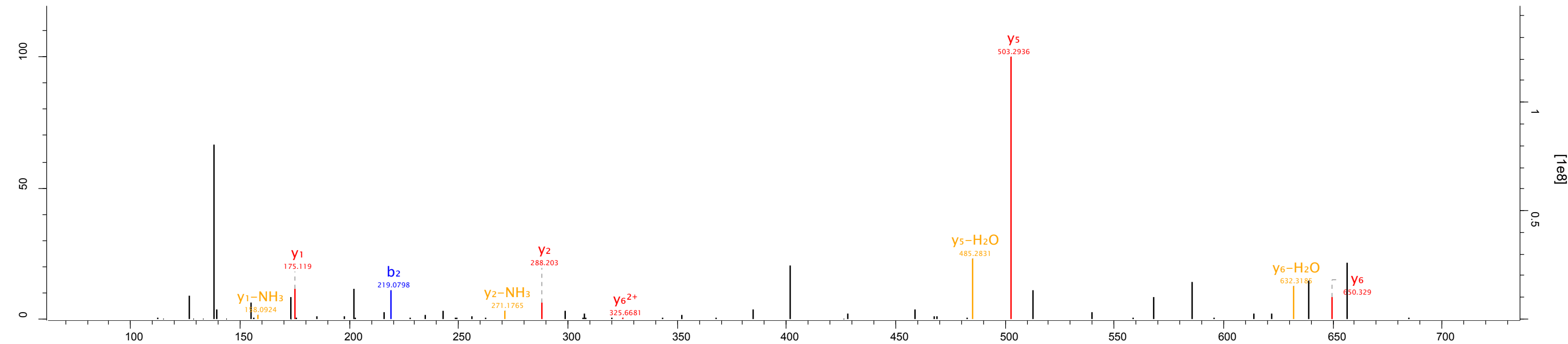
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 Scan: 10002 Method: FTMS; HCD Score: 63.08 m/z: 379.89 Gene names: C1orf21



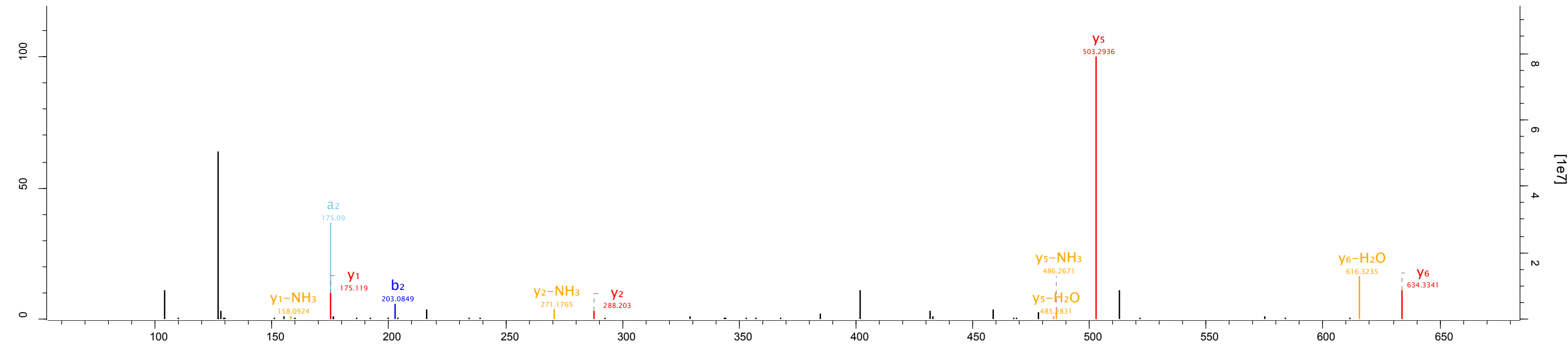
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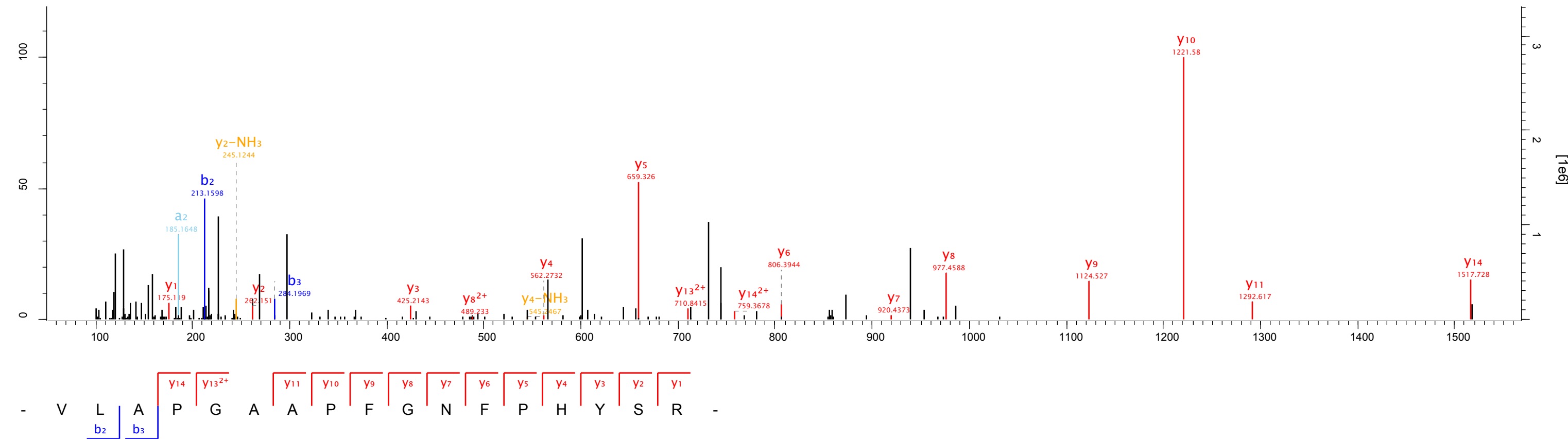


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Raw file 20180707_MaS_A375SR_ML_proteome_2_22 Scan 6392 Method FTMS; HCD Score 79.45 m/z 353.19

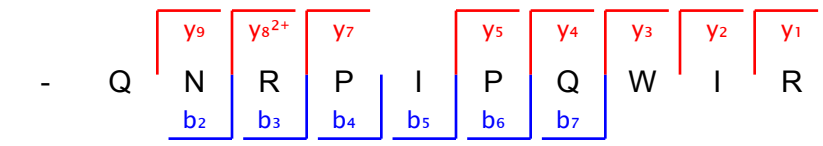
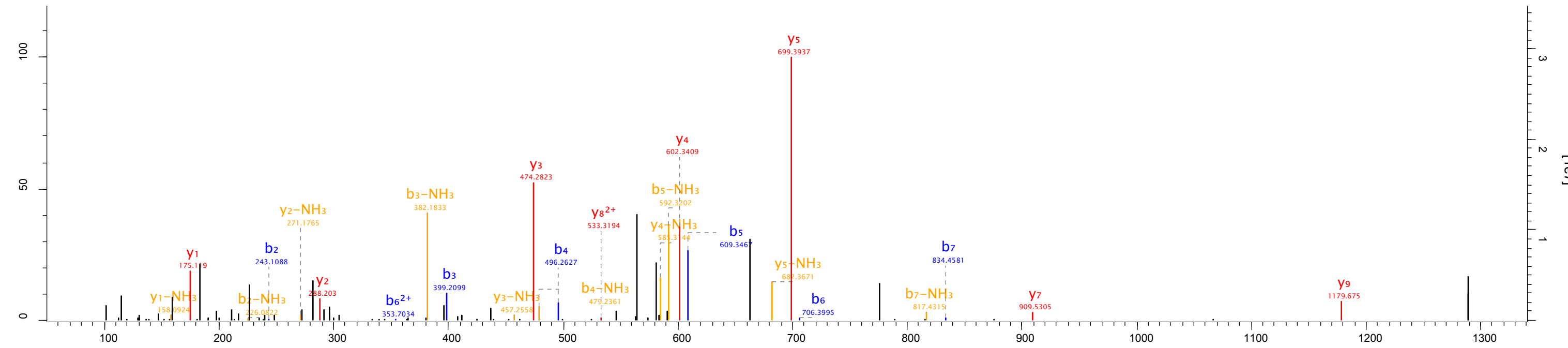




Raw file

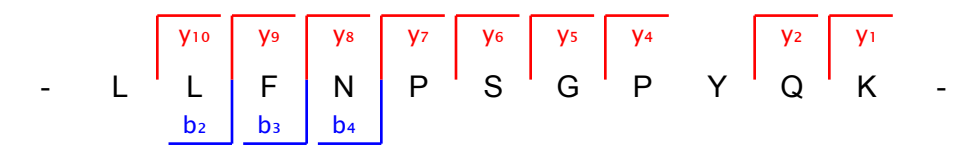
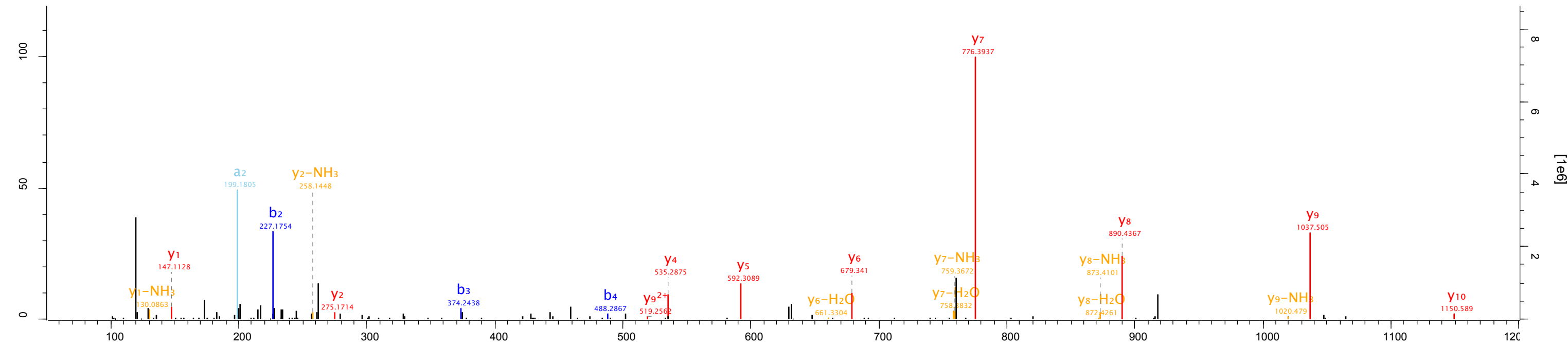
20180707_MaS_A375SR_ML_proteome_2_24

Scan	Method	Score	m/z	Gene names
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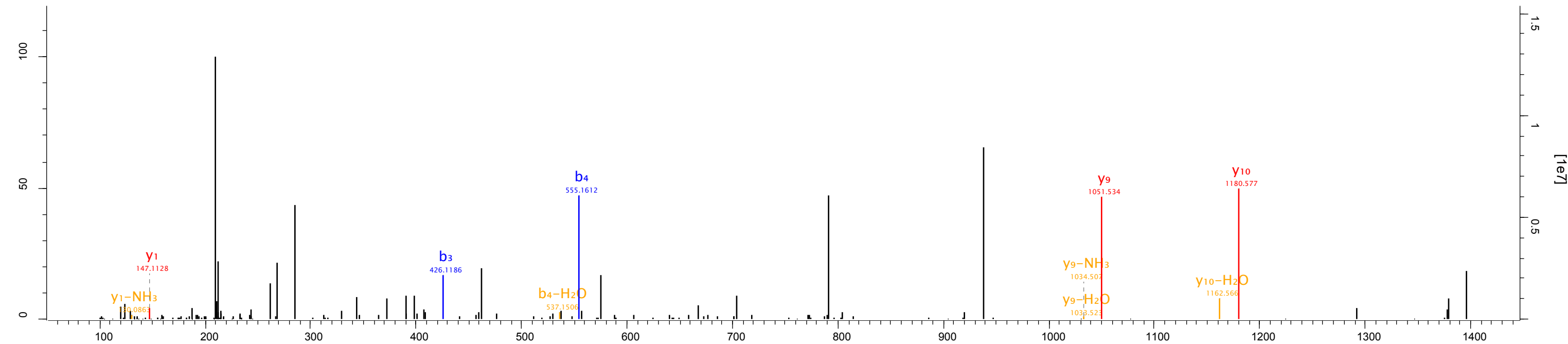


Raw file
20180707_MaS_A375SR_ML_proteome_2_24

Scan 19842 Method FTMS; HCD Score 110.39 m/z 632.84 Gene names CKLF



Raw file 20180707_MaS_A375SR_ML_proteome_2_24 Scan 28242 Method FTMS; HCD Score 42.84 m/z 803.85



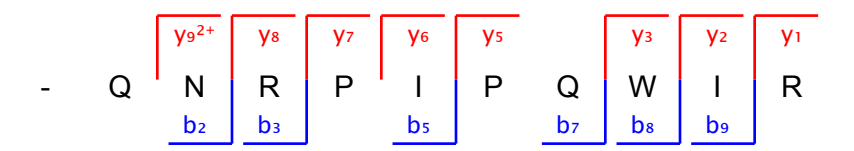
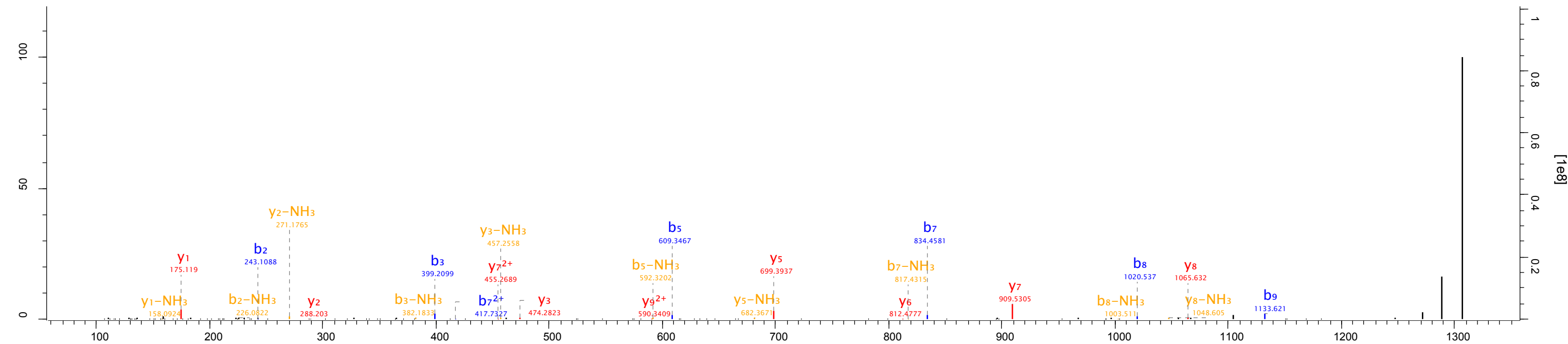
- OX M OX M M E M E S I L D S L K -

Fragmentation mapping:

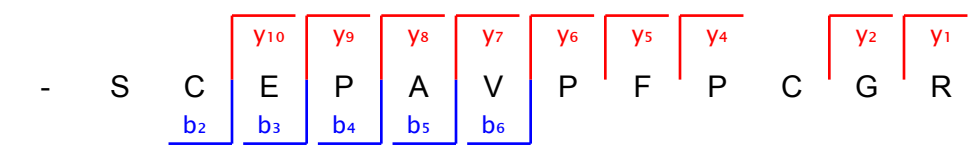
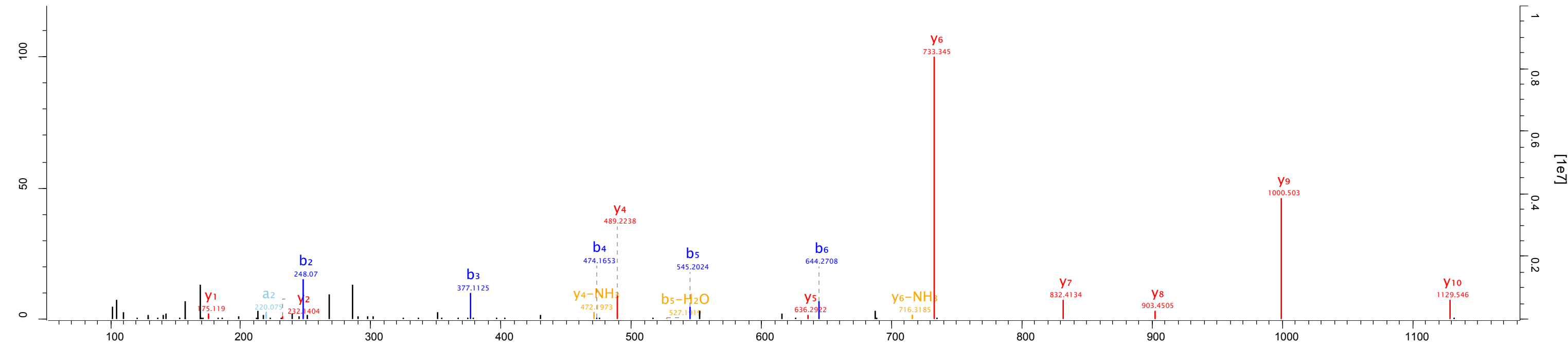
- b3: M
- b4: M E
- y9: M
- y10: E M
- y1: K

Raw file
20180707_MaS_A375SR_ML_proteome_2_25

Scan 16232 Method FTMS; HCD Score 152.06 m/z 654.37 Gene names RPL39P5;RPL39

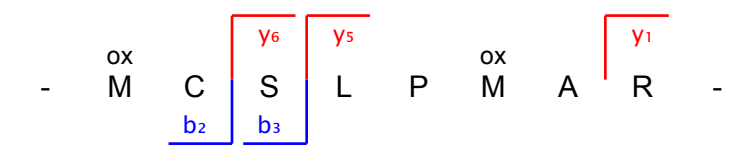
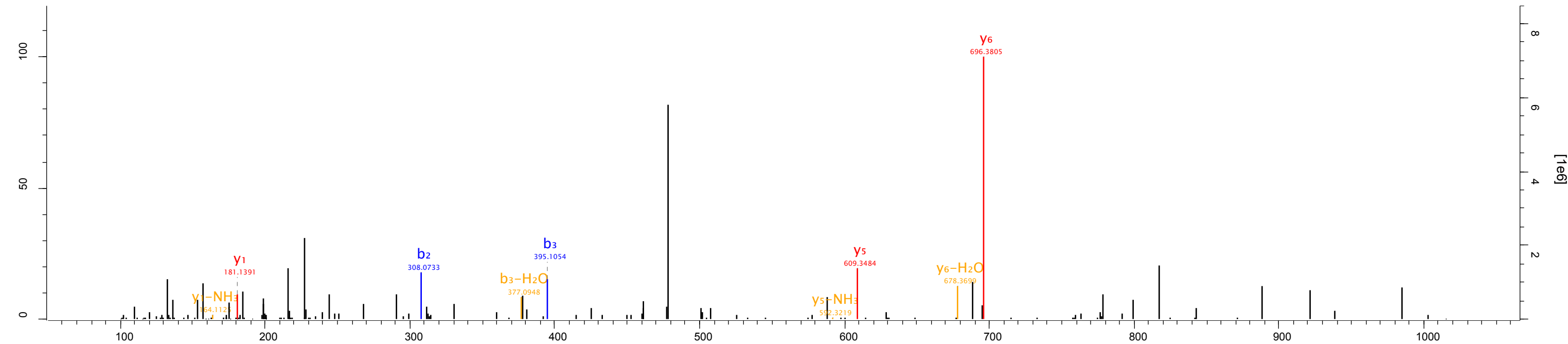


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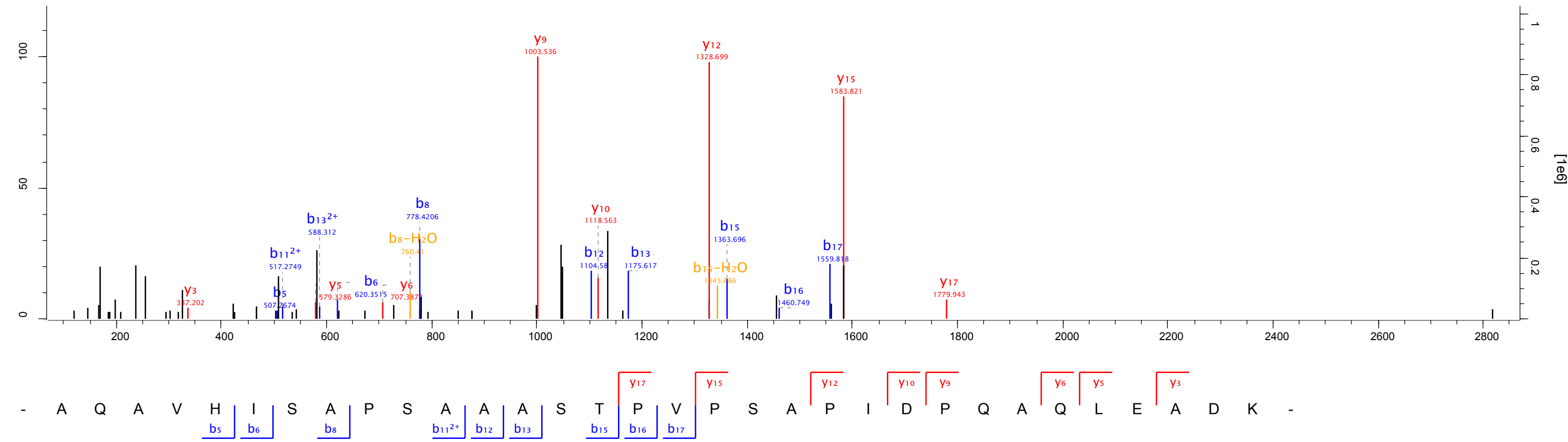
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20180707_MaS_A375SR_ML_proteome_2_25

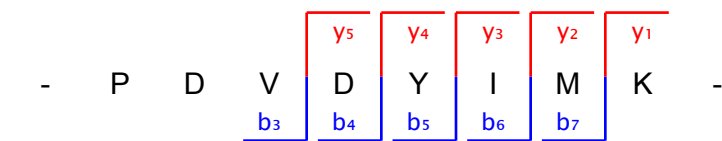
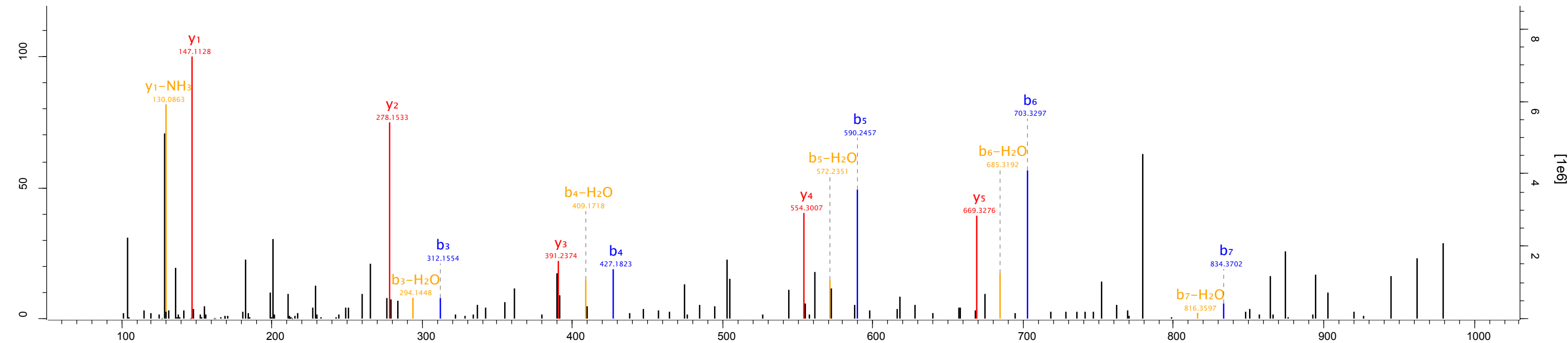
Scan 9032 Method FTMS; HCD Score 46.43 m/z 502.23 Gene names IL1F10



Raw file
20180707_MaS_A375SR_ML_proteome_2_26

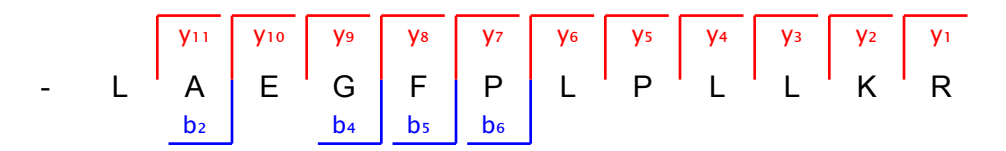
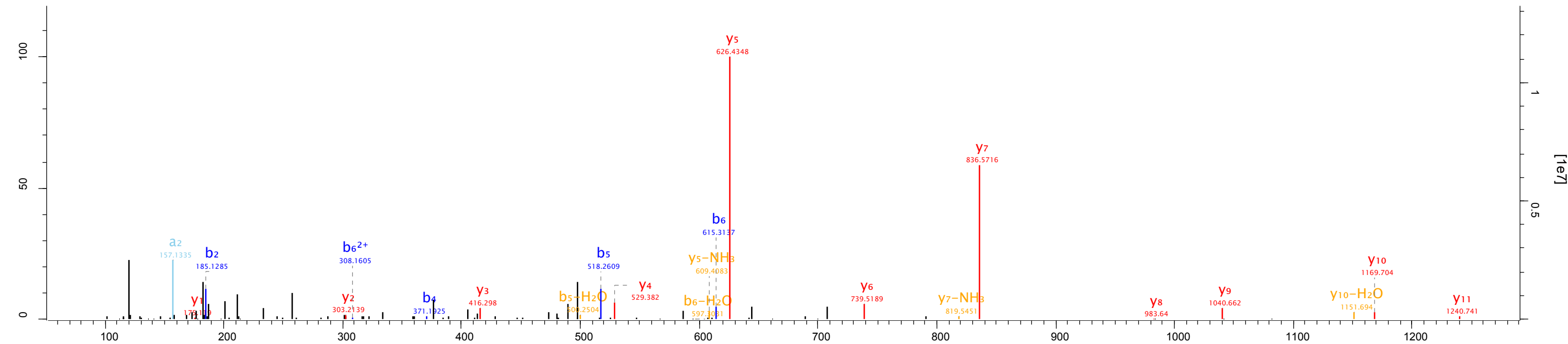
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Method: FTMS; HCD
Score: 50.89
m/z: 1048.22
Gene names: PKNOX2





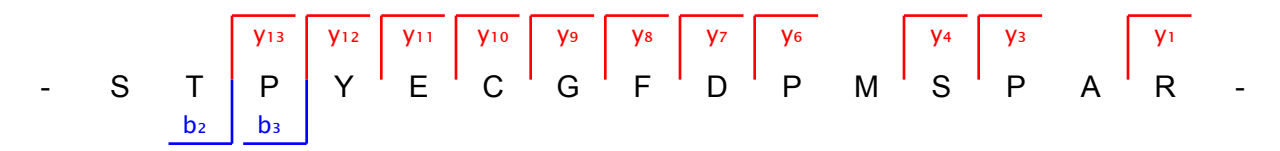
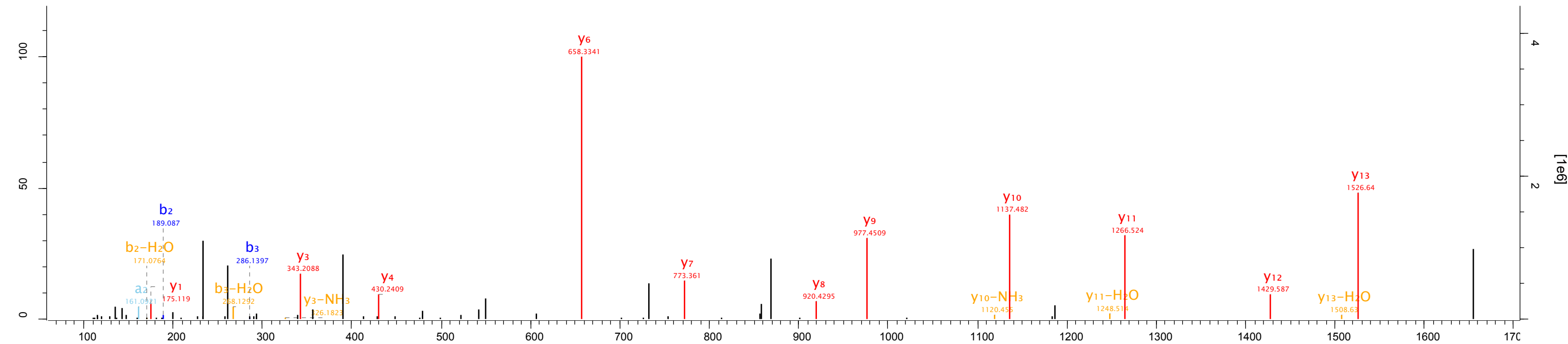
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20180707_MaS_A375SR_ML_proteome_2_27

Scan 27442 Method FTMS; HCD Score 102.4 m/z 452.28 Gene names LBP



Raw file
20180707_MaS_A375SR_ML_proteome_2_28

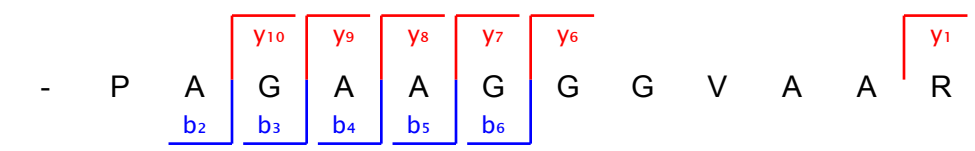
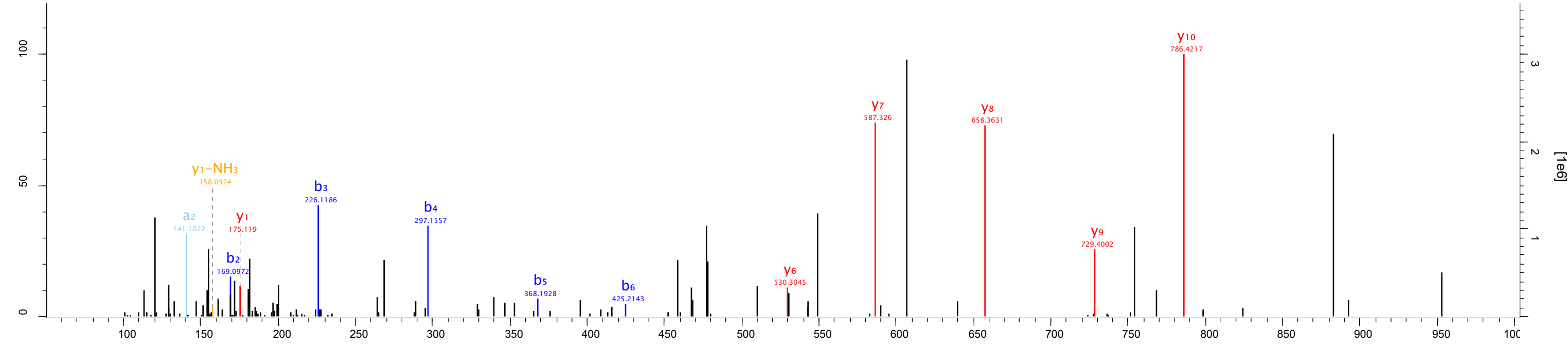
Scan 19552 Method FTMS; HCD Score 80.63 m/z 857.86 Gene names MT-ND3



Raw file

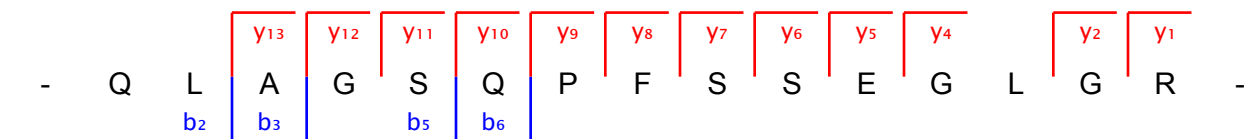
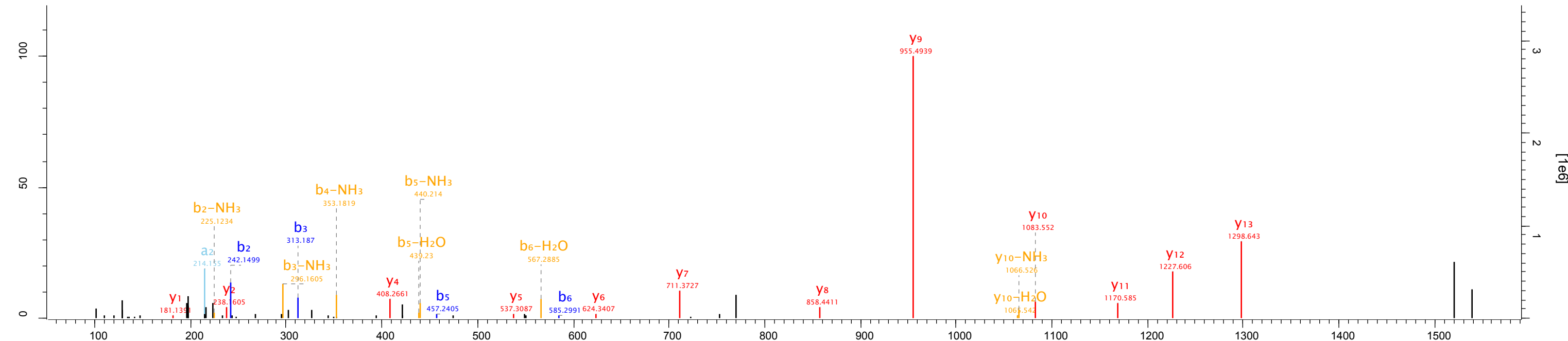
20180707_MaS_A375SR_ML_proteome_2_28

Scan	Method	Score	m/z	Gene names
6412	FTMS; HCD	47.84	477.76	EPM2A

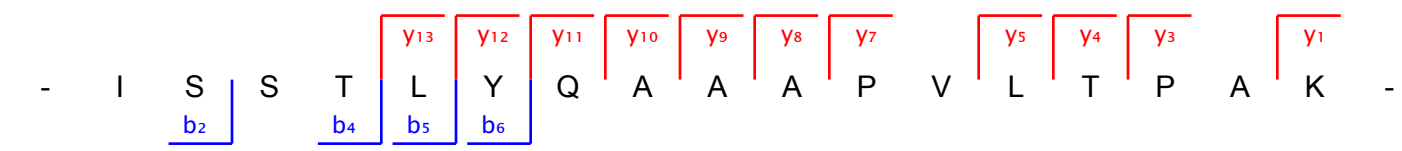
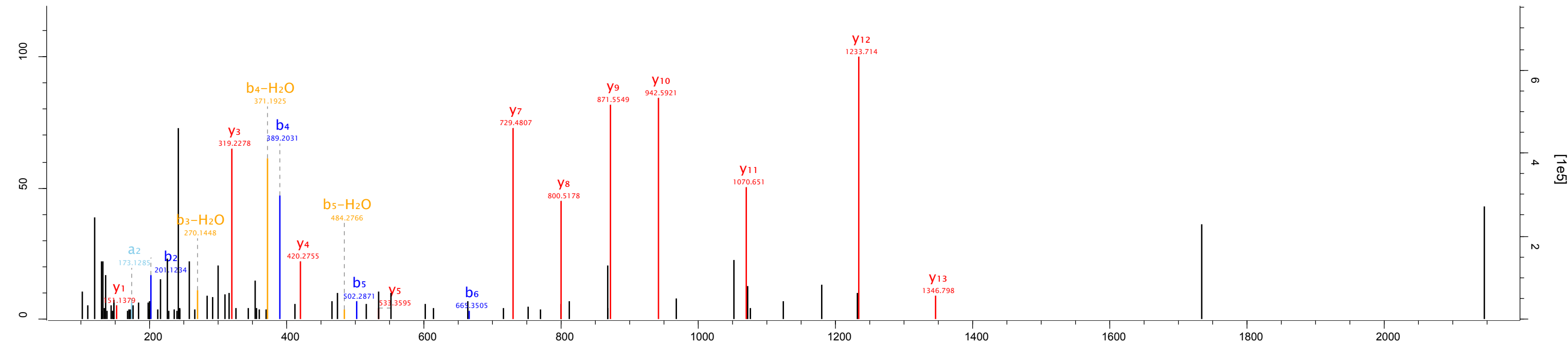


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20180707_MaS_A375SR_ML_proteome_2_29

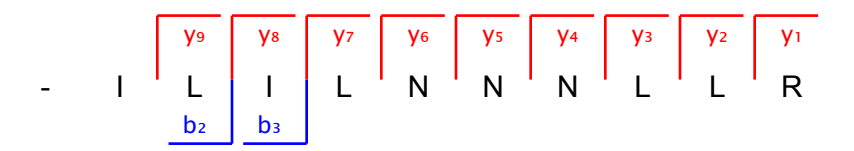
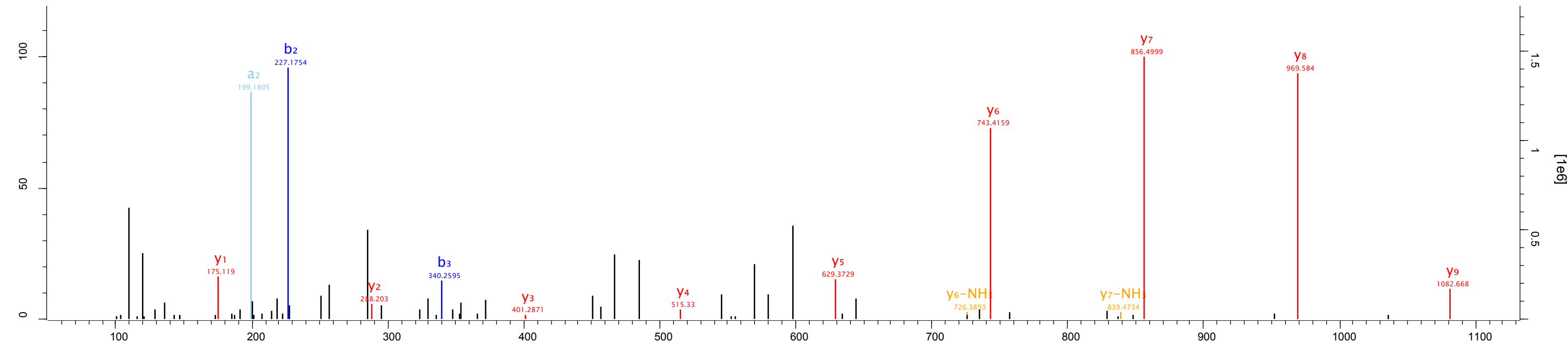
Scan 17092 Method FTMS; HCD Score 97.77 m/z 770.9 Gene names PLXNB3



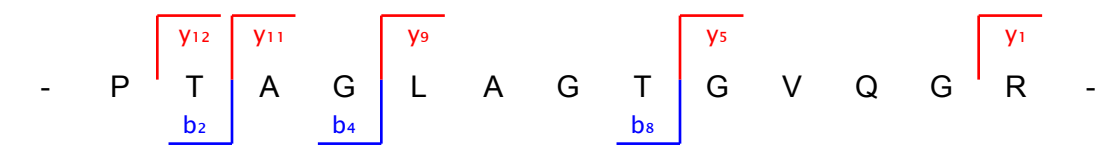
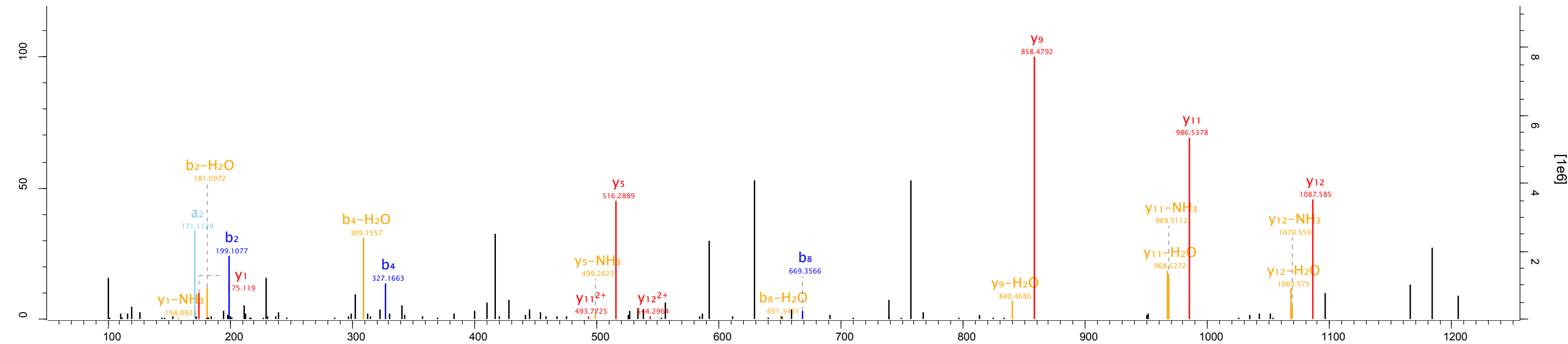
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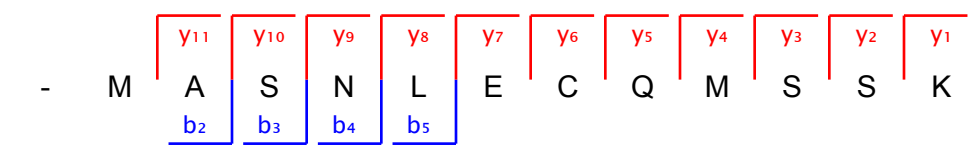
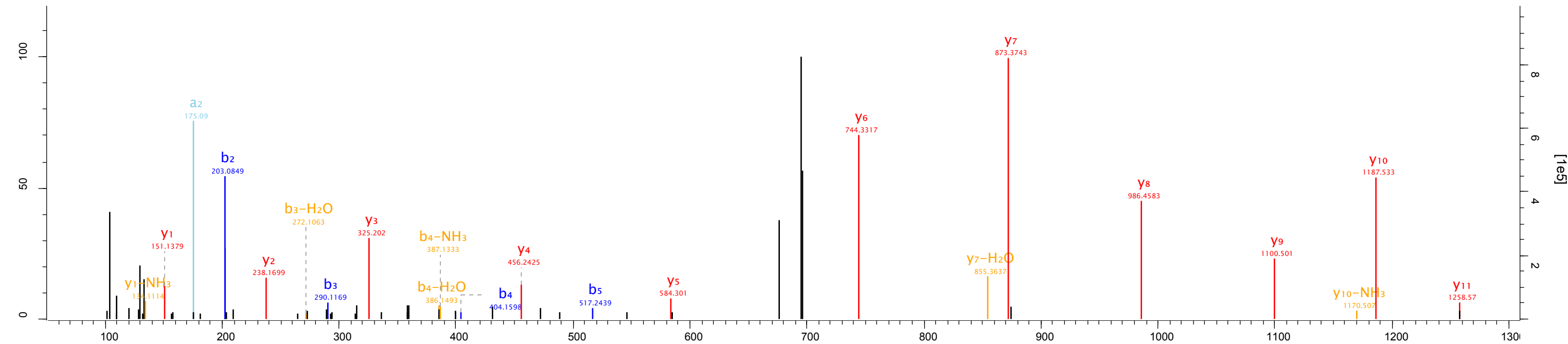
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 Scan 28622 Method FTMS; HCD Score 72.61 m/z 598.38 Gene names SLITRK1



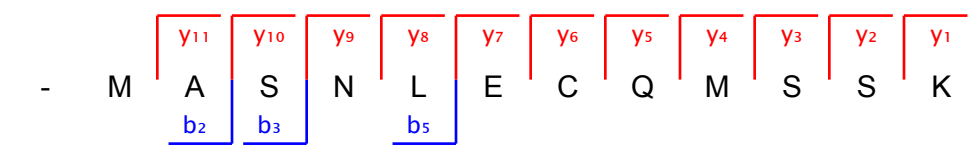
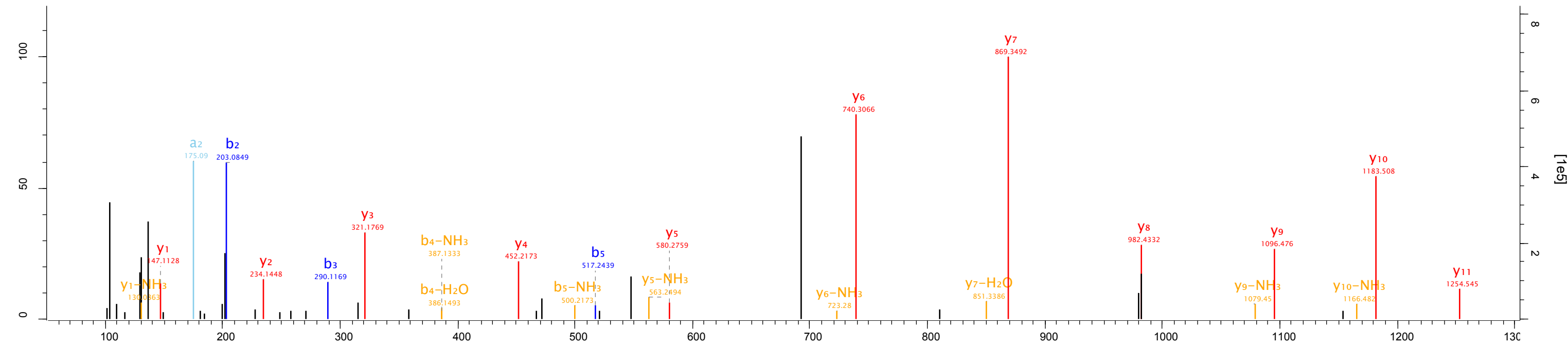
Raw file 20180707_MaS_A375SR_ML_proteome_2_30
 Scan 8362 Method FTMS; HCD Score 99.75 m/z 592.82



Raw file: 20180707_MaS_A375SR_ML_proteome_20
 Scan: 10802 Method: FTMS; HCD Score: 98.94 m/z: 695.81 Gene names: KIAA1549L

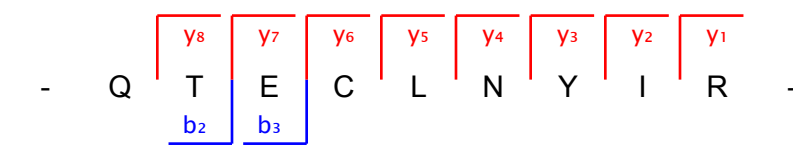
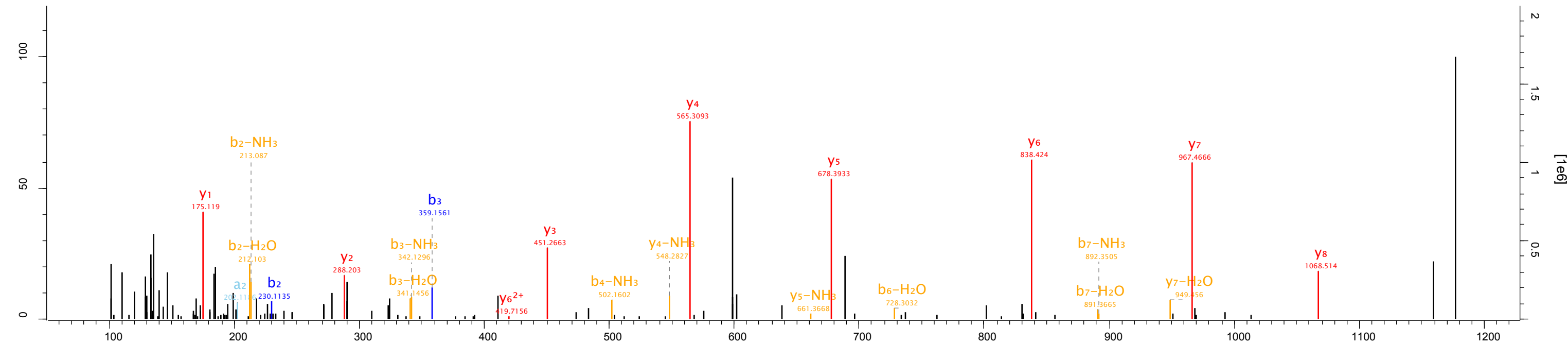


Raw file: 20180707_MaS_A375SR_ML_proteome_20
 Scan: 10822 Method: FTMS; HCD Score: 111.79 m/z: 693.3 Gene names: KIAA1549L

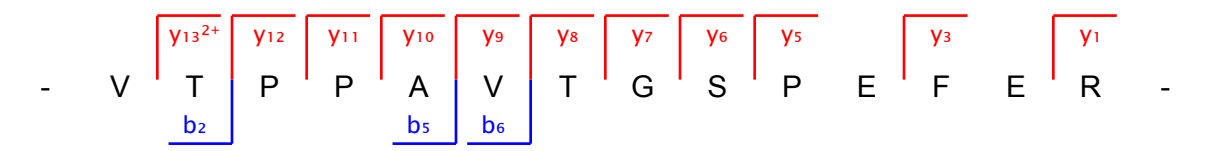
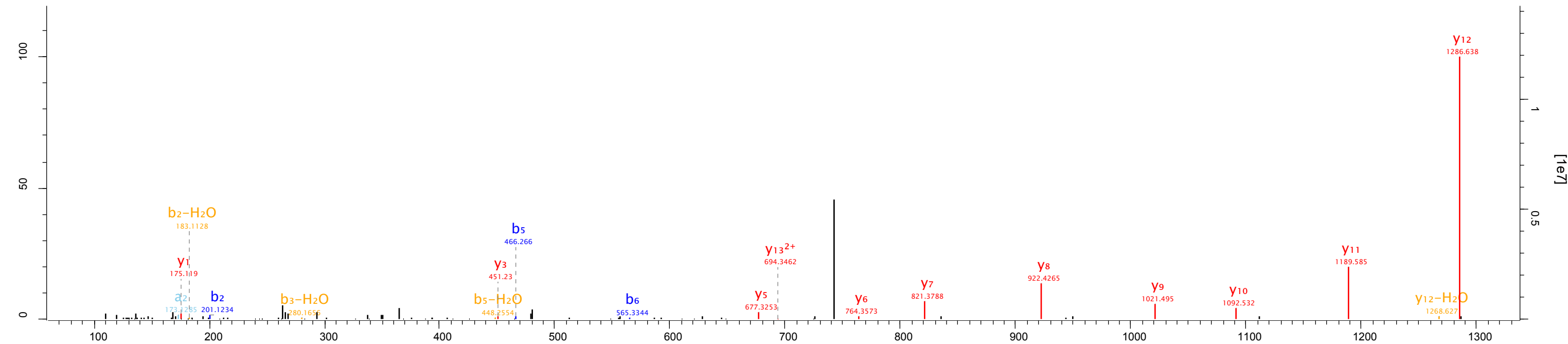


Raw file
20180707_MaS_A375SR_ML_proteome_20

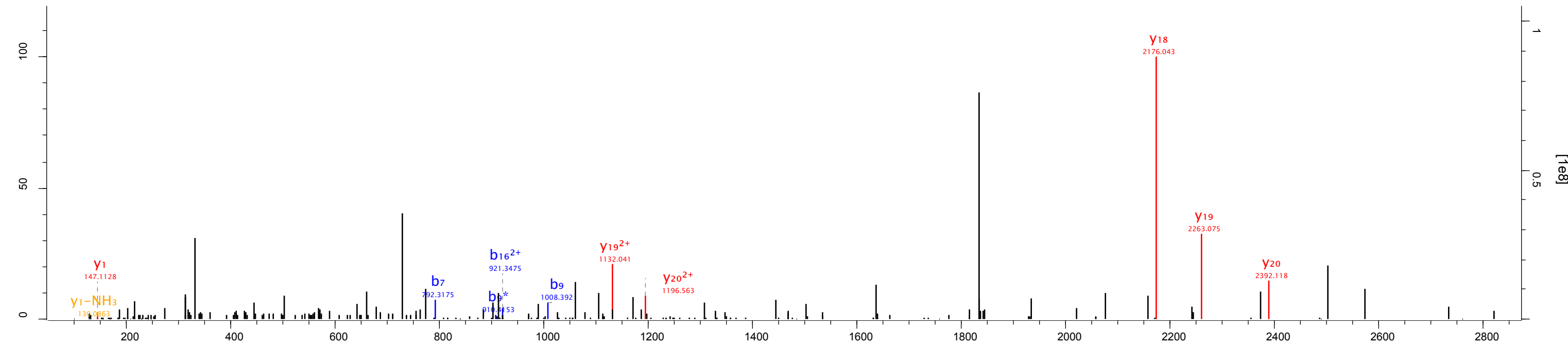
Scan: 14342
Method: FTMS; HCD
Score: 103.55
m/z: 599.29
Gene names: SEMA4D



Raw file 20180707_MaS_A375SR_ML_proteome_20 Scan 16812 Method FTMS; HCD Score 60.66 m/z 743.88 Gene names MGST2



Raw file 20180707_MaS_A375SR_ML_proteome_20
 Scan 19832 Method FTMS; HCD Score 54 m/z 1062.15



- L P P S S T E E S E S S H A L F D H K L Q V L T N K -

Fragmentation mapping (red boxes):

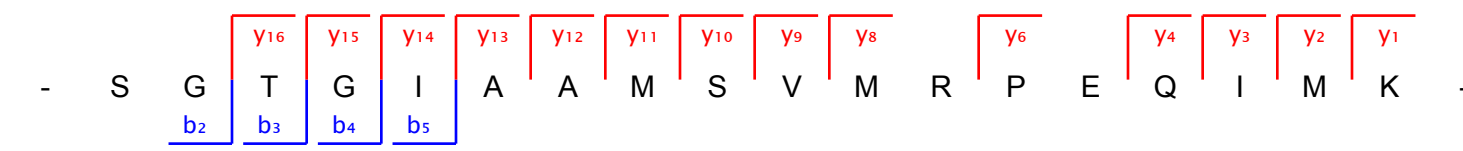
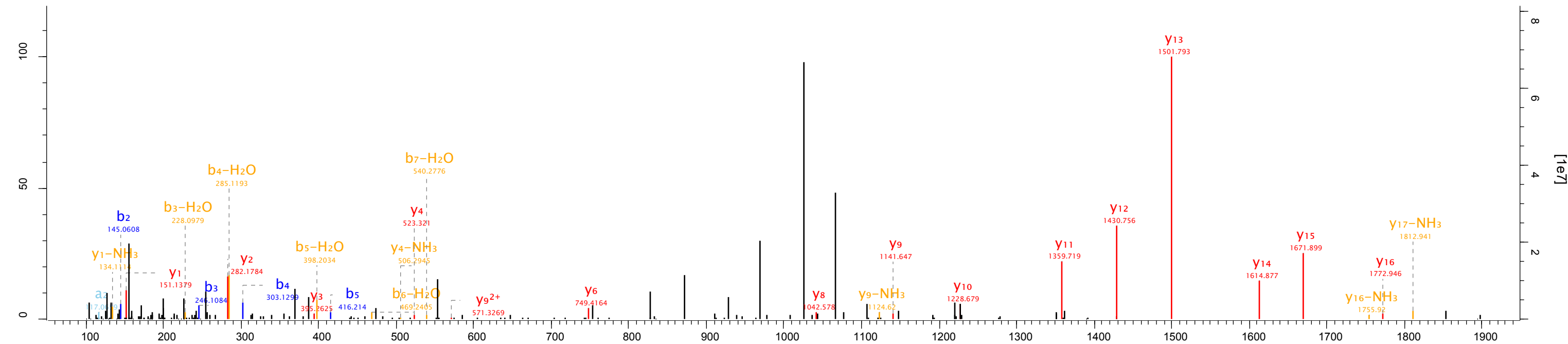
- y20: E (residues 18-19)
- y19: S (residue 20)
- y18: E (residue 21)
- y1: K (residue 26)

Fragmentation mapping (blue boxes):

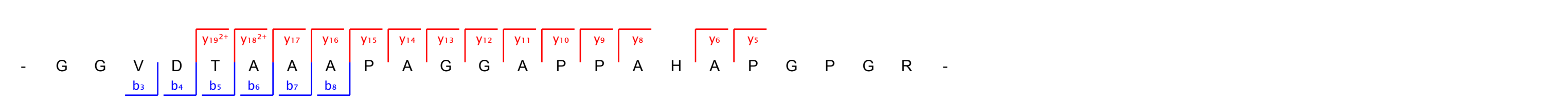
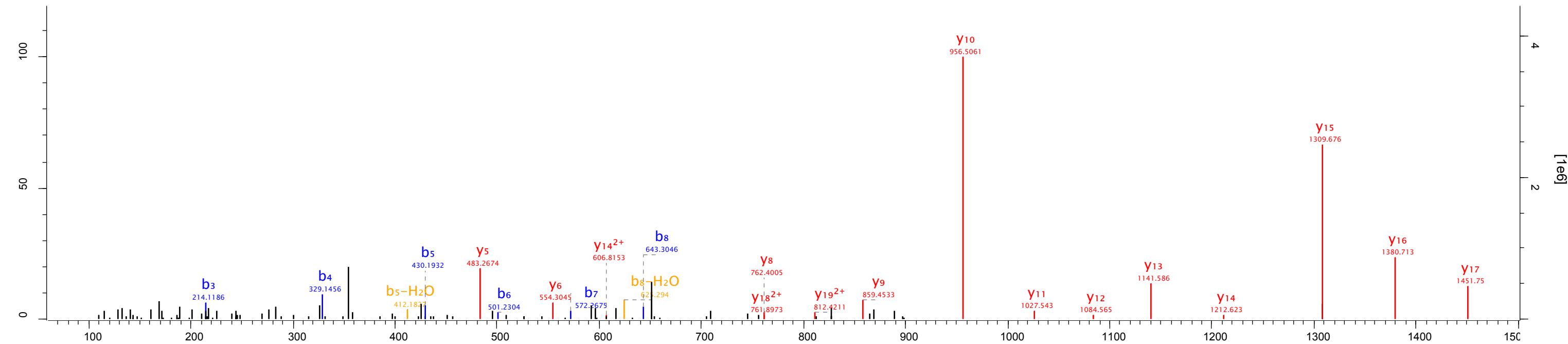
- b7: E (residues 18-19)
- b9: S (residues 20-21)
- b16²⁺: L (residue 23)

Raw file
20180707_MaS_A375SR_ML_proteome_20

Scan Method Score m/z Gene names
23672 FTMS; HCD 81.51 640.34 ATP6V0C



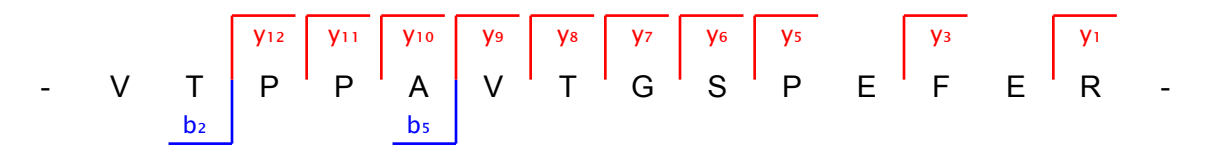
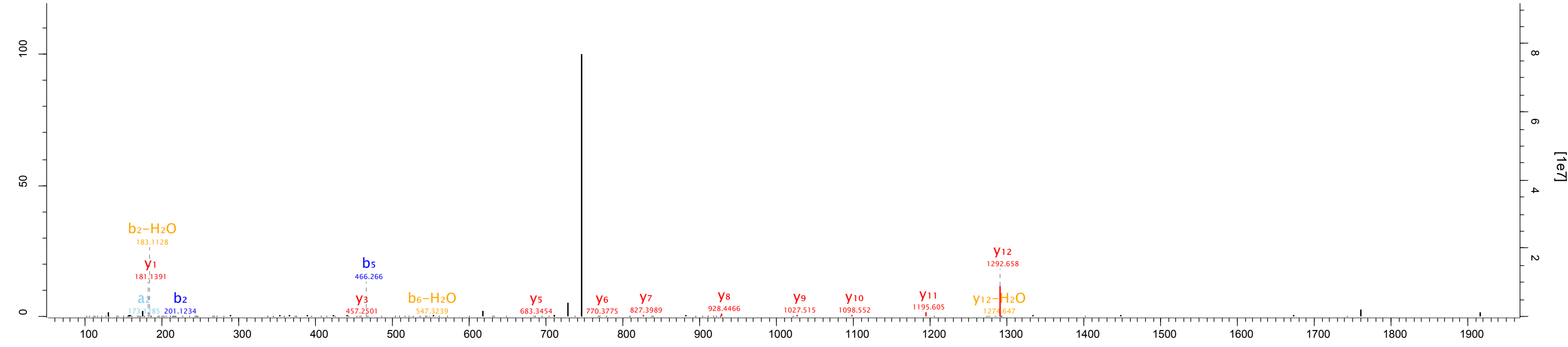
20180707_MaS_A375SR_ML_proteome_20



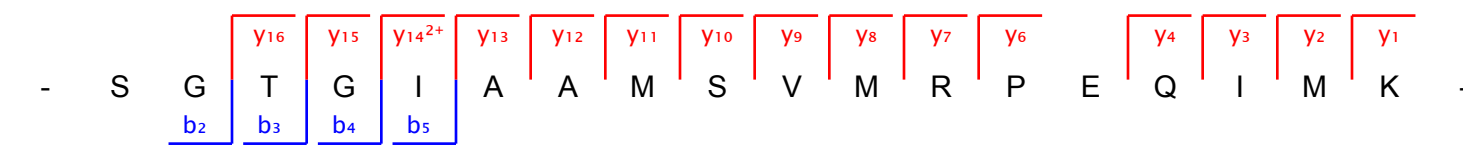
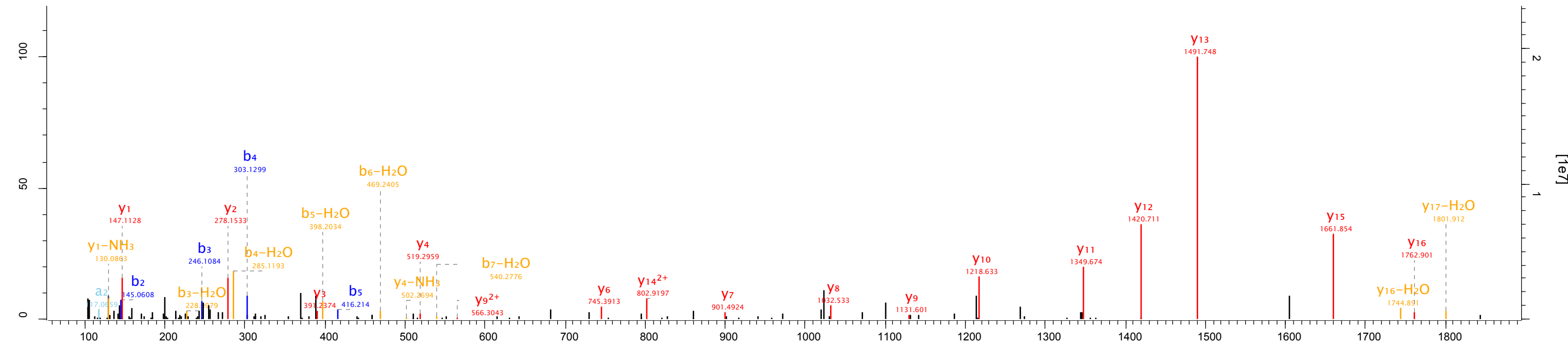
Raw file

20180707_MaS_A375SR_ML_proteome_21

Scan	Method	Score	m/z	Gene names
17212	FTMS; HCD	34.18	746.89	MGST2

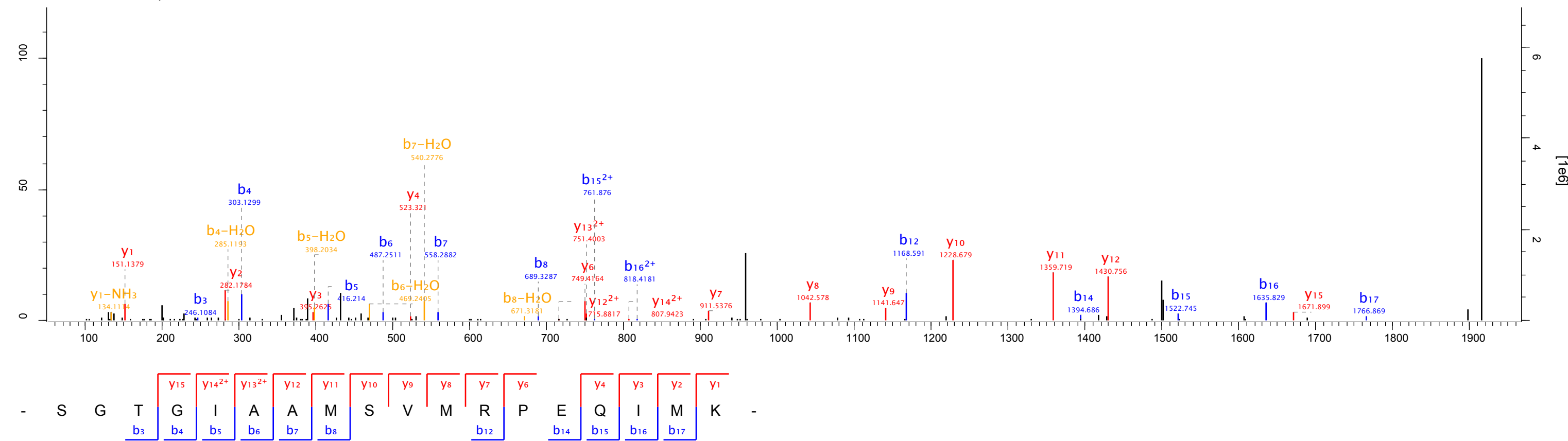


Raw file 20180707_MaS_A375SR_ML_proteome_21 Scan 23922 Method FTMS; HCD Score 98.06 m/z 636.32 Gene names ATP6V0C

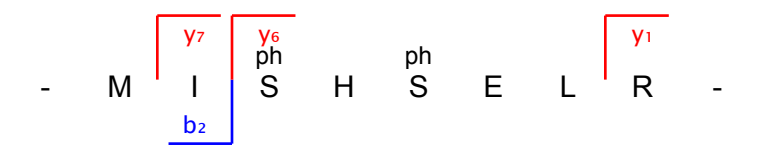
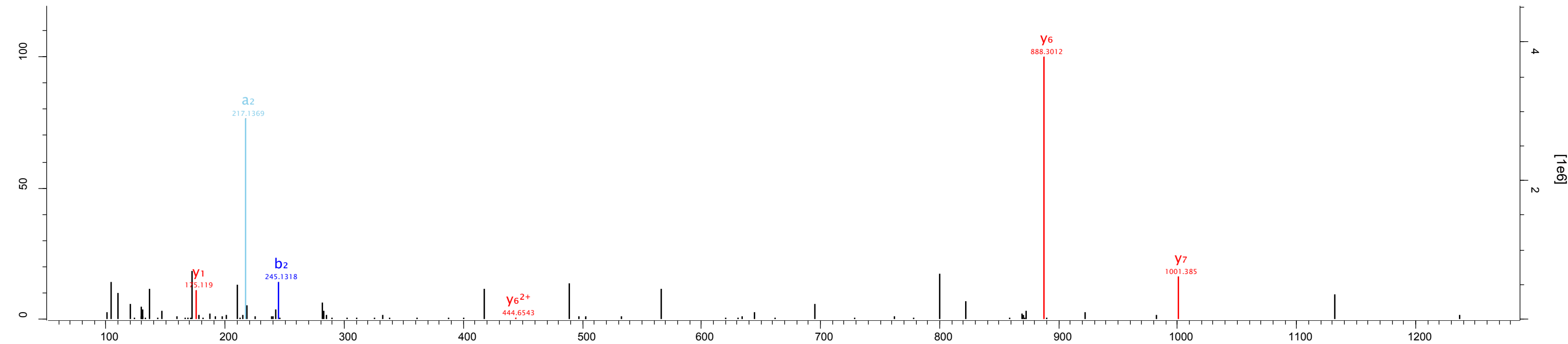


Raw file
20180707_MaS_A375SR_ML_proteome_21

Scan: 23952
Method: FTMS; HCD
Score: 164.53
m/z: 959
Gene names: ATP6V0C



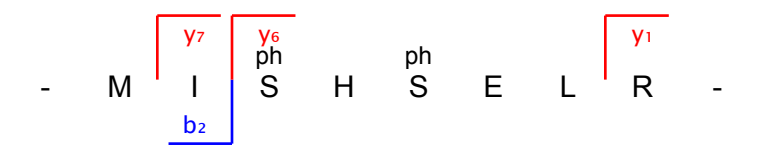
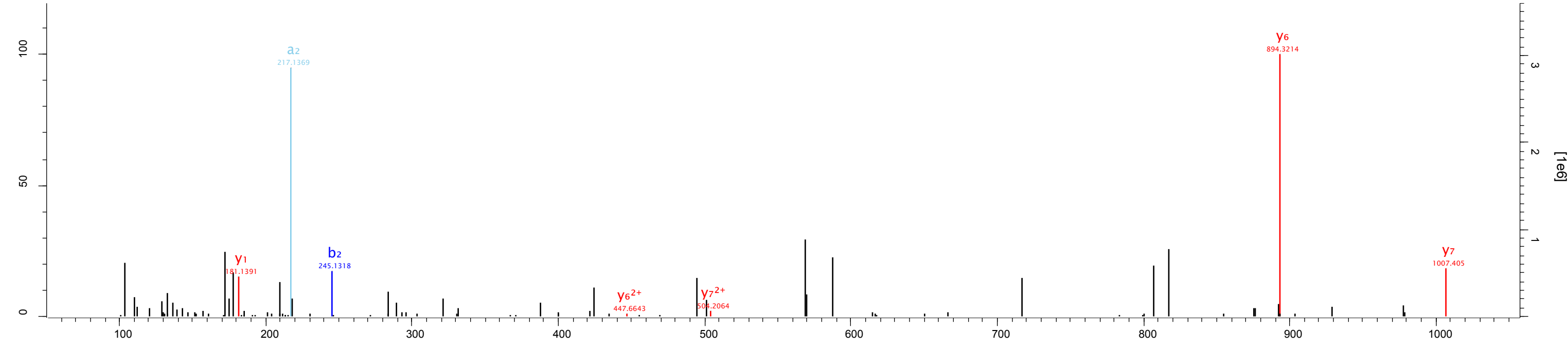
Raw file 20180707_MaS_A375SR_ML_proteome_21 Scan 9522 Method FTMS; HCD Score 54.2 m/z 566.72 Gene names PSPHP1



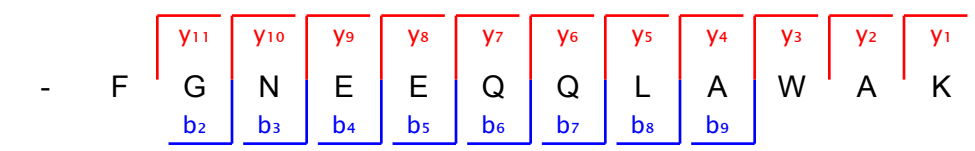
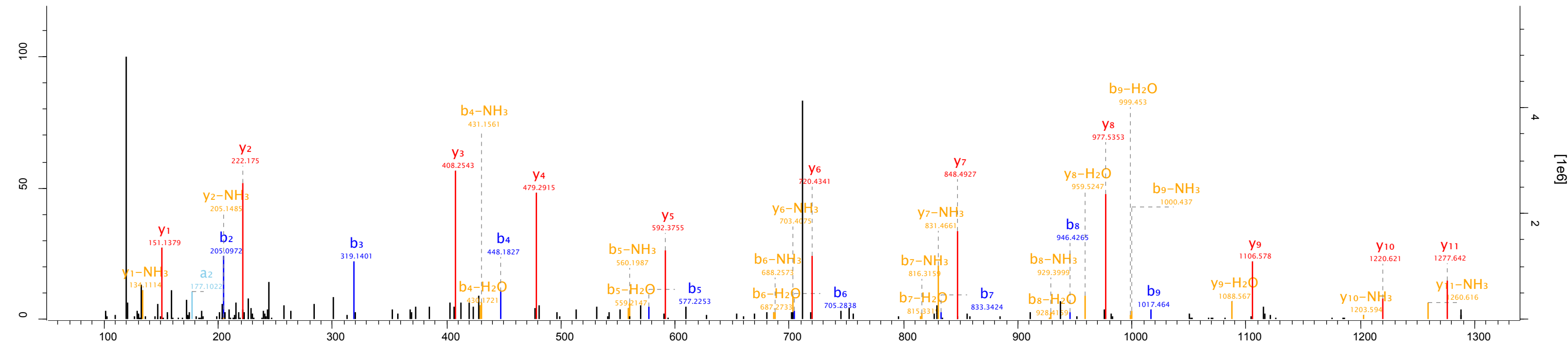
Raw file

20180707_MaS_A375SR_ML_proteome_21

Scan: 9542
Method: FTMS; HCD
Score: 60.76
m/z: 569.73
Gene names: PSPHP1

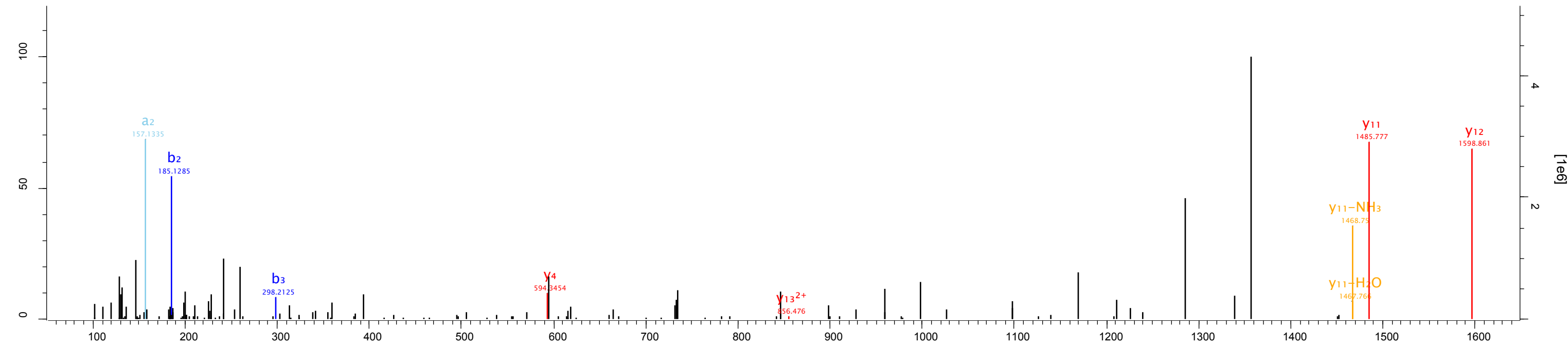


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 Scan: 17312 Method: FTMS; HCD Score: 225.79 m/z: 712.86 Gene names: SPATA22

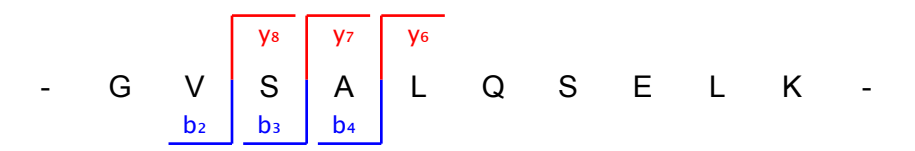
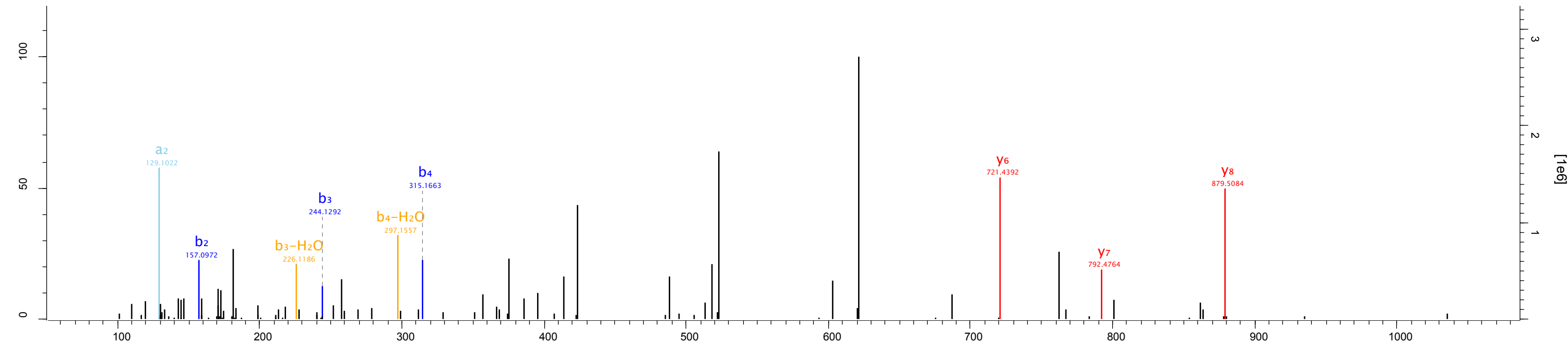


Raw file
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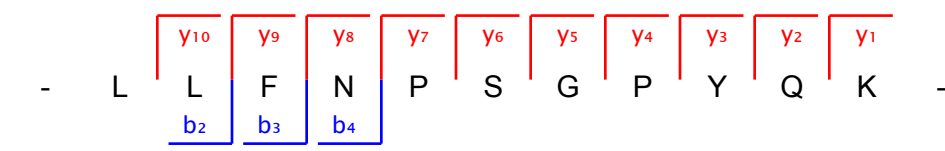
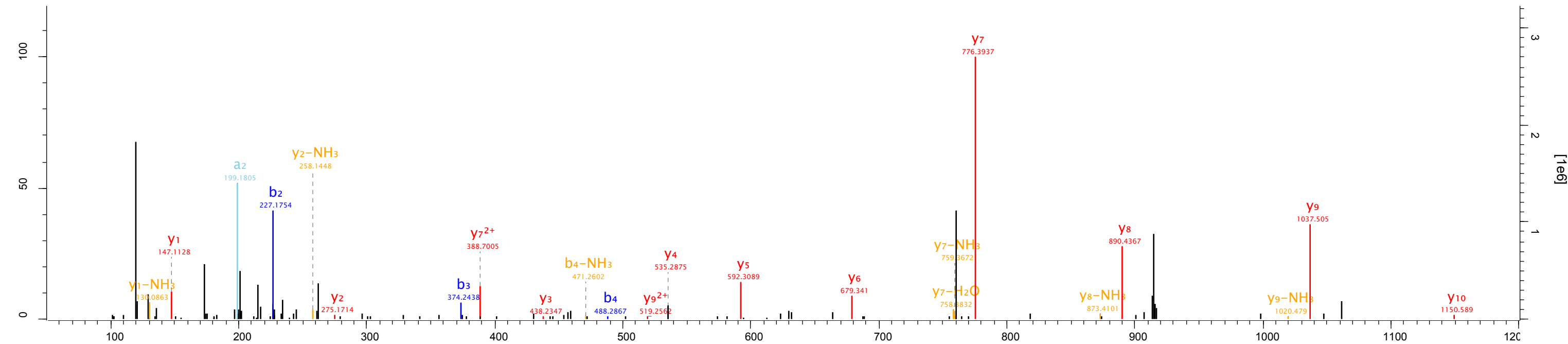
Scan 21652 Method FTMS; HCD Score 40.48 m/z 595



Raw file 20180707_MaS_A375SR_ML_proteome_23 Scan 11042 Method FTMS; HCD Score 52.58 m/z 518.3

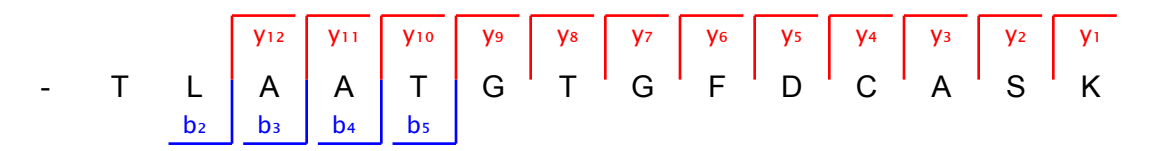
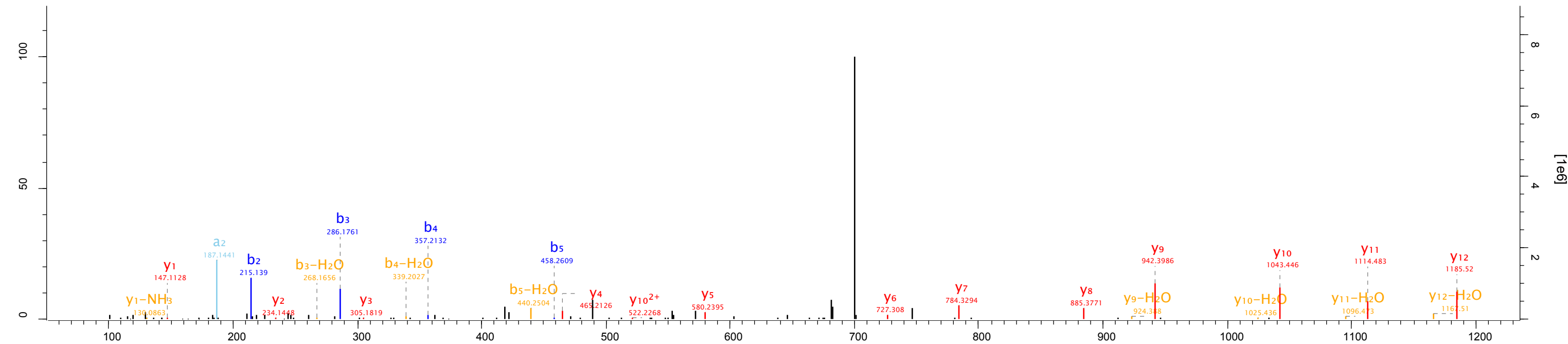


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 20180707_MaS_A375SR_ML_proteome_23
 Scan: 19662 Method: FTMS; HCD Score: 100.82 m/z: 632.34 Gene names: CKLF

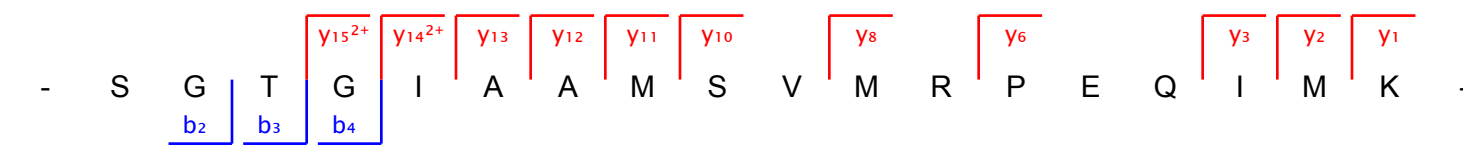
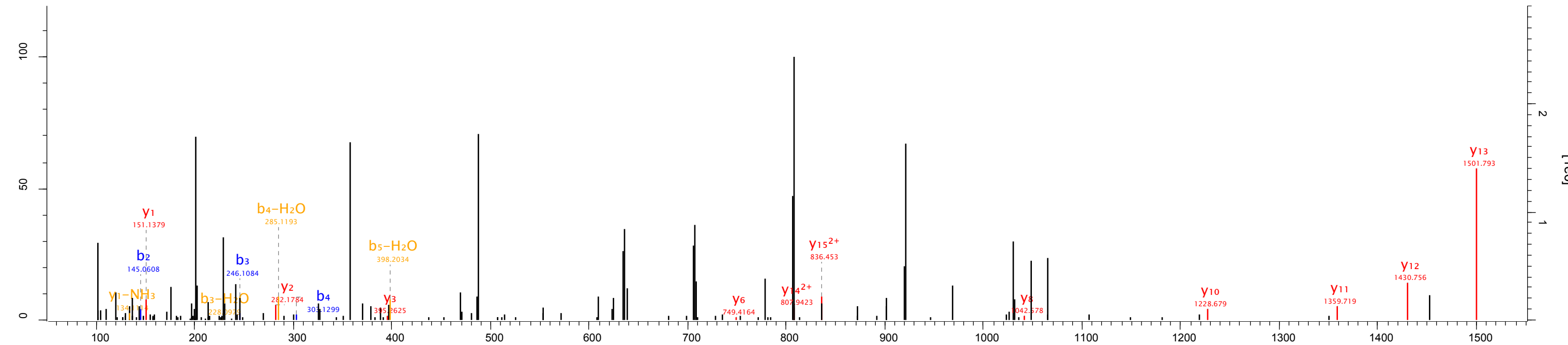


Raw file
20180707_MaS_A375SR_ML_proteome_24

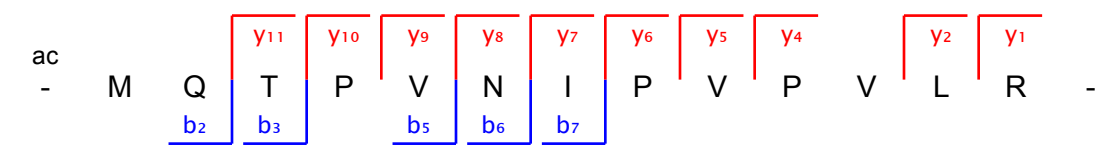
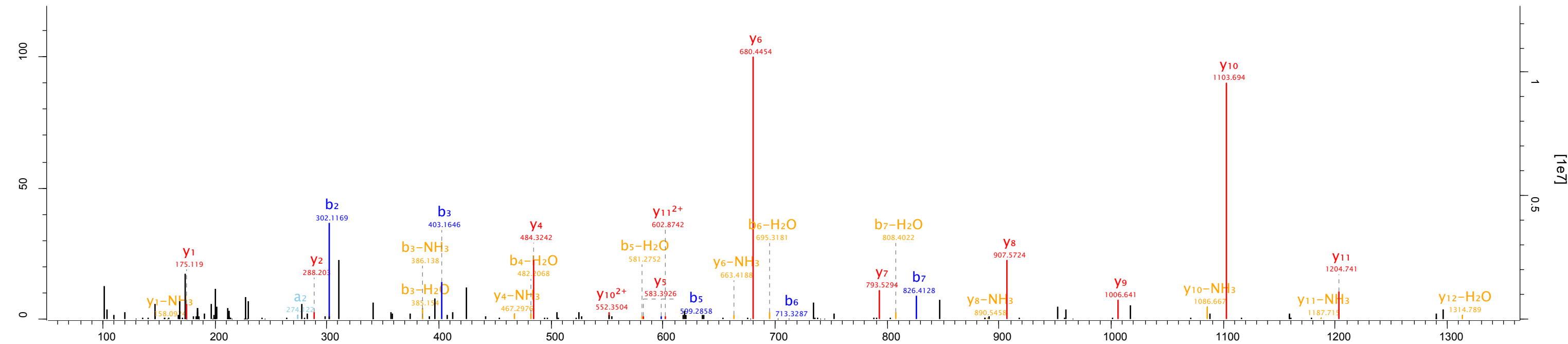
Scan: 12412
Method: FTMS; HCD
Score: 88.56
m/z: 700.33
Gene names: ODC1



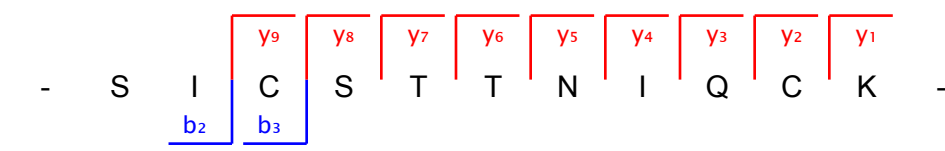
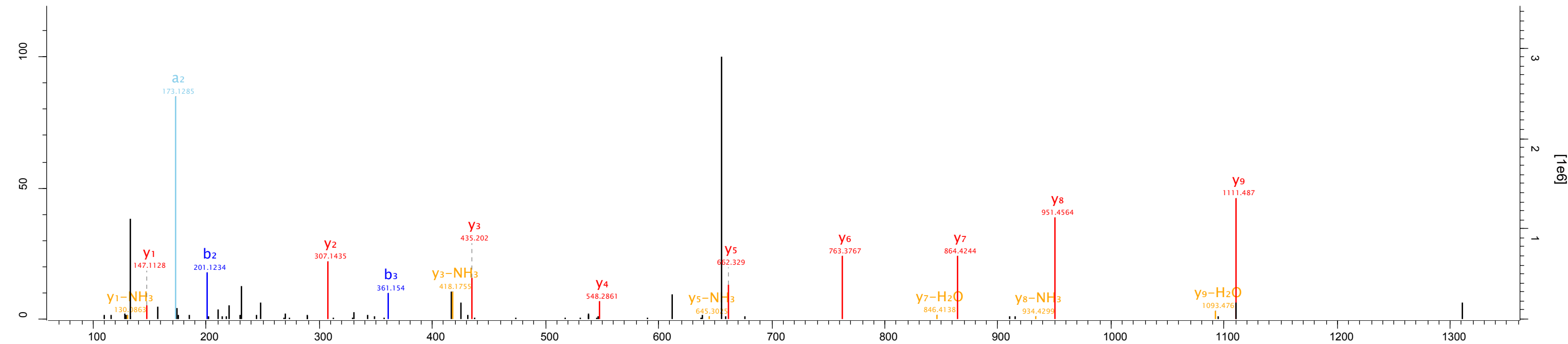
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 Scan: 22752 Method: FTMS; HCD Score: 17.56 m/z: 639.67 Gene names: ATP6V0C



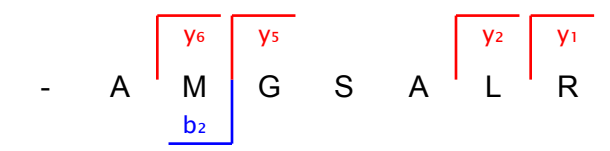
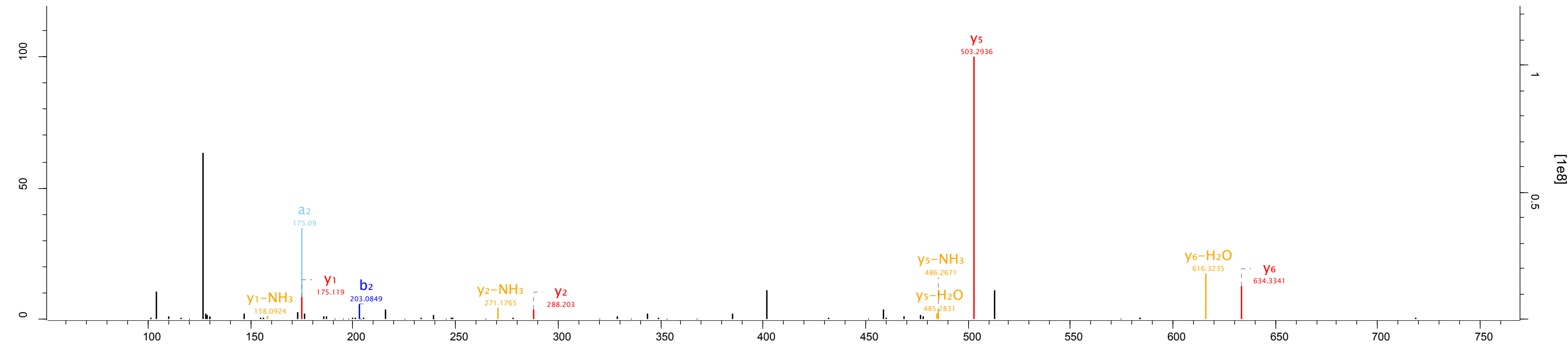
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 Scan: 29272 Method: FTMS; HCD Score: 118.37 m/z: 753.43 Gene names: GEMIN7



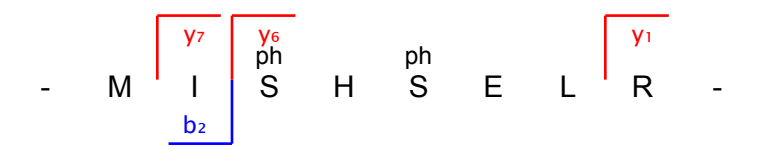
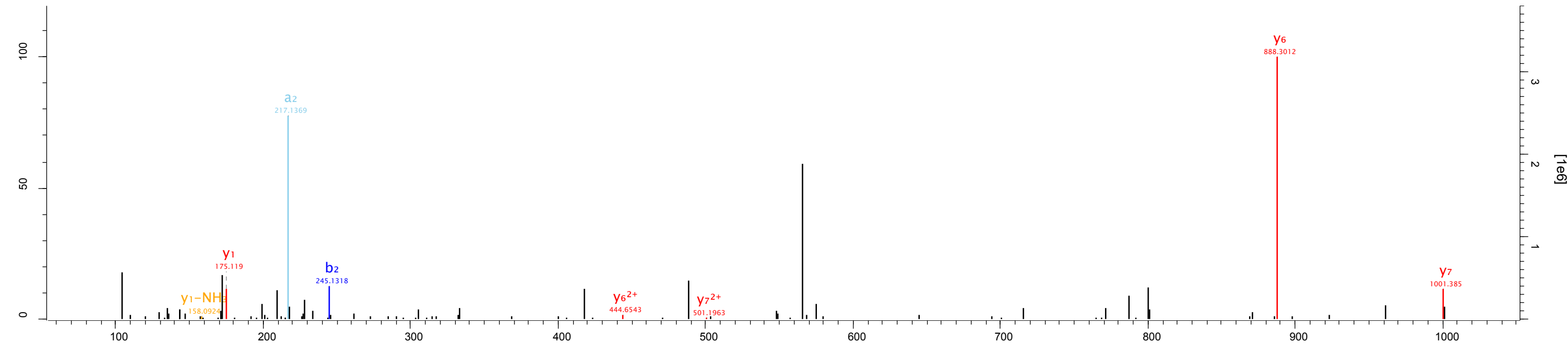
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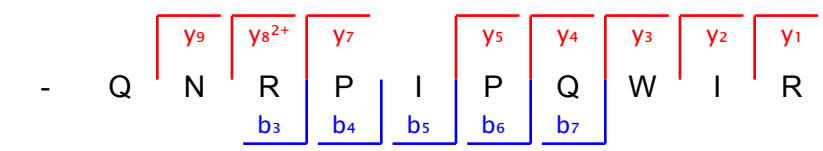
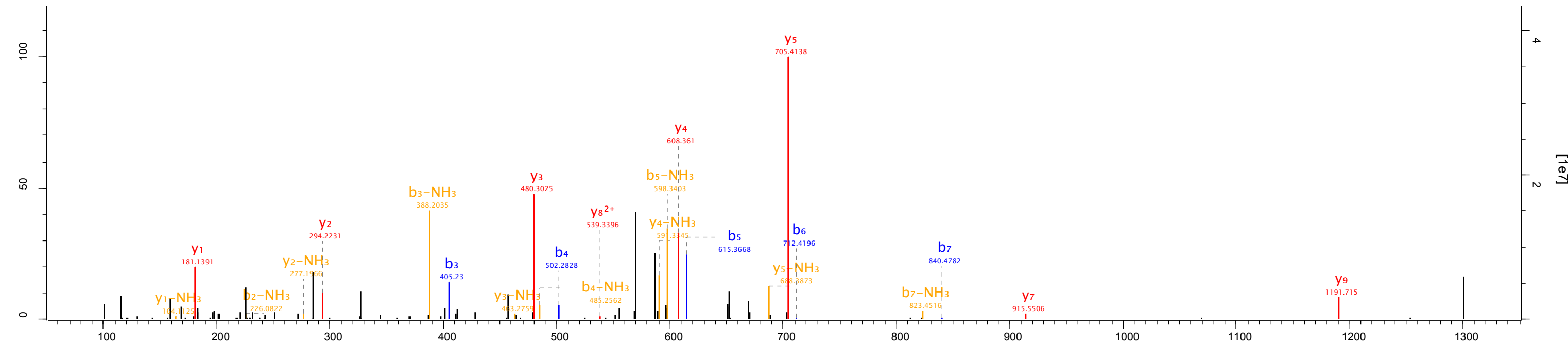
Raw file: 20180707_MaS_A375SR_ML_proteome_25
 Scan: 6052 Method: FTMS; HCD Score: 79.45 m/z: 353.19



Raw file: 20180707_MaS_A375SR_ML_proteome_25
 Scan: 9122 Method: FTMS; HCD Score: 50.13 m/z: 566.72 Gene names: PSPHP1

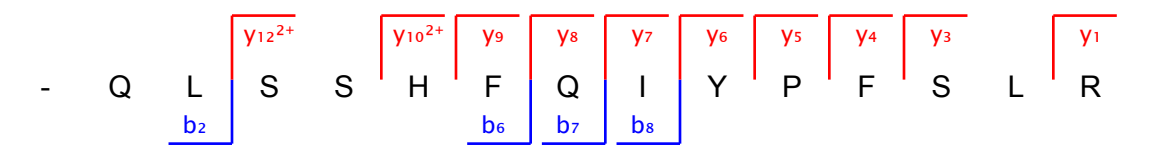
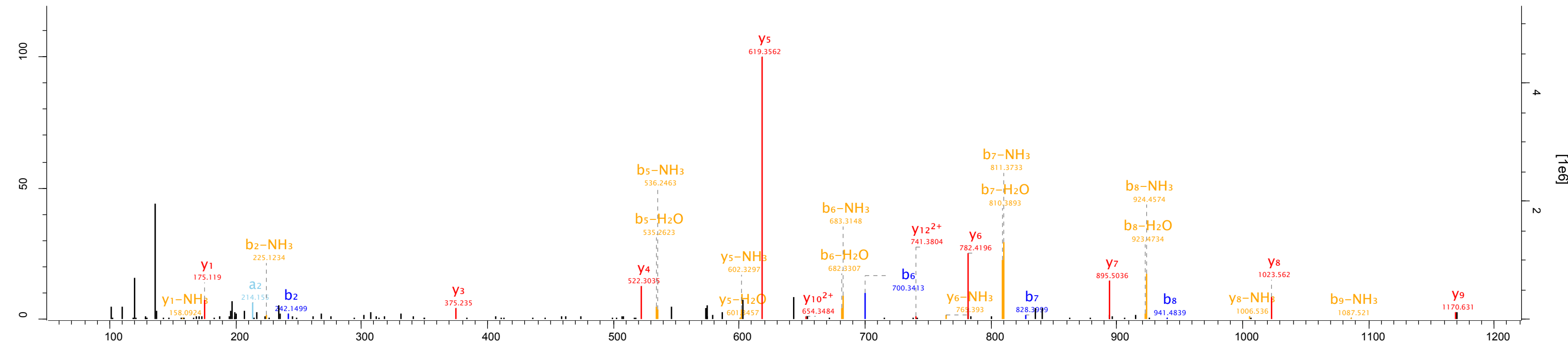


Raw file: 20180707_MaS_A375SR_ML_proteome_26
 Scan: 15932 Method: FTMS; HCD Score: 131.11 m/z: 440.6 Gene names: RPL39P5;RPL39

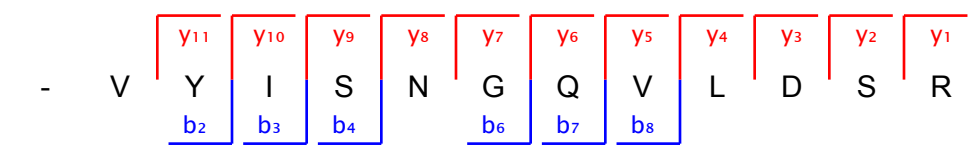
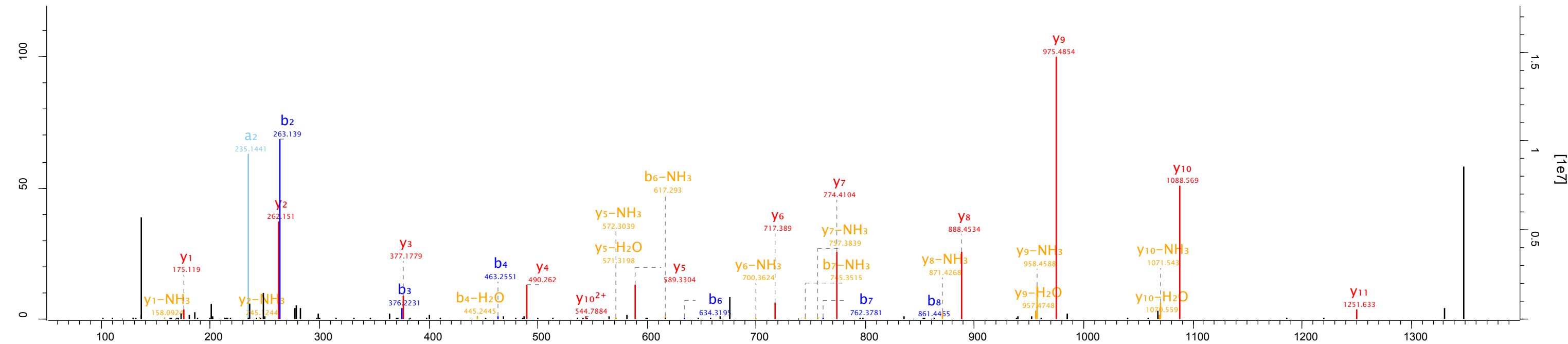


Raw file
20180707_MaS_A375SR_ML_proteome_26

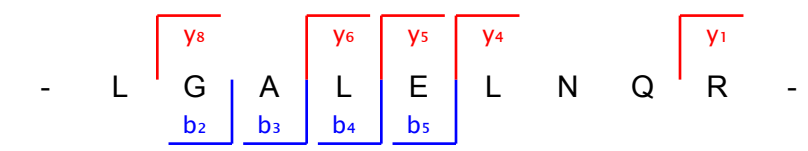
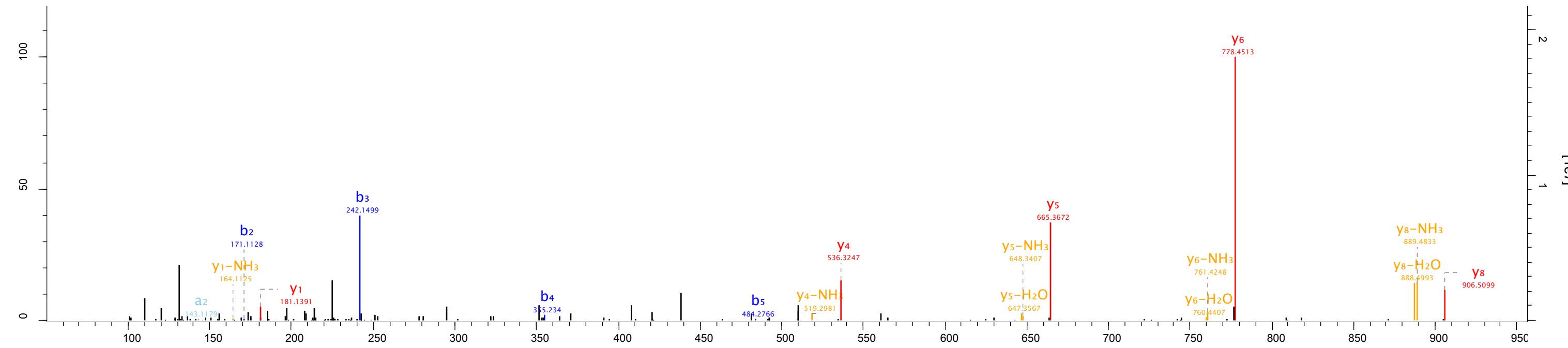
Scan 27162 Method FTMS; HCD Score 97.27 m/z 574.97 Gene names EPT1



Raw file: 20180707_MaS_A375SR_ML_proteome_27
 Scan: 14462 Method: FTMS; HCD Score: 161.48 m/z: 675.85 Gene names: SELK

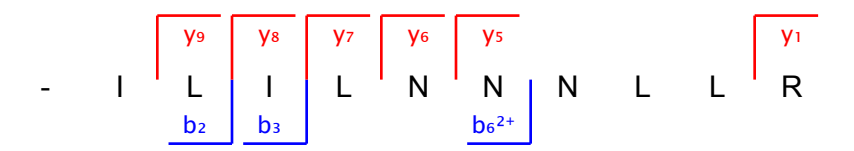
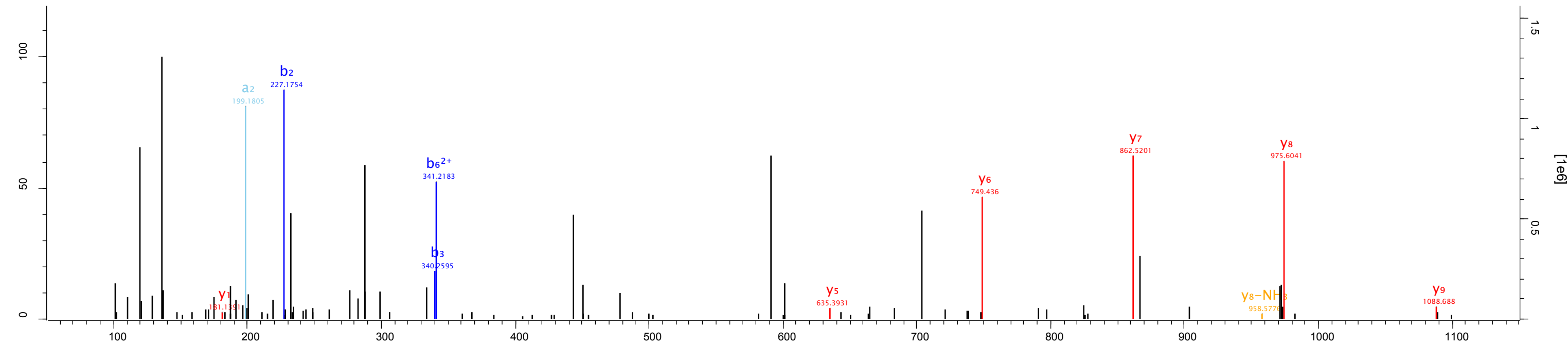


Raw file: 20180707_MaS_A375SR_ML_proteome_29
 Scan: 13602 Method: FTMS; HCD Score: 91.07 m/z: 510.3 Gene names: TBC1D30

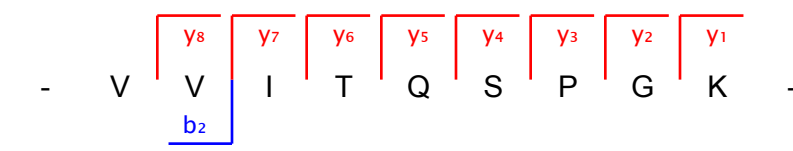
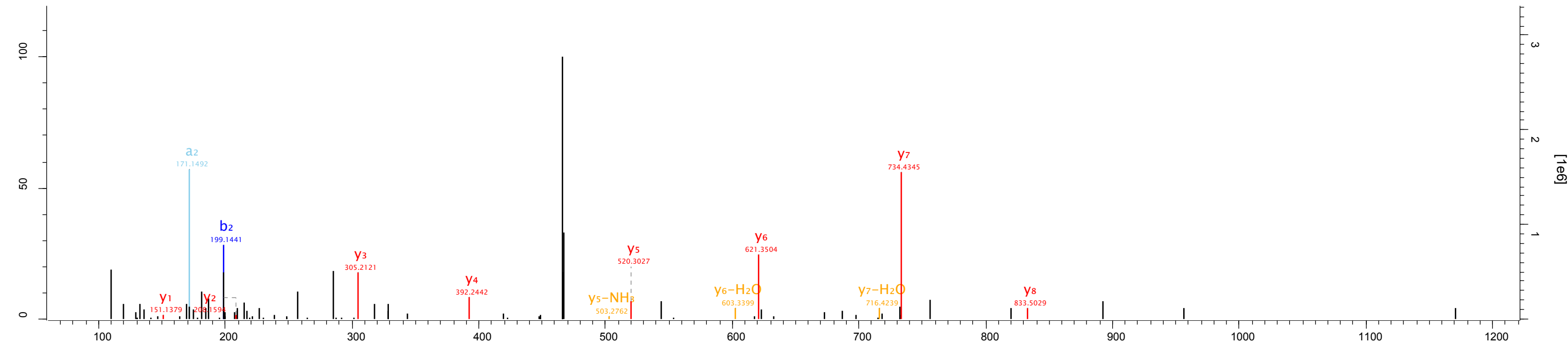


Raw file
20180707_MaS_A375SR_ML_proteome_29

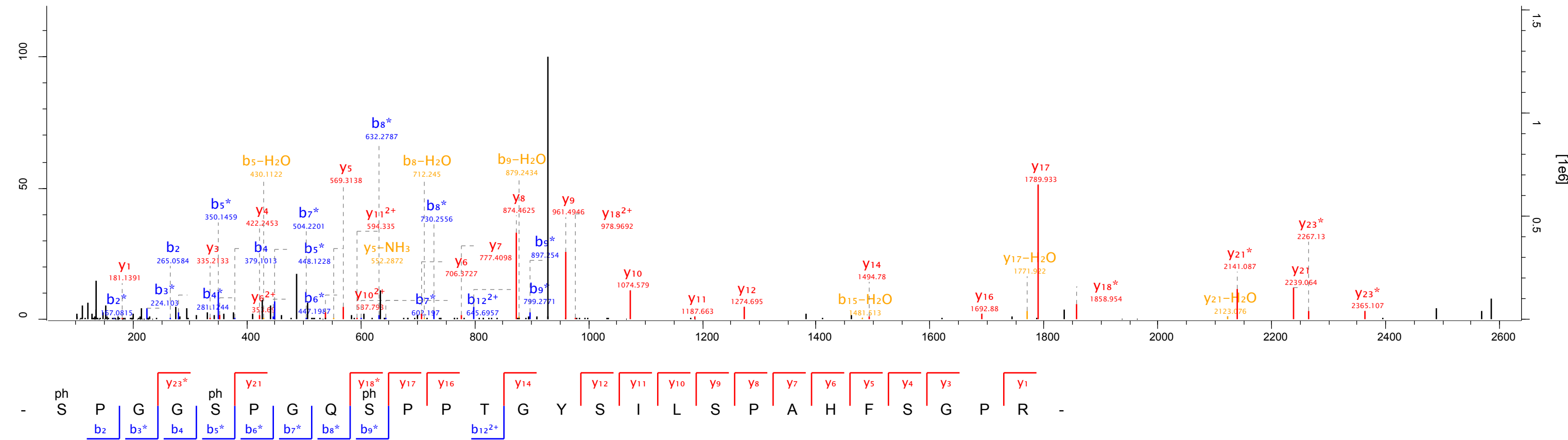
Scan 27542 Method FTMS; HCD Score 56.43 m/z 601.39 Gene names SLITRK1



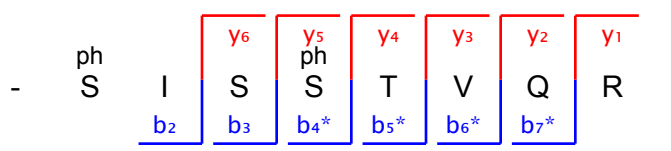
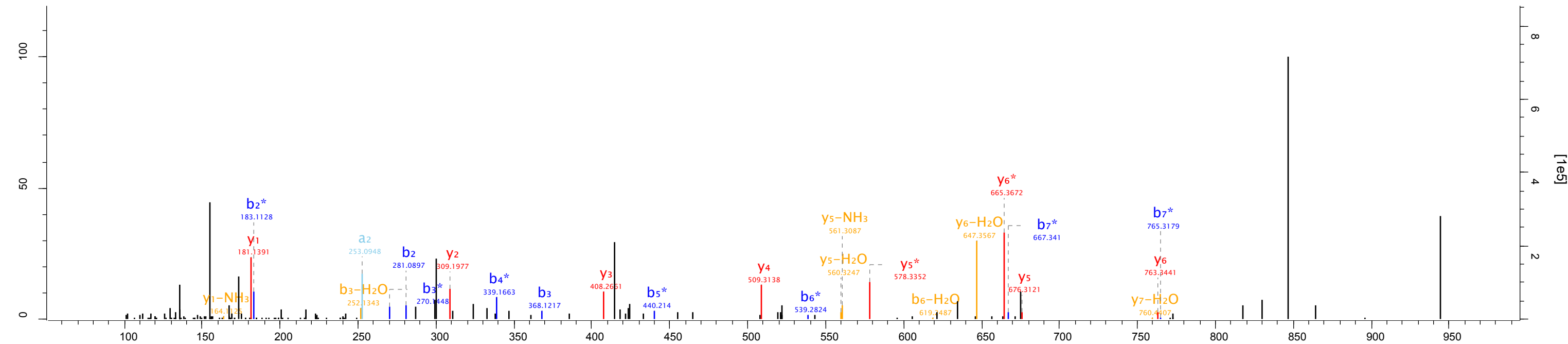
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 Scan: 6882 Method: FTMS; HCD Score: 52.49 m/z: 466.79 Gene names: FAM11A;TMEM185A;TMEM185B



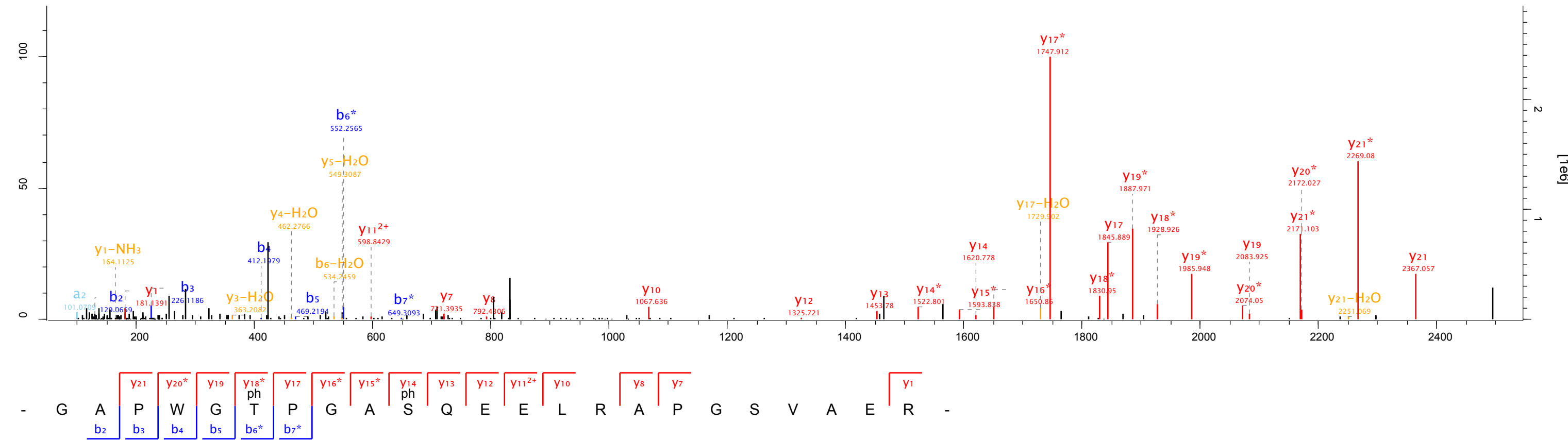
Raw file Scan Method Score m/z Gene names
 20150812_A375SR_Phospho_BR1_02 25863 FTMS; HCD 65.5 929.06 HECA



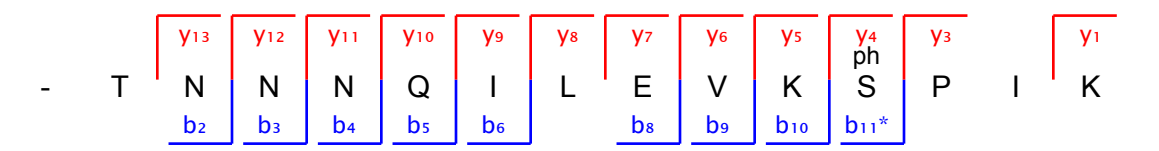
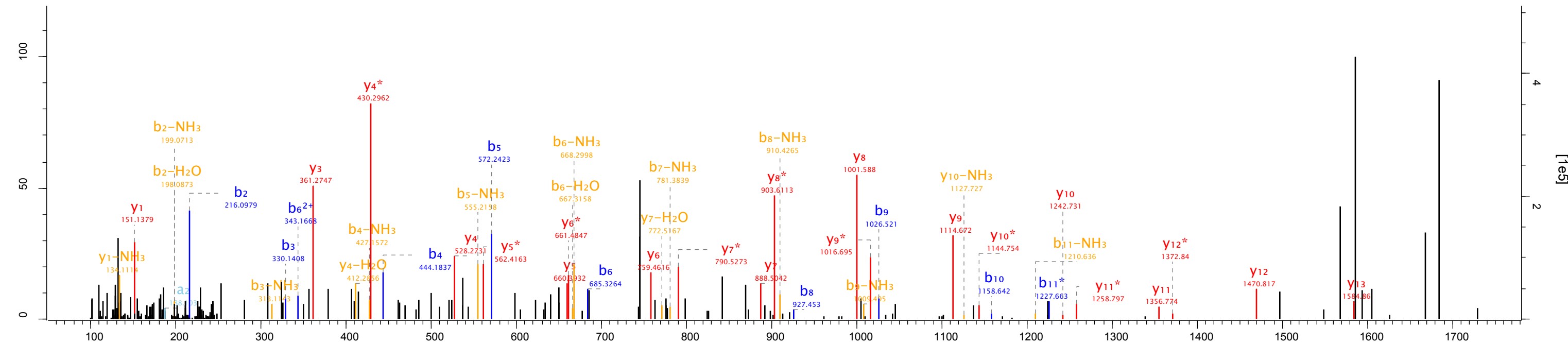
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 Scan: 8433 Method: FTMS; HCD Score: 109.39 m/z: 522.22 Gene names: RHBDF2



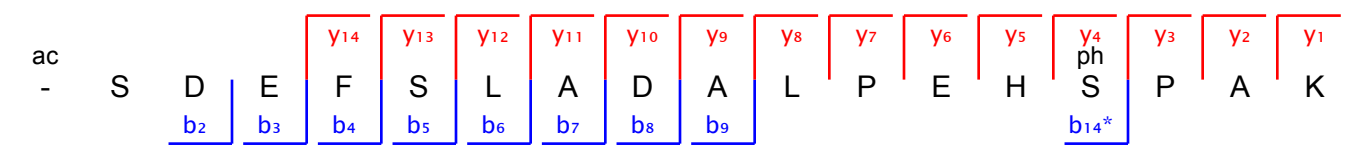
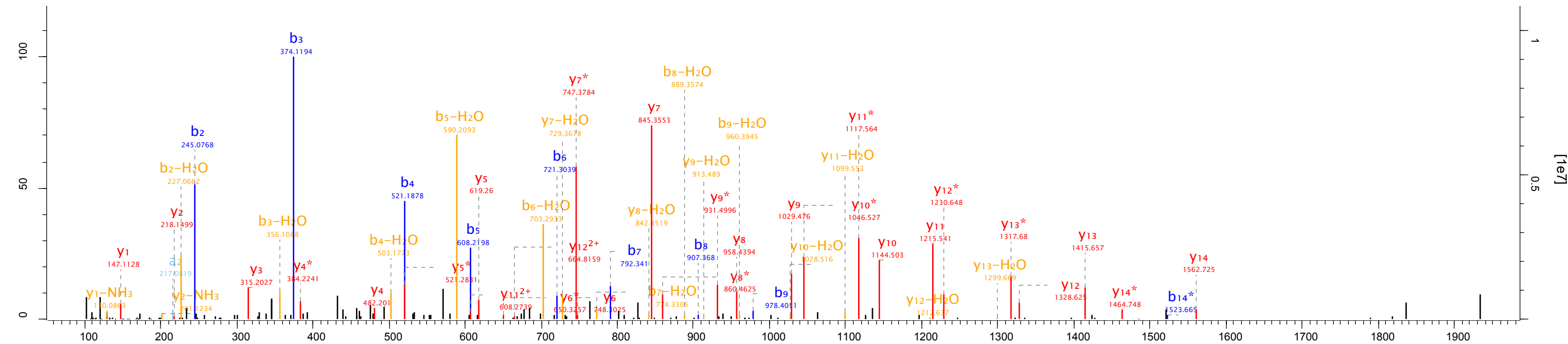
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 Scan: 19853 Method: FTMS; HCD Score: 82.41 m/z: 832.71 Gene names: SPEG



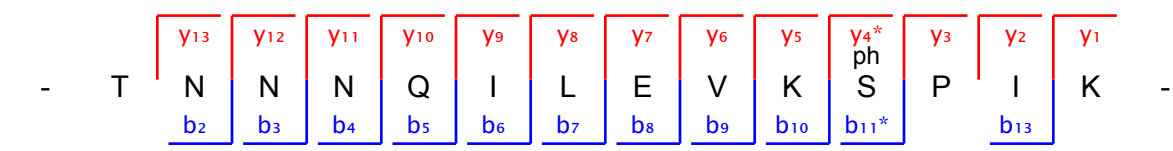
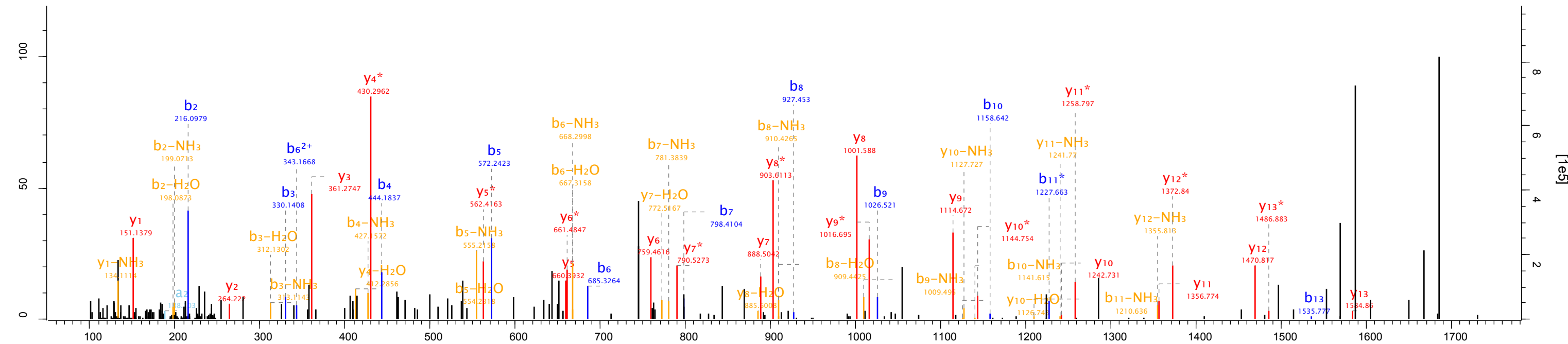
Raw file 20150812_A375SR_Phospho_BR1_04 Scan 13613 Method FTMS; HCD Score 190.67 m/z 843.46 Gene names MLLT3



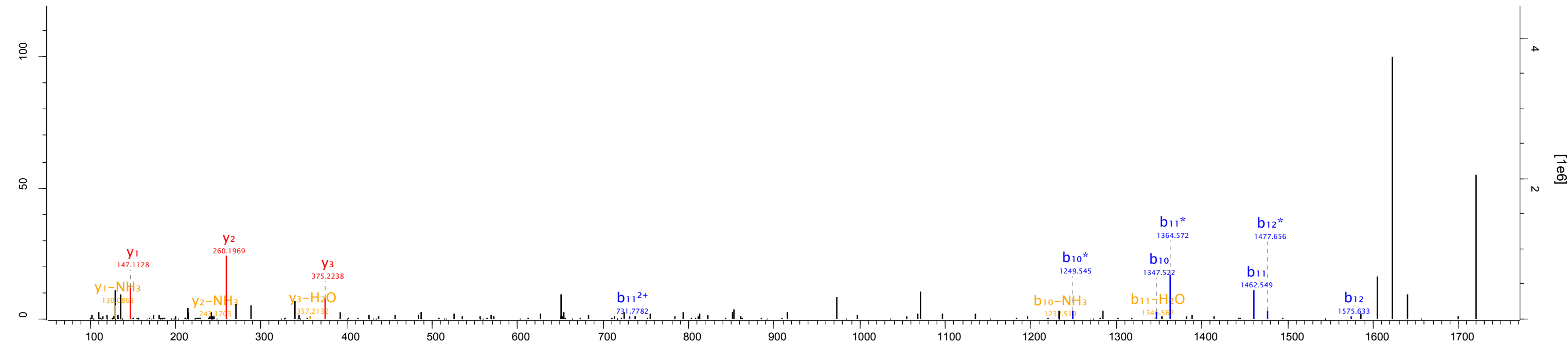
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 Scan: 24353 Method: FTMS; HCD Score: 283.64 m/z: 968.93 Gene names: MAPK11P1L



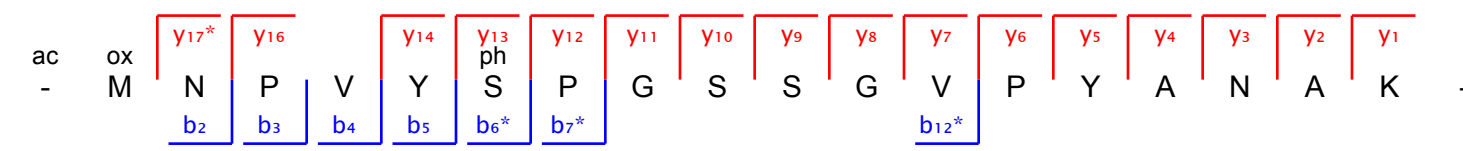
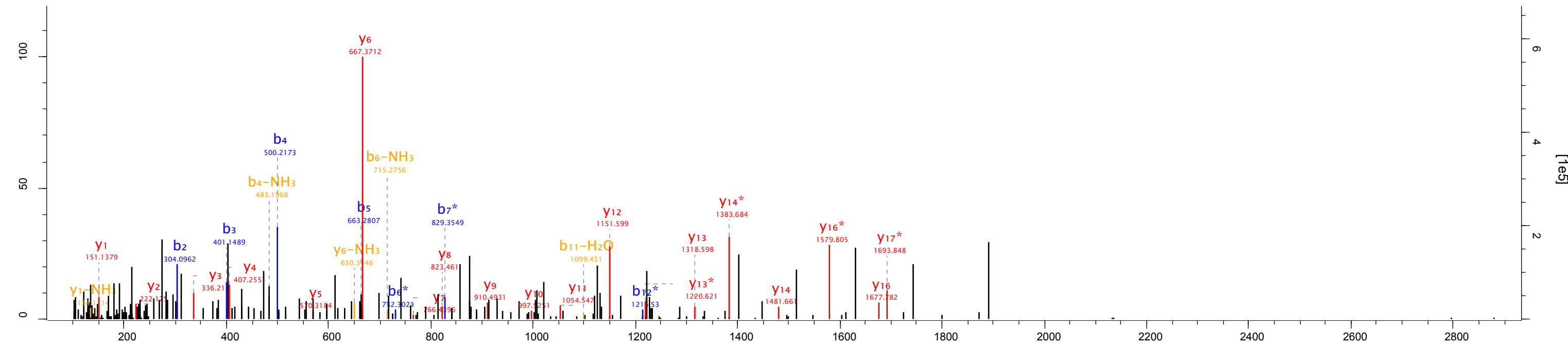
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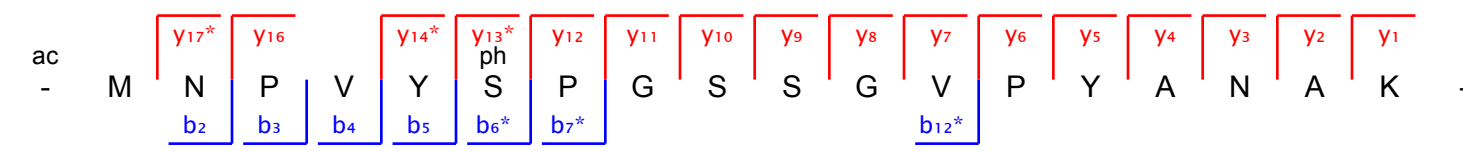
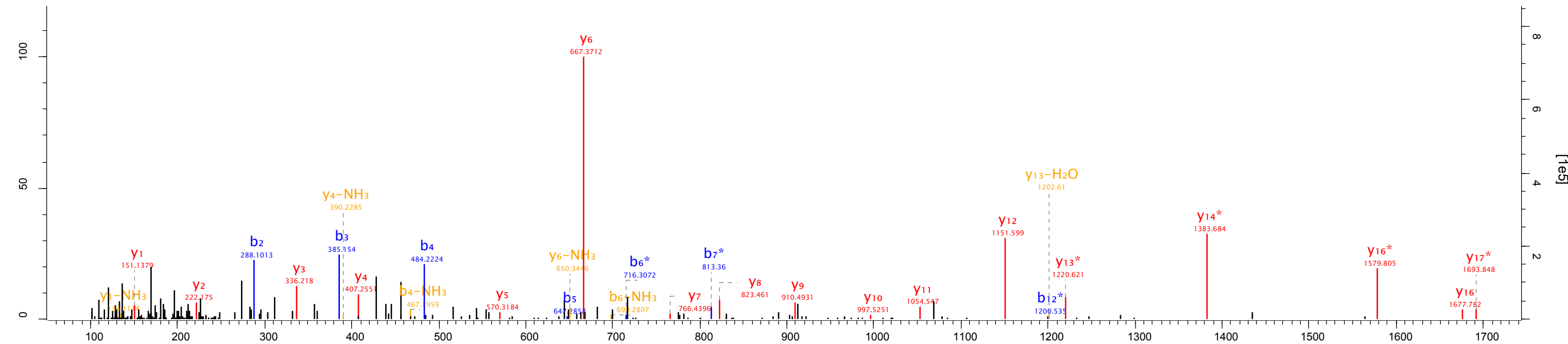
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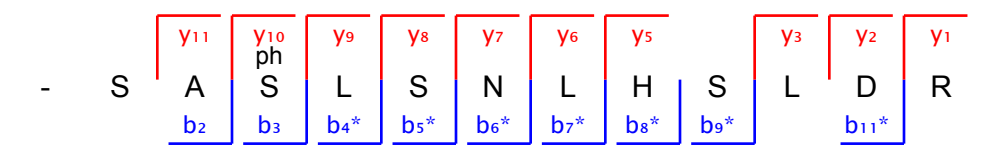
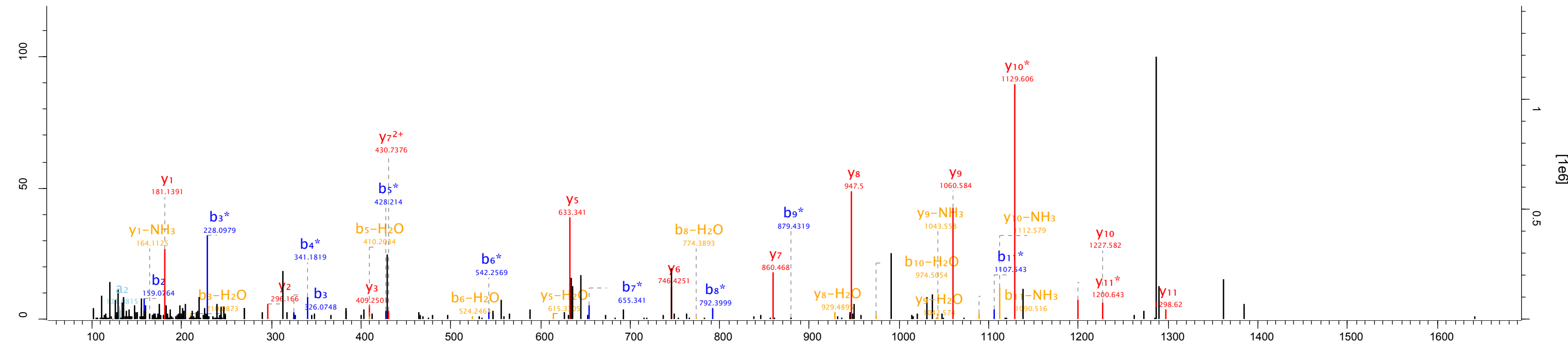
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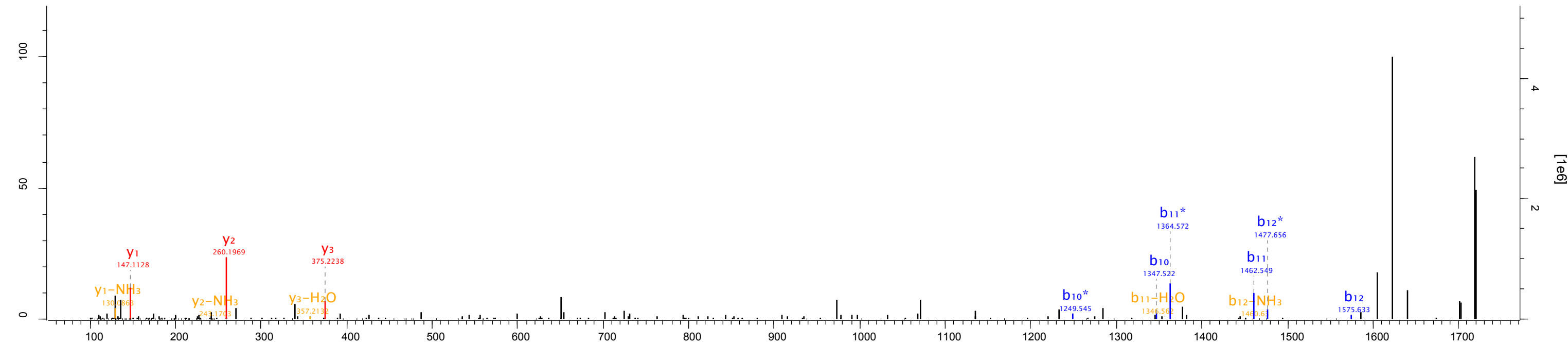
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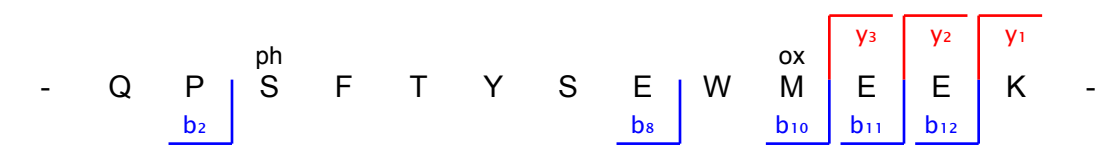
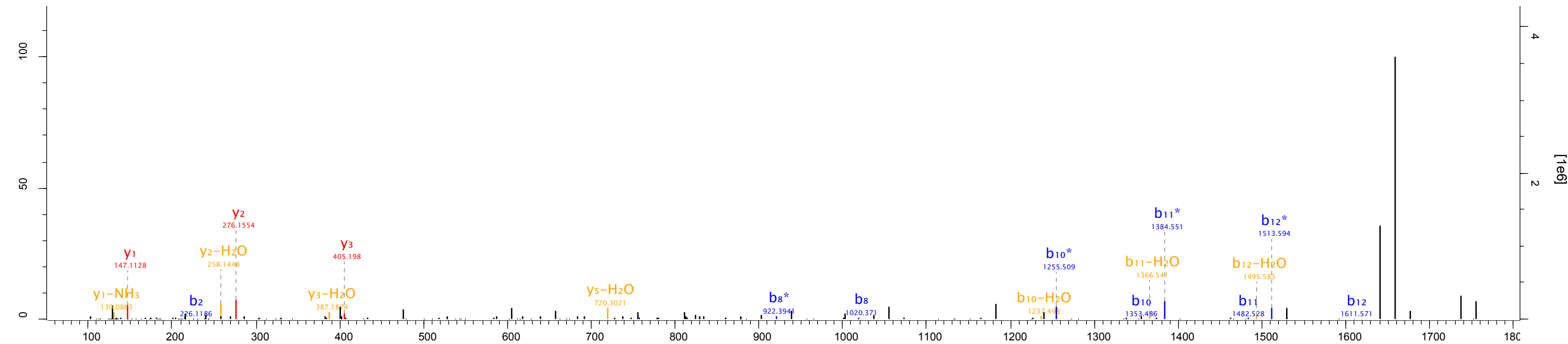
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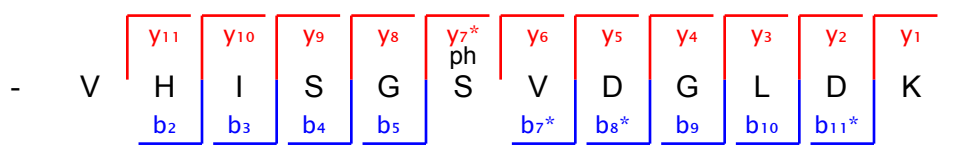
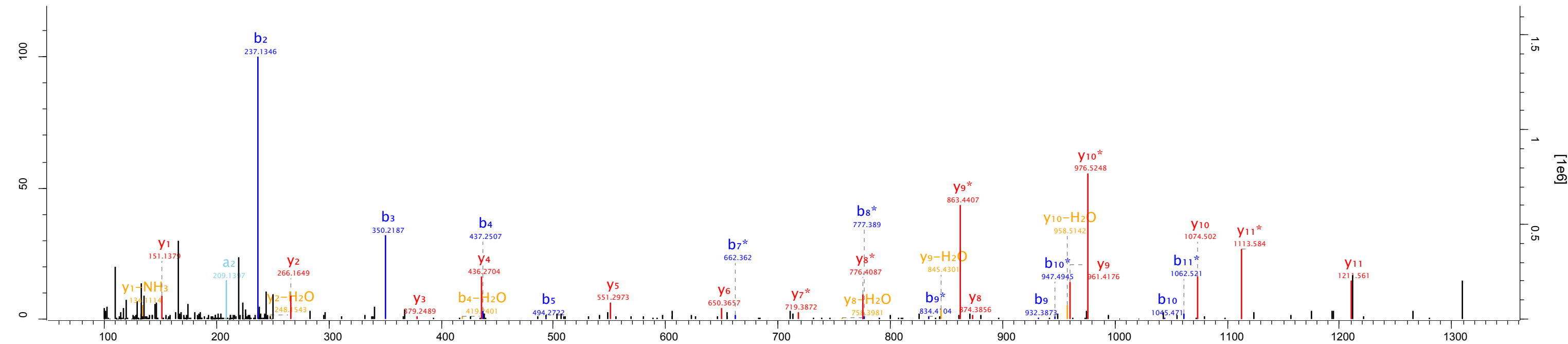
Raw file 20150812_A375SR_Phospho_BR1_06 Scan 14953 Method FTMS; HCD Score 42.31 m/z 861.37



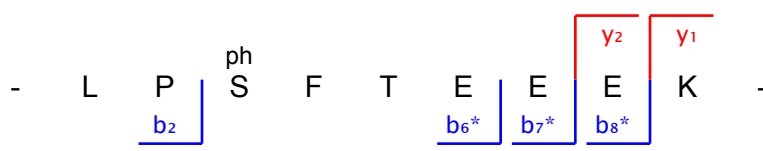
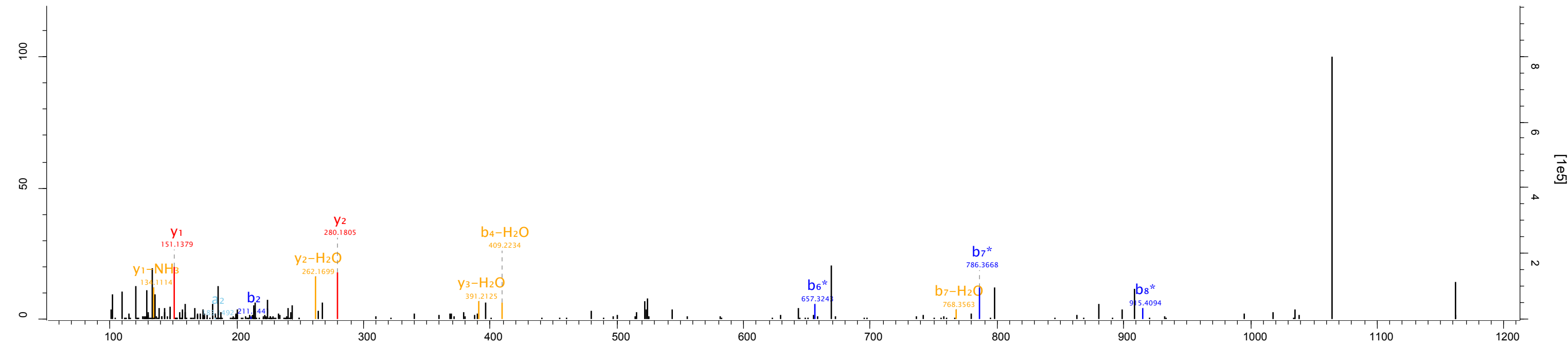
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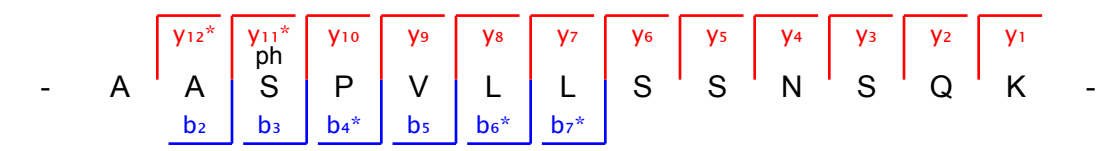
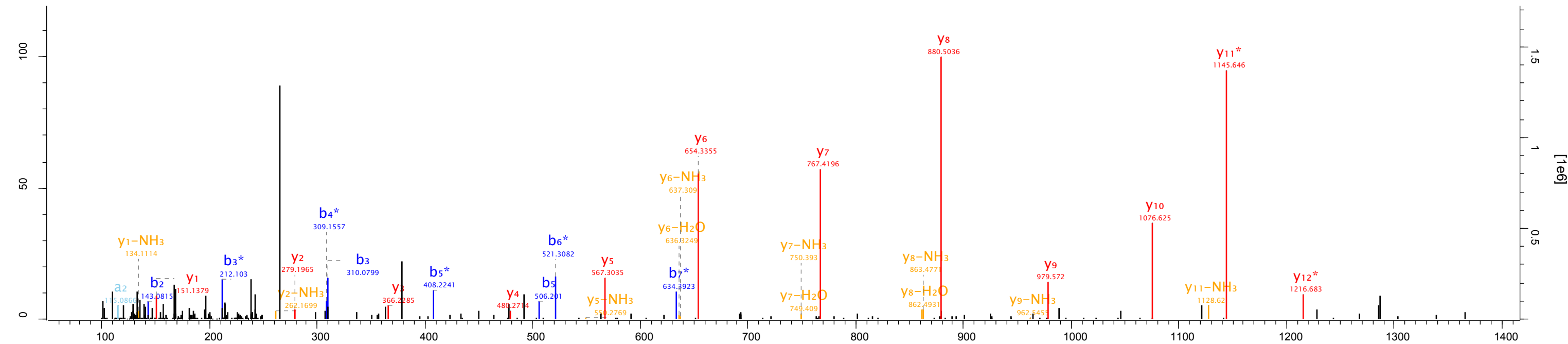
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 Scan: 12603 Method: FTMS; HCD Score: 101.8 m/z: 655.82 Gene names: PHACTR2



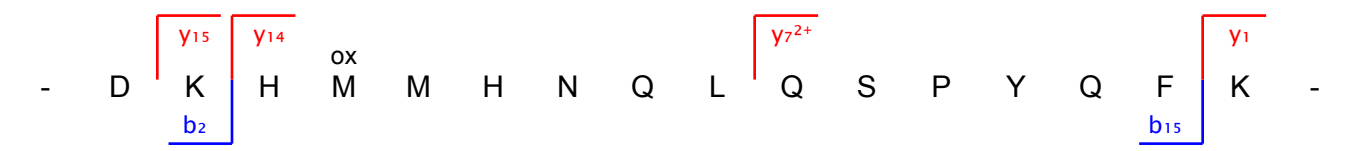
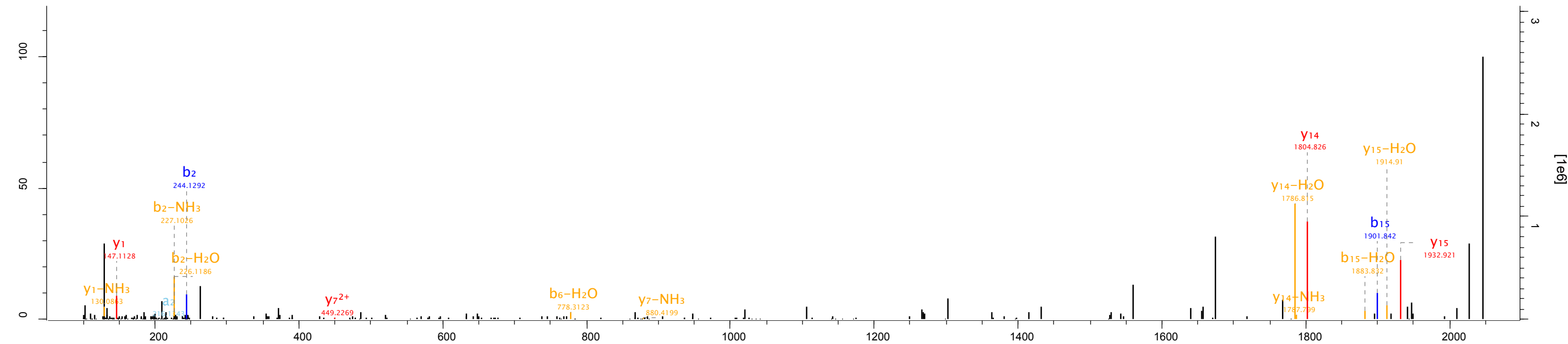
Raw file 20150812_A375SR_Phospho_BR1_07 Scan 16303 Method FTMS; HCD Score 46.84 m/z 582.26 Gene names LCT



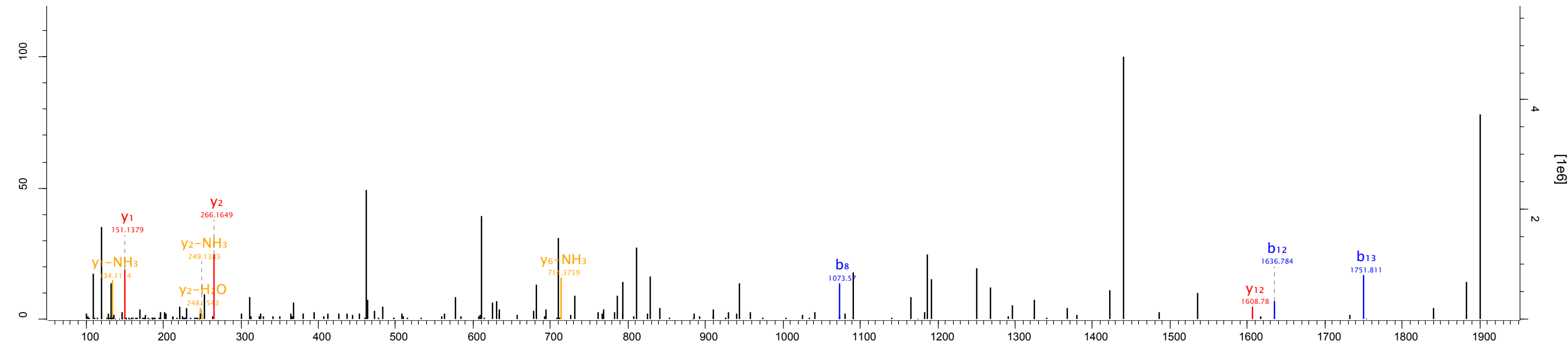
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 Scan: 11103 Method: FTMS; HCD Score: 98.51 m/z: 693.35 Gene names: ELK3



Raw file: 20150812_A375SR_Phospho_BR1_08
 Scan: 5403 Method: FTMS; HCD Score: 47.04 m/z: 683.65



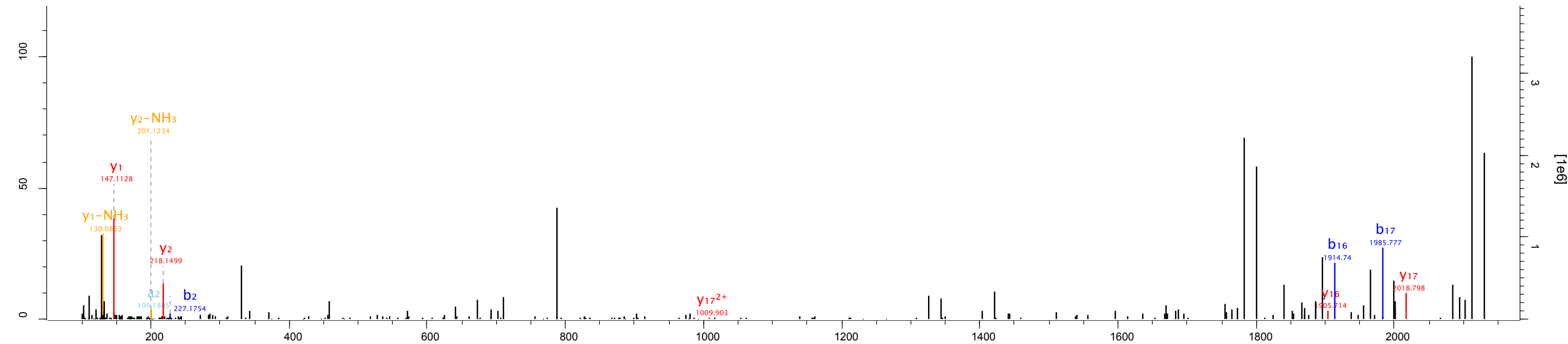
Raw file 20150812_A375SR_Phospho_BR1_09 Scan 20553 Method FTMS; HCD Score 44.51 m/z 634.99 Gene names C1orf61



- R M Y F I W L G W I P S D K -

Fragmentation labels: y12 (above Y), b8 (below G), b12 (below S), b13 (below D), y2 (above D), y1 (above K).

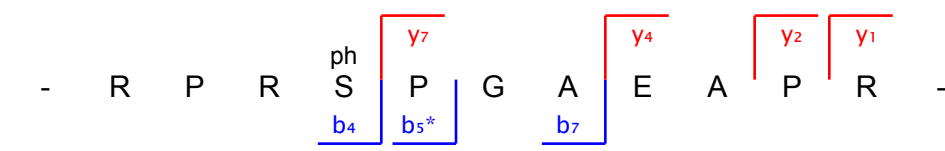
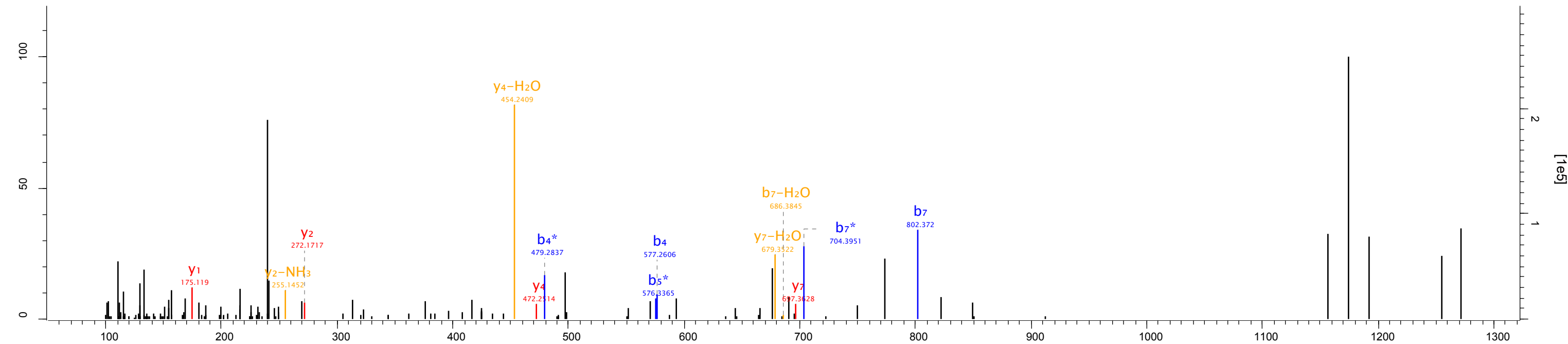
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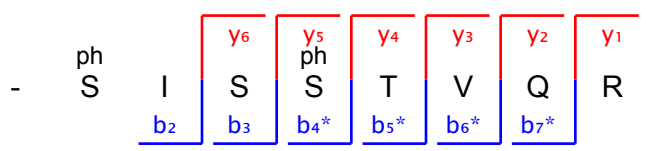
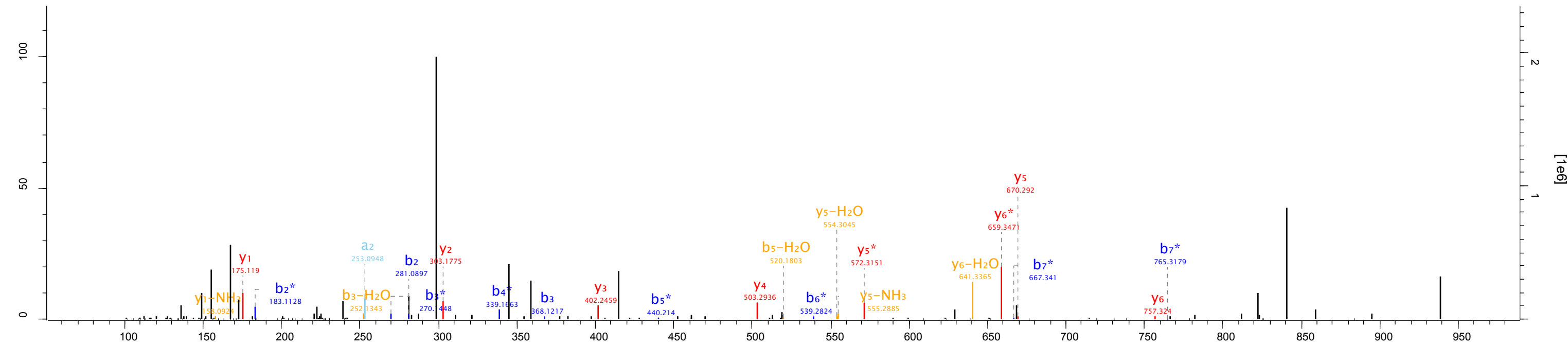
- L L L E C T Y G A L E S A G V P A K -

Fragmentation labels: b₂ (under the first L), y₁₇ (over the first L), y₁₆ (over the second L), b₁₆ (under P), y₂ (over A), b₁₇ (under A), y₁ (over K).

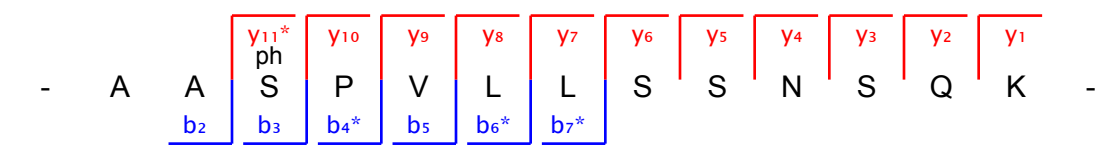
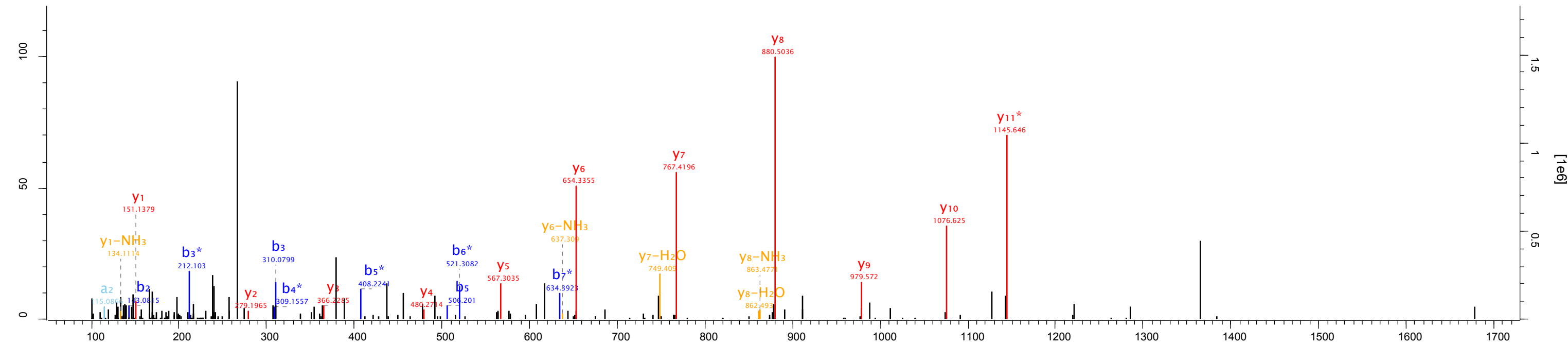
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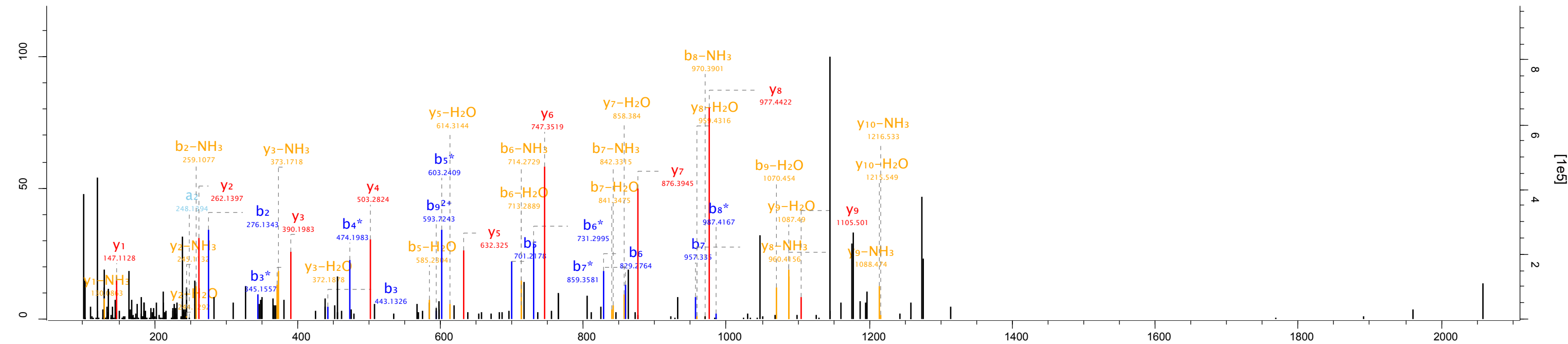
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 Scan: 8073 Method: FTMS; HCD Score: 91.69 m/z: 519.21 Gene names: RHBD2



Raw file
 20150814_A375SR_Phospho_BR2_03
 Scan 10623 Method FTMS; HCD Score 63.55 m/z 693.35 Gene names ELK3

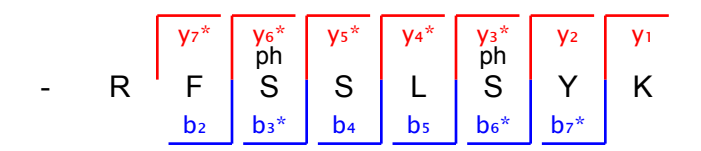
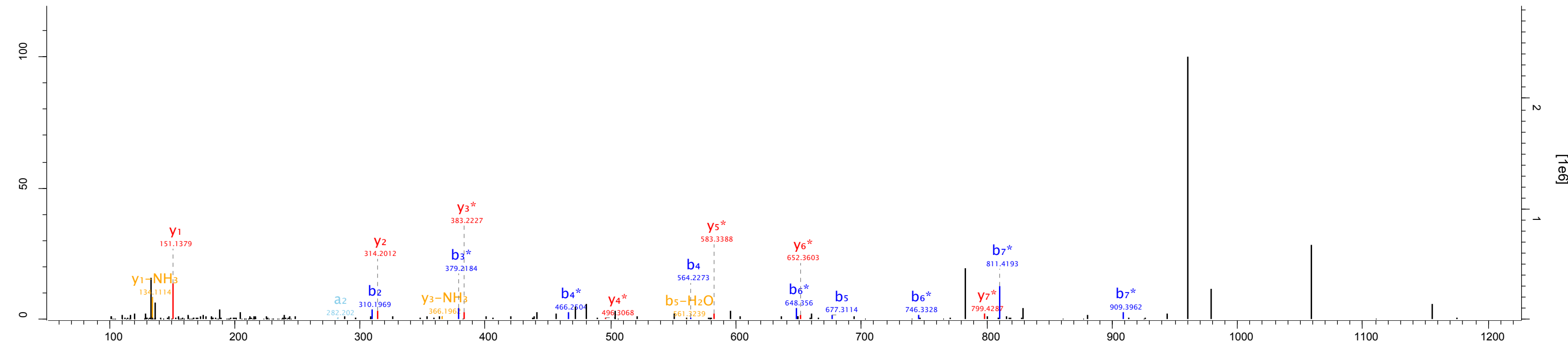


Raw file 20150814_A375SR_Phospho_BR2_03 Scan 11713 Method FTMS; HCD Score 131.98 m/z 687.95

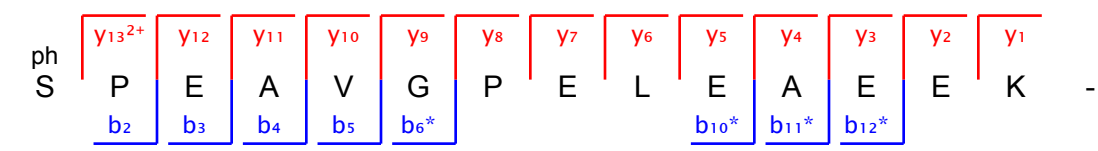
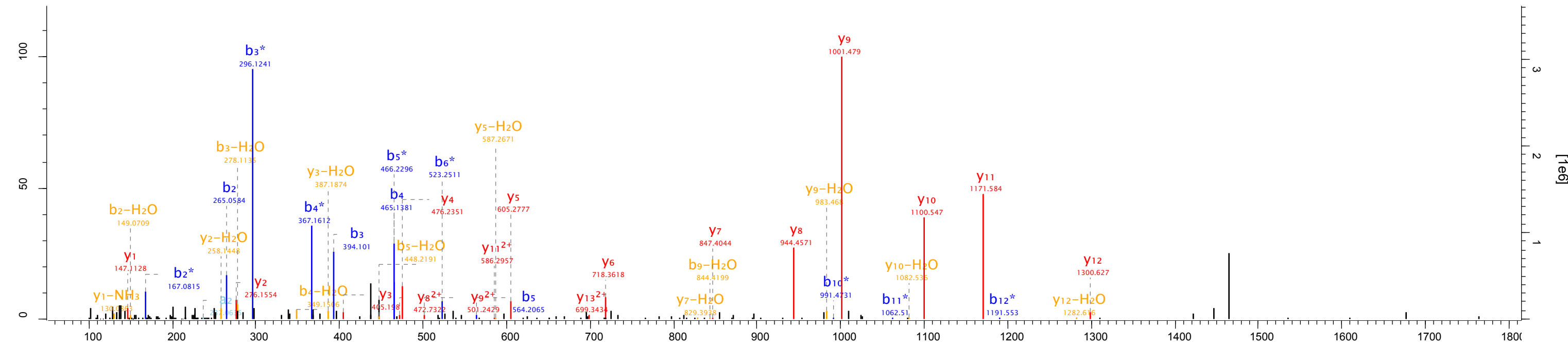


- F Q S E E Q Q Q T E D E L Q D K -
 (Labels below the sequence: b2, b3, b4*, b5, b6, b7, b8*, b9²⁺ are under the first 8 residues; y9, y8, y7, y6, y5, y4, y3, y2, y1 are under the last 9 residues)

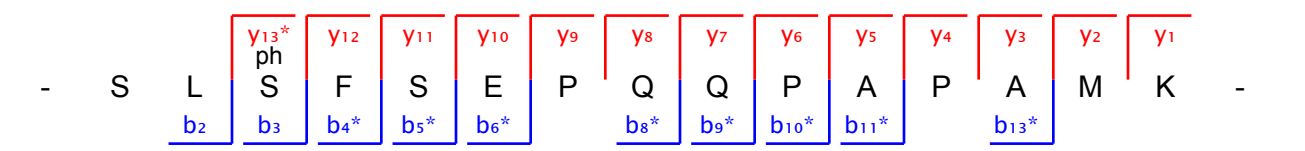
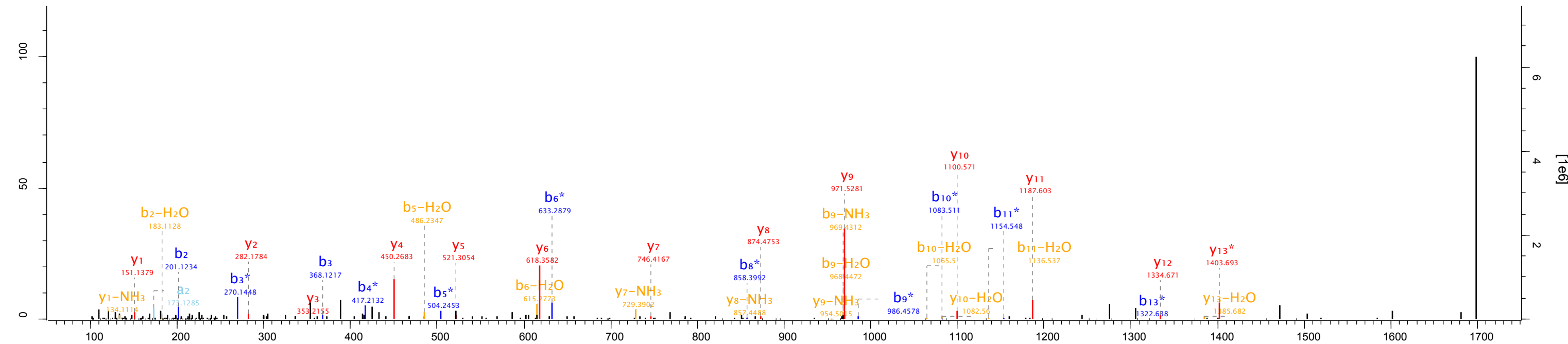
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 20150814_A375SR_Phospho_BR2_03 12063 FTMS; HCD 78.32 579.26 PAG1



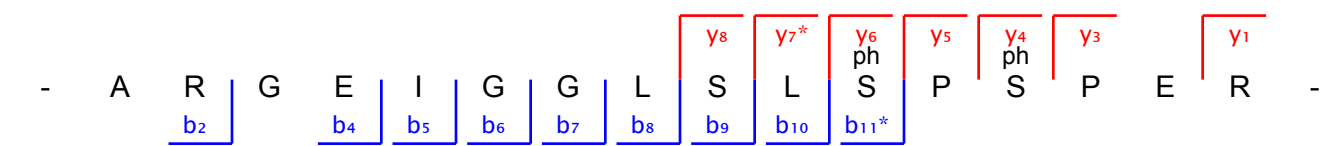
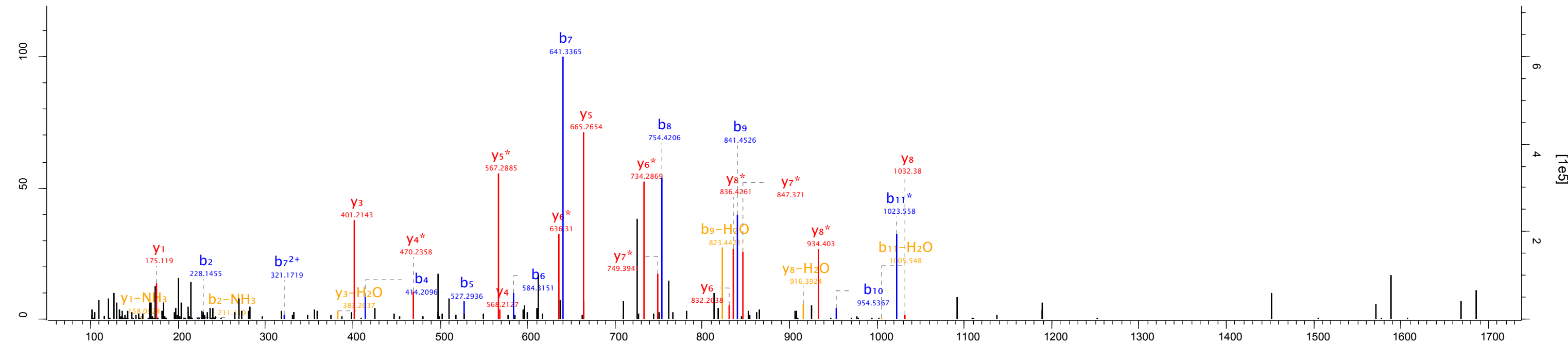
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 Scan: 13383 Method: FTMS; HCD Score: 164.48 m/z: 782.84 Gene names: PWWP2A



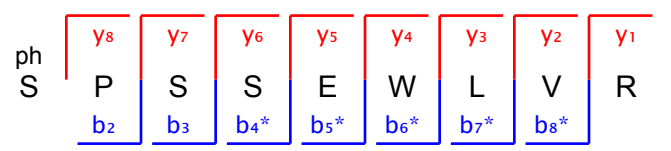
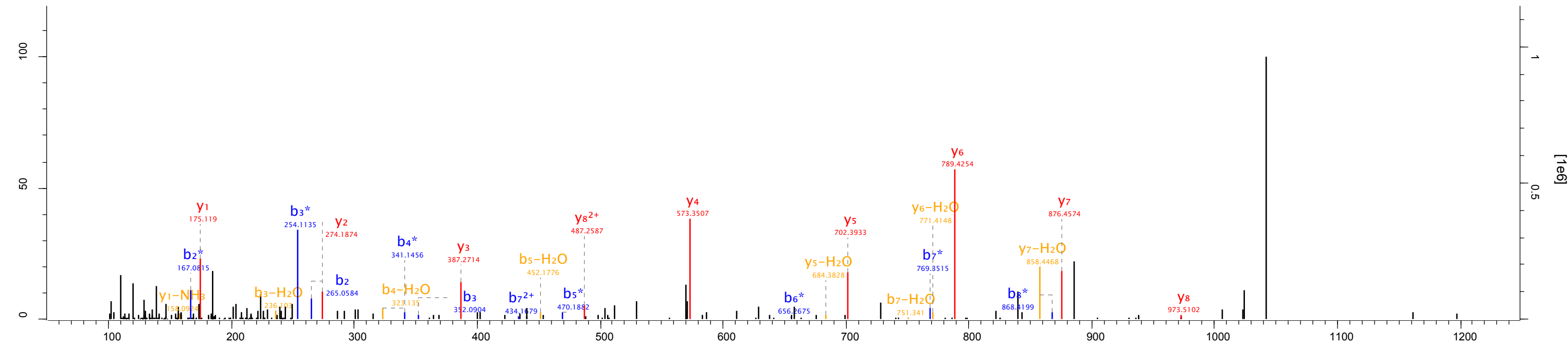
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 Scan: 16243 Method: FTMS; HCD Score: 132.25 m/z: 851.4 Gene names: ZNF395



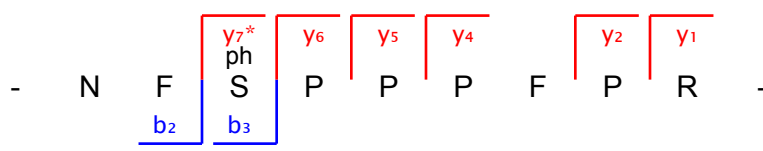
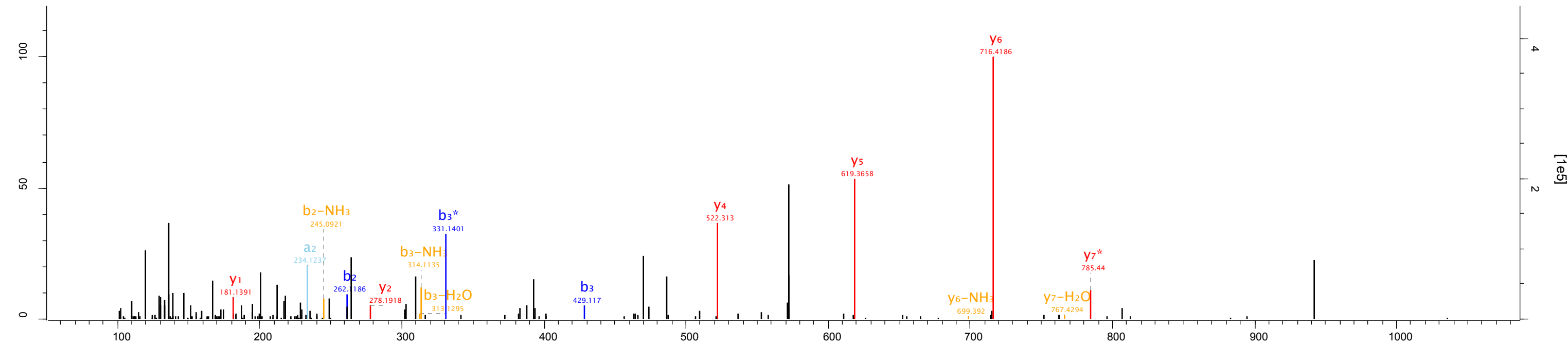
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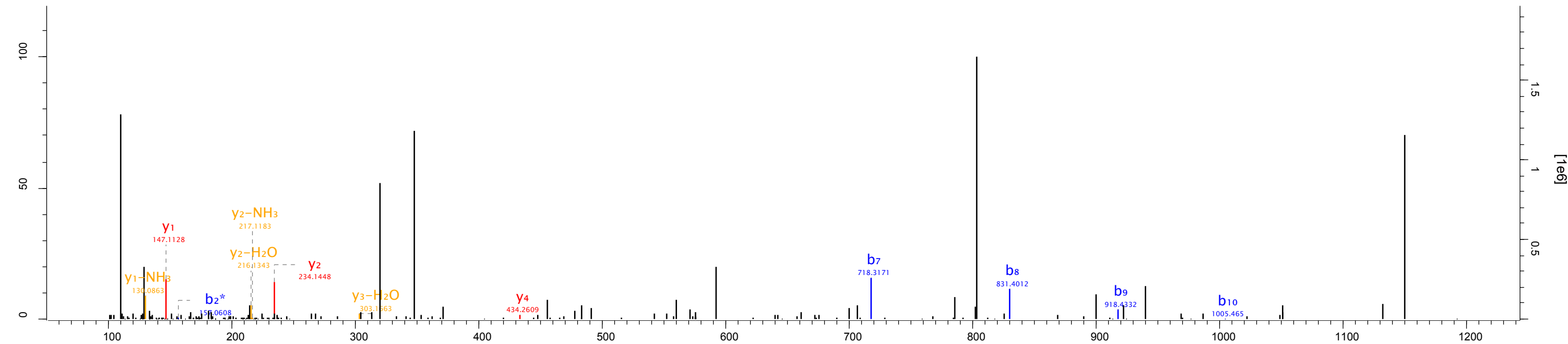
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 Scan: 19373 Method: FTMS; HCD Score: 46.52 m/z: 572.77 Gene names: CCDC125

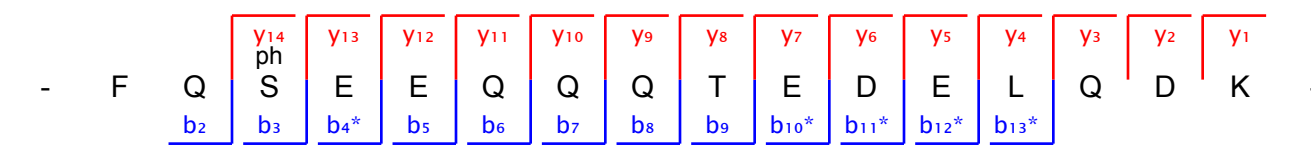
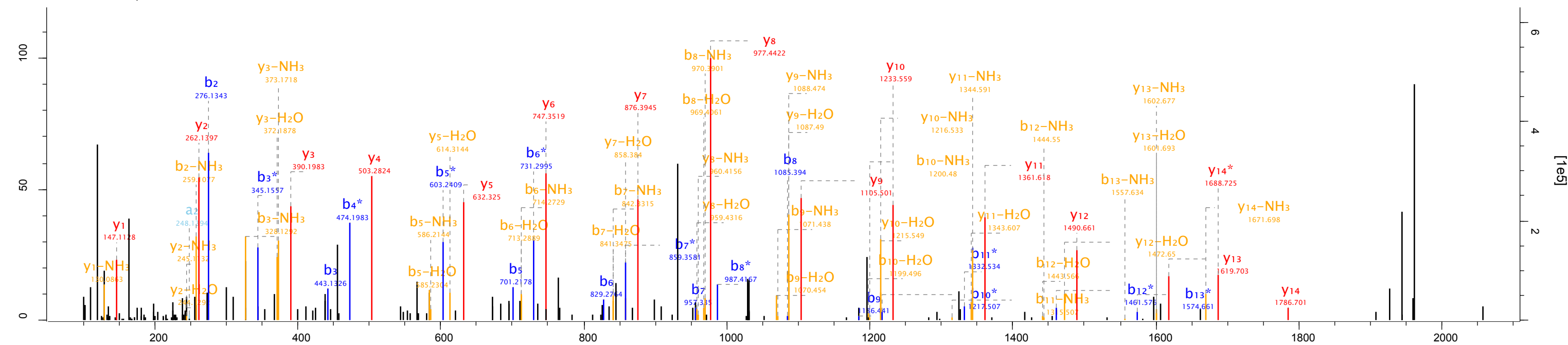


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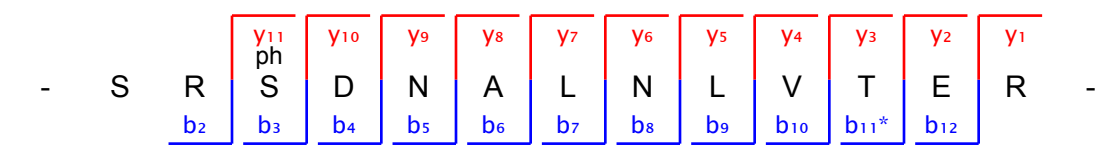
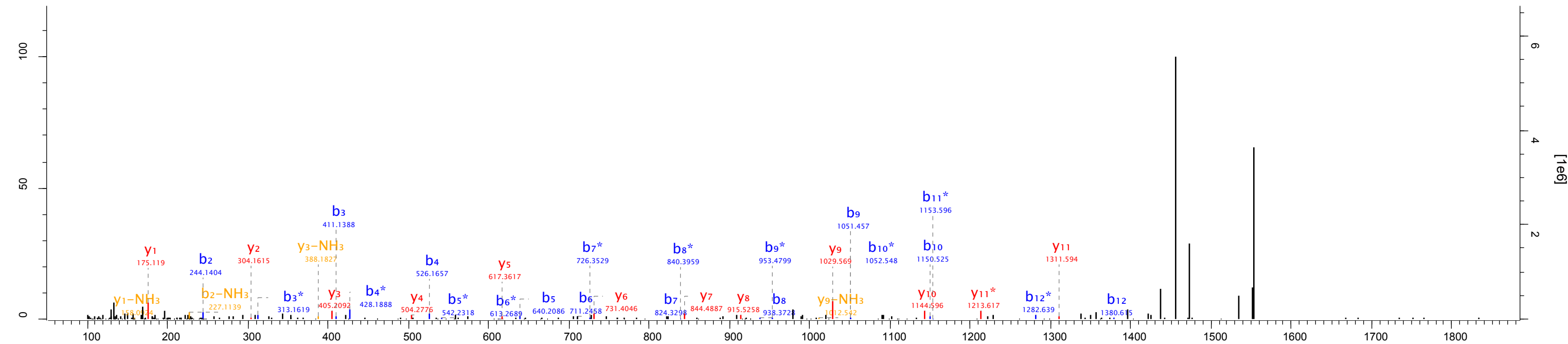


Raw file
20150814_A375SR_Phospho_BR2_04

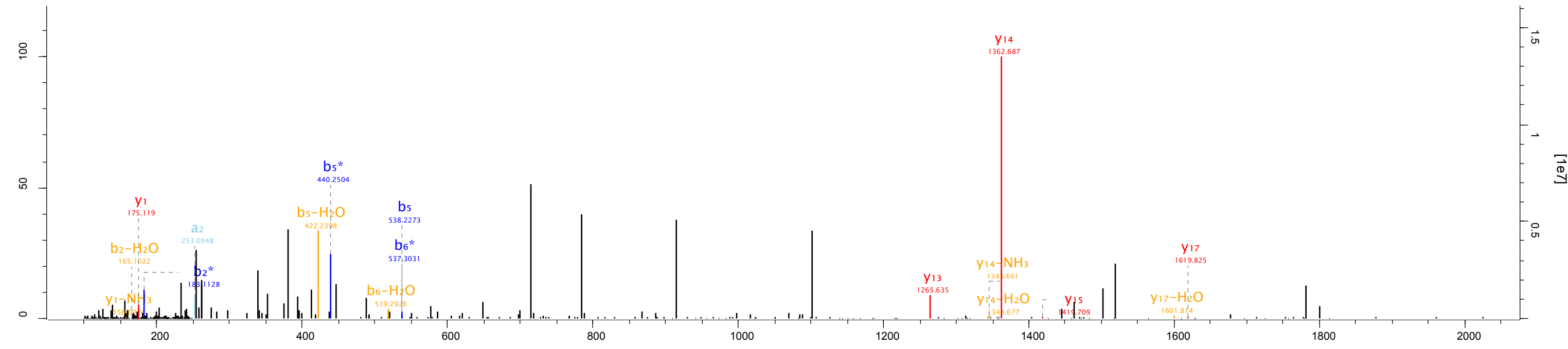
Scan 11703 Method FTMS; HCD Score 323.57 m/z 1031.42



Raw file: 20150814_A375SR_Phospho_BR2_04
 Scan: 14643 Method: FTMS; HCD Score: 75.25 m/z: 777.87 Gene names: PRICKLE1



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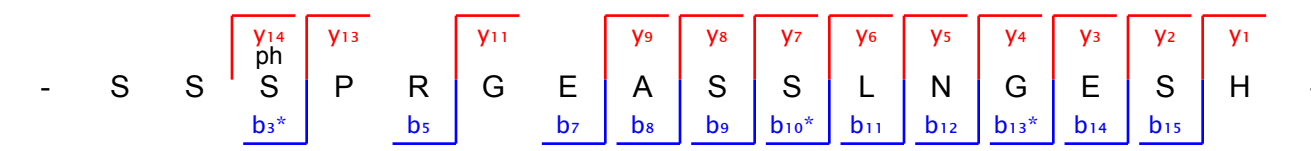
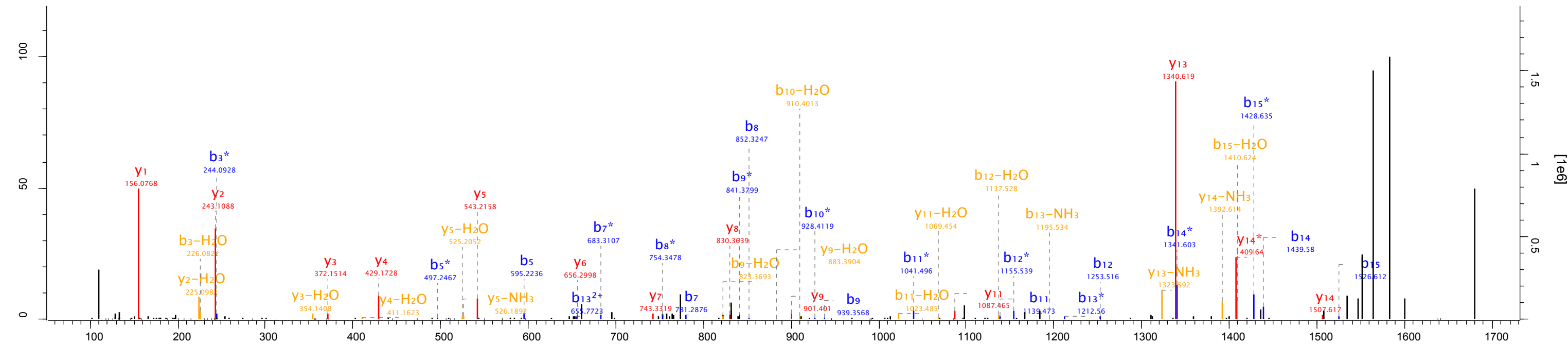


- ph S L S L G P S Q E P A P G G G R G P R -

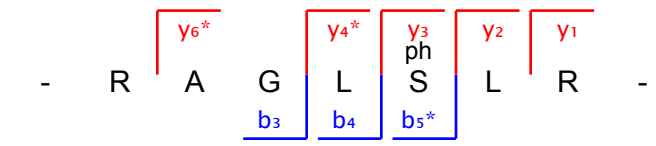
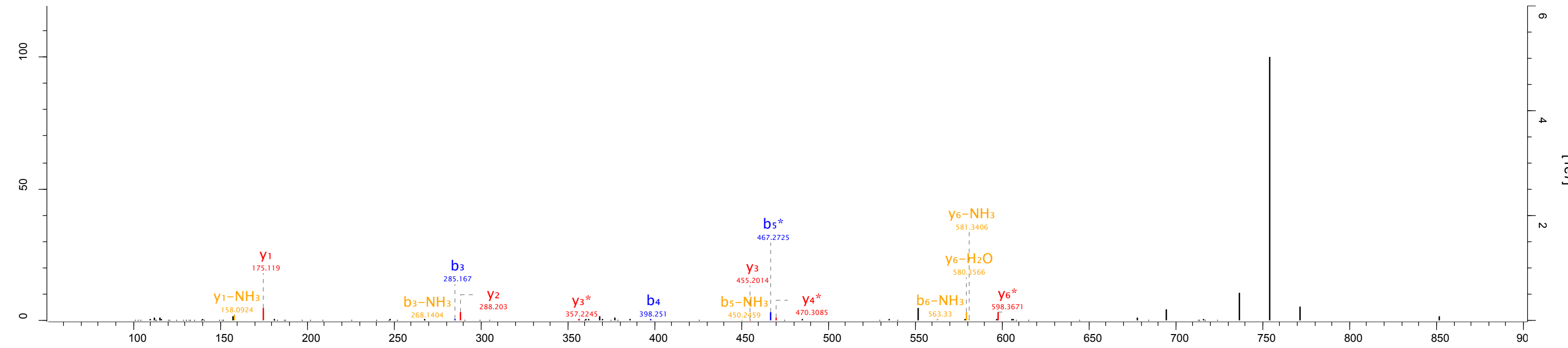
Fragmentation mapping (b and y ions):

- b₂*: L S
- y₁₇: S
- b₅: G
- y₁₅: G
- b₆*: P
- y₁₄: P
- y₁₃: S
- y₁: R

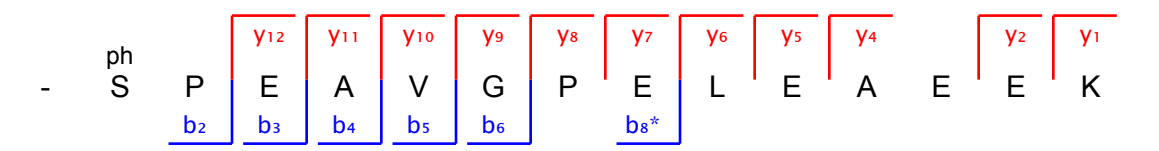
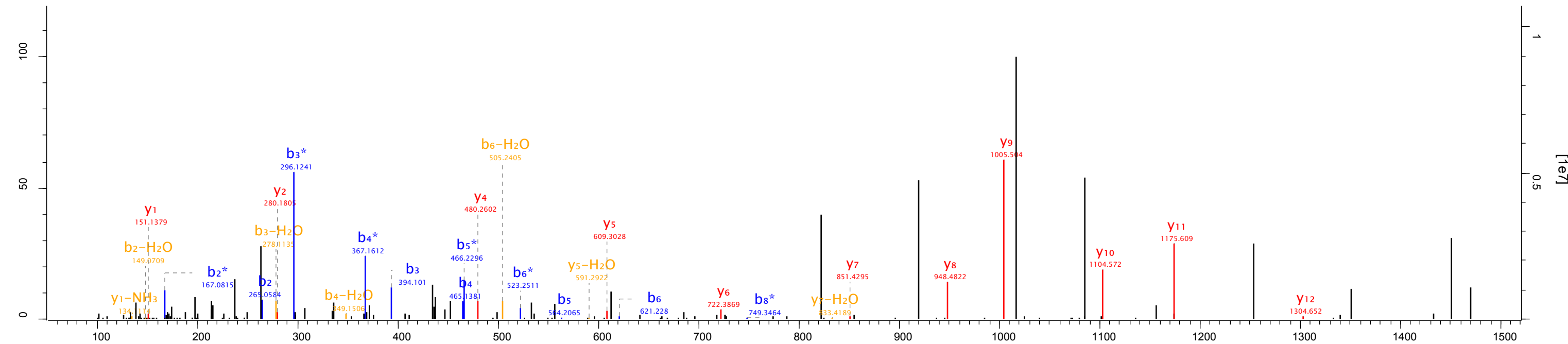
Raw file: 20150814_A375SR_Phospho_BR2_04
 Scan: 5583 Method: FTMS; HCD Score: 195.36 m/z: 841.34 Gene names: YAF2



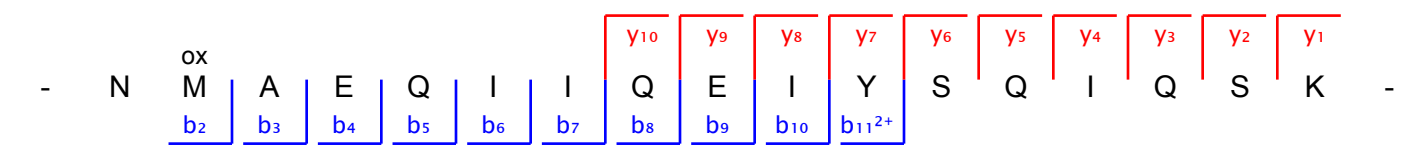
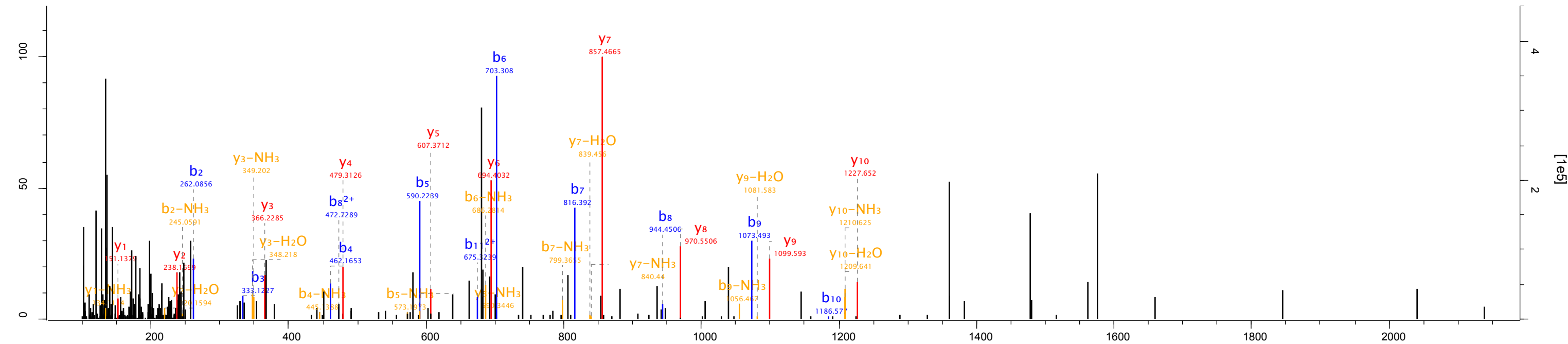
Raw file 20150814_A375SR_Phospho_BR2_04 Scan 5653 Method FTMS; HCD Score 70.06 m/z 426.73



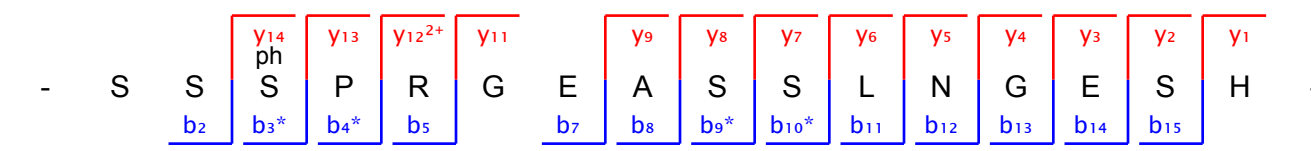
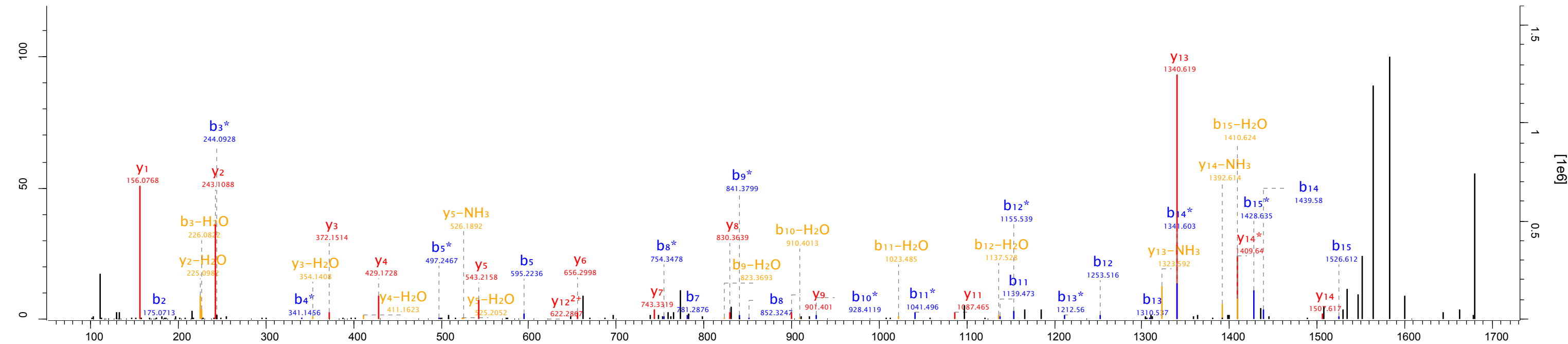
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 Scan: 13673 Method: FTMS; HCD Score: 66.55 m/z: 784.86 Gene names: PWWP2A



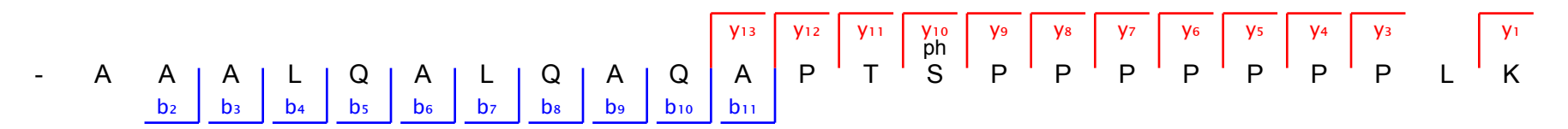
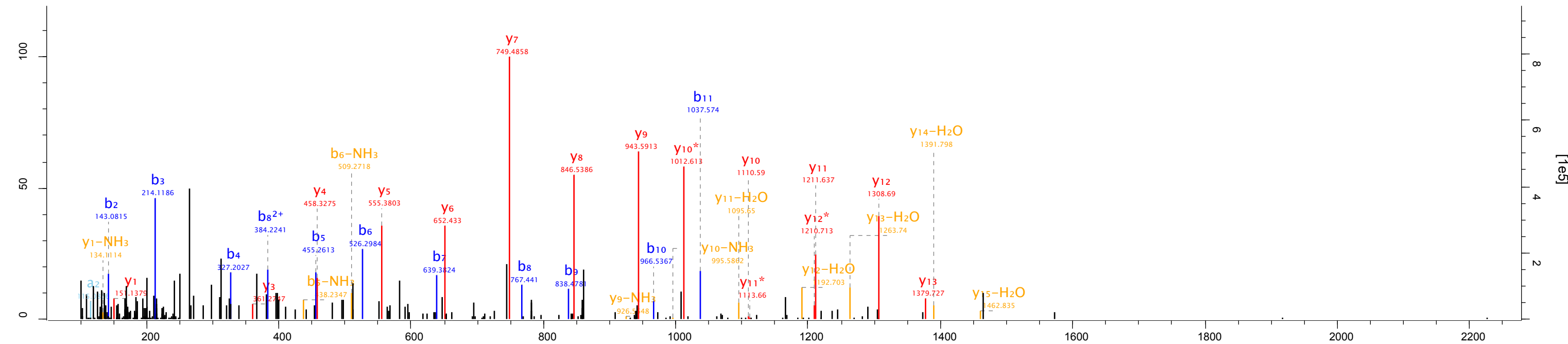
Raw file: 20150814_A375SR_Phospho_BR2_05
 Scan: 28843 Method: FTMS; HCD Score: 119.08 m/z: 682.02 Gene names: TKT



Raw file: 20150814_A375SR_Phospho_BR2_05
 Scan: 6003 Method: FTMS; HCD Score: 142.54 m/z: 841.34 Gene names: YAF2

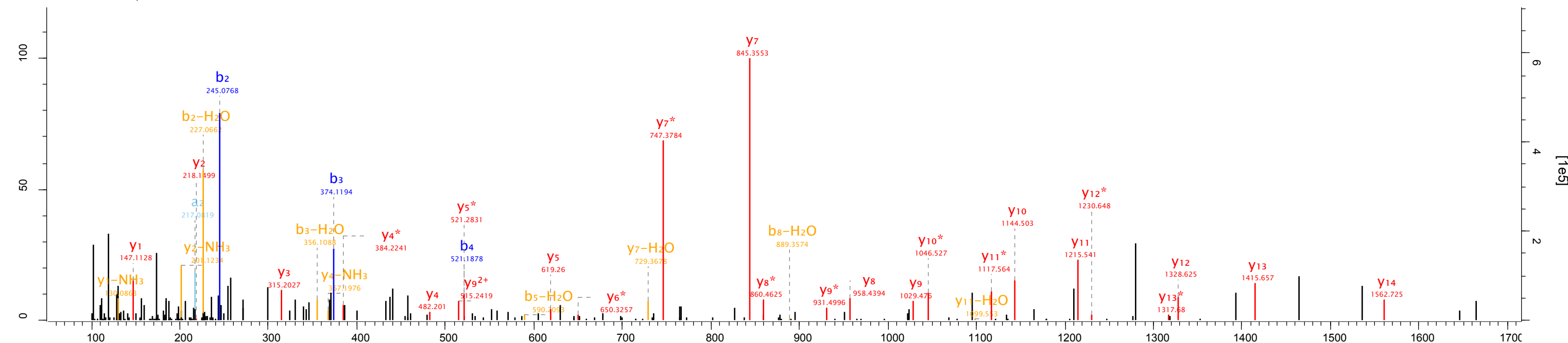


Raw file 20150814_A375SR_Phospho_BR2_06 Scan 21253 Method FTMS; HCD Score 89.3 m/z 782.76 Gene names ZNF579



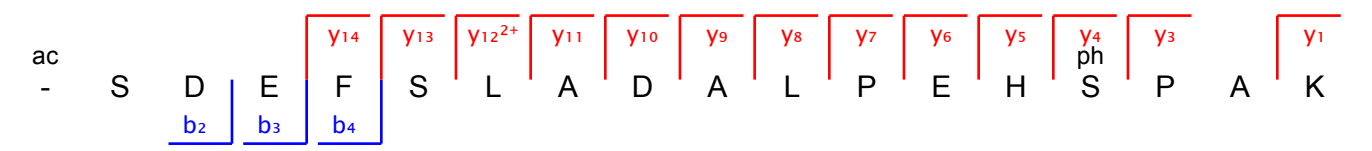
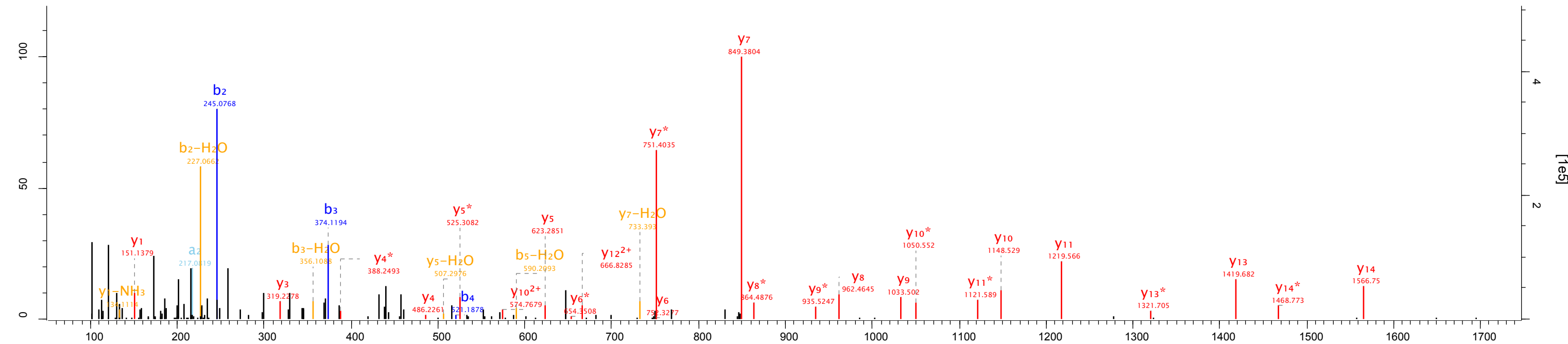
Raw file
20150814_A375SR_Phospho_BR2_06

Scan 24083 Method FTMS; HCD Score 107.83 m/z 646.29 Gene names MAPK11P1L

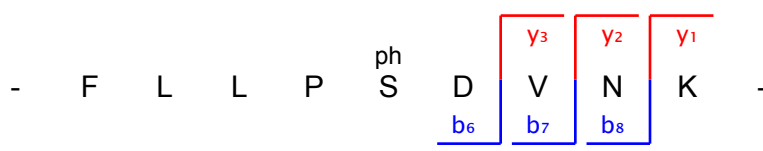
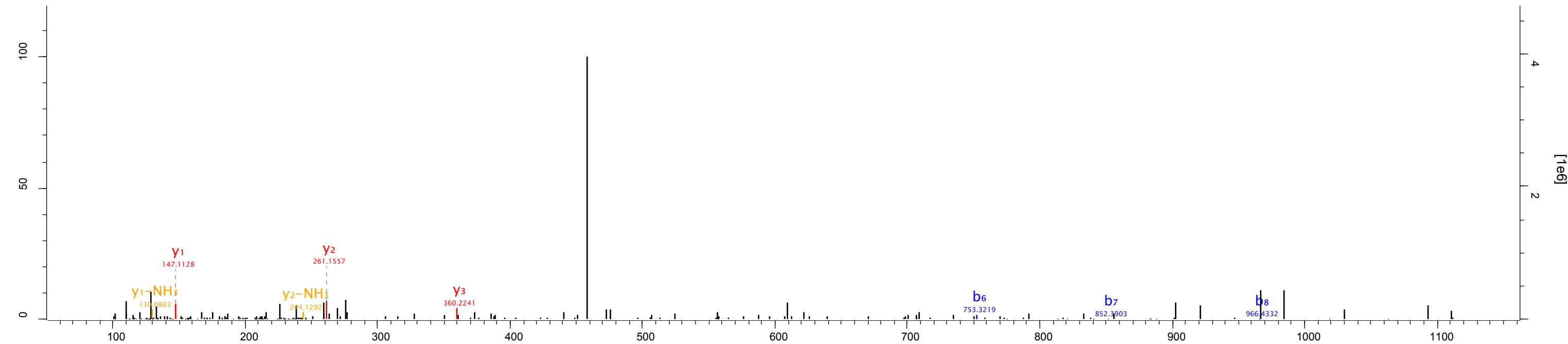


ac
- S D E F S L A D A L P E H S P A K -
b2 b3 b4

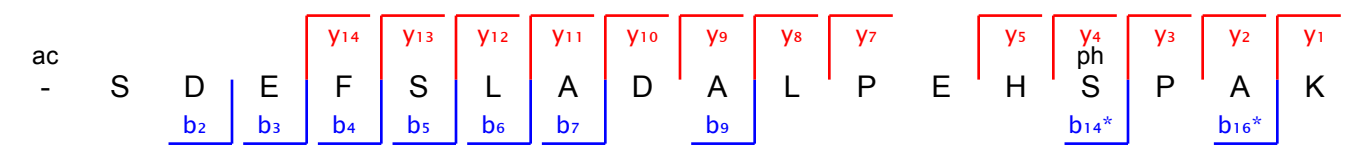
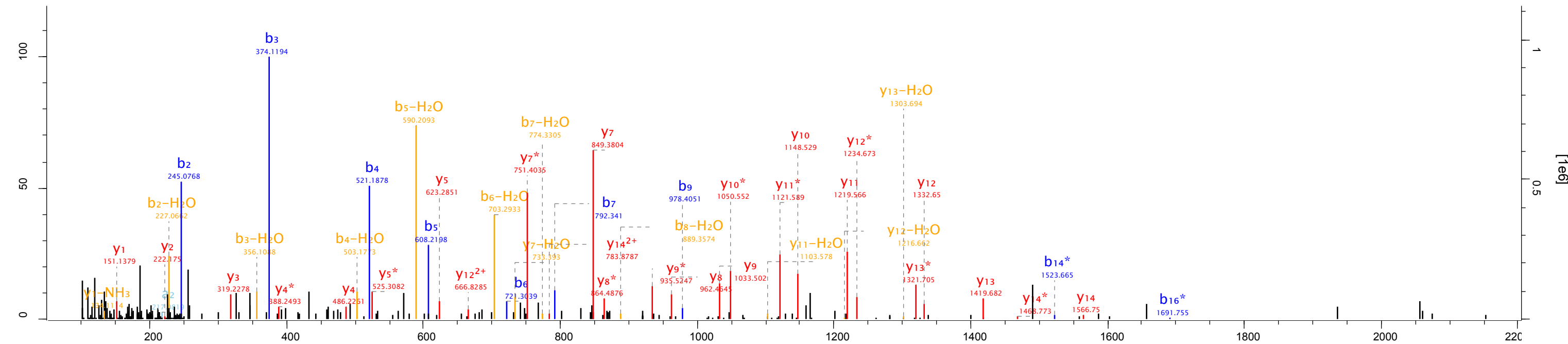
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 Scan: 23553 Method: FTMS; HCD Score: 105.51 m/z: 647.63 Gene names: MAPK11P1L



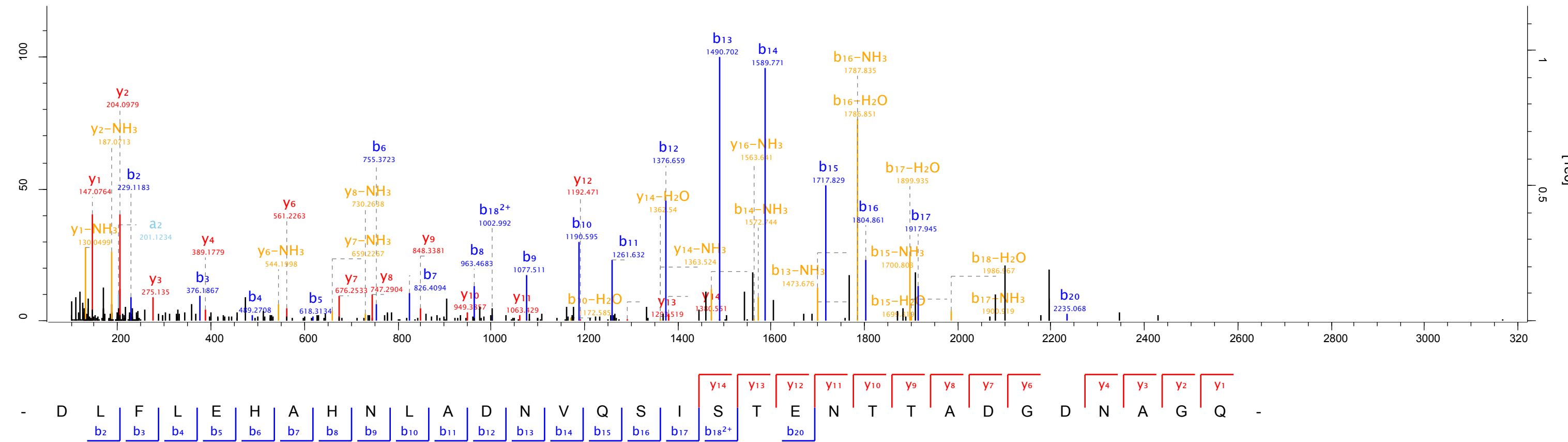
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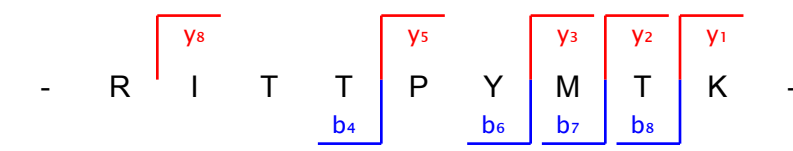
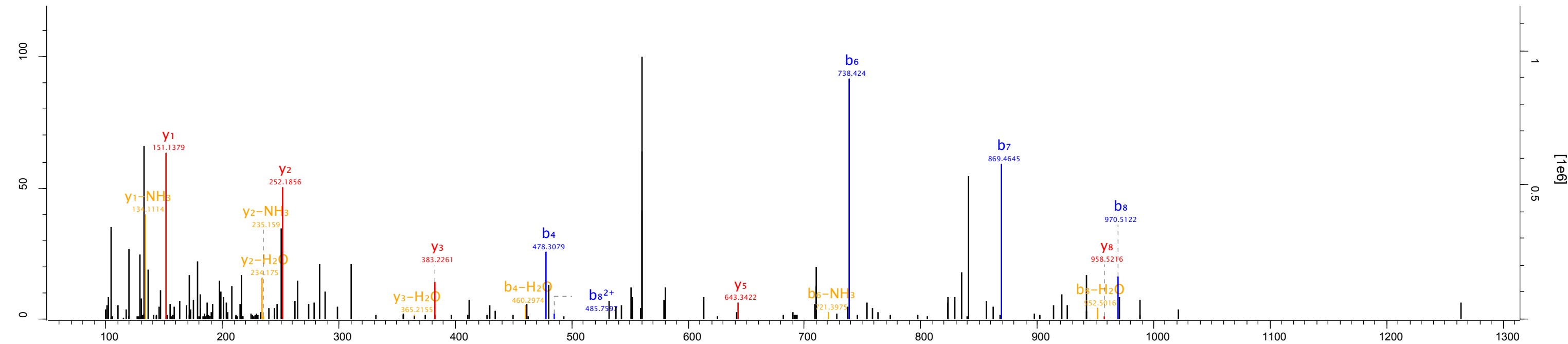
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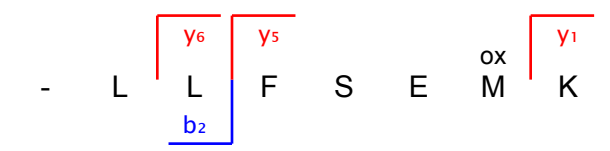
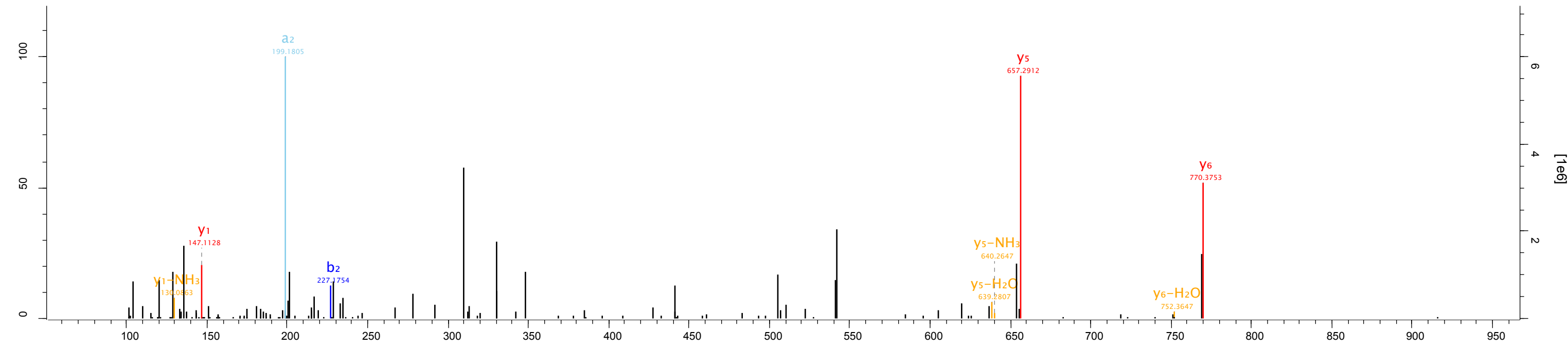
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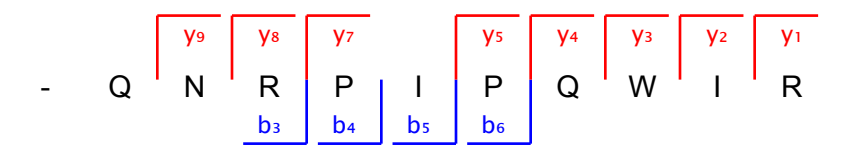
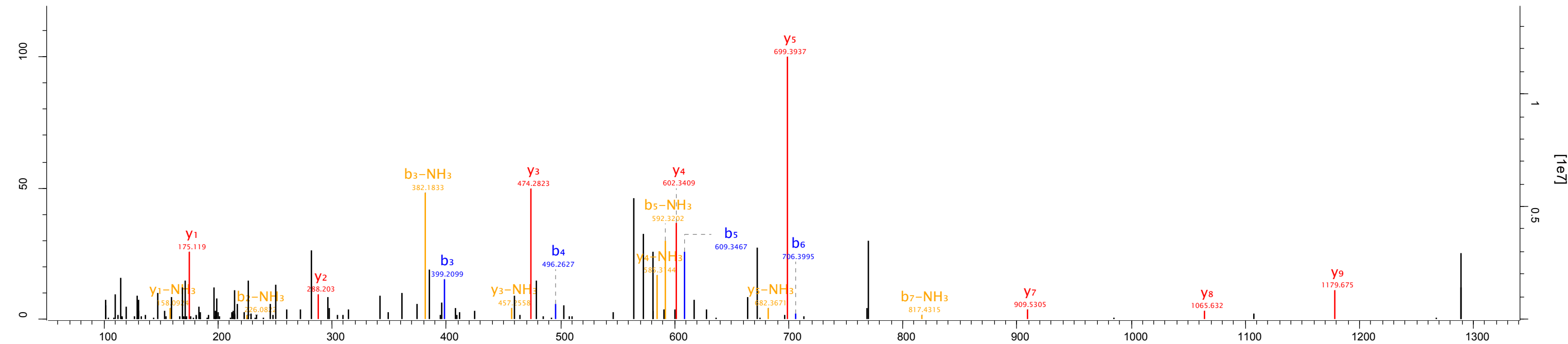
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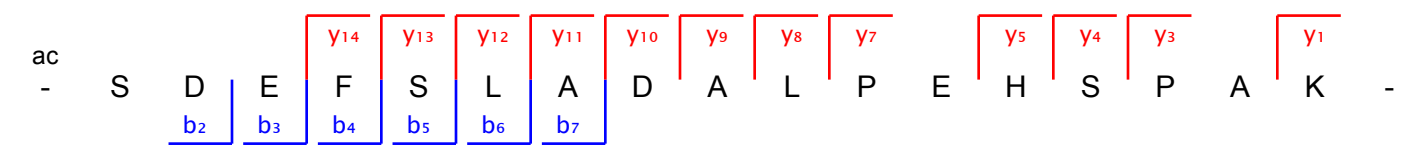
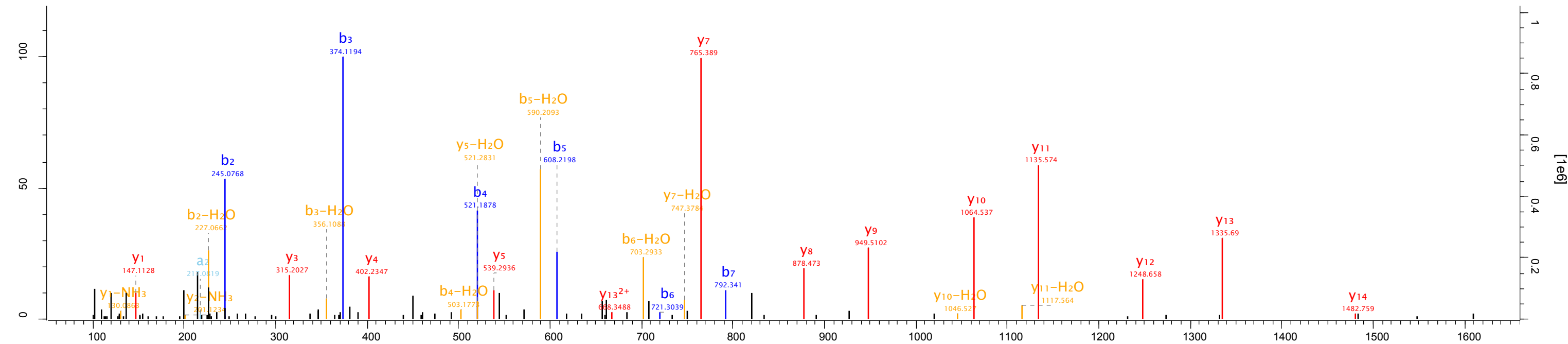
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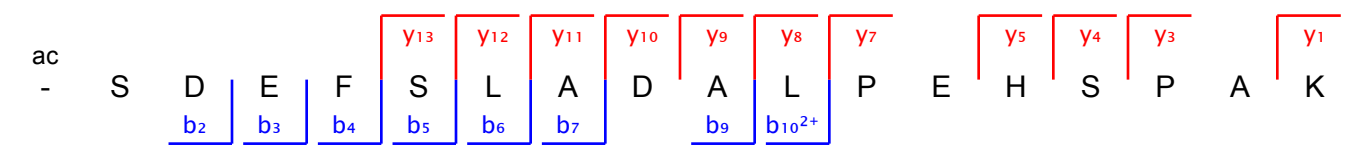
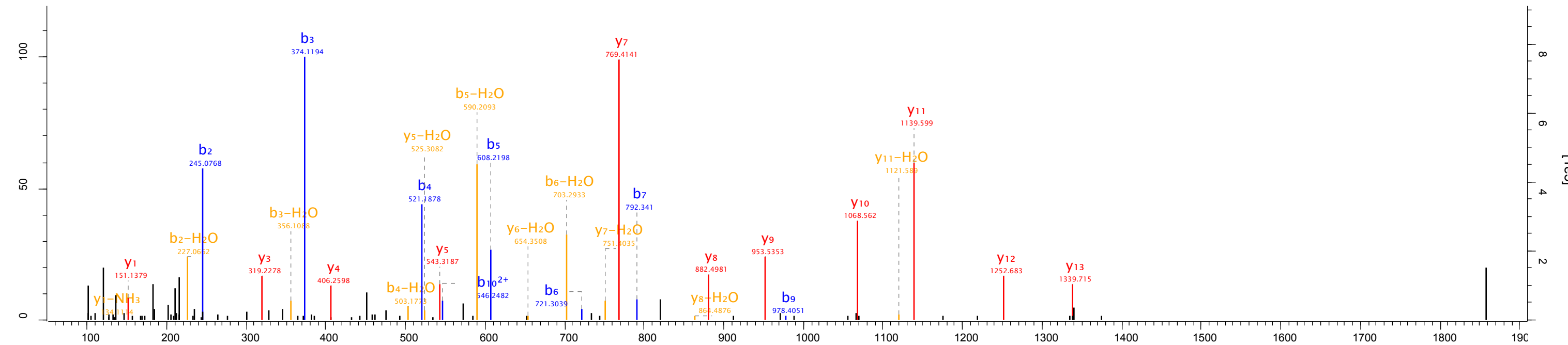
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 Scan: 38593 Method: FTMS; HCD Score: 89.03 m/z: 436.58 Gene names: RPL39P5;RPL39



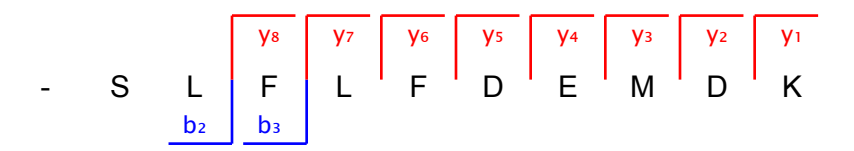
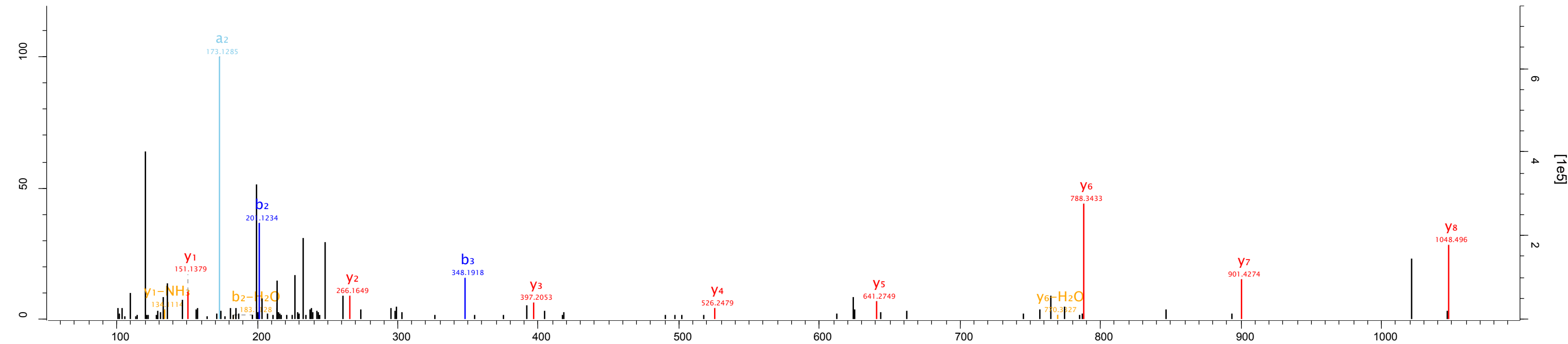
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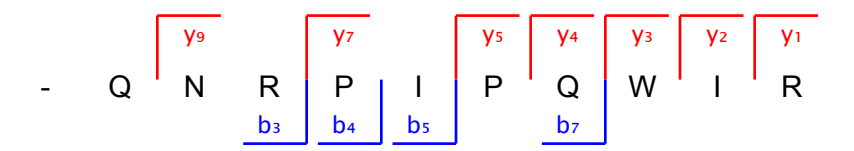
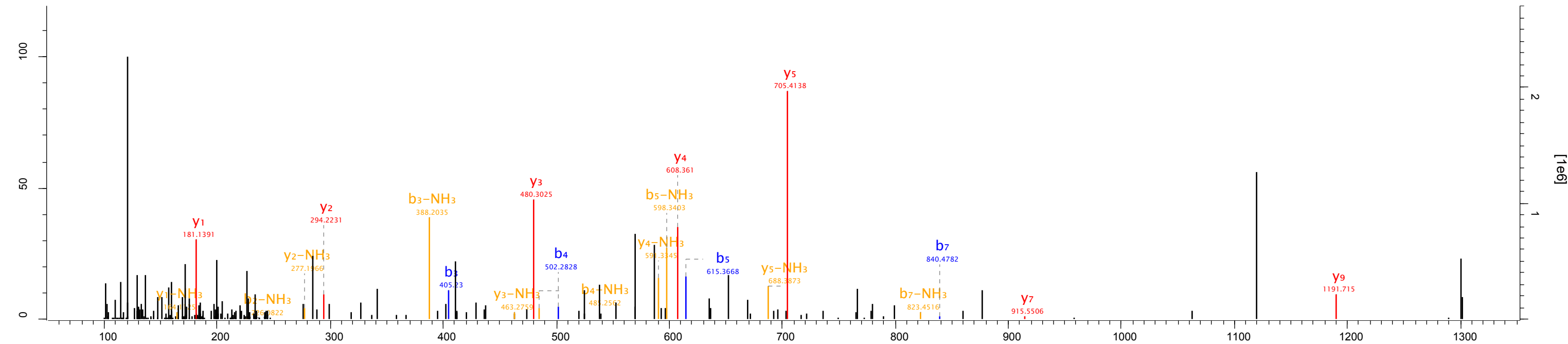
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 Gene names: MAPK11P1L



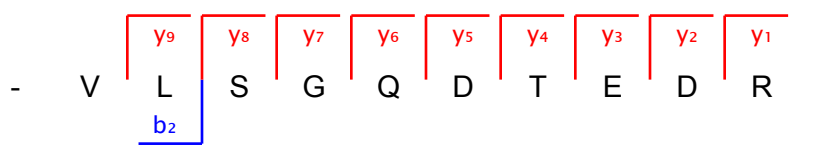
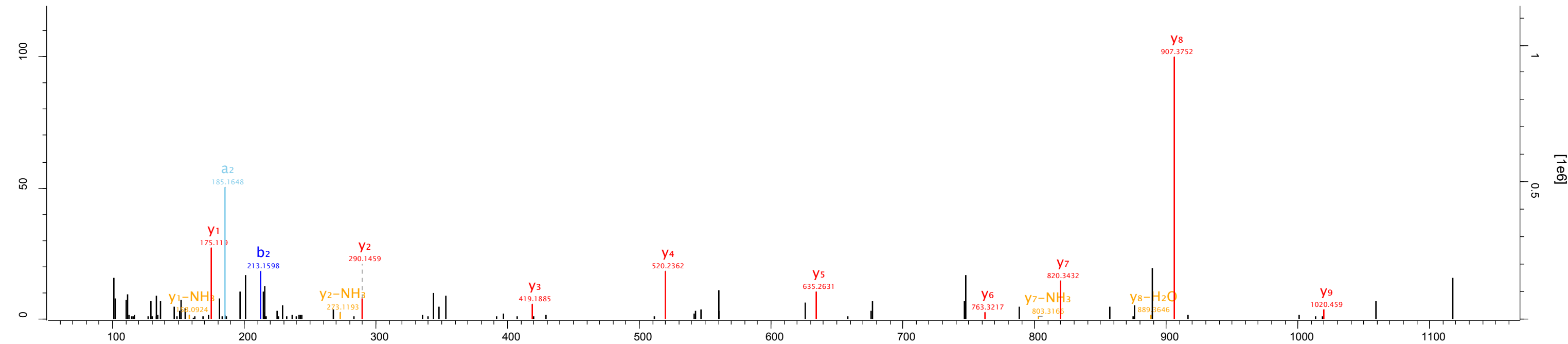
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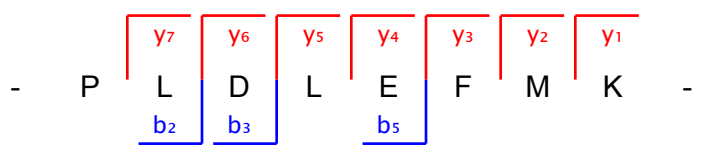
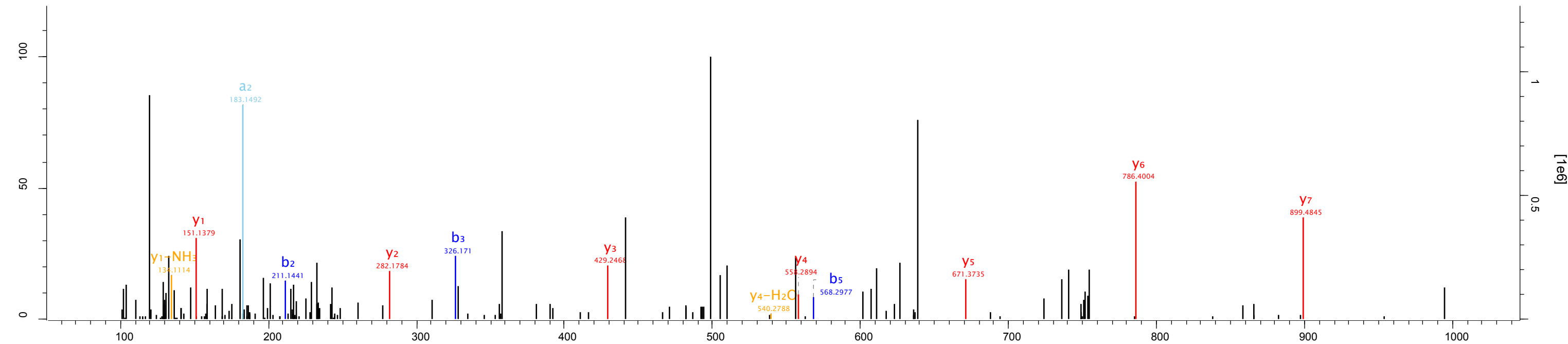
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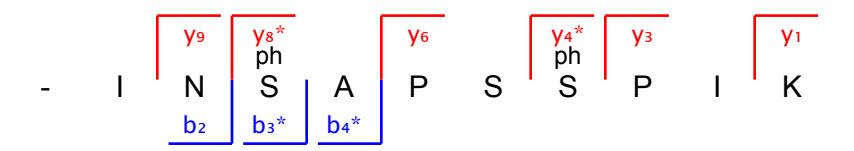
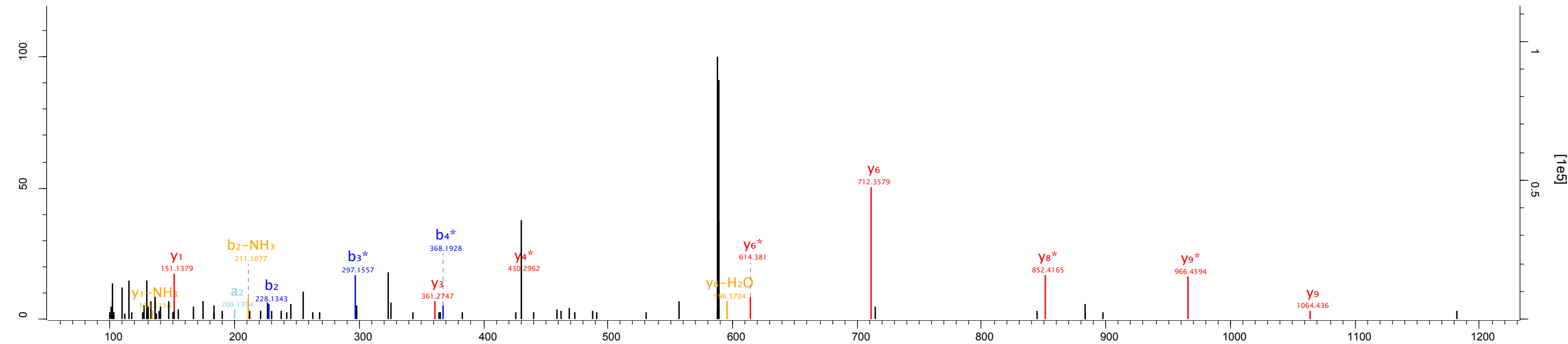
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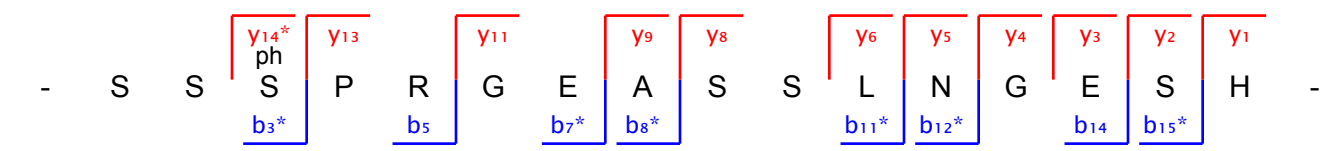
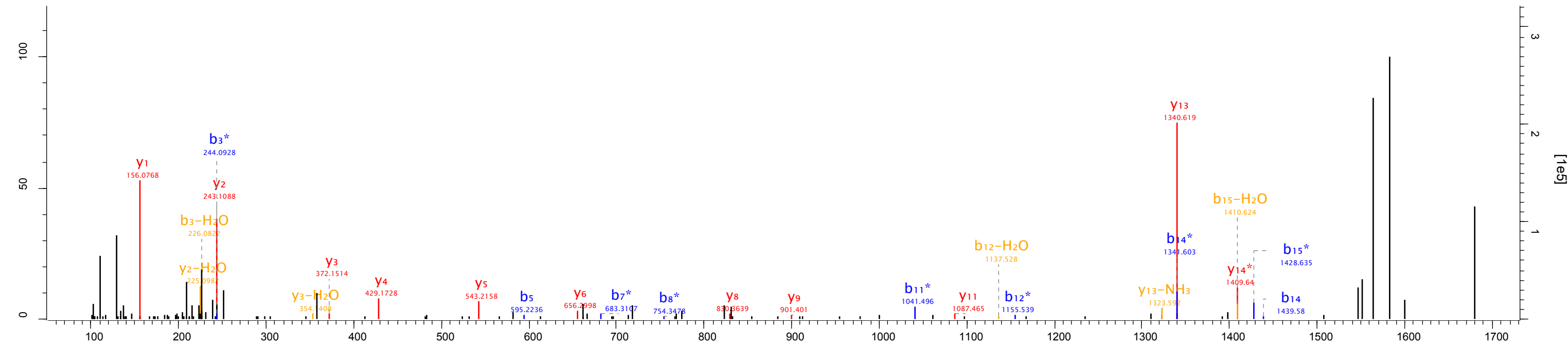
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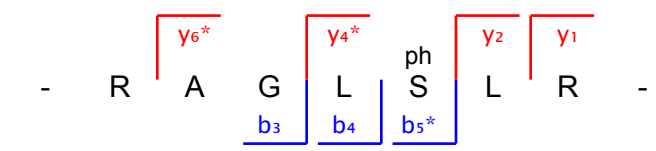
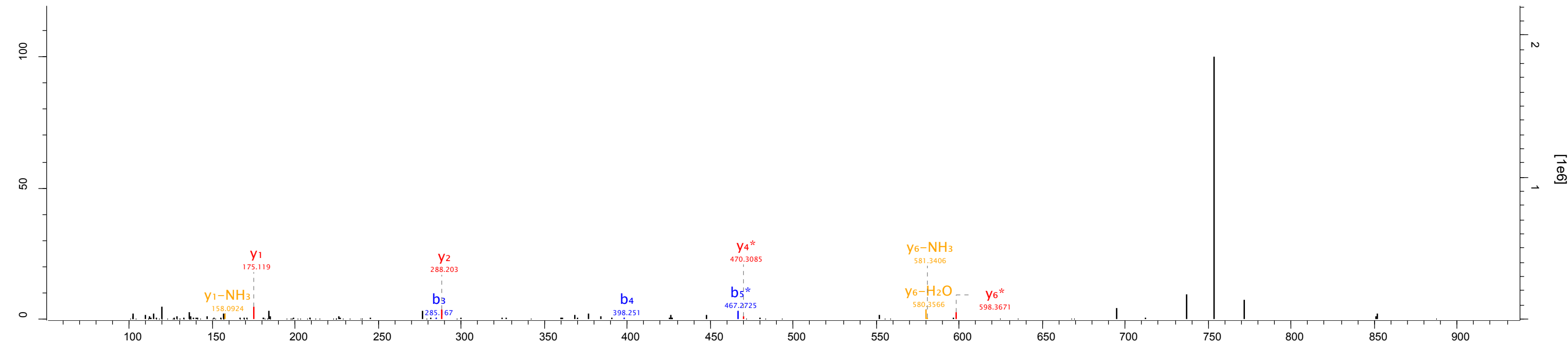
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 Scan: 6093 Method: FTMS; HCD Score: 40.28 m/z: 589.26 Gene names: E2F8



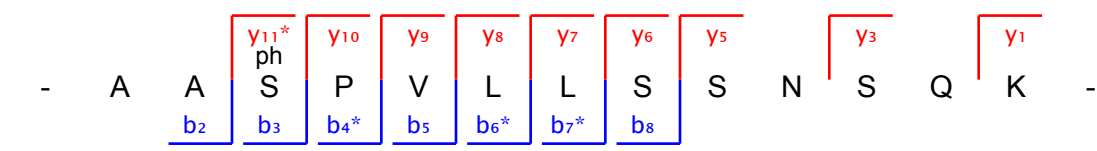
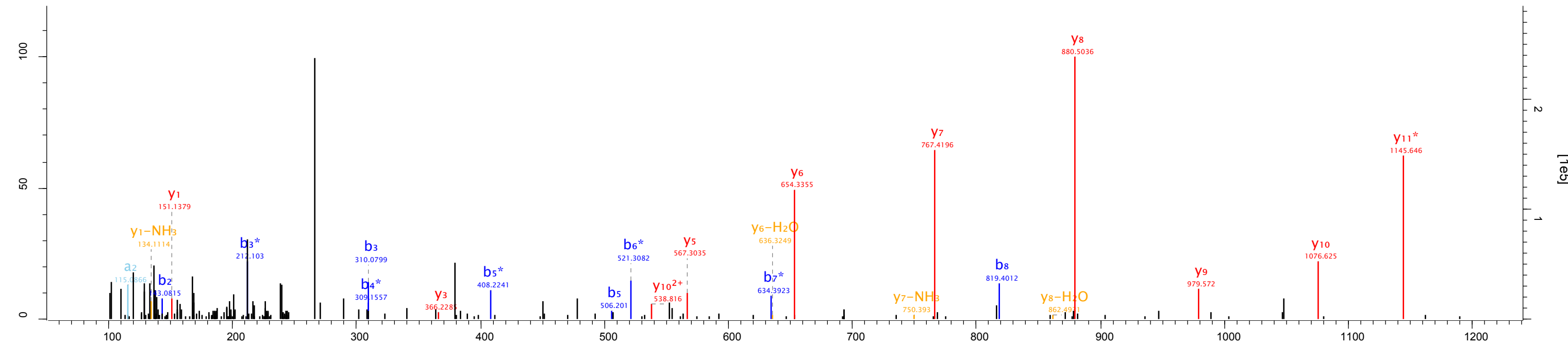
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 Scan: 6053 Method: FTMS; HCD Score: 84.97 m/z: 841.35 Gene names: YAF2



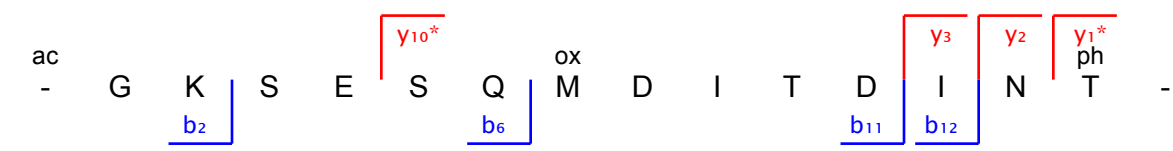
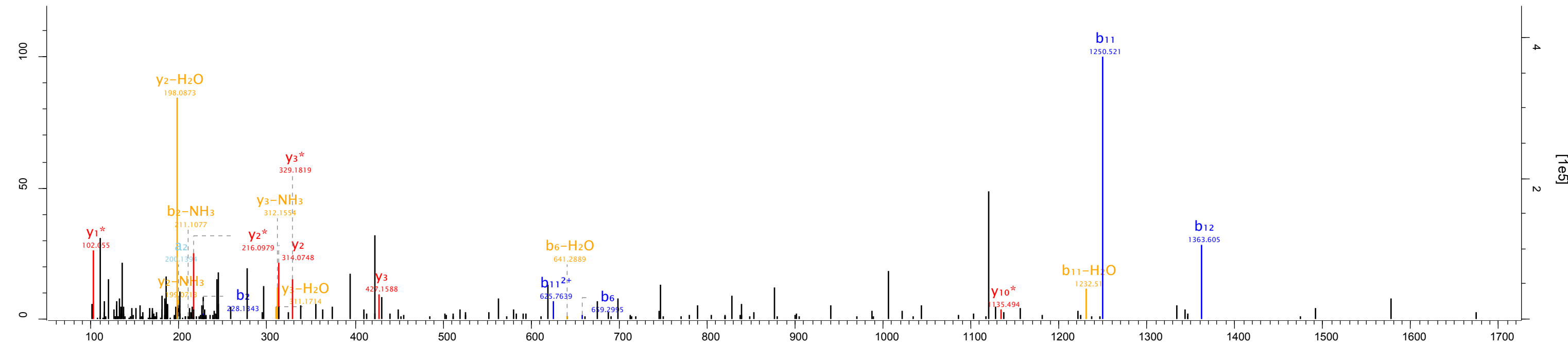
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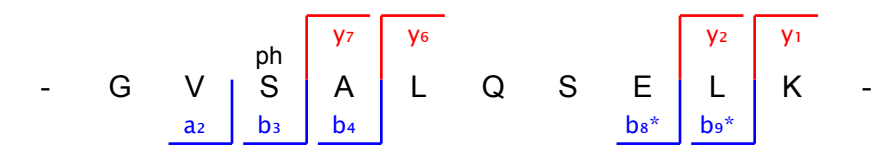
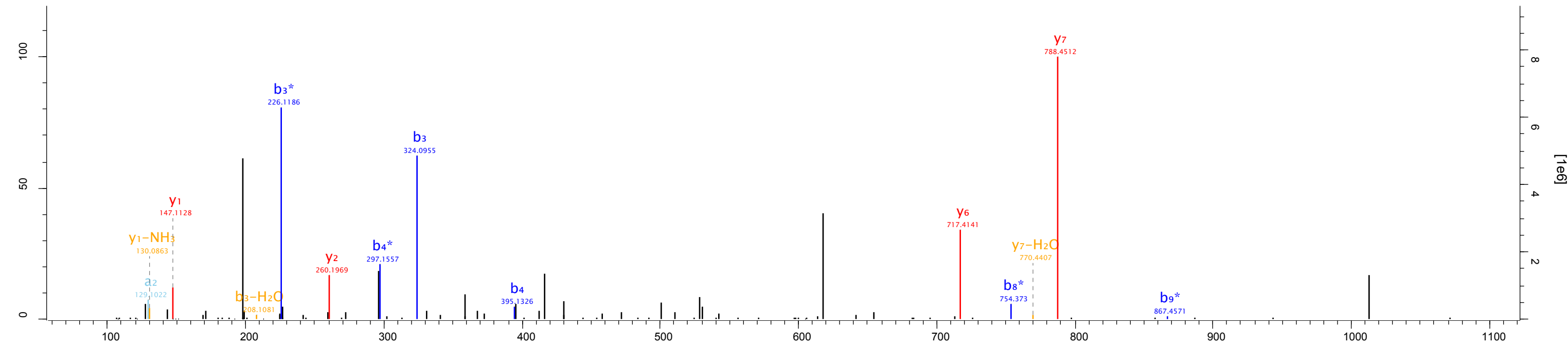
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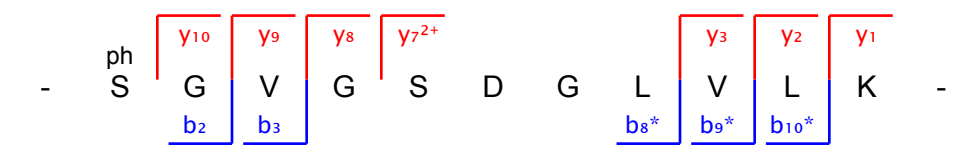
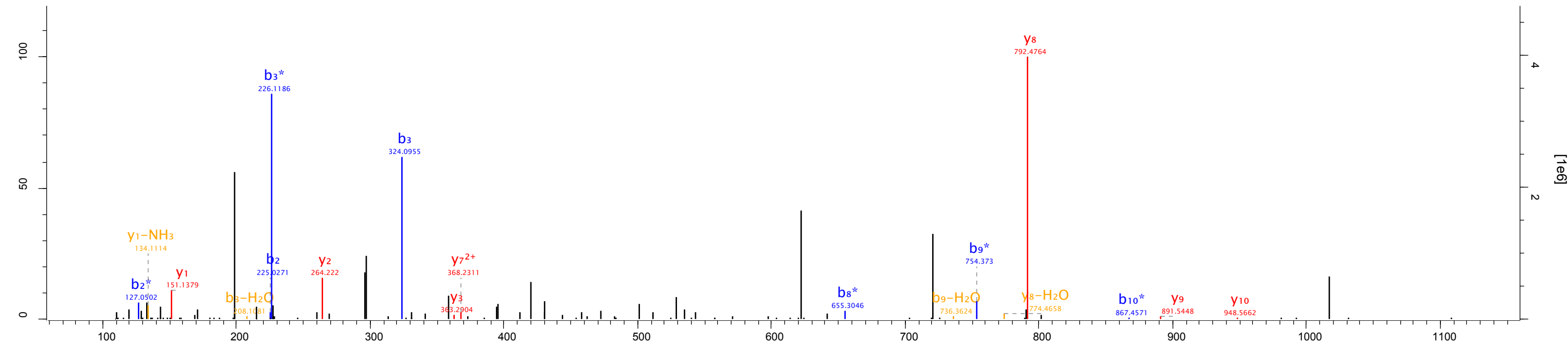
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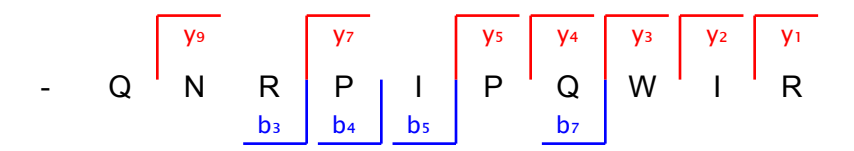
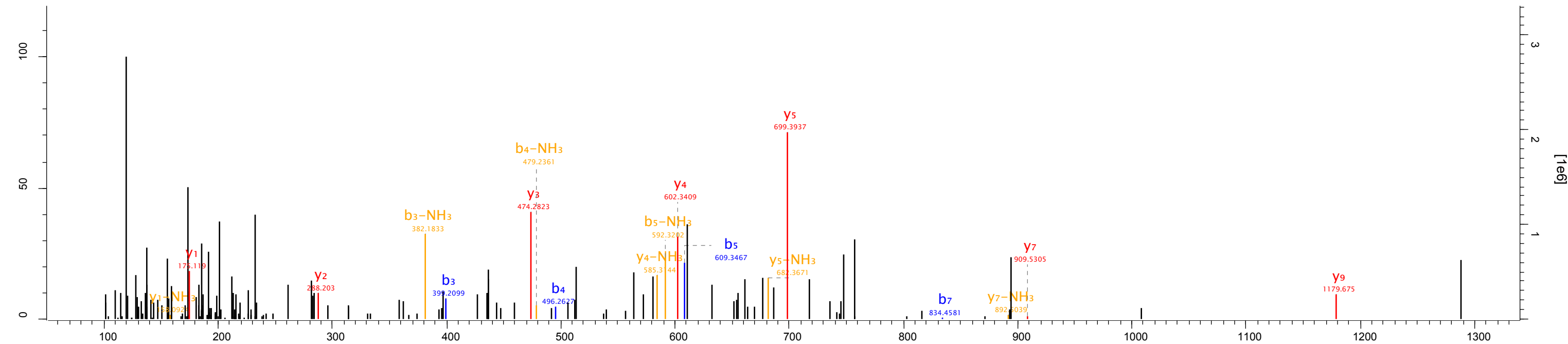
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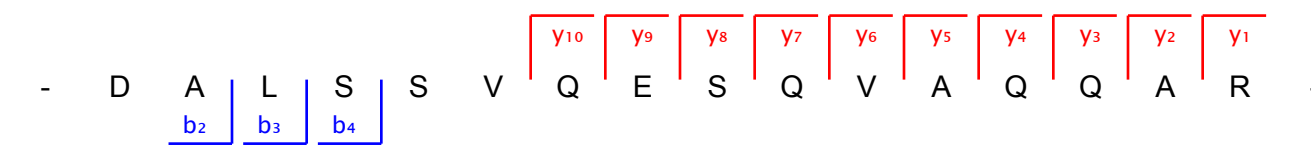
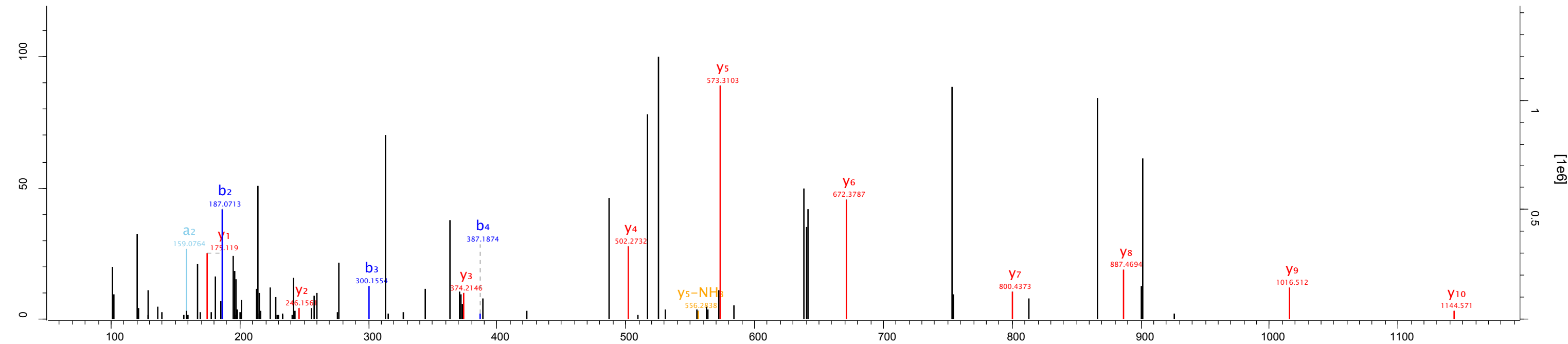


Raw file Scan Method Score m/z Gene names
 20150822_A375SR-Proteome_BR3 45023 FTMS; HCD 78.94 436.58 RPL39P5;RPL39



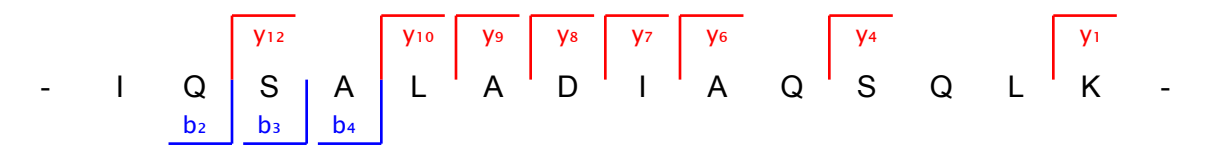
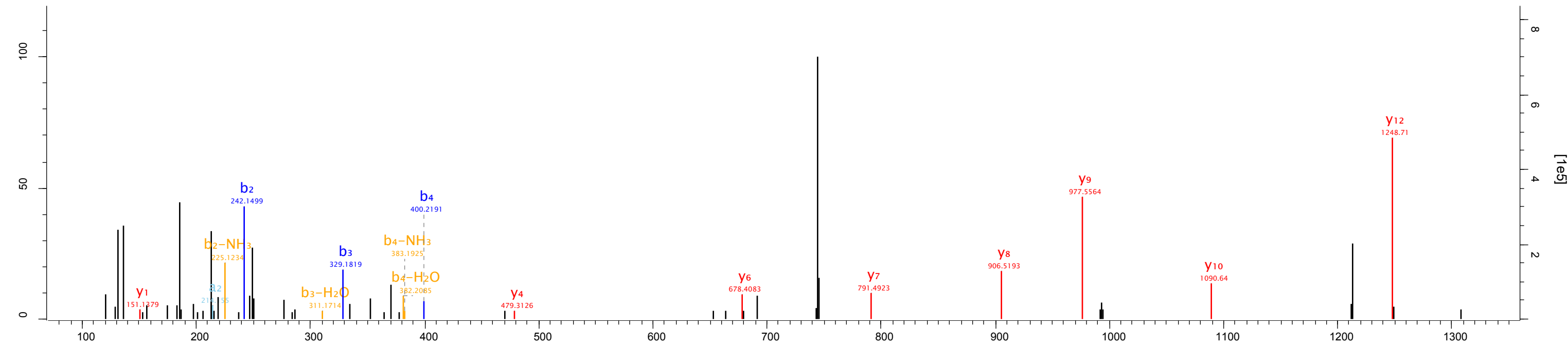
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20180707_MaS_A375SR_LM_proteome_01

Scan 12923 Method FTMS; HCD Score 34.39 m/z 572.96 Gene names APOC3



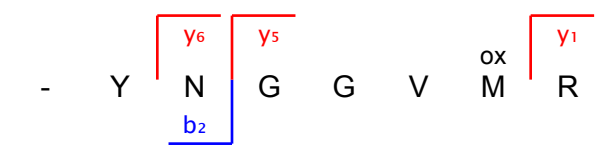
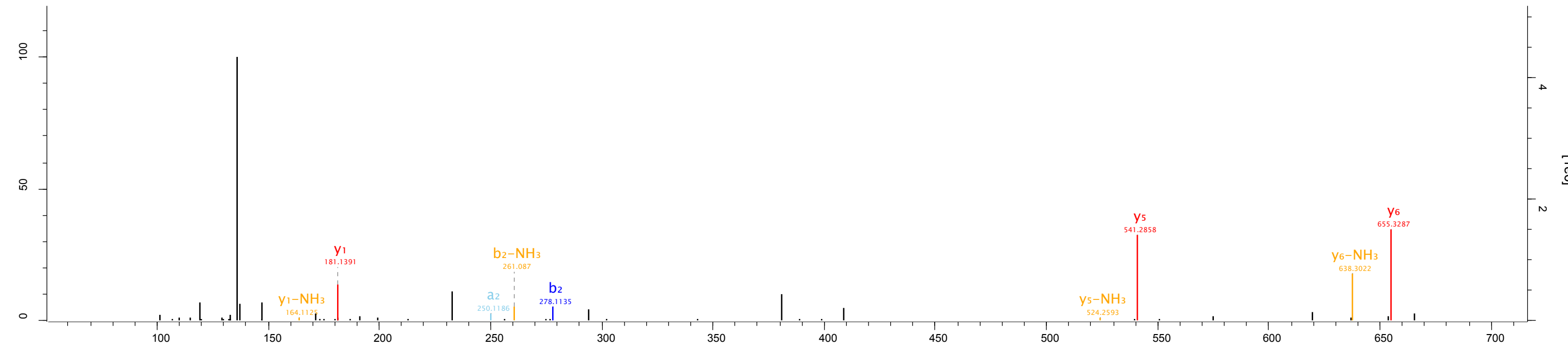
Raw file
20180707_MaS_A375SR_LM_proteome_01

Scan: 20823
Method: FTMS; HCD
Score: 52.53
m/z: 745.93
Gene names: MED21



Raw file
20180707_MaS_A375SR_LM_proteome_01

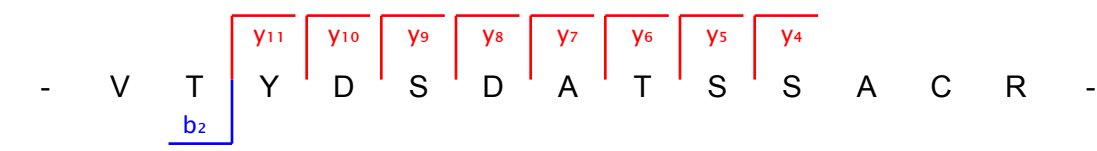
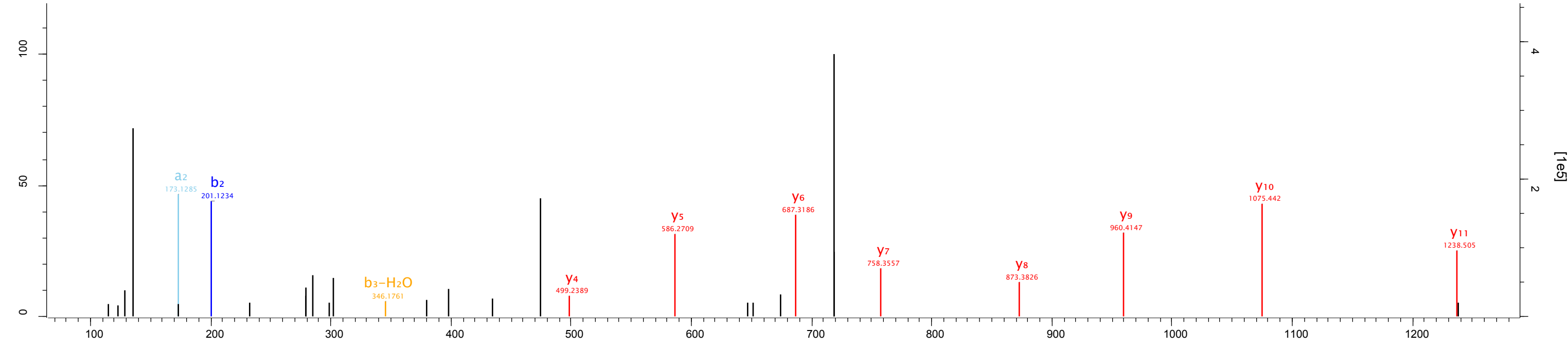
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5033	FTMS; HCD	59.64	409.7	KCNN2



Raw file

20180707_MaS_A375SR_LM_proteome_06

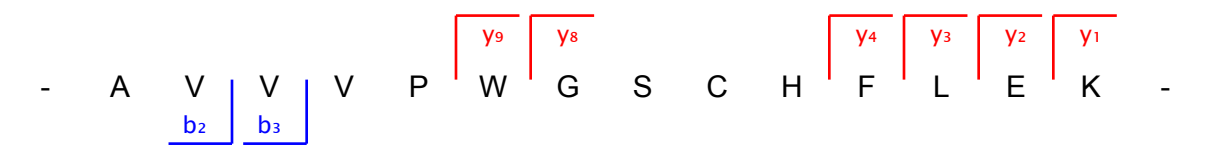
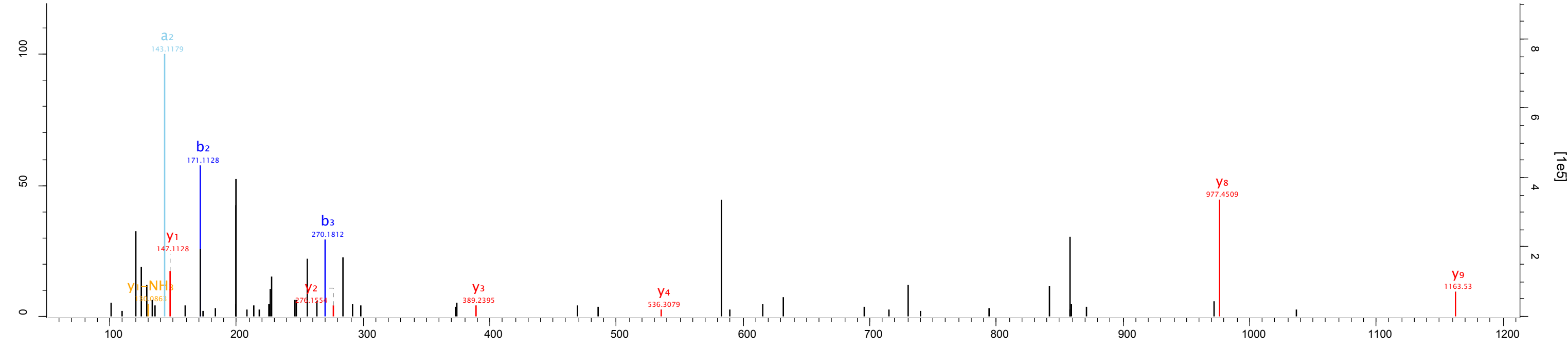
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6813	FTMS; HCD	42.32	719.81	LEPROT



Raw file

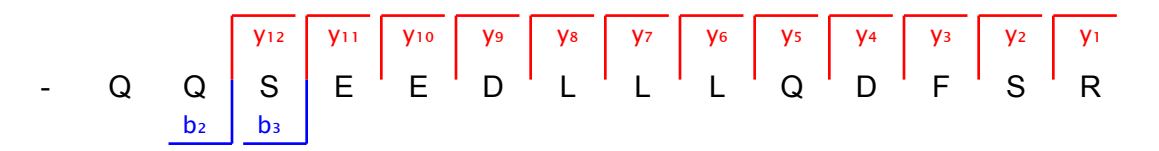
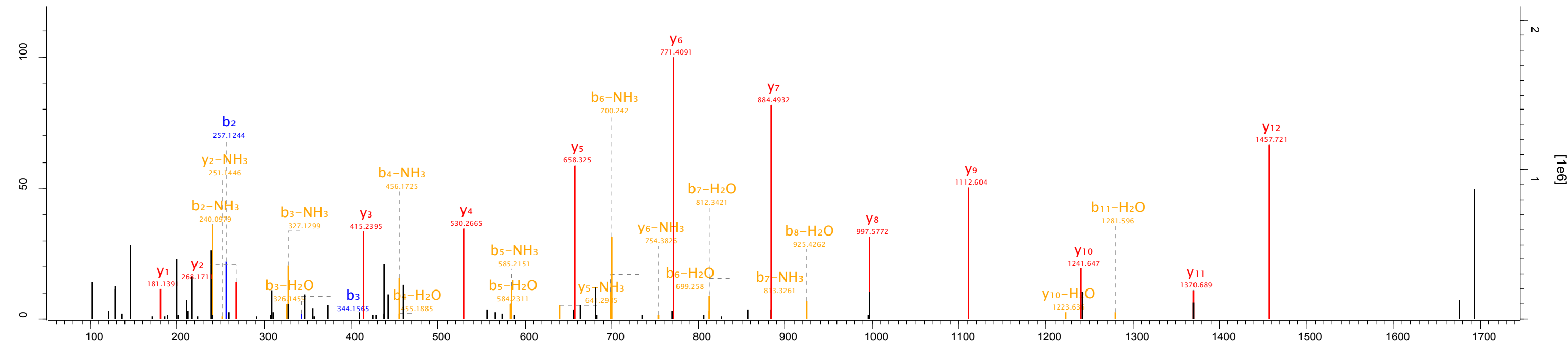
20180707_MaS_A375SR_LM_proteome_07

Scan	Method	Score	m/z	Gene names
24313	FTMS; HCD	17.25	543.61	SPPL2A

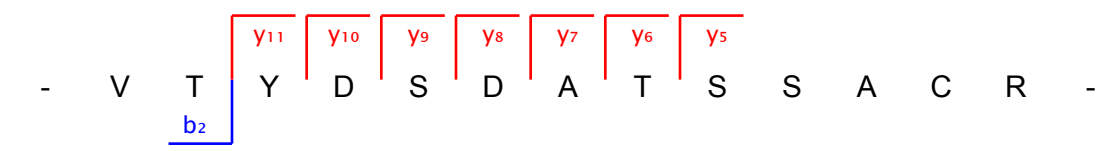
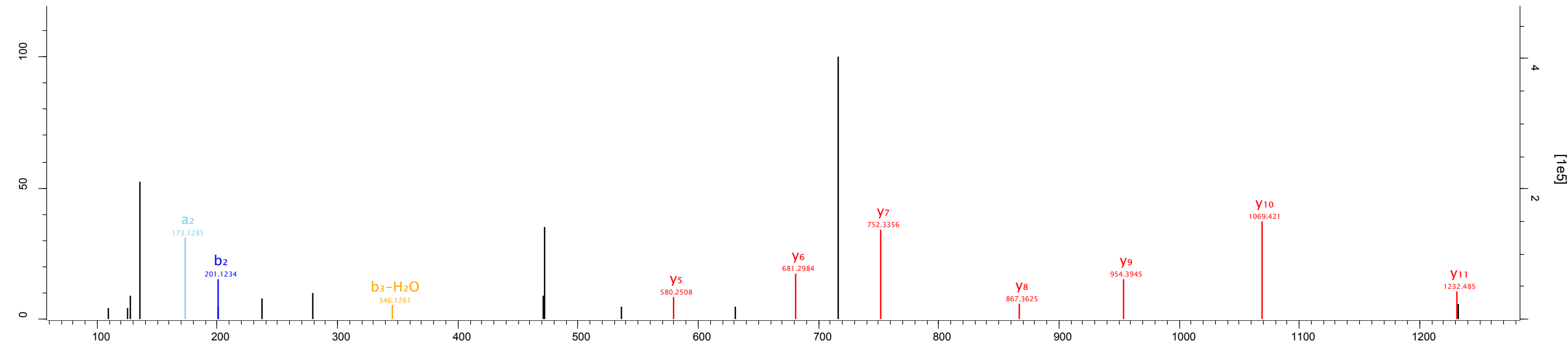


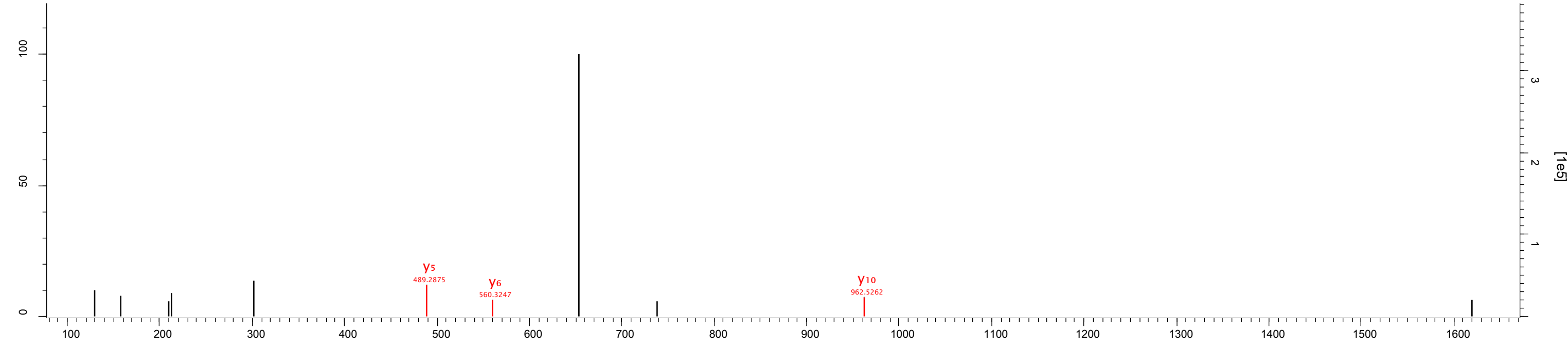
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20180707_MaS_A375SR_LM_proteome_07

Scan 26923 Method FTMS; HCD Score 75.32 m/z 857.42 Gene names SSR3



Raw file 20180707_MaS_A375SR_LM_proteome_07 Scan 6713 Method FTMS; HCD Score 36.29 m/z 716.8 Gene names LEPROT





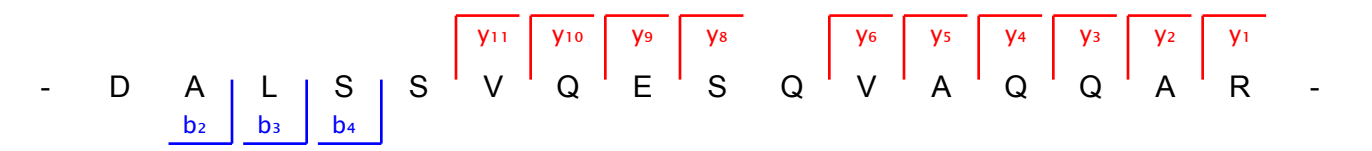
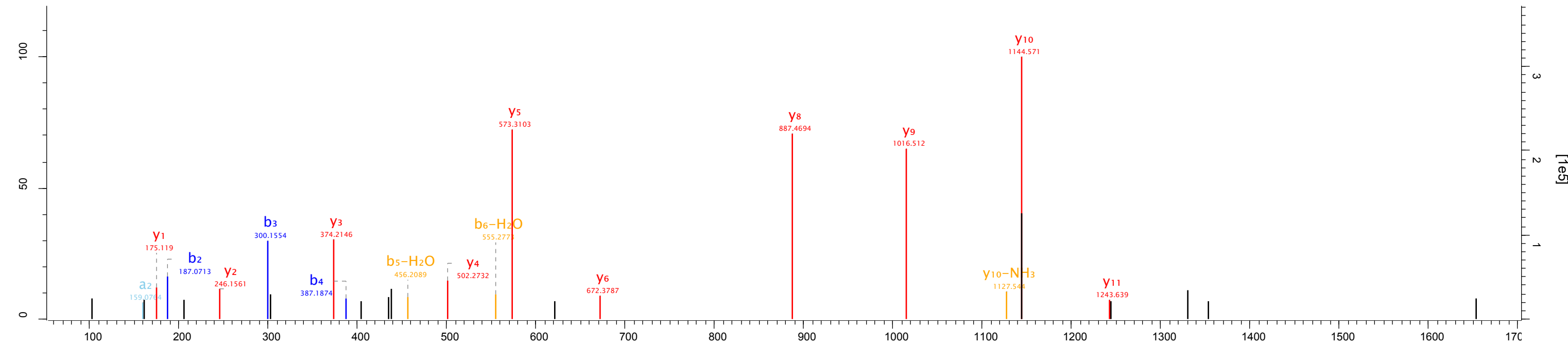
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y10

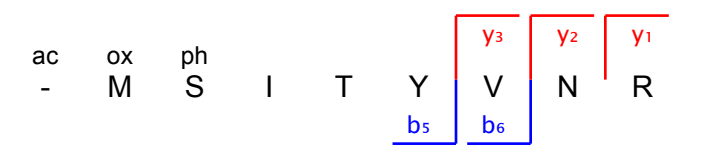
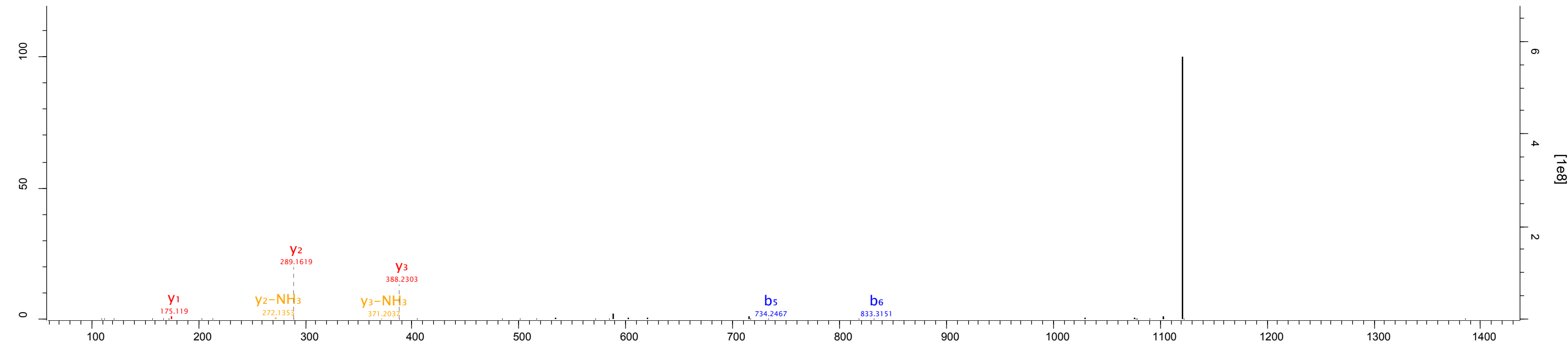
y6

y5

Raw file 20180707_MaS_A375SR_LM_proteome_16 Scan 12883 Method FTMS; HCD Score 55.01 m/z 859.43 Gene names APOC3

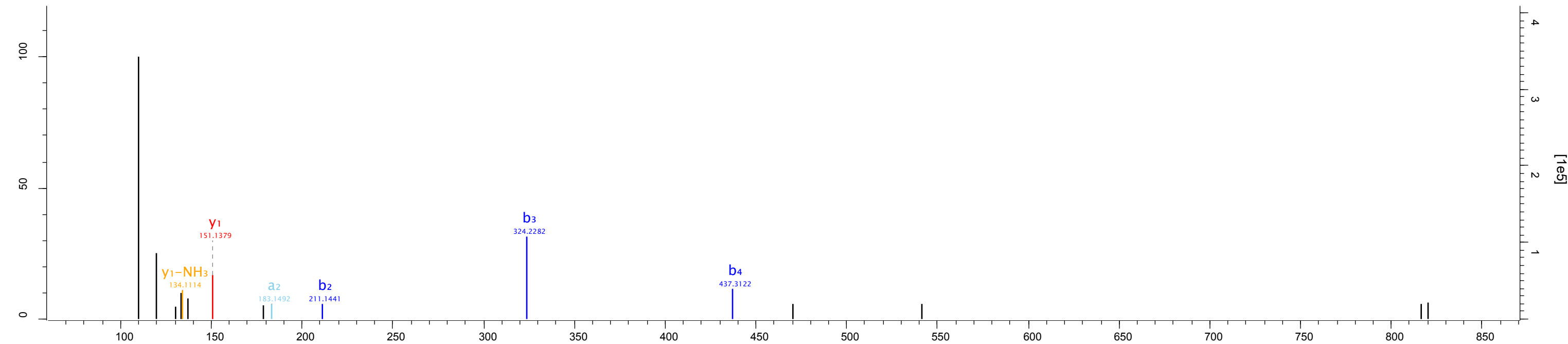


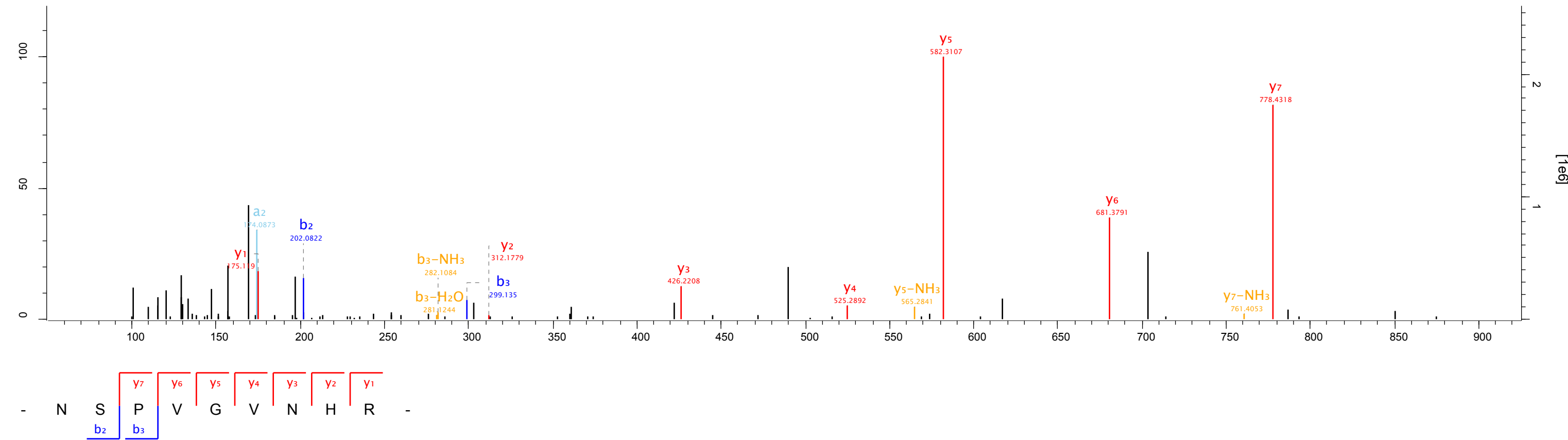
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Raw file
20180707_MaS_A375SR_LM_proteome_19

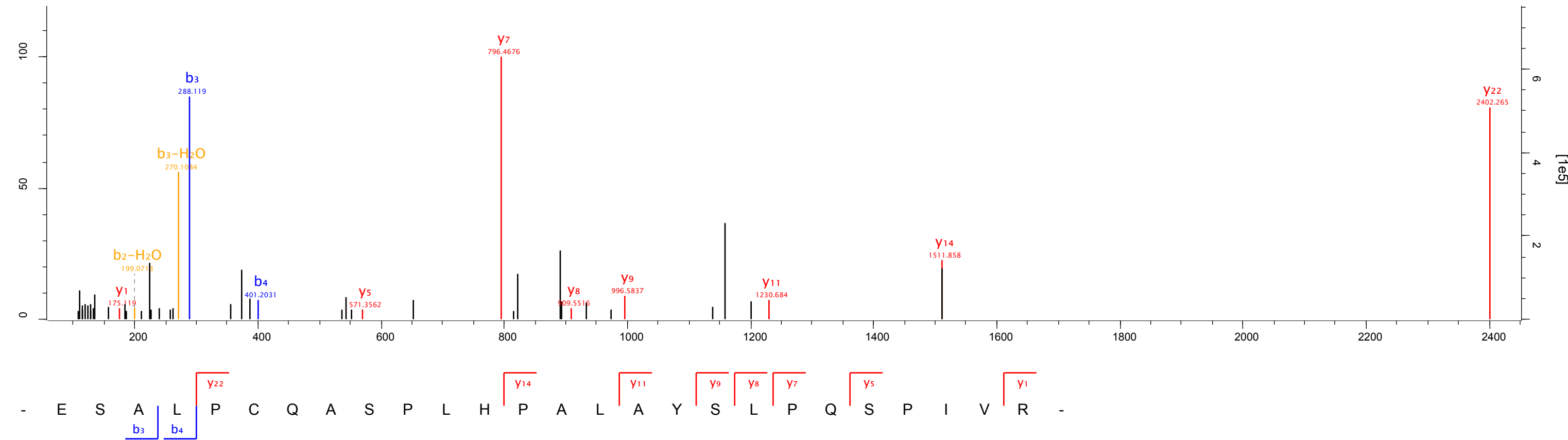
Scan	Method	Score	m/z	Gene names
24333	FTMS; HCD	11.58	486.29	IL1R1





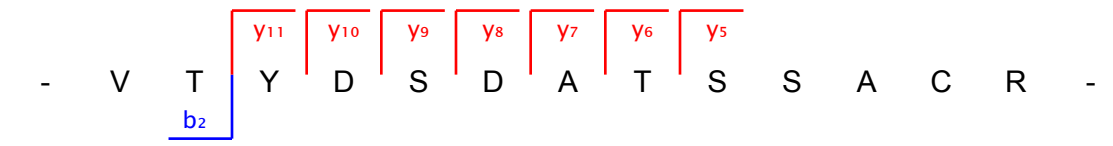
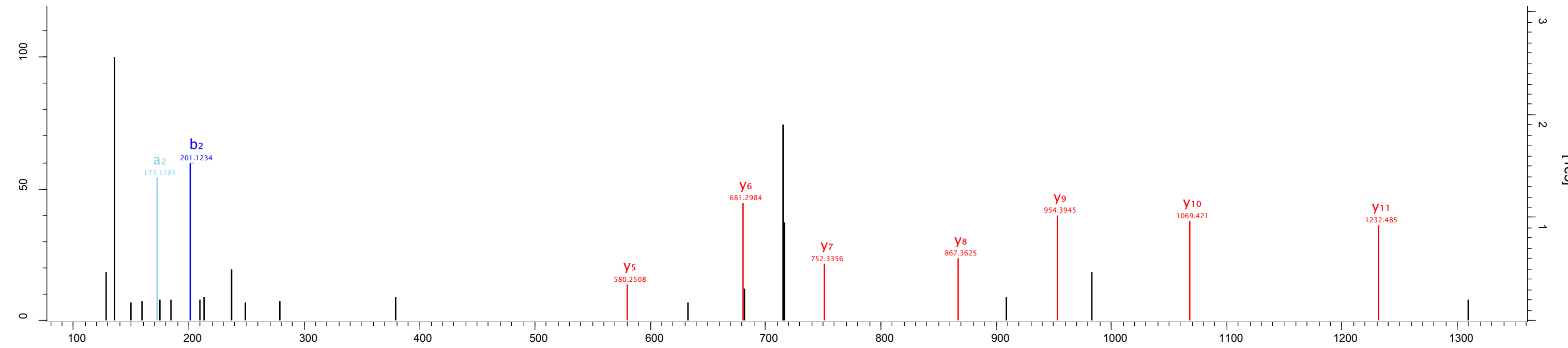
Raw file
20180707_MaS_A375SR_LM_proteome_21

Scan: 26743
Method: FTMS; HCD
Score: 15.52
m/z: 935.16
Gene names: C1orf85



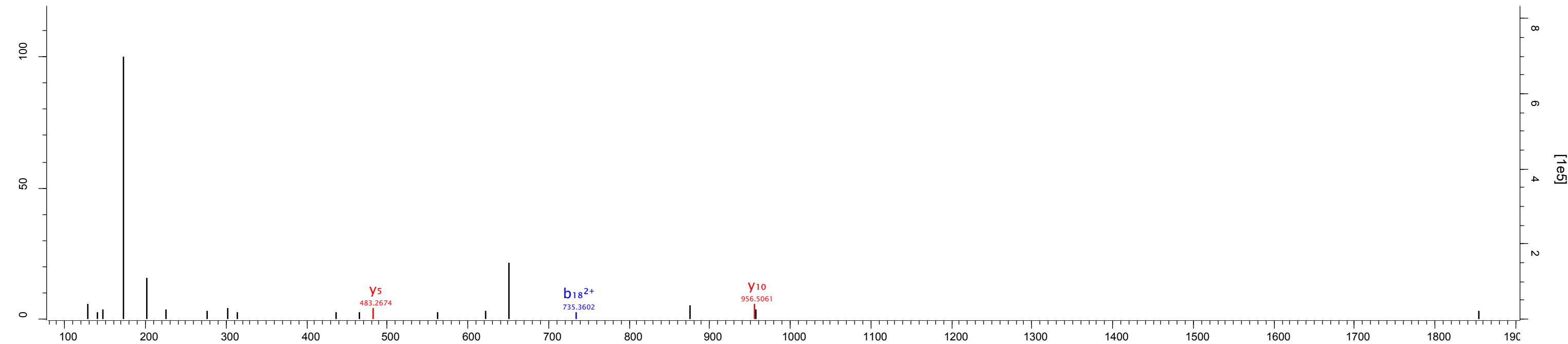
Raw file
20180707_MaS_A375SR_LM_proteome_22

Scan Method Score m/z Gene names
6863 FTMS; HCD 36.29 716.8 LEPROT



Raw file
20180707_MaS_A375SR_LM_proteome_22

Scan	Method	Score	m/z	Gene names
9183	FTMS; HCD	2.04	651.33	LAGE3



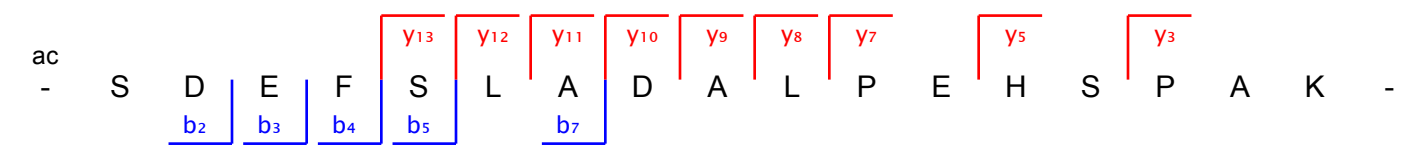
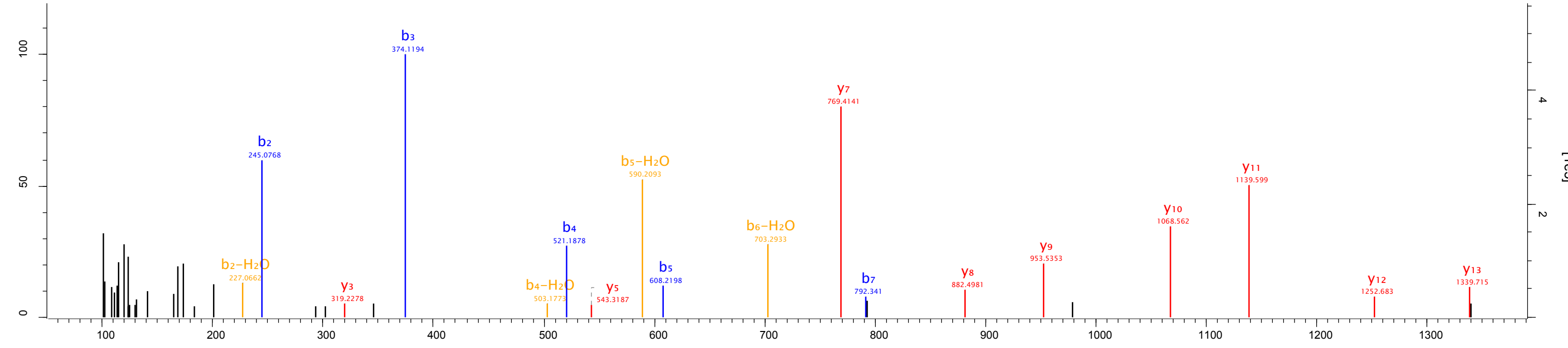
- G G V D T A A A P A G G A P P A H A P G P G R -

Annotations on the peptide sequence:
- y10 (red bracket) spans from the 13th residue (A) to the 18th residue (P).
- b18²⁺ (blue bracket) spans from the 13th residue (A) to the 18th residue (P).
- y5 (red bracket) spans from the 18th residue (P) to the 21st residue (G).

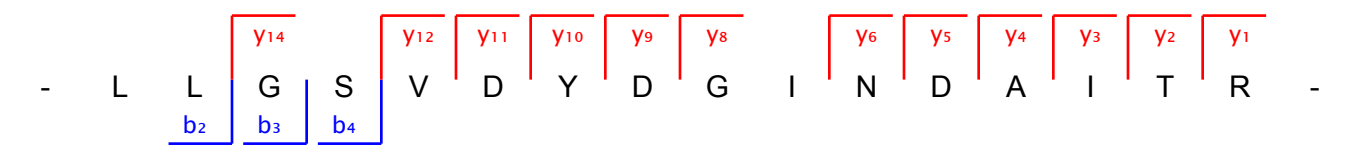
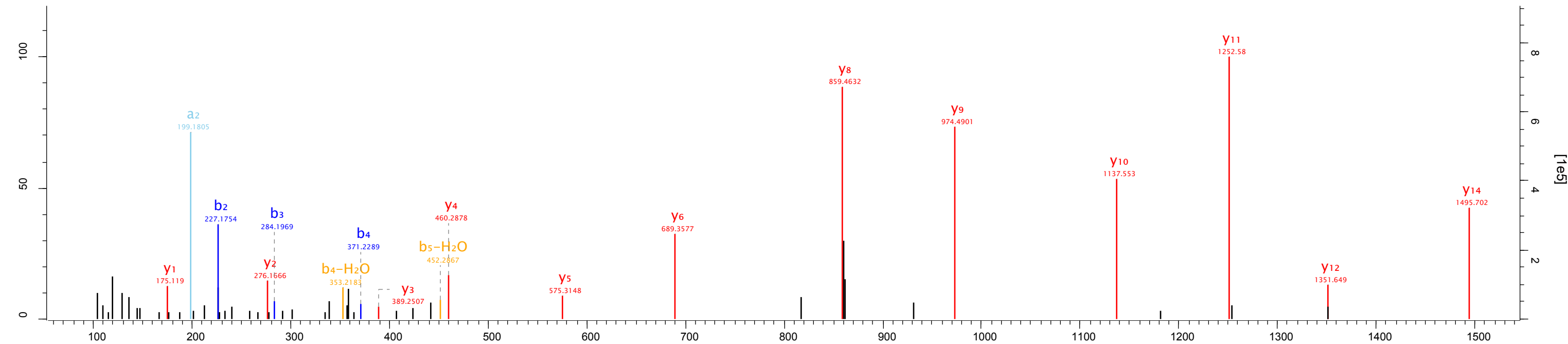
Raw file

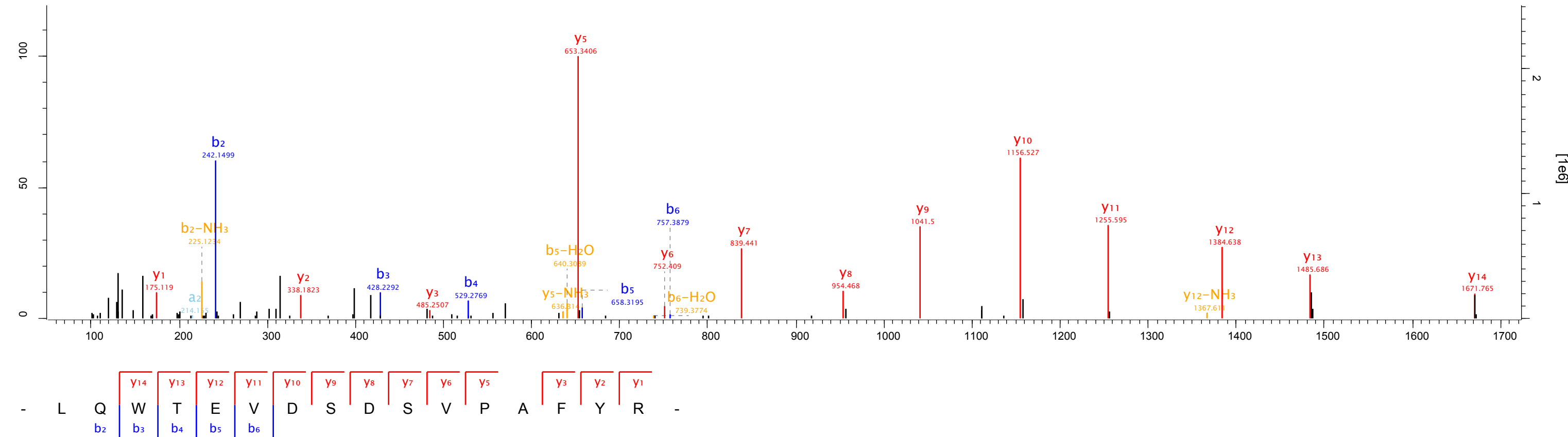
20180707_MaS_A375SR_LM_proteome_29

Scan	Method	Score	m/z	Gene names
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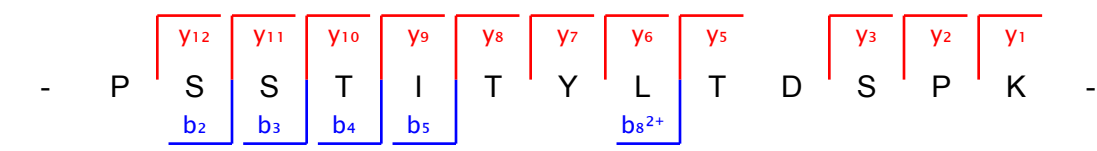
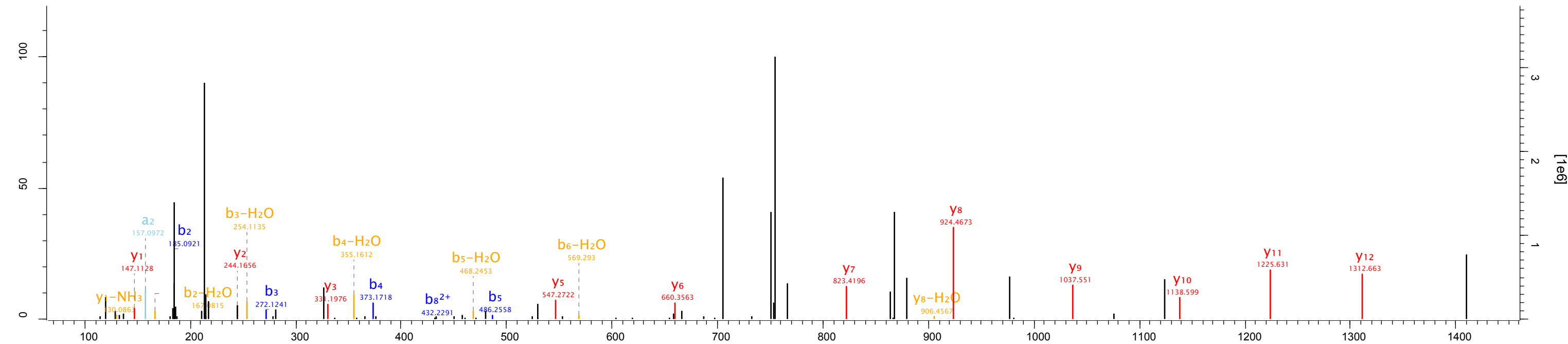


Raw file: 20180707_MaS_A375SR_ML_proteome_01
 Scan: 23163 Method: FTMS; HCD Score: 66.83 m/z: 861.94 Gene names: PIK3C2B

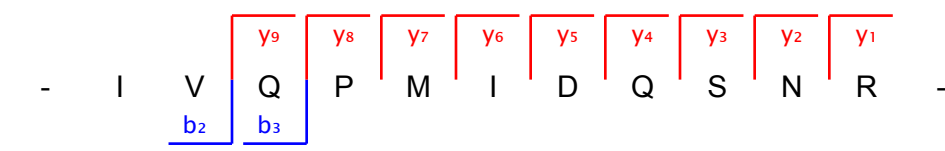
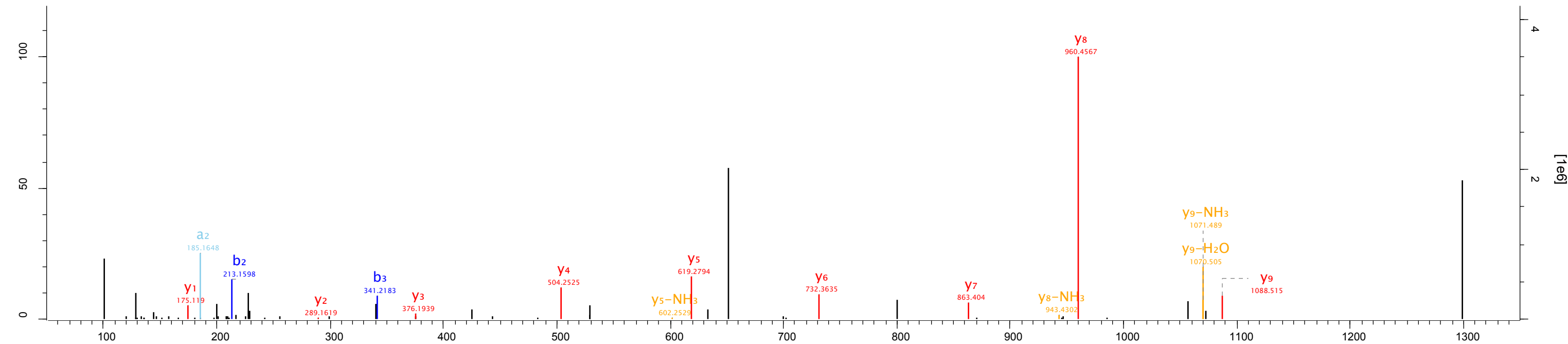




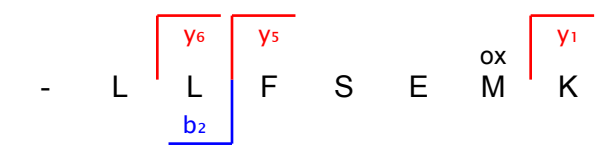
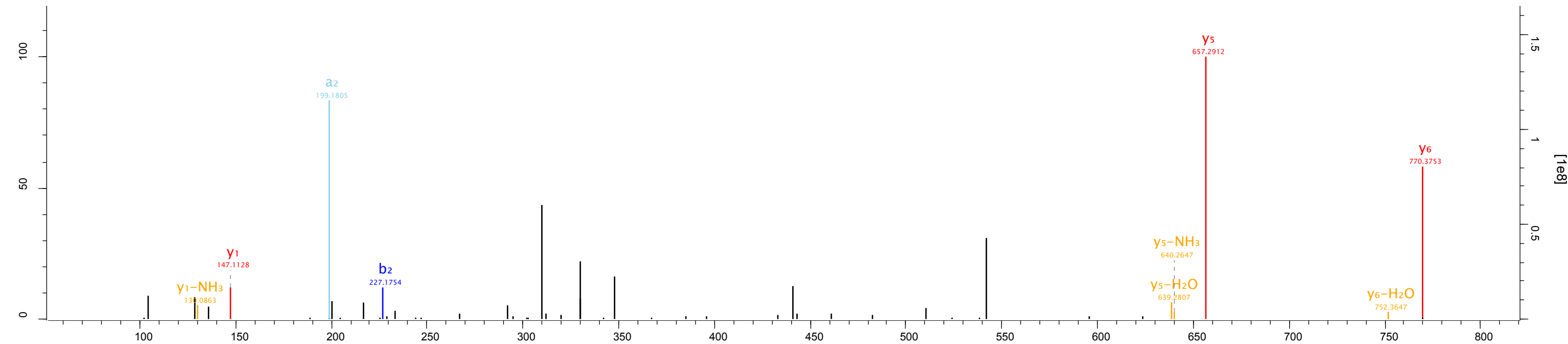
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Raw file: 20180707_MaS_A375SR_ML_proteome_03
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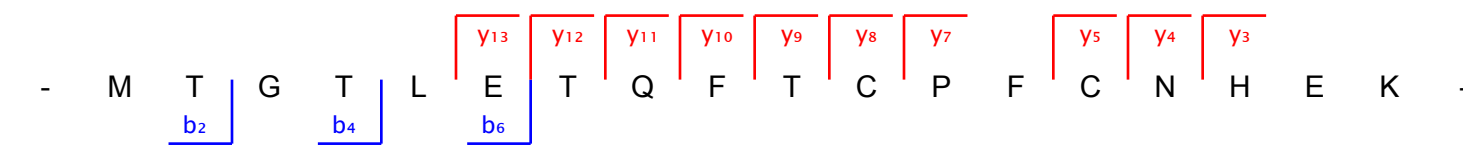
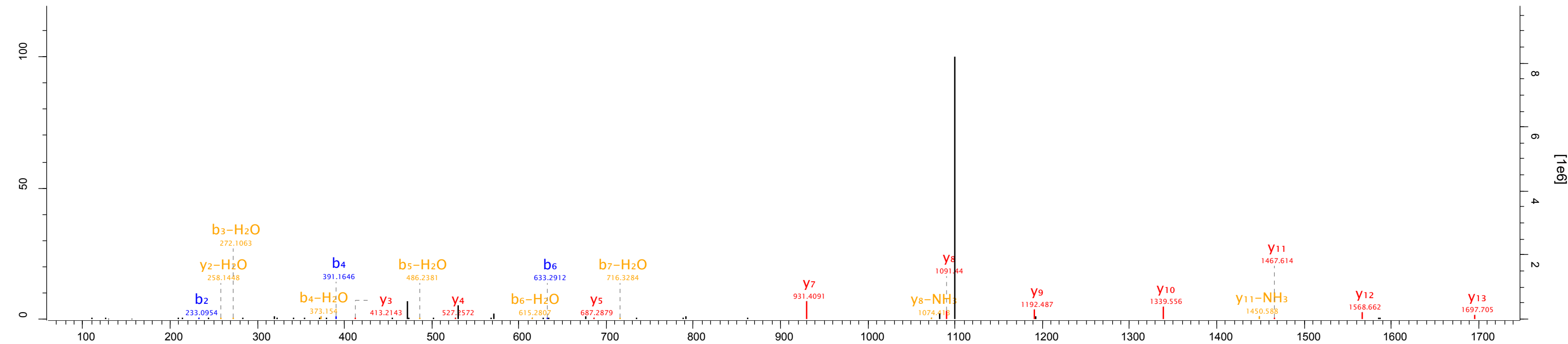


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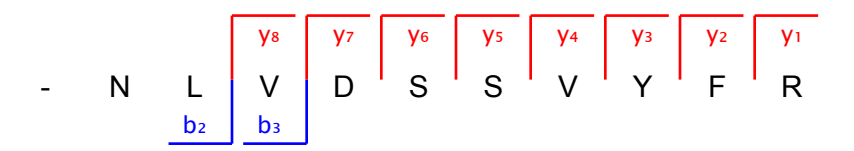
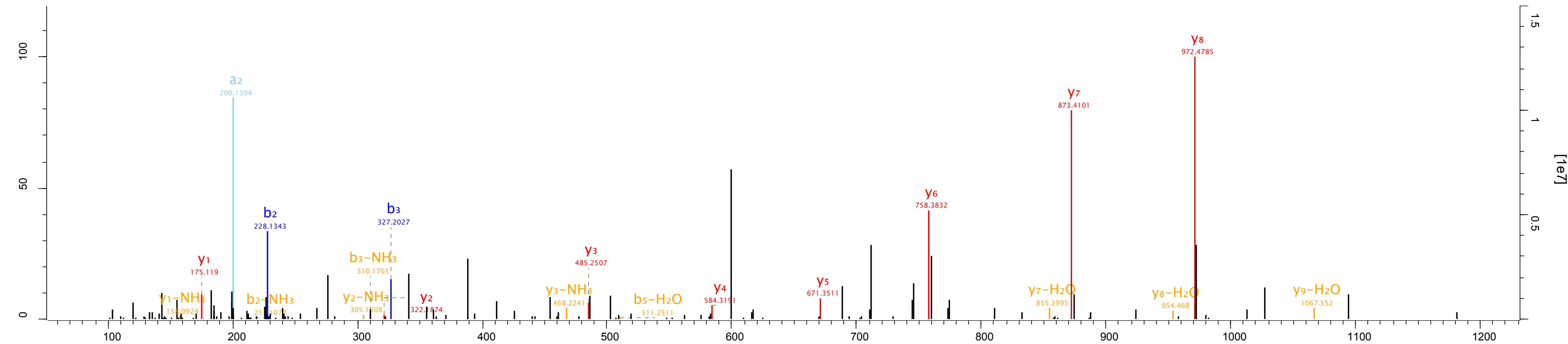


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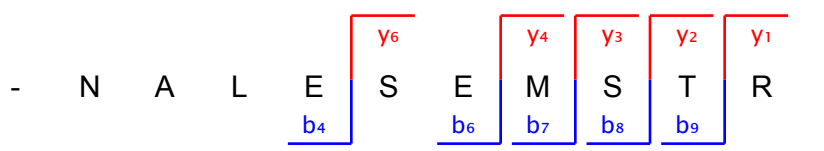
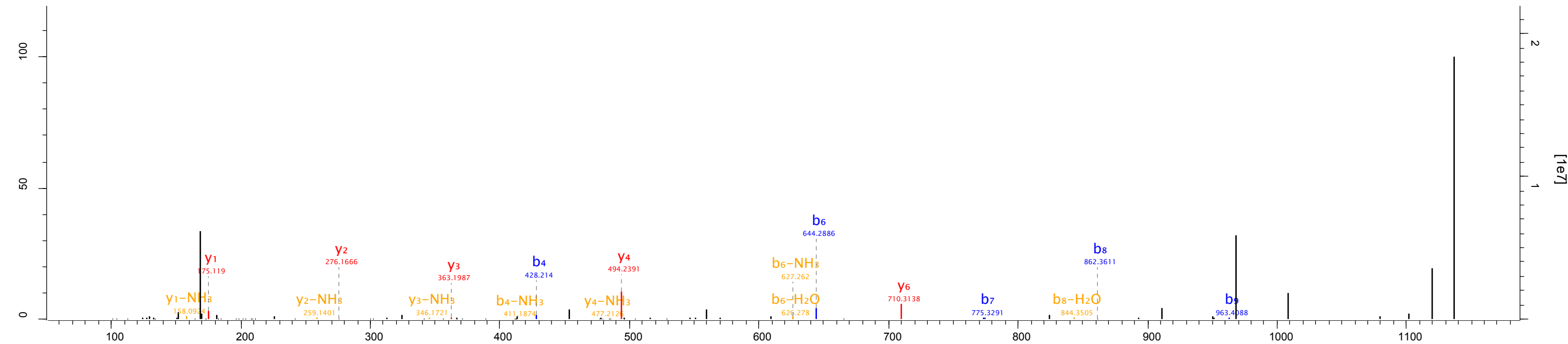
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20180707_MaS_A375SR_ML_proteome_04

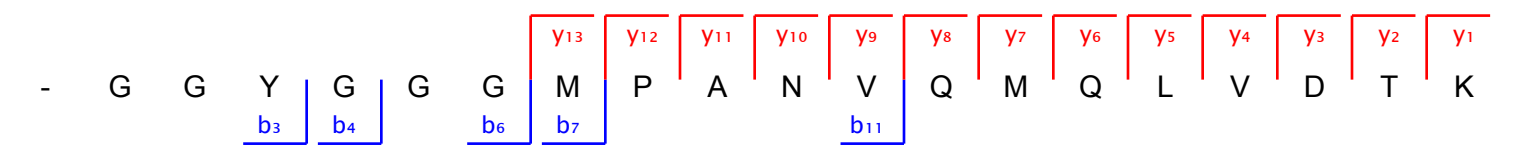
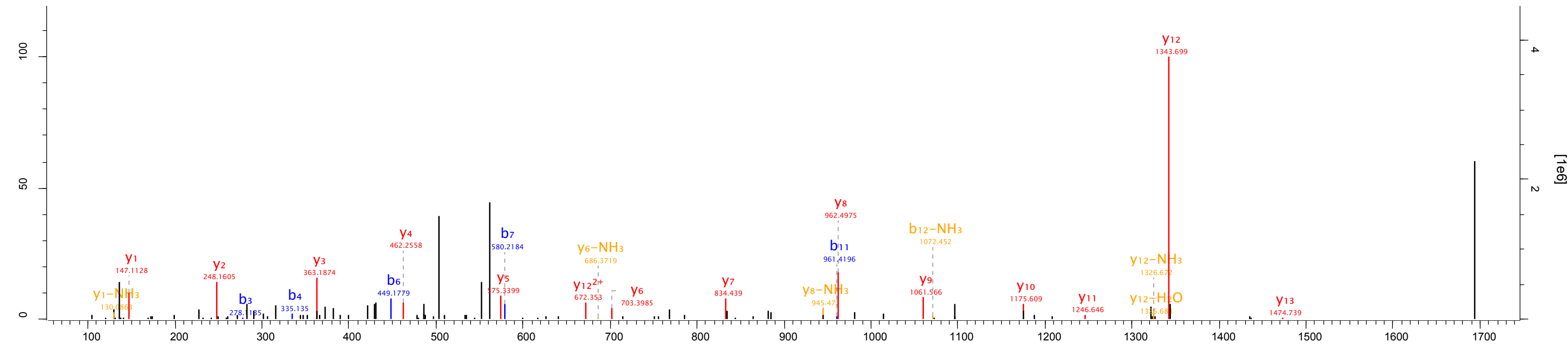


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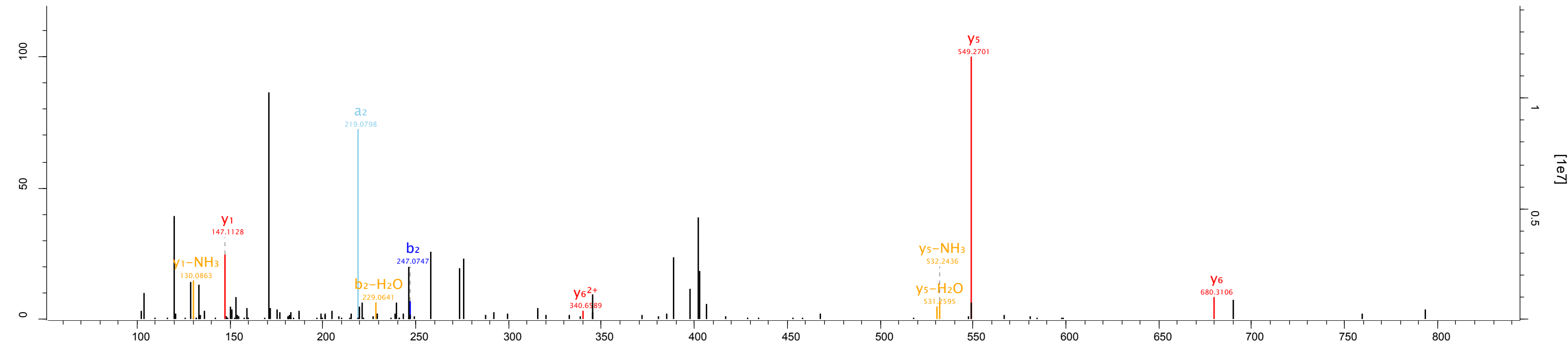


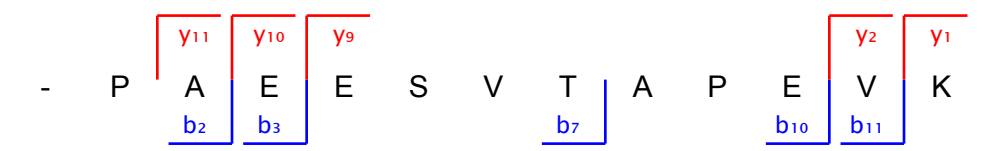
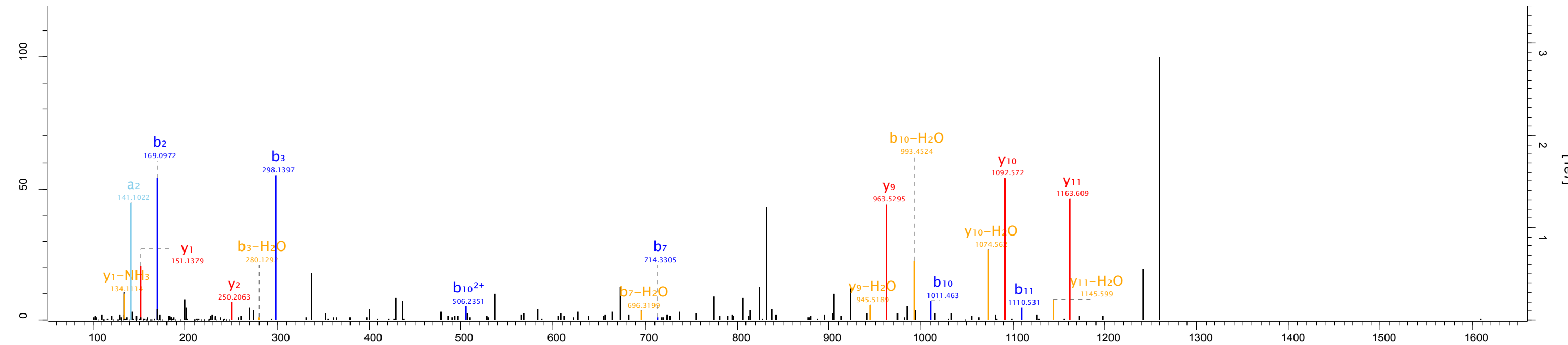
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Scan 23023 Method FTMS; HCD Score 95.41 m/z 962.46 Gene names CDC42SE2

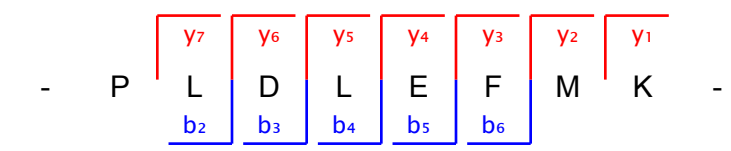
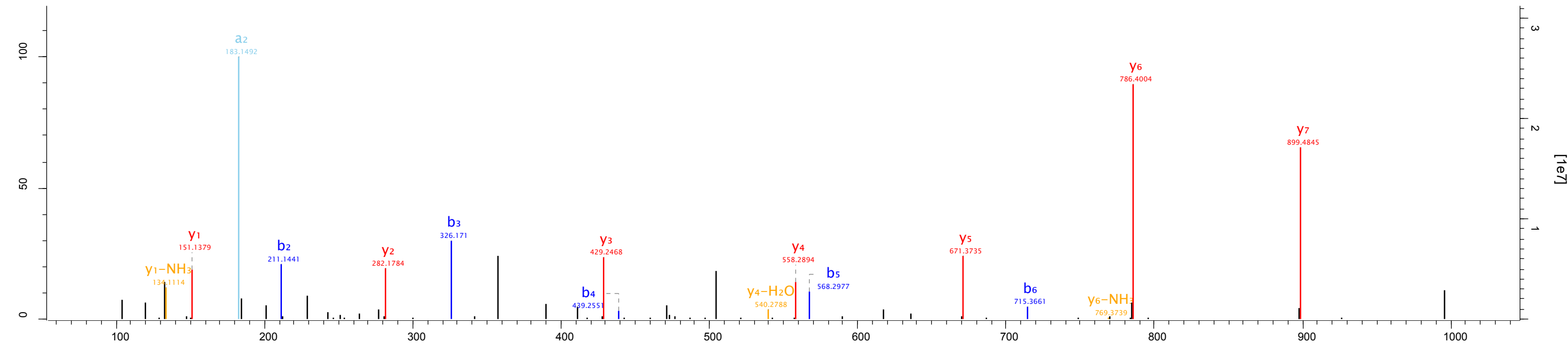


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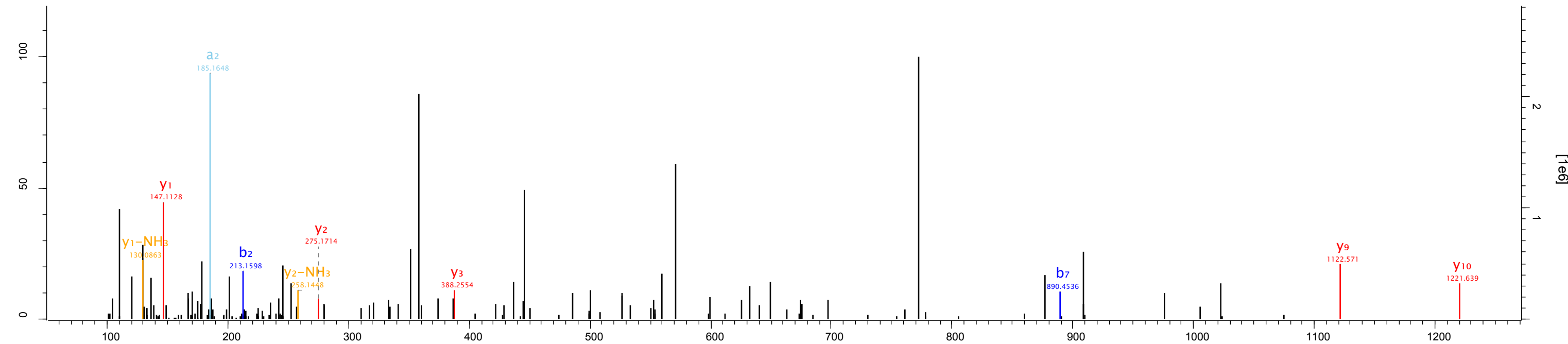


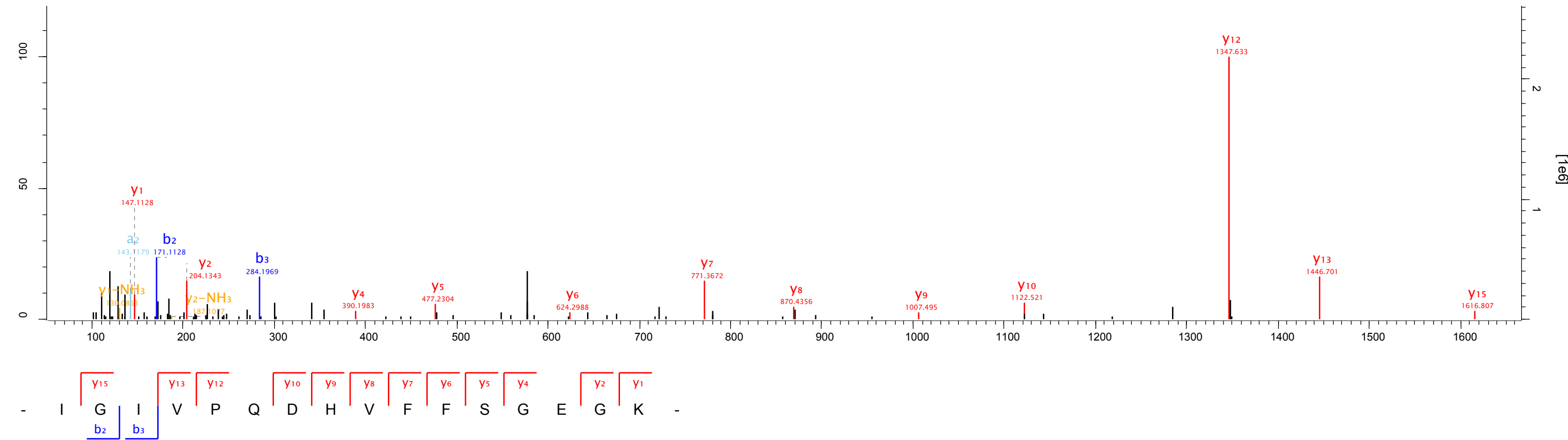
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Raw file
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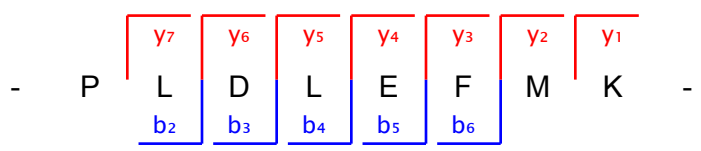
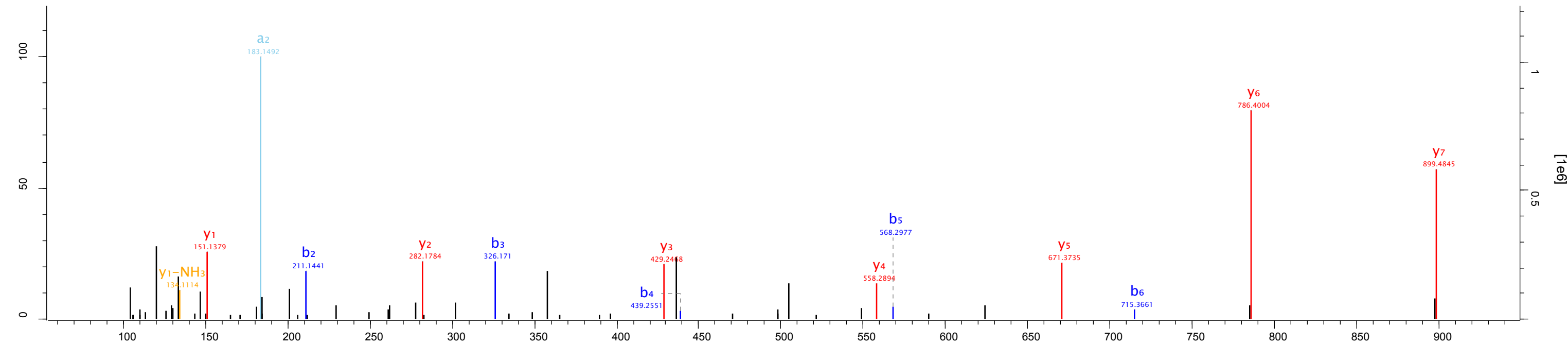
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m/z: 445.58
Gene names: GREB1L



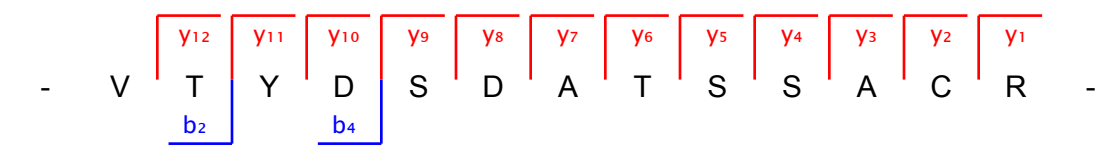
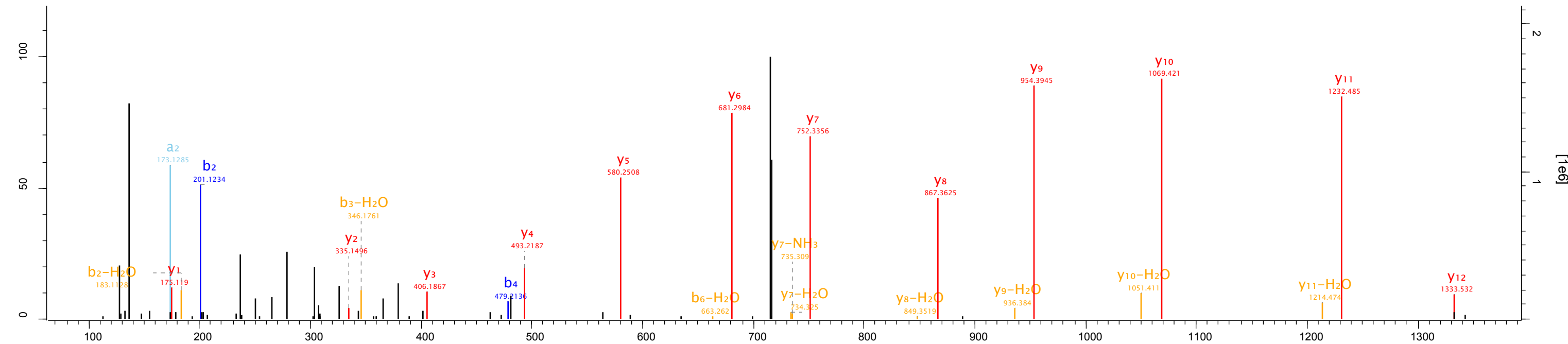


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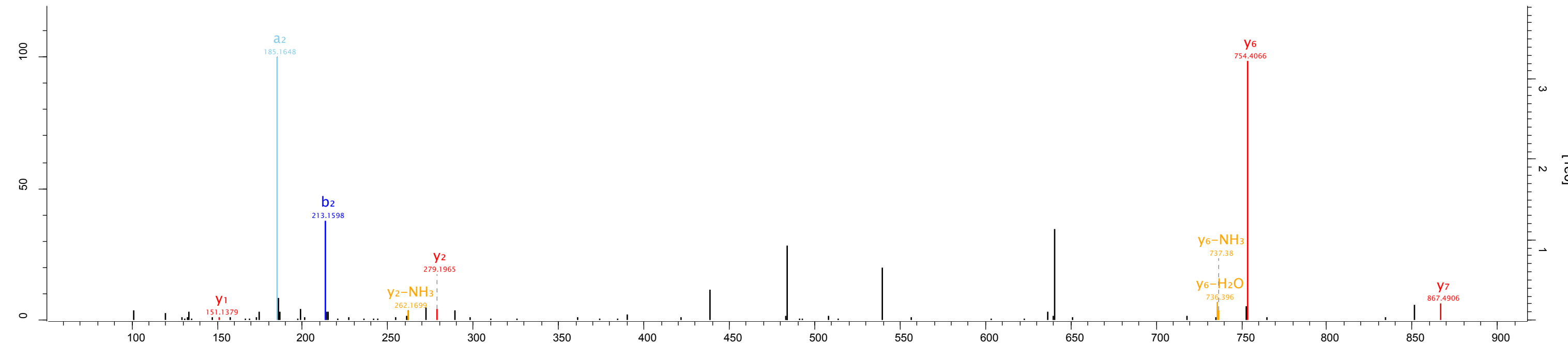
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Score: 97.43
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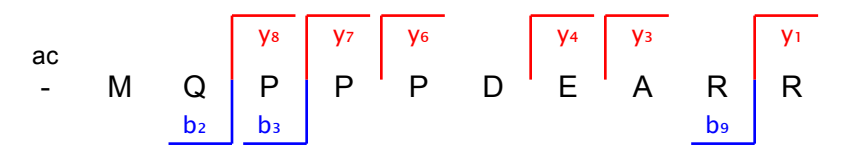
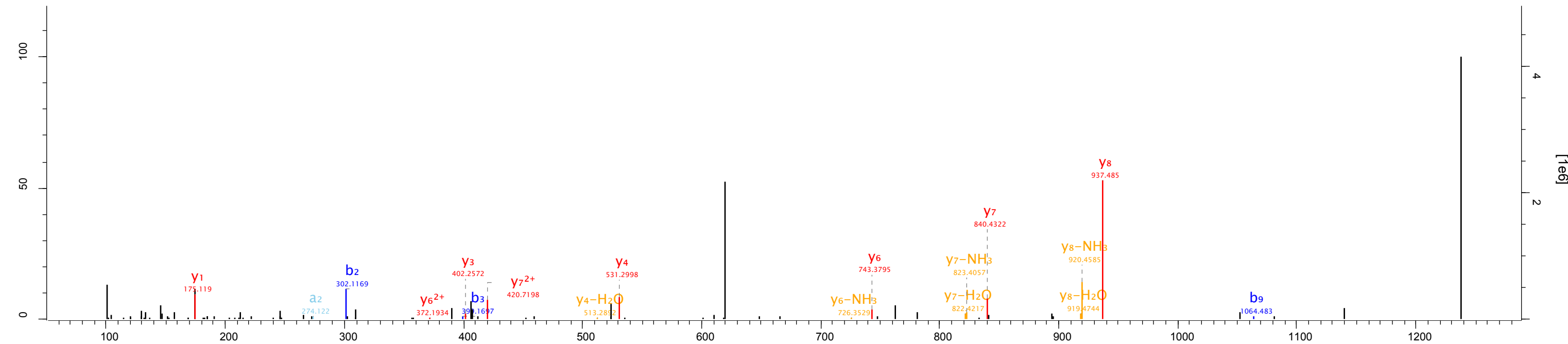


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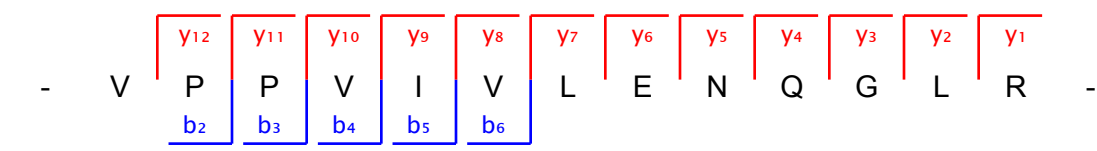
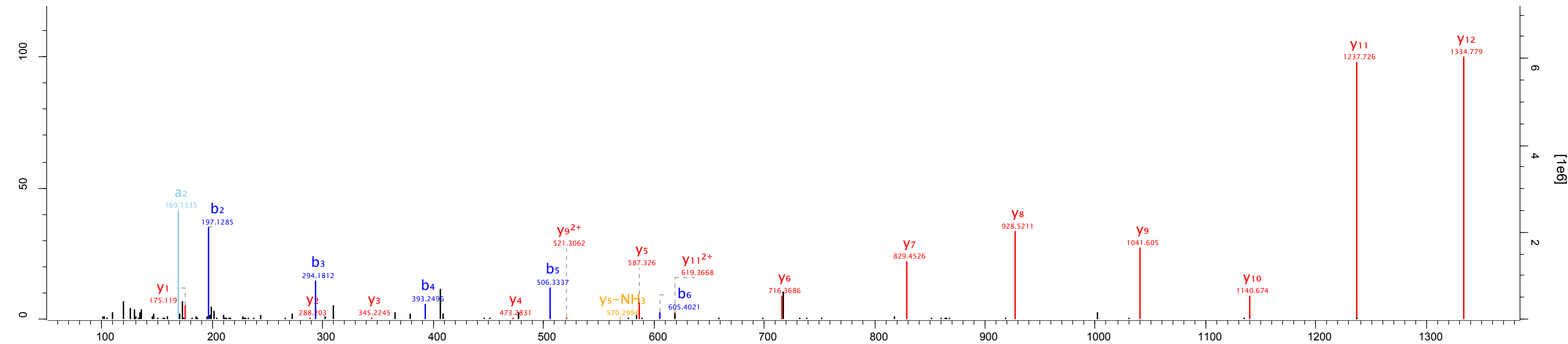


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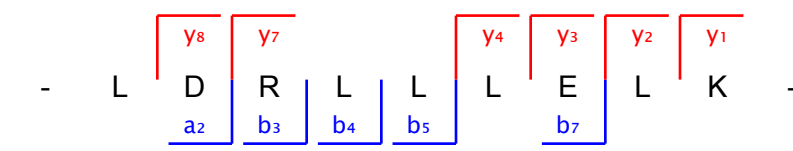
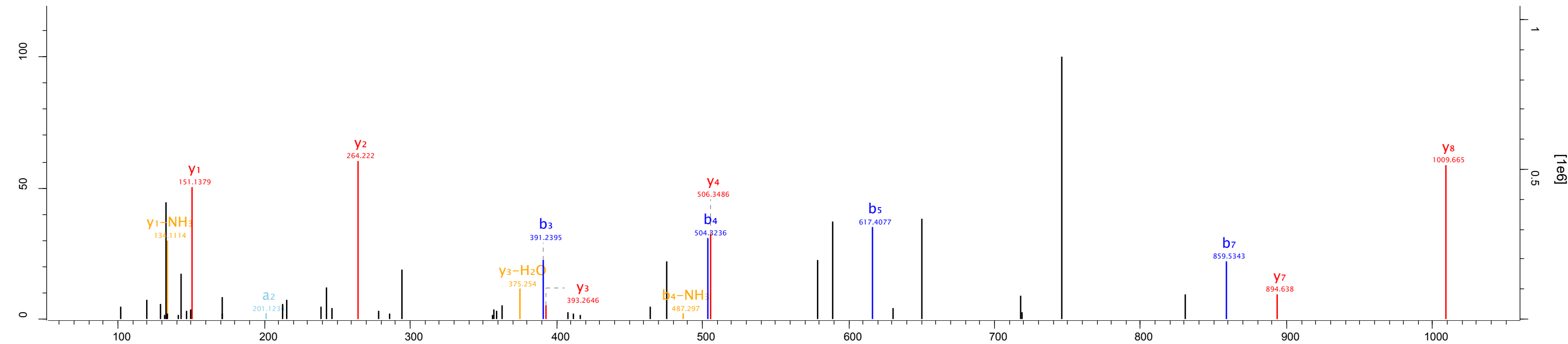
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8793 FTMS; HCD 94.41 619.8 SLC17A9

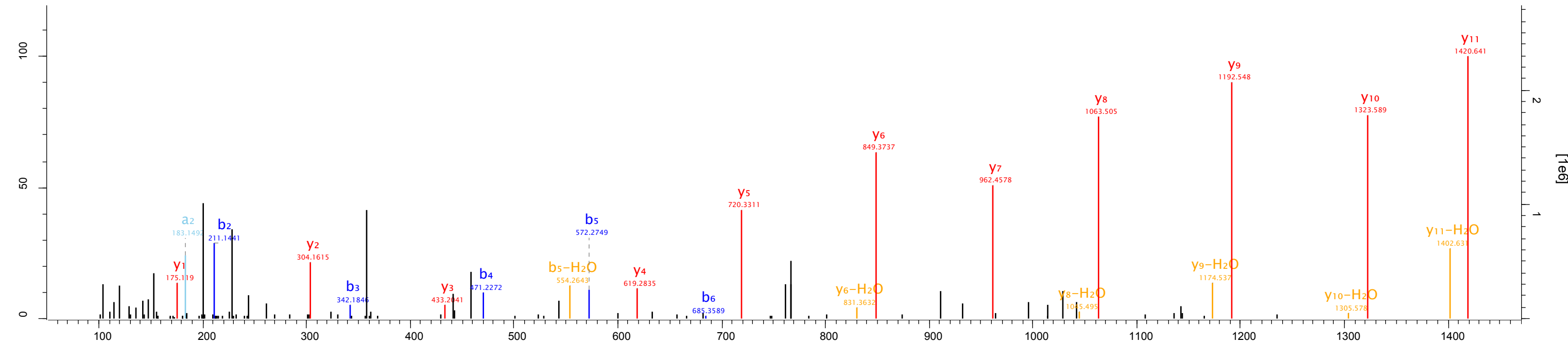


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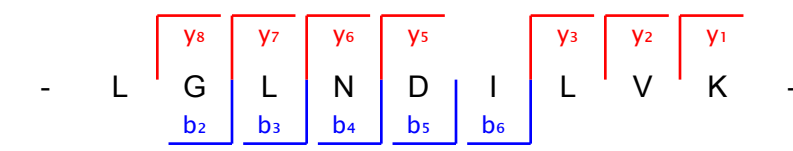
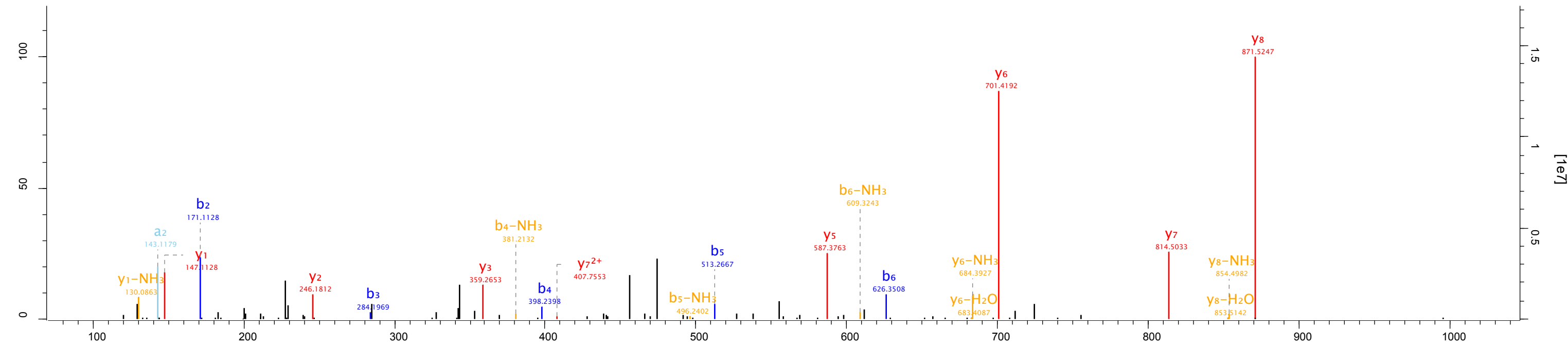


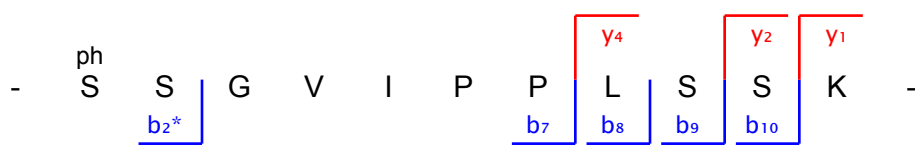
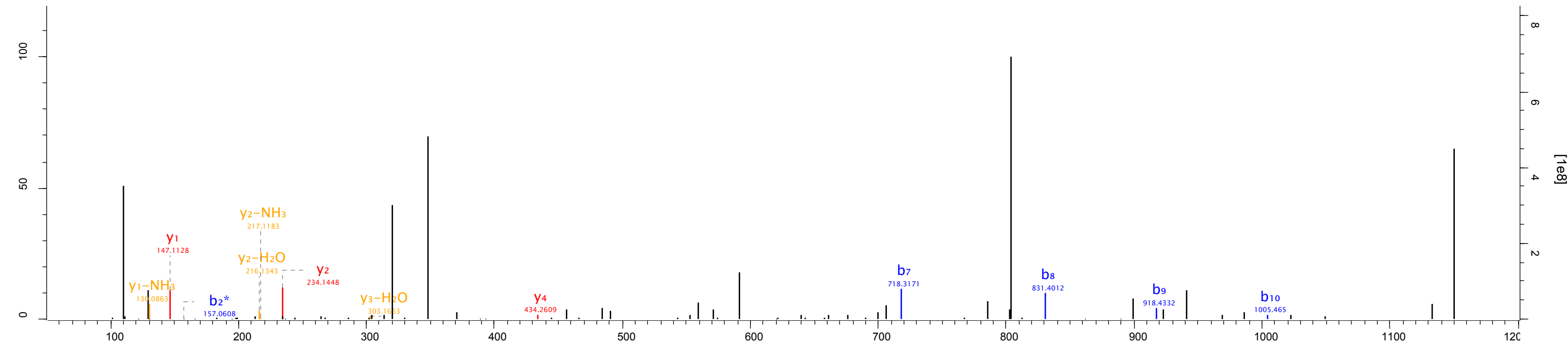


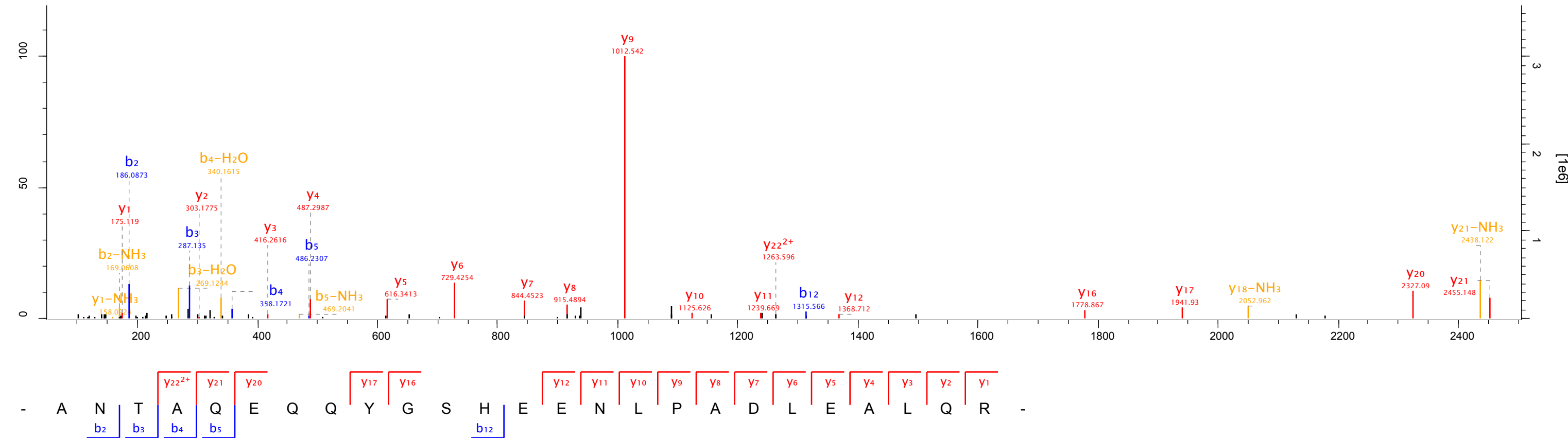
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P M E T L E T W E E R -
b₂ b₃ b₄ b₅ b₆

Raw file
20180707_MaS_A375SR_ML_proteome_11

Scan Method Score m/z Gene names
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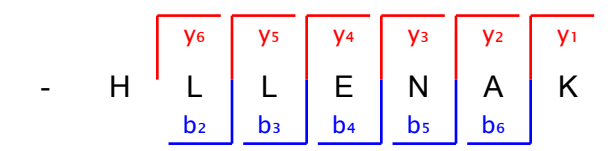
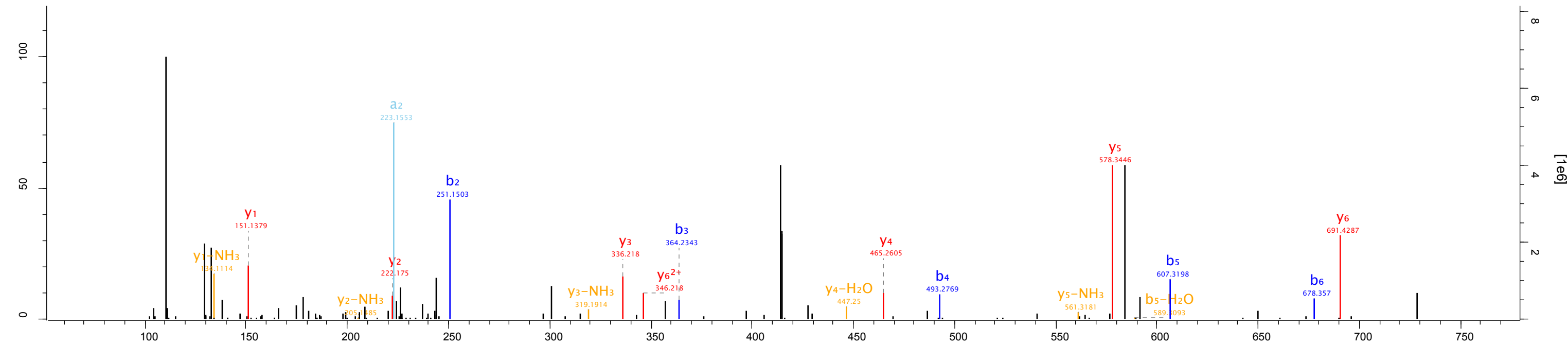






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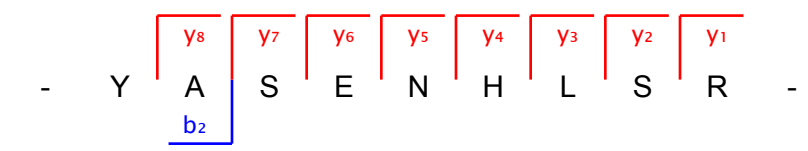
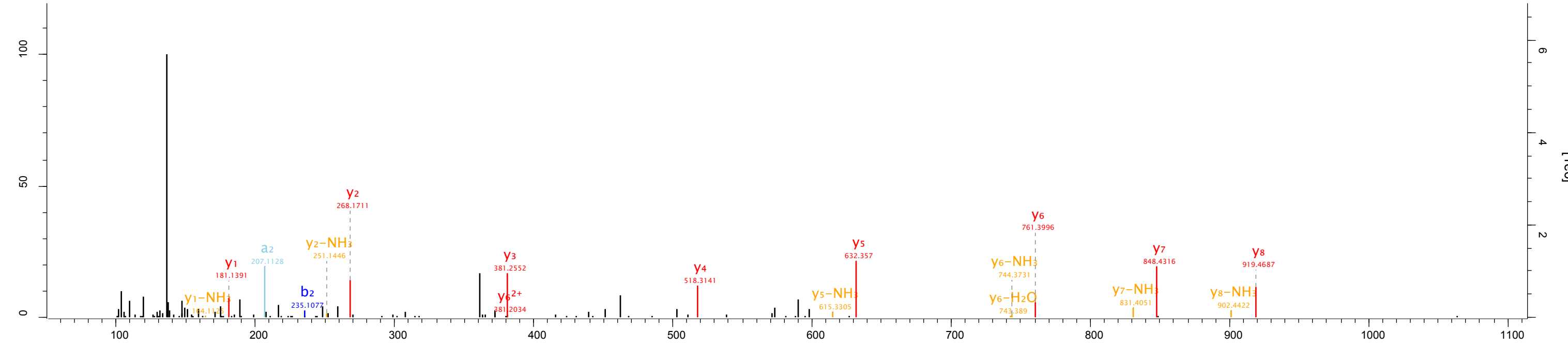
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Raw file

Scan Method Score m/z Gene names

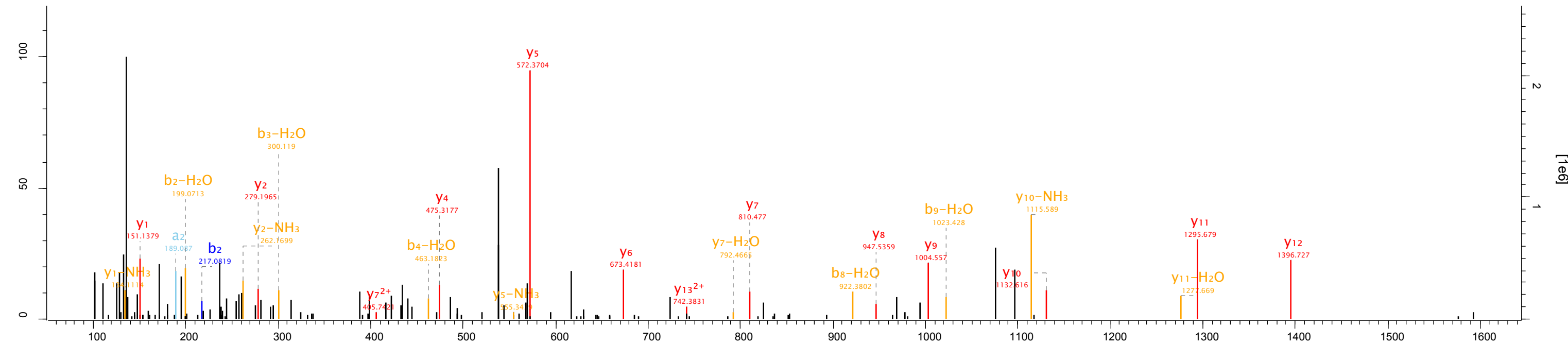
20180707_MaS_A375SR_ML_proteome_12 3033 FTMS; HCD 89.05 361.51 TM4SF1



Raw file

20180707_MaS_A375SR_ML_proteome_12

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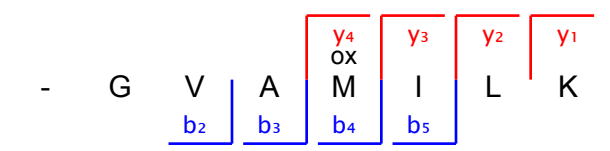
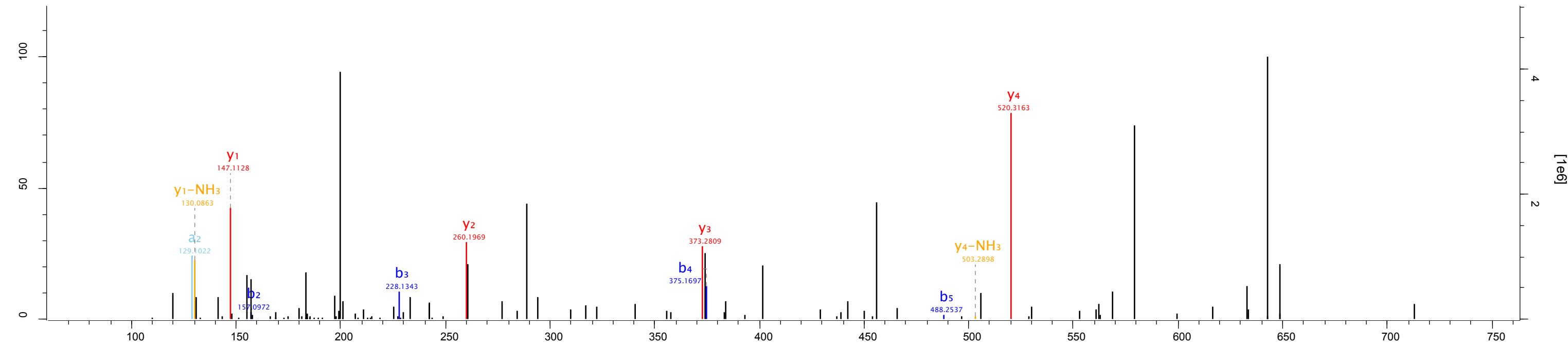


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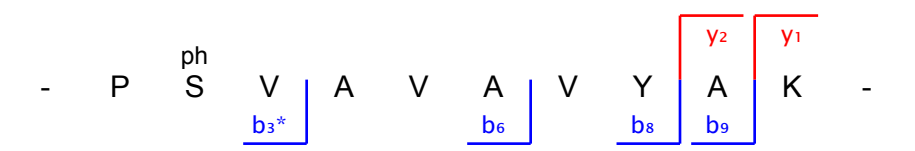
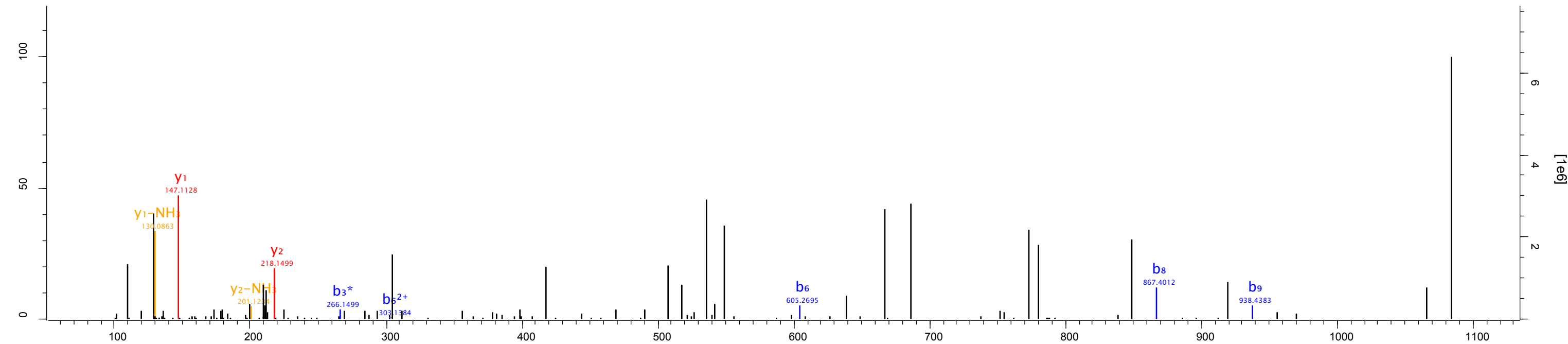
b₂

S T Y Q G H H T P P V Q K

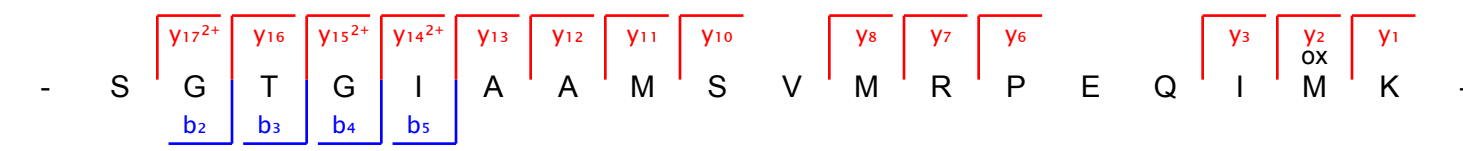
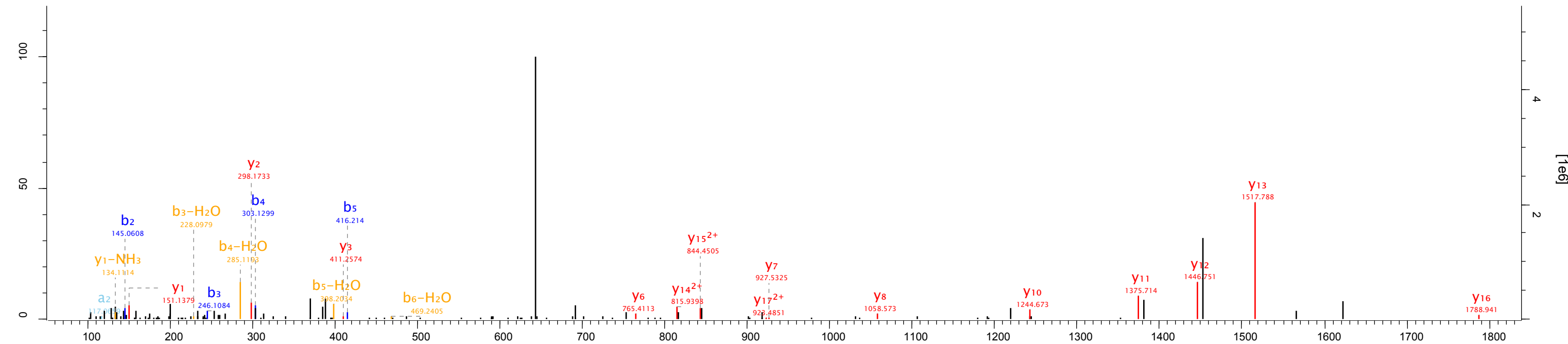
Raw file 20180707_MaS_A375SR_ML_proteome_13 Scan 15703 Method FTMS; HCD Score 66.99 m/z 374.22



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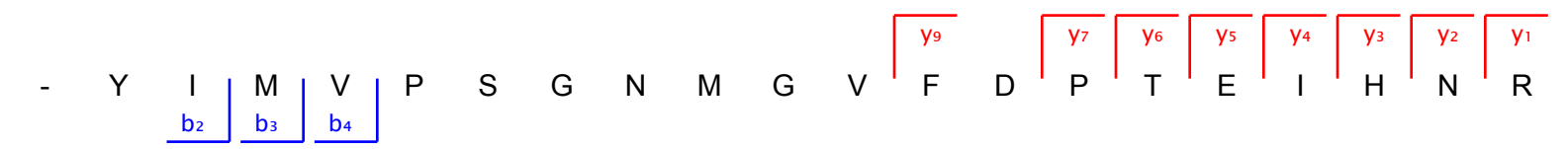
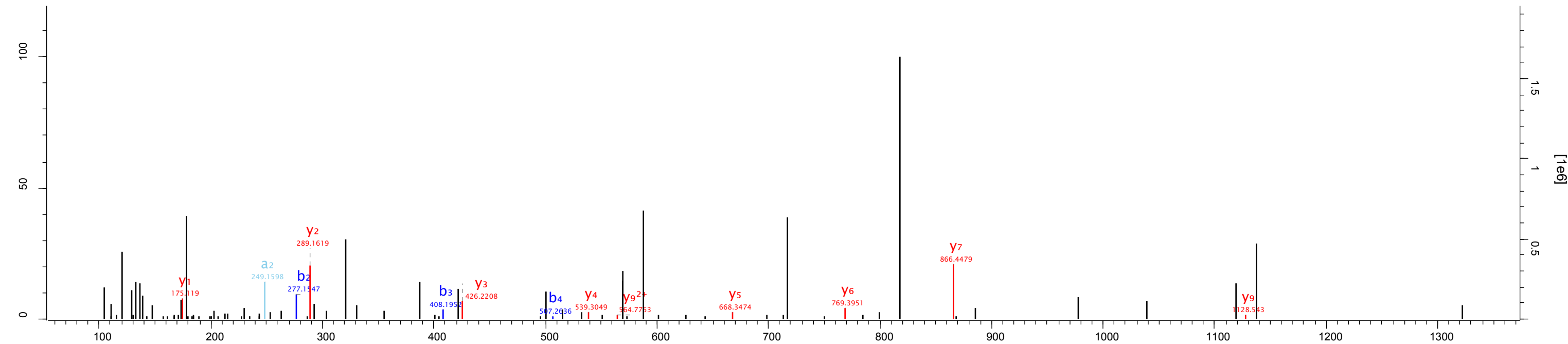


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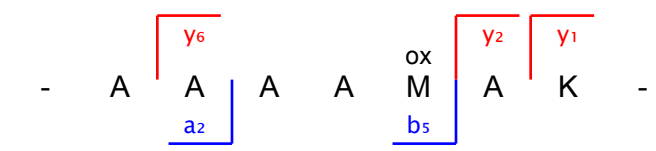
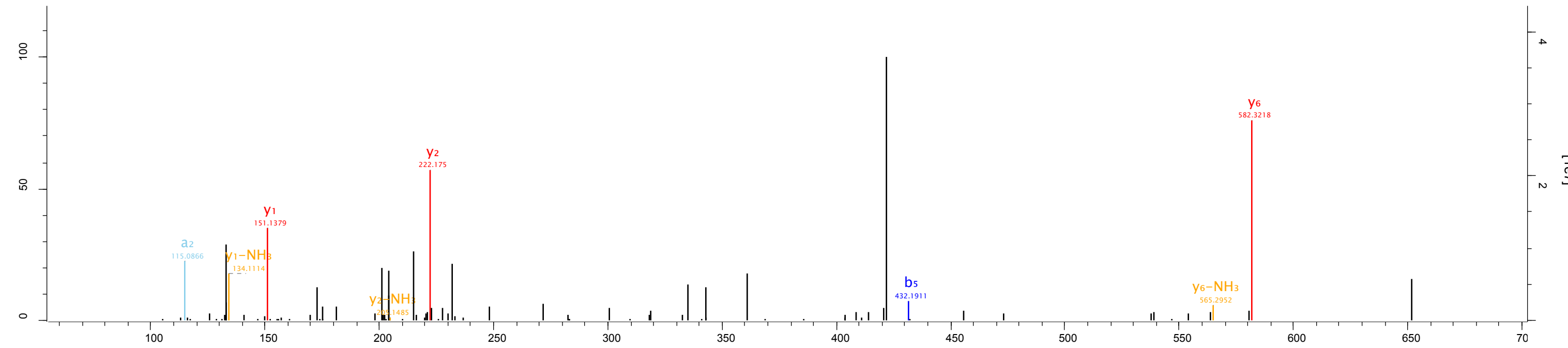


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20180707_MaS_A375SR_ML_proteome_13

Scan Method Score m/z Gene names
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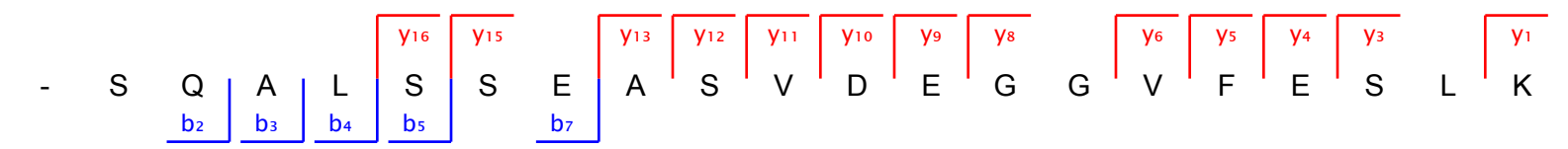
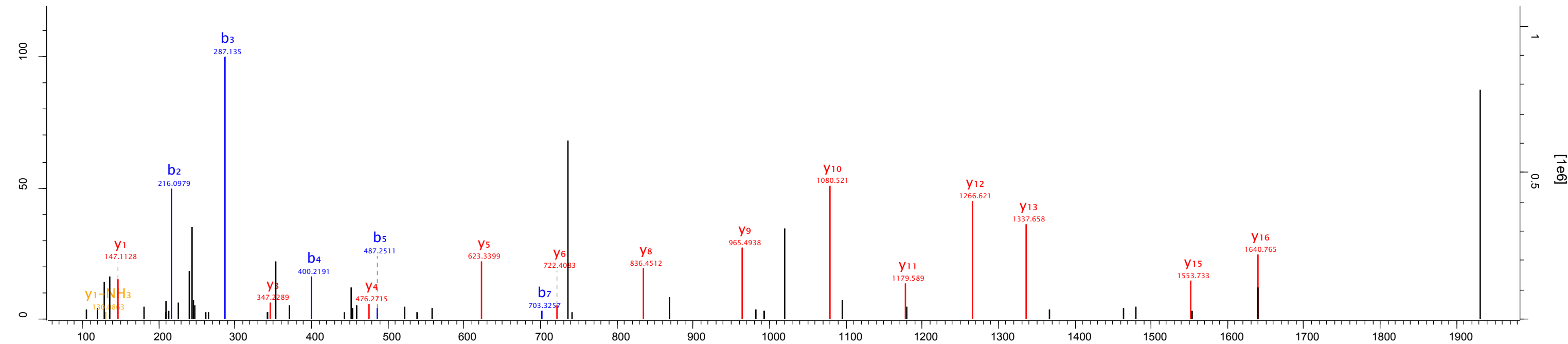


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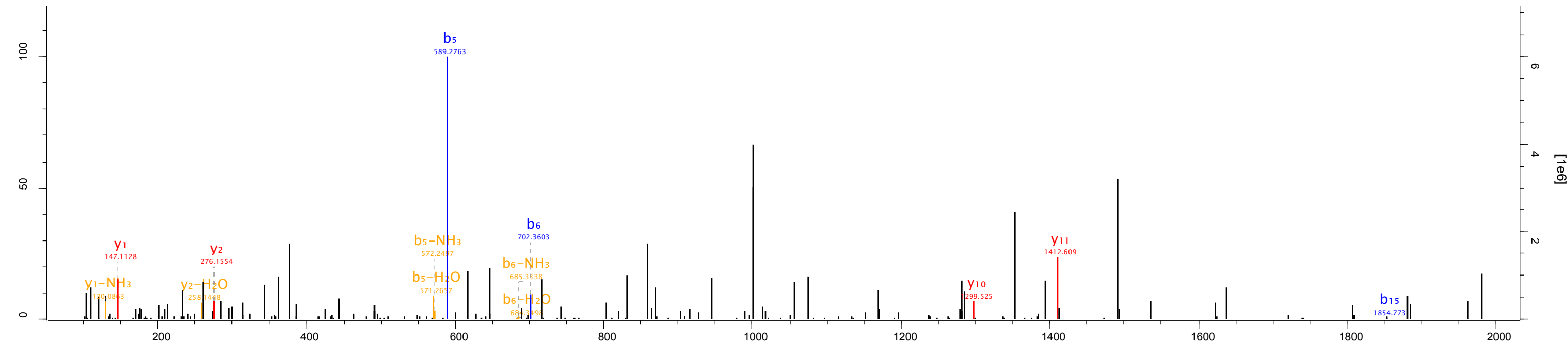


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m/z: 1020.49
Gene names: RNFT2



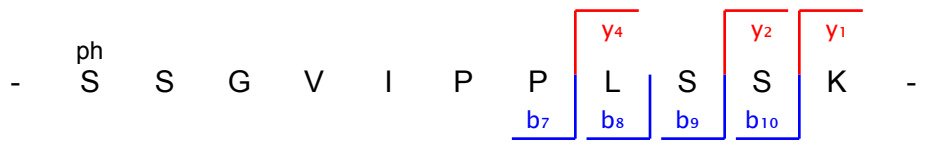
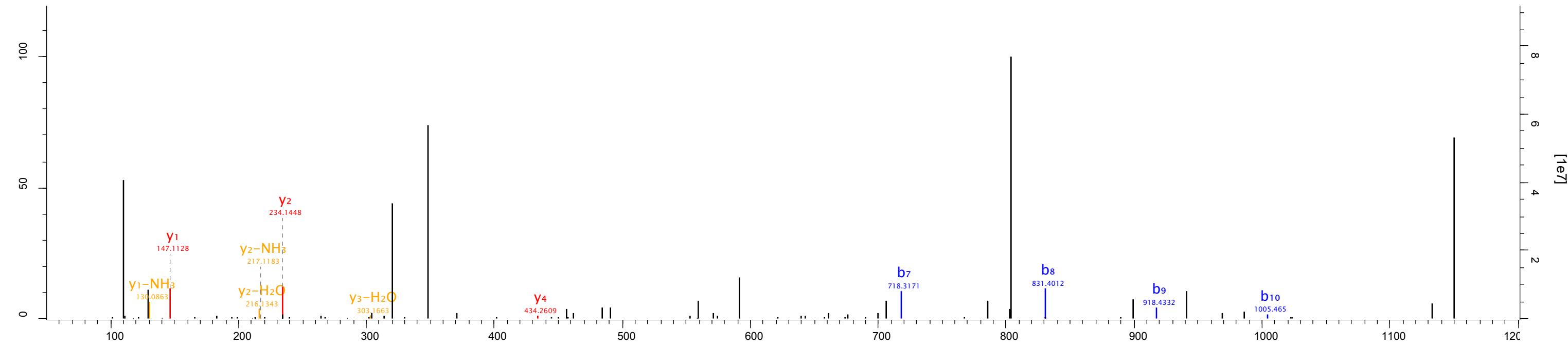
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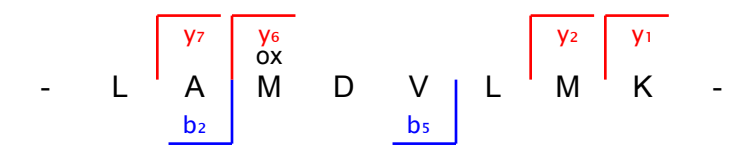
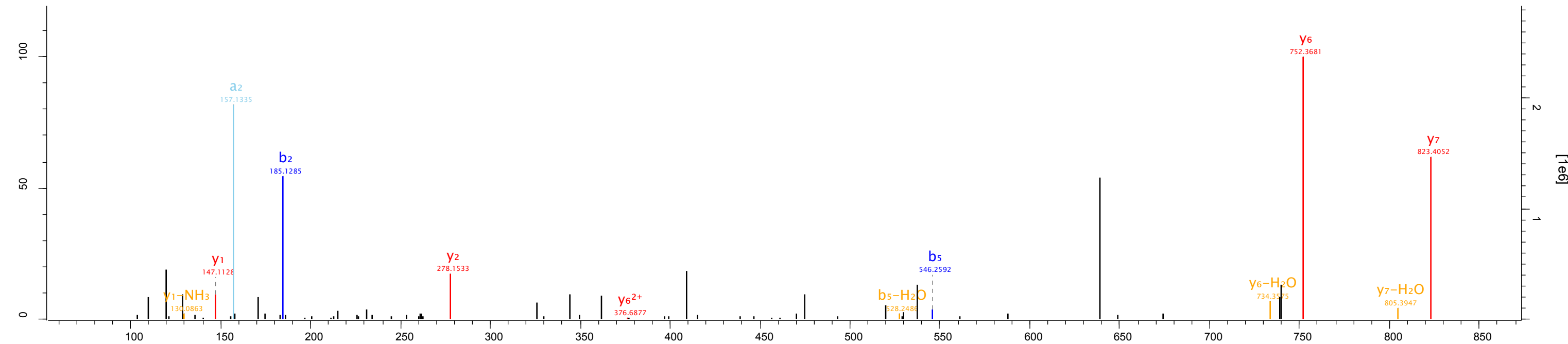
Fragmentation sites are indicated by brackets below the sequence:

- Red brackets: y₁₁ (L), y₁₀ (LQ), y₂ (E), y₁ (EK)
- Blue brackets: b₅ (TR), b₆ (TL), b₁₅ (E)

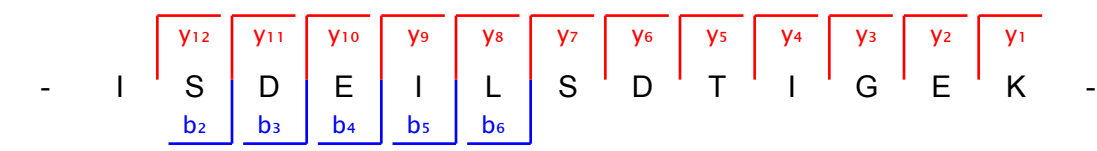
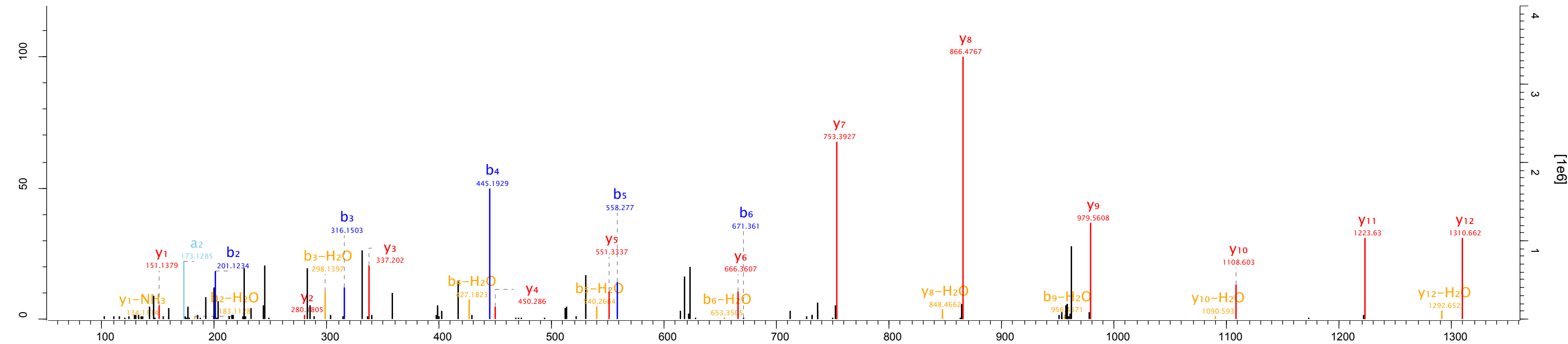


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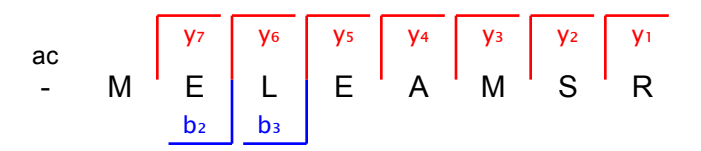
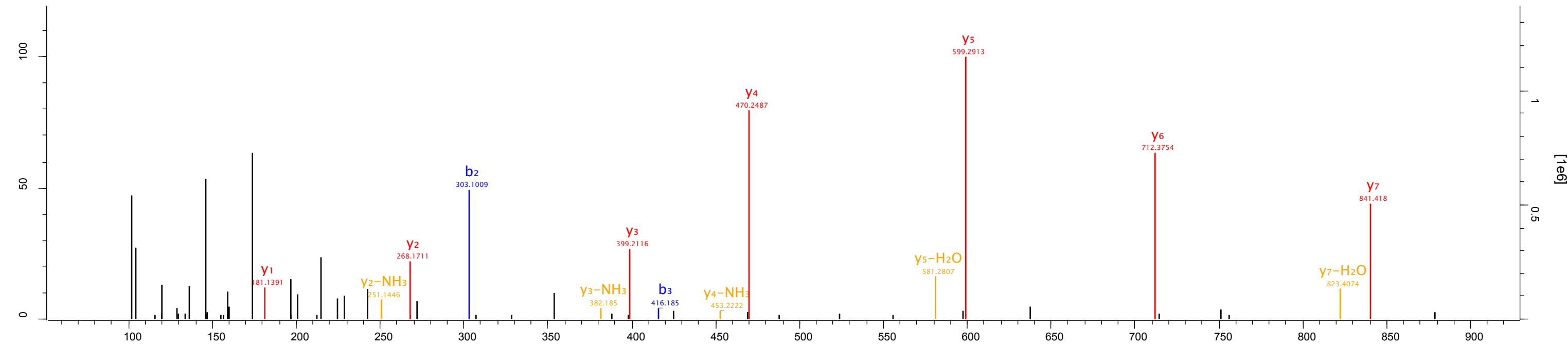


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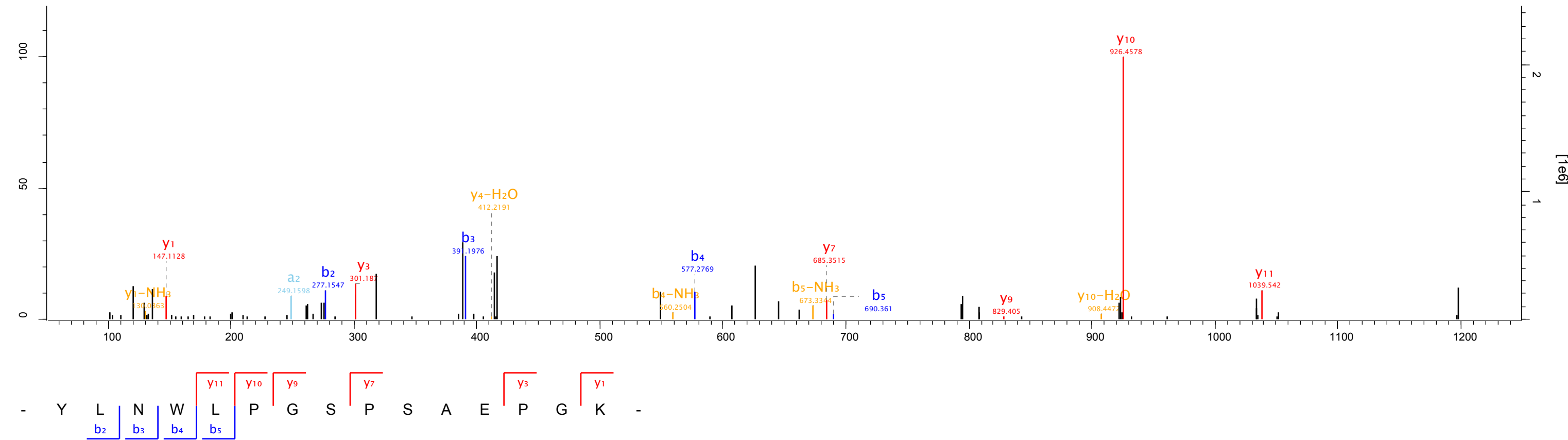


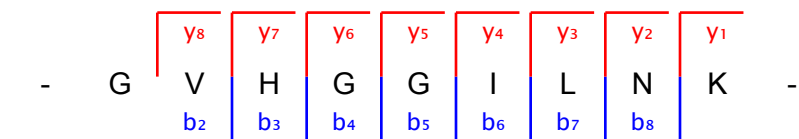
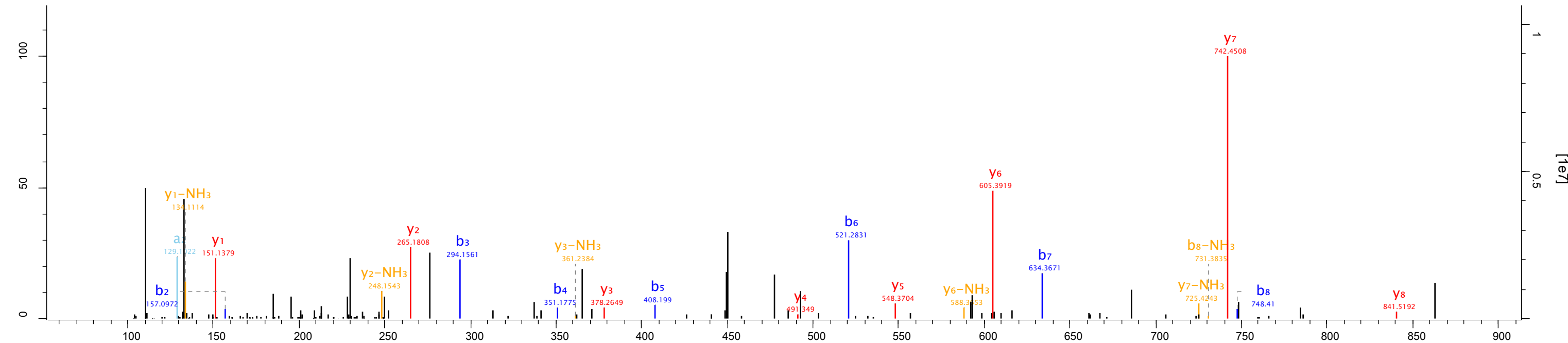
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Scan 25533 Method FTMS; HCD Score 74.46 m/z 507.74 Gene names TMEM258

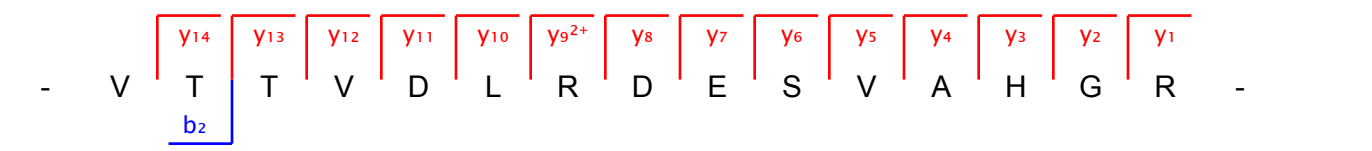
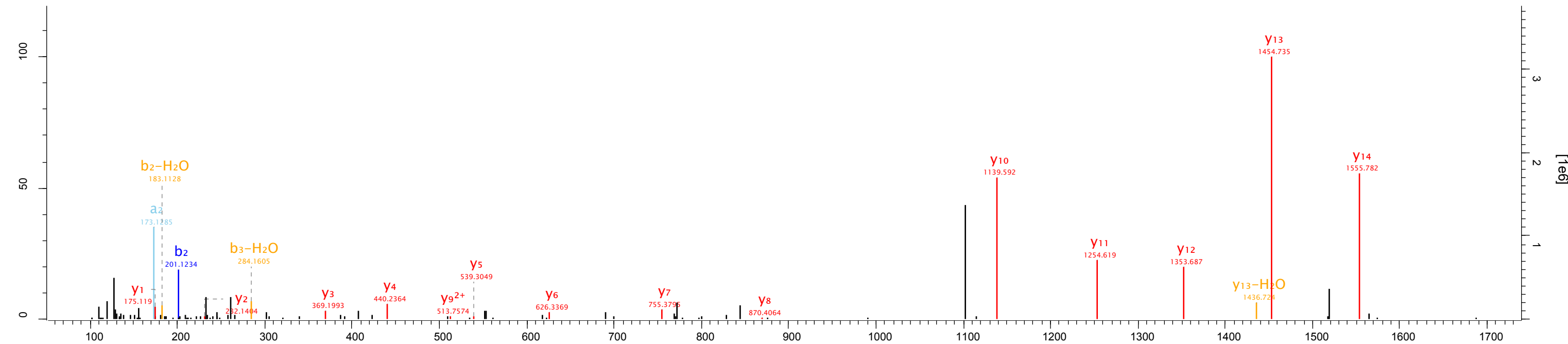


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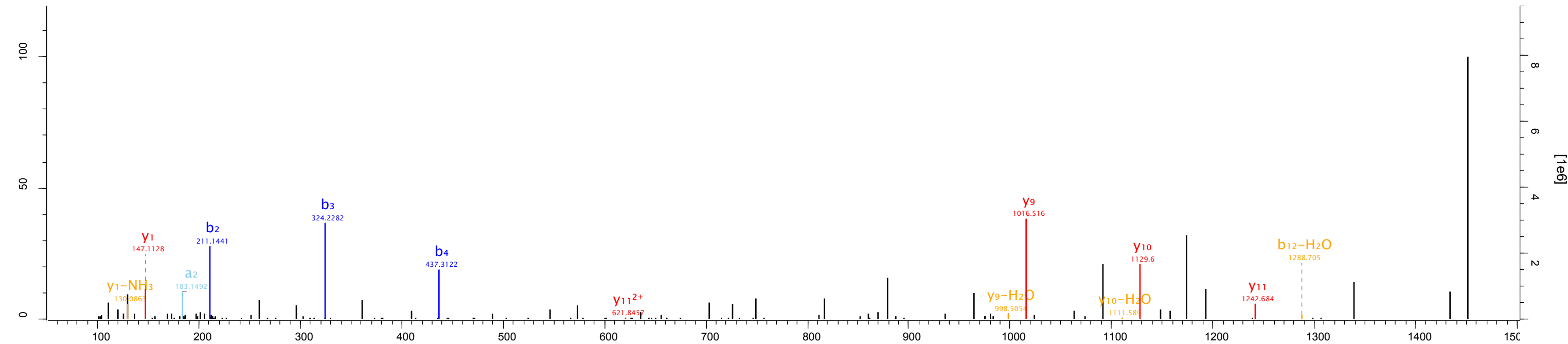




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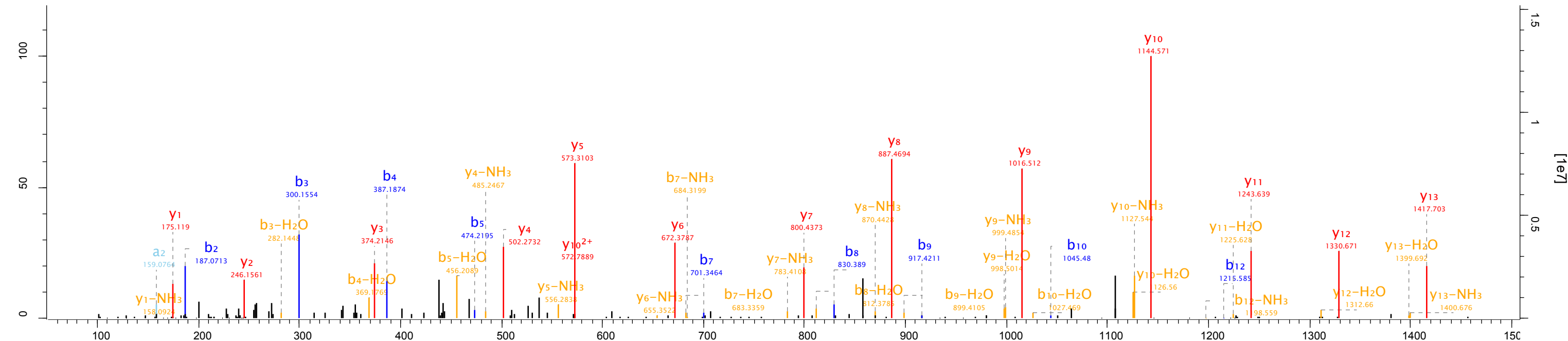


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Raw file
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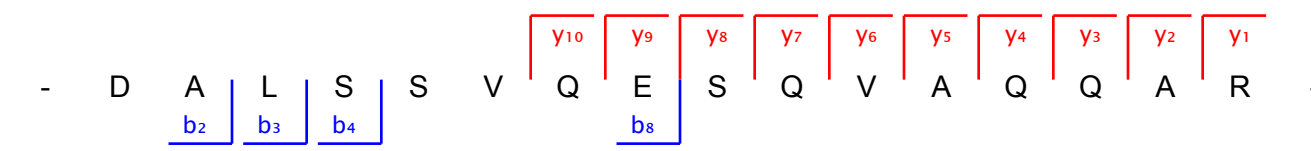
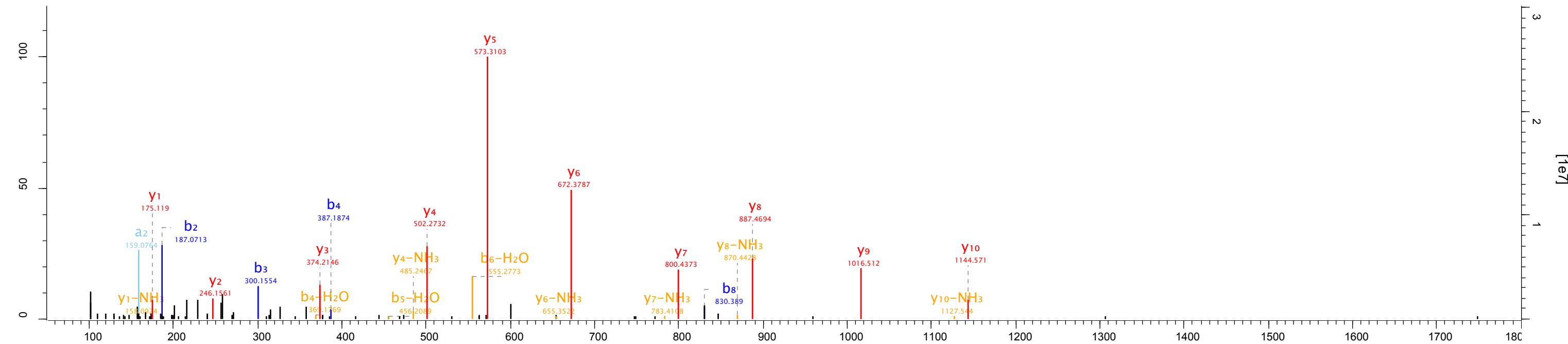
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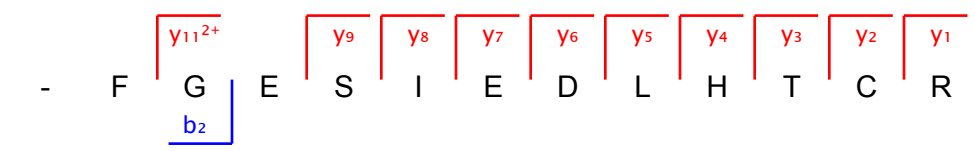
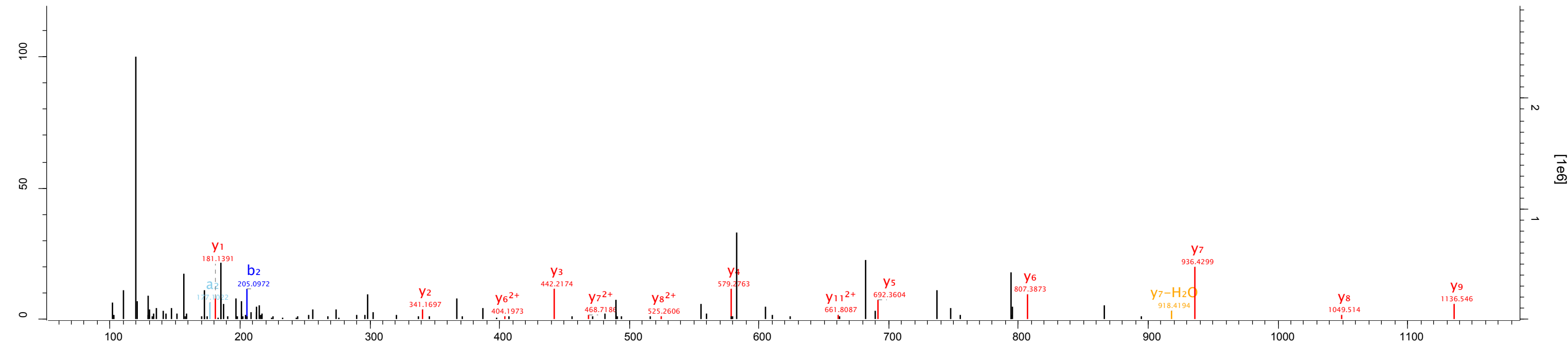
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Scan 14513 Method FTMS; HCD Score 87.52 m/z 572.96 Gene names APOC3



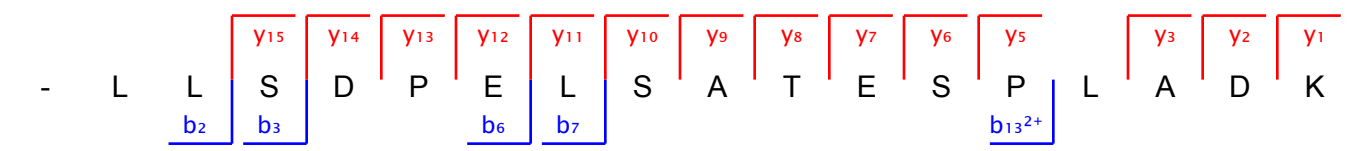
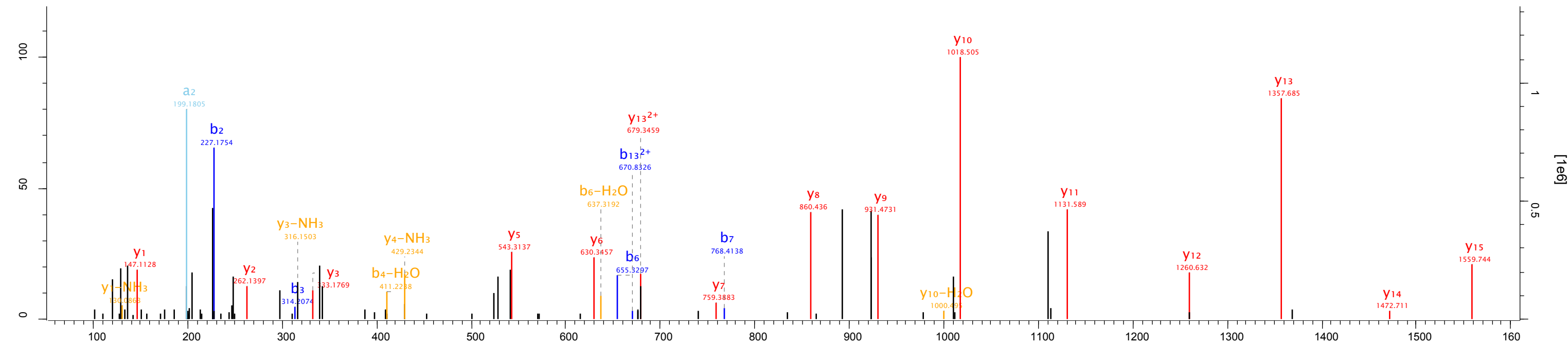
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Scan Method Score m/z Gene names
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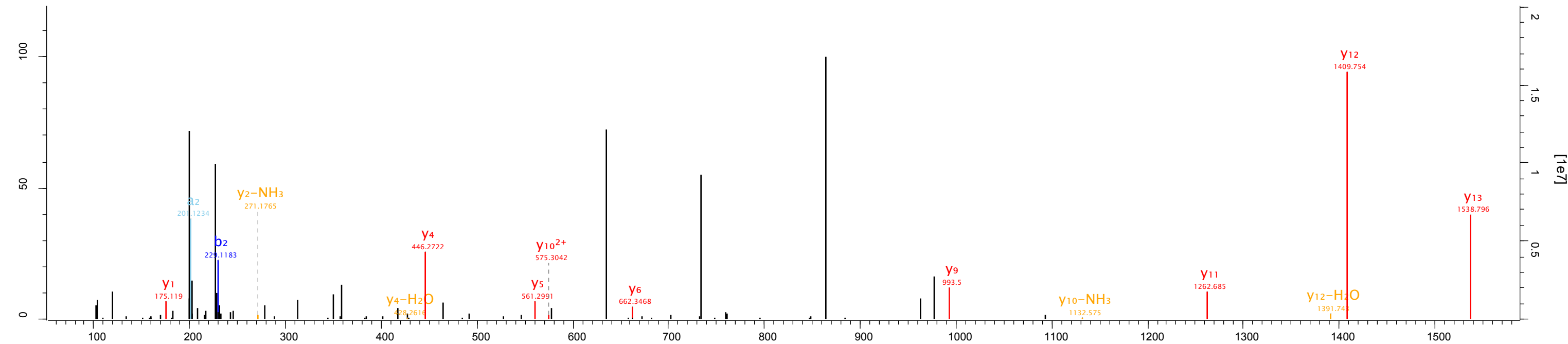
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Scan 22793 Method FTMS; HCD Score 107.98 m/z 893.46 Gene names BICC1

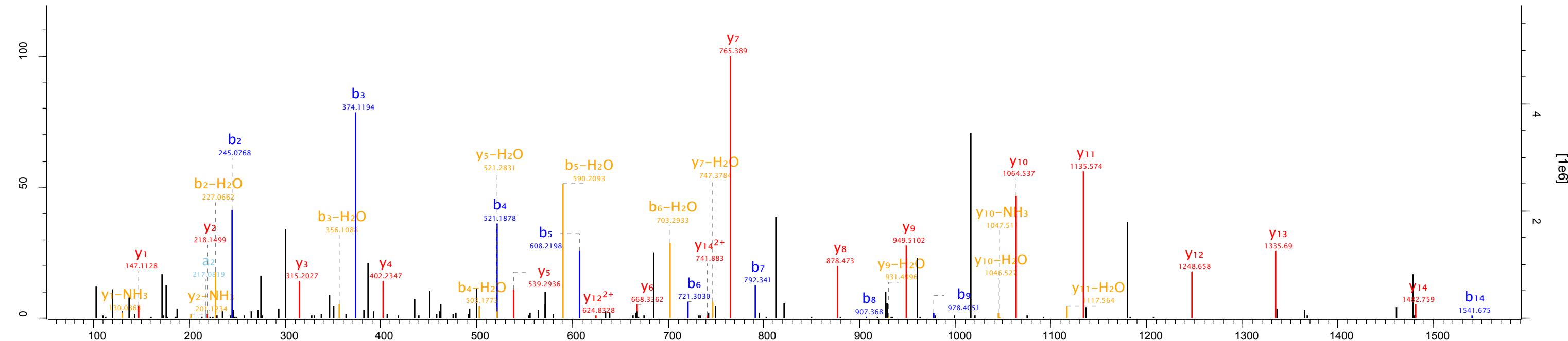


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Scan 23093 Method FTMS; HCD Score 40.28 m/z 546.96 Gene names PVRL1



- V E F L R P S F T D G T I R -
b2



ac

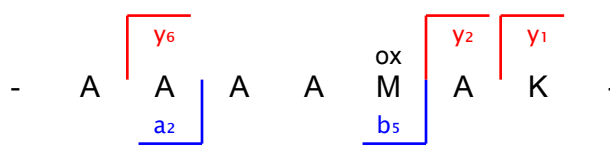
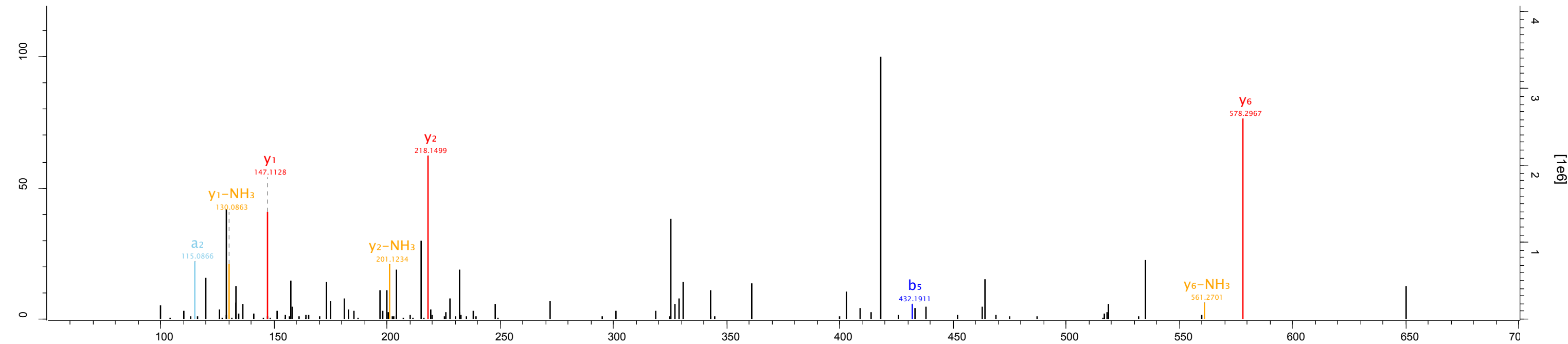
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b₂ b₃ b₄ b₅ b₆ b₇ b₈ b₉ b₁₄

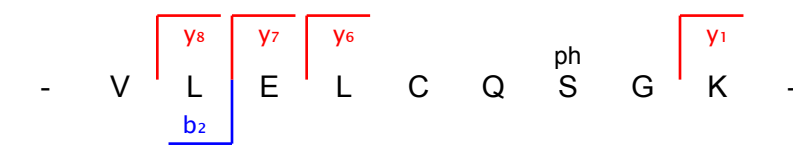
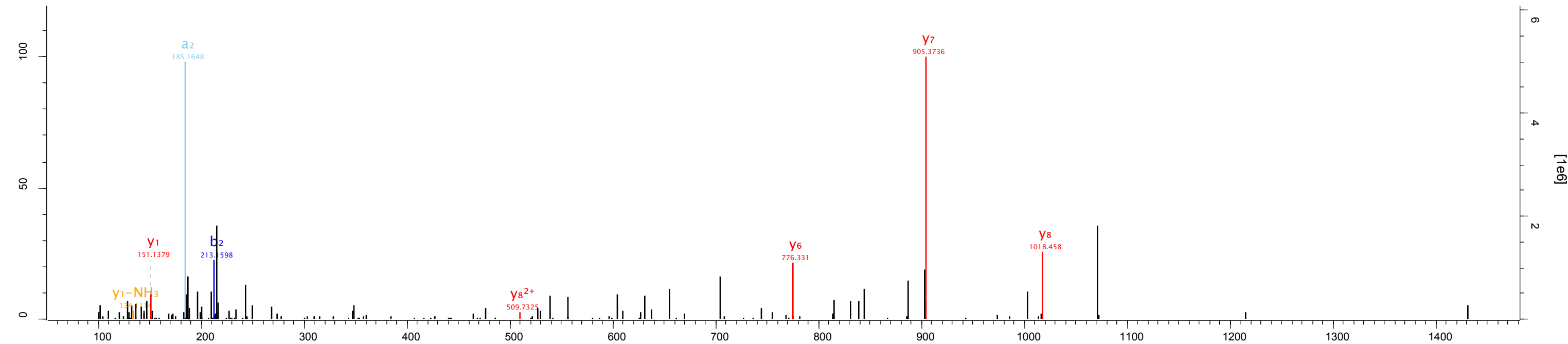
y₁₄ y₁₃ y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

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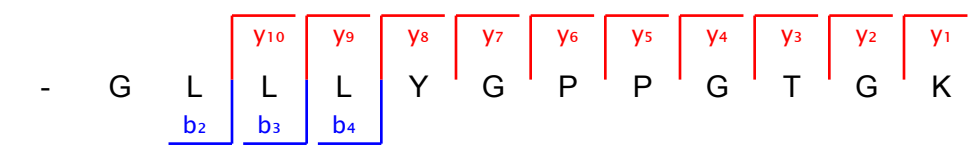
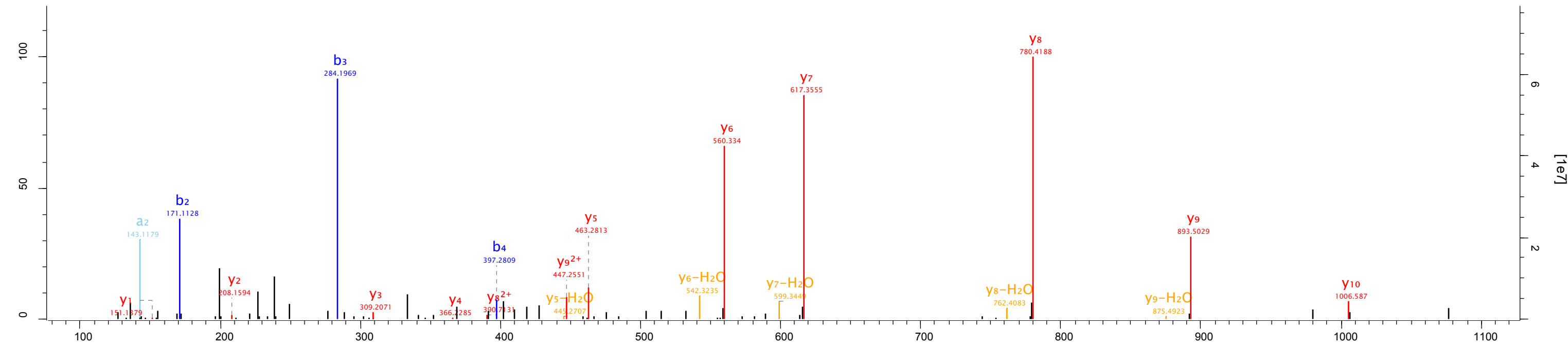
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Raw file 20180707_MaS_A375SR_ML_proteome_19 Scan 12813 Method FTMS; HCD Score 41.88 m/z 559.27

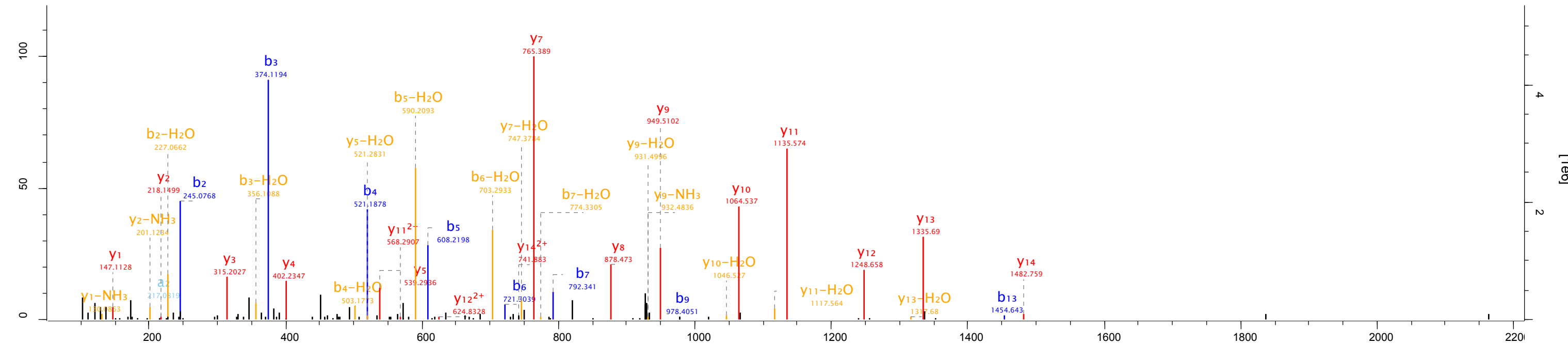


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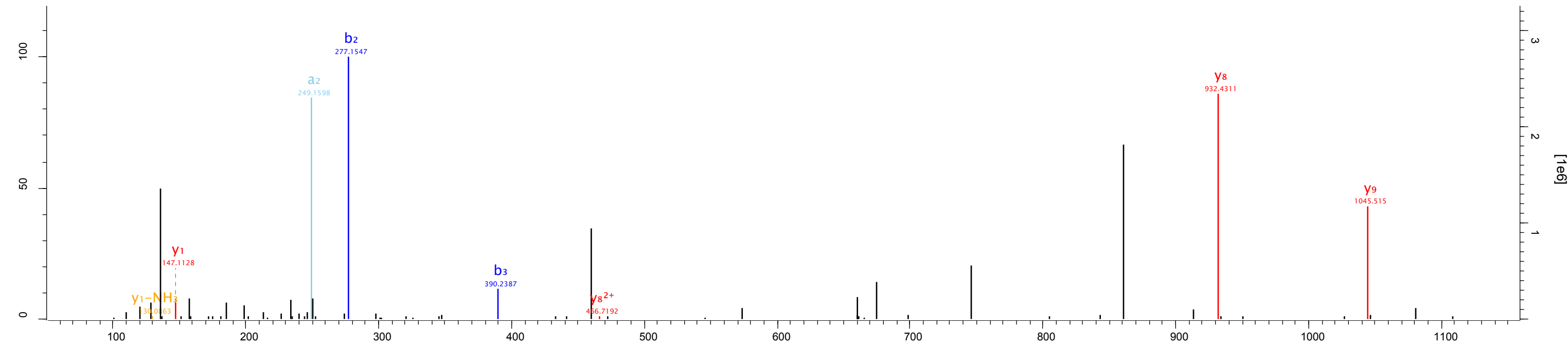
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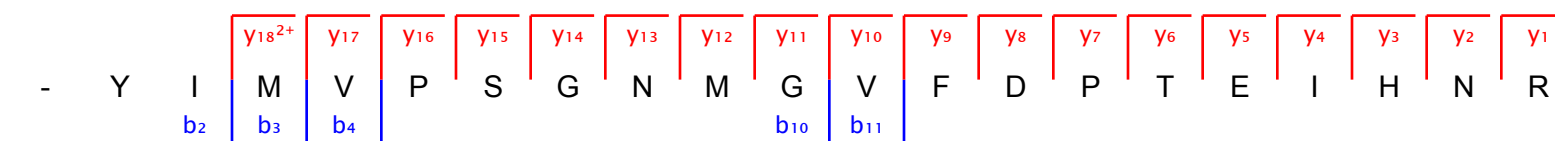
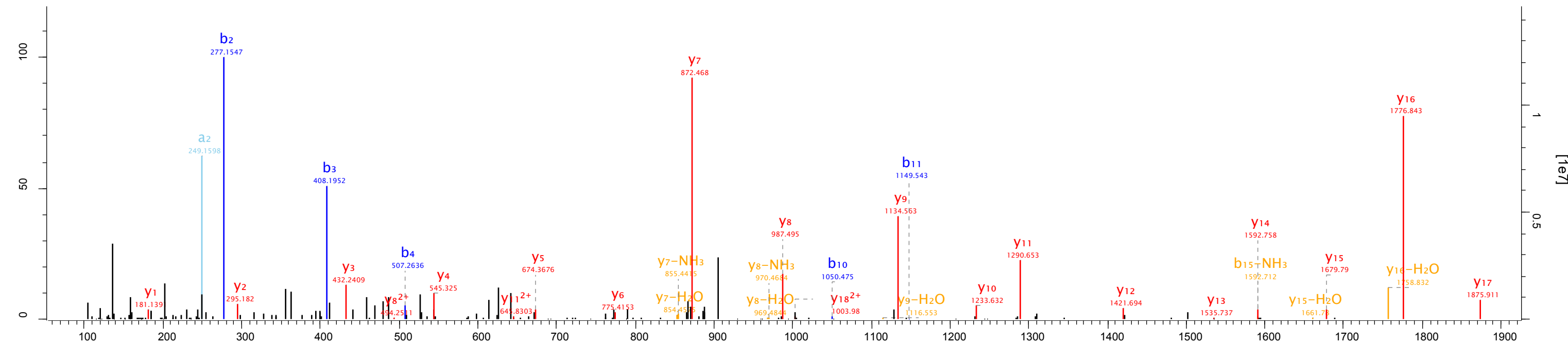
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b2 b3 b4 b5 b6 b7 b9 b13

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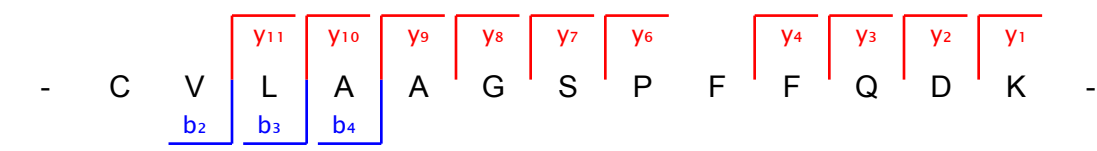
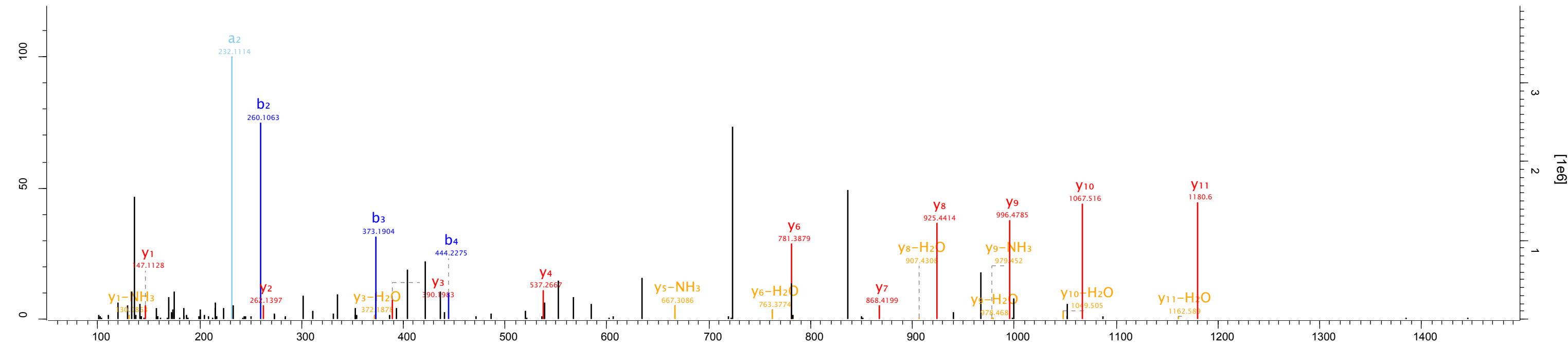


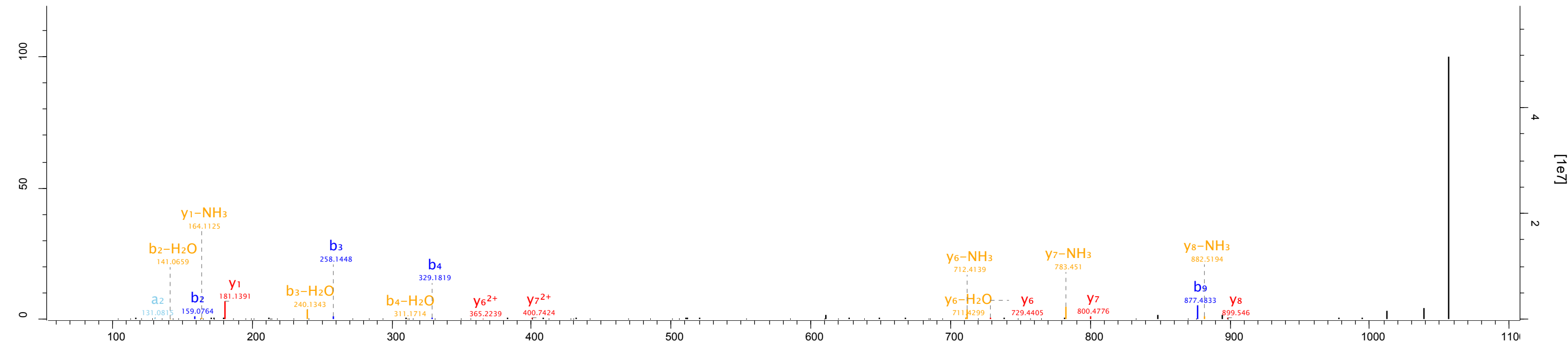
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20180707_MaS_A375SR_ML_proteome_2_02

Scan 27003 Method FTMS; HCD Score 121.77 m/z 761.7 Gene names CNIH4



Raw file: 20180707_MaS_A375SR_ML_proteome_2_03
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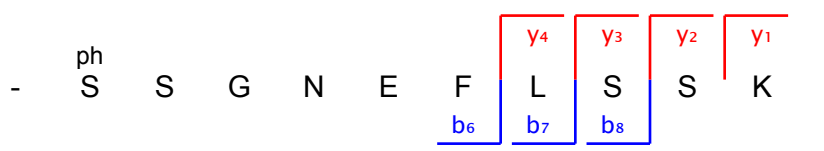
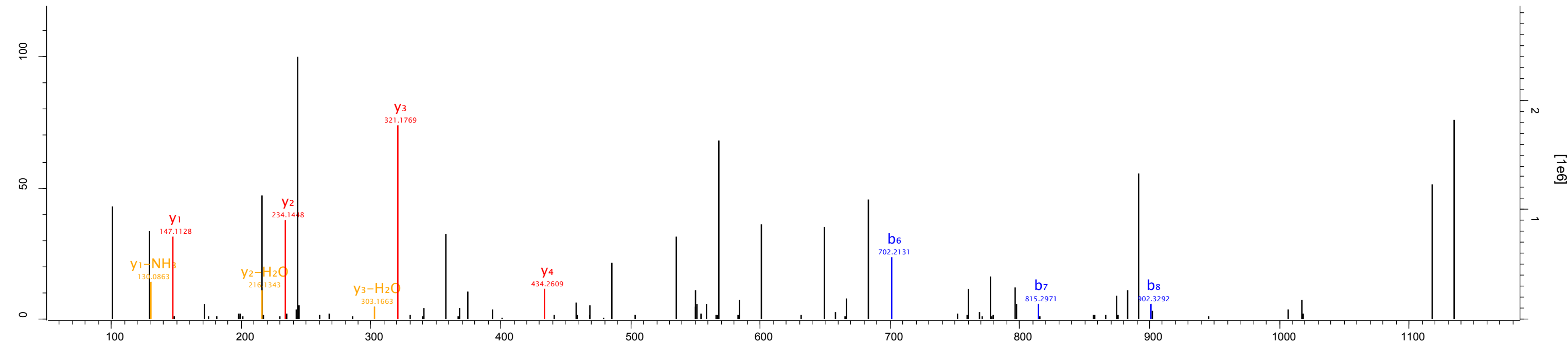


- A S V A L S G E R R -

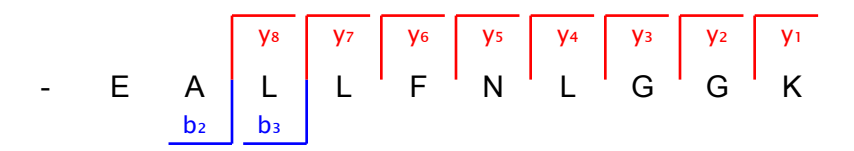
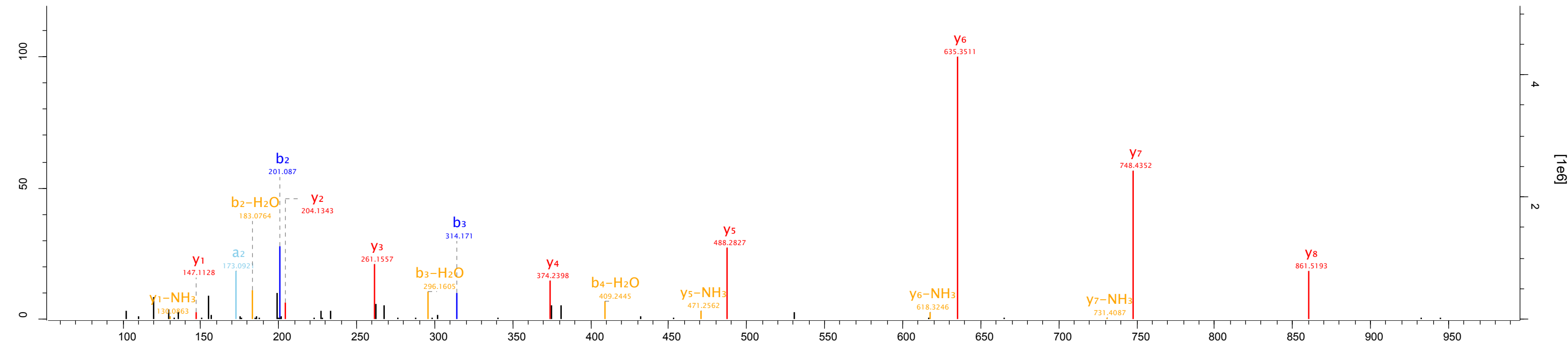
Fragmentation sites are indicated by boxes and labels:

- Red boxes above the sequence: y₈ (V), y₇ (A), y₆ (L), y₁ (R).
- Blue boxes below the sequence: b₂ (S), b₃ (V), b₄ (A), b₉ (R).

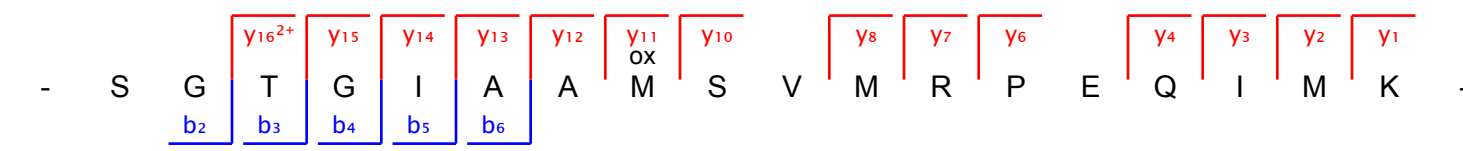
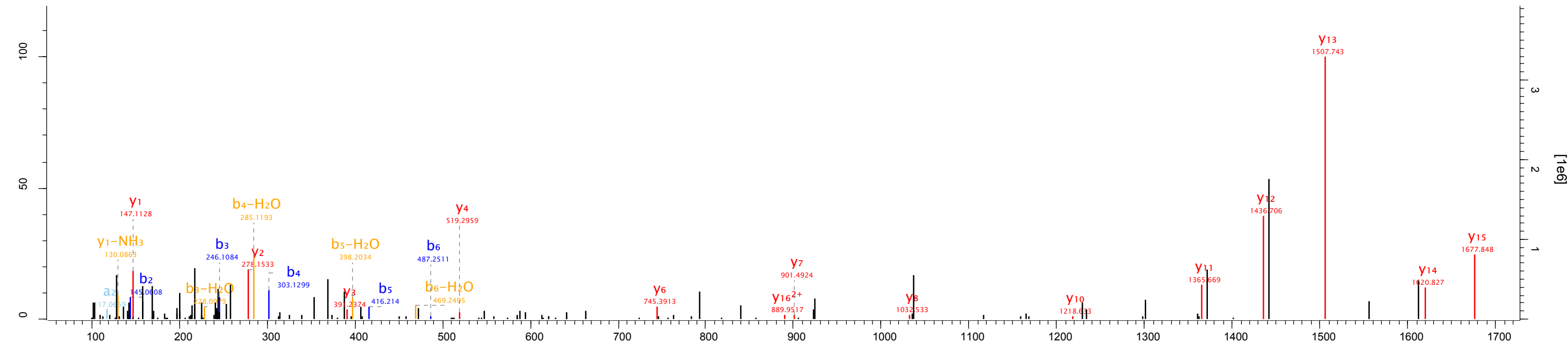
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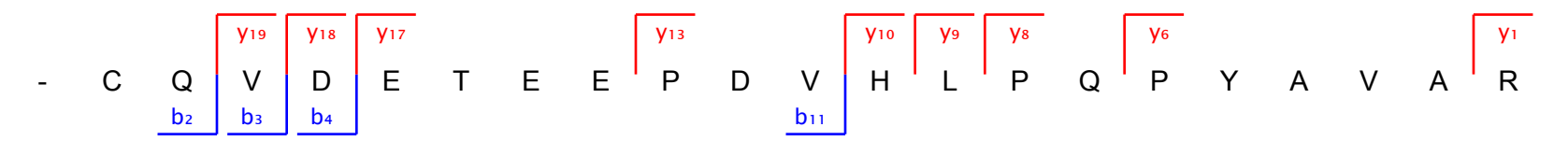
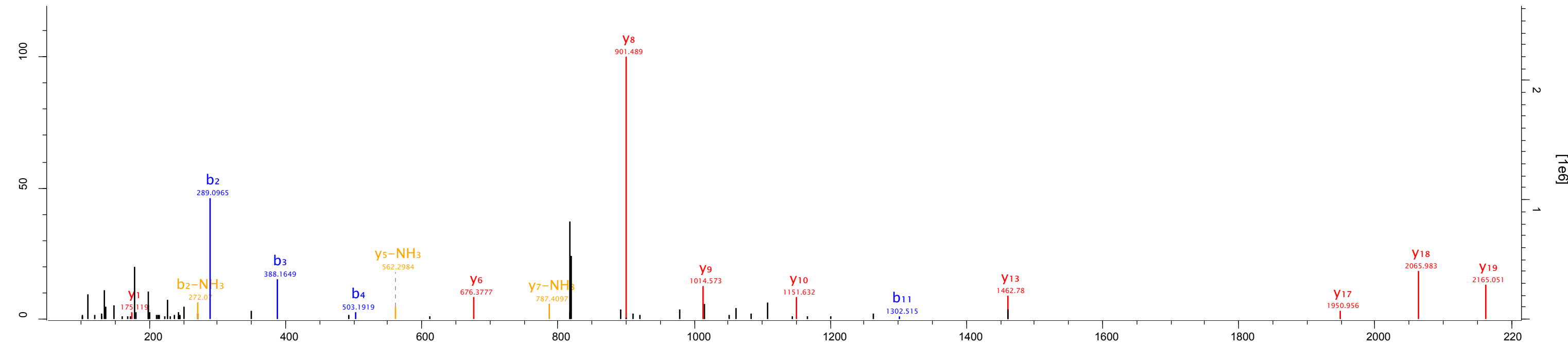


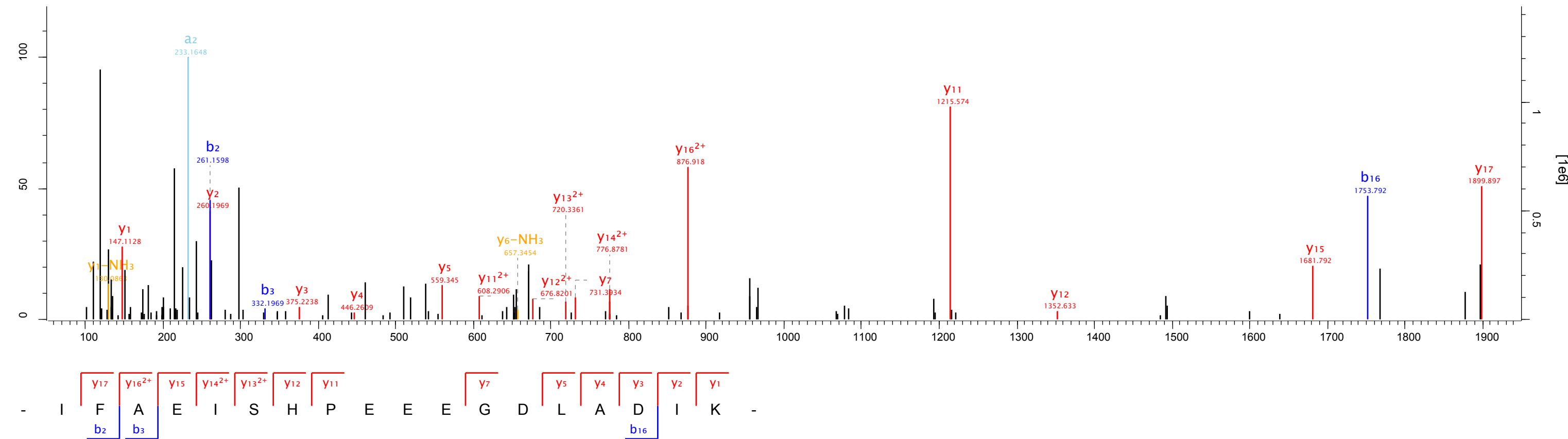
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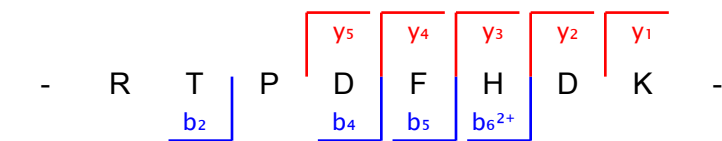
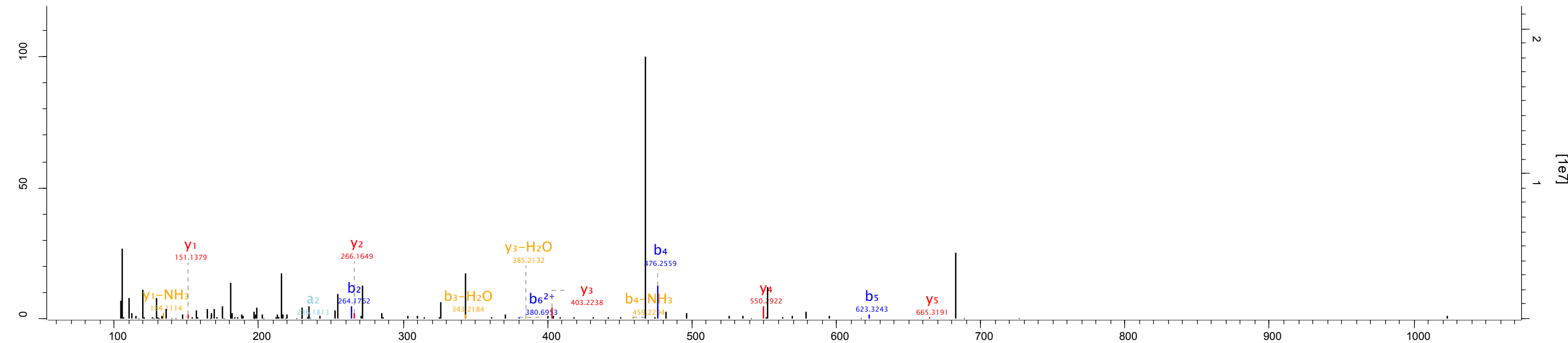


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20180707_MaS_A375SR_ML_proteome_2_05

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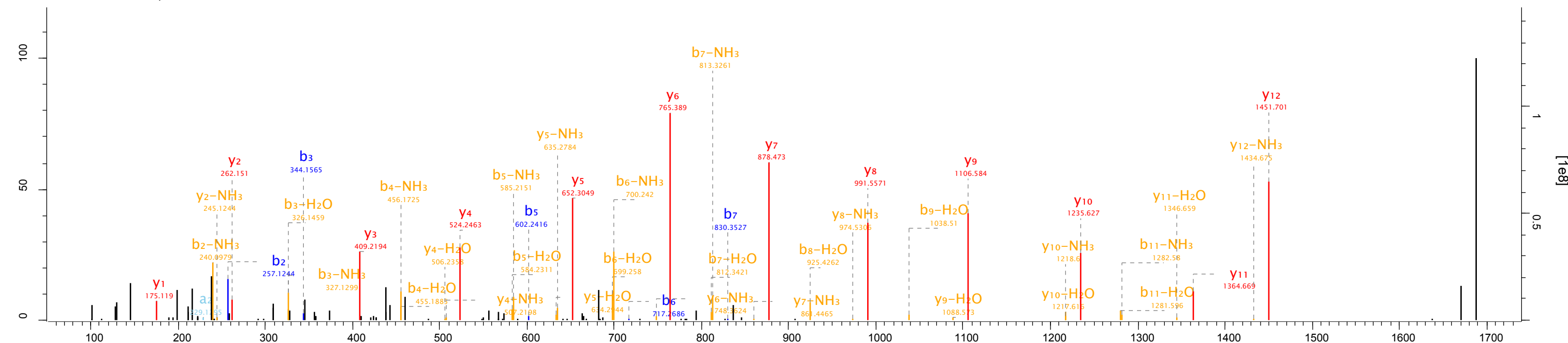






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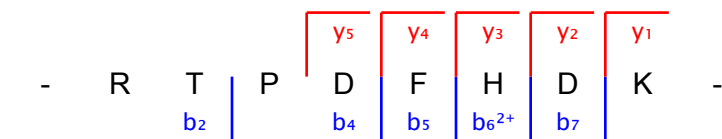
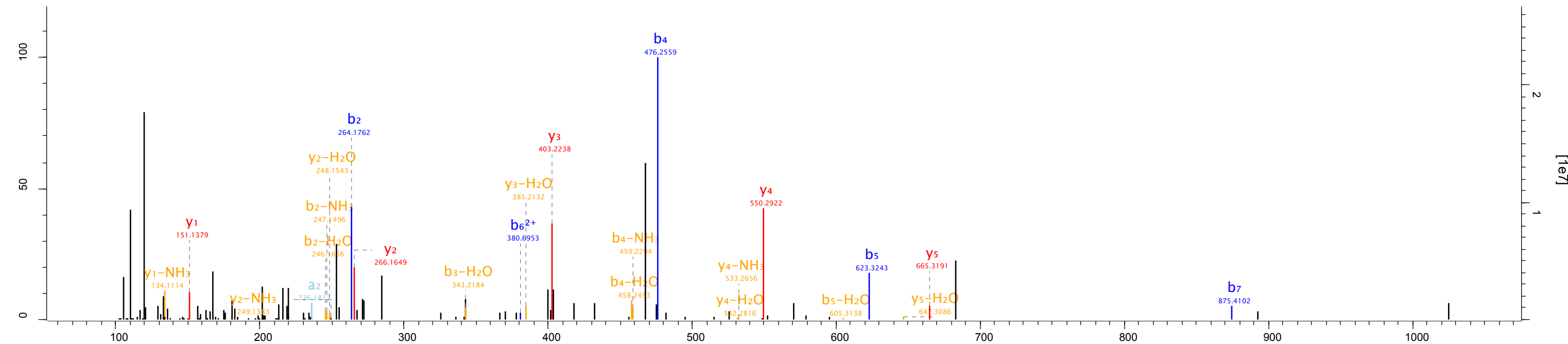


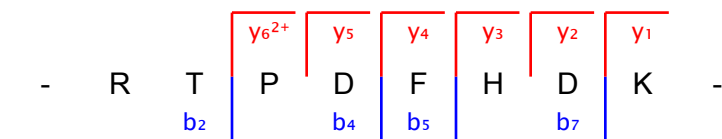
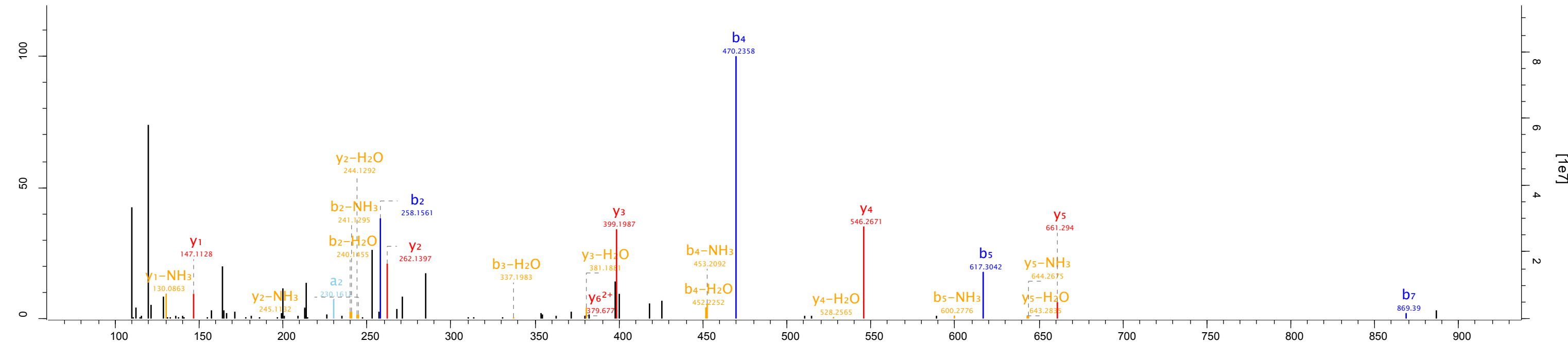
- Q Q S E E D L L L Q D F S R -

Peptide sequence: Q Q S E E D L L L Q D F S R

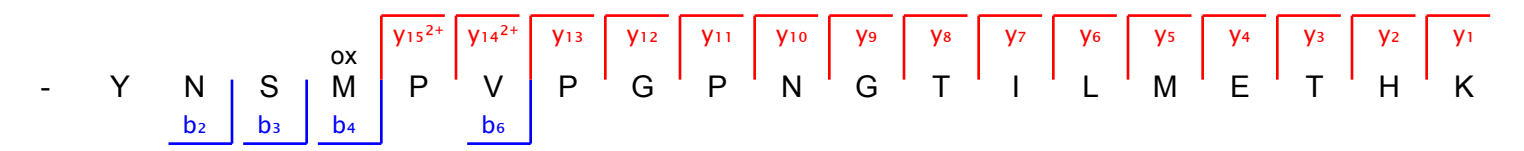
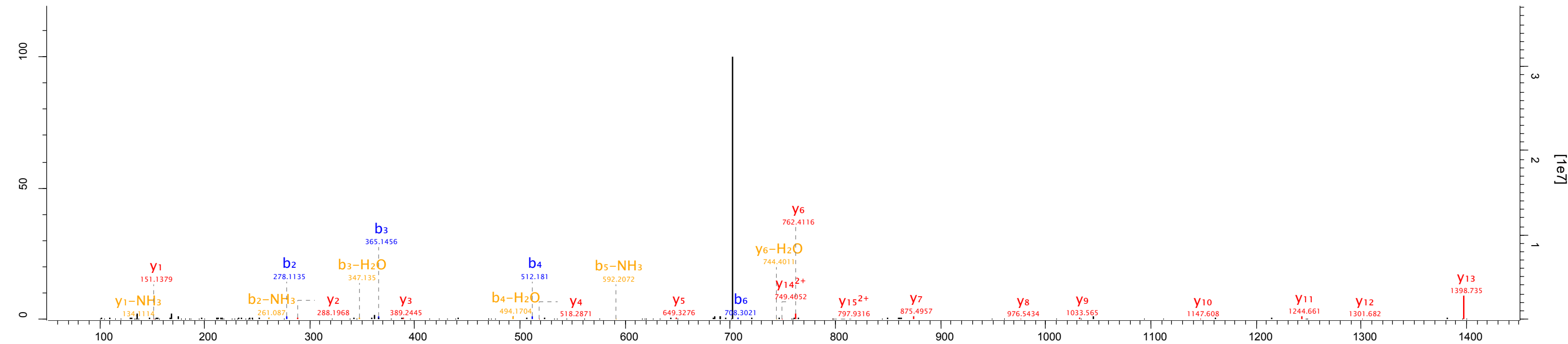
Fragmentation sites (b and y ions) are indicated by brackets below the sequence:

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- b3: Q S
- b5: E E
- b6: E D
- b7: E D L

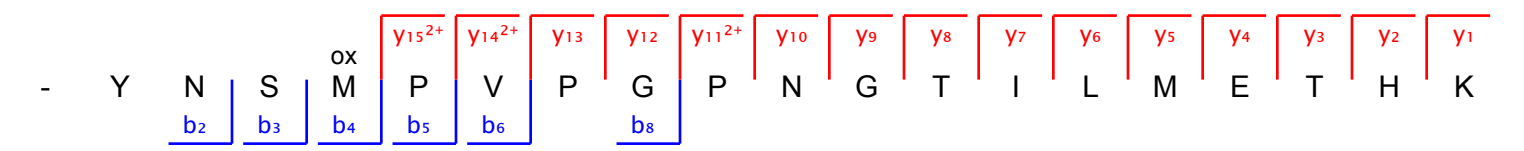
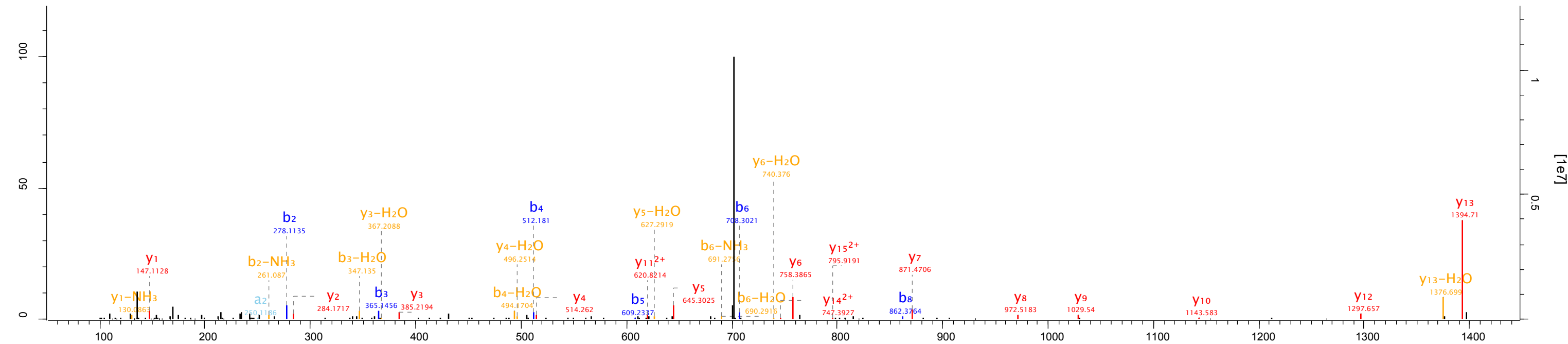




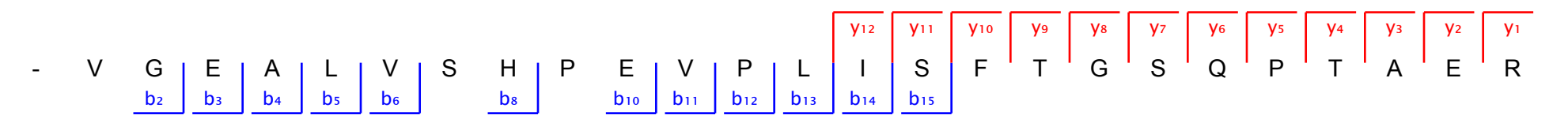
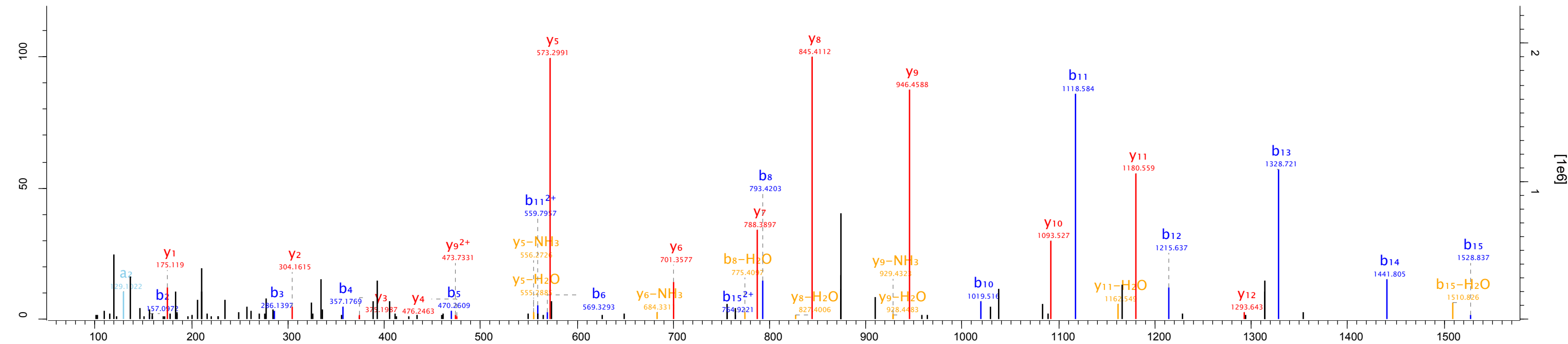
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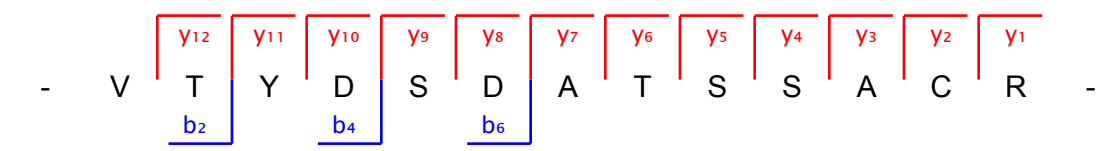
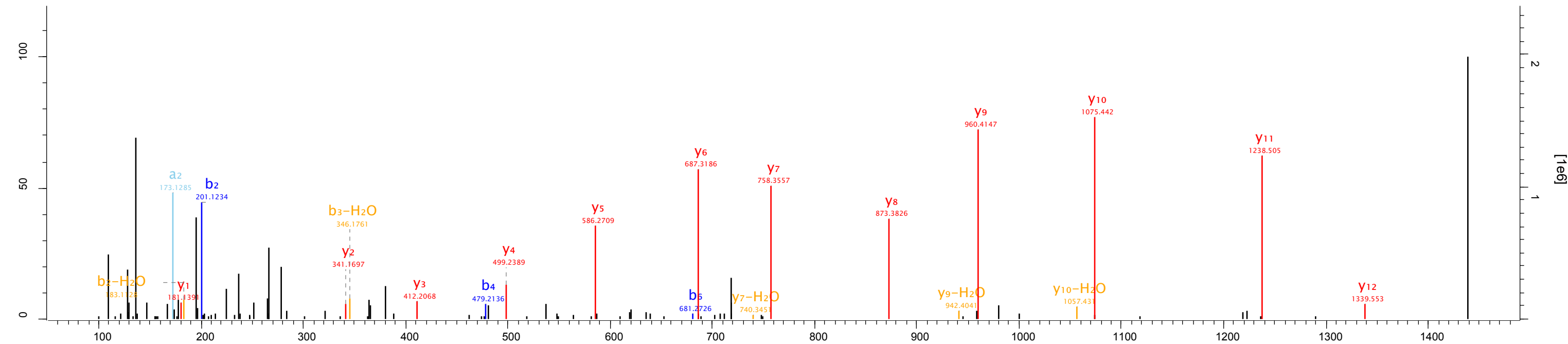
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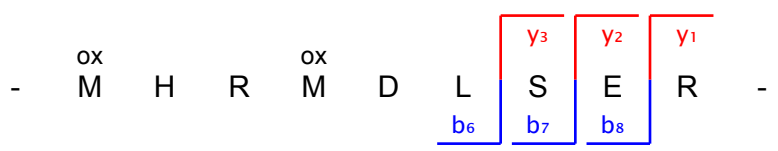
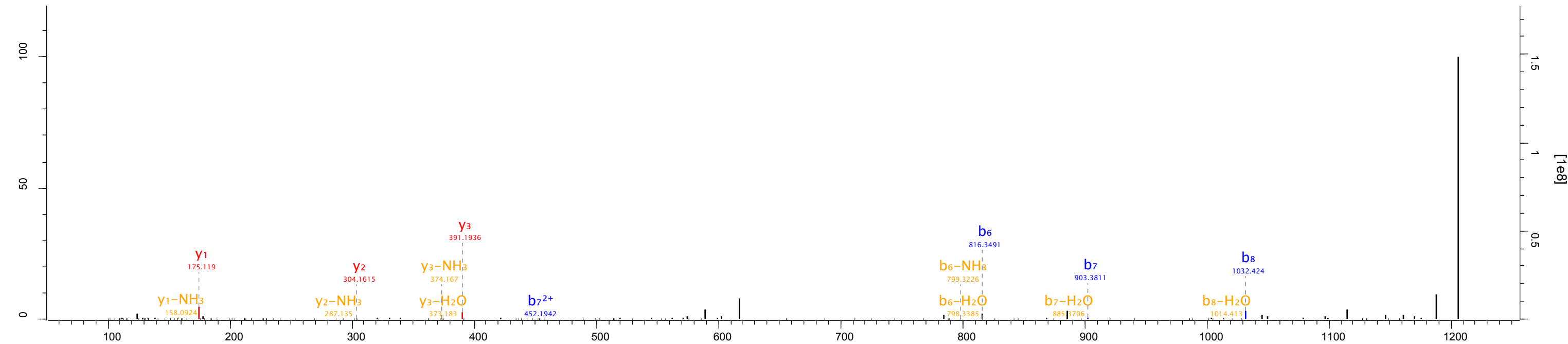
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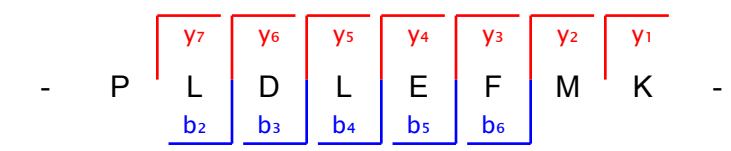
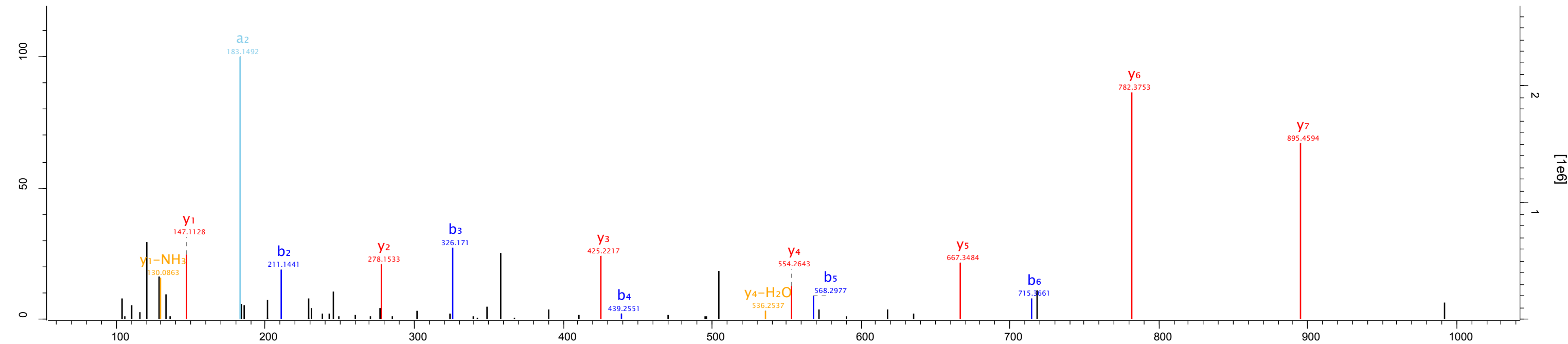
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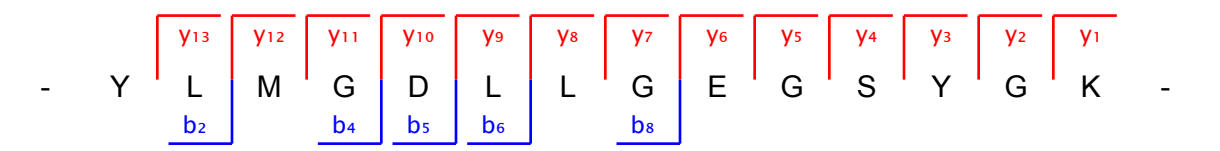
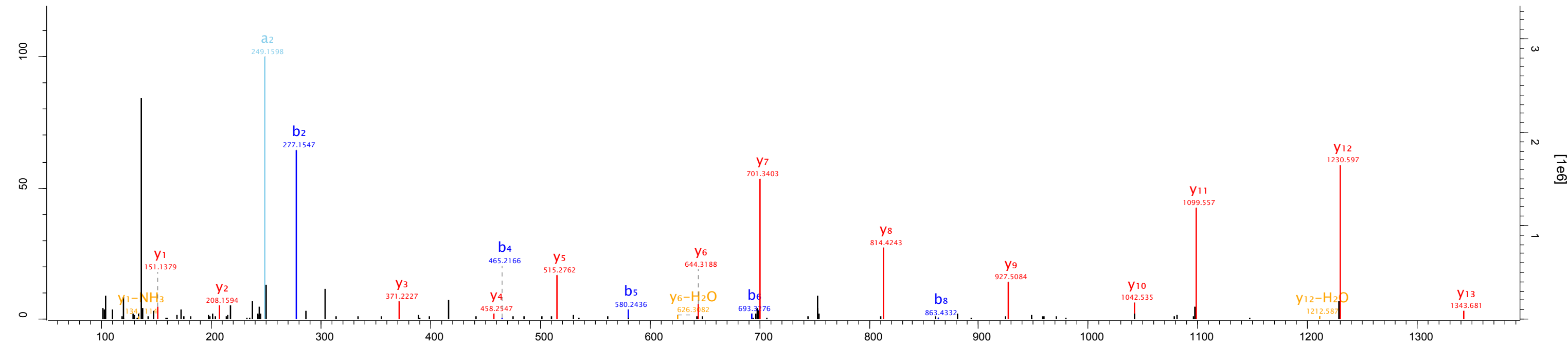


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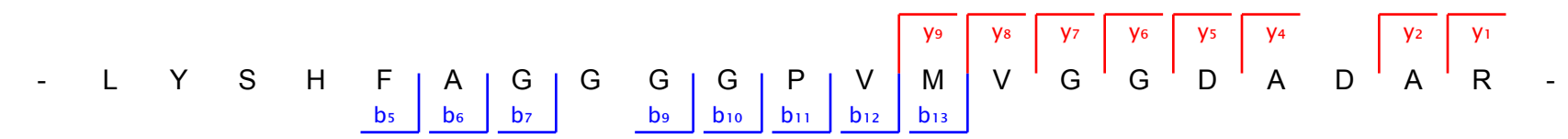
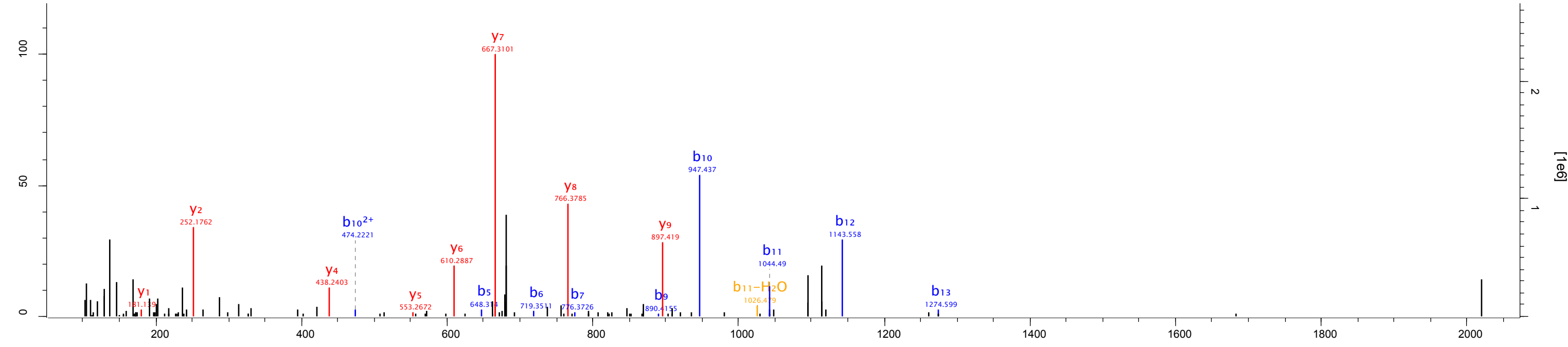


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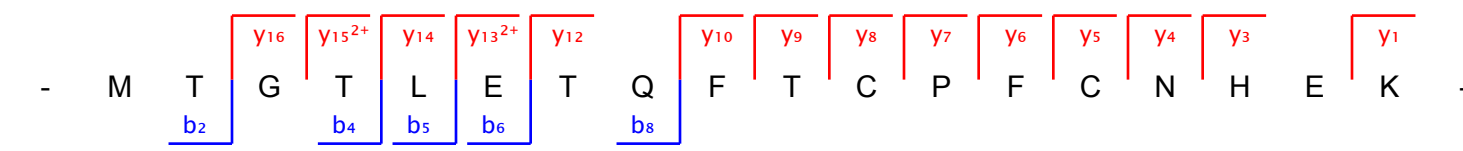
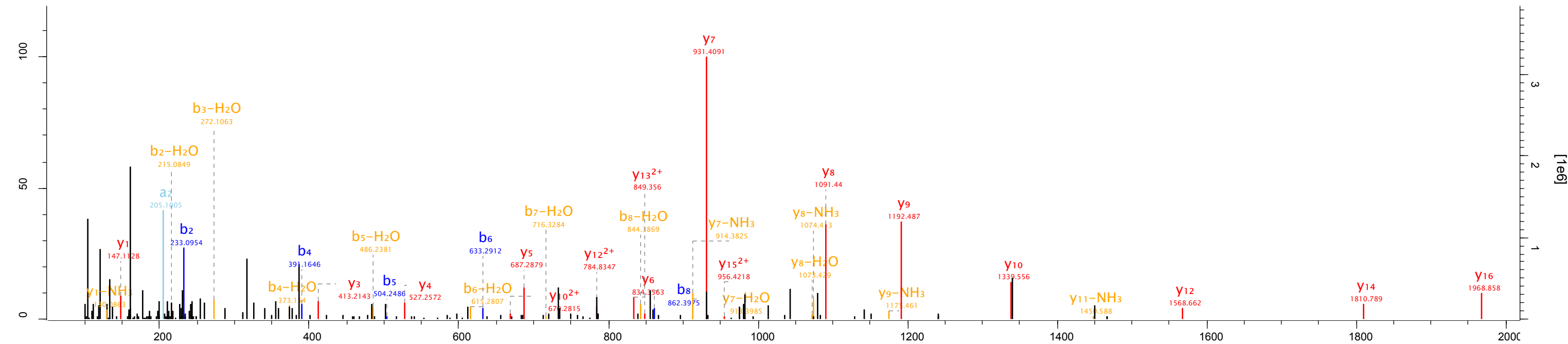


20180707_MaS_A375SR_ML_proteome_2_11 17343 FTMS; HCD 35.09 681 UFSP1

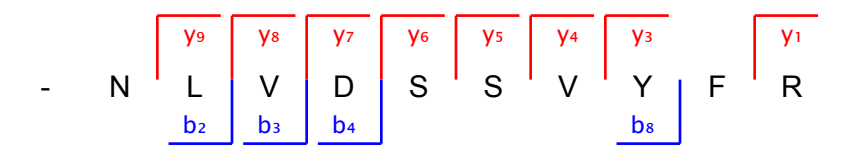
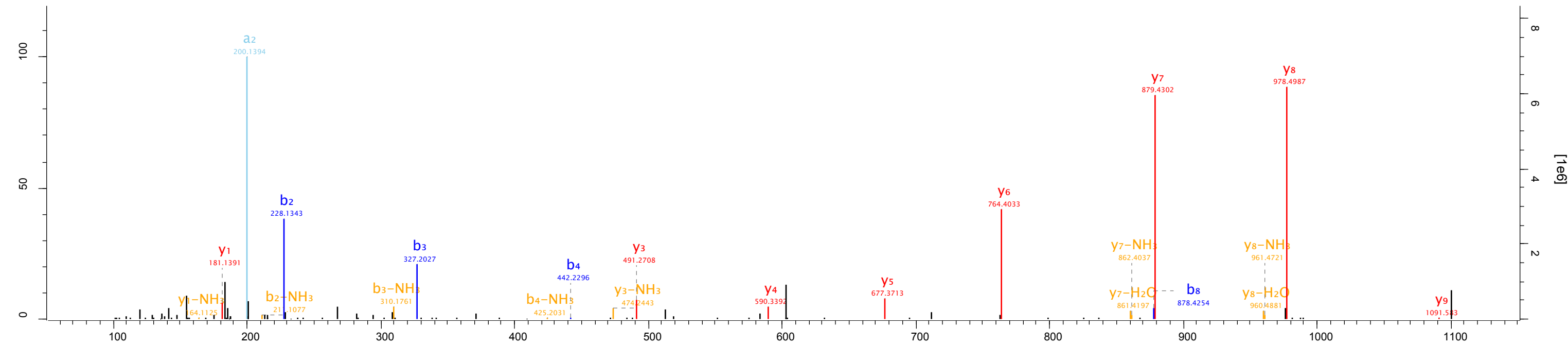


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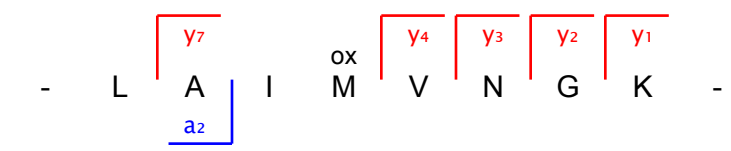
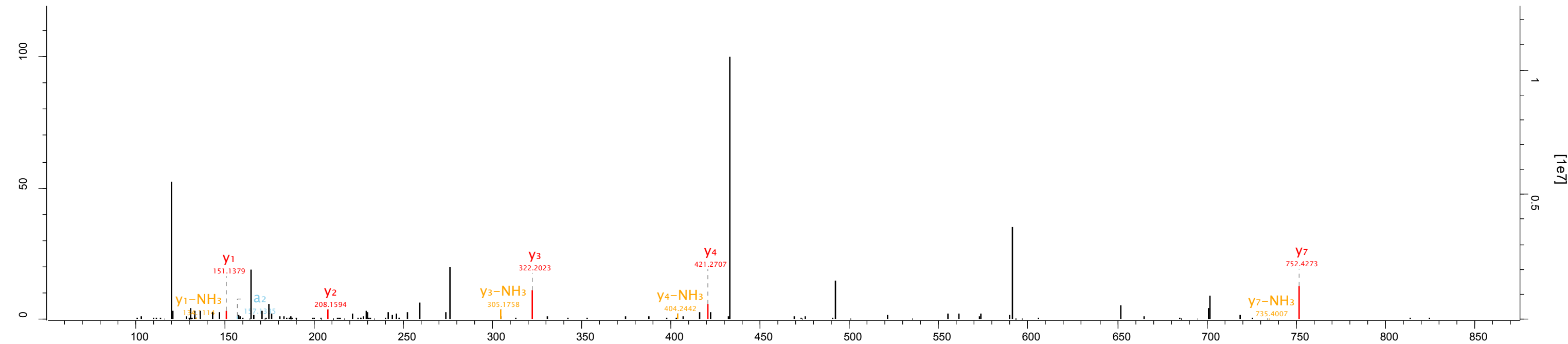


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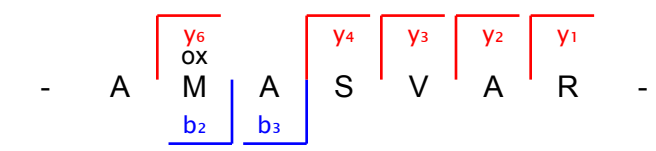
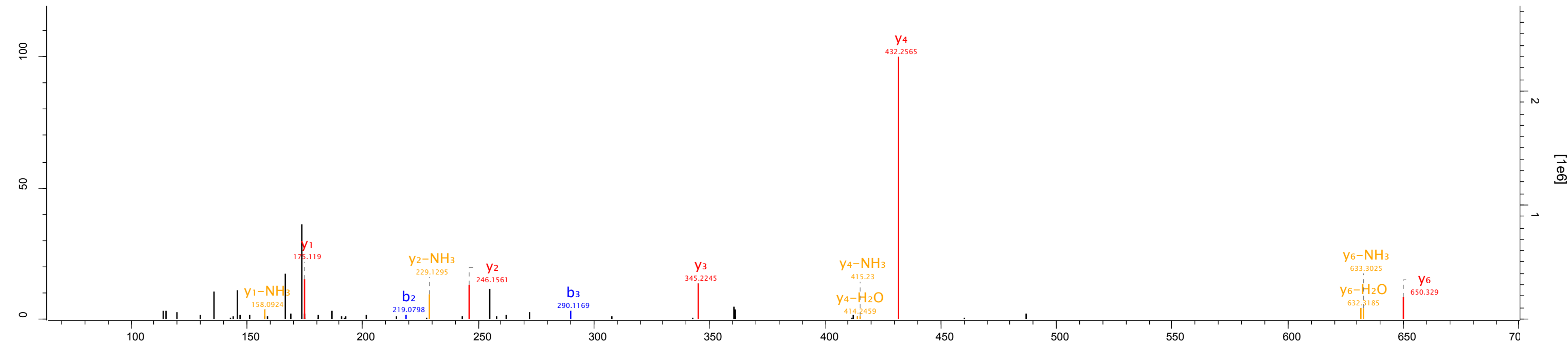


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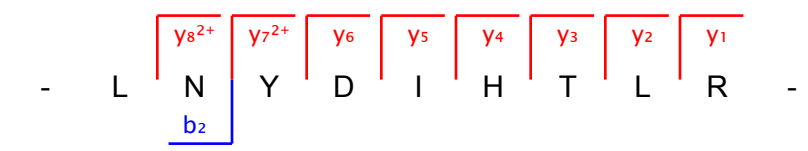
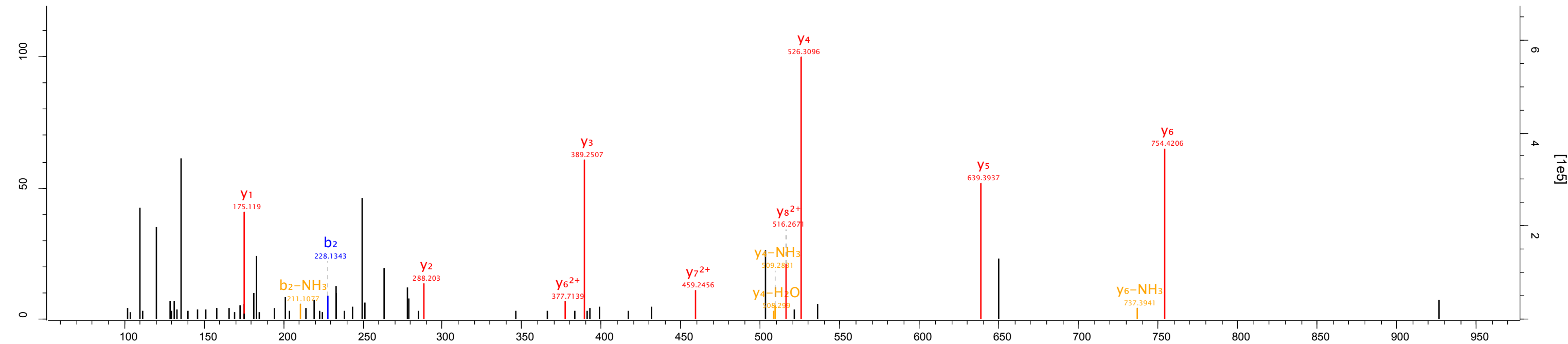
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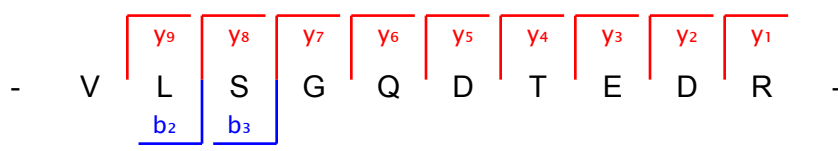
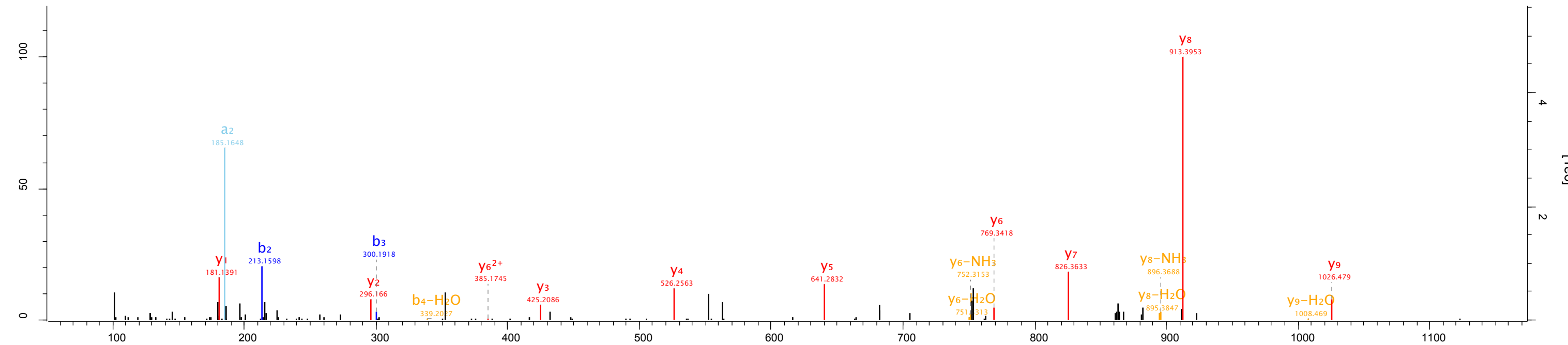
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Scan 14823 Method FTMS; HCD Score 68.37 m/z 382.54 Gene names MREG



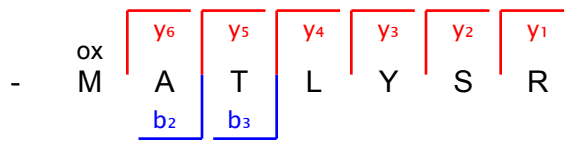
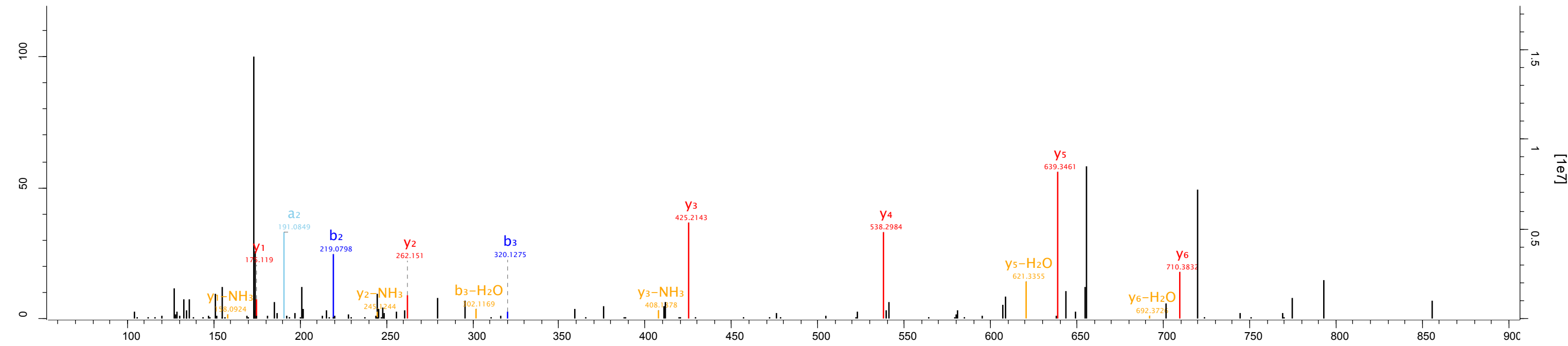
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Scan Method Score m/z Gene names
4843 FTMS; HCD 60.26 563.28 SFT2D2

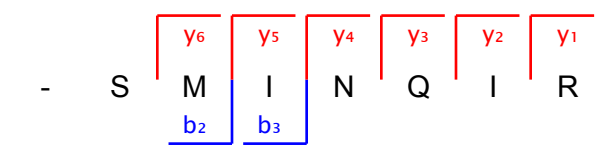
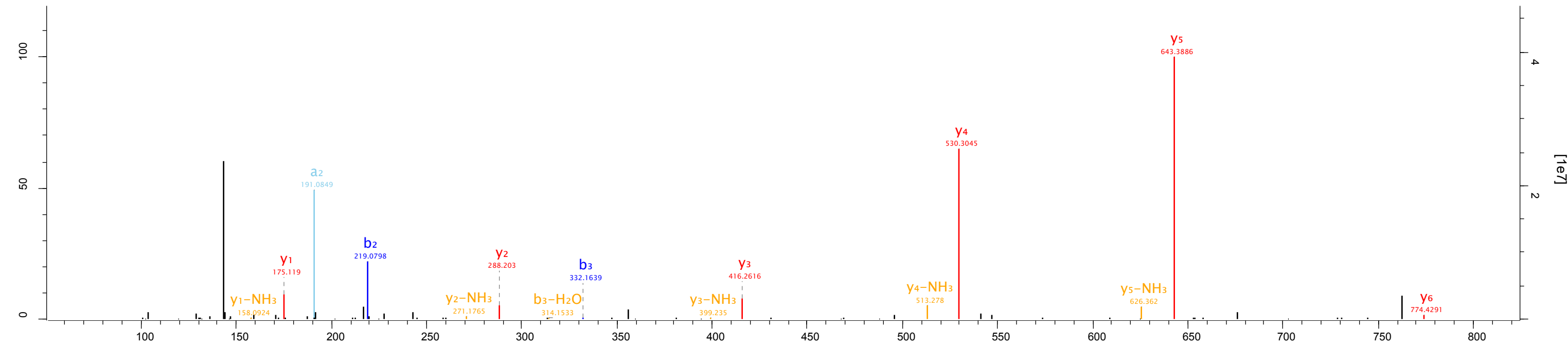


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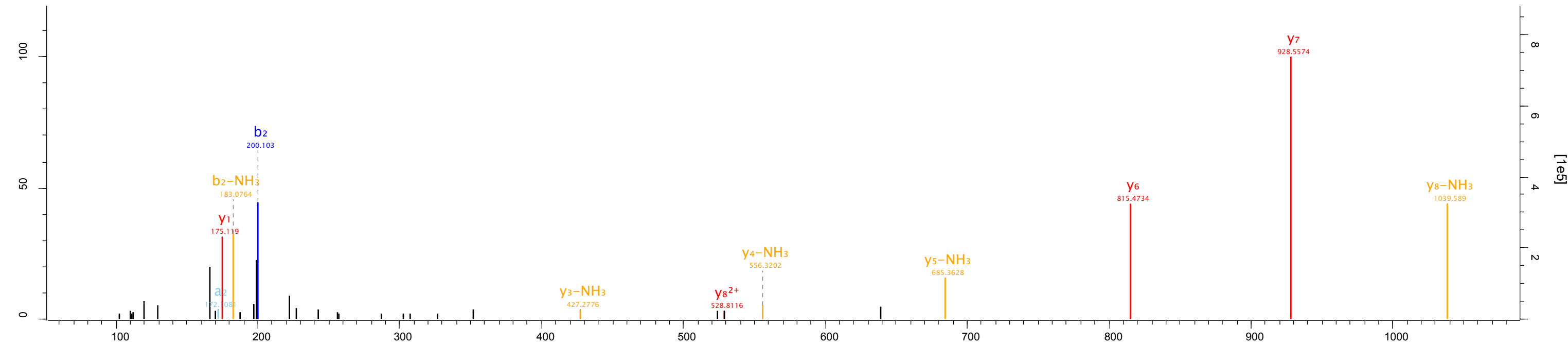


Raw file 20180707_MaS_A375SR_ML_proteome_2_15 Scan 12313 Method FTMS; HCD Score 111.28 m/z 431.23



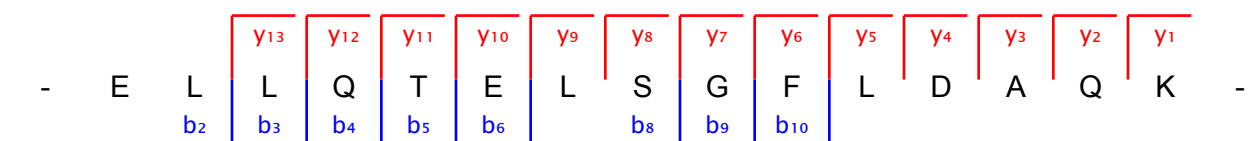
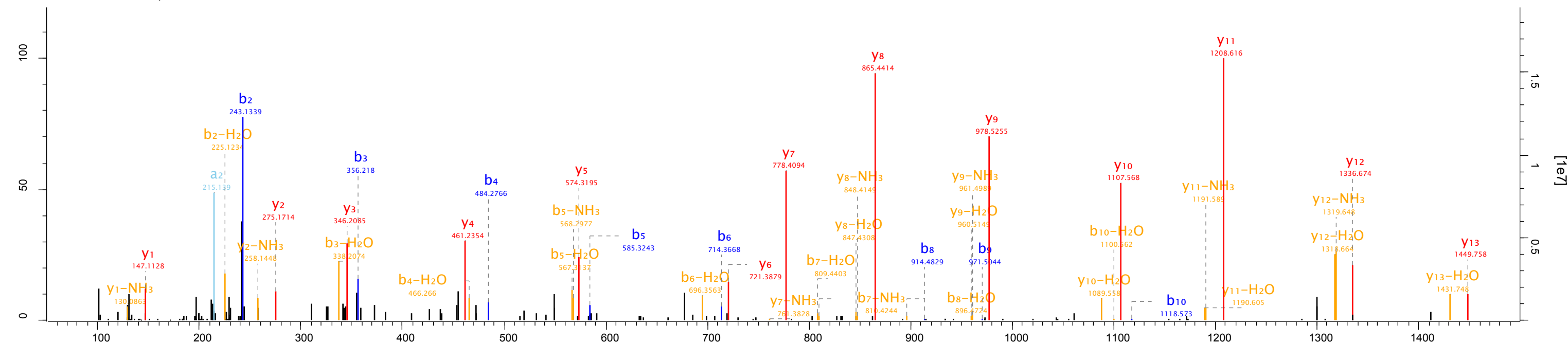
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Scan 16713 Method FTMS; HCD Score 31.42 m/z 376.56 Gene names PNKD

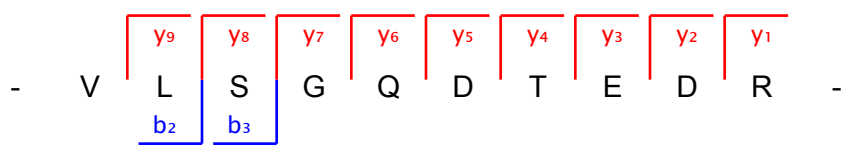
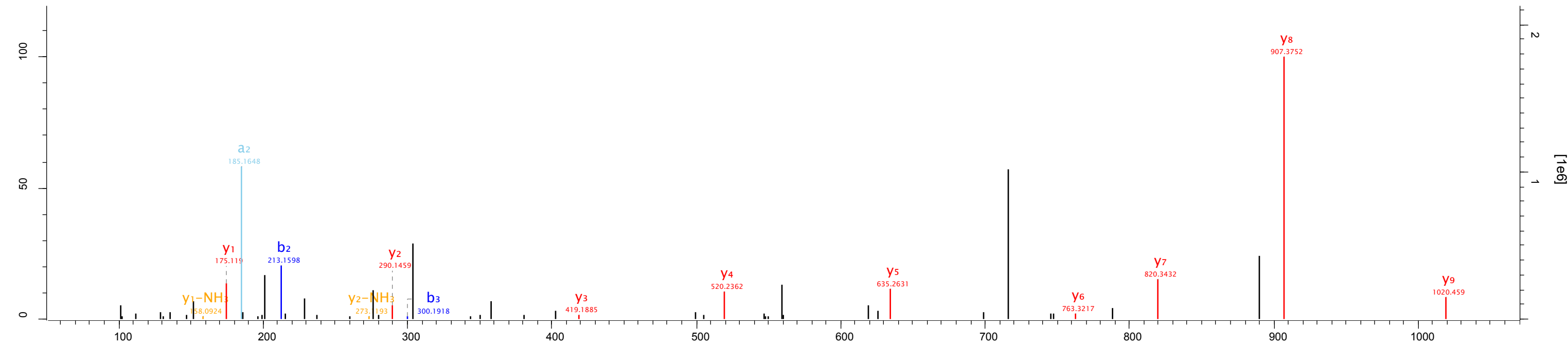


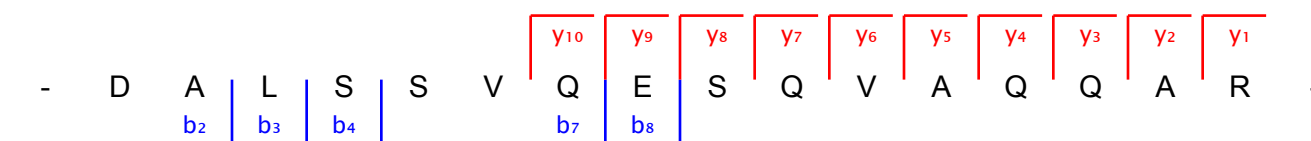
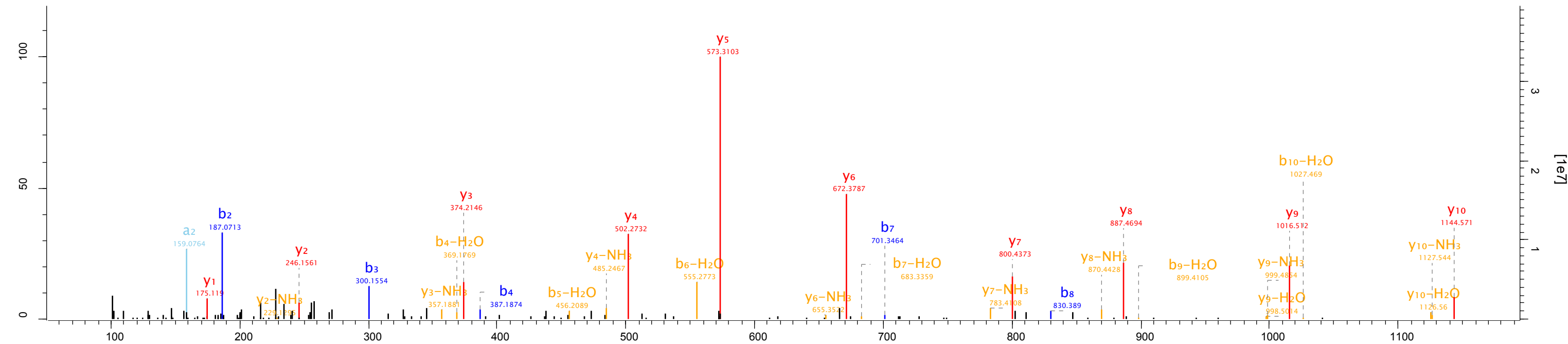
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20180707_MaS_A375SR_ML_proteome_2_15

Scan 29433 Method FTMS; HCD Score 230.86 m/z 846.45 Gene names S100A1



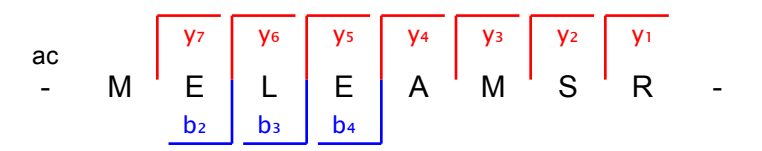
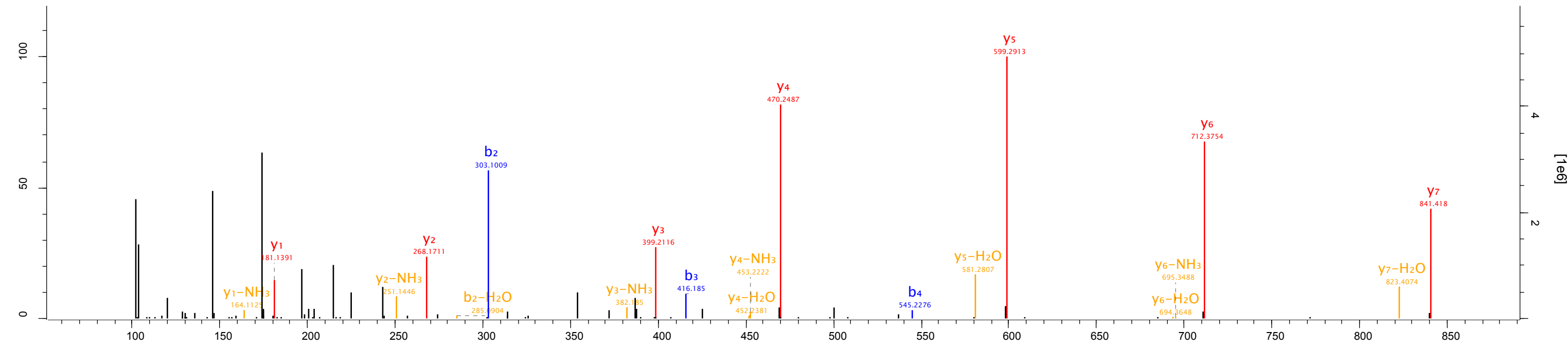
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 Scan: 4773 Method: FTMS; HCD Score: 50.95 m/z: 560.27 Gene names: SFT2D2





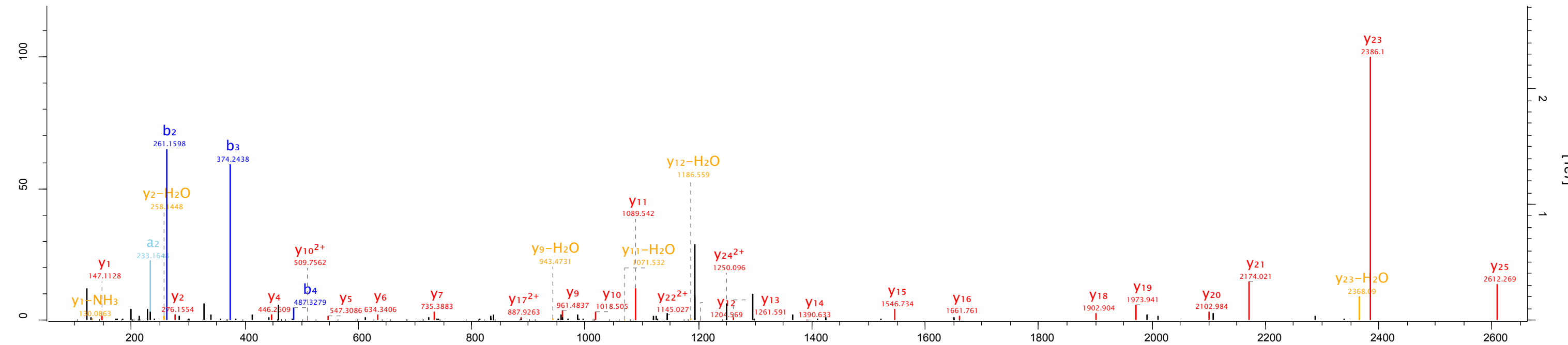
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Scan: 25663
Method: FTMS; HCD
Score: 119.21
m/z: 507.74
Gene names: TMEM258



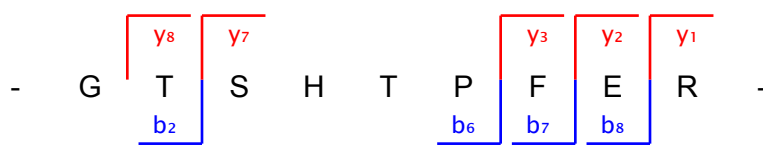
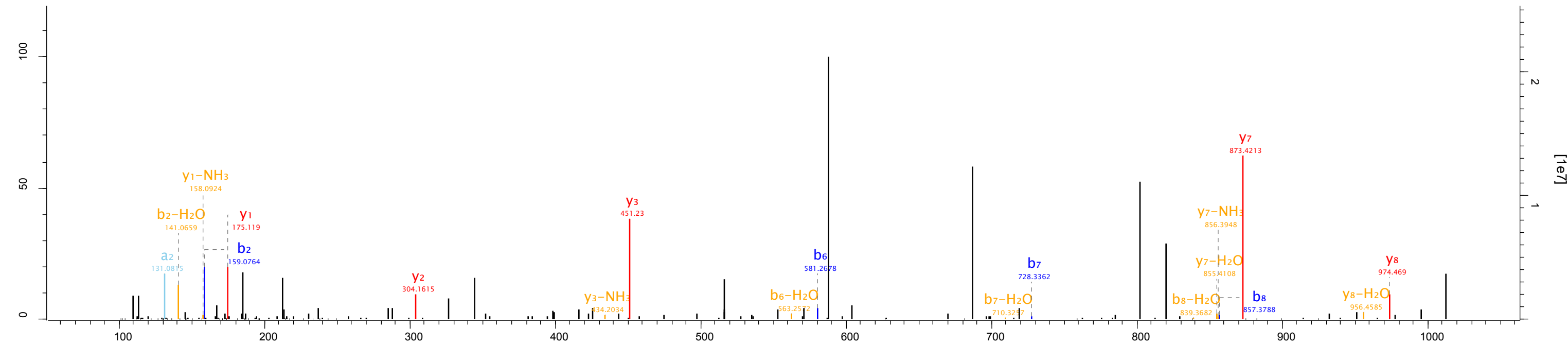
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Scan 27613 Method FTMS; HCD Score 100.23 m/z 958.48 Gene names TMEM128



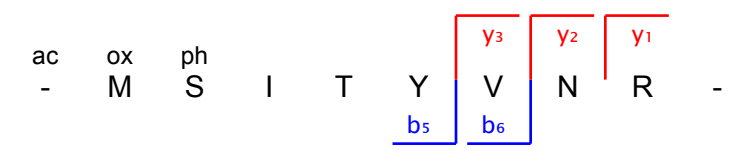
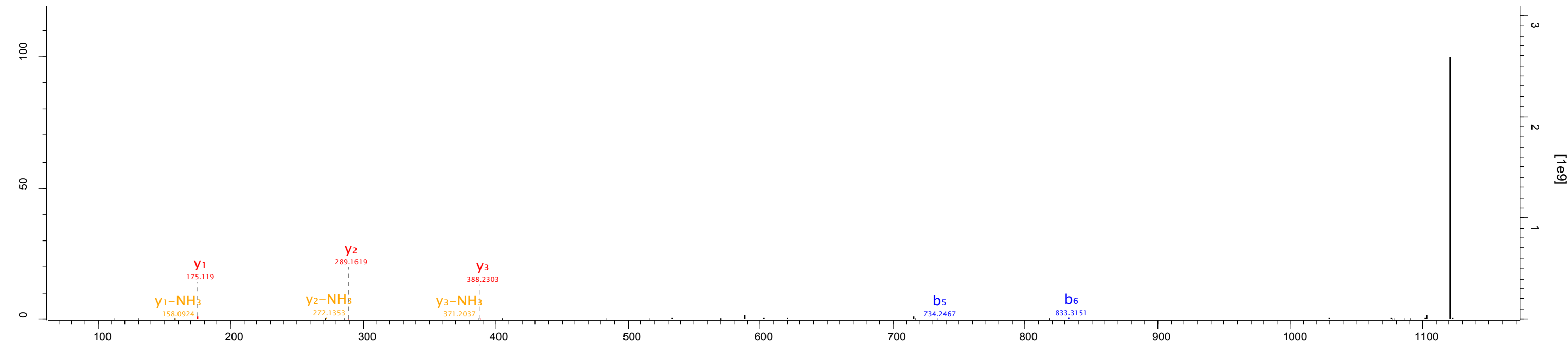
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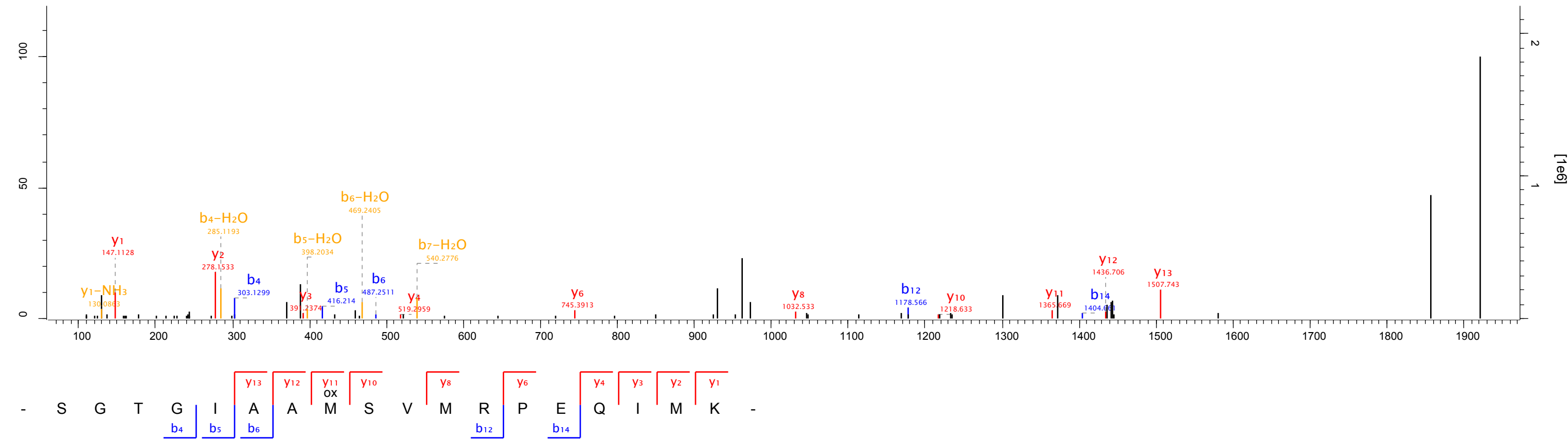


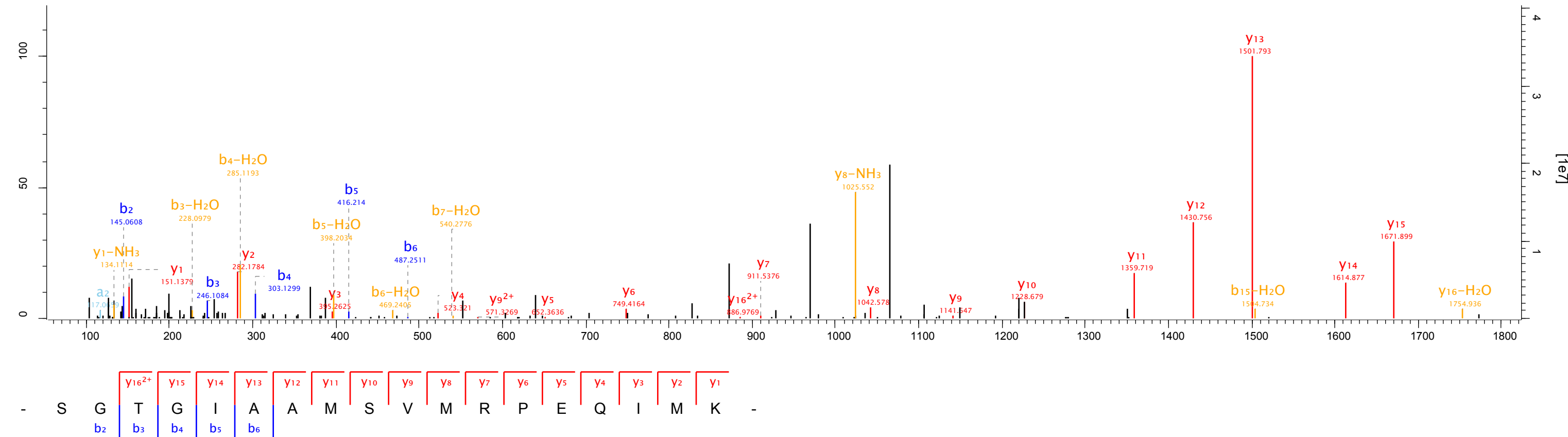
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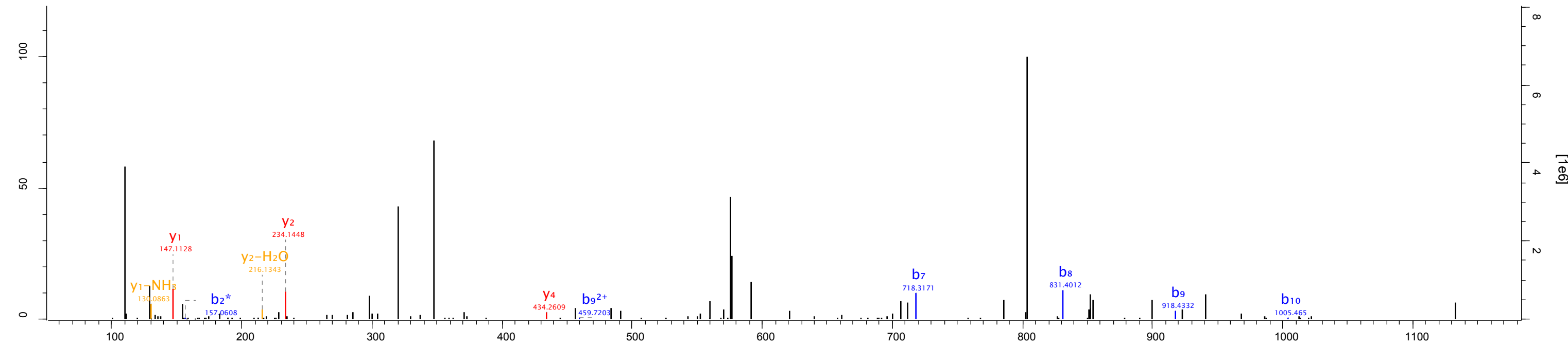
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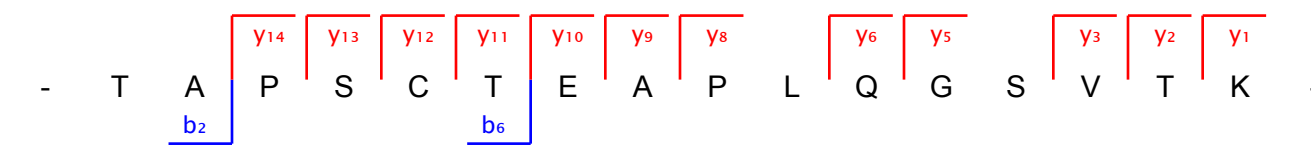
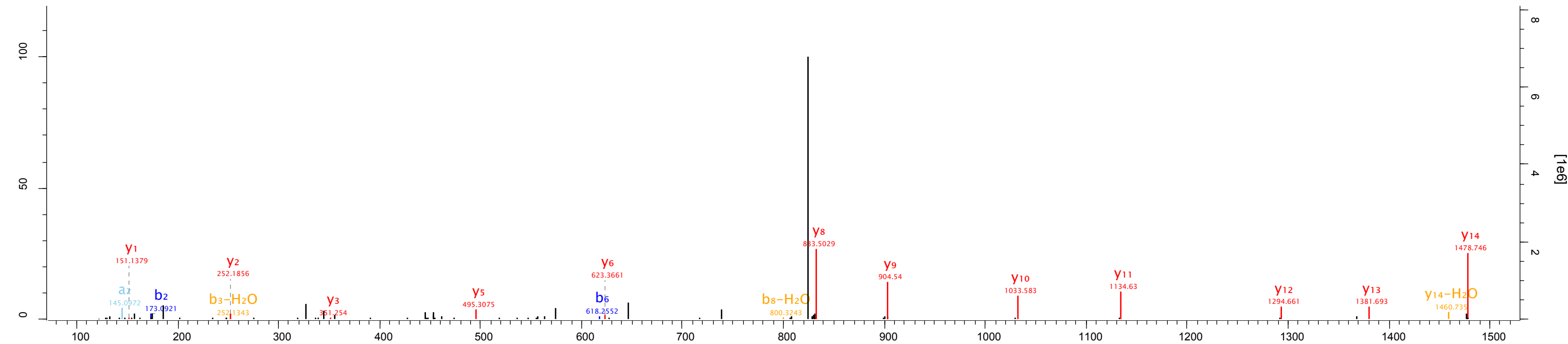
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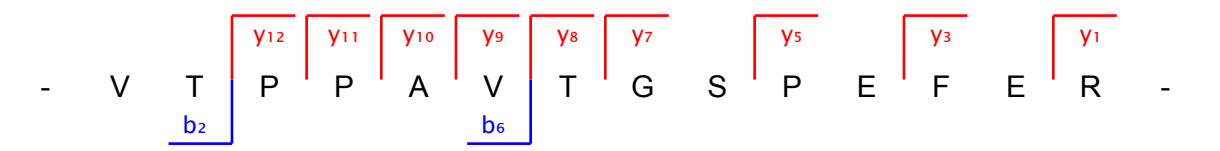
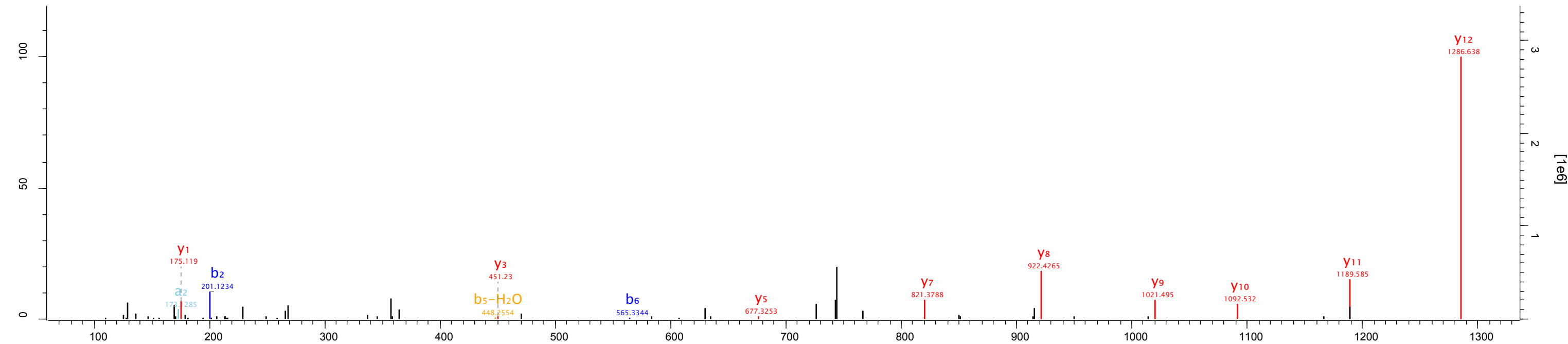




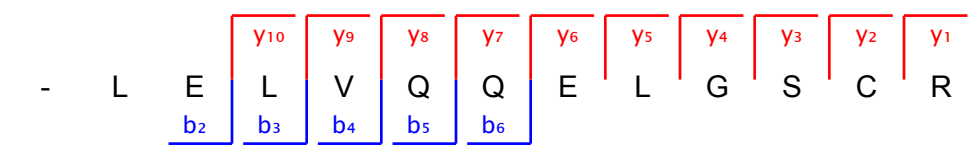
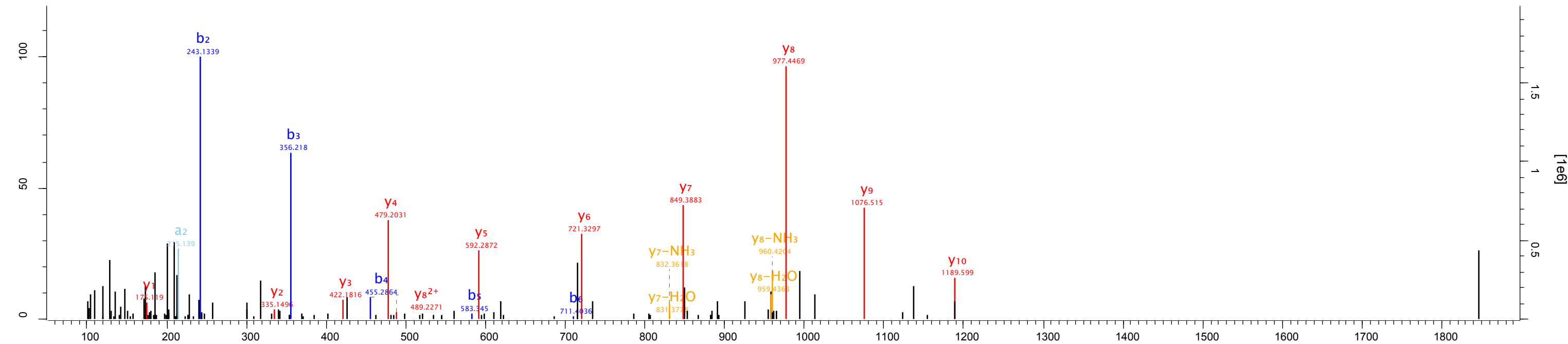
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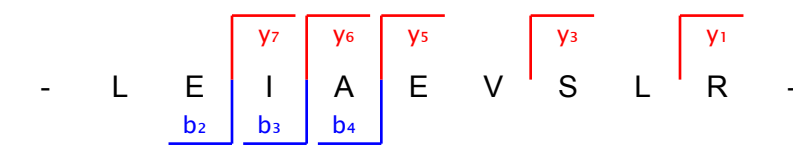
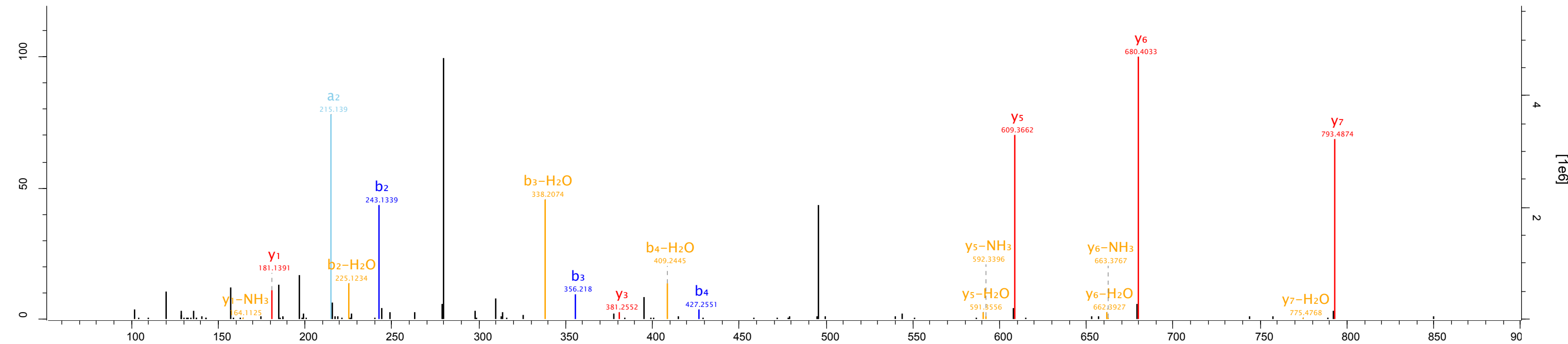
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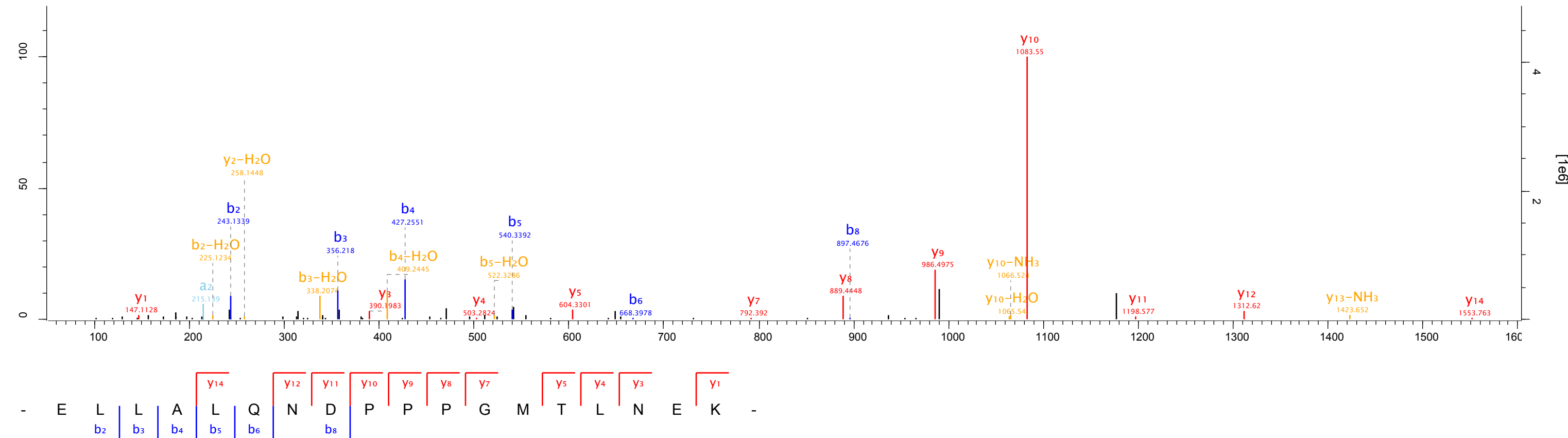


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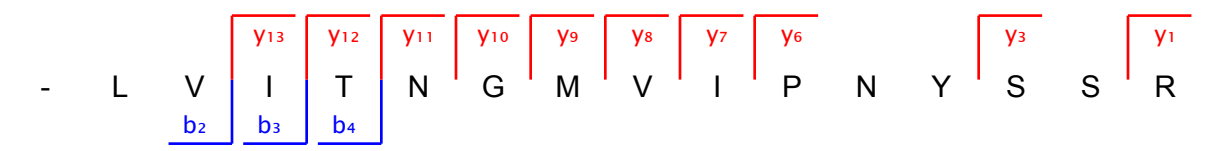
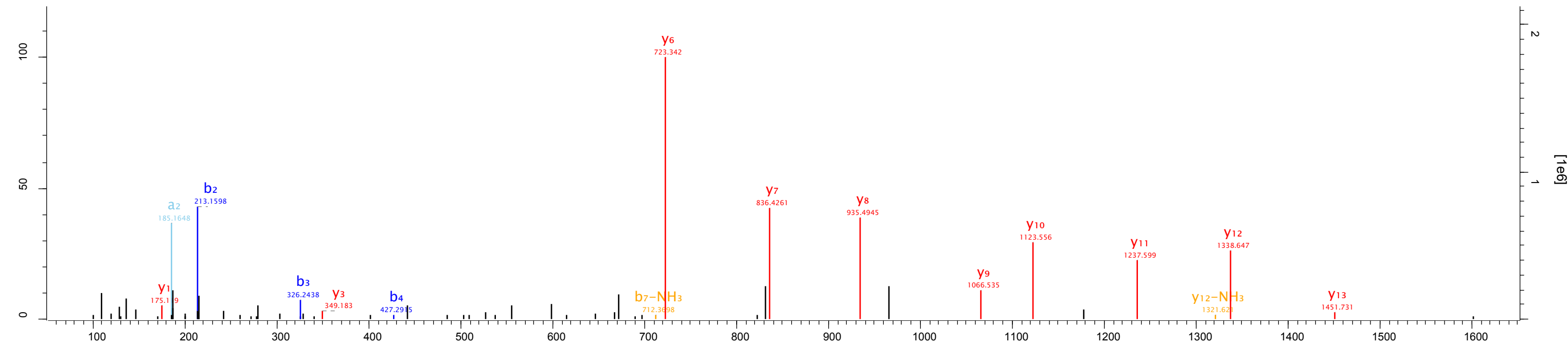
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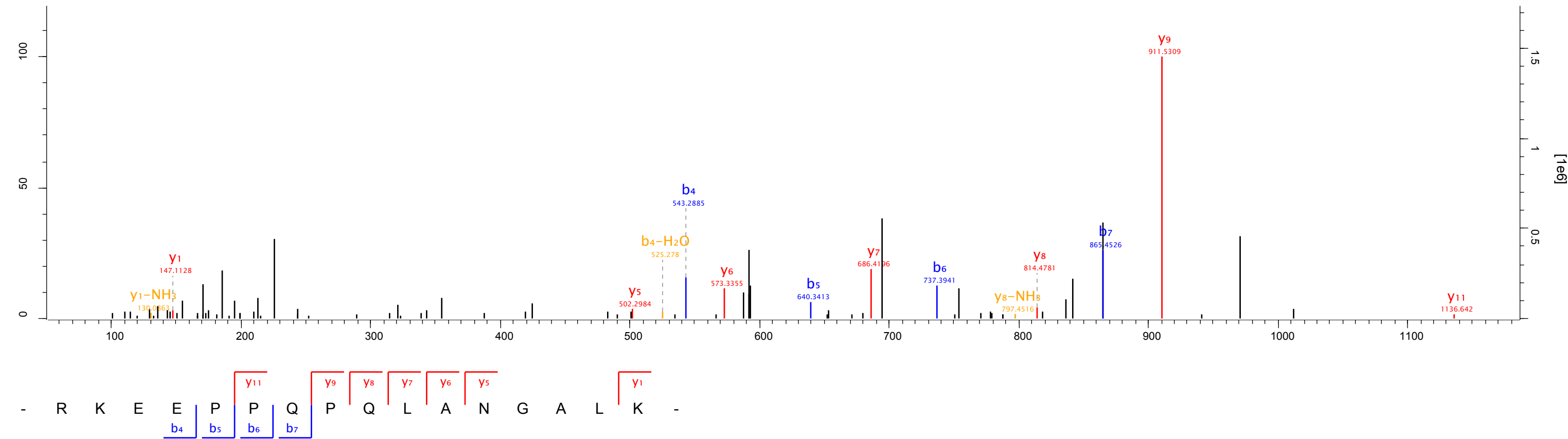
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Scan 25583 Method FTMS; HCD Score 65.37 m/z 832.44 Gene names UROC1



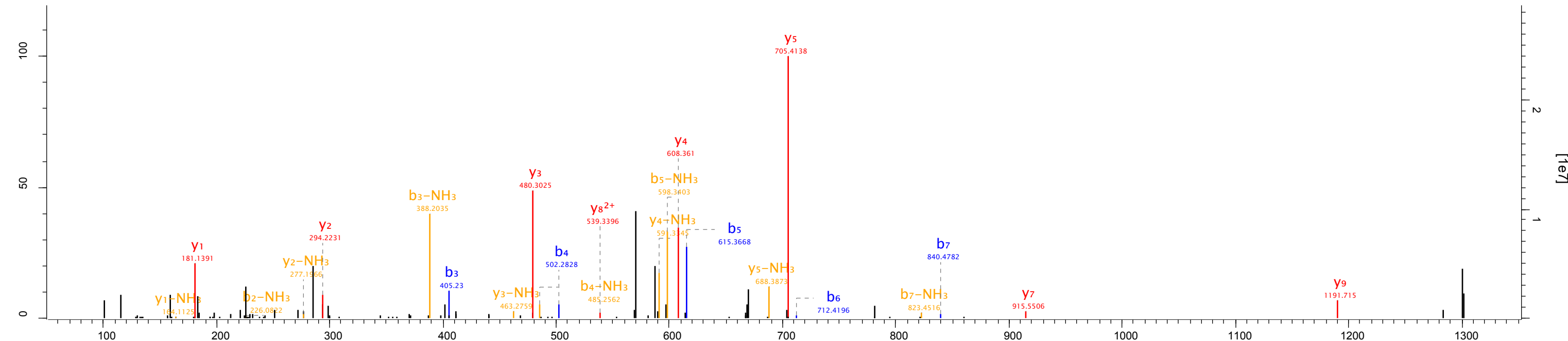
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Scan	Method	Score	m/z	Gene names
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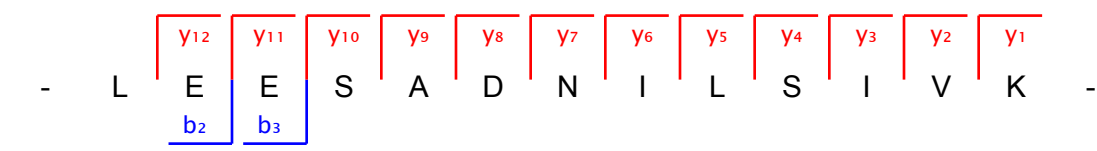
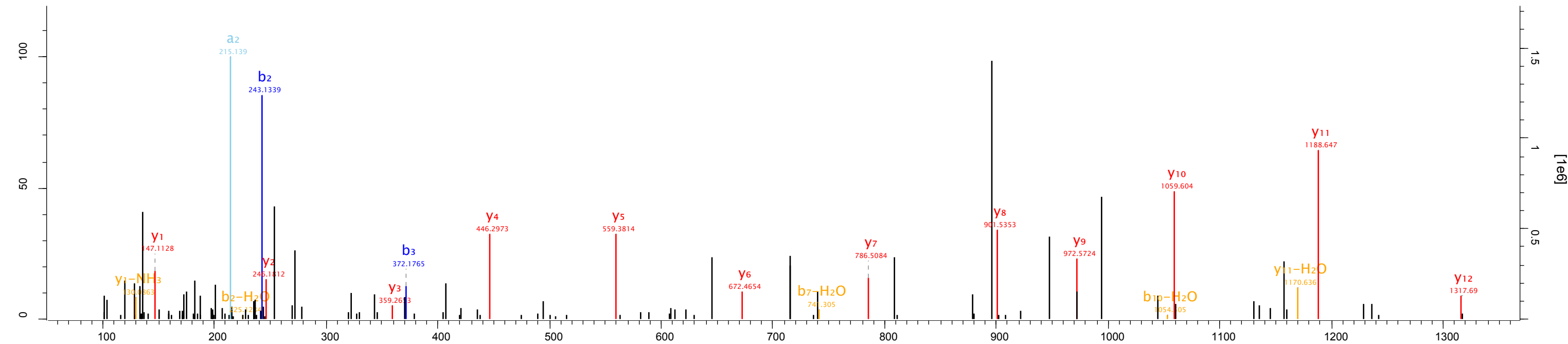
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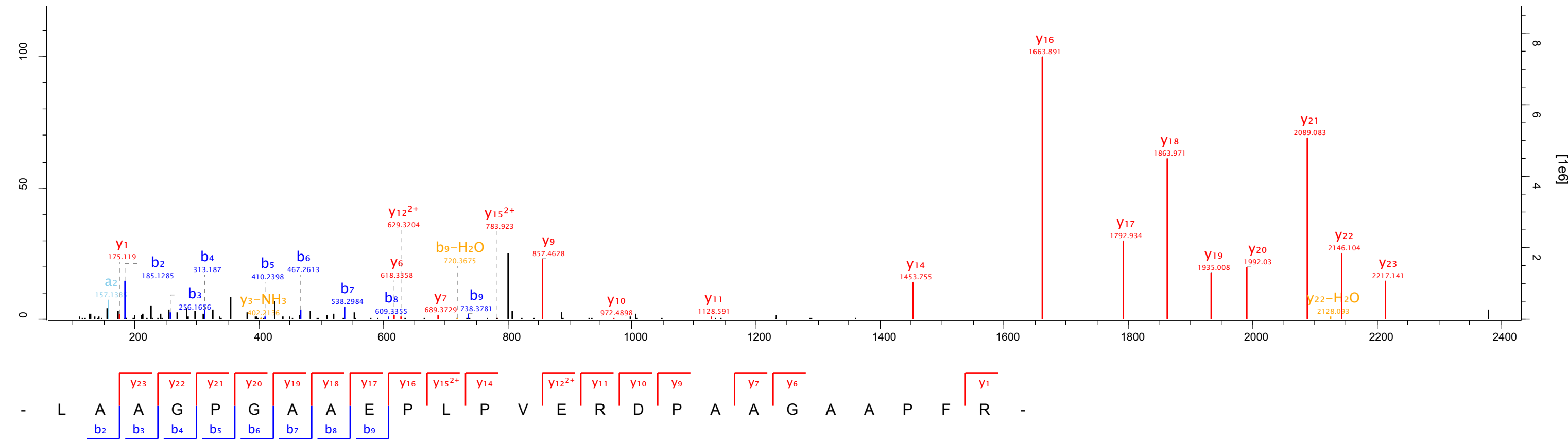
Scan 15613 Method FTMS; HCD Score 143.7 m/z 440.6 Gene names RPL39P5;RPL39



- Q N R P I P Q W I R -
 b3 b4 b5 b6 b7

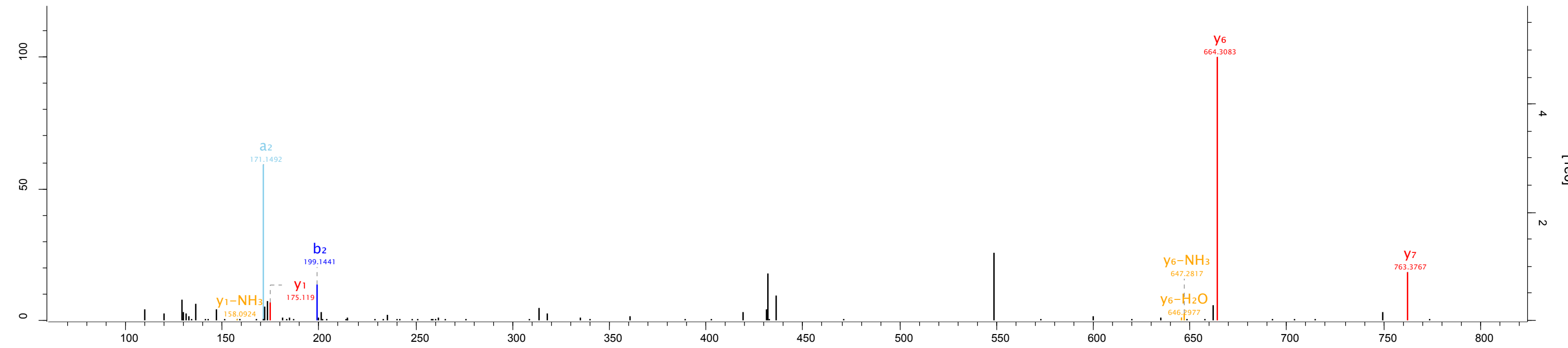
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 Scan: 27523 Method: FTMS; HCD Score: 66.22 m/z: 715.89 Gene names: RFXAP

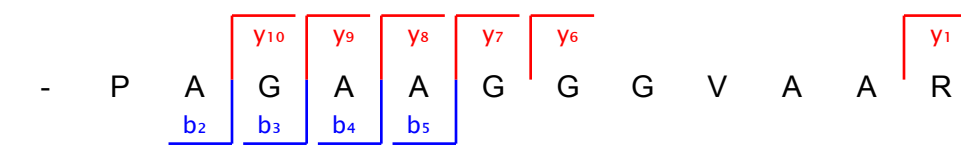
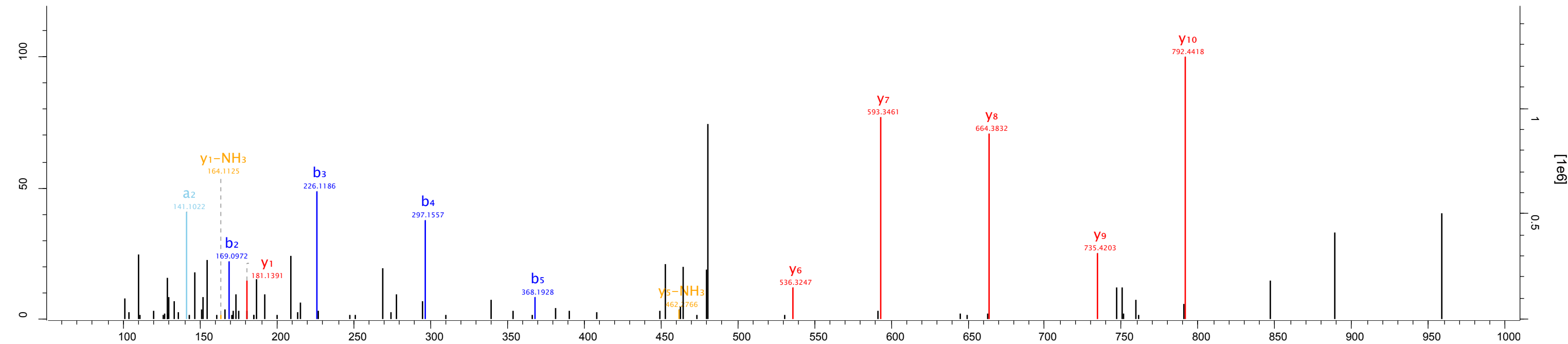




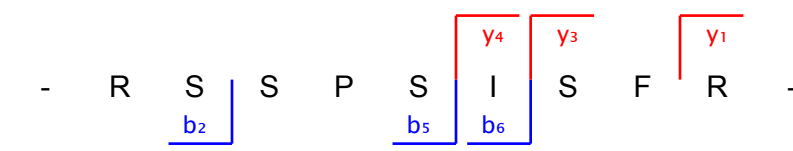
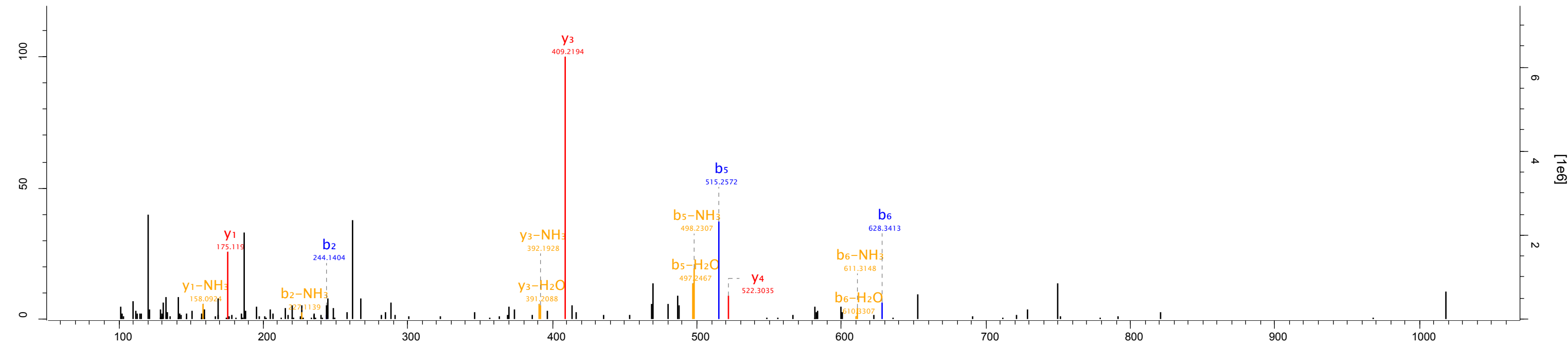
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20180707_MaS_A375SR_ML_proteome_2_27

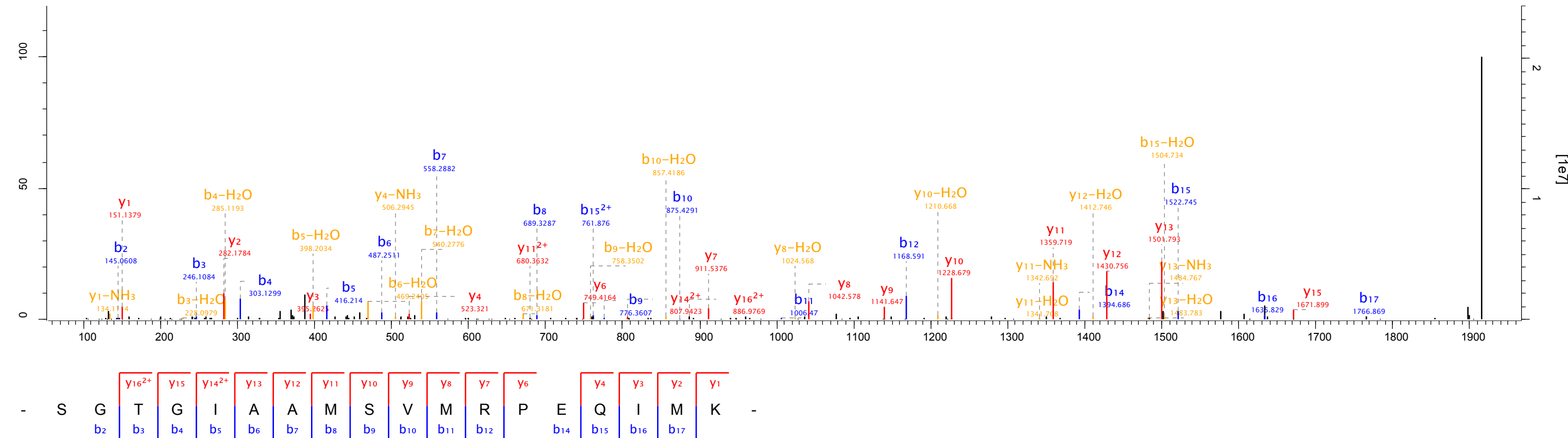
Scan 9293 Method FTMS; HCD Score 40.27 m/z 431.73



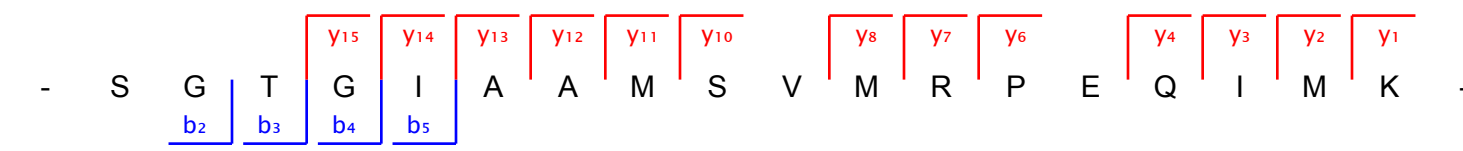
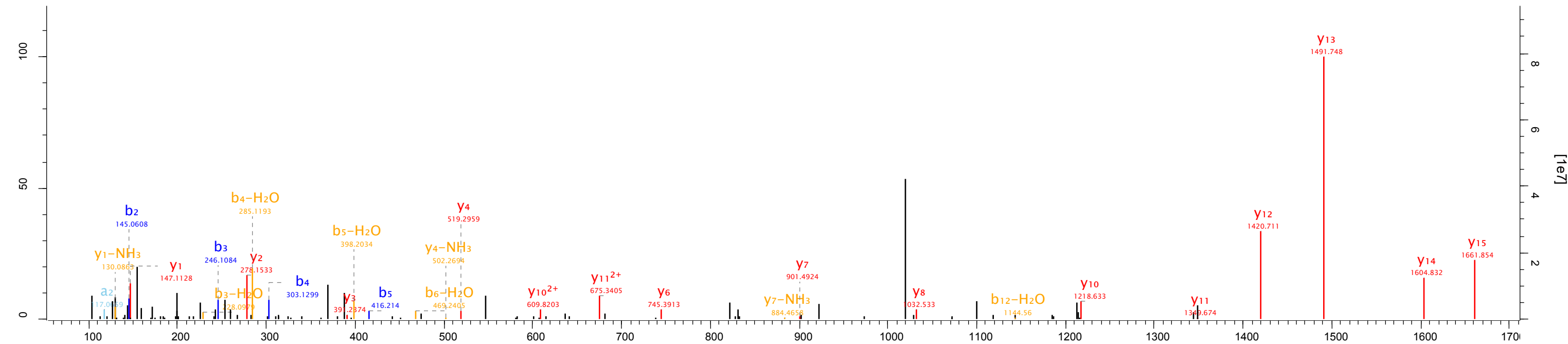


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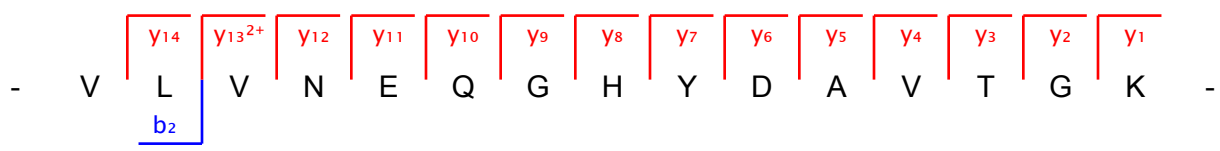
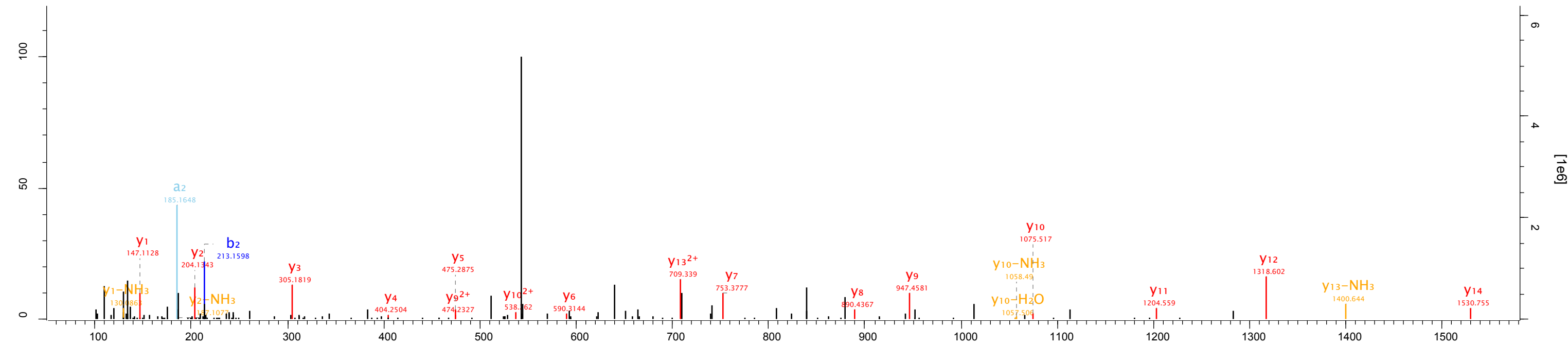


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 Scan: 23703 Method: FTMS; HCD Score: 92.63 m/z: 636.66 Gene names: ATP6V0C

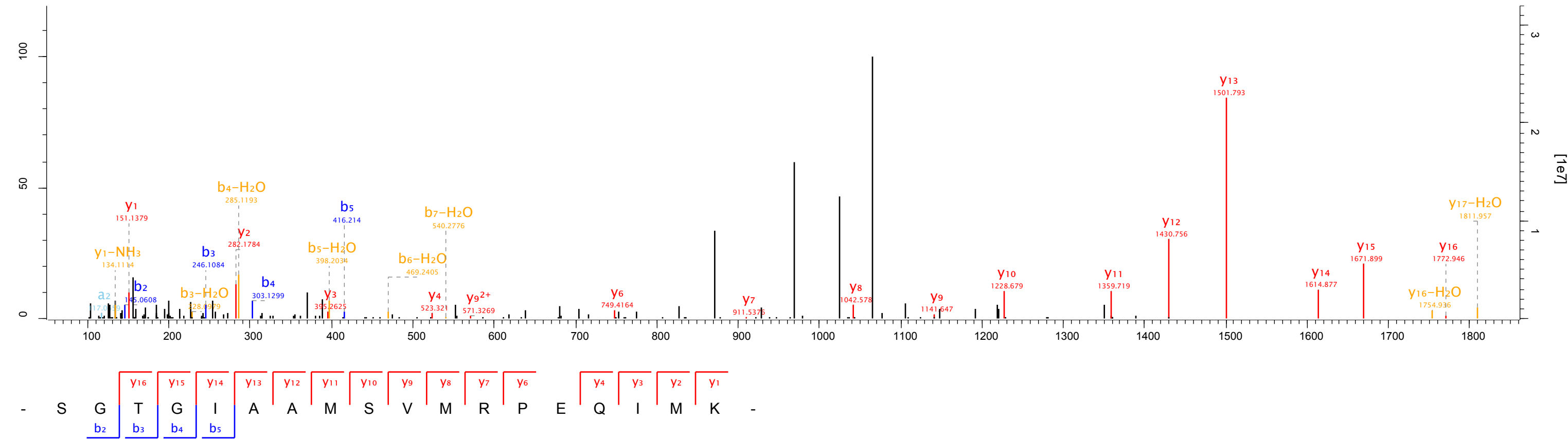


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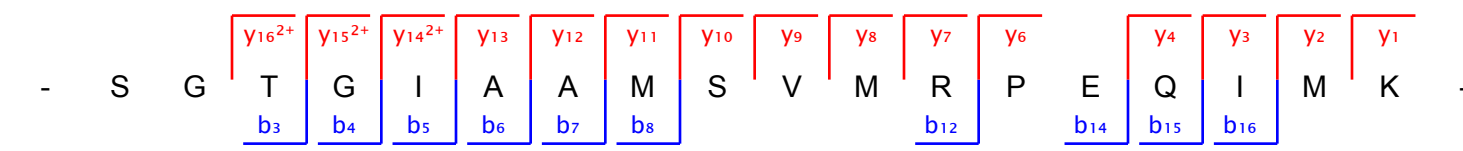
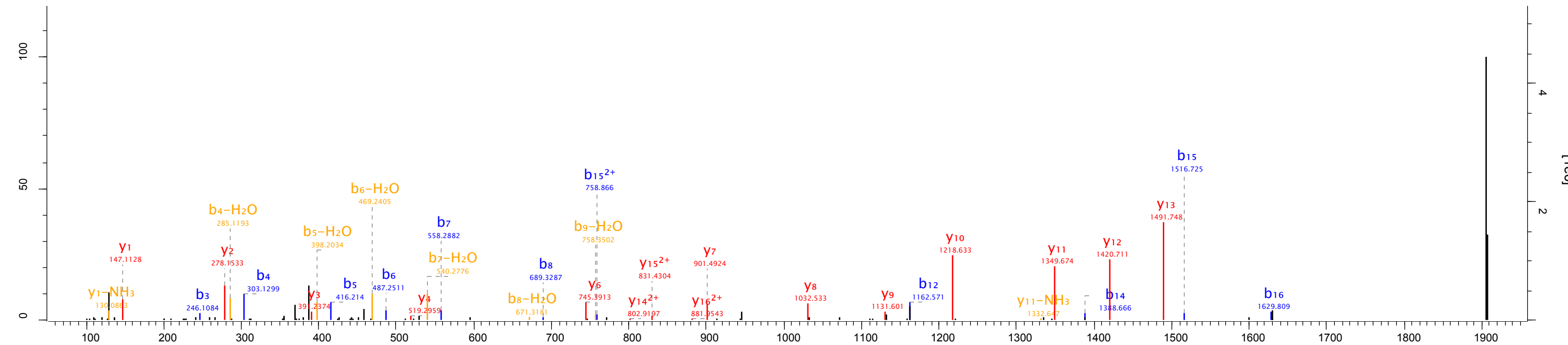
Scan 11213 Method FTMS; HCD Score 70.2 m/z 543.95 Gene names C1QTNF5



Raw file: 20180707_MaS_A375SR_ML_proteome_21
 Scan: 23913 Method: FTMS; HCD Score: 80.86 m/z: 640.01 Gene names: ATP6V0C

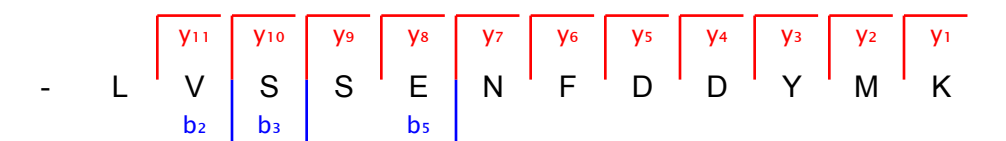
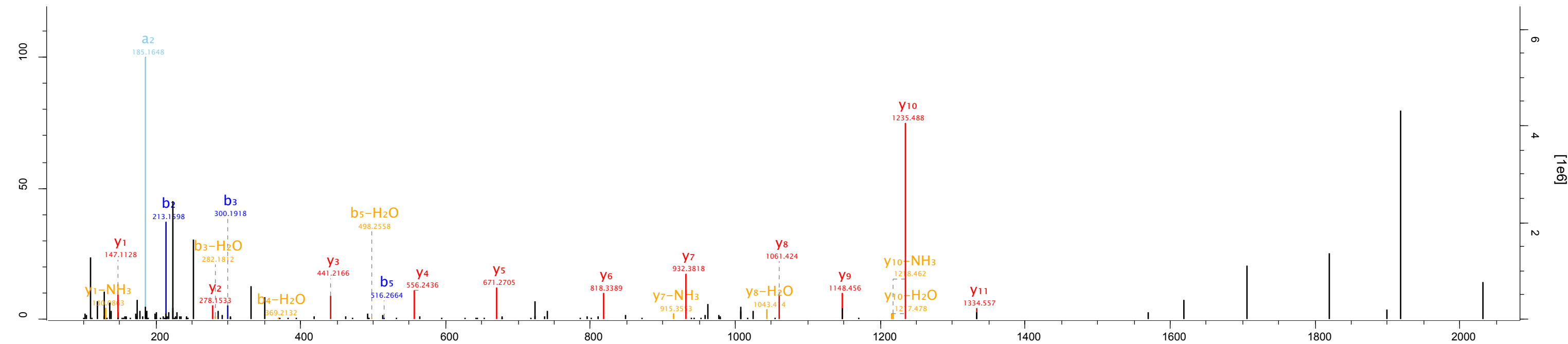


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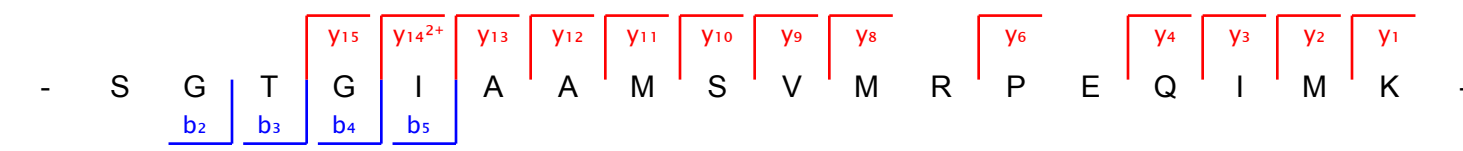
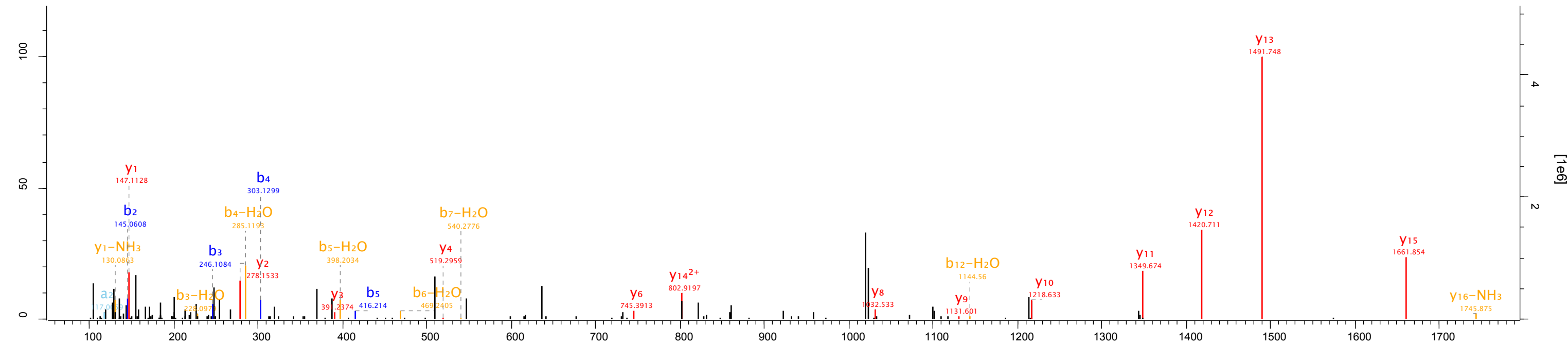


Raw file
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Scan 18963 Method FTMS; HCD Score 105.65 m/z 724.33 Gene names FABP4;PMP2

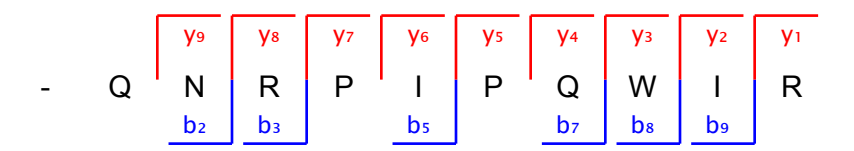
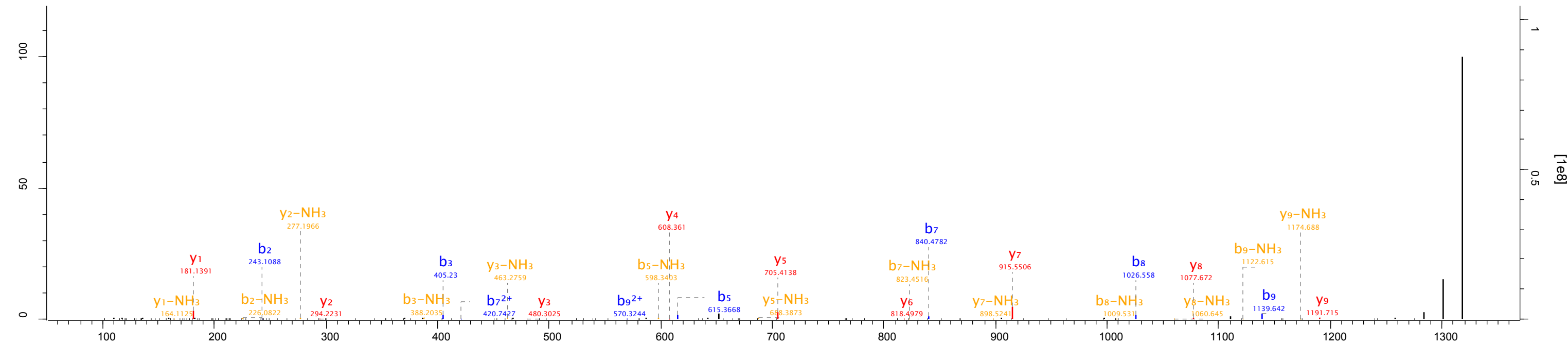


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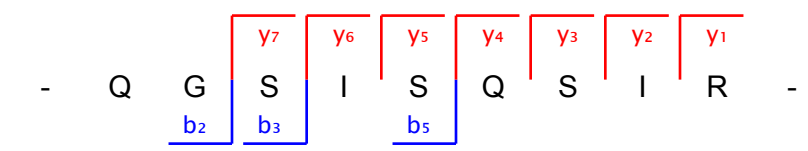
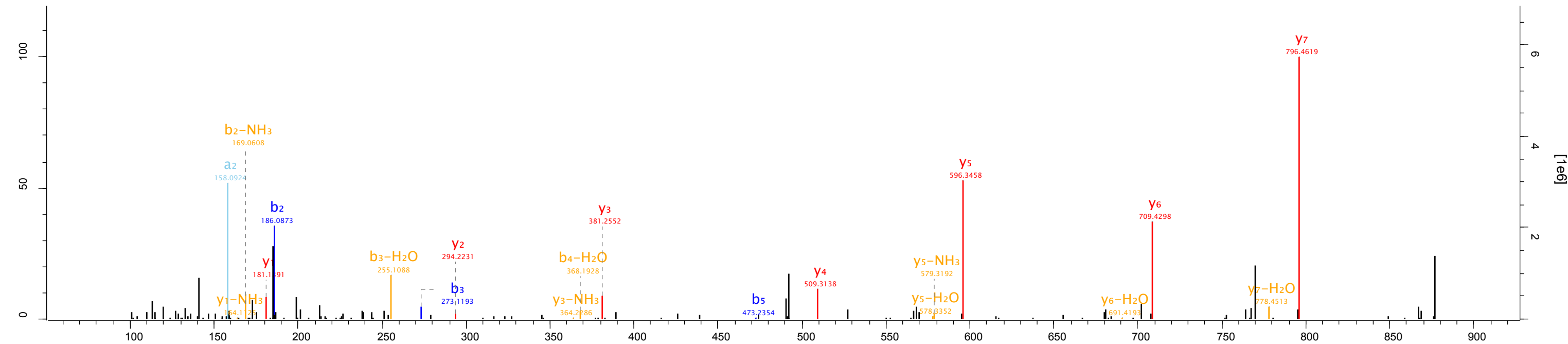


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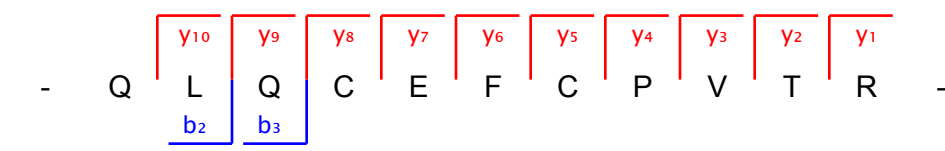
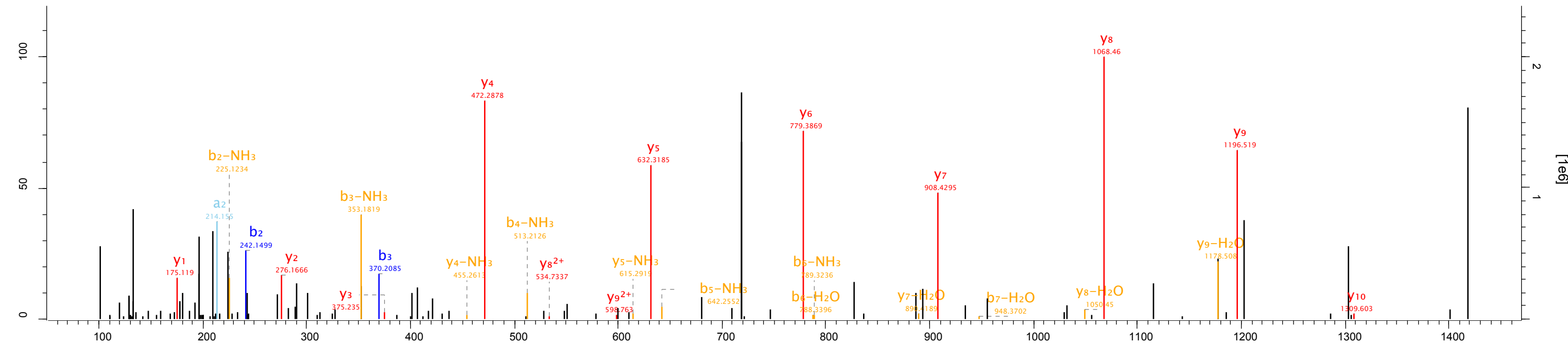
Scan 16553 Method FTMS; HCD Score 210.6 m/z 660.39 Gene names RPL39P5;RPL39



Raw file 20180707_MaS_A375SR_ML_proteome_25 Scan 9573 Method FTMS; HCD Score 72.37 m/z 491.27

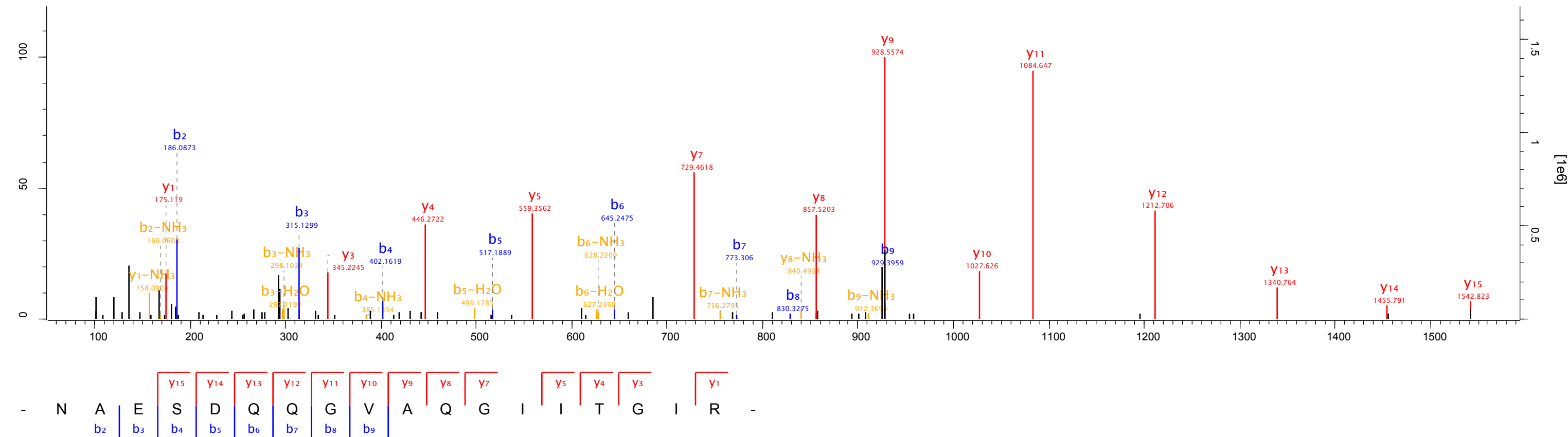


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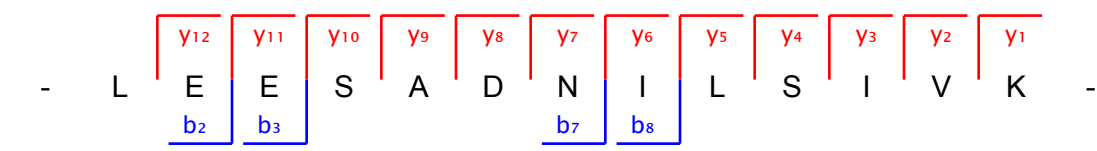
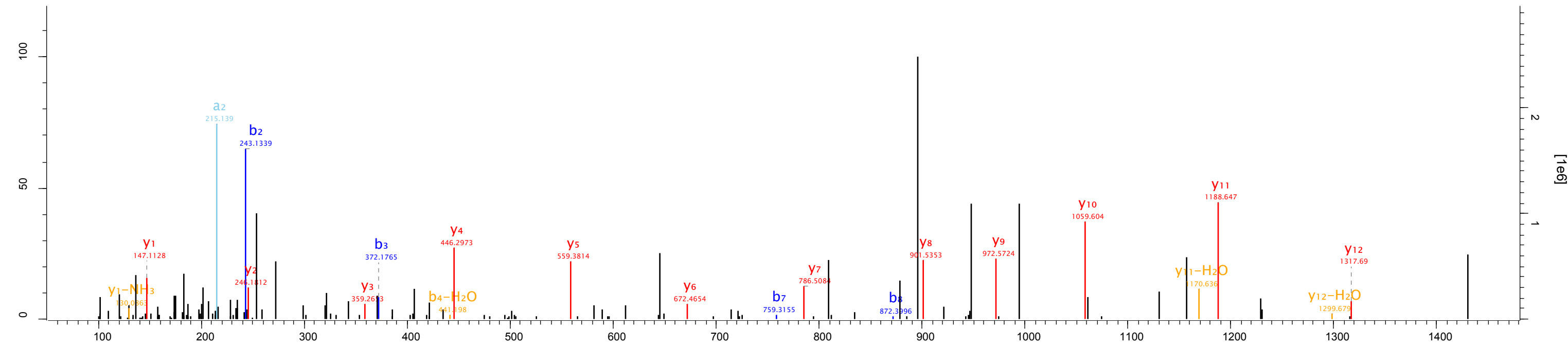


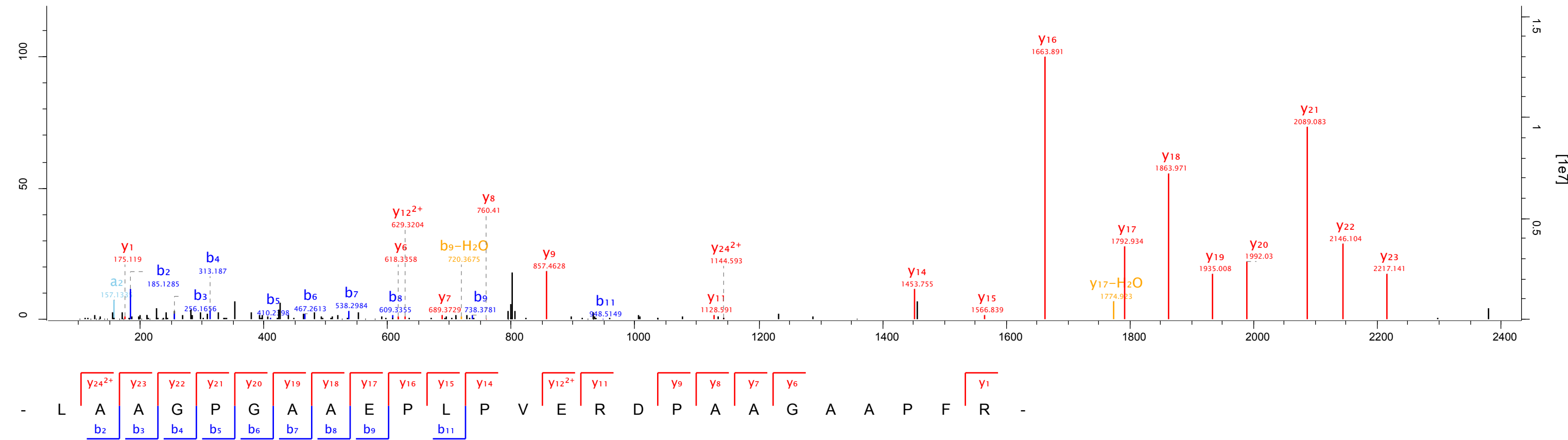
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20180707_MaS_A375SR_ML_proteome_26

Scan 21273 Method FTMS; HCD Score 110.56 m/z 928.98 Gene names HIATL1

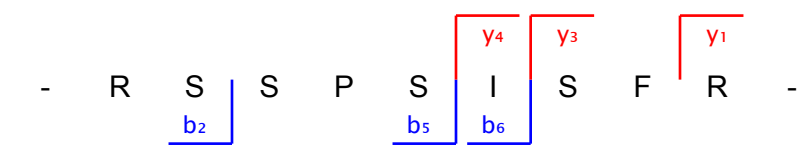
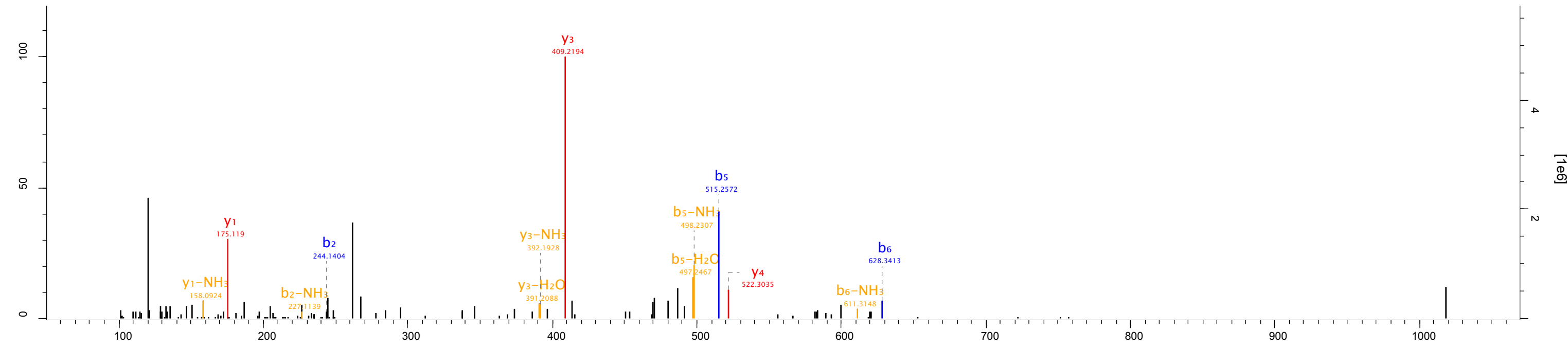


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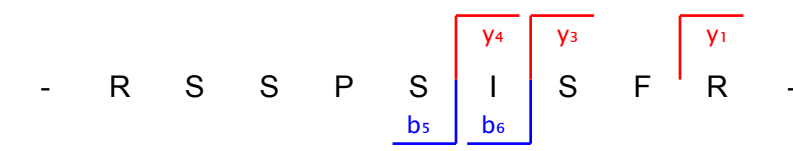
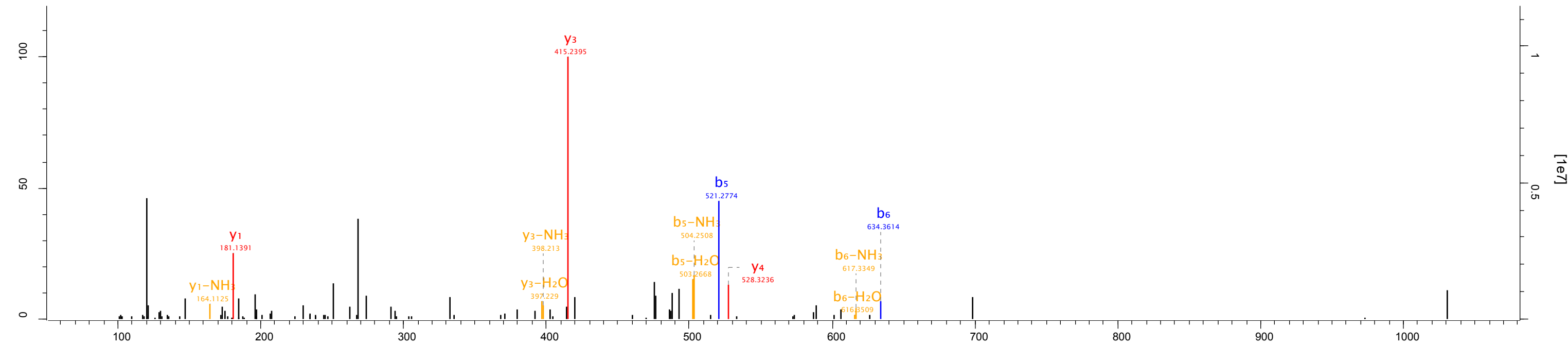




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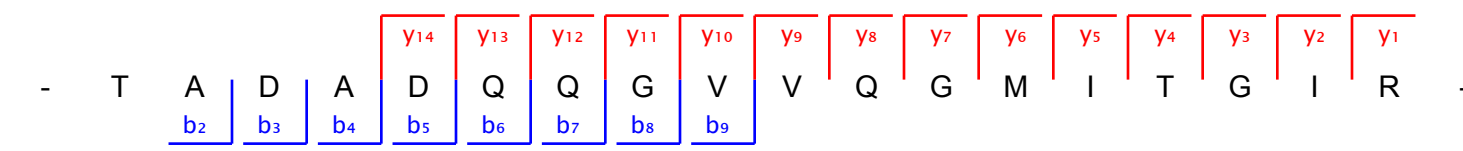
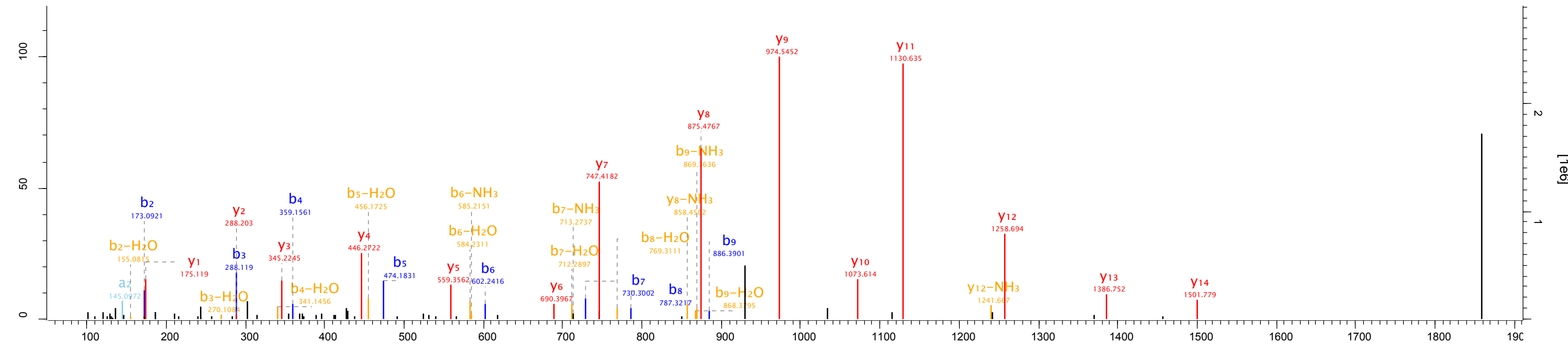


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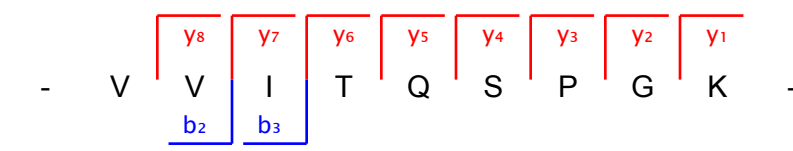
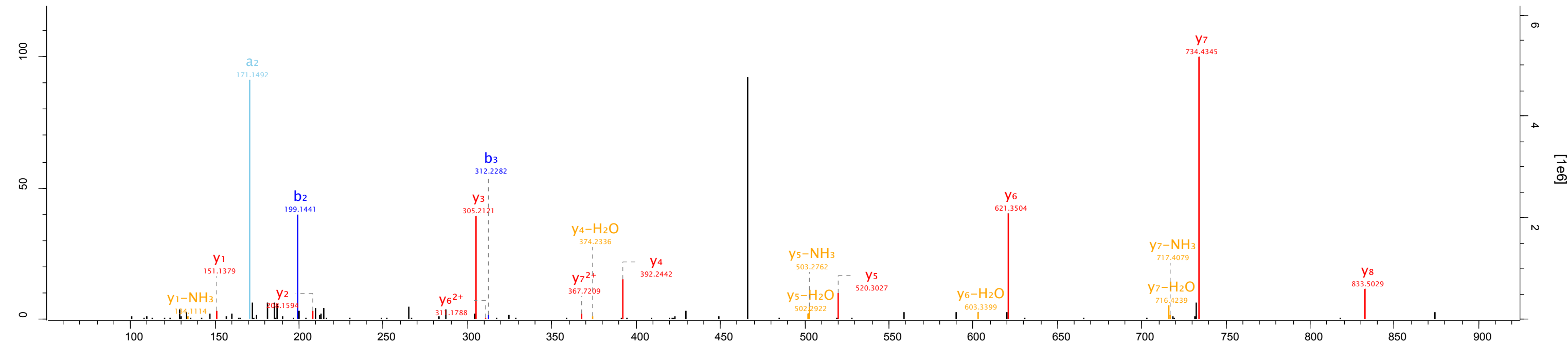


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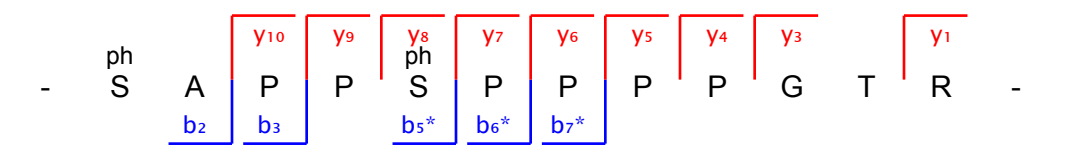
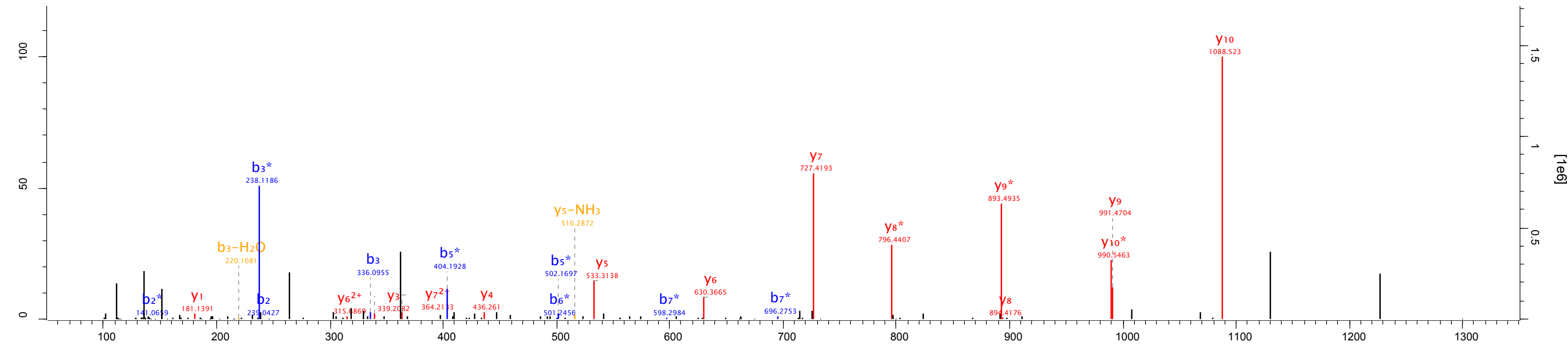
Scan 23323 Method FTMS; HCD Score 167.14 m/z 930.97 Gene names HIAT1



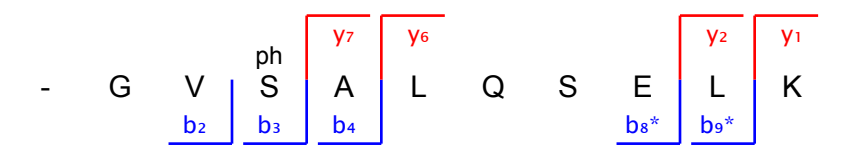
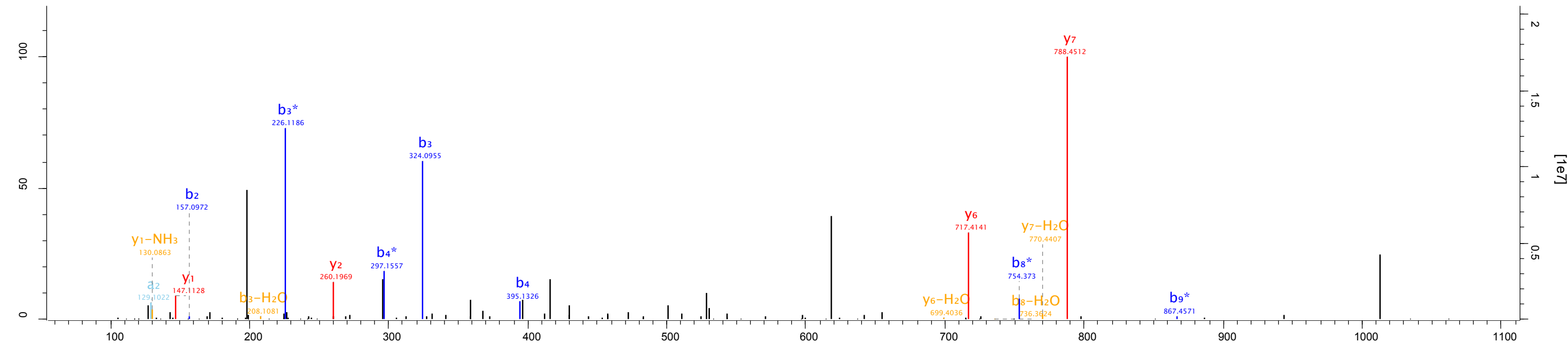
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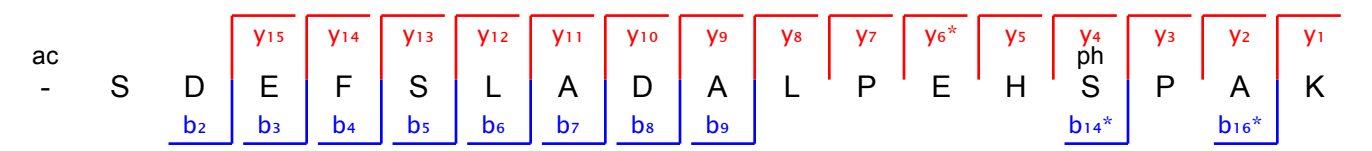
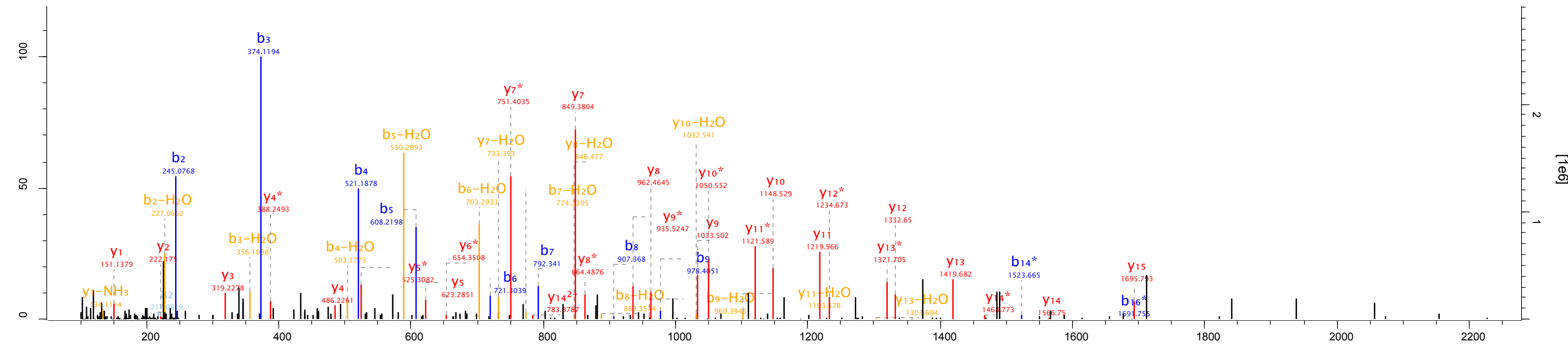
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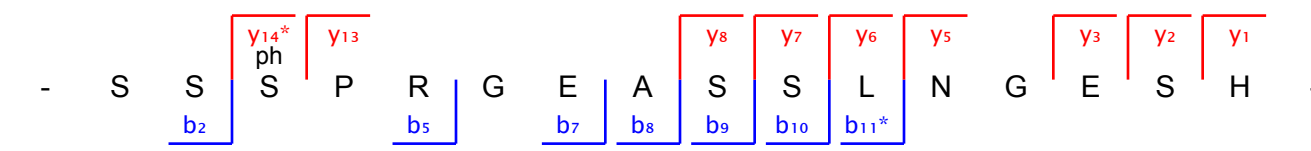
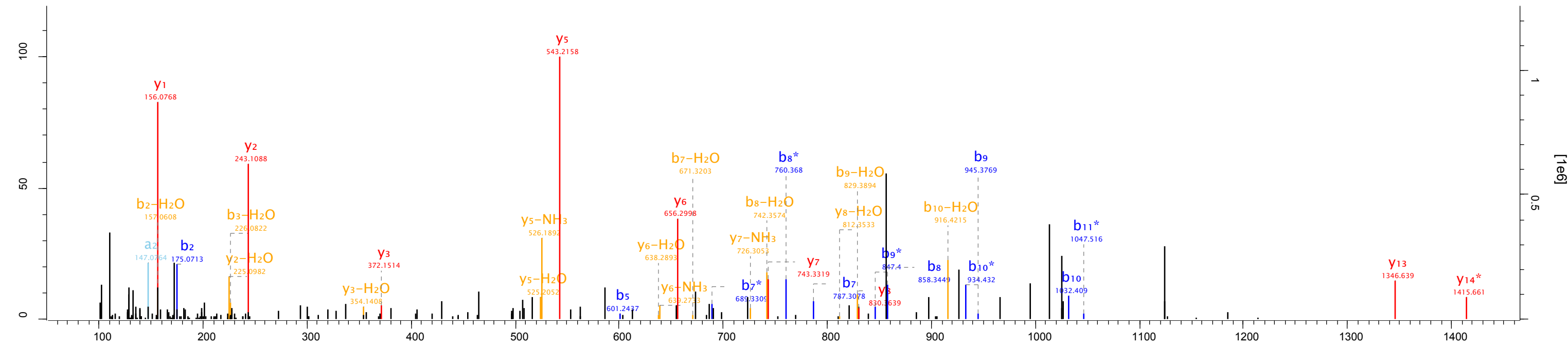
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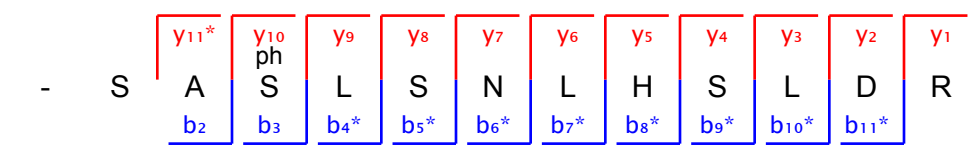
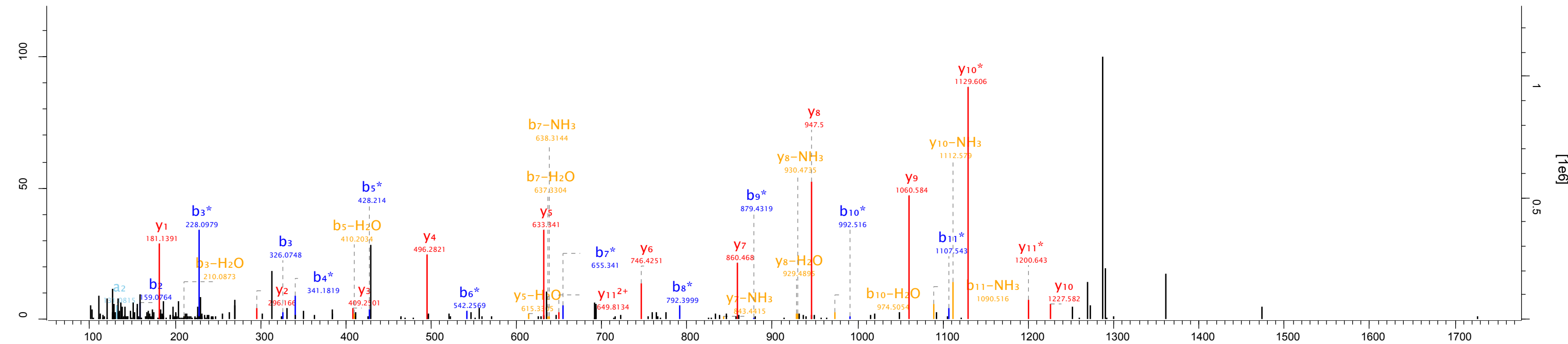
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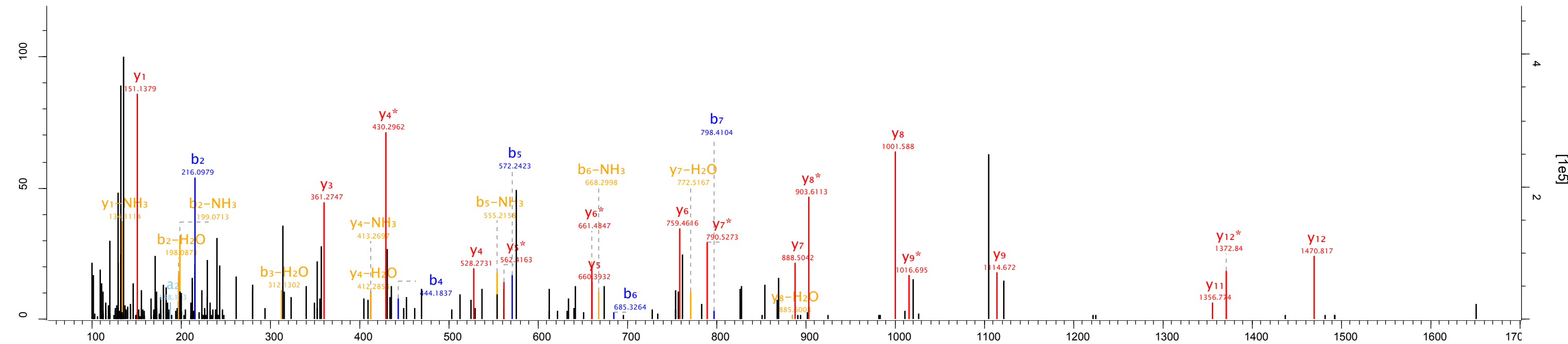
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Raw file 20150812_A375SR_Phospho_BR1_05 Scan 13554 Method FTMS; HCD Score 94.45 m/z 562.64 Gene names MLLT3



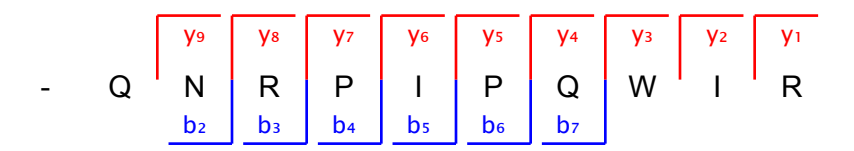
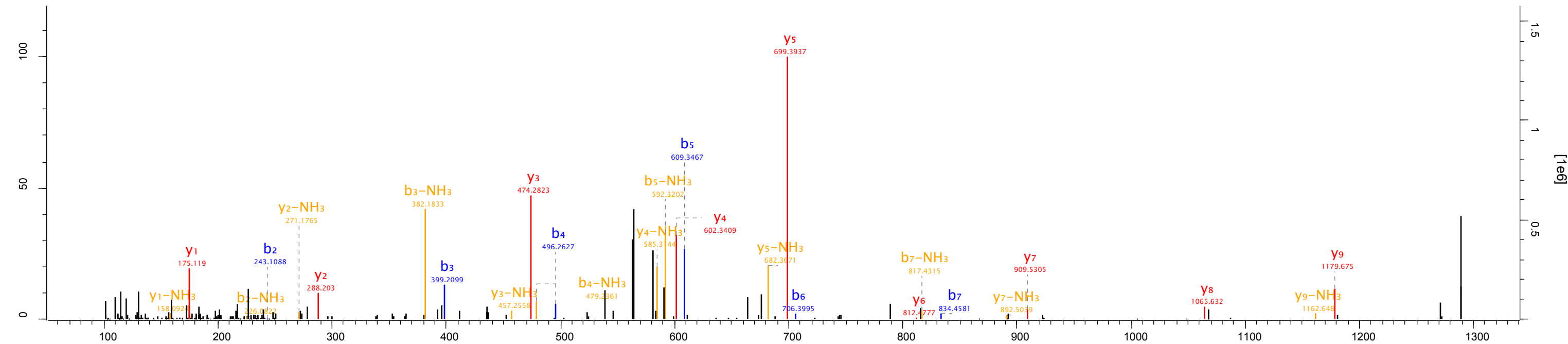
- T N N Q I L E V K S P I K -

Peptide sequence: T N N Q I L E V K S P I K

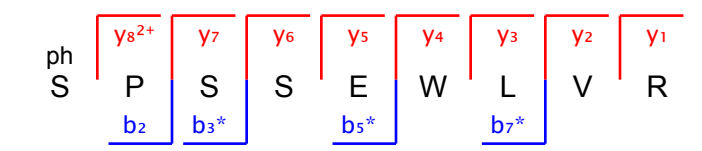
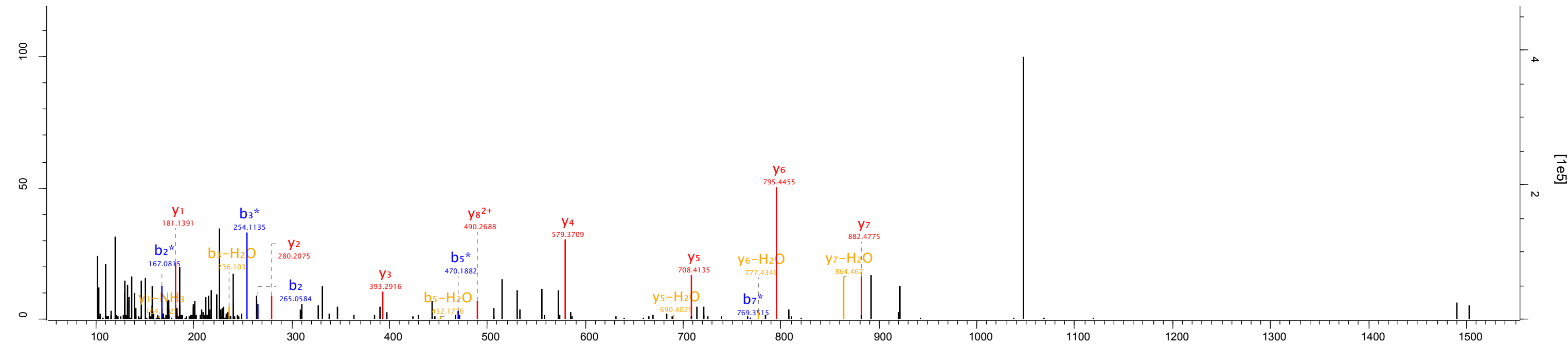
Fragmentation sites (b and y ions) are indicated by brackets below the sequence:

- b2: N
- b4: NN
- b5: NQ
- b6: NQI
- b7: NQIL
- y1: K
- y3: SP
- y4: Sph
- y5: K
- y6: V
- y7: E
- y8: IL
- y9: IQ
- y11: NN
- y12: NN

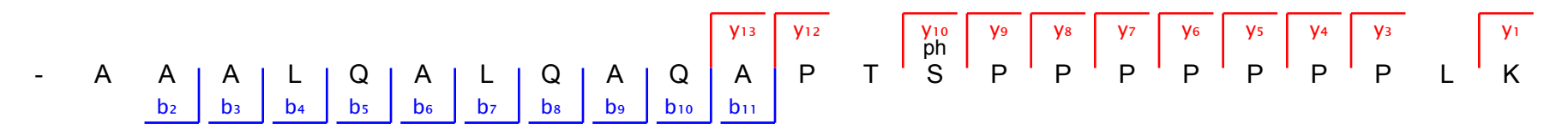
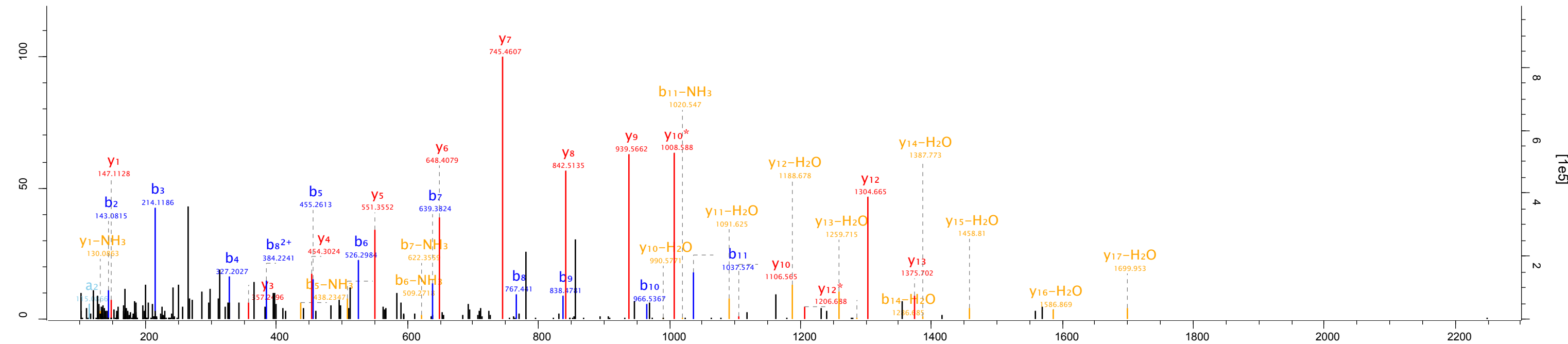
Raw file: 20150812_A375SR_Phospho_BR1_05
 Scan: 14294 Method: FTMS; HCD Score: 145.9 m/z: 436.58 Gene names: RPL39P5;RPL39



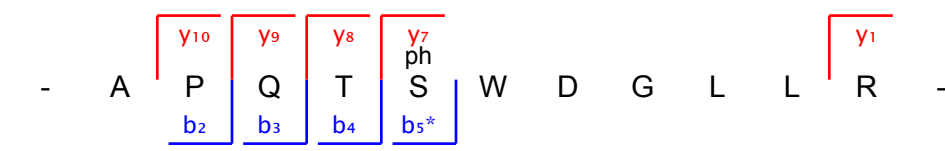
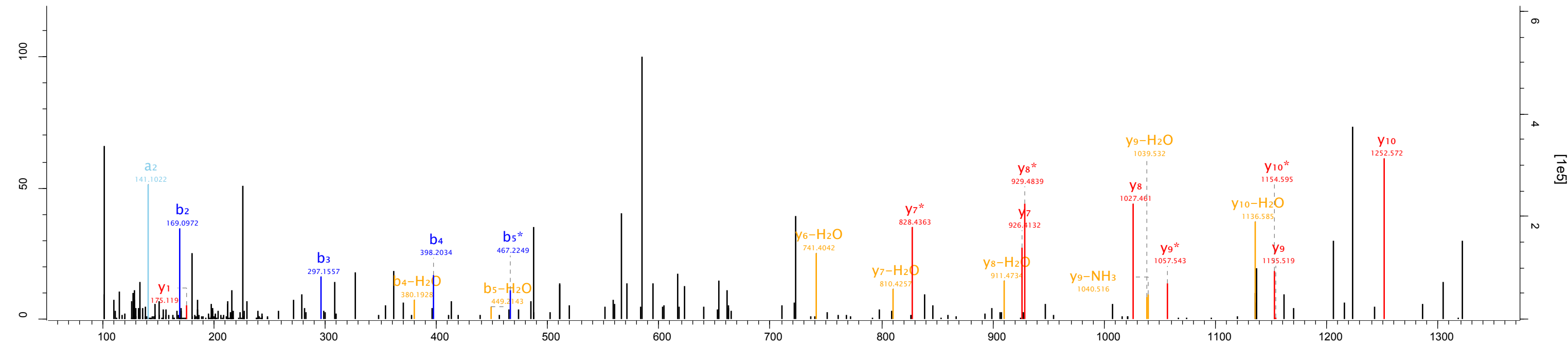
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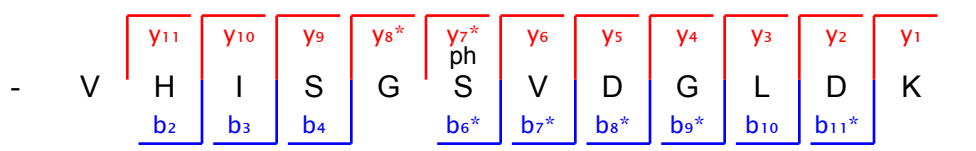
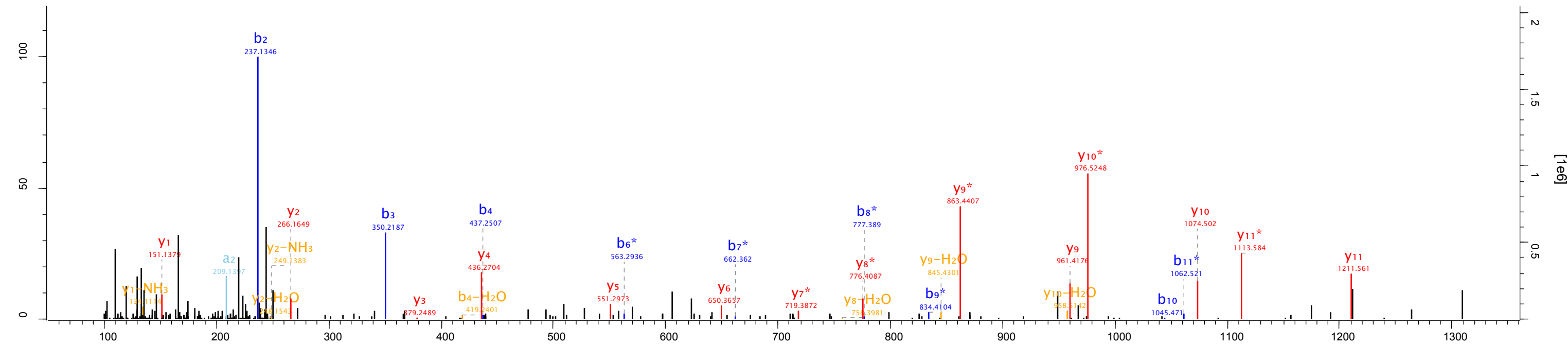
Raw file 20150812_A375SR_Phospho_BR1_05 Scan 21224 Method FTMS; HCD Score 82.64 m/z 781.42 Gene names ZNF579



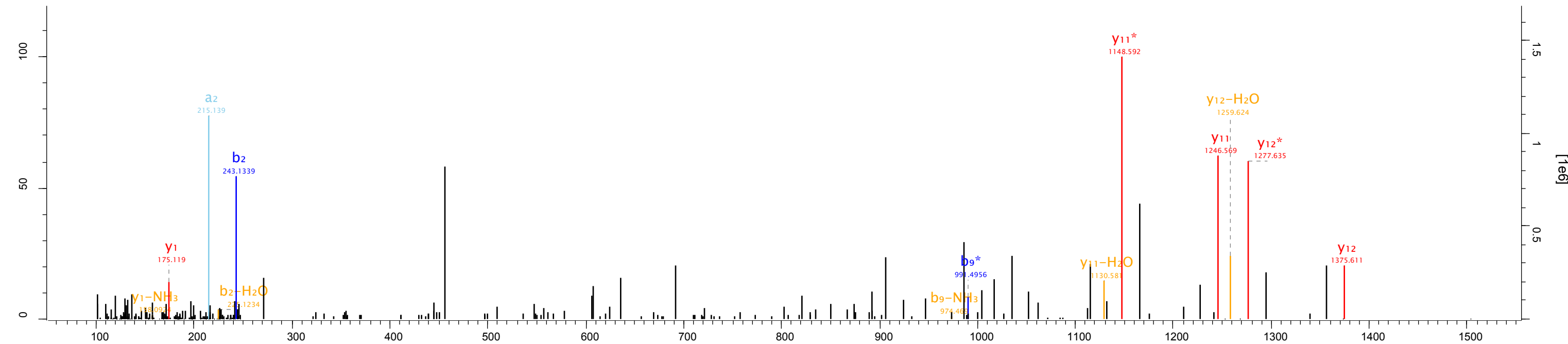
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 Scan: 5374 Method: FTMS; HCD Score: 106.32 m/z: 662.31 Gene names: PLA2G4E



Raw file 20150812_A375SR_Phospho_BR1_06 Scan 12304 Method FTMS; HCD Score 87.09 m/z 655.82 Gene names PHACTR2



Raw file Scan Method Score m/z
 20150812_A375SR_Phospho_BR1_06 9194 FTMS; HCD 44.93 496.9

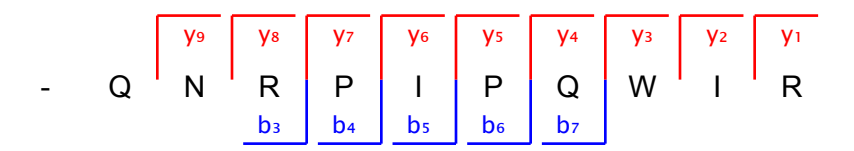
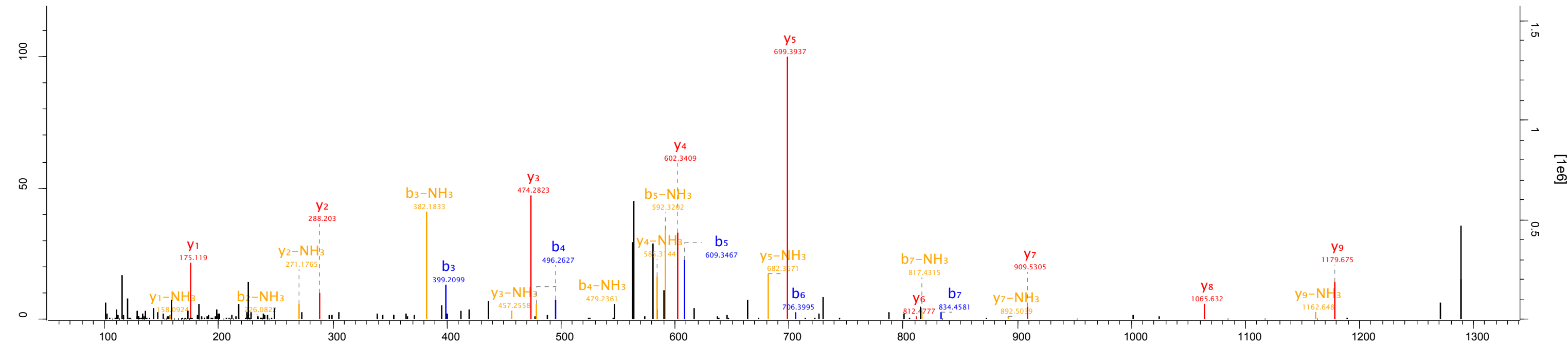


- L E S T P H S R T A G P R -

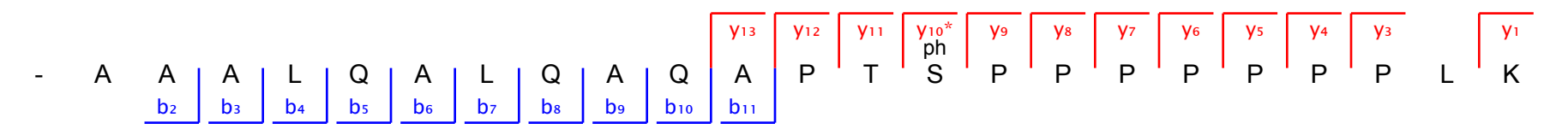
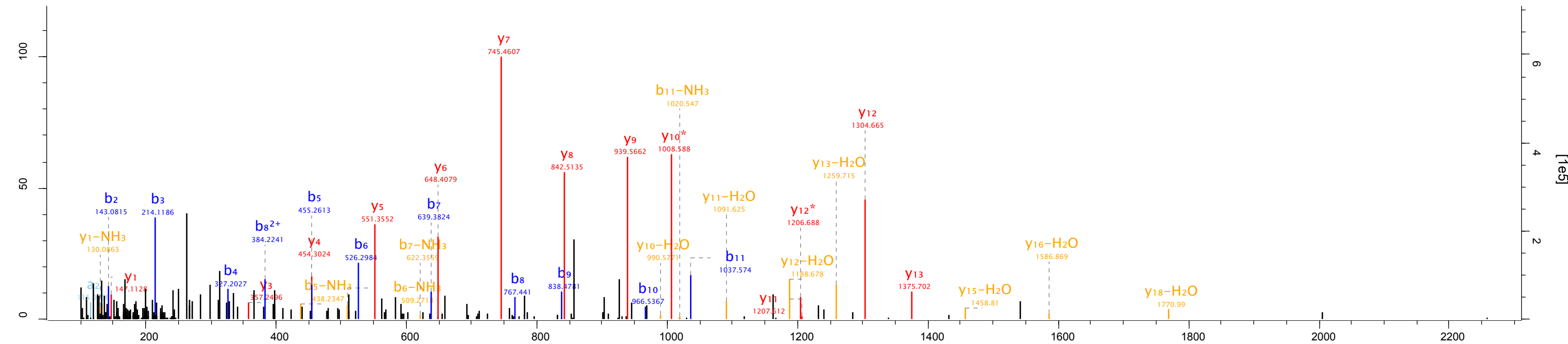
Fragmentation mapping:

- Red brackets above the sequence:
 - y12 above E
 - y11-ph above S
 - y1 above R
- Blue brackets below the sequence:
 - b2 below E
 - b9* below T

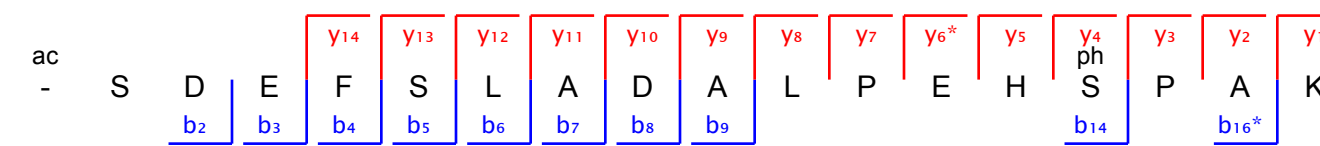
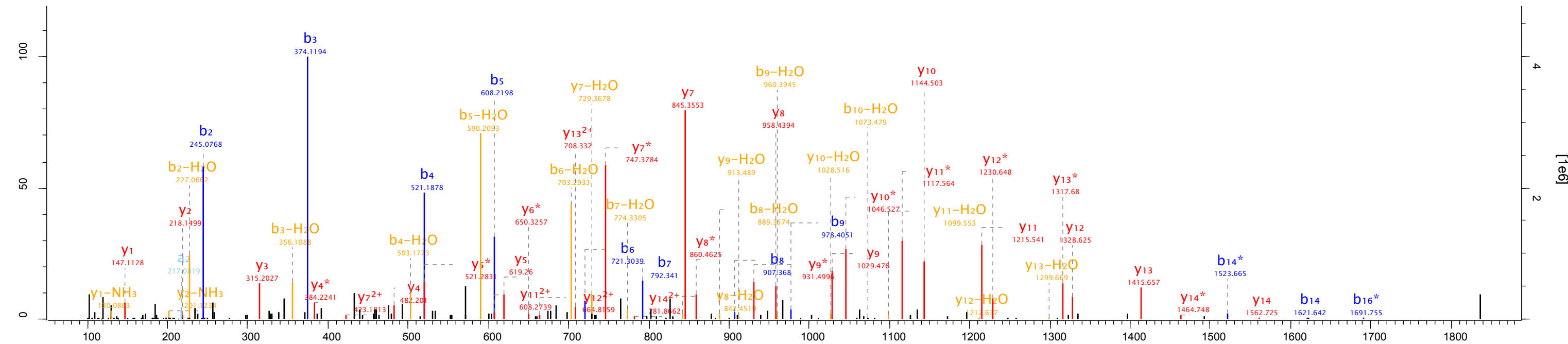
Raw file: 20150812_A375SR_Phospho_BR1_07
 Scan: 14884 Method: FTMS; HCD Score: 175.91 m/z: 436.58 Gene names: RPL39P5;RPL39



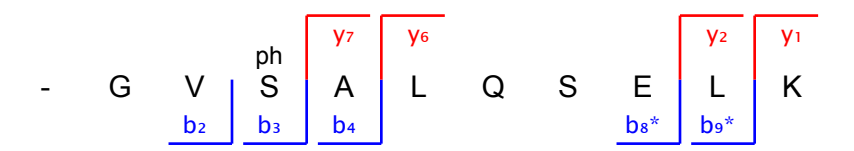
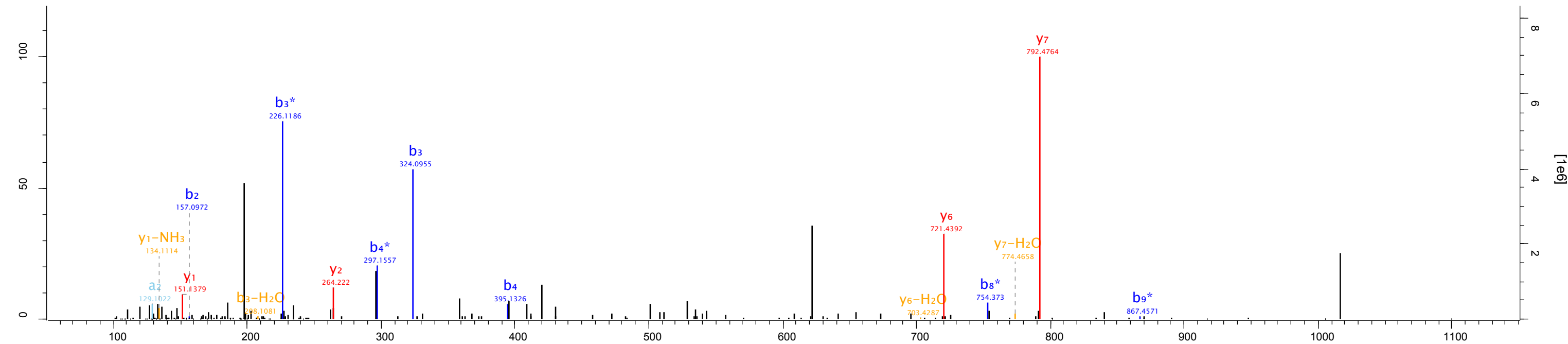
Raw file 20150812_A375SR_Phospho_BR1_07 Scan 21584 Method FTMS; HCD Score 75.53 m/z 781.42 Gene names ZNF579



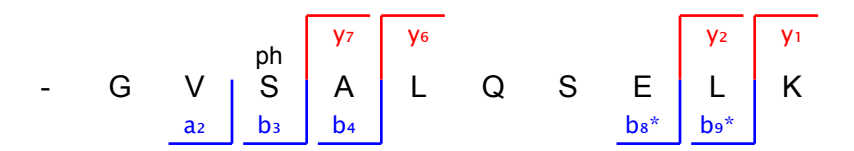
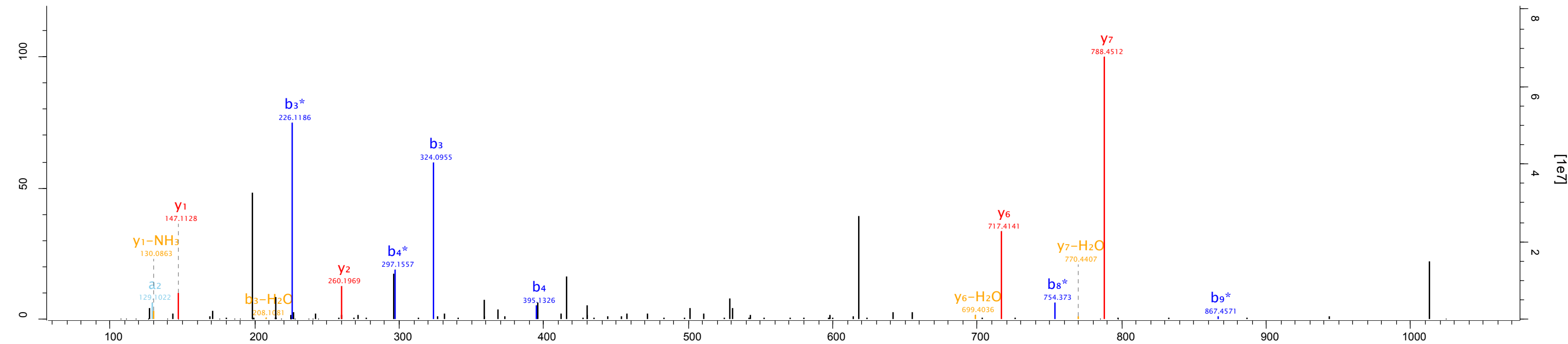
Raw file Scan Method Score m/z Gene names
 20150812_A375SR_Phospho_BR1_07 24684 FTMS; HCD 291.68 968.42 MAPK11P1L



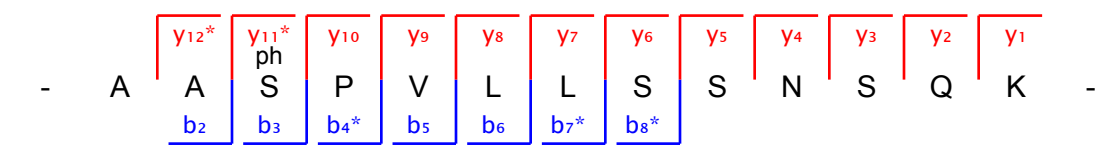
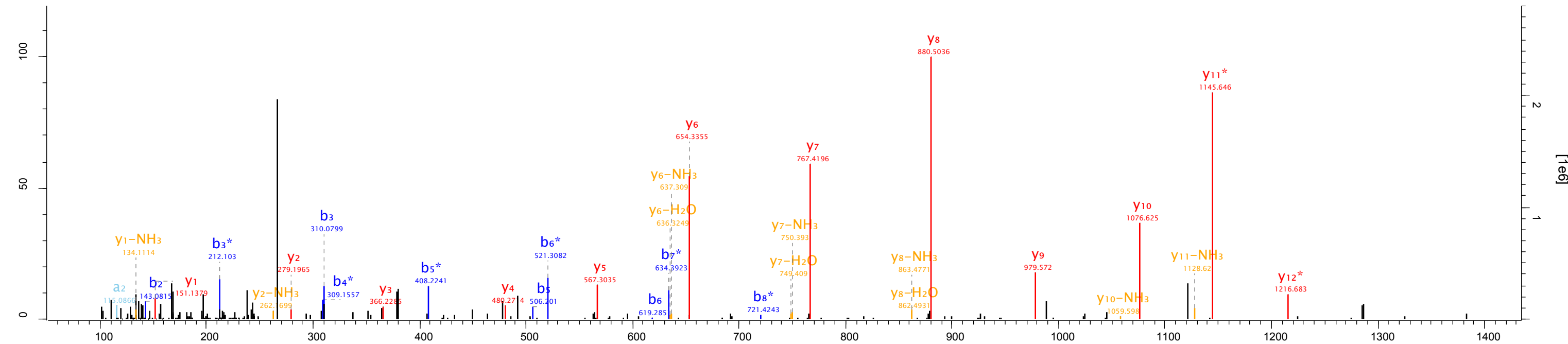
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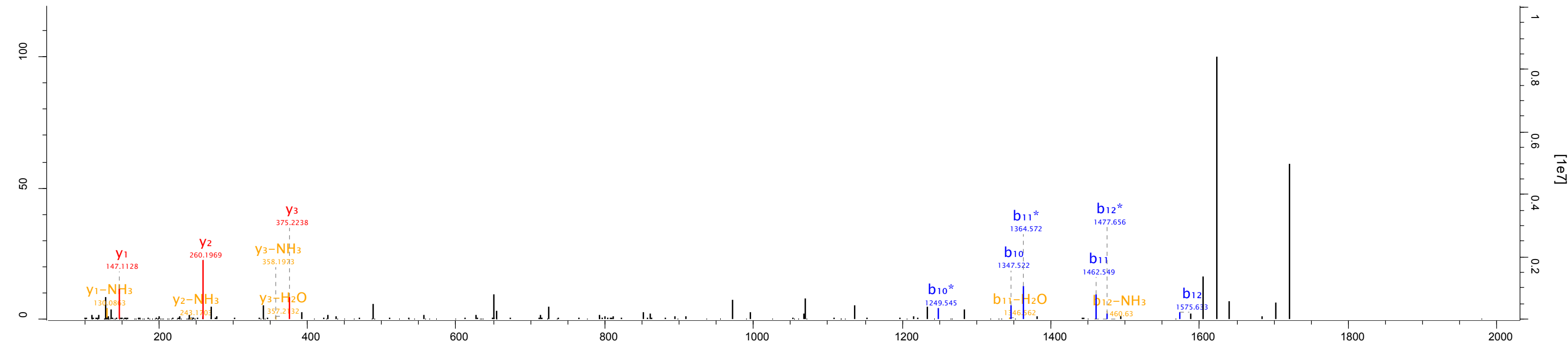
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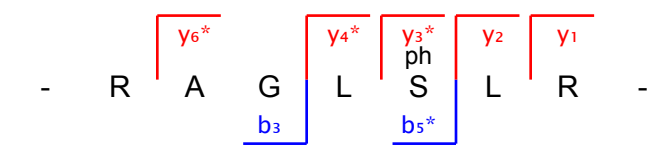
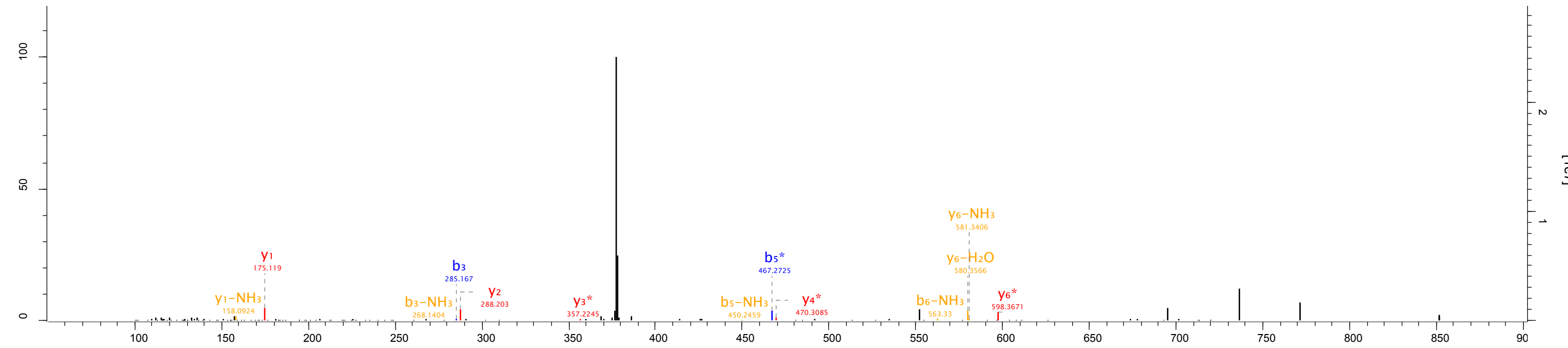
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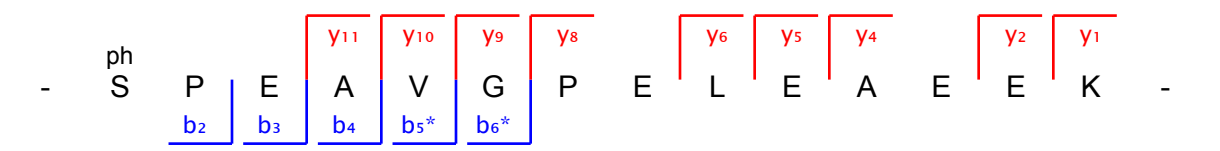
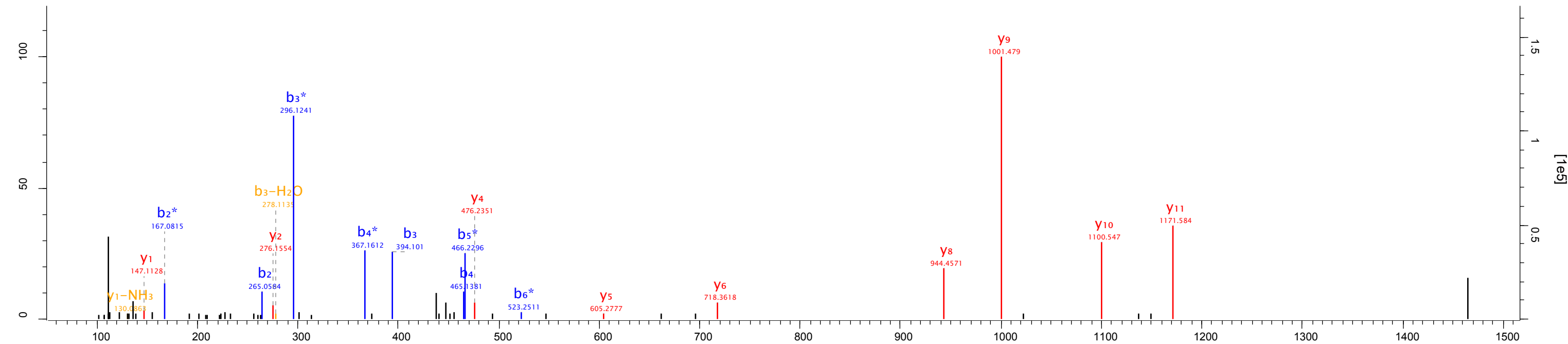
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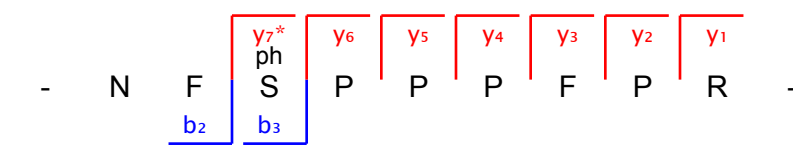
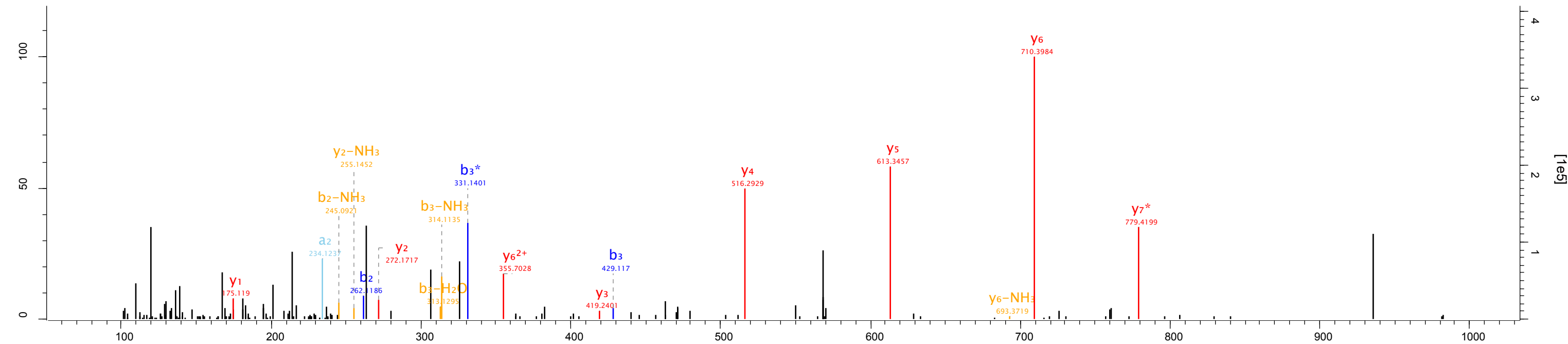
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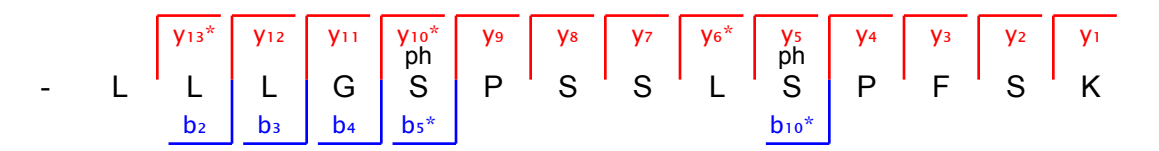
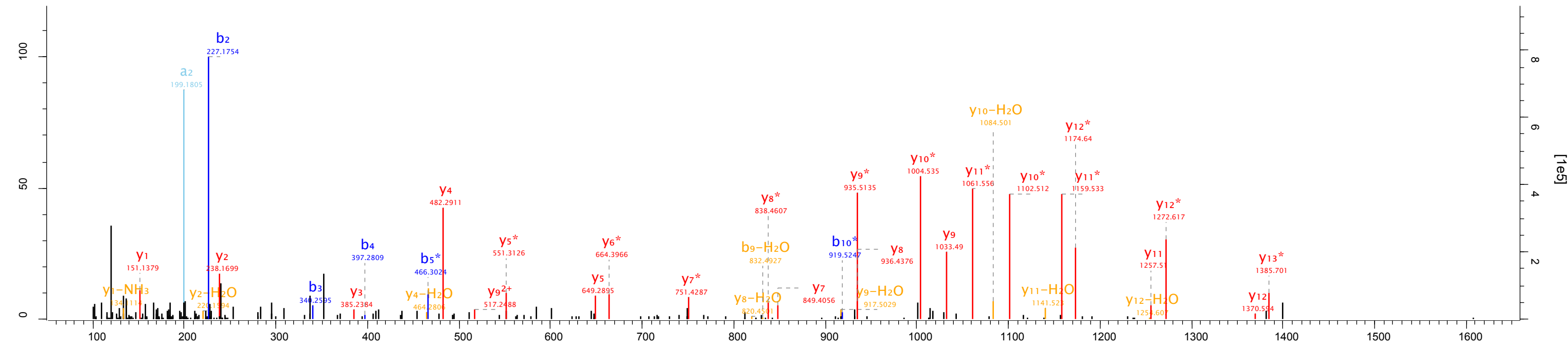
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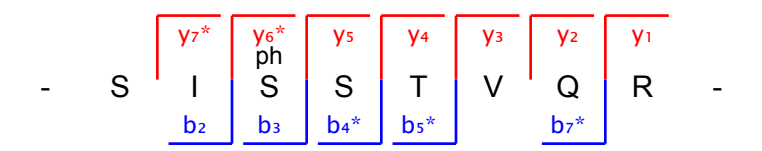
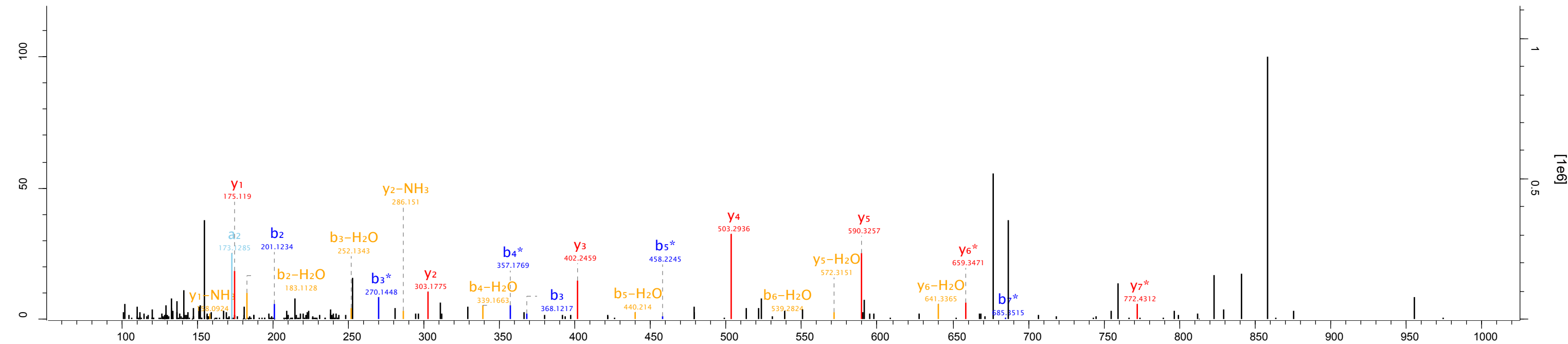
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Raw file Scan Method Score m/z Gene names
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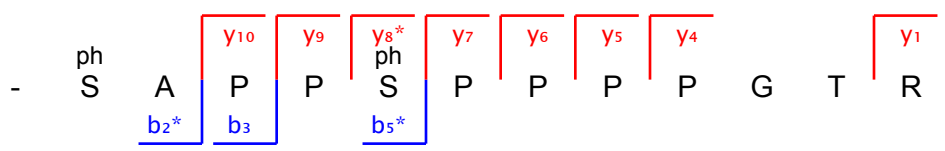
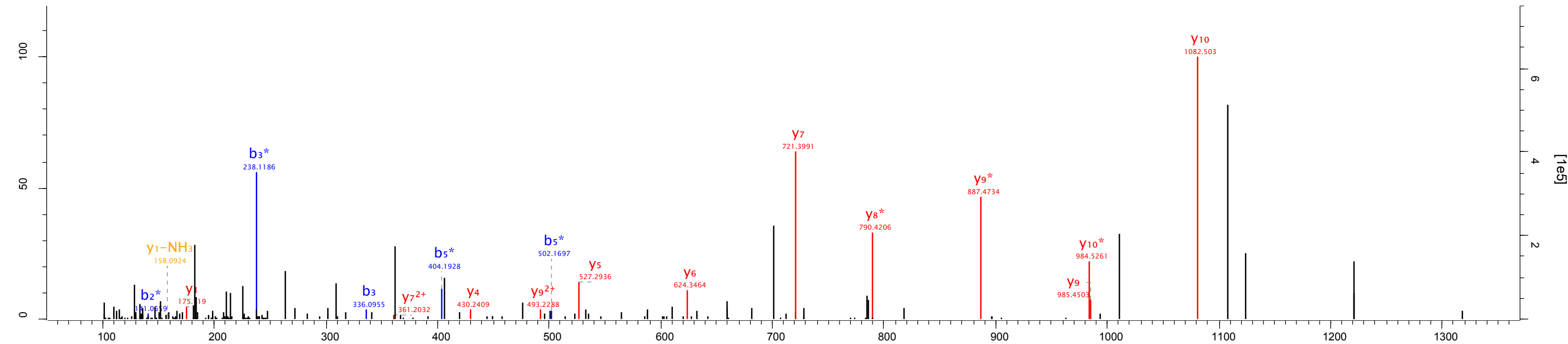
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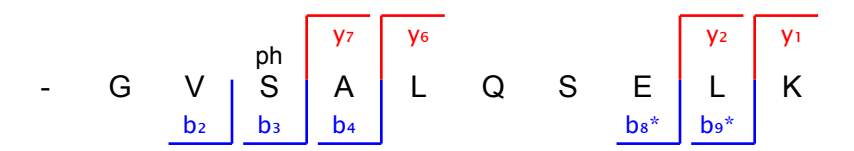
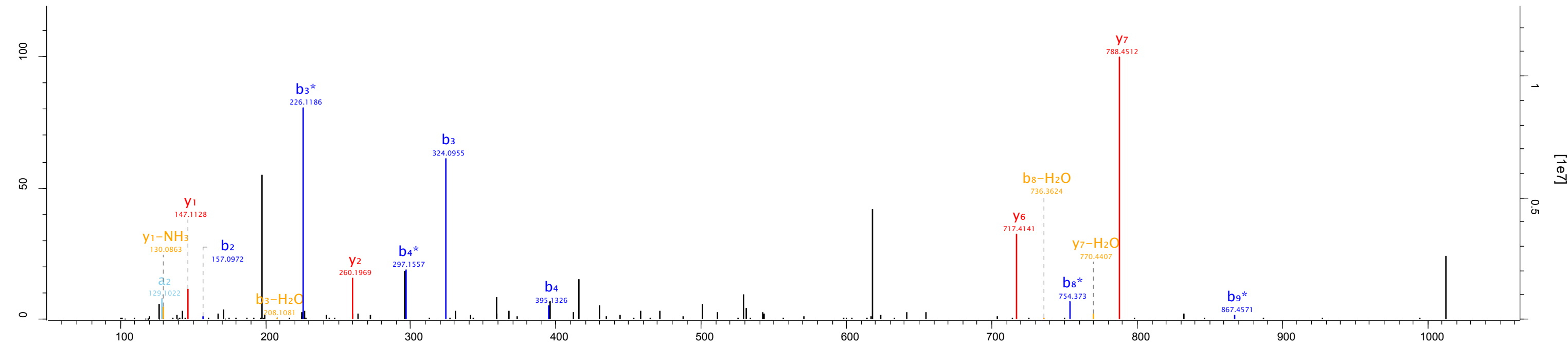
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20150814_A375SR_Phospho_BR2_03

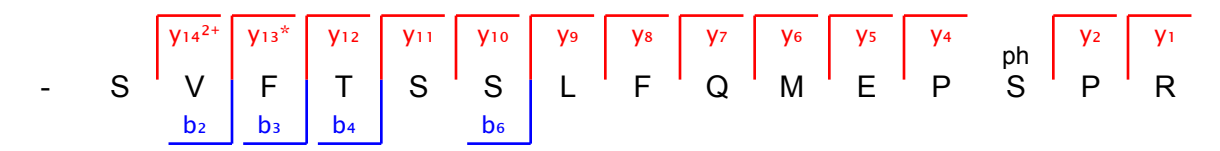
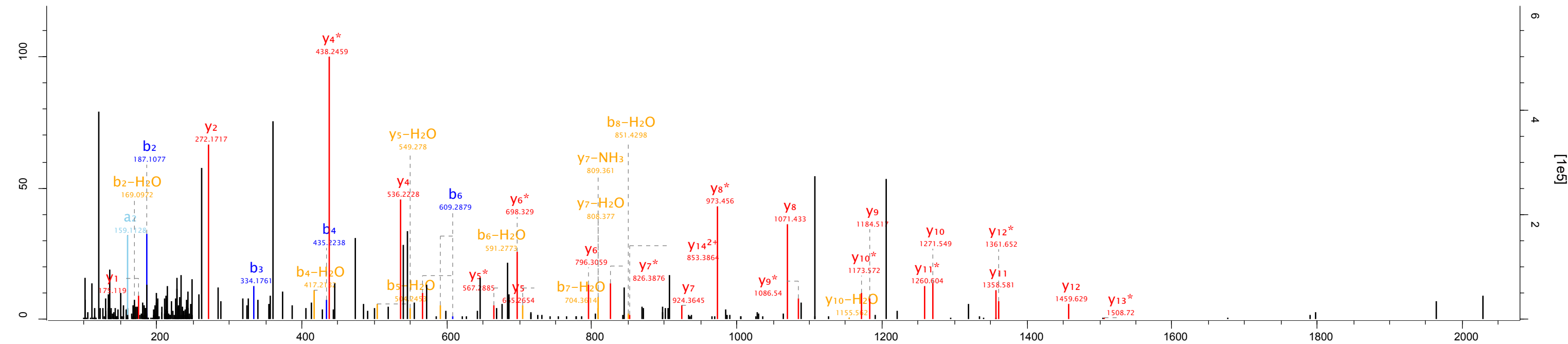
Scan	Method	Score	m/z	Gene names
5794	FTMS; HCD	48.29	660.77	GPSM3



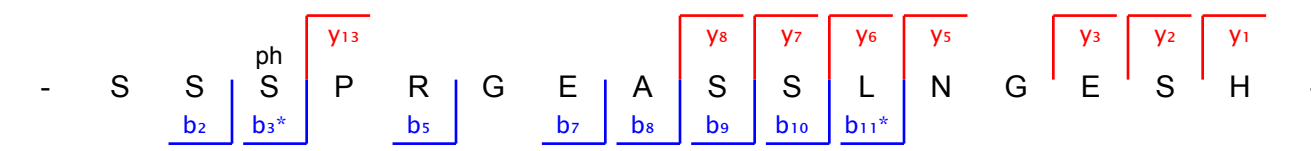
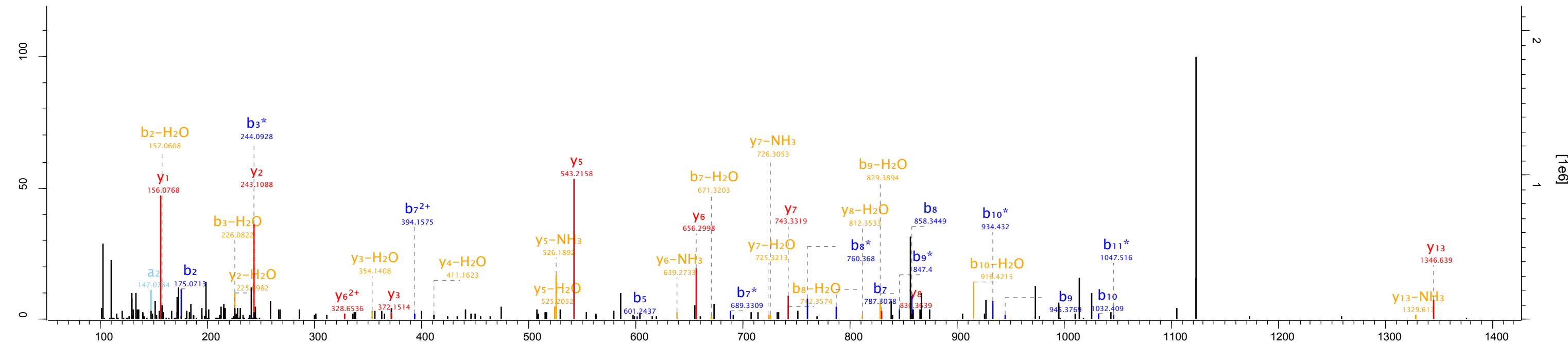
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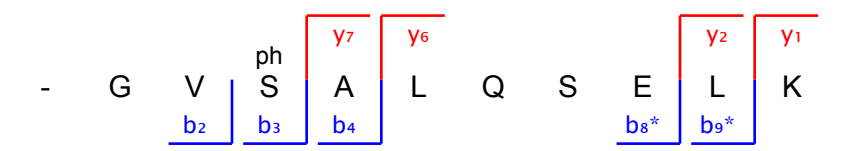
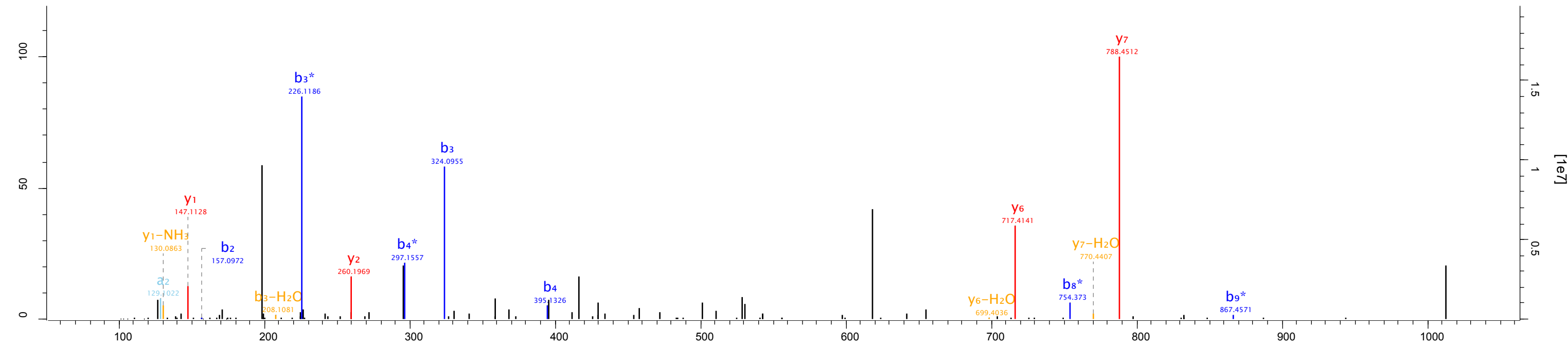
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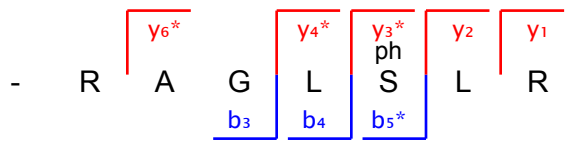
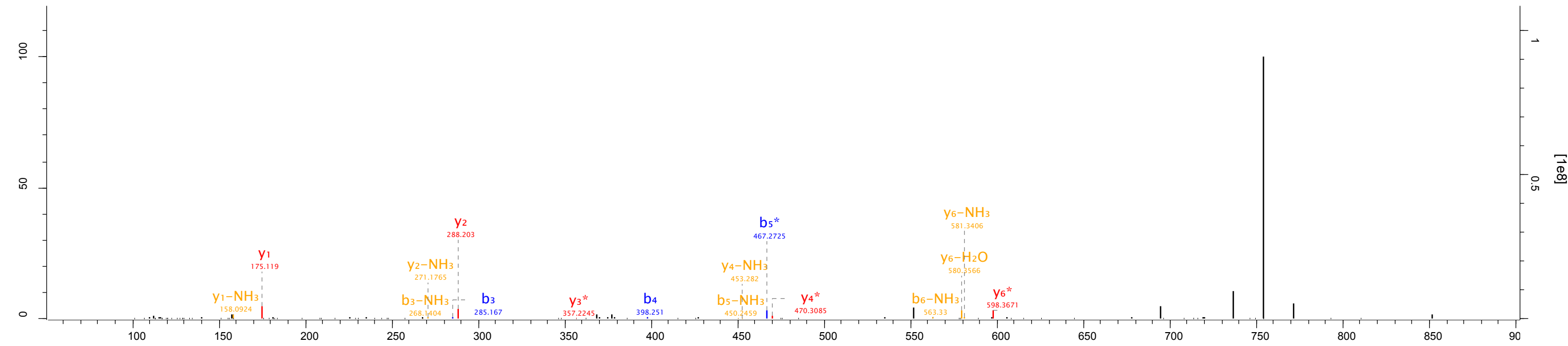
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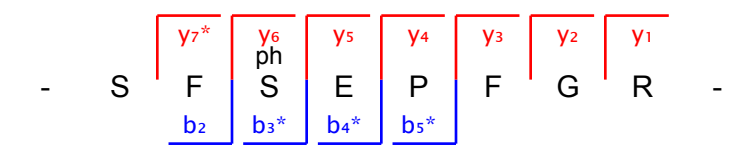
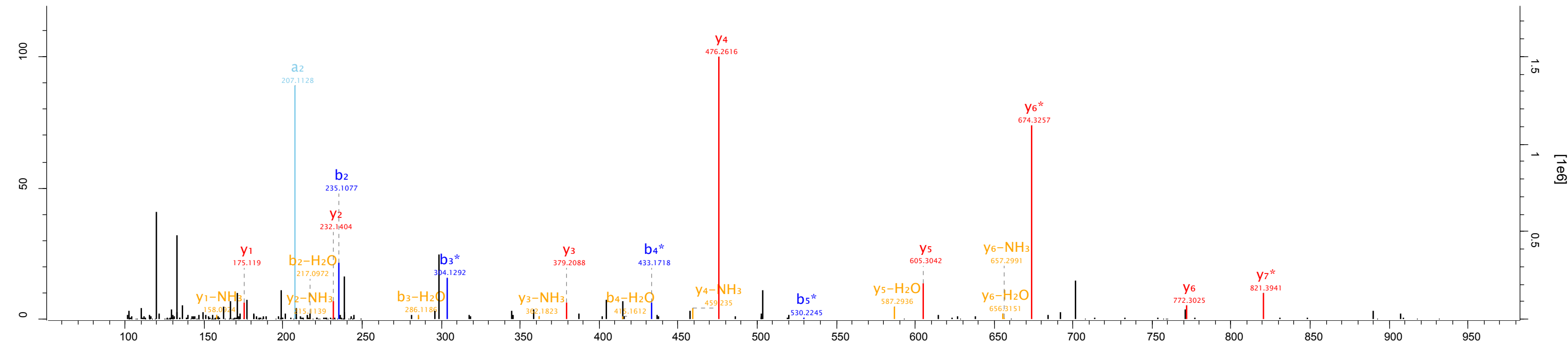
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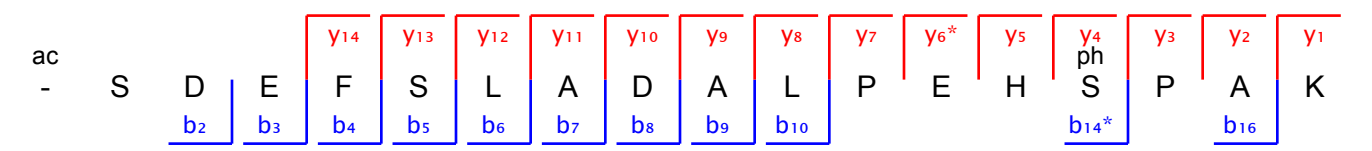
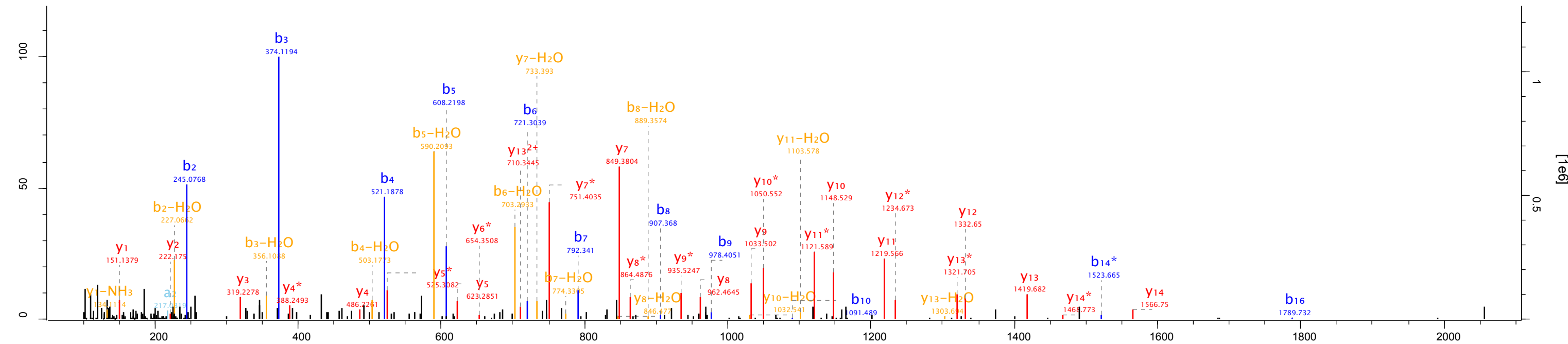
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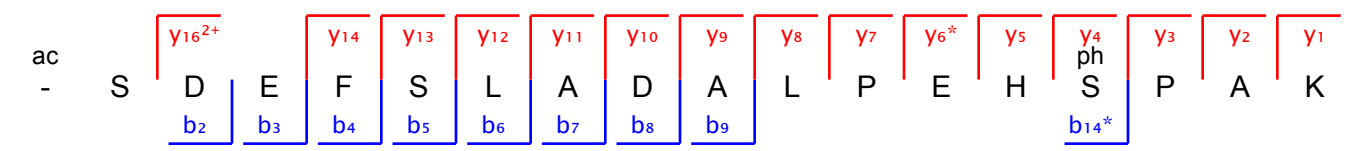
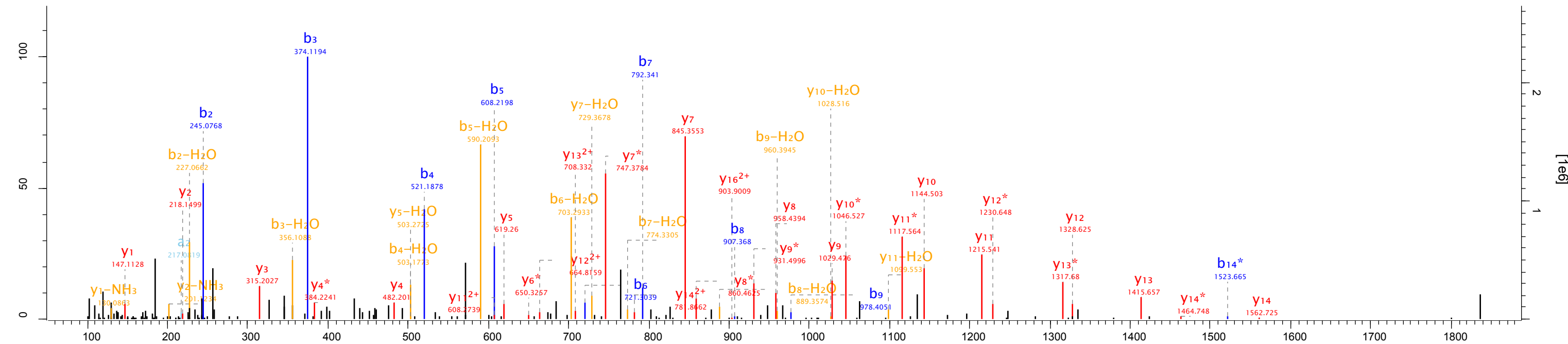
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 Method: FTMS; HCD
 Score: 89.61
 m/z: 503.71
 Gene names: MLF1



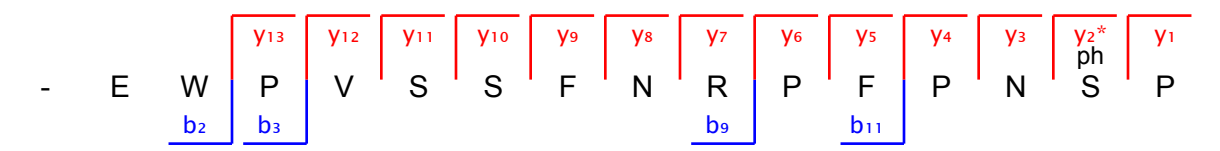
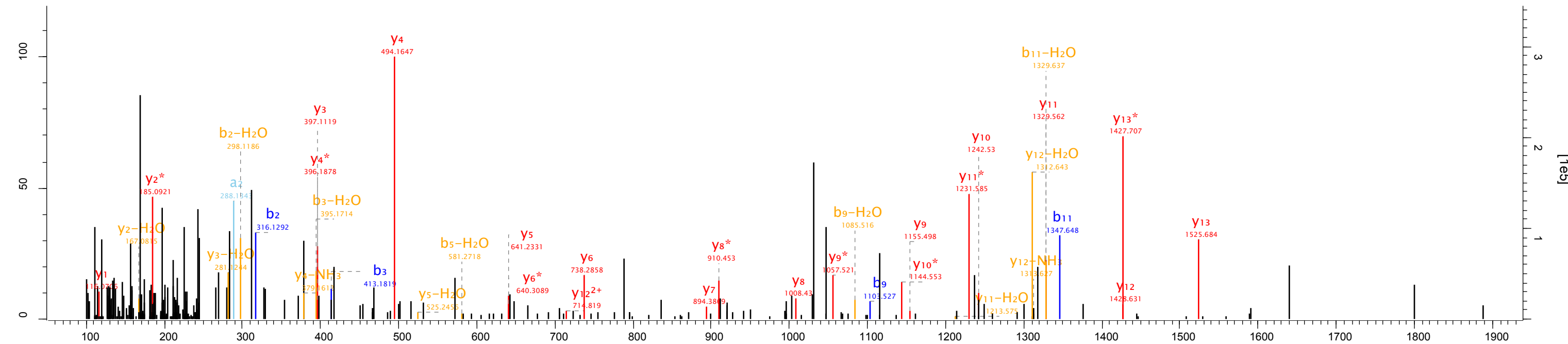
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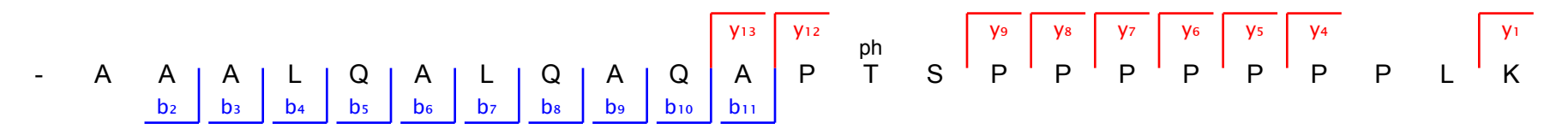
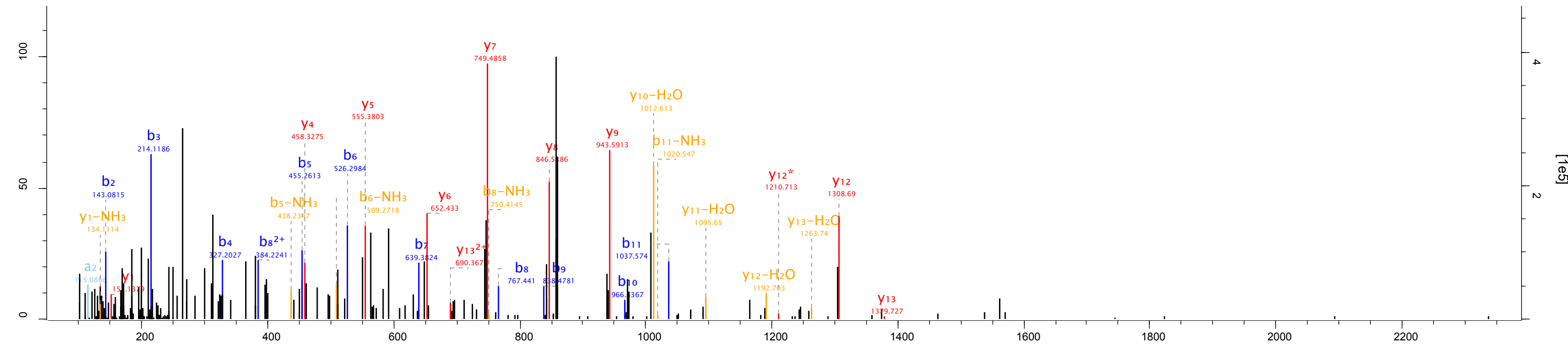
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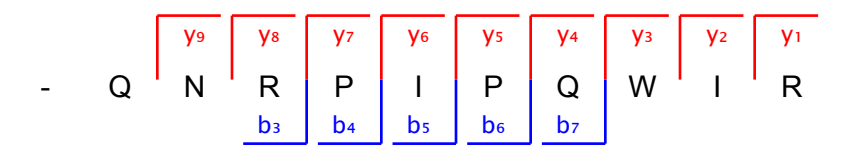
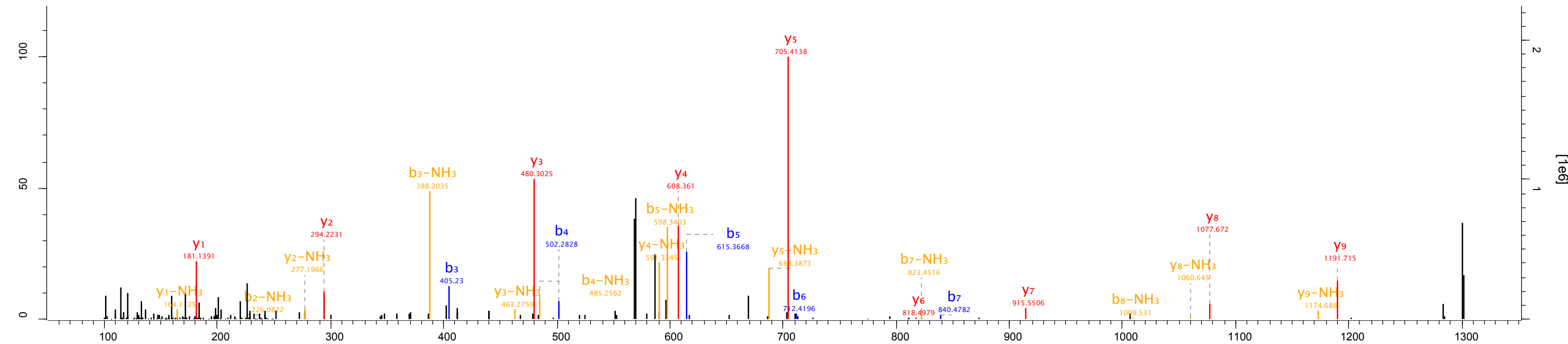
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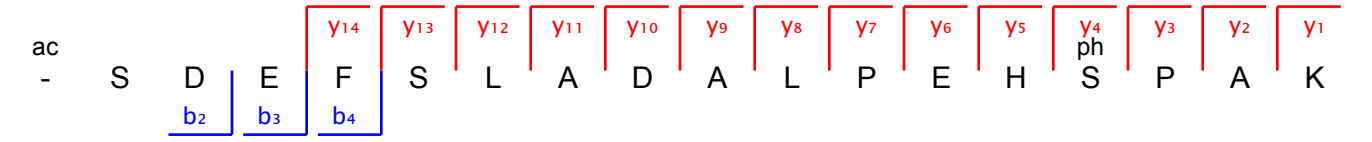
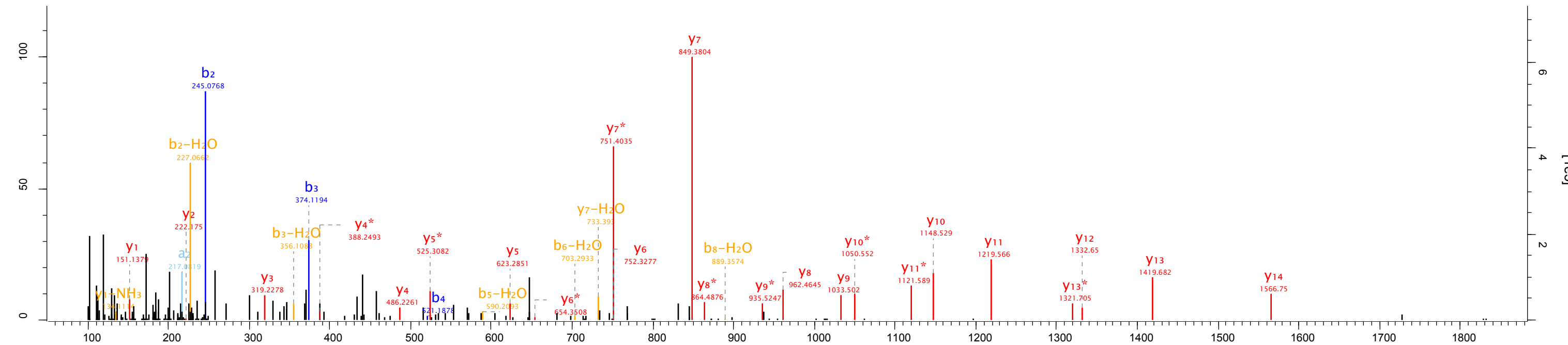
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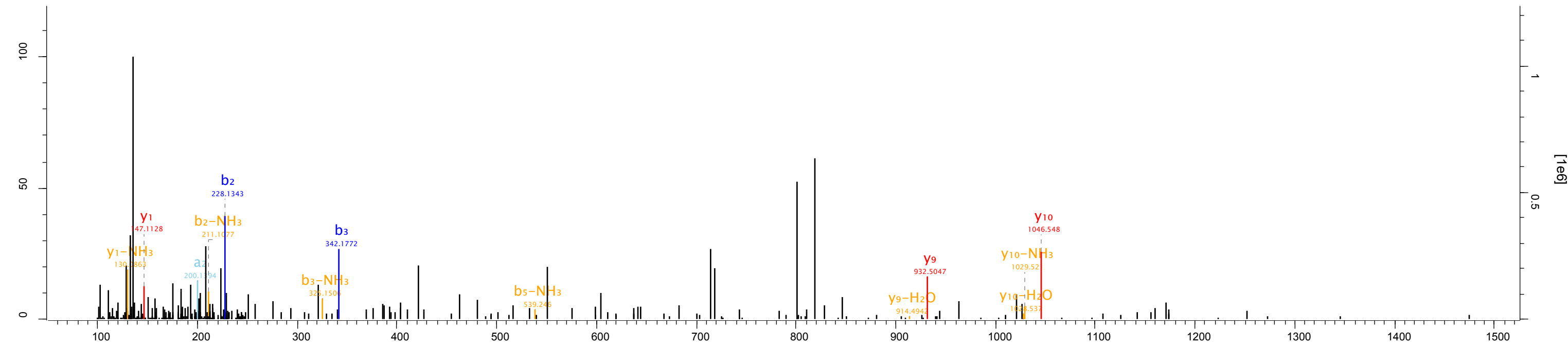
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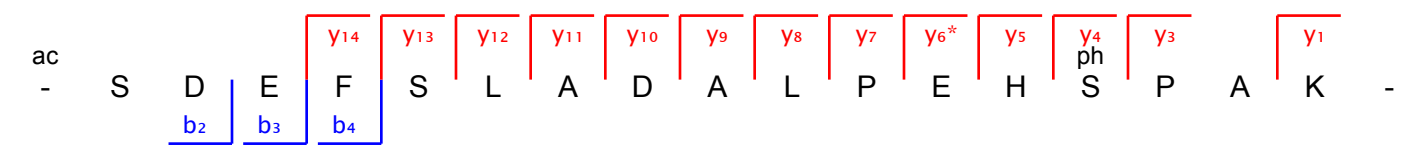
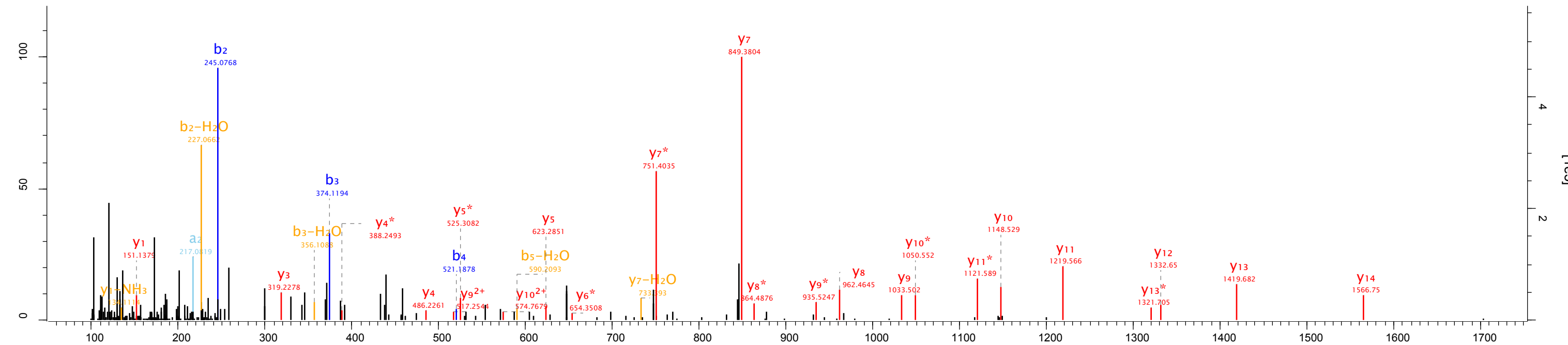
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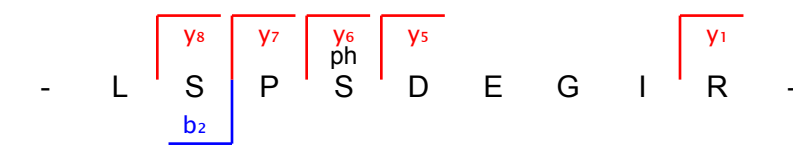
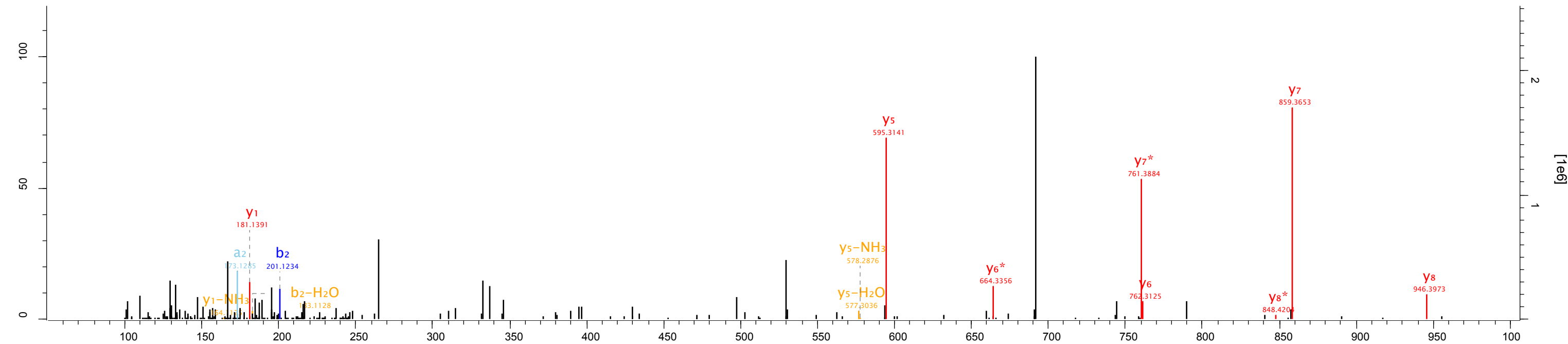
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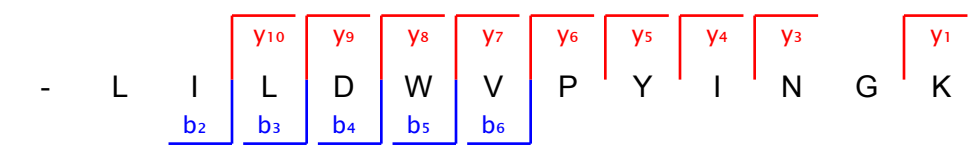
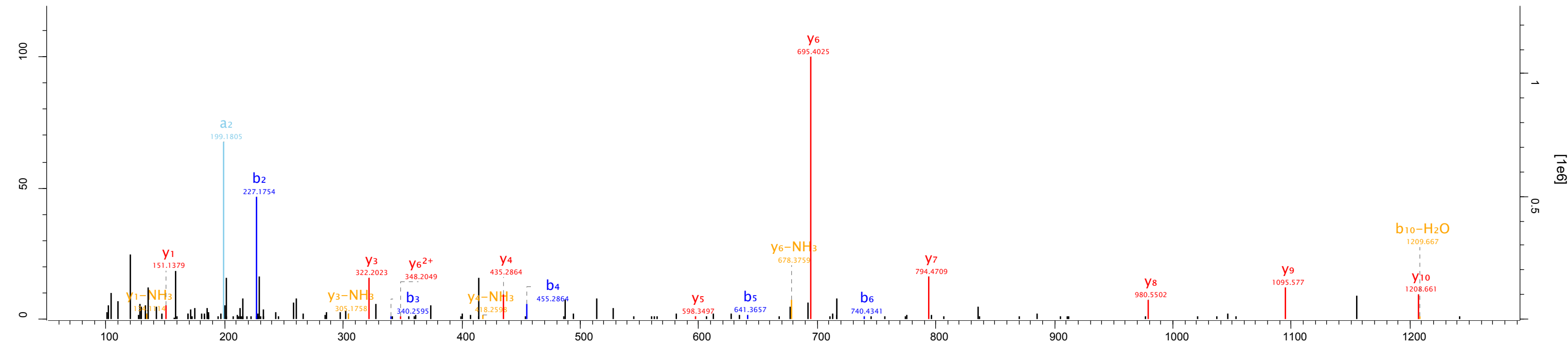
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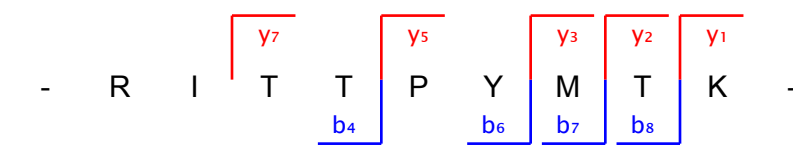
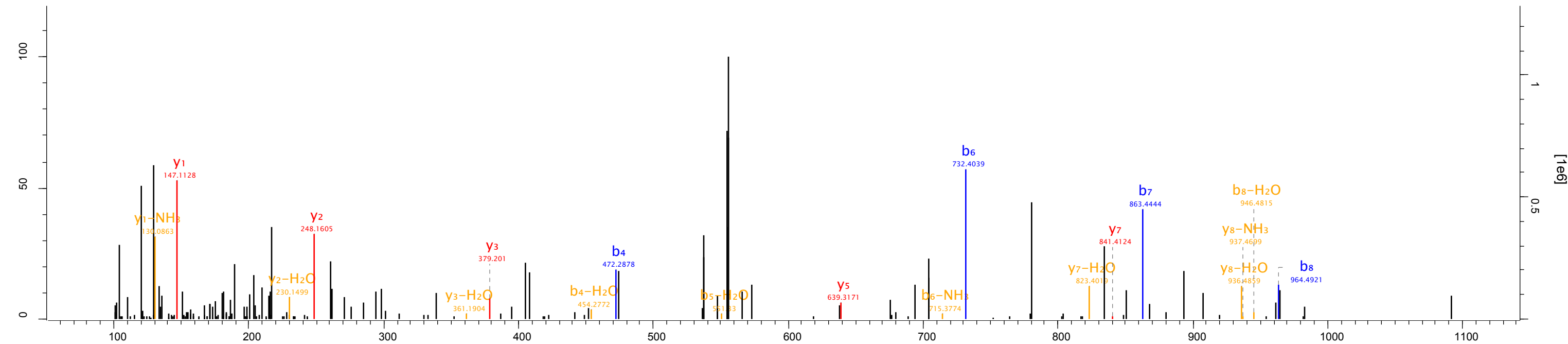
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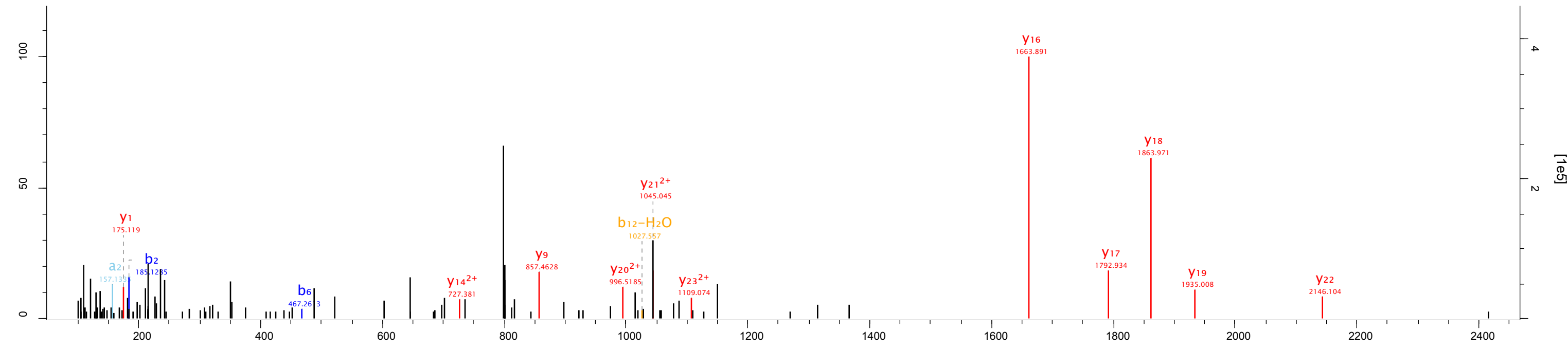
Raw file Scan Method Score m/z Gene names
 20150818_A375SR-Proteome_BR1 116014 FTMS; HCD 63.47 717.92 UQCR11



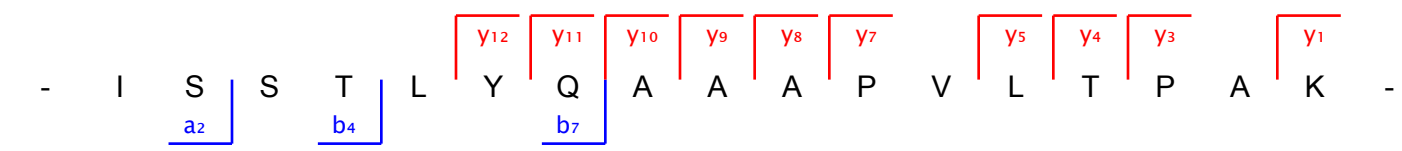
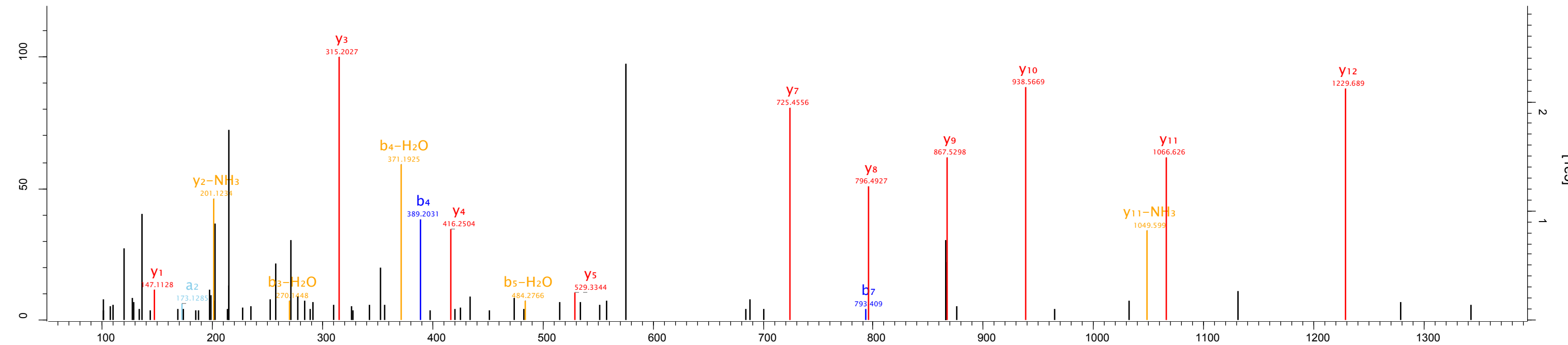
Raw file: 20150818_A375SR-Proteome_BR1
 Scan: 15644 Method: FTMS; HCD Score: 54.09 m/z: 555.8 Gene names: POLR2F



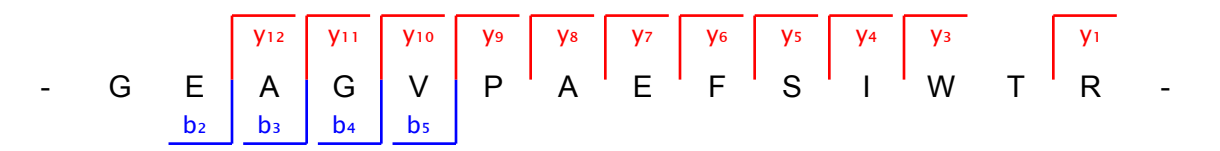
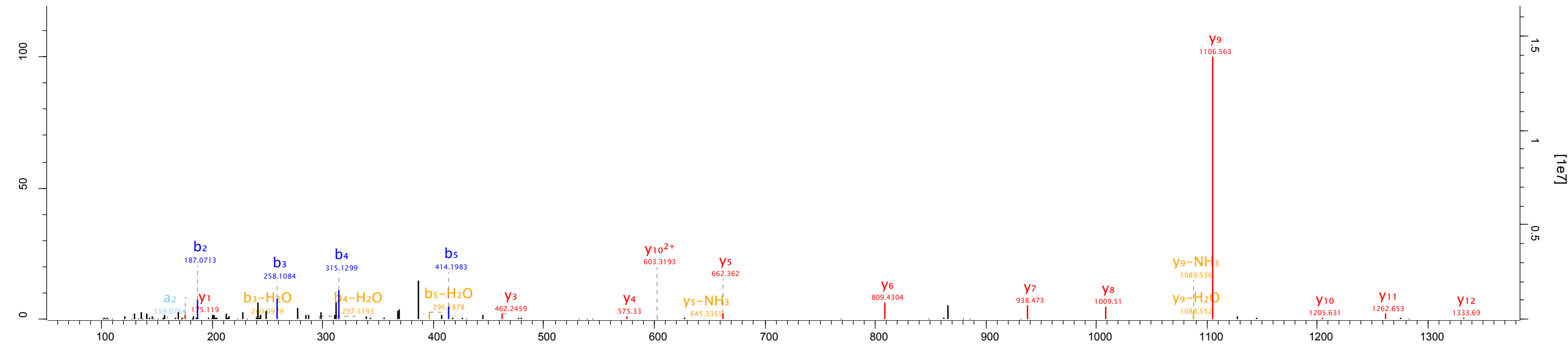
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 Scan: 64894 Method: FTMS; HCD Score: 34.25 m/z: 801.09 Gene names: ZNF511



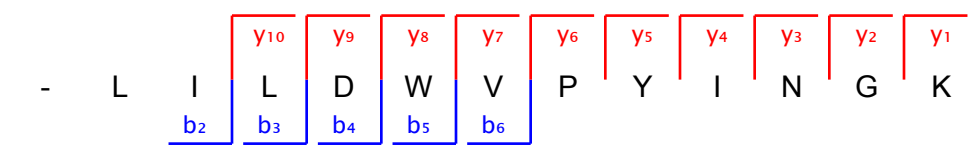
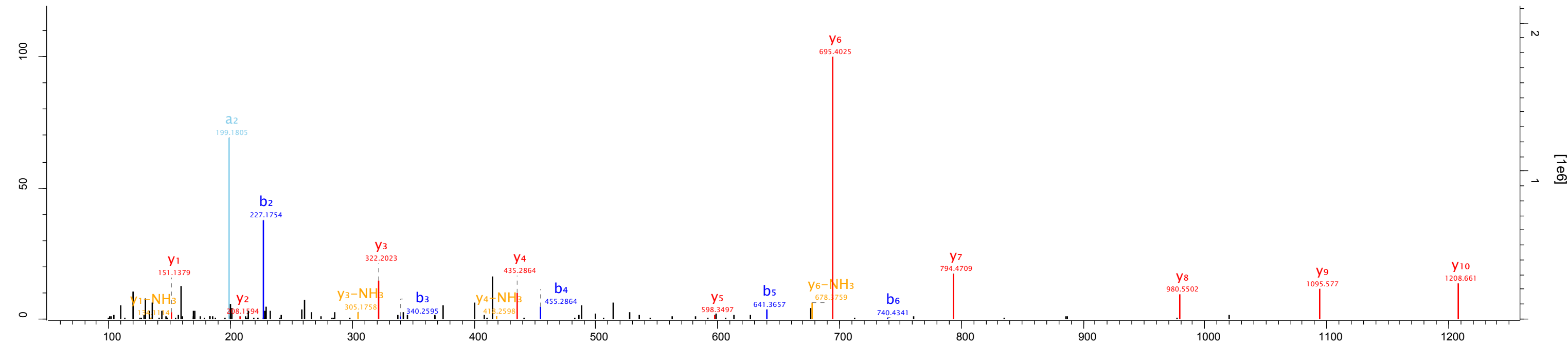
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 Scan: 69994 Method: FTMS; HCD Score: 65.23 m/z: 866.49 Gene names: KRTCAP2



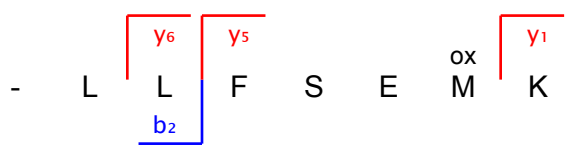
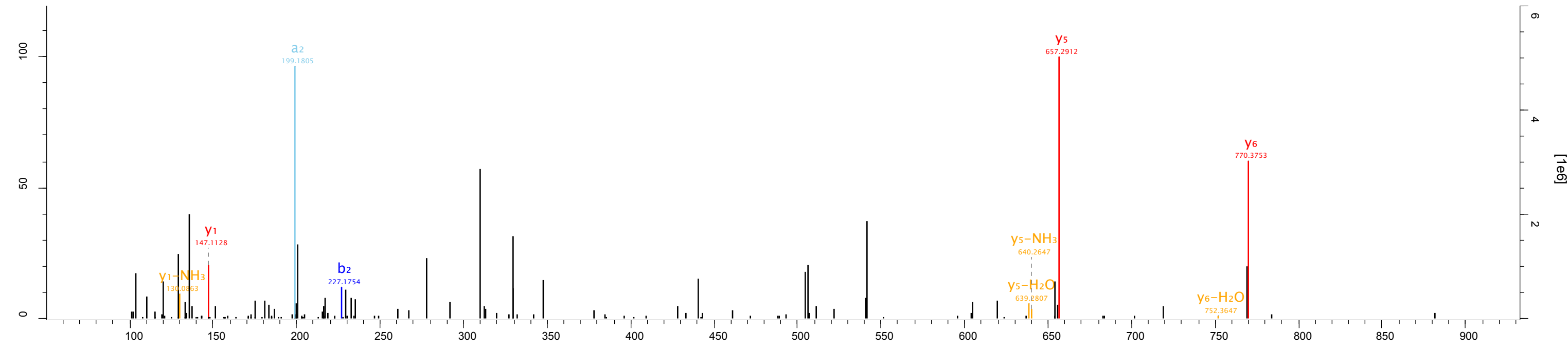
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 Scan: 86444 Method: FTMS; HCD Score: 90.71 m/z: 760.38 Gene names: FLNB



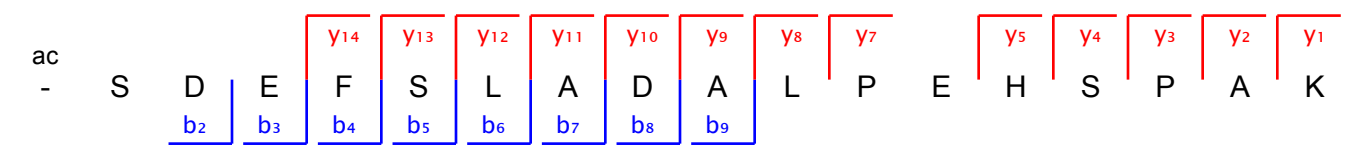
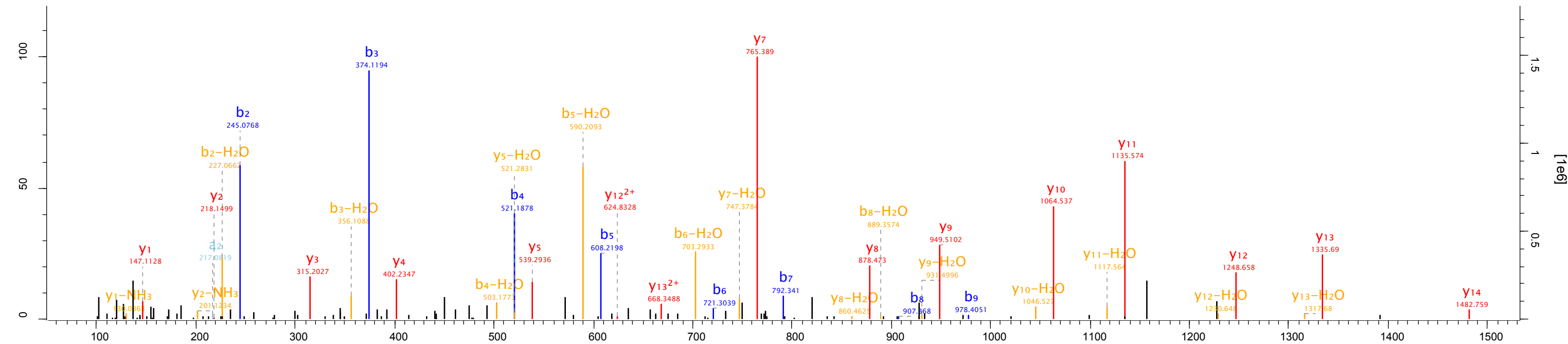
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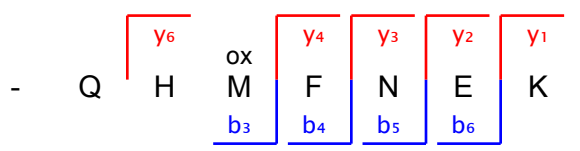
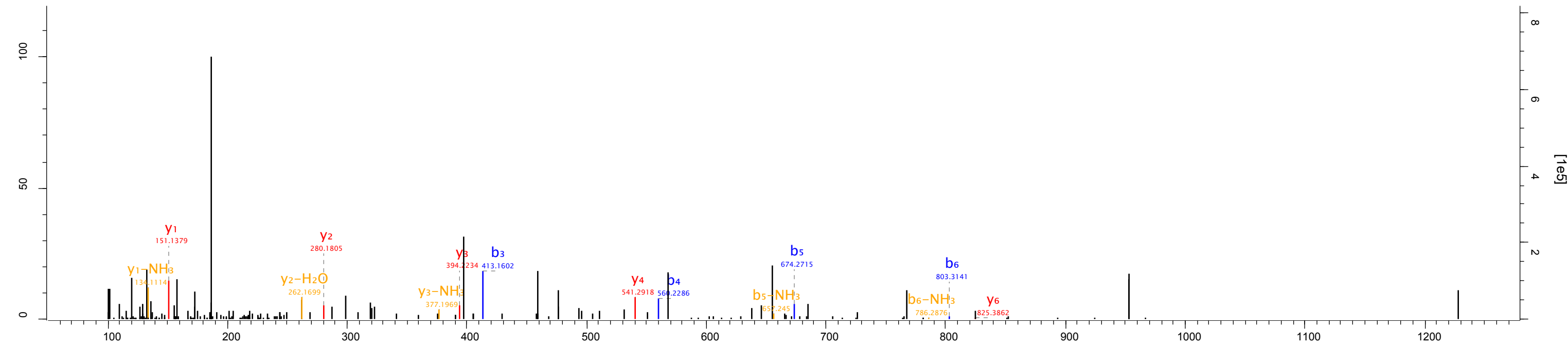
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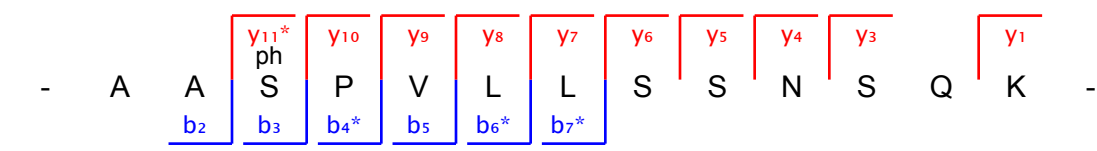
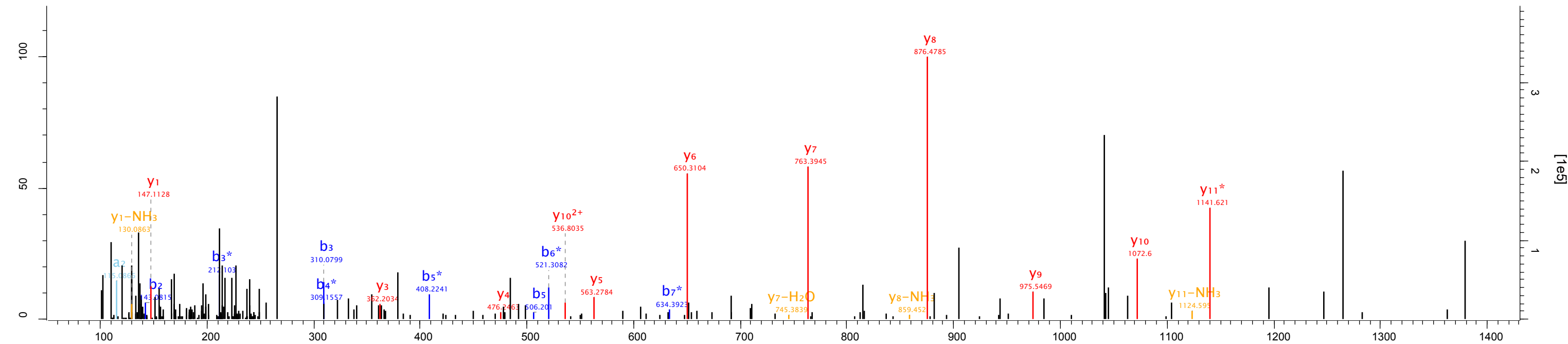
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 Scan: 78684 Method: FTMS; HCD Score: 177.04 m/z: 928.44 Gene names: MAPK11P1L



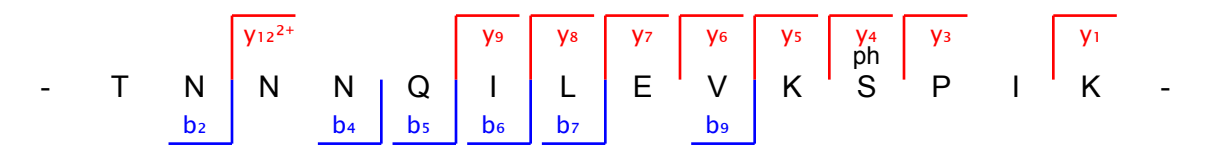
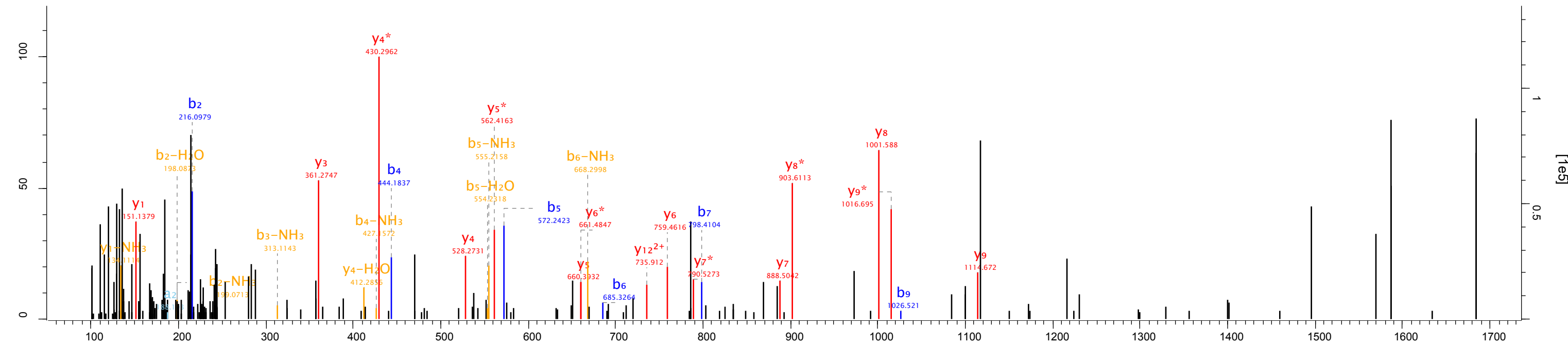
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 Scan: 9694 Method: FTMS; HCD Score: 89.75 m/z: 477.23 Gene names: GPR64



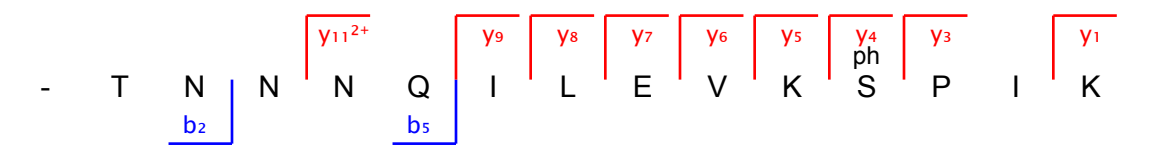
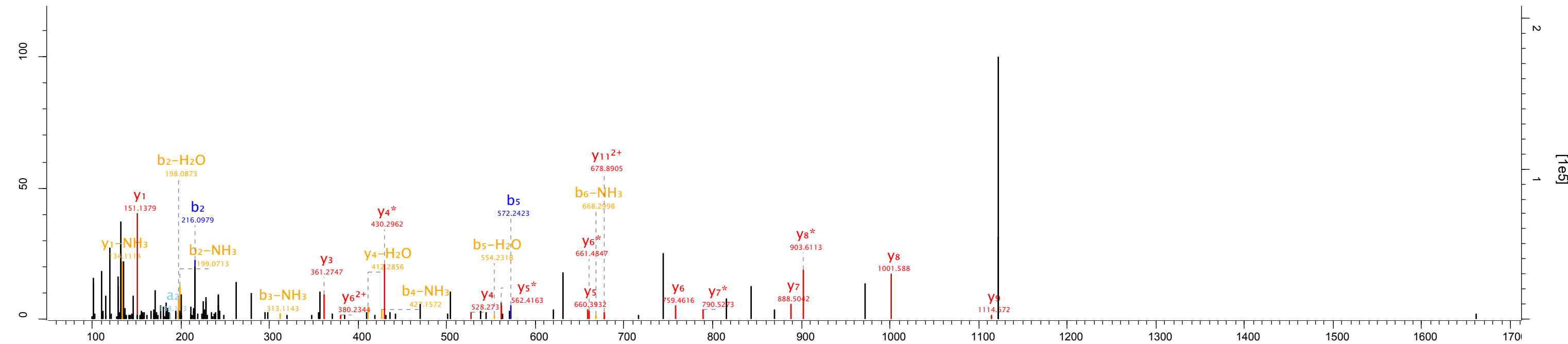
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 Scan: 11174 Method: FTMS; HCD Score: 44.82 m/z: 691.34 Gene names: ELK3



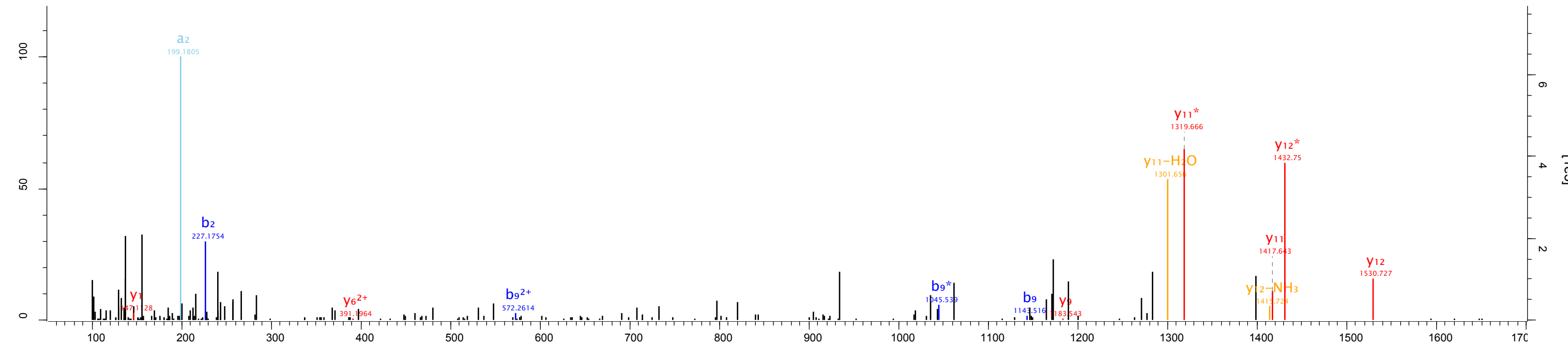
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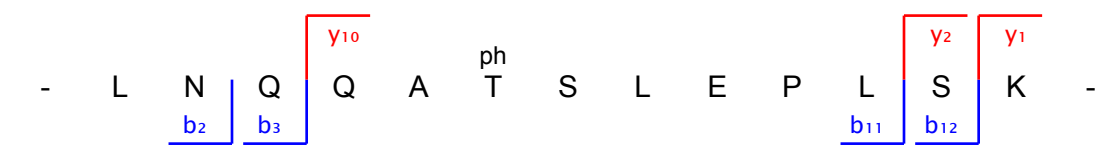
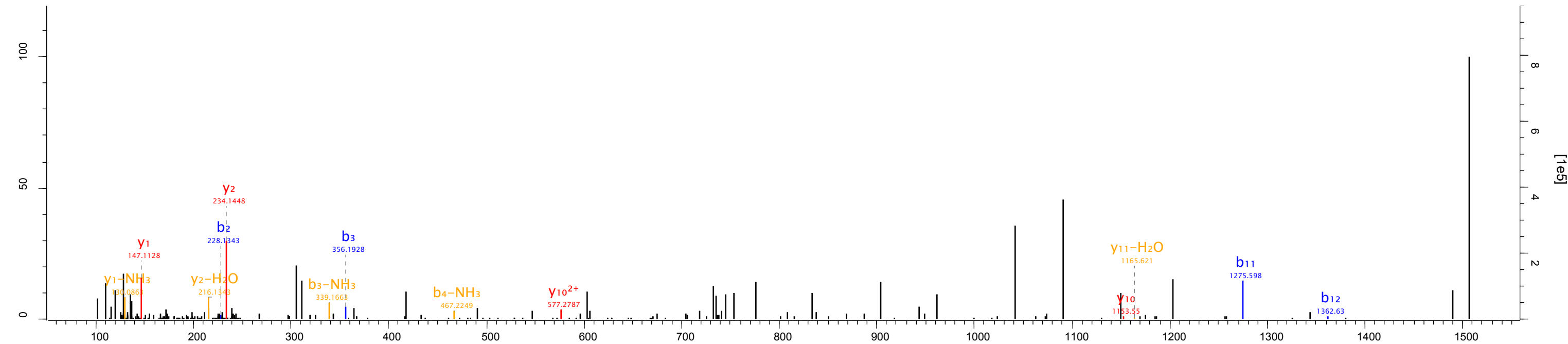
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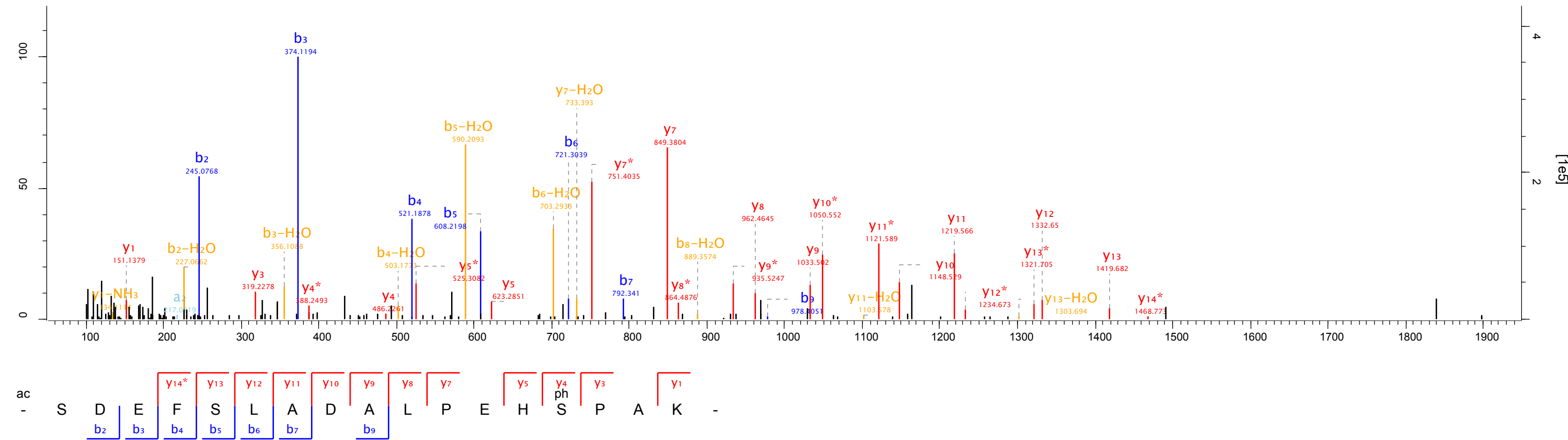
- I L S F E L C S L E K P K -

Fragmentation mapping:
 - Red brackets above: y12 (L-S), y11 (S-F), y9 (E-L), y6²⁺ (C-S), y1 (P-K)
 - Blue brackets below: b2 (L-S), b9 (C-S)

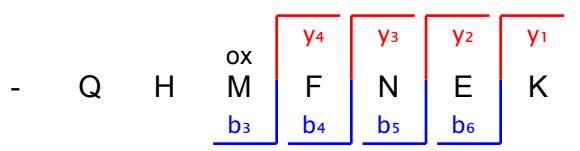
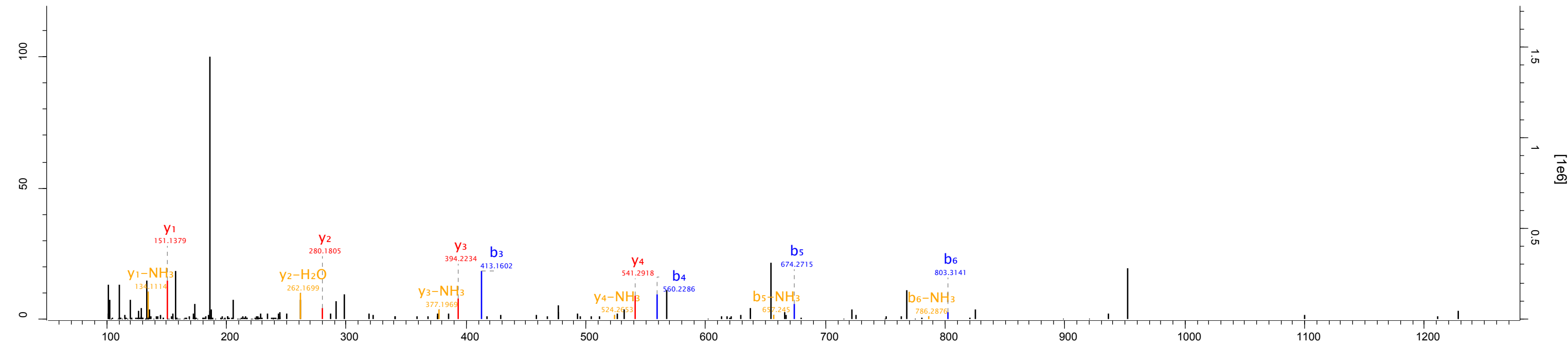
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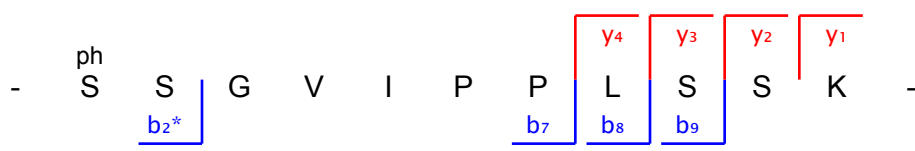
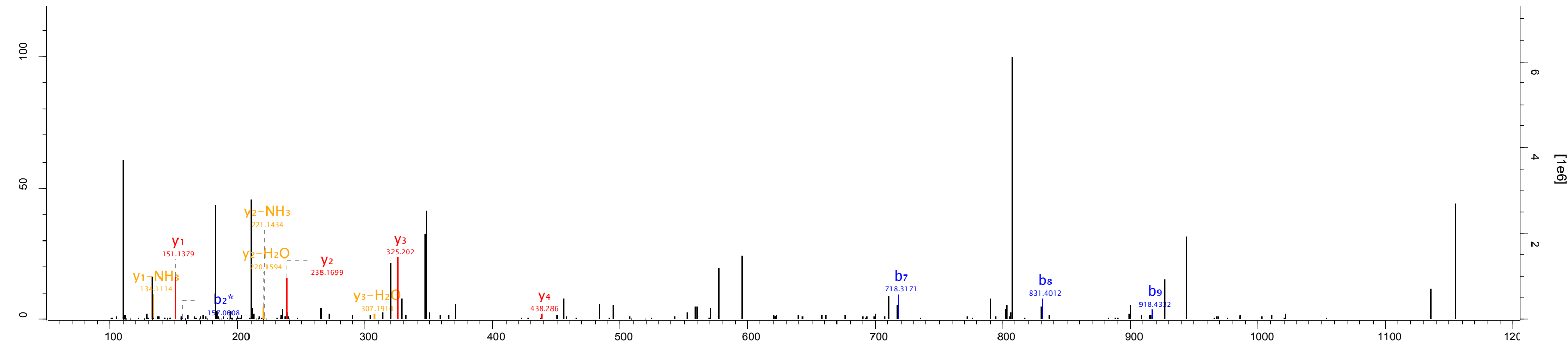
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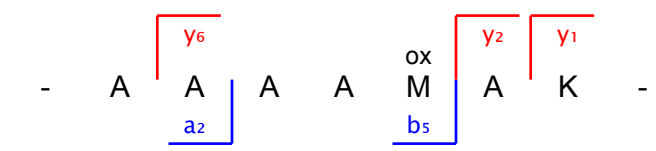
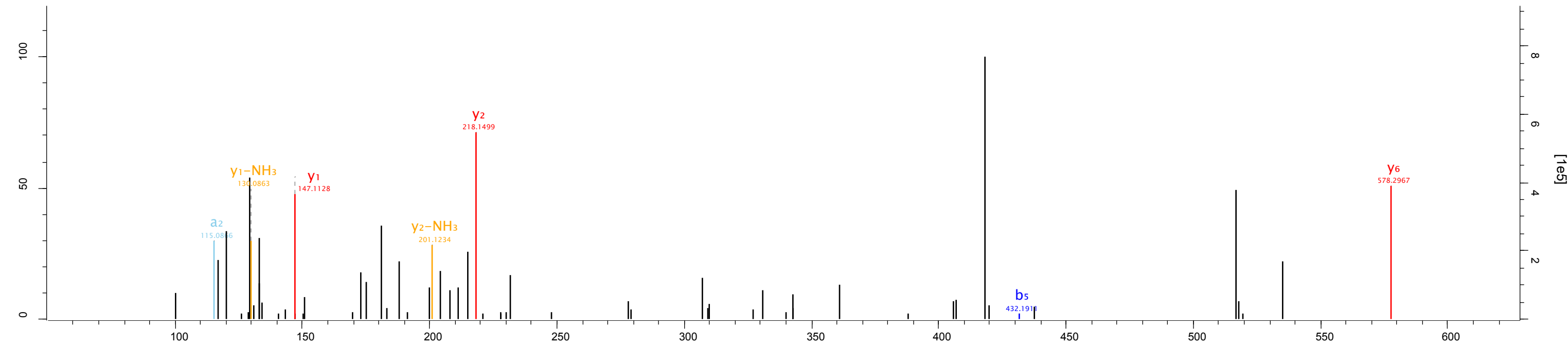
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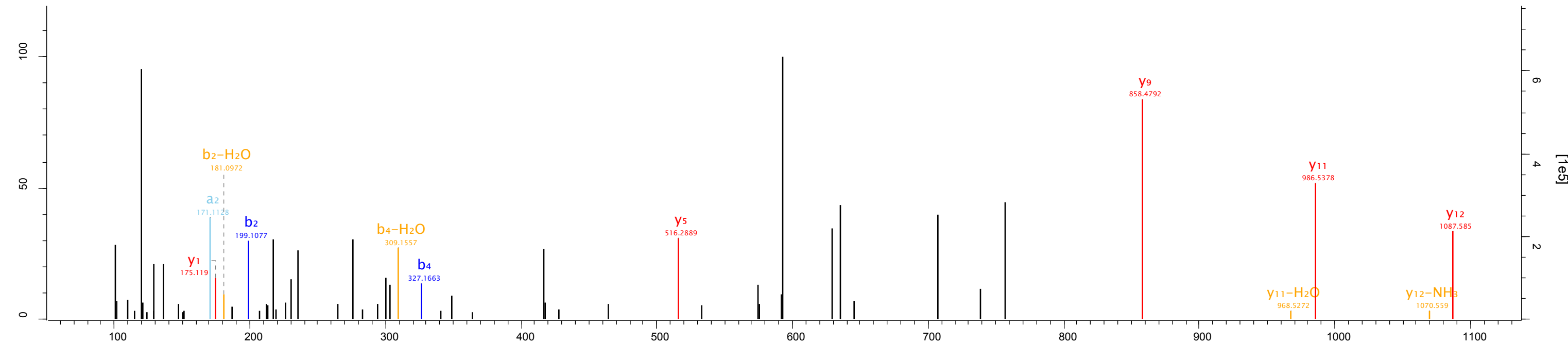
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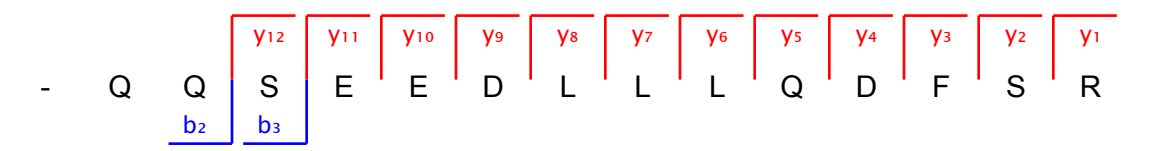
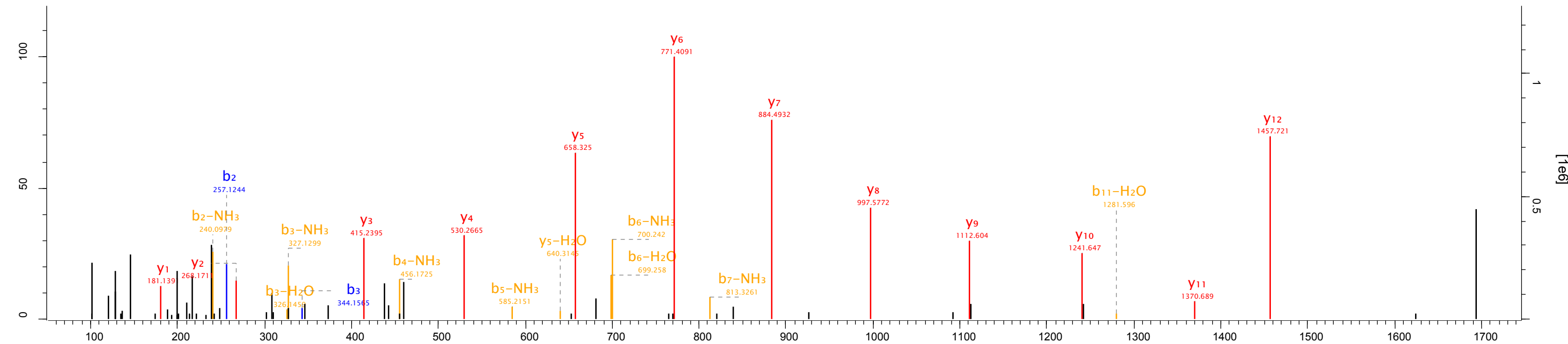
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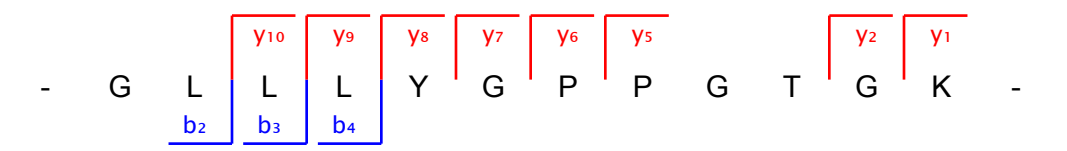
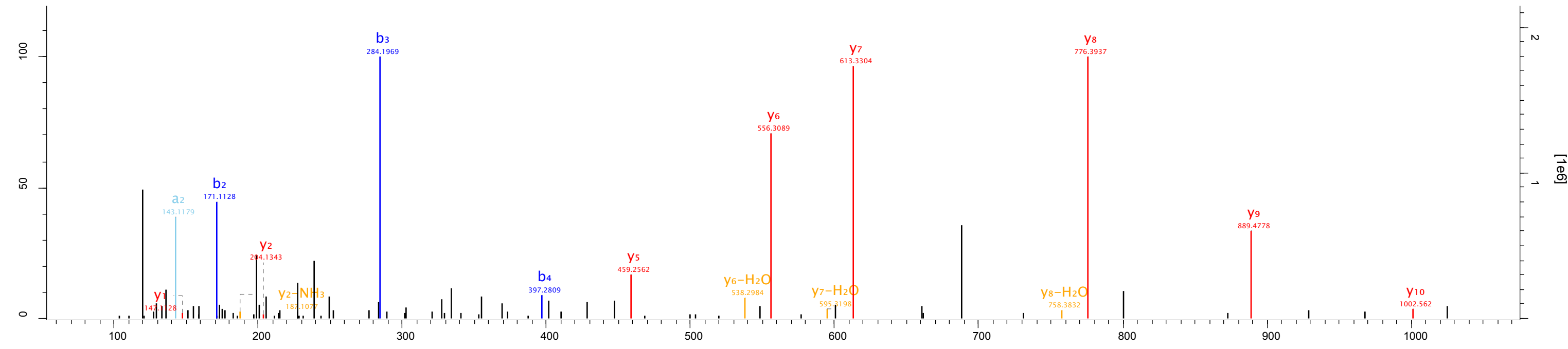
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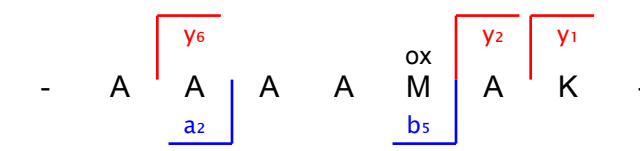
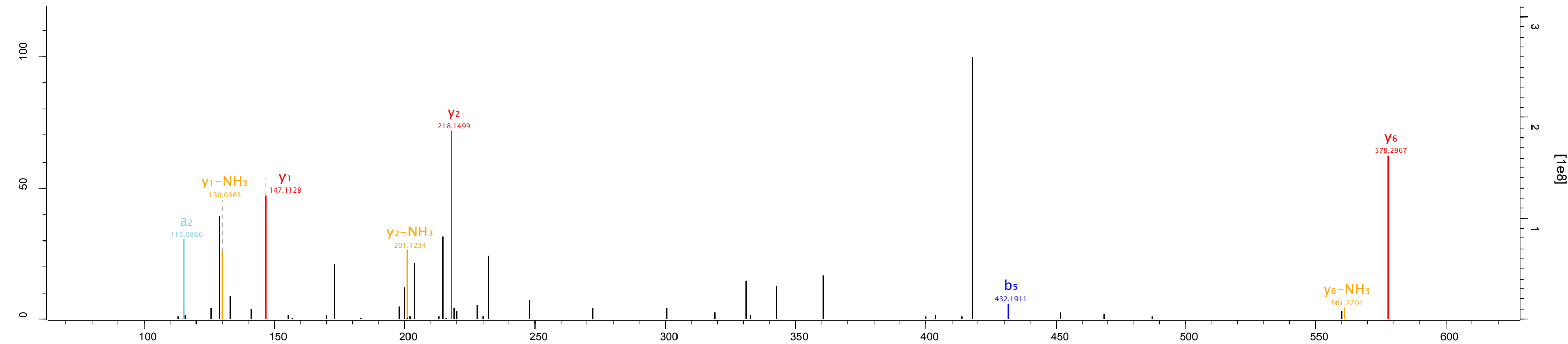
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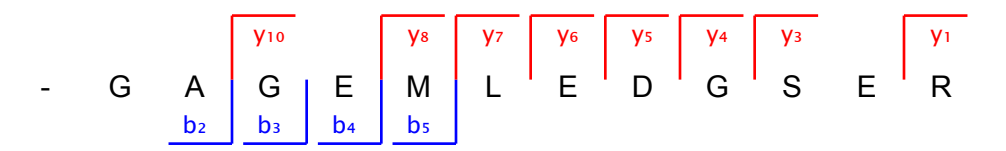
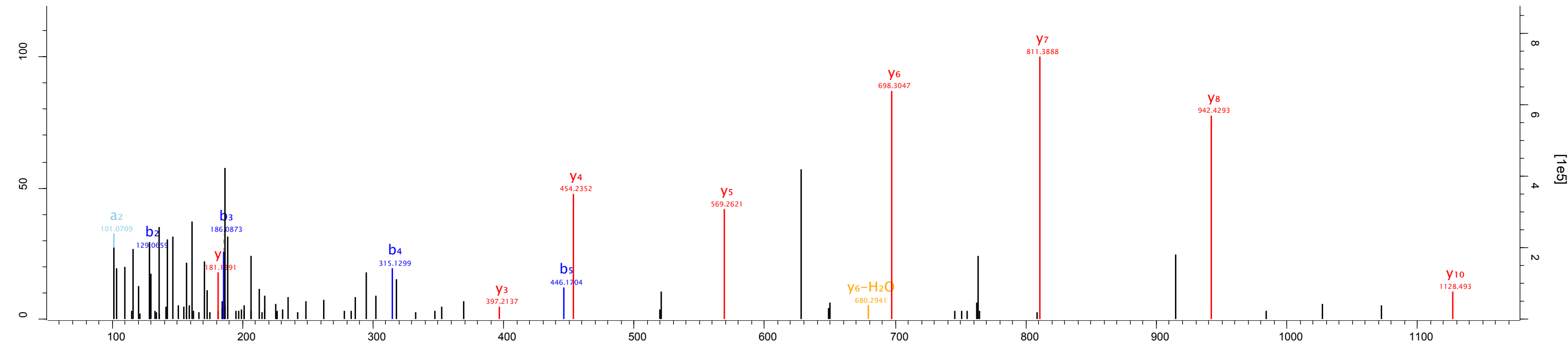
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 Scan: 21004 Method: FTMS; HCD Score: 65.18 m/z: 586.84 Gene names: KATNAL2



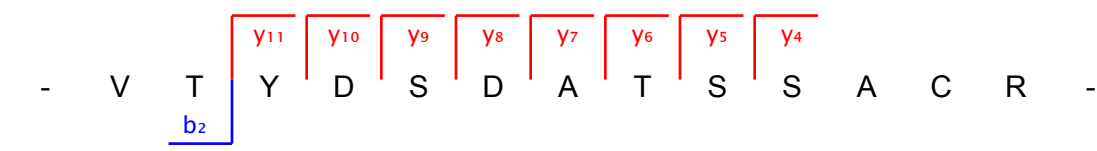
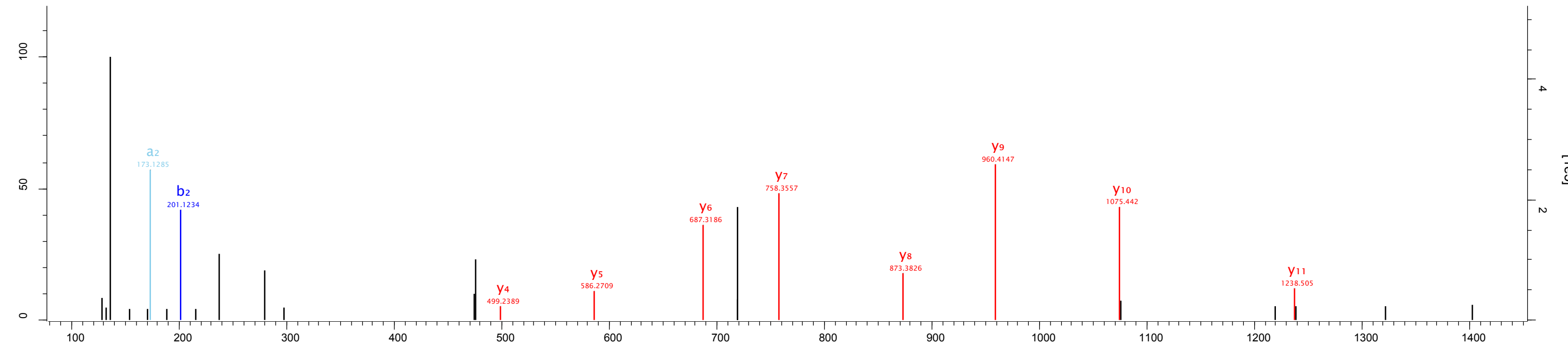
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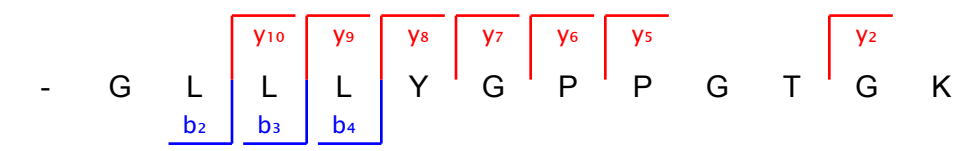
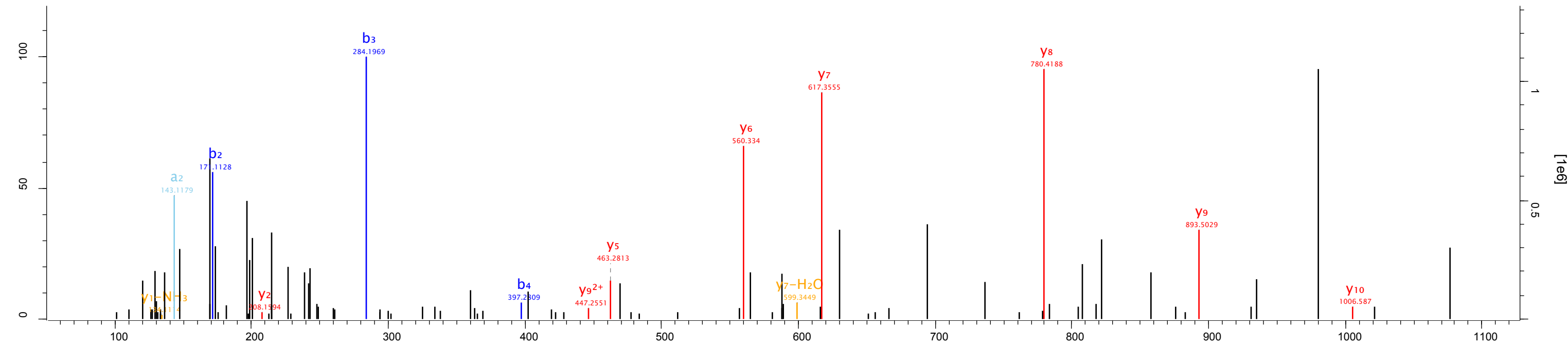
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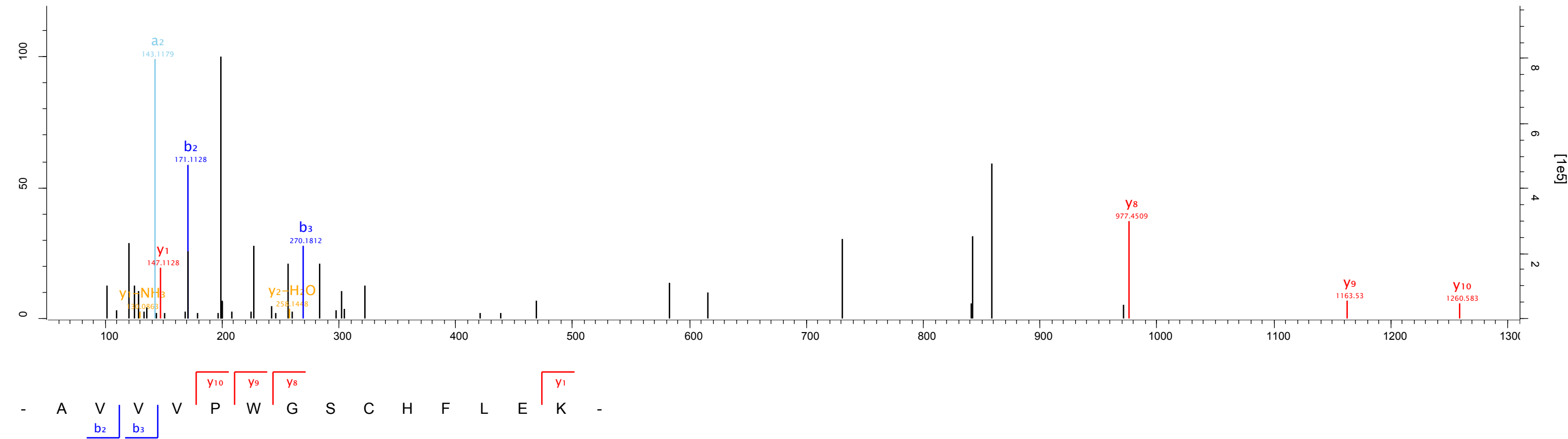


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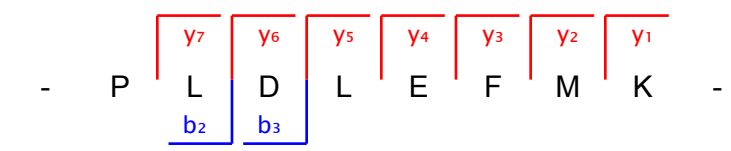
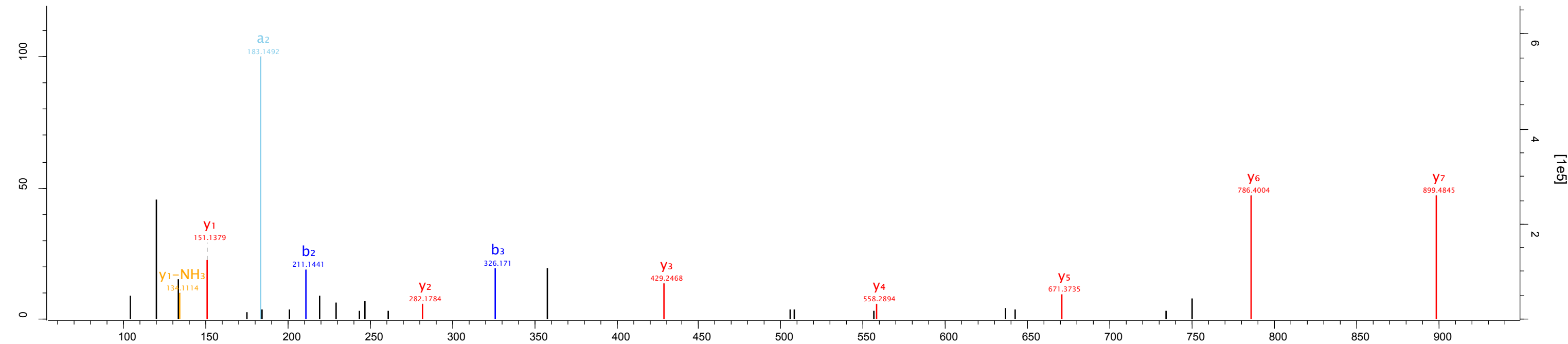
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 Scan: 21744 Method: FTMS; HCD Score: 48.57 m/z: 588.85 Gene names: KATNAL2





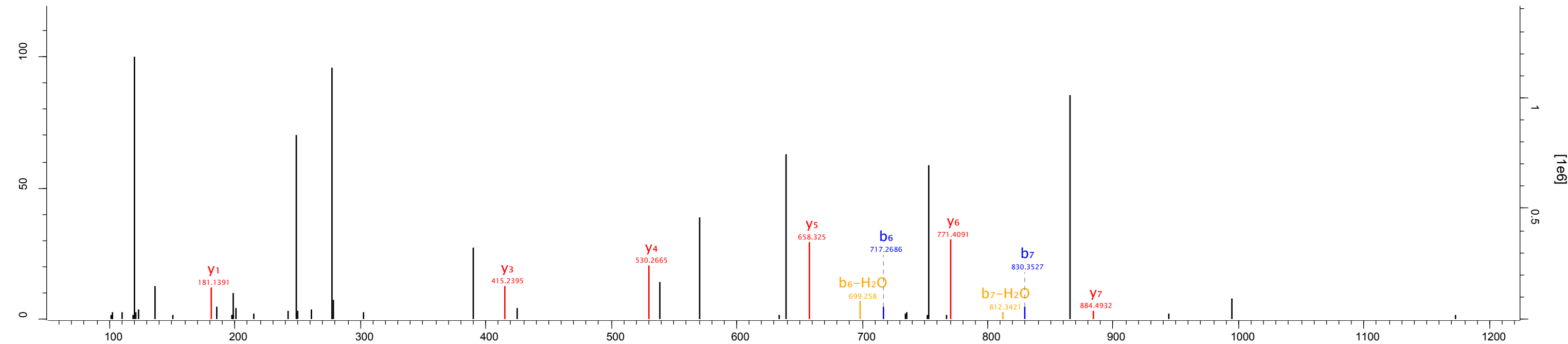
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20180707_MaS_A375SR_LM_proteome_22

Scan: 25184
Method: FTMS; HCD
Score: 61.68
m/z: 498.77
Gene names: SEPT3



Raw file
20180707_MaS_A375SR_LM_proteome_22

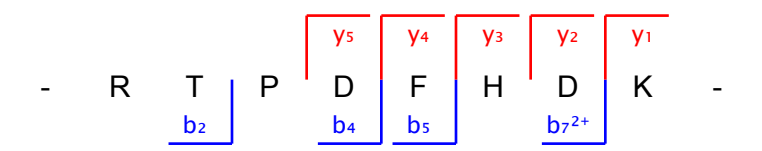
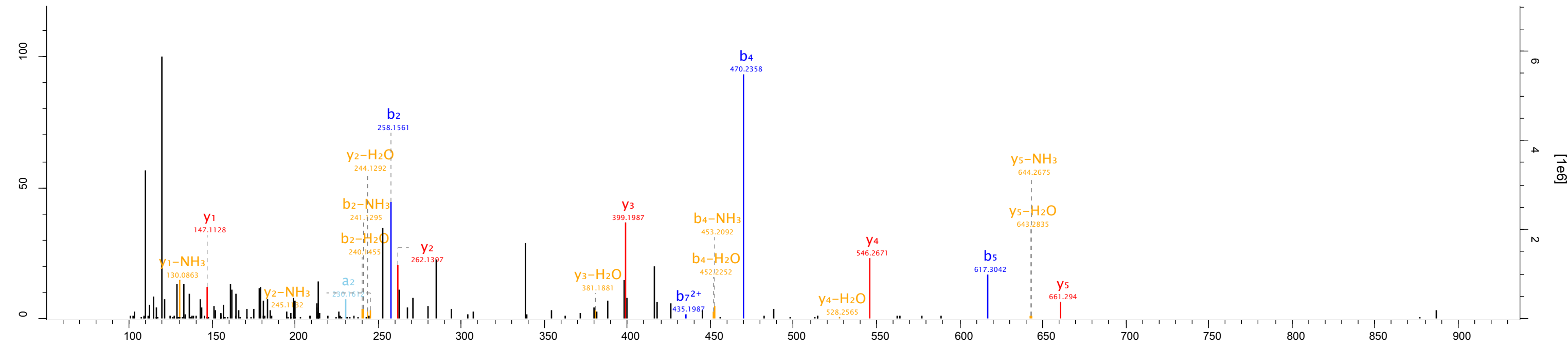
Scan 27514 Method FTMS; HCD Score 33.84 m/z 571.95 Gene names SSR3



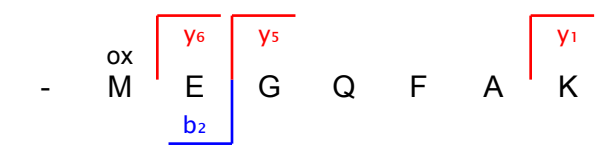
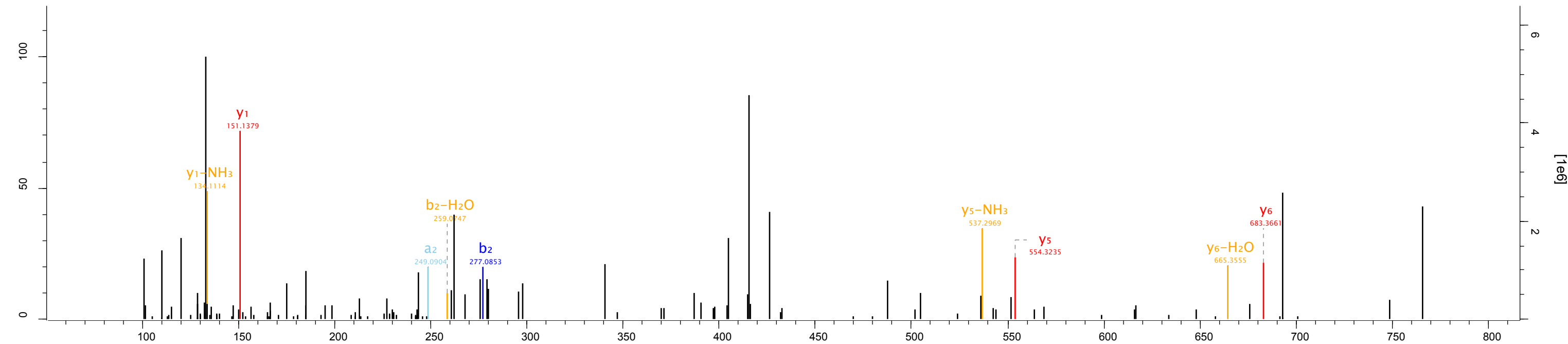
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b₆ b₇ y₇ y₆ y₅ y₄ y₃ y₁

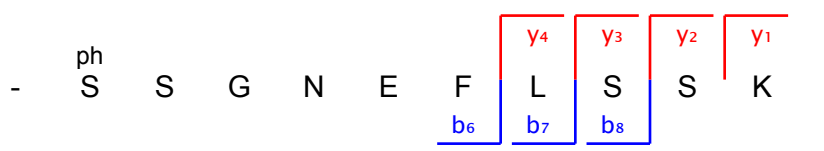
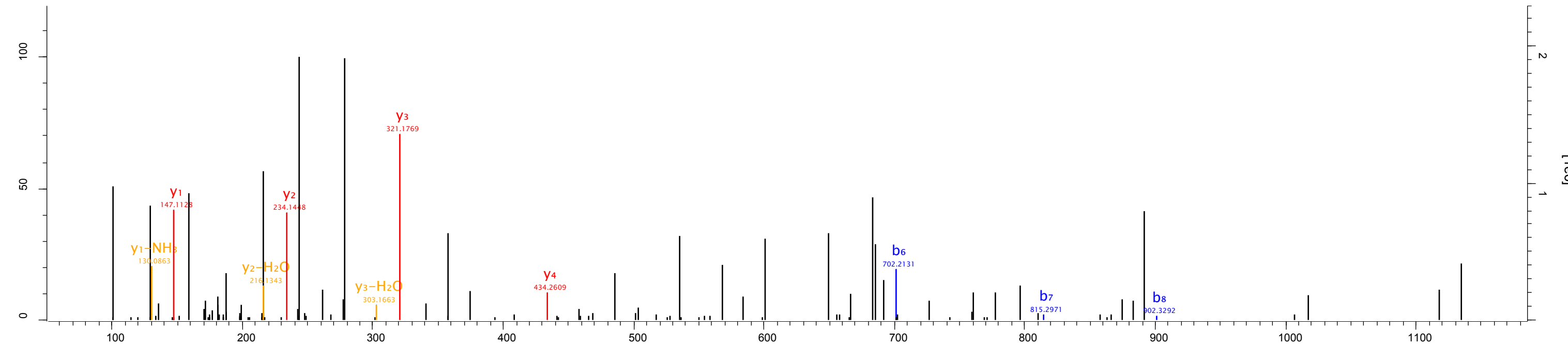
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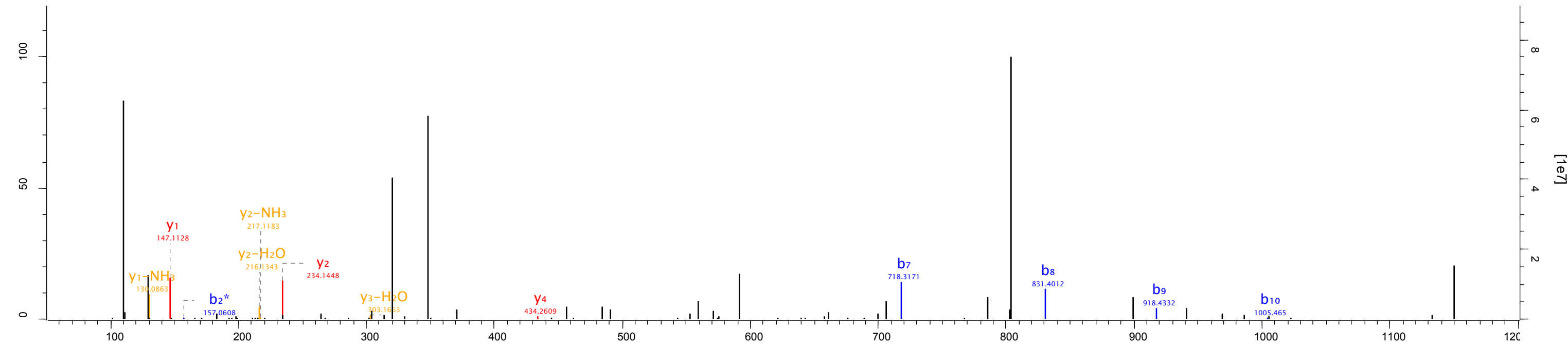
Raw file 20180707_MaS_A375SR_LM_proteome_25 Scan 3844 Method FTMS; HCD Score 64.78 m/z 415.7



Raw file: 20180707_MaS_A375SR_LM_proteome_26
 Scan: 3724 Method: FTMS; HCD Score: 57.35 m/z: 568.24 Gene names: MAP3K19

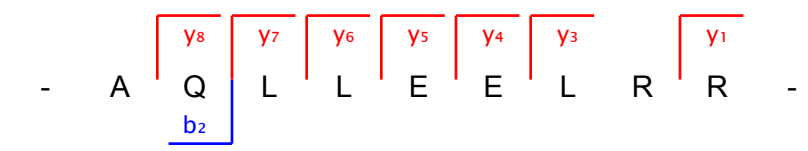
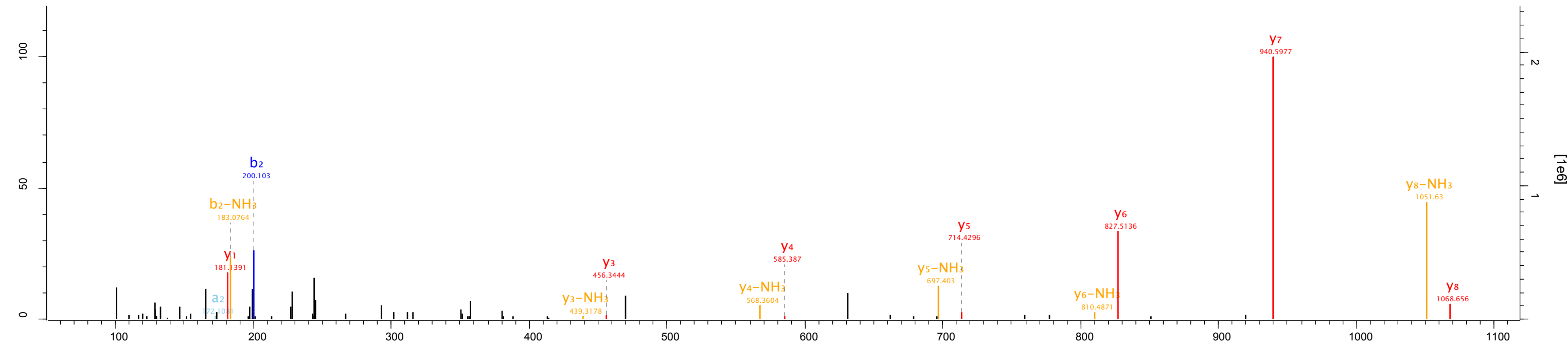


Raw file 20180707_MaS_A375SR_LM_proteome_28 Scan 8564 Method FTMS; HCD Score 66.06 m/z 576.29

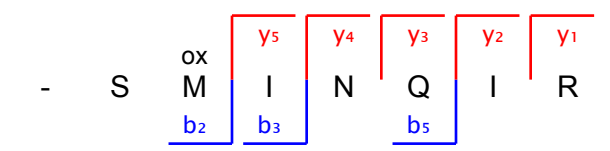
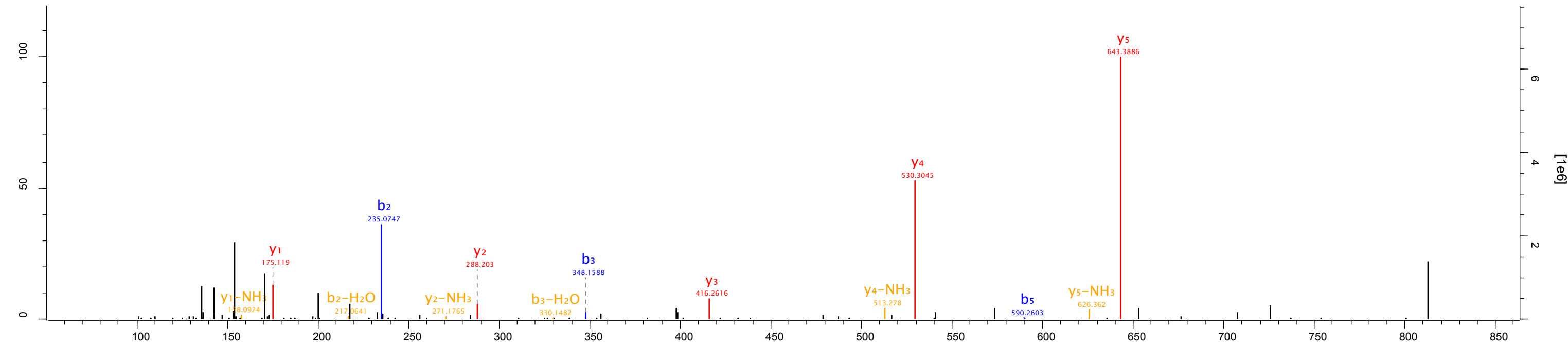


Raw file
20180707_MaS_A375SR_ML_proteome_01

Scan	Method	Score	m/z	Gene names
15054	FTMS; HCD	82.29	380.57	PNKD



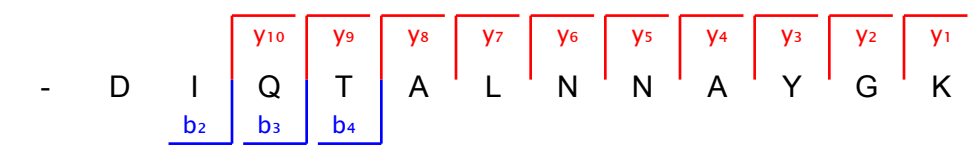
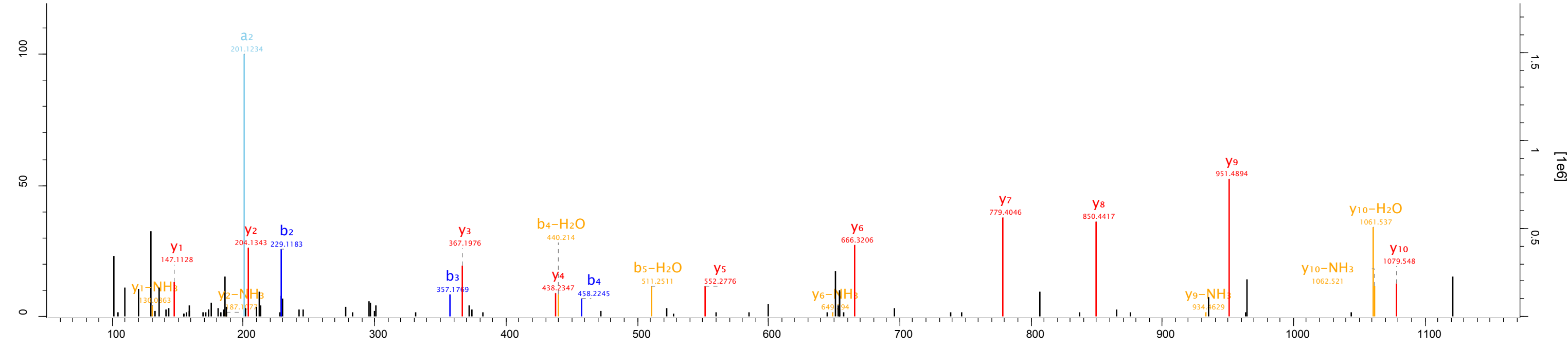
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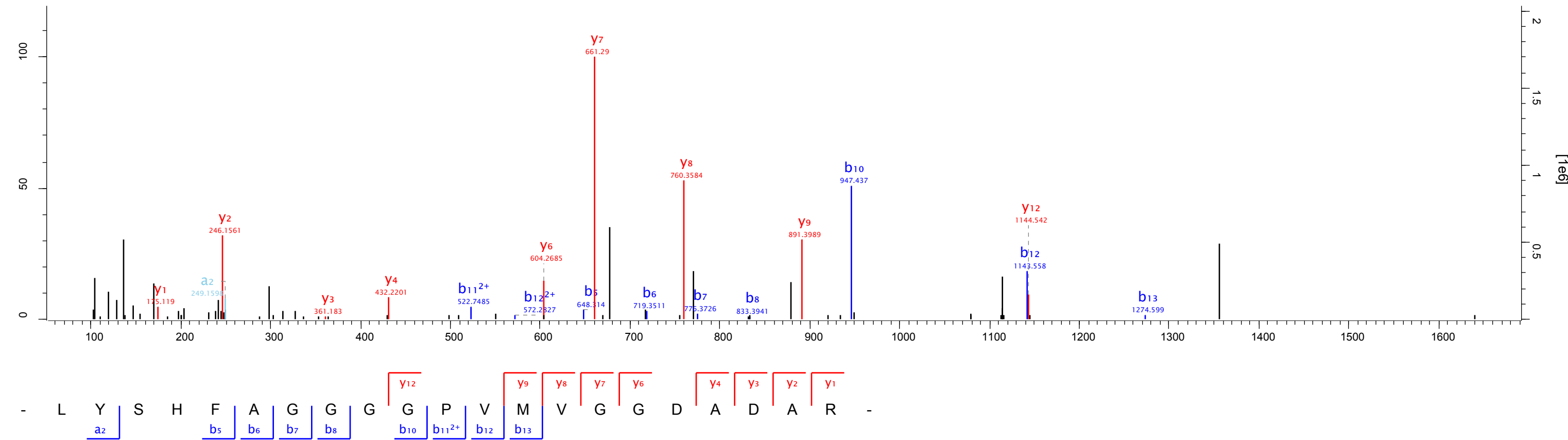


Raw file

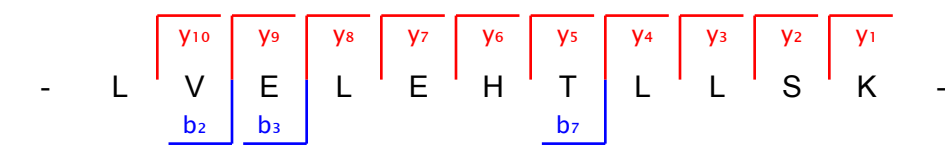
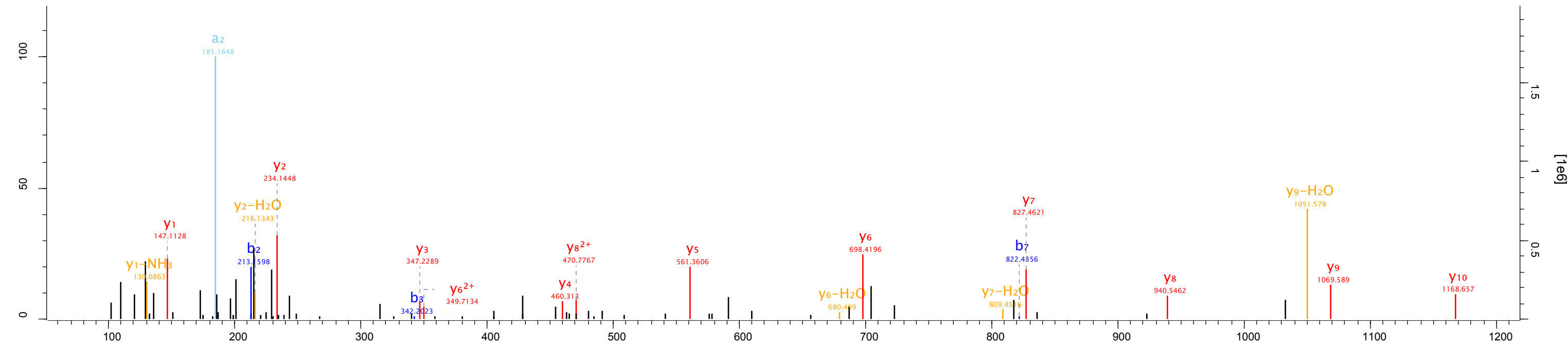
20180707_MaS_A375SR_ML_proteome_02

Scan	Method	Score	m/z	Gene names
16034	FTMS; HCD	96.6	654.33	PLEKHA8;PLEKHA8P1



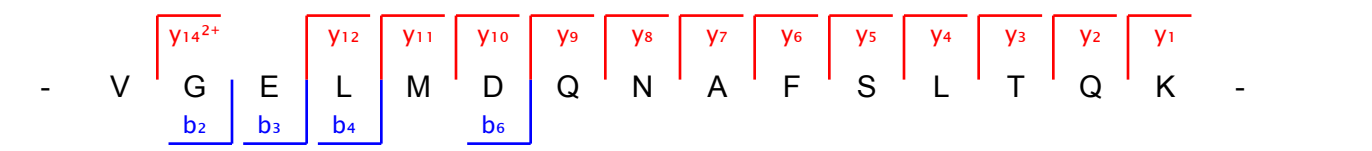
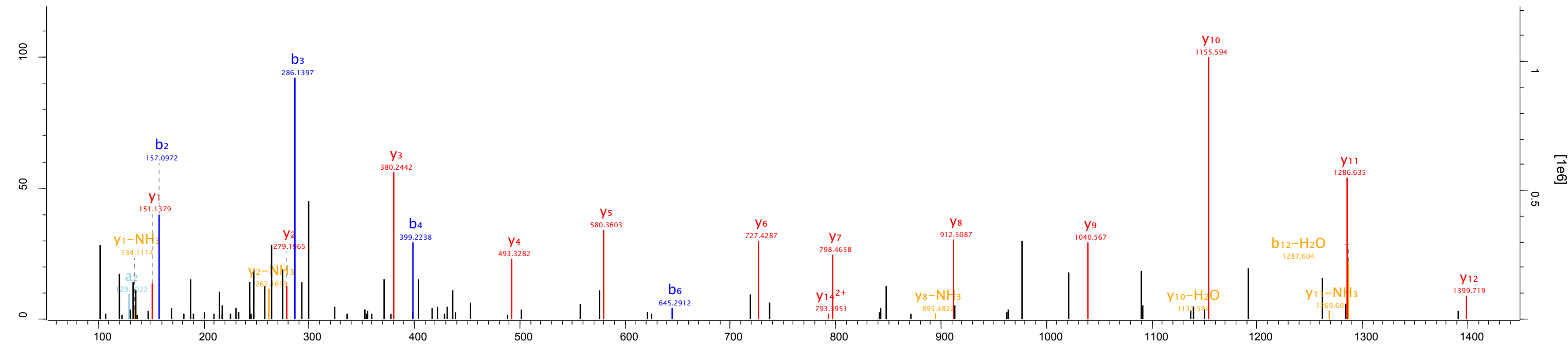


Raw file: 20180707_MaS_A375SR_ML_proteome_04
 Scan: 19664 Method: FTMS; HCD Score: 127.87 m/z: 428.25 Gene names: CT83



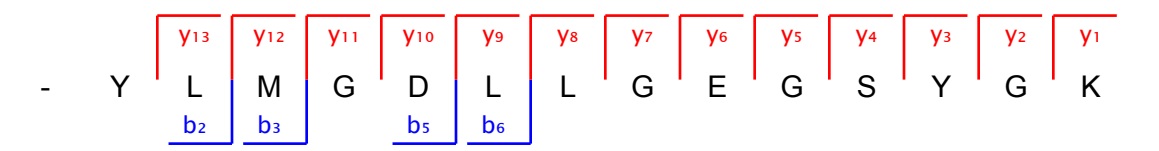
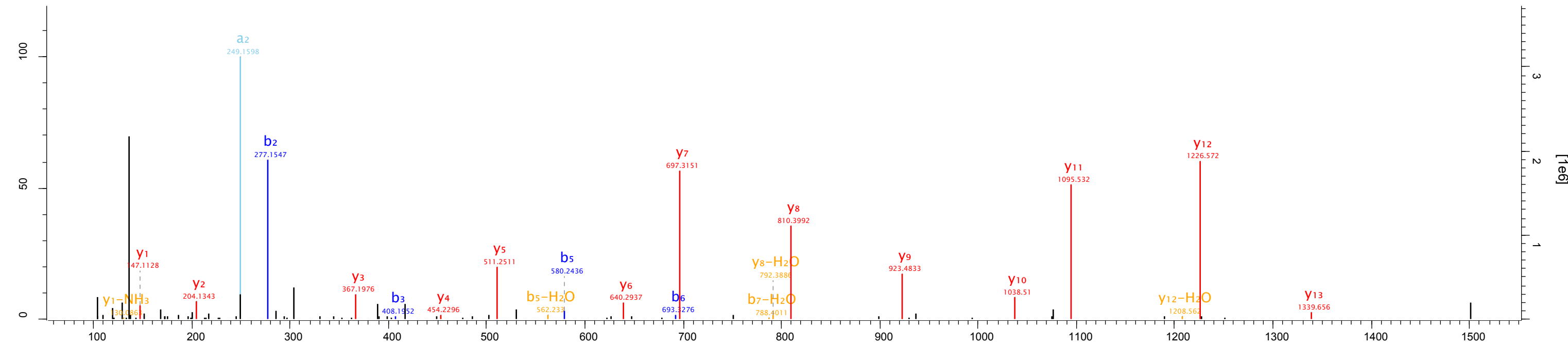
Raw file
20180707_MaS_A375SR_ML_proteome_05

Scan 24744 Method FTMS; HCD Score 70.13 m/z 842.93 Gene names GTF2H5

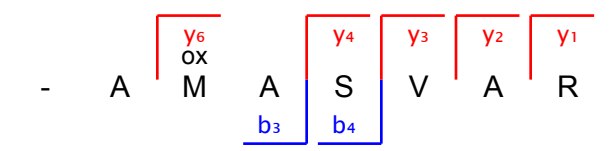
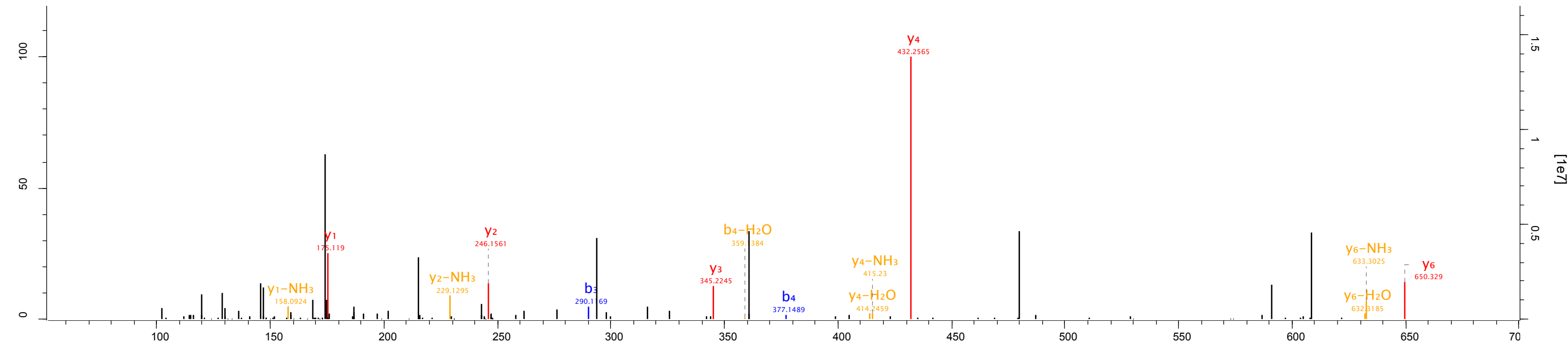


Raw file
20180707_MaS_A375SR_ML_proteome_06

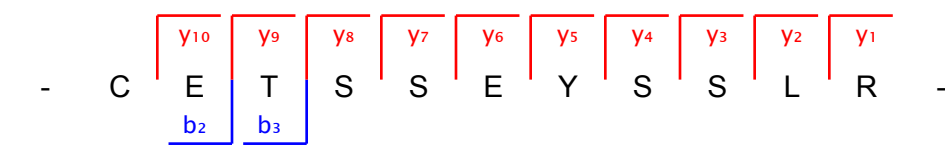
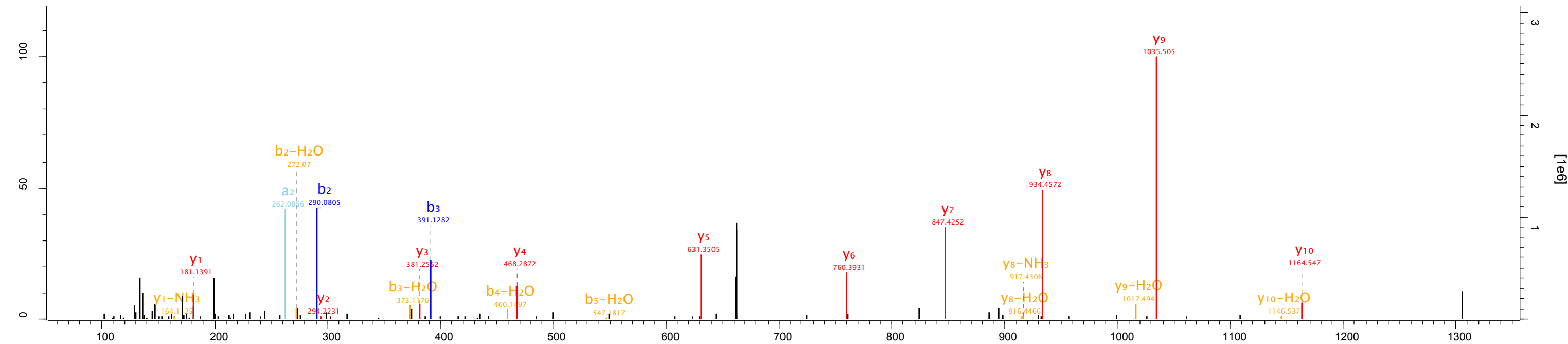
Scan 27664 Method FTMS; HCD Score 111.83 m/z 751.86 Gene names STK11



Raw file 20180707_MaS_A375SR_ML_proteome_06 Scan 7344 Method FTMS; HCD Score 82.39 m/z 361.69 Gene names ART4

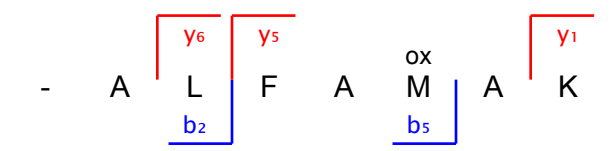
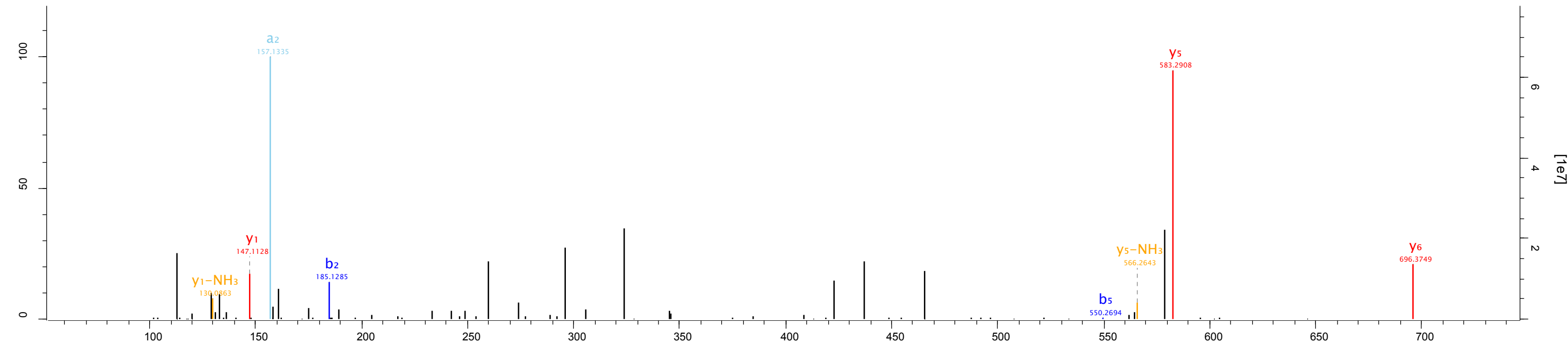


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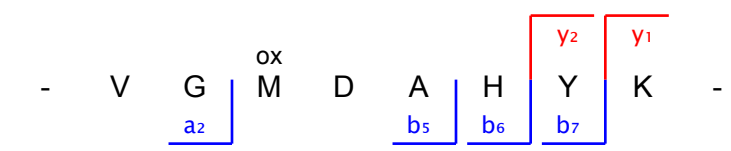
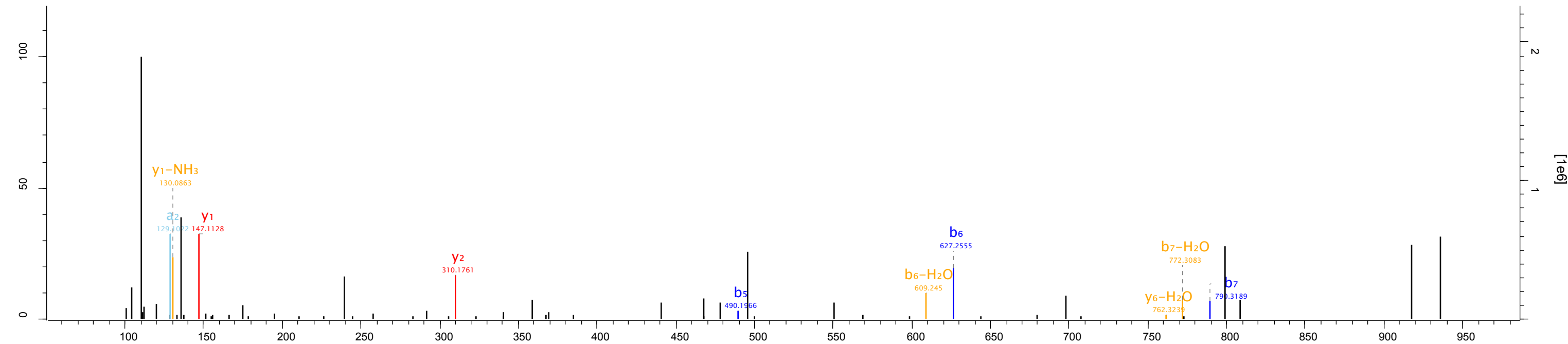
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Scan 12574 Method FTMS; HCD Score 56.51 m/z 384.21 Gene names RASD1



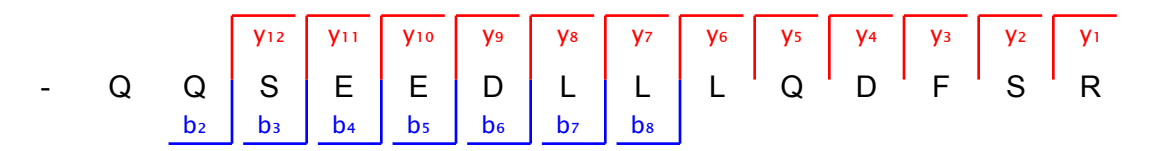
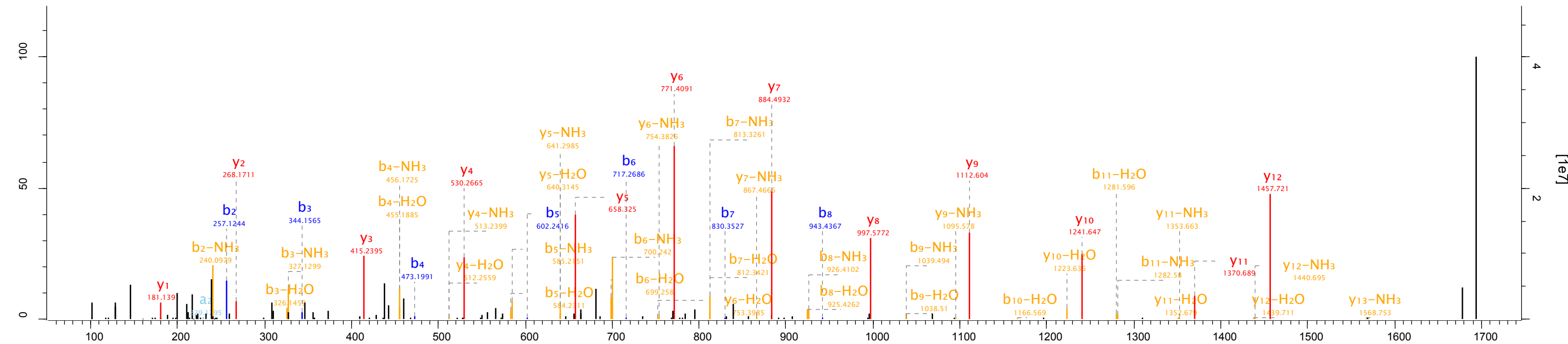
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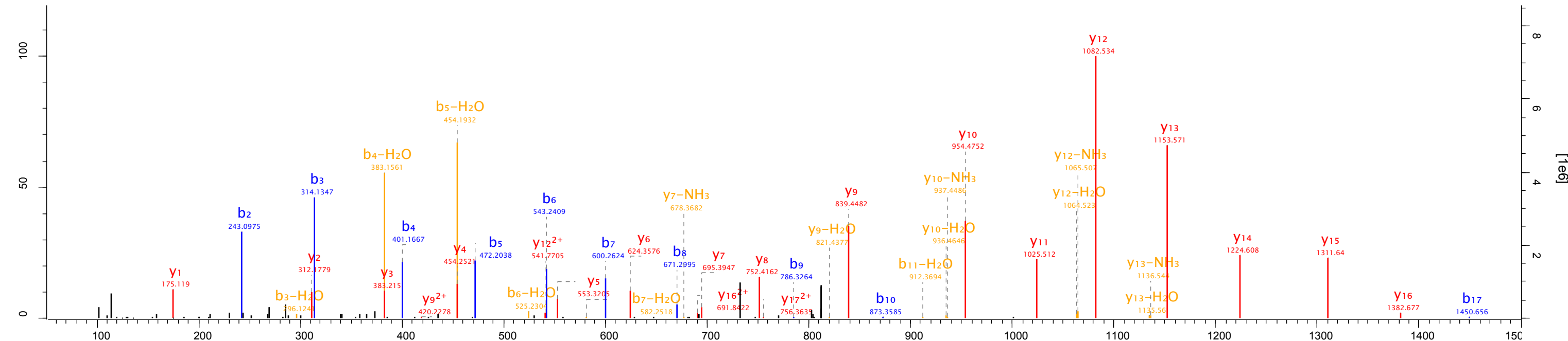
Scan 2894 Method FTMS; HCD Score 60.76 m/z 468.72



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Scan 26594 Method FTMS; HCD Score 226.88 m/z 857.42 Gene names SSR3





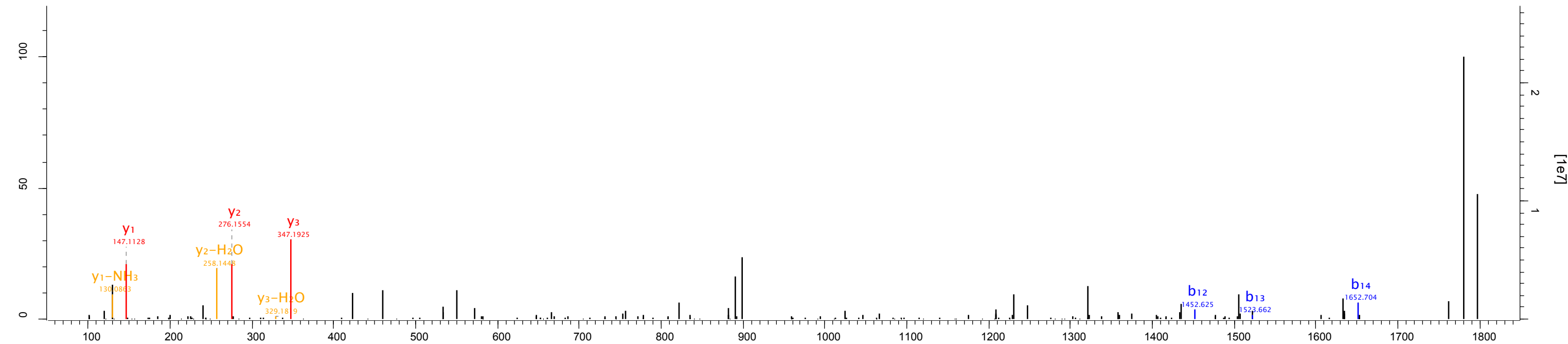
ac - A E A S A A G A D S G A A V A A H R -

Fragmentation scheme showing b and y ions for the peptide sequence: A E A S A A G A D S G A A V A A H R.

Red boxes indicate y ions: y17²⁺, y16, y15, y14, y13, y12, y11, y10, y9, y8, y7, y6, y5, y4, y3, y2, y1.

Blue boxes indicate b ions: b2, b3, b4, b5, b6, b7, b8, b9, b10, b17.

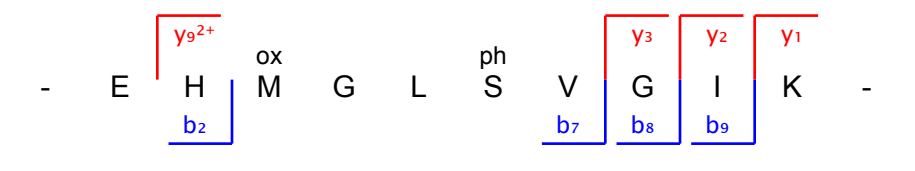
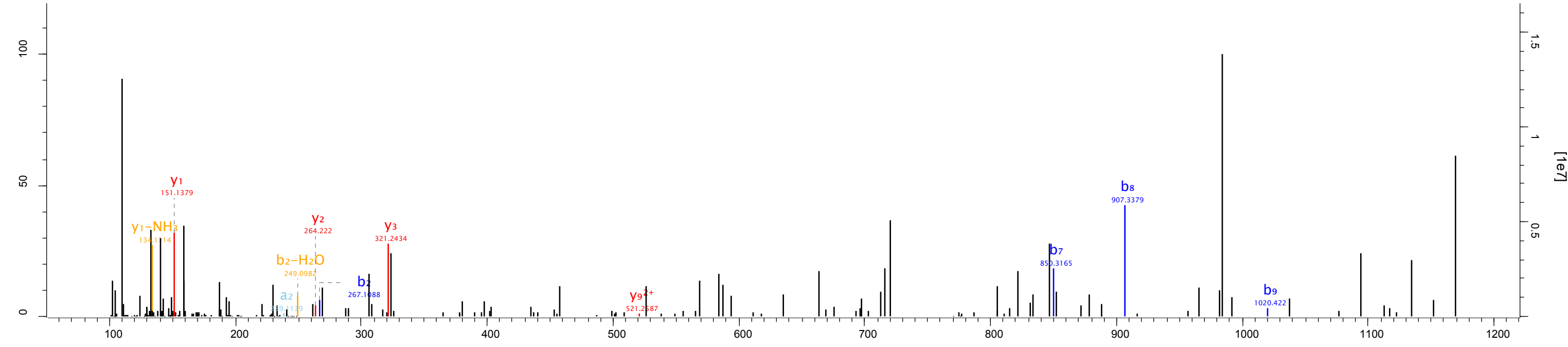
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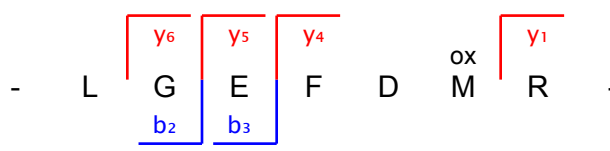
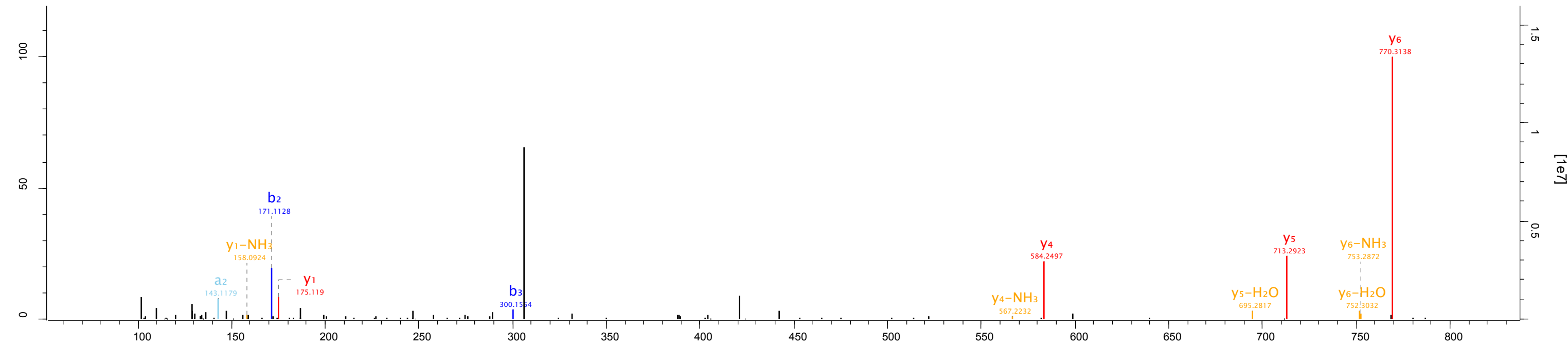
ac ox ph ph
 - M F L L T G G V S L K S A E K -

b₁₂ b₁₃ b₁₄

y₃ y₂ y₁

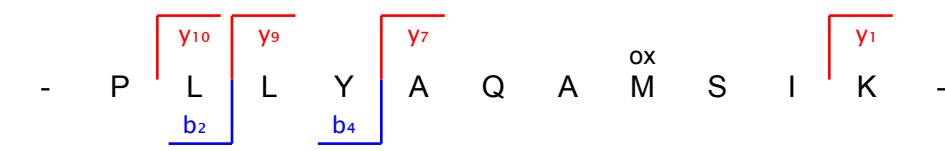
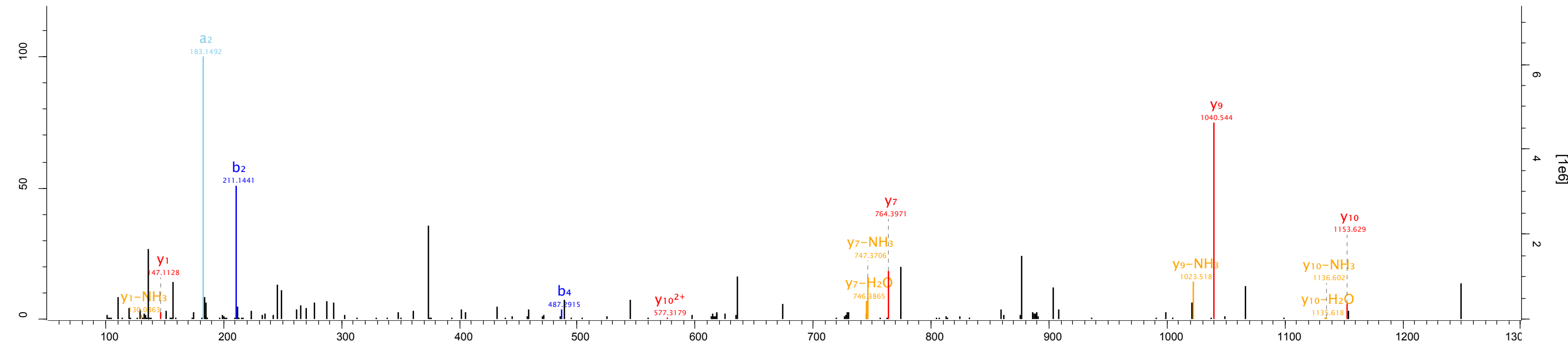


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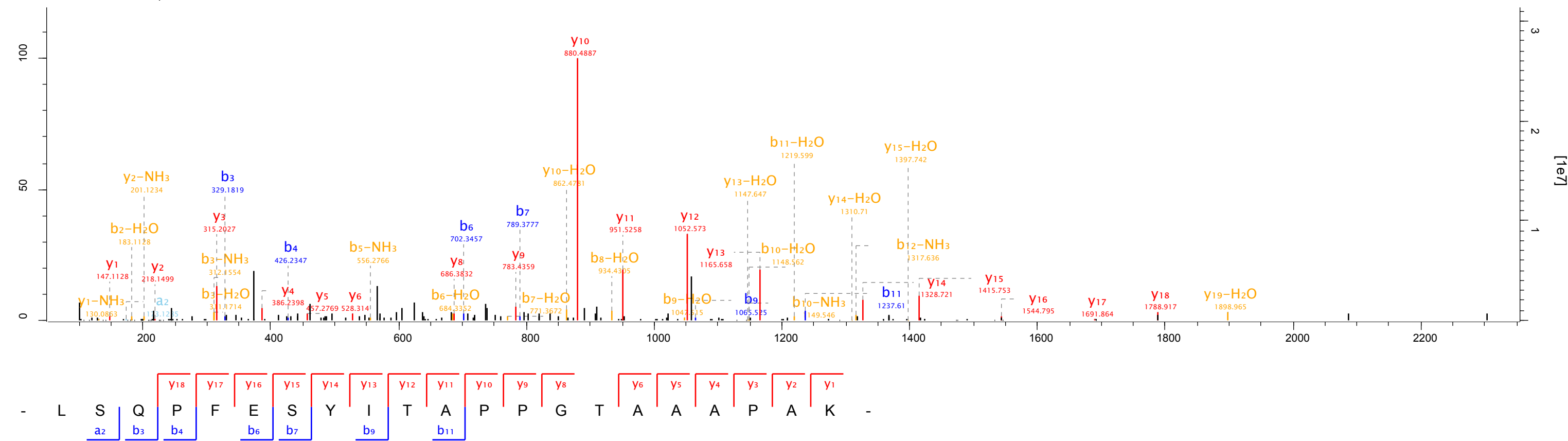
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Scan 17694 Method FTMS; HCD Score 59.07 m/z 625.85 Gene names OR9G1;OR9G9

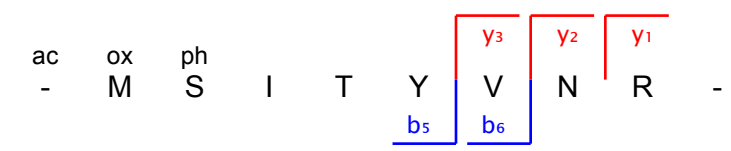
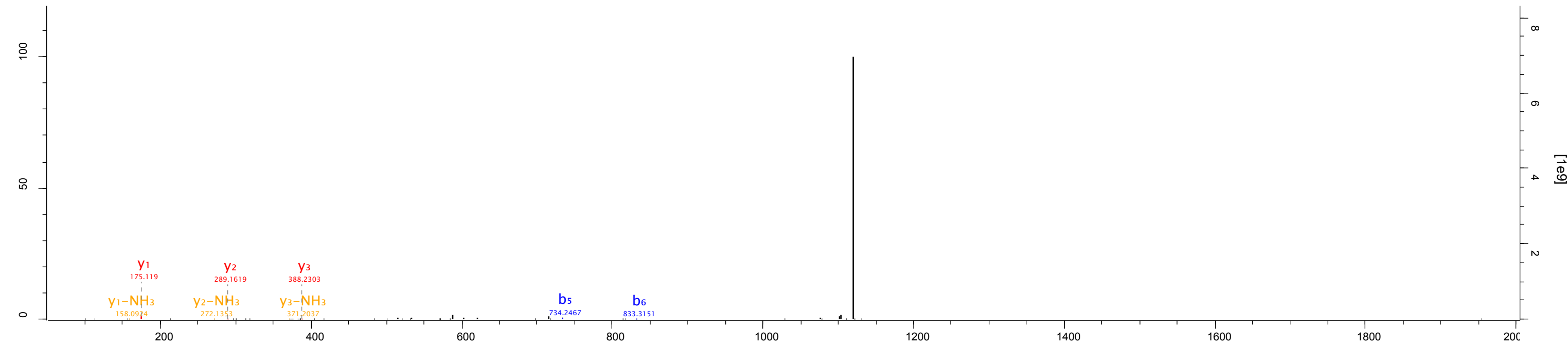


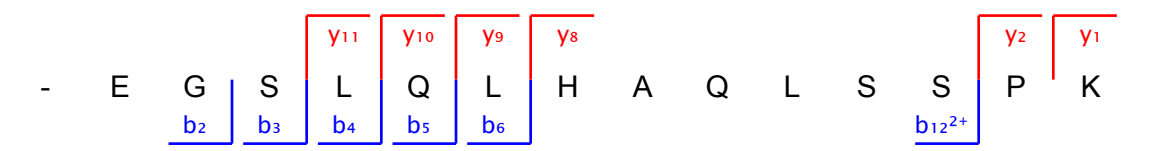
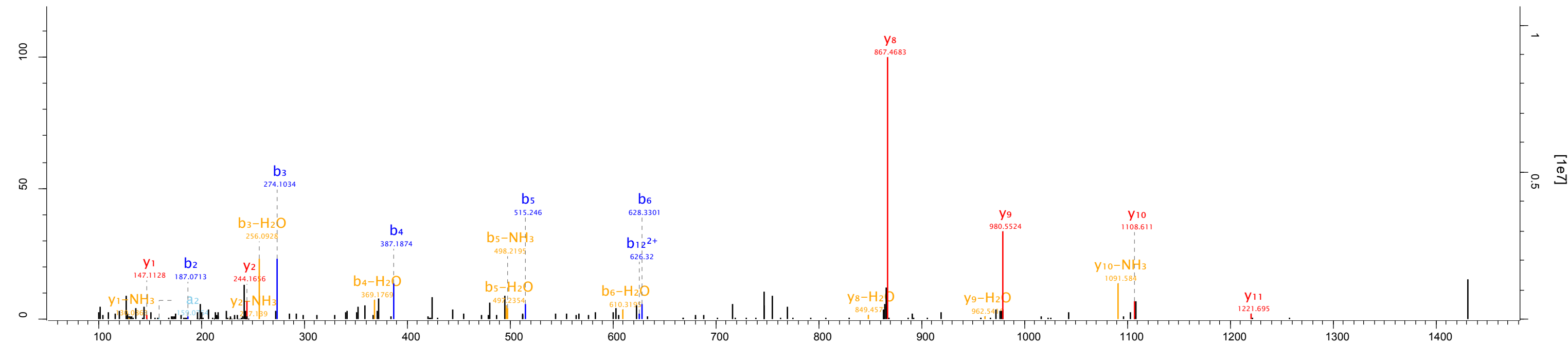
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Scan 25584 Method FTMS; HCD Score 96.88 m/z 1059.55 Gene names TMEM261



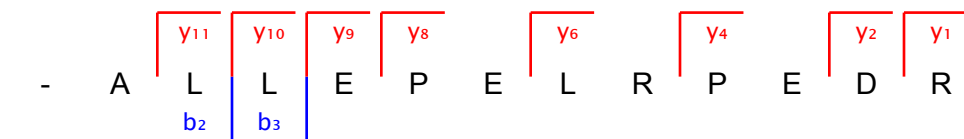
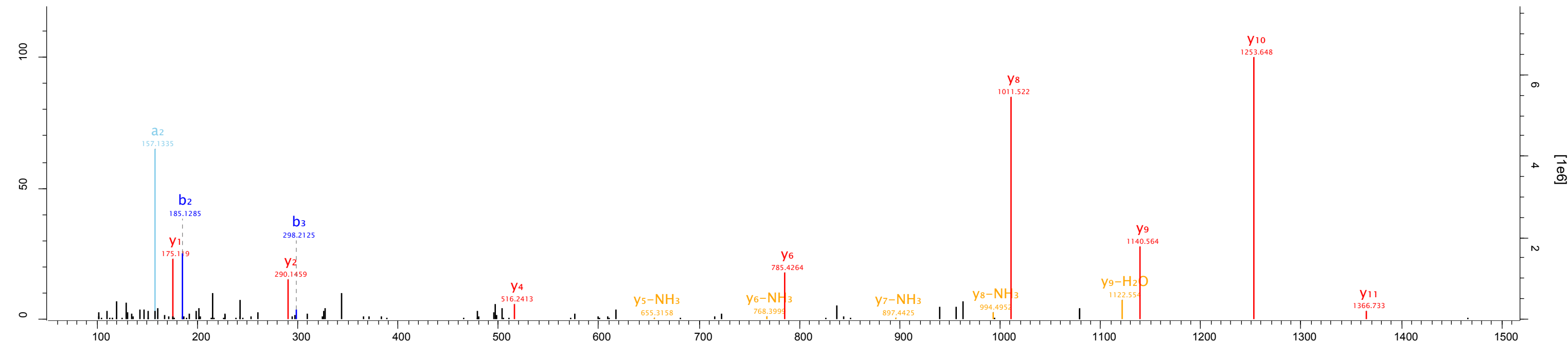
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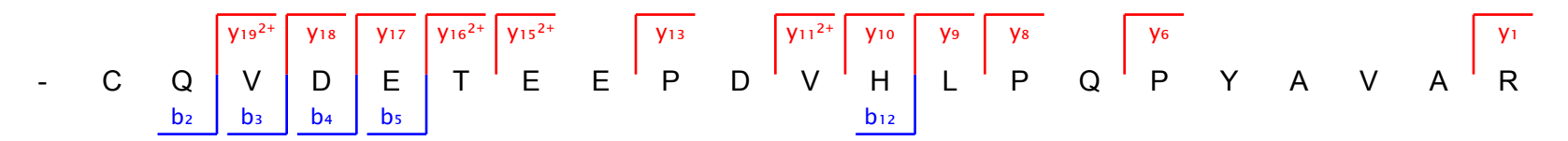
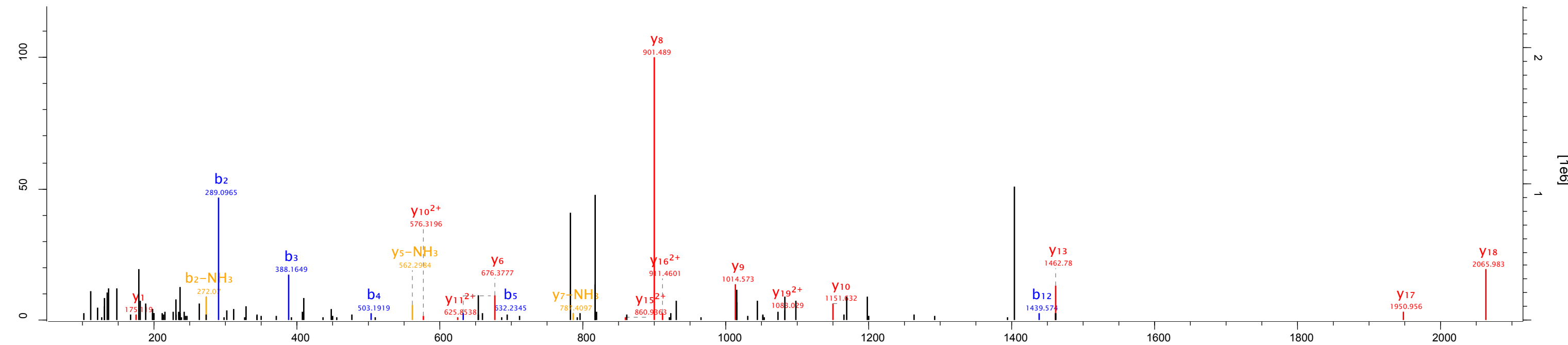




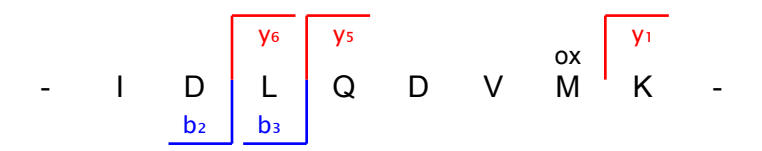
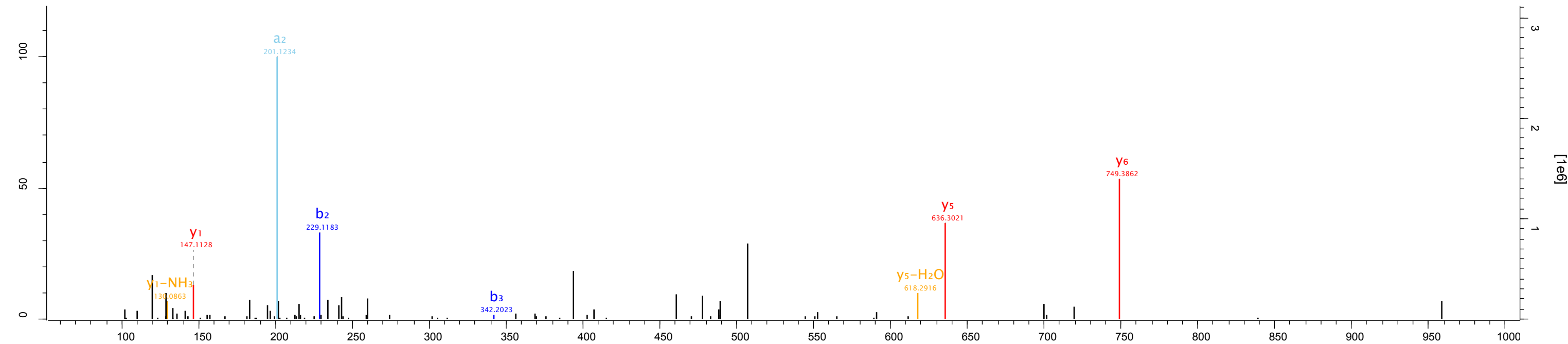
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20180707_MaS_A375SR_ML_proteome_15

Scan 16944 Method FTMS; HCD Score 73.44 m/z 479.93 Gene names ECE2



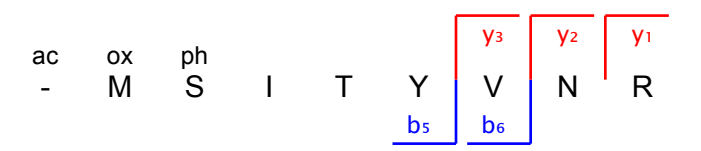
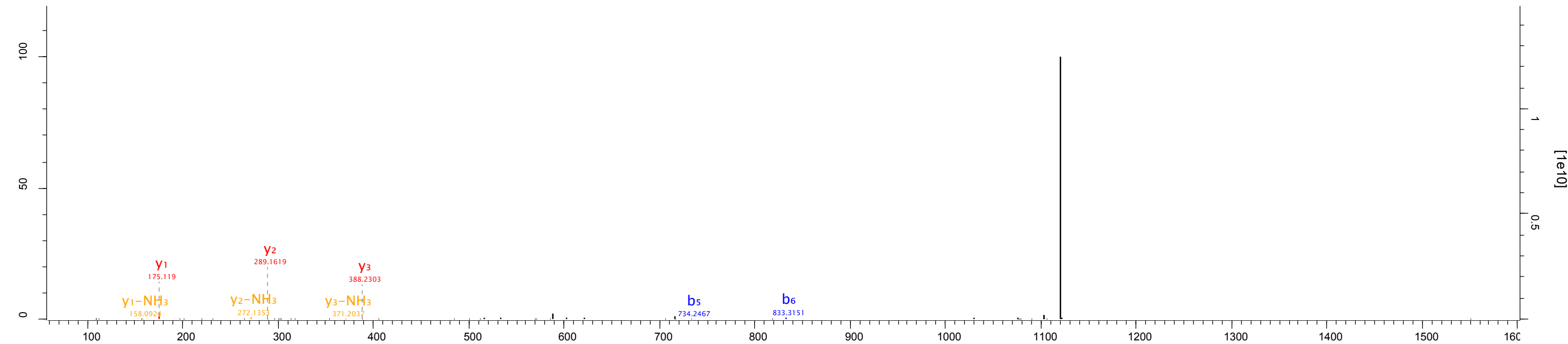


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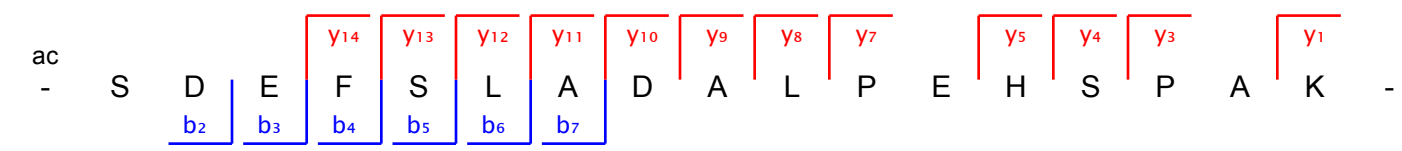
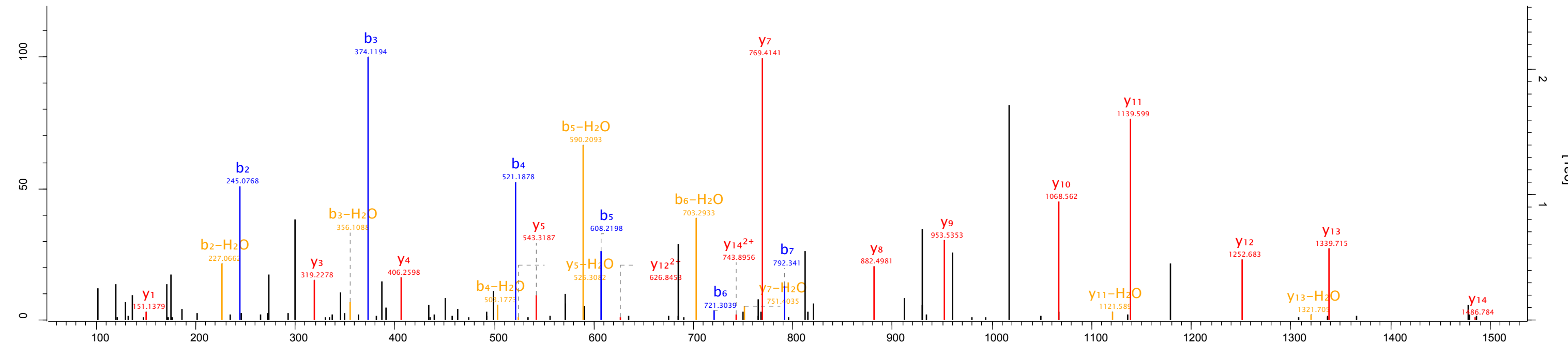


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20180707_MaS_A375SR_ML_proteome_17

Scan	Method	Score	m/z
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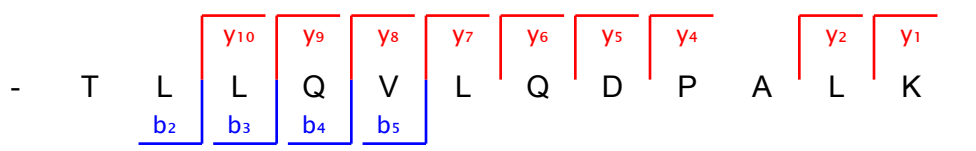
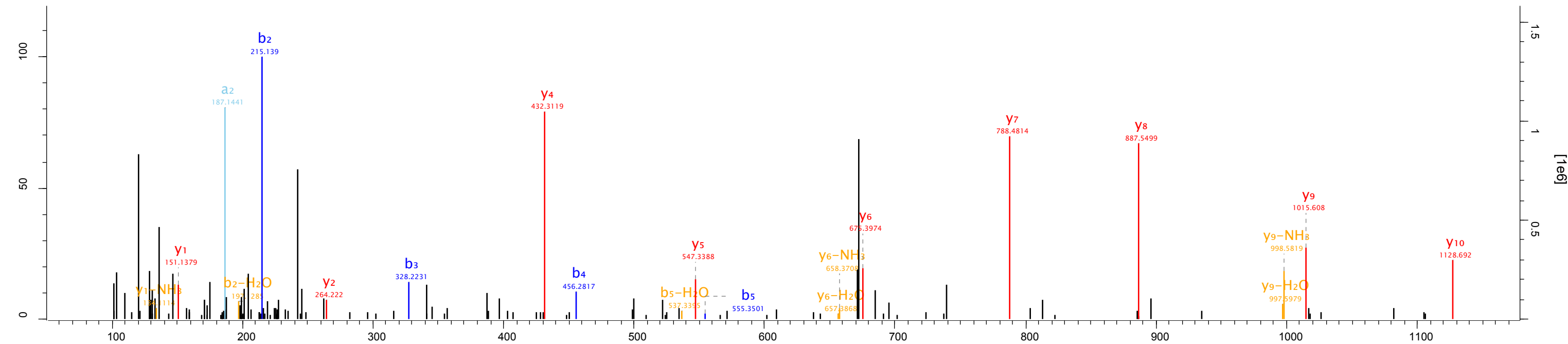


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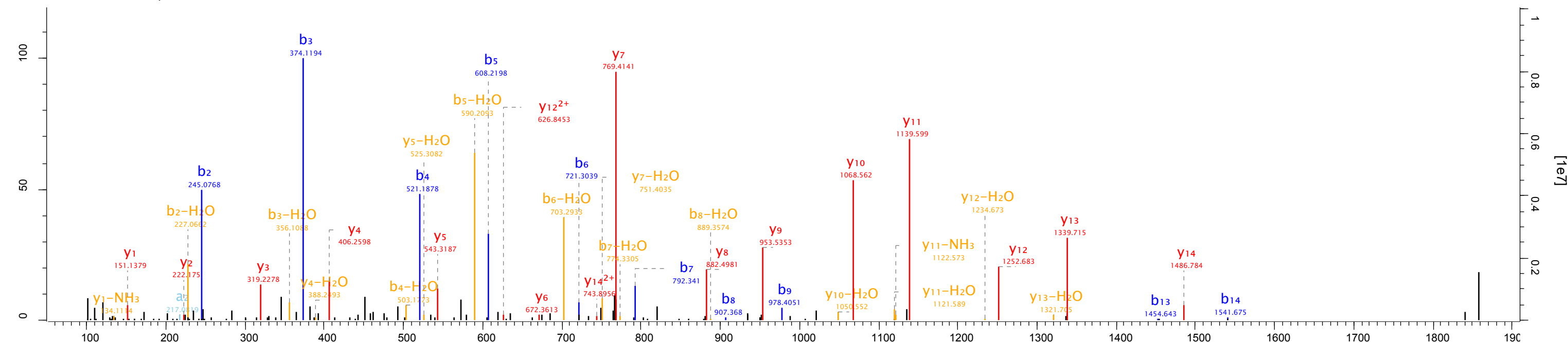
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20180707_MaS_A375SR_ML_proteome_18

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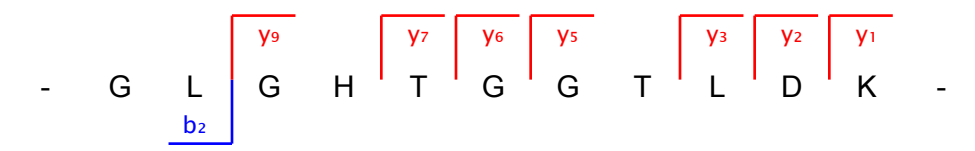
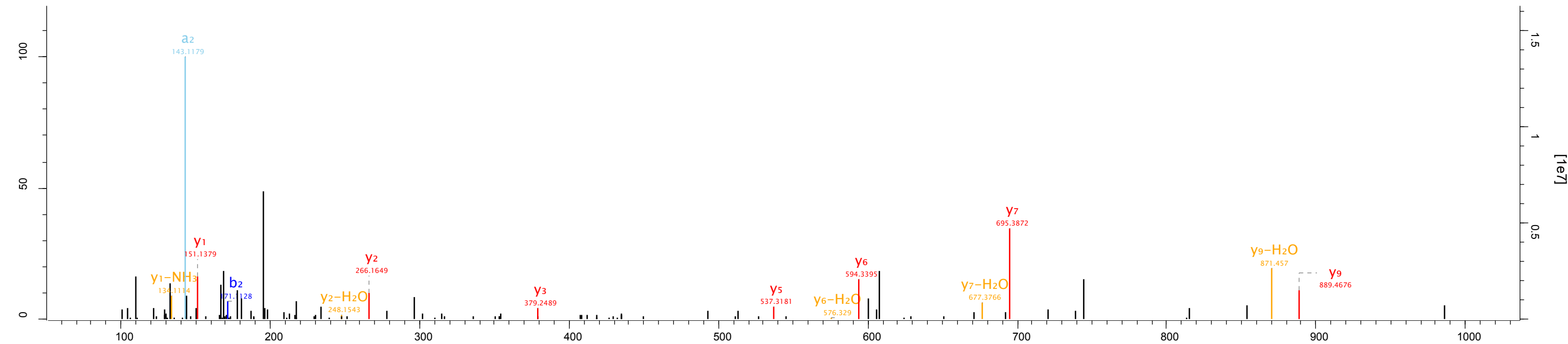
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Scan 26374 Method FTMS; HCD Score 191.15 m/z 930.45 Gene names MAPK11P1L



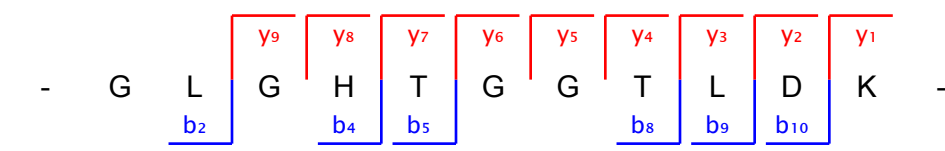
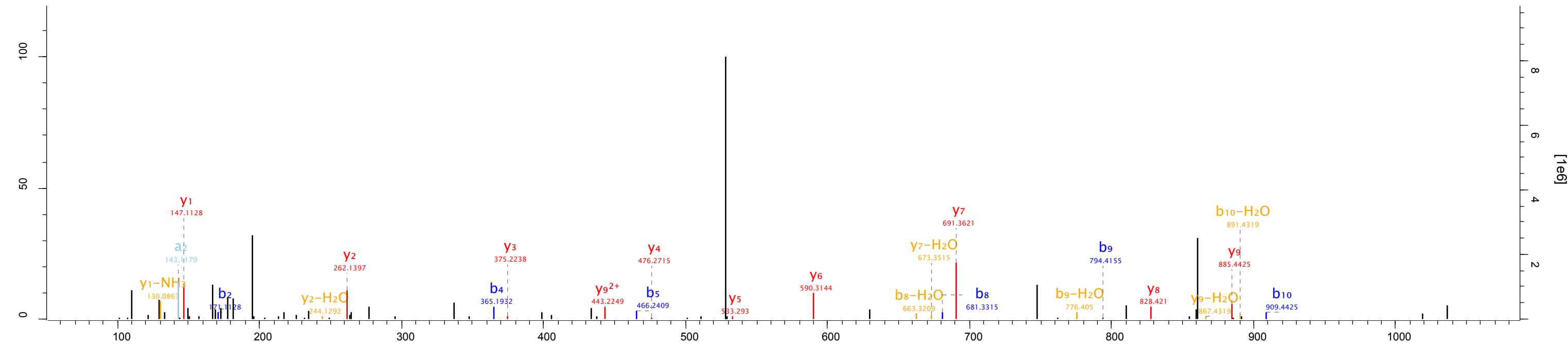
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b2 b3 b4 b5 b6 b7 b8 b9 b13 b14

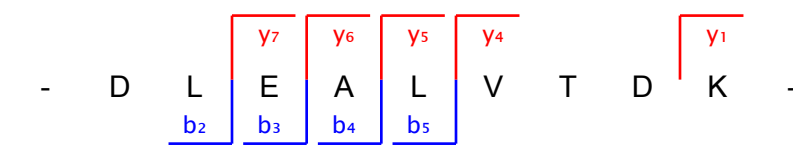
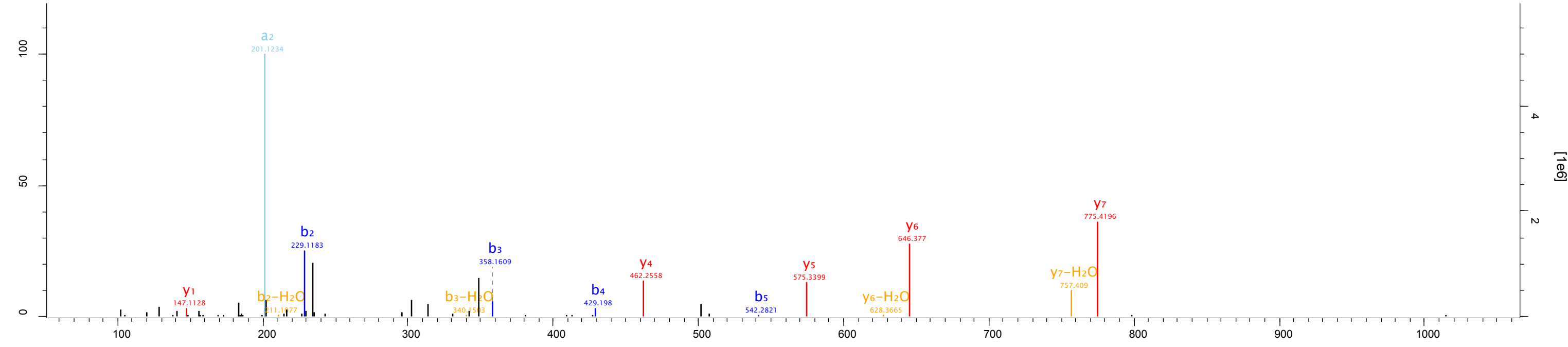
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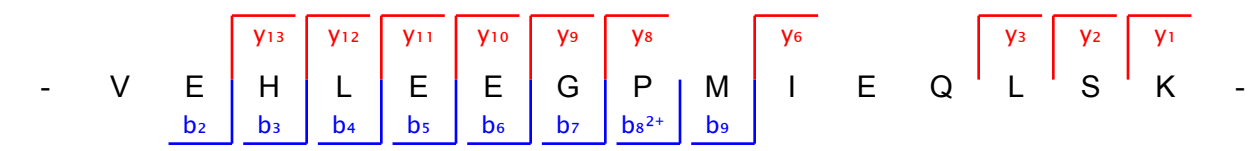
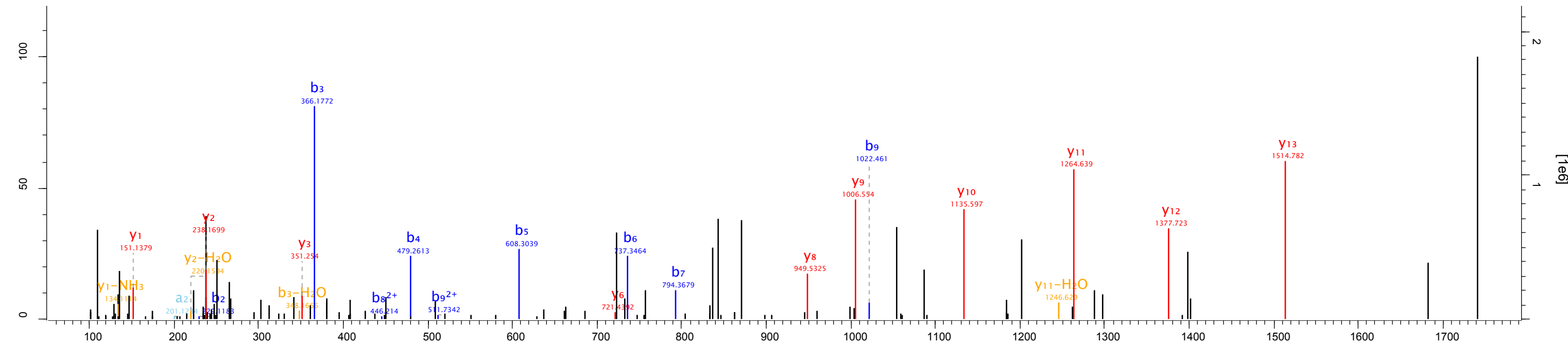
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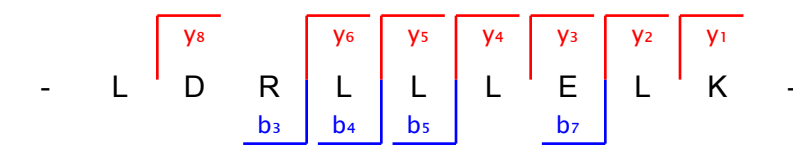
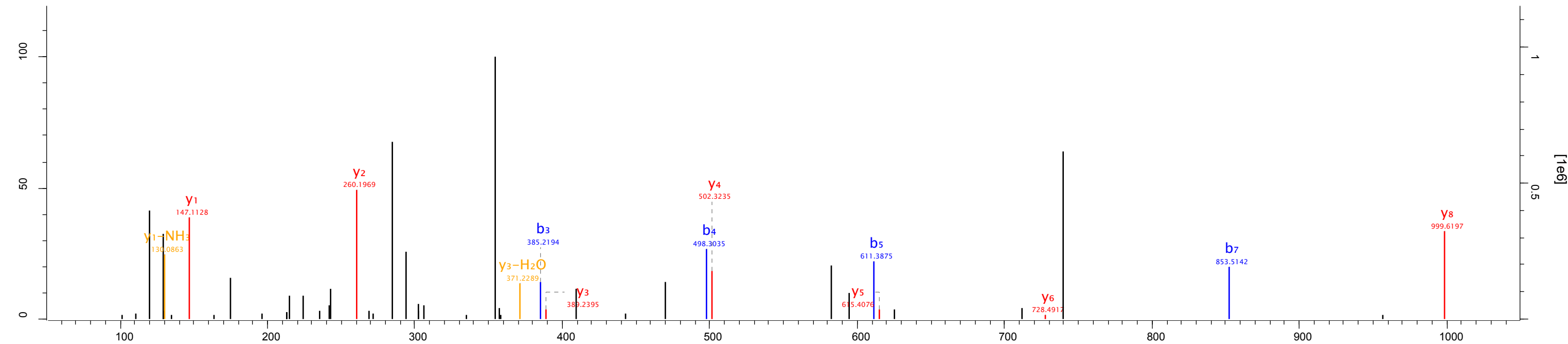




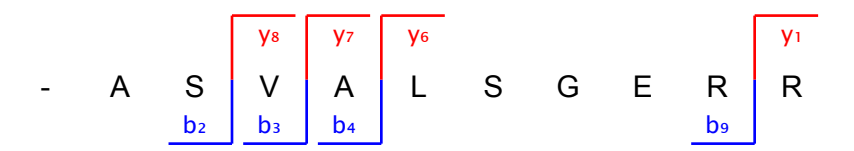
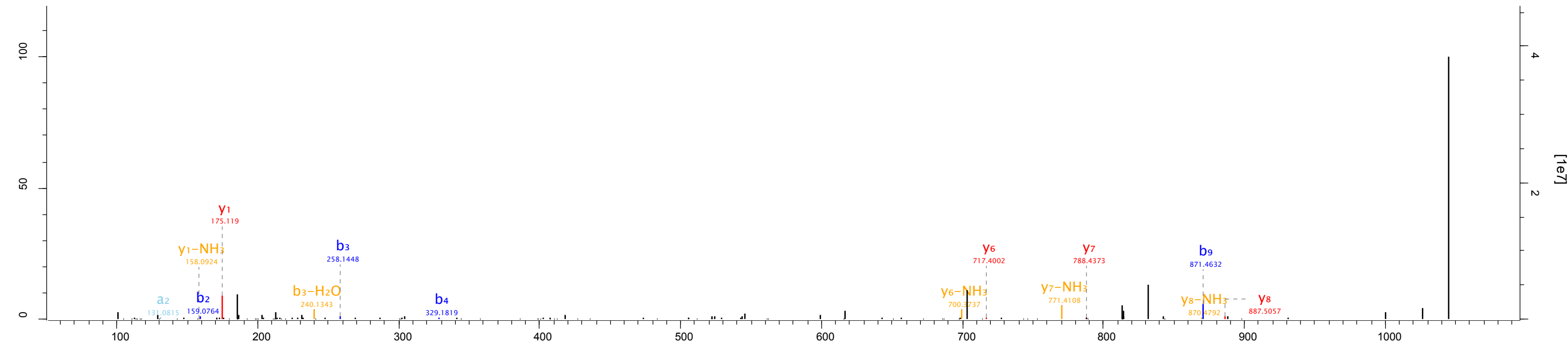
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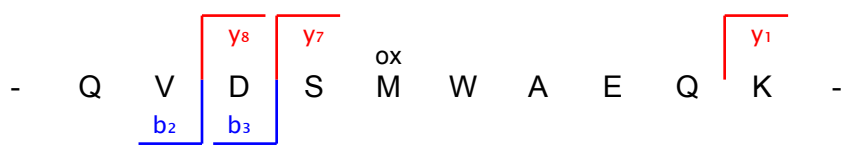
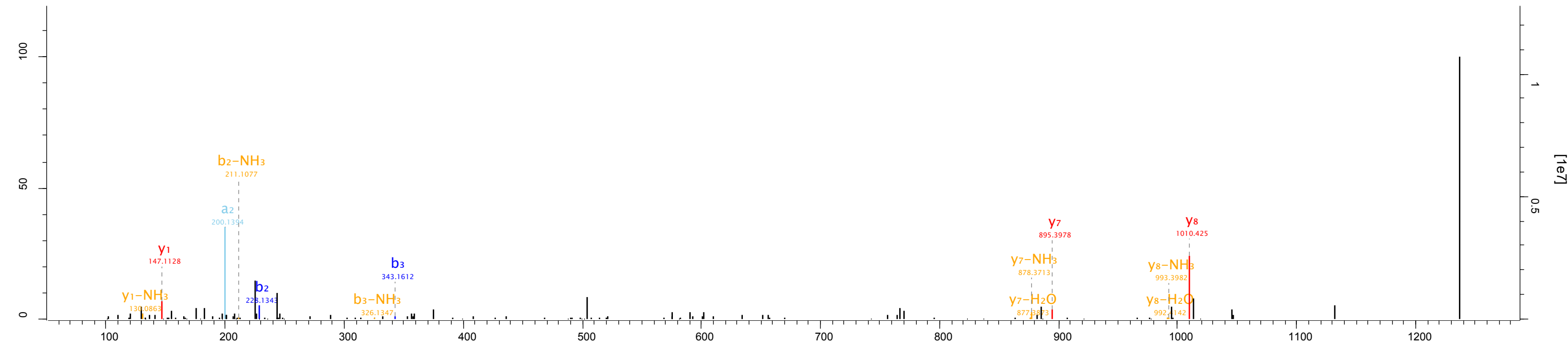
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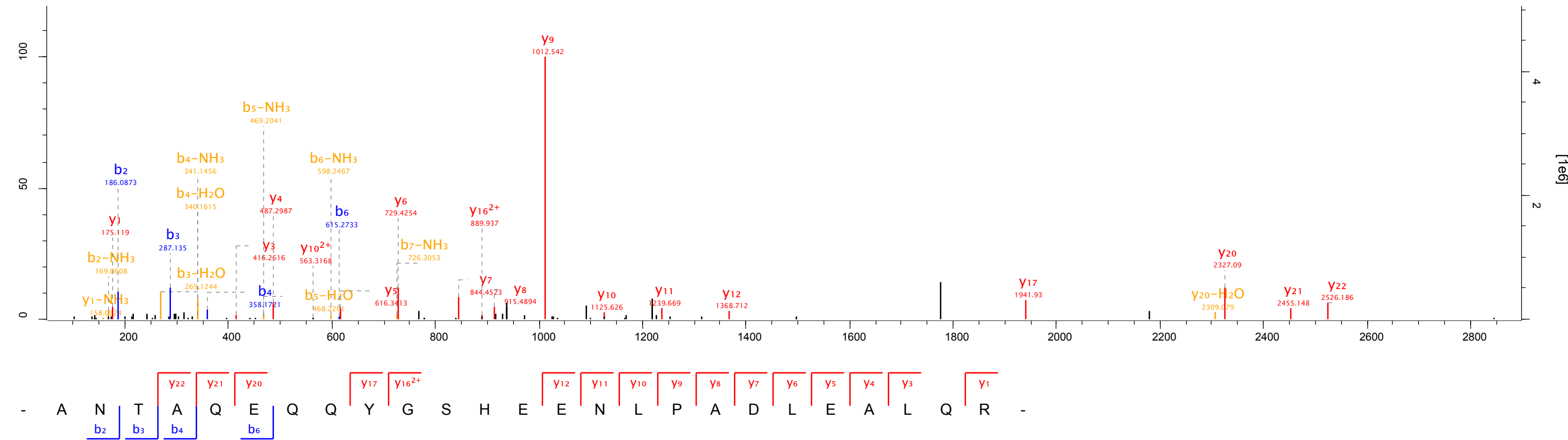


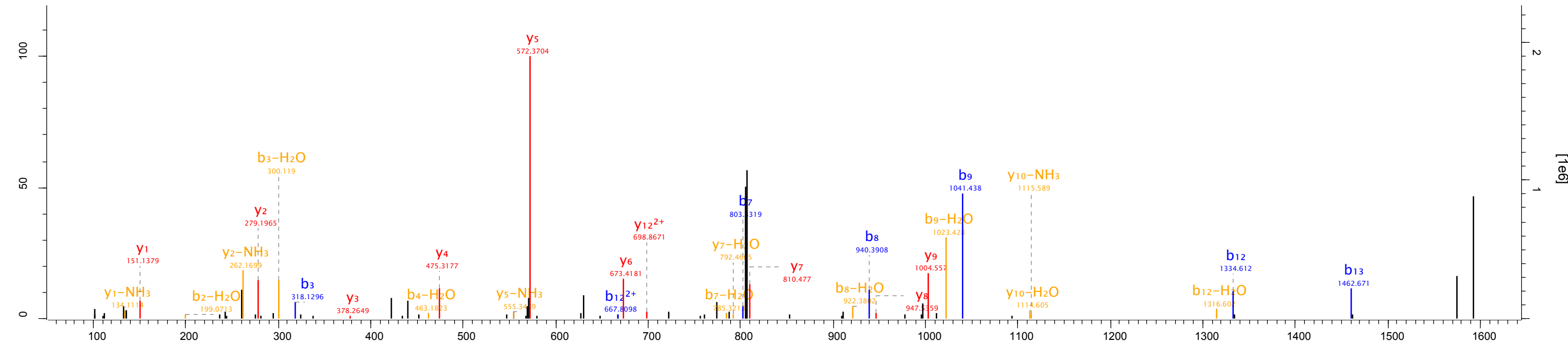
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 Scan: 12434 Method: FTMS; HCD Score: 40.72 m/z: 619.28 Gene names: GHRH



Raw file
20180707_MaS_A375SR_ML_proteome_2_04

Scan: 21854
Method: FTMS; HCD
Score: 117.62
m/z: 938.44
Gene names: IFT43;DKFZp686P0738;GJC1



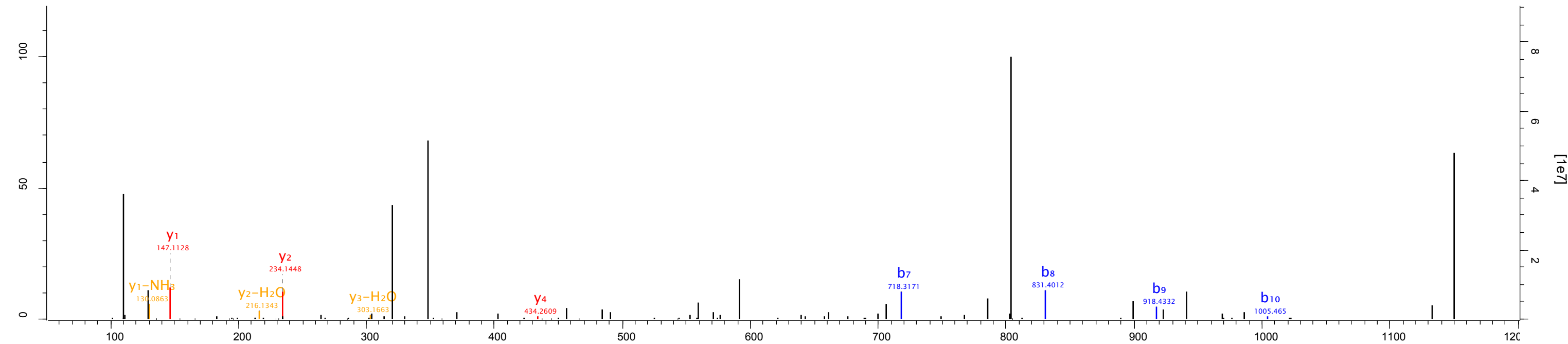


- E S y12²⁺ T Y Q y9 y8 y7 y6 y5 y4 y3 y2 y1 -

b3 b7 b8 b9 b12 b13

Raw file
20180707_MaS_A375SR_ML_proteome_2_04

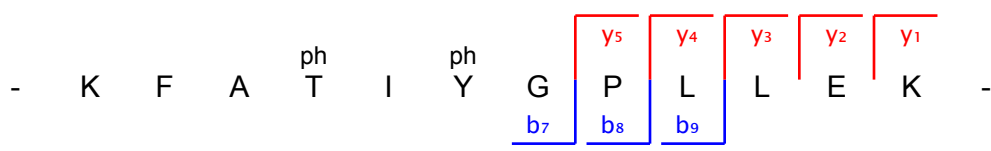
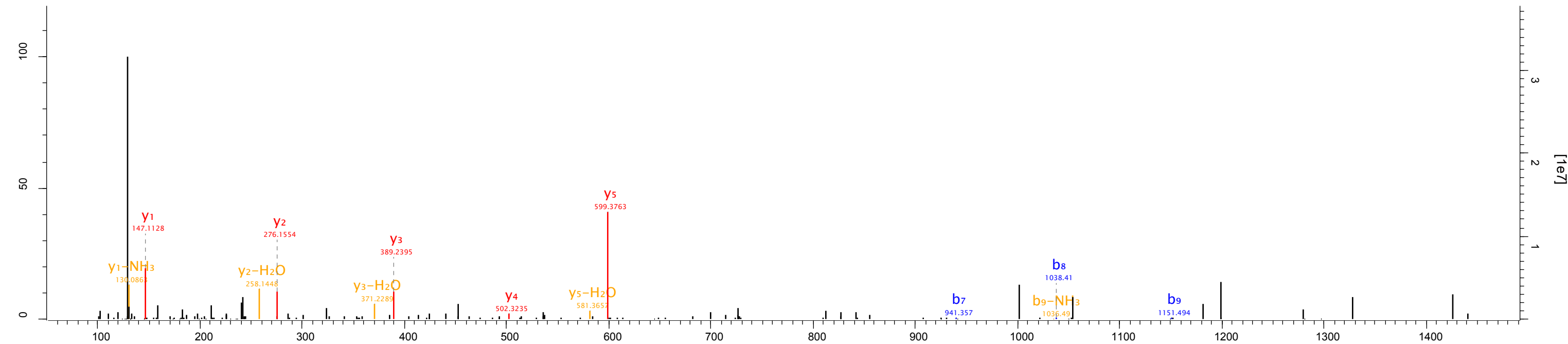
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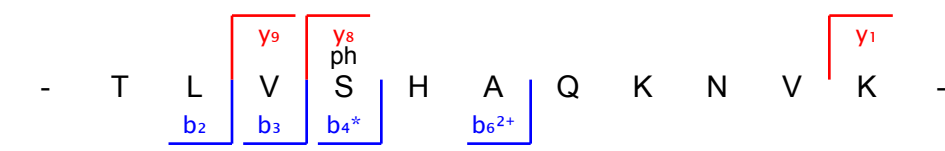
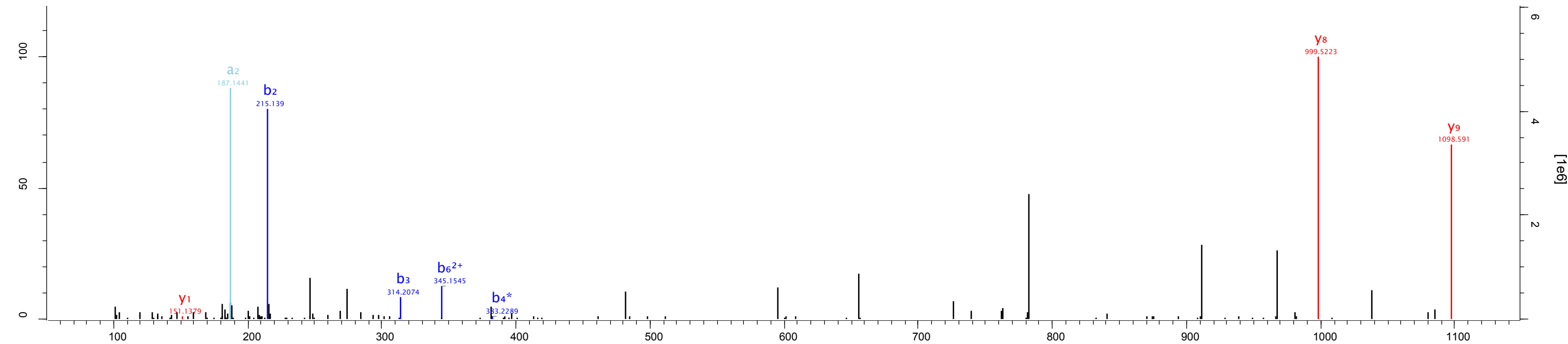
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 b7 b8 b9 b10

Raw file
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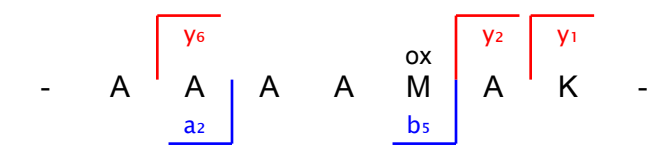
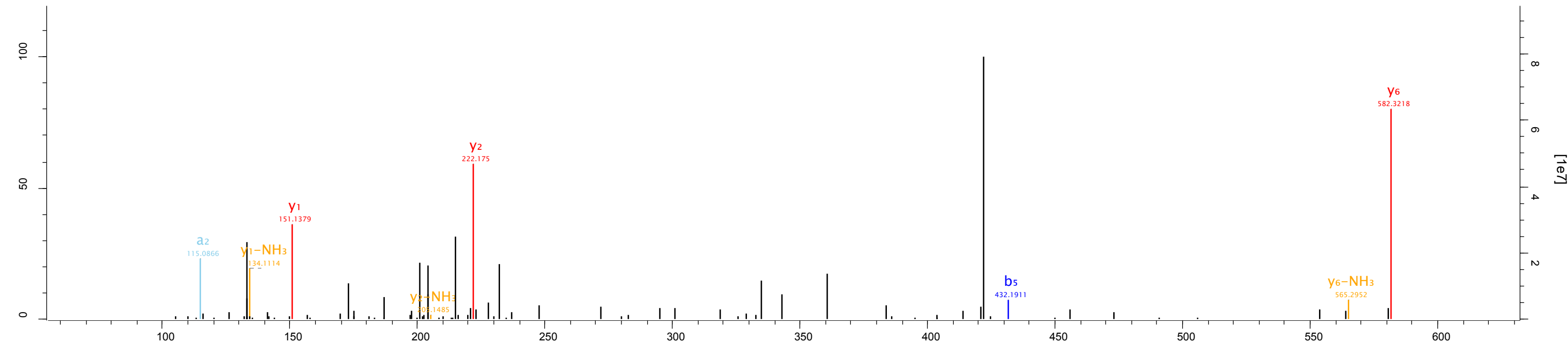
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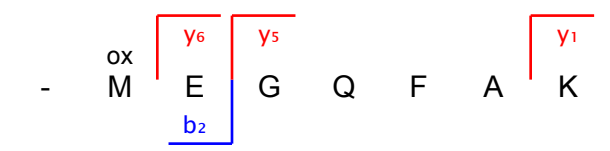
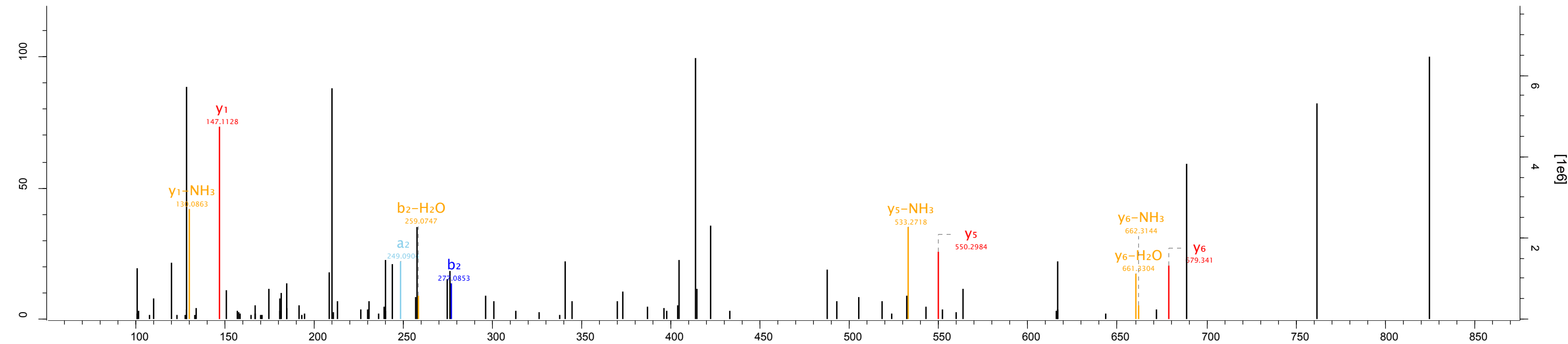
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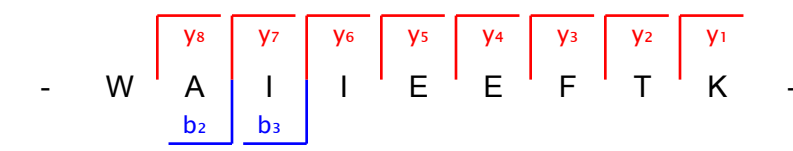
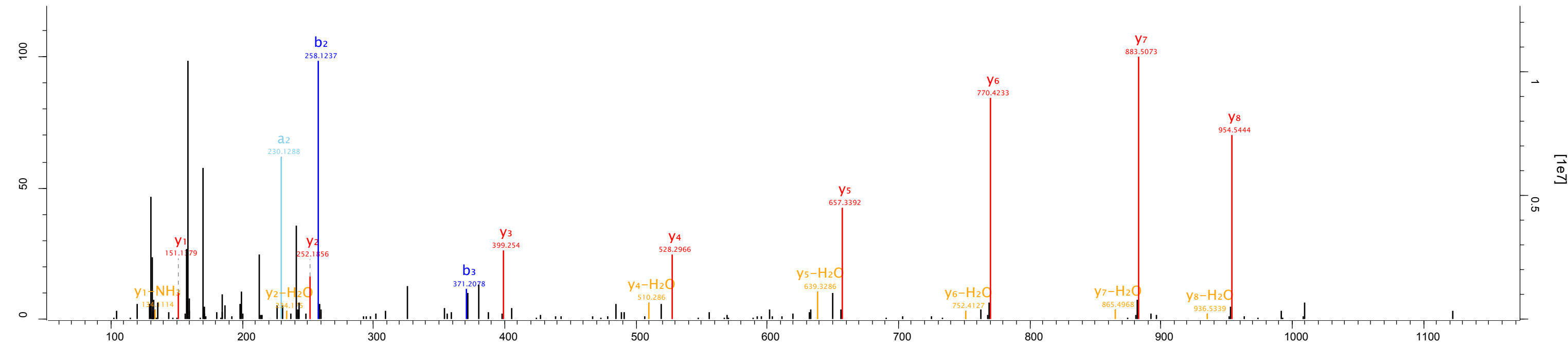
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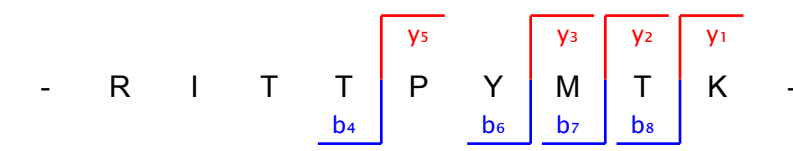
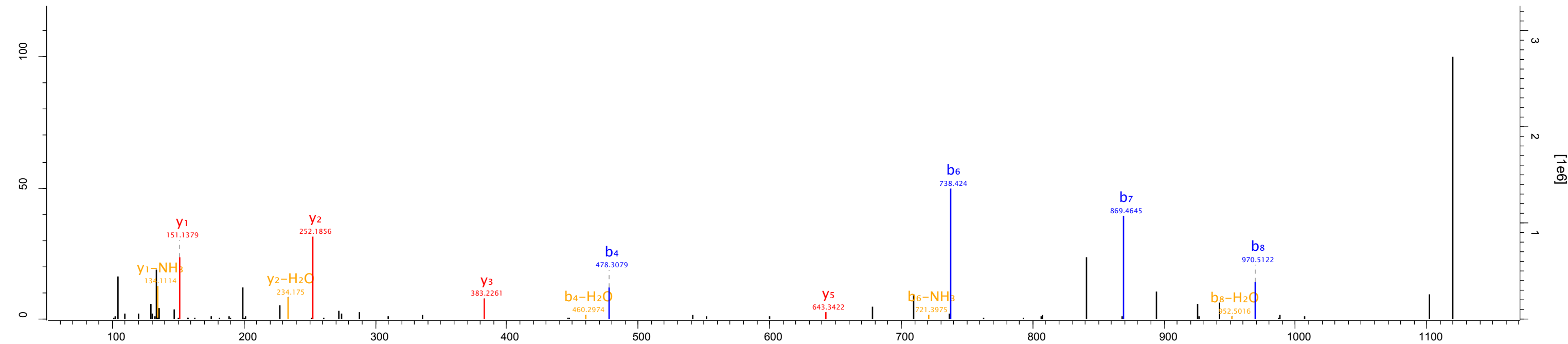
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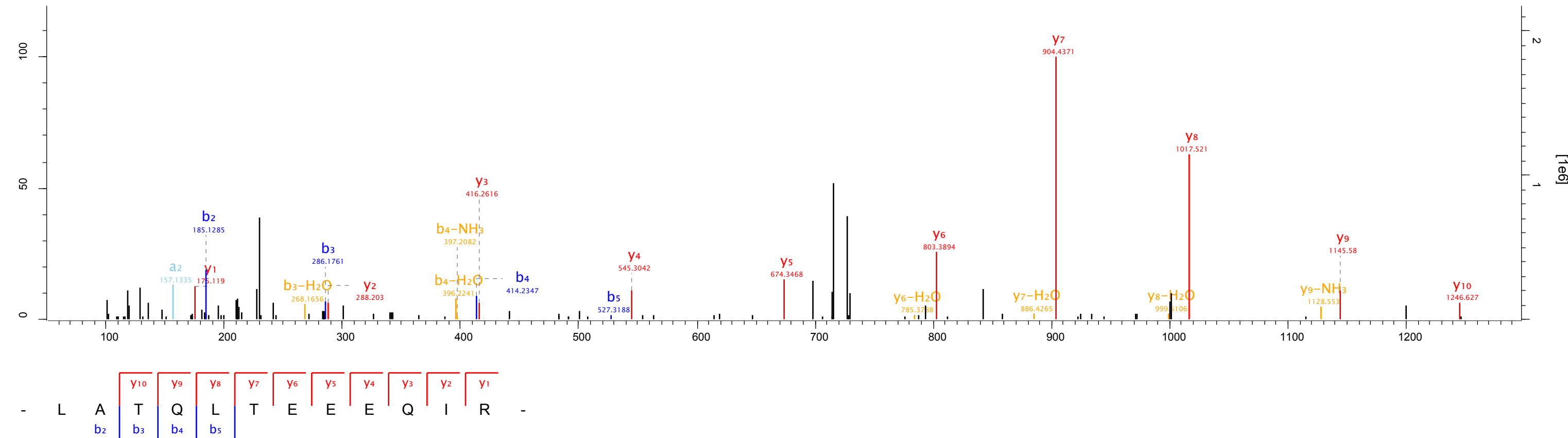


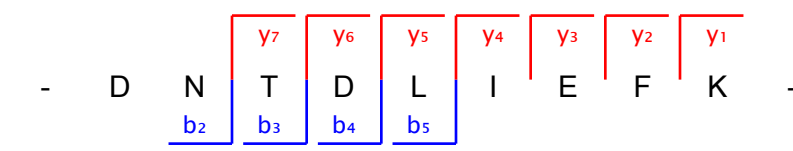
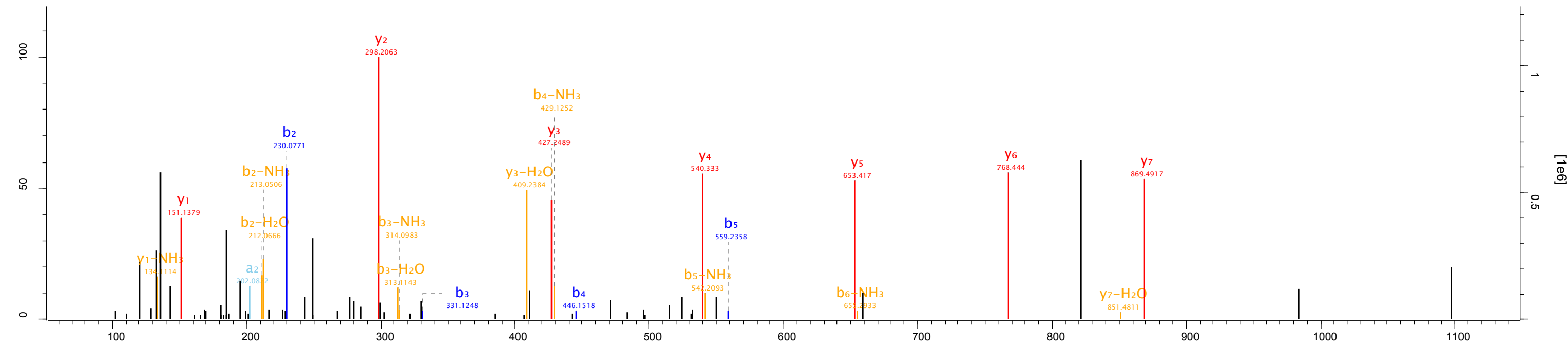
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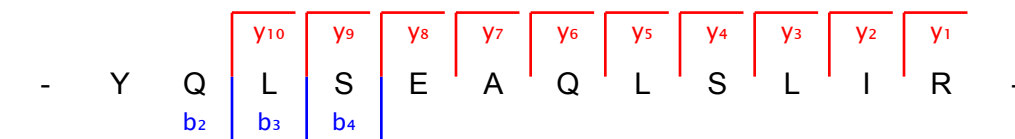
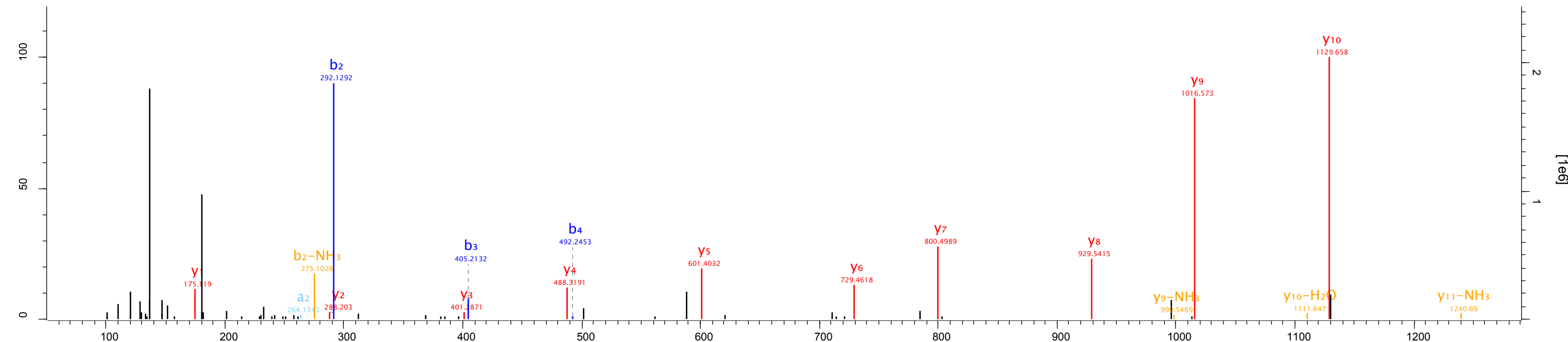


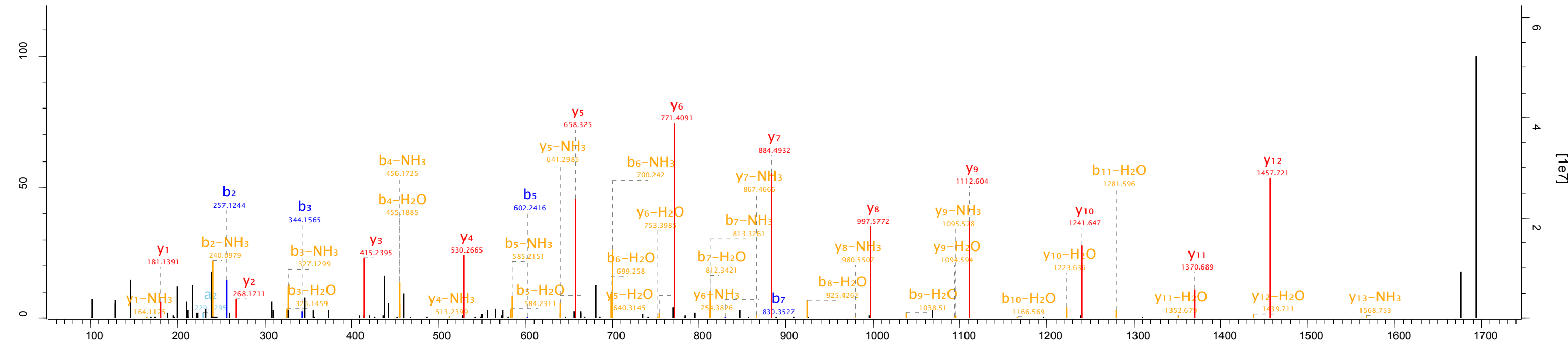




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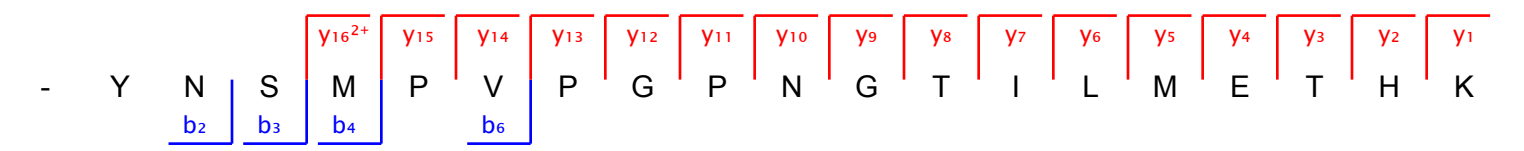
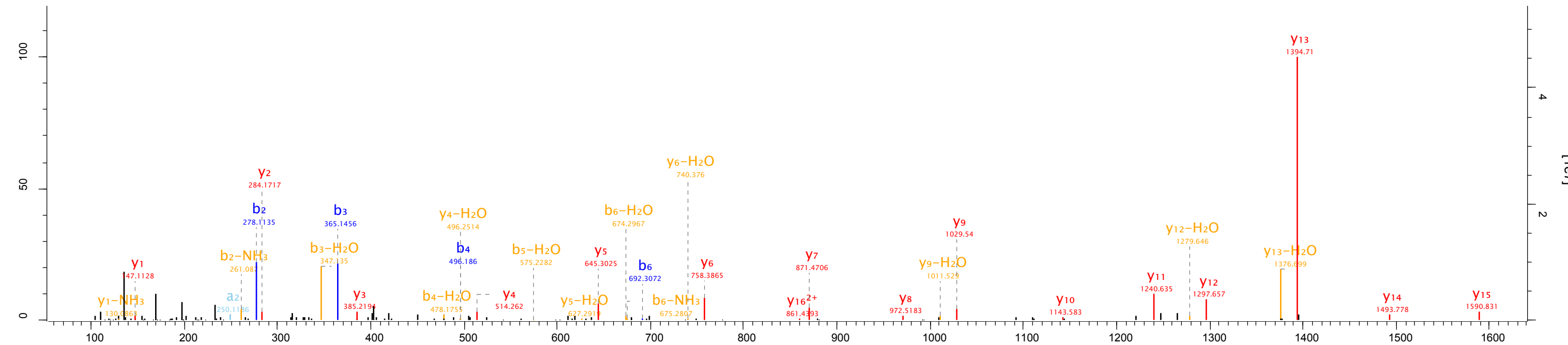




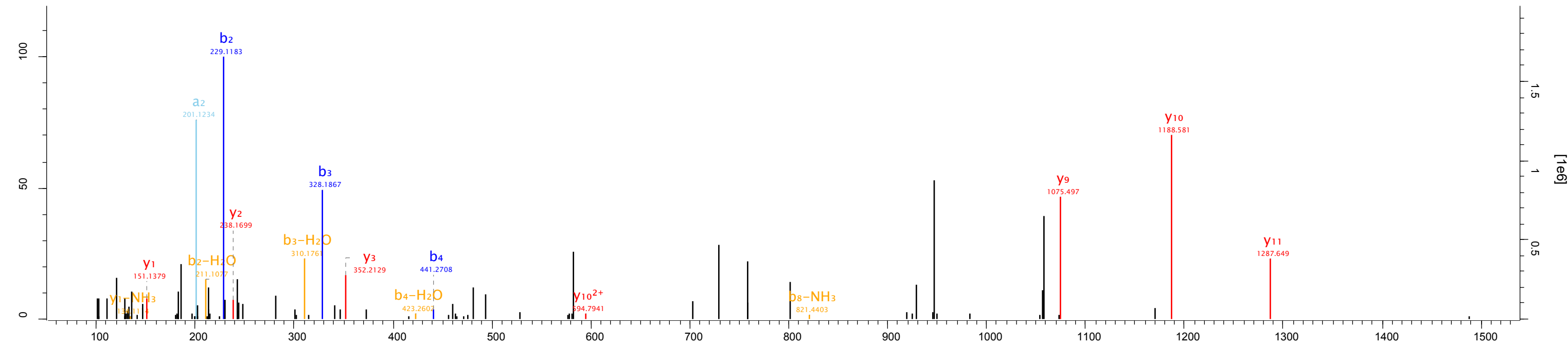
- Q Q S E E D L L L Q D F S R -

b₂
b₃
b₅
b₇
y₁₂
y₁₁
y₁₀
y₉
y₈
y₇
y₆
y₅
y₄
y₃
y₂
y₁

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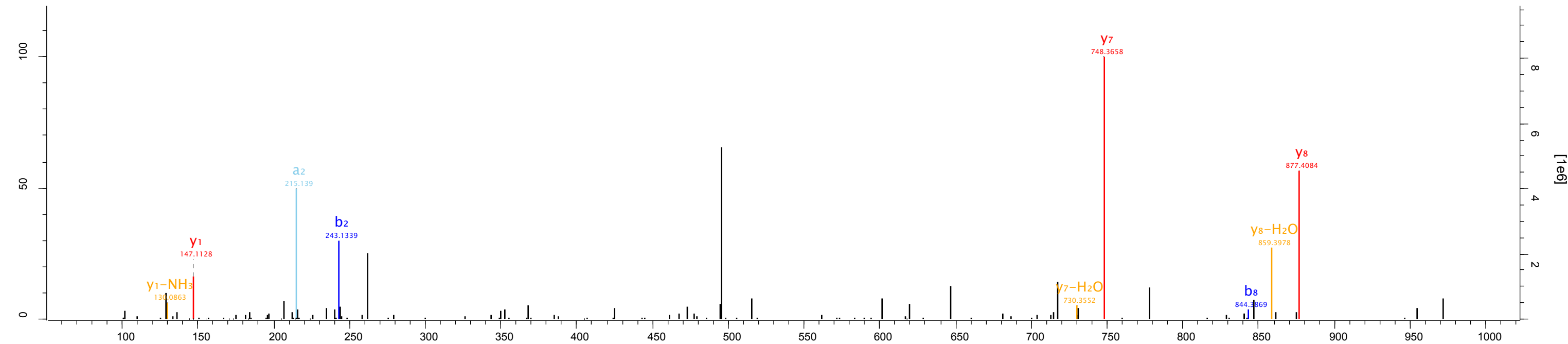


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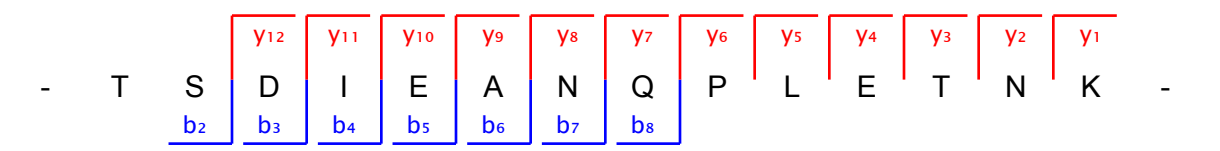
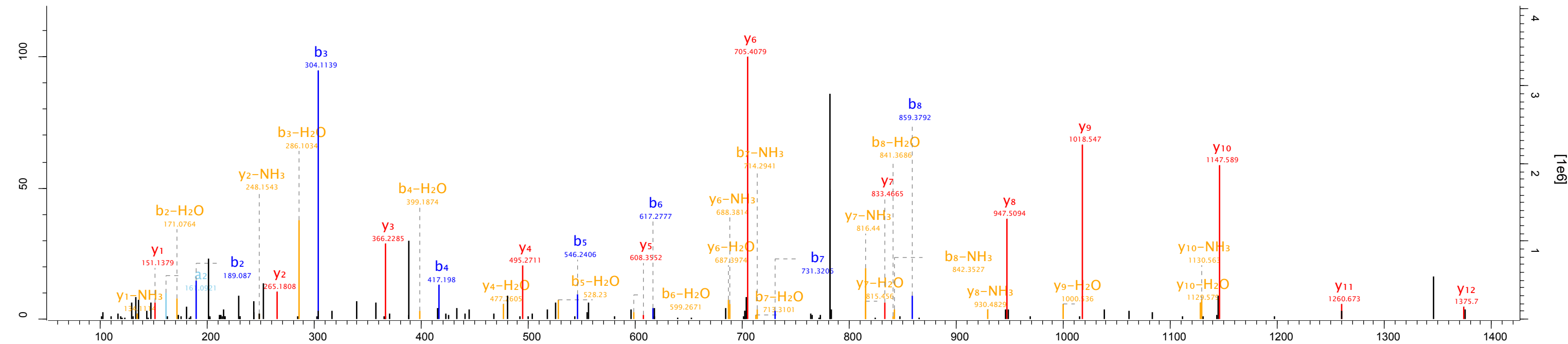
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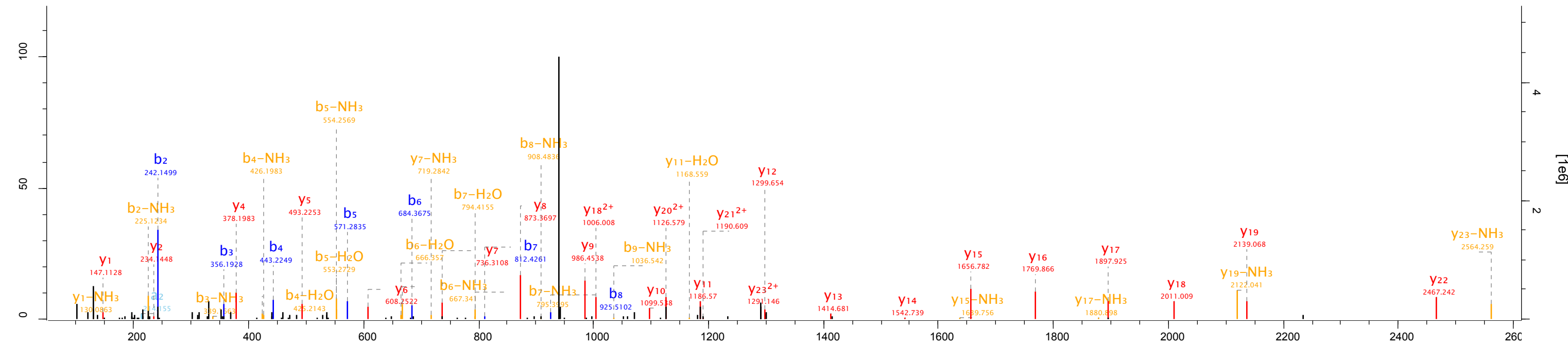
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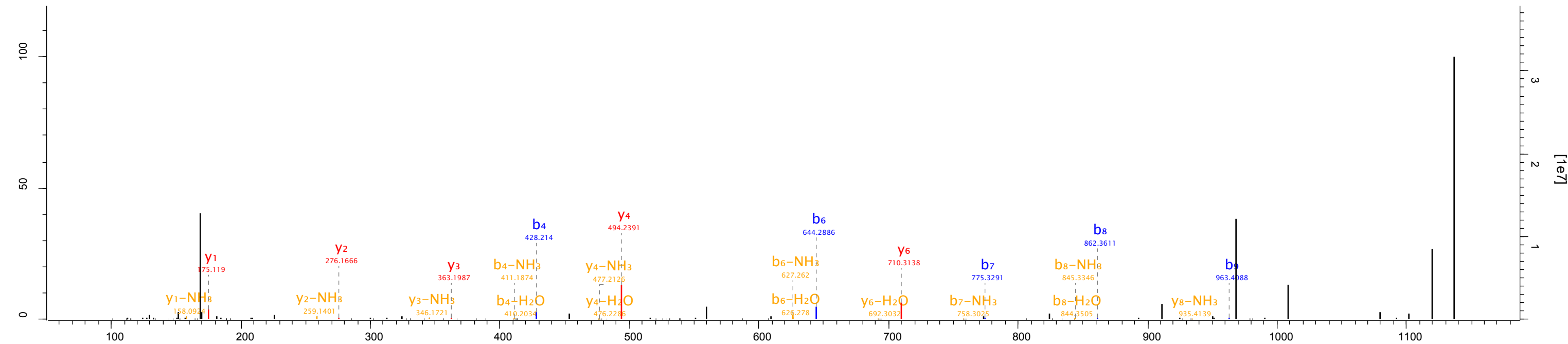
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Scan 28444 Method FTMS; HCD Score 182.02 m/z 941.82 Gene names PKNOX1



- I Q N S Q L Q L Q L N Q D L S I L H Q D D G S S K -

Fragmentation map showing b and y ion series for the peptide sequence: I Q N S Q L Q L Q L N Q D L S I L H Q D D G S S K. The b ion series (blue) and y ion series (red) are indicated by brackets below the sequence.



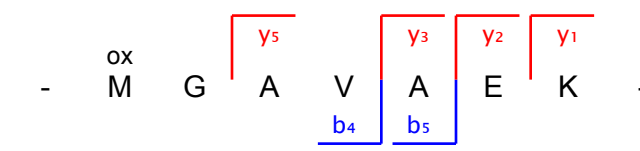
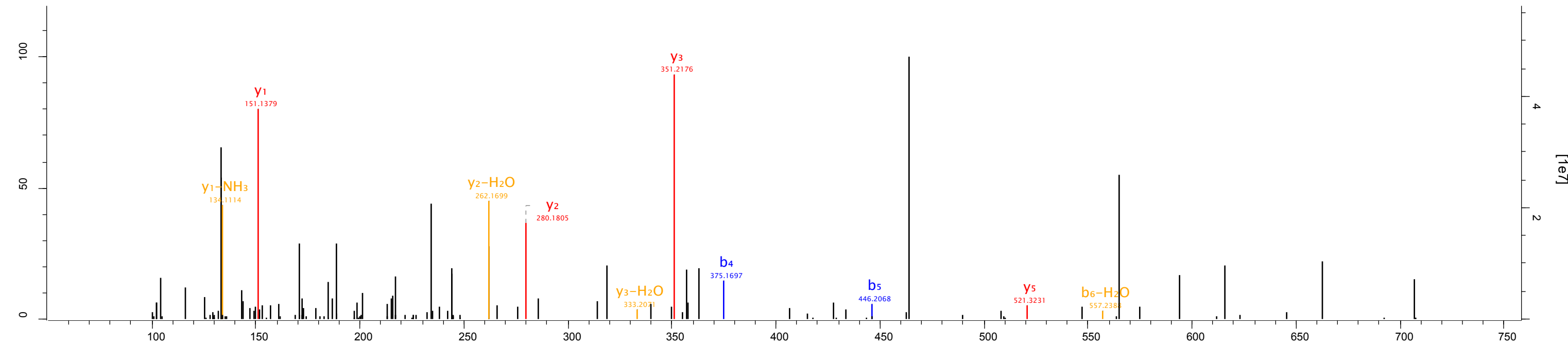
- N A L E S E M S T R -

b₄ y₆ b₆ y₄ y₃ y₂ y₁

b₇ b₈ b₉

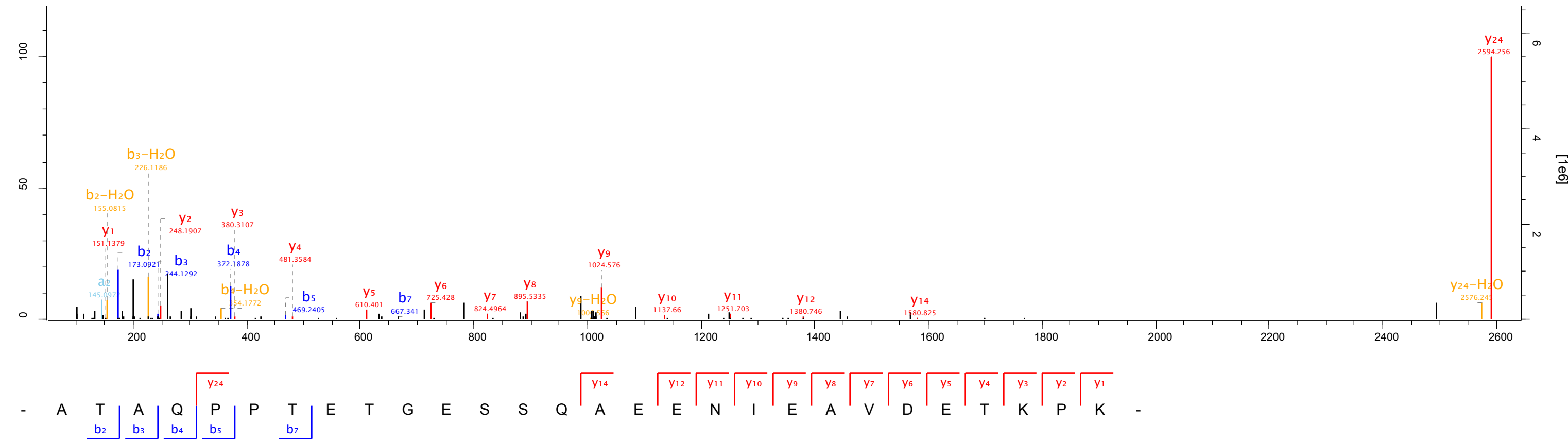
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20180707_MaS_A375SR_ML_proteome_2_11

Scan 3494 Method FTMS; HCD Score 53.55 m/z 363.19

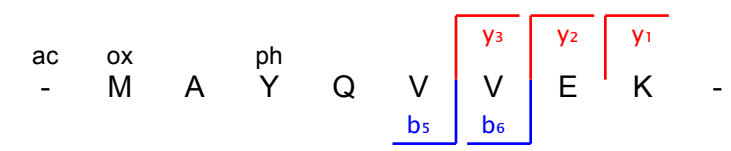
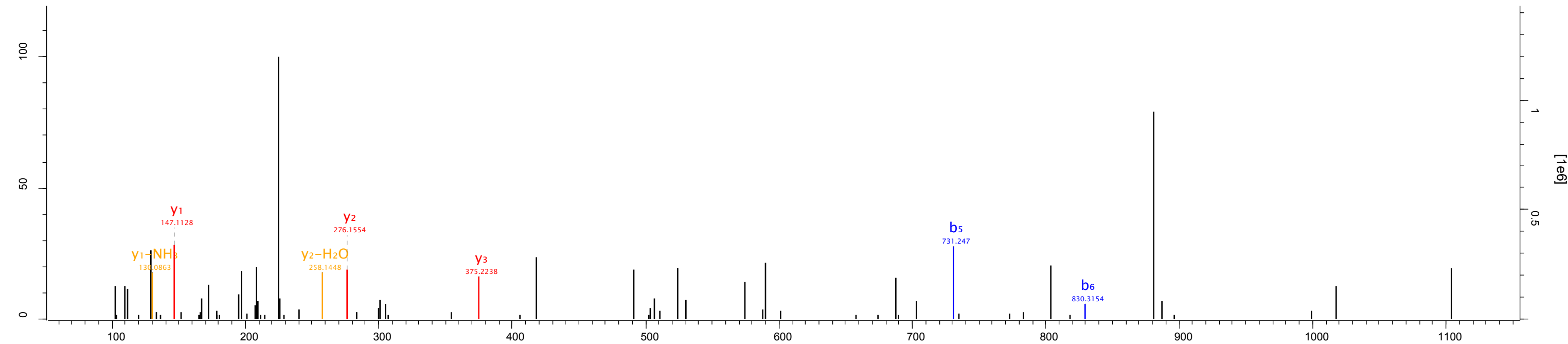


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20180707_MaS_A375SR_ML_proteome_2_12

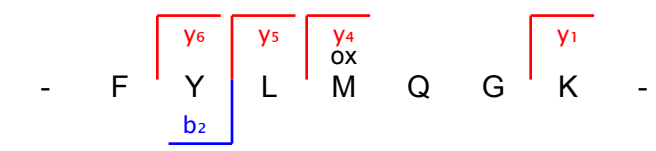
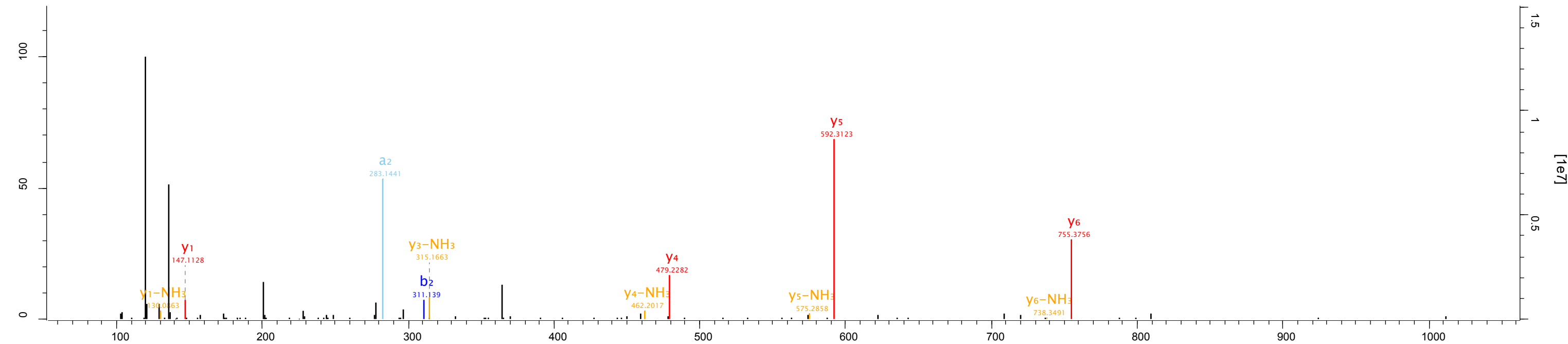
Scan 17904 Method FTMS; HCD Score 65.25 m/z 989.49 Gene names GAP43



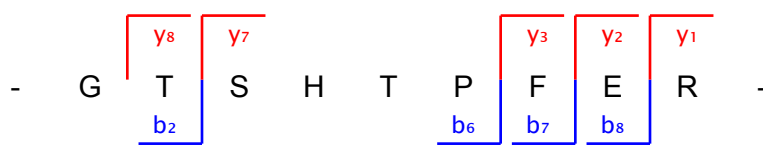
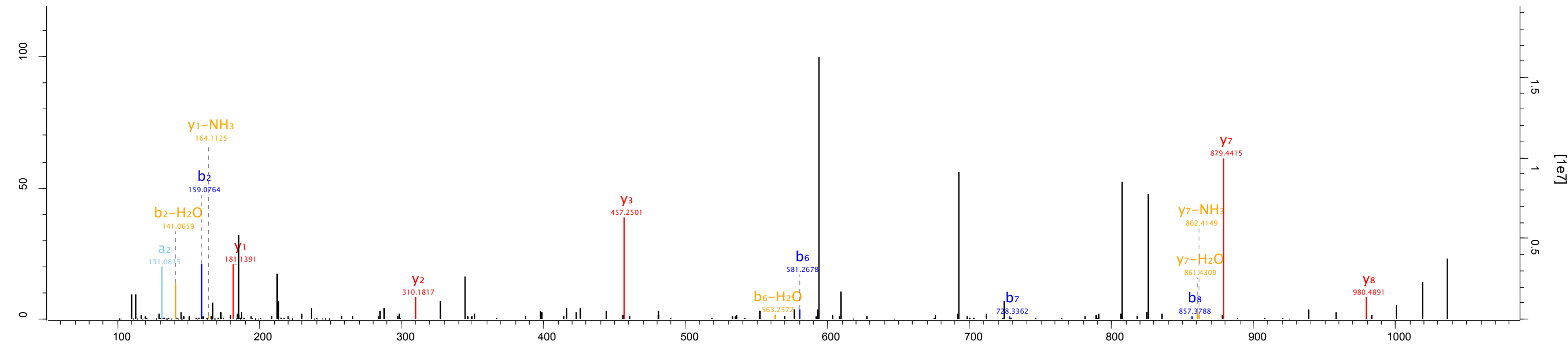
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 20180707_MaS_A375SR_ML_proteome_2_15
 Scan 7994 Method FTMS; HCD Score 42.6 m/z 553.24



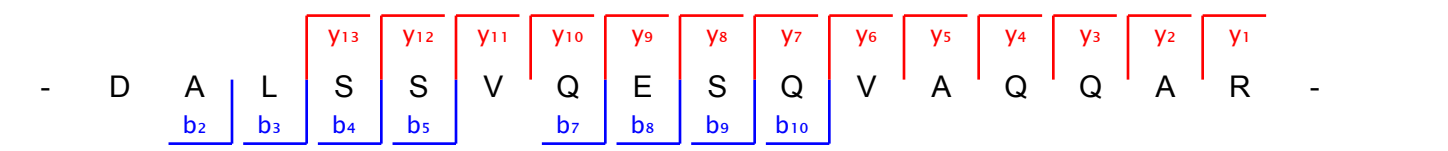
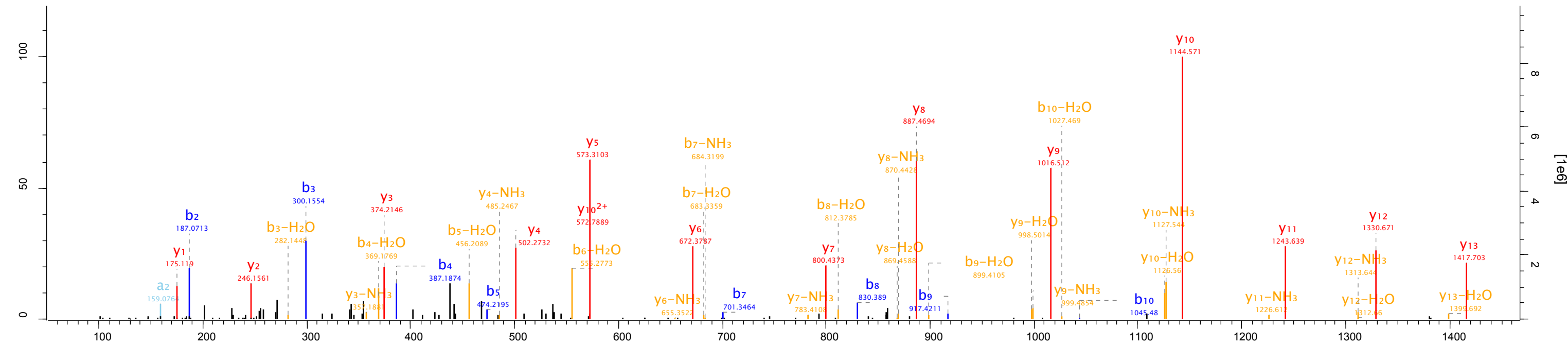
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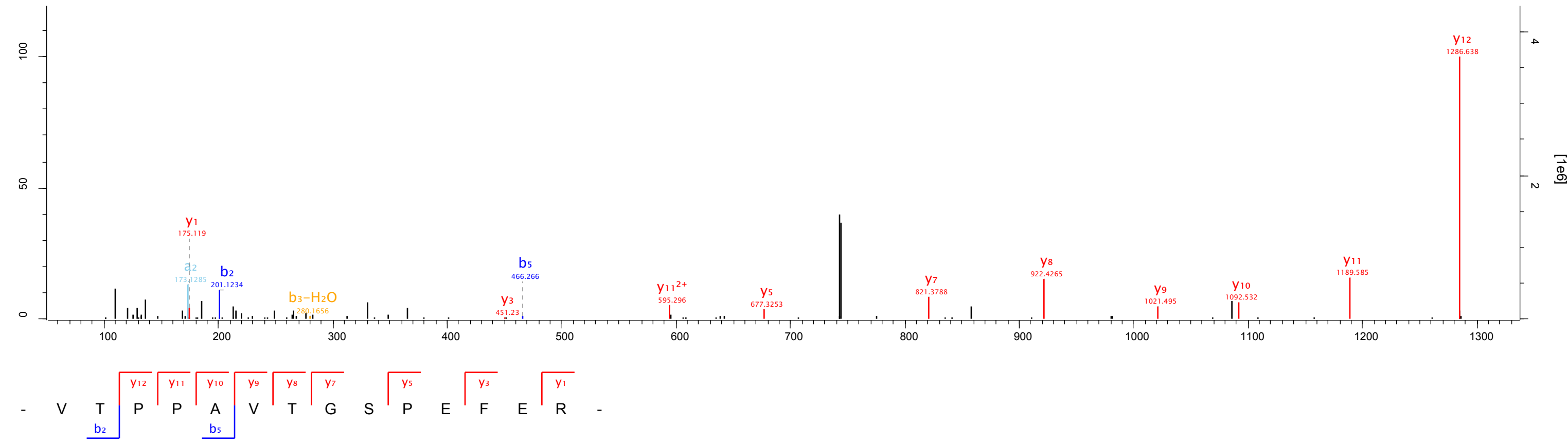


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 Scan: 14874 Method: FTMS; HCD Score: 254.18 m/z: 858.93 Gene names: APOC3



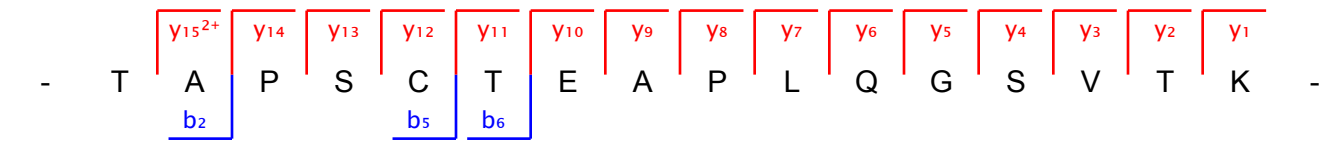
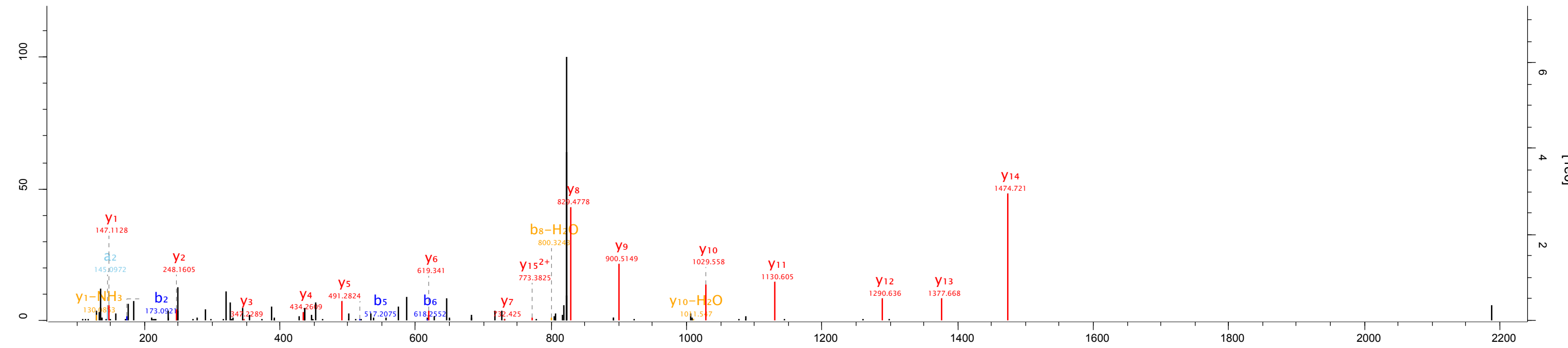
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20180707_MaS_A375SR_ML_proteome_2_18

Scan 16804 Method FTMS; HCD Score 53.3 m/z 743.88 Gene names MGST2

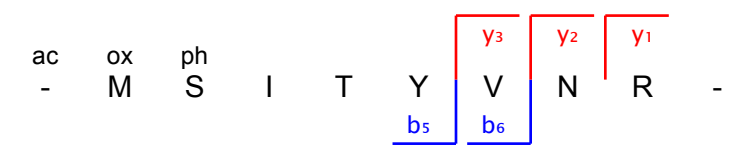
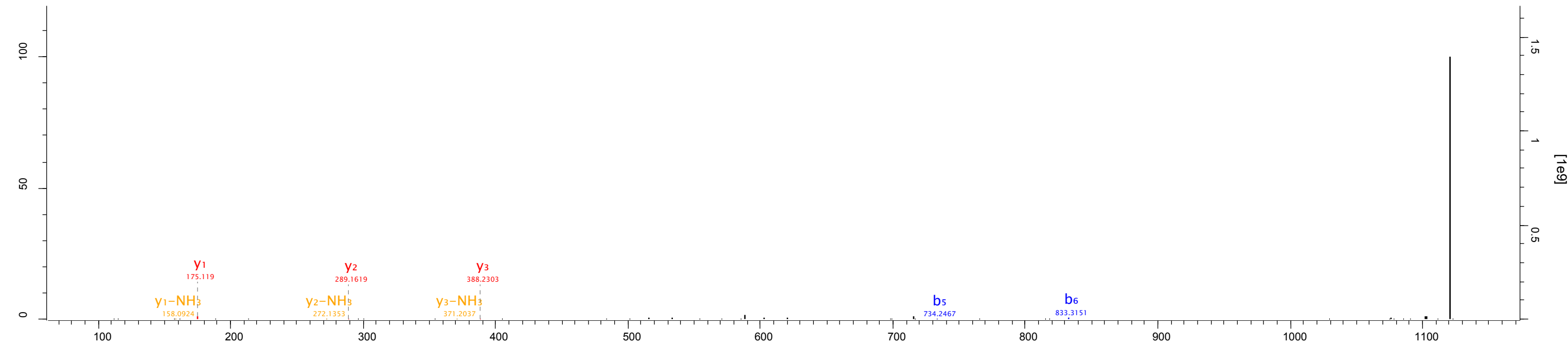


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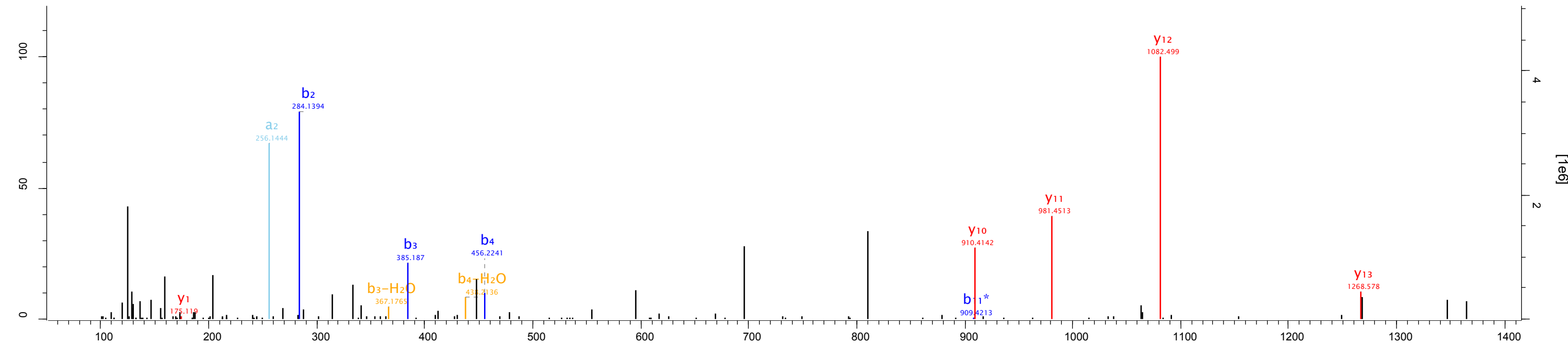
Scan 11604 Method FTMS; HCD Score 43.95 m/z 823.9 Gene names MKRN1

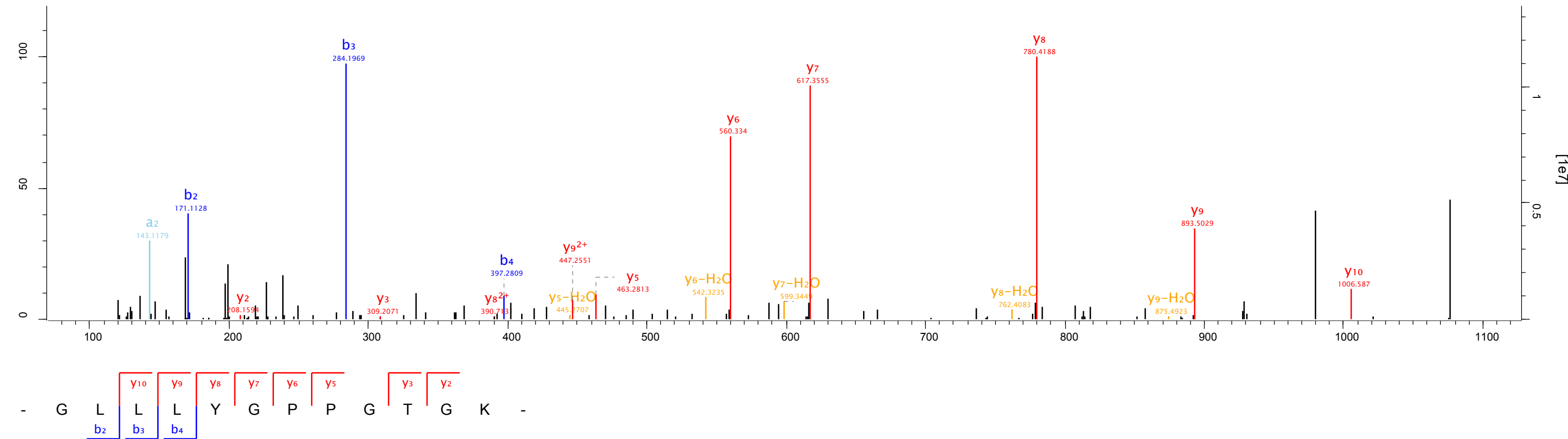


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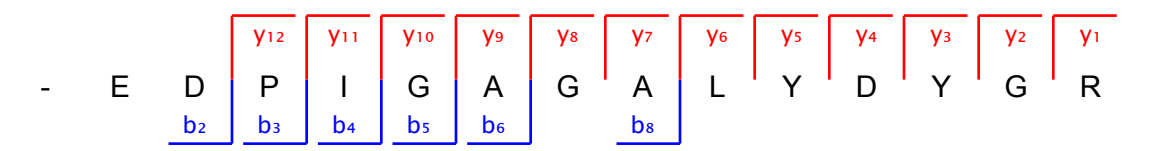
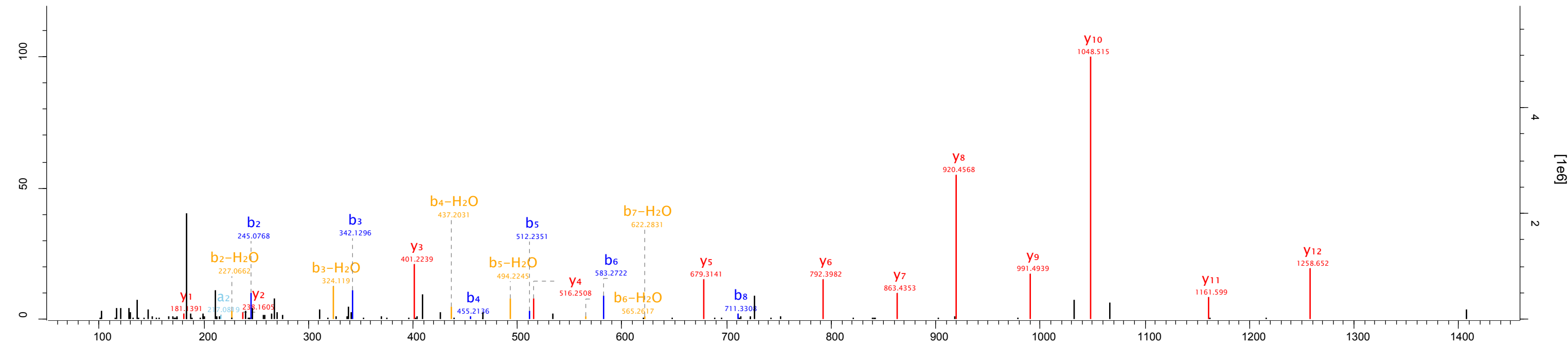


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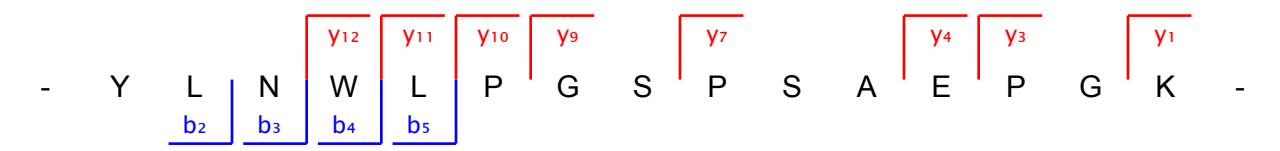
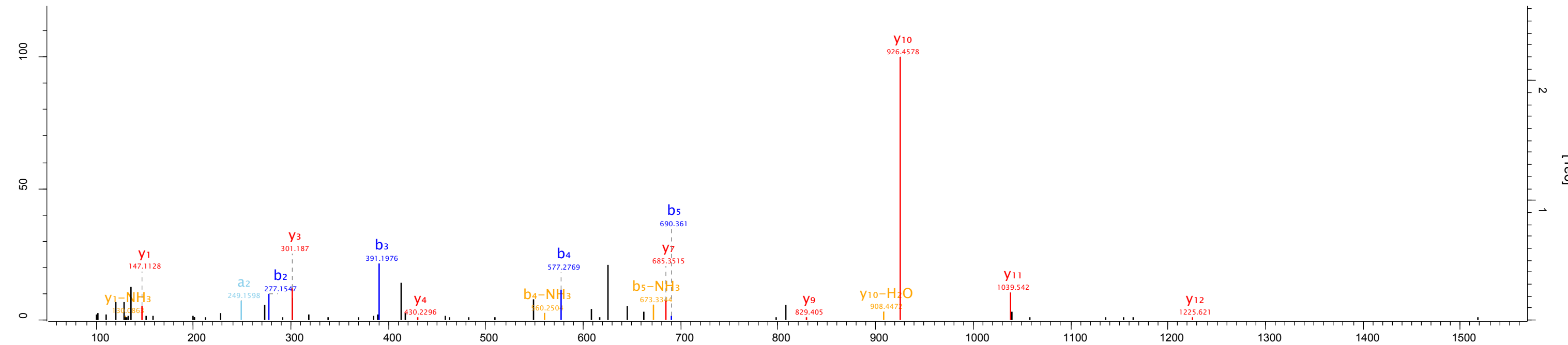


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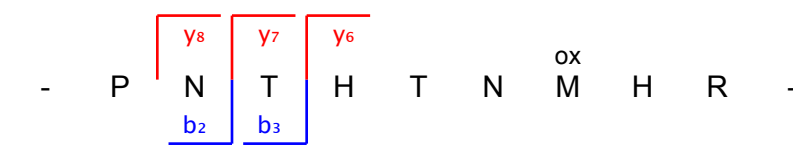
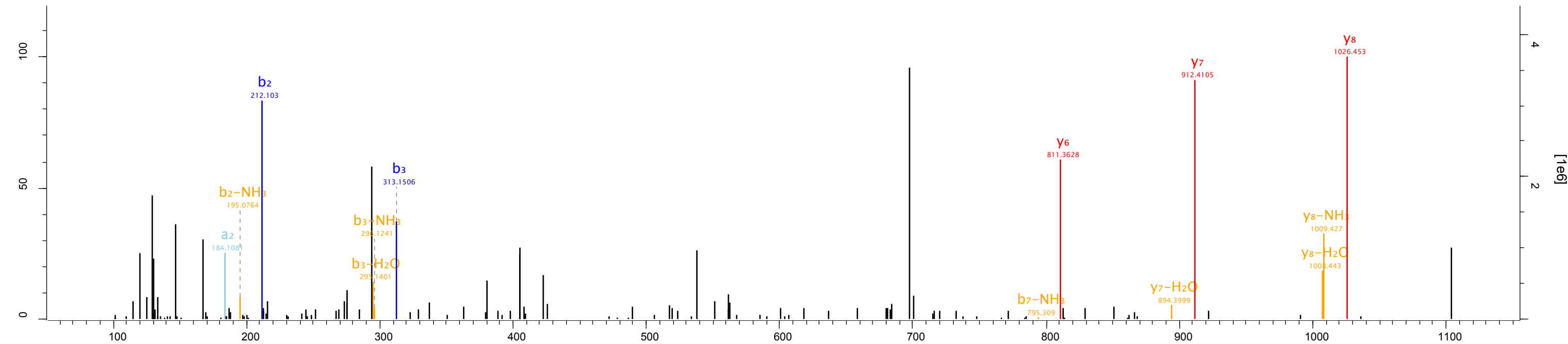


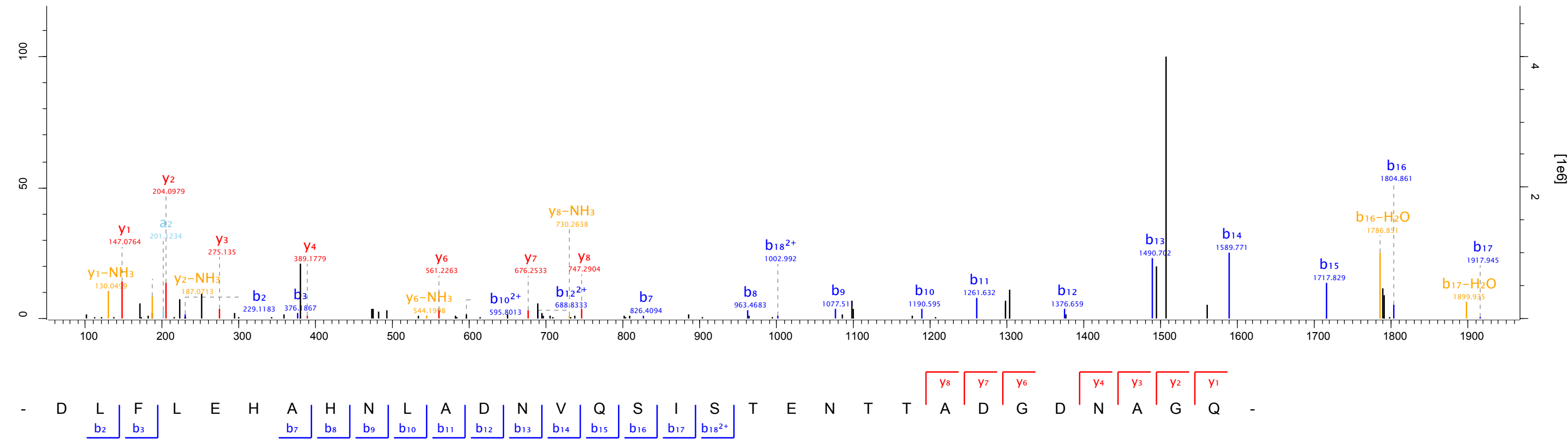
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Scan 26114 Method FTMS; HCD Score 76.76 m/z 808.41 Gene names MRC1



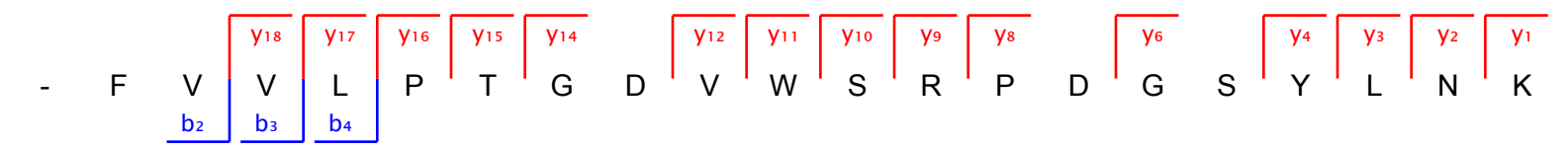
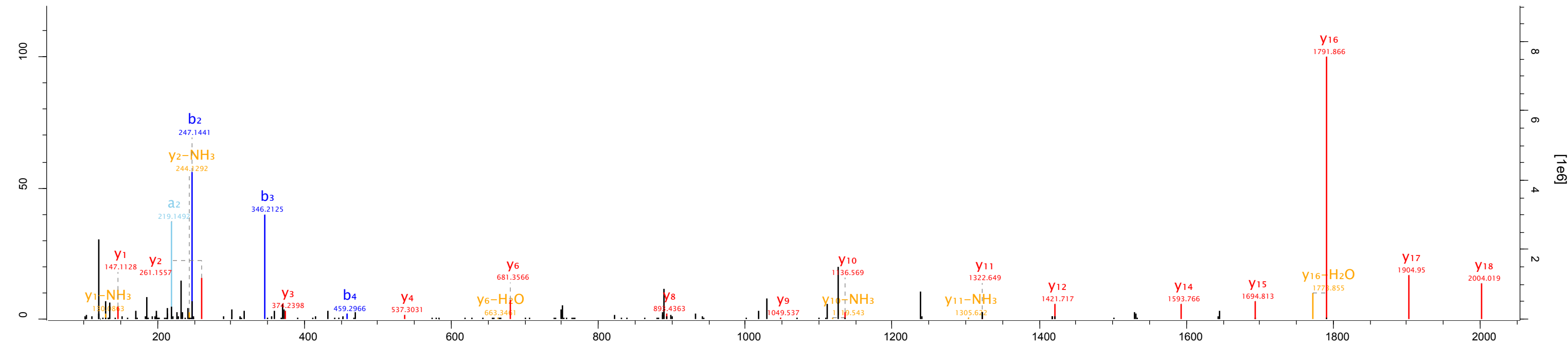
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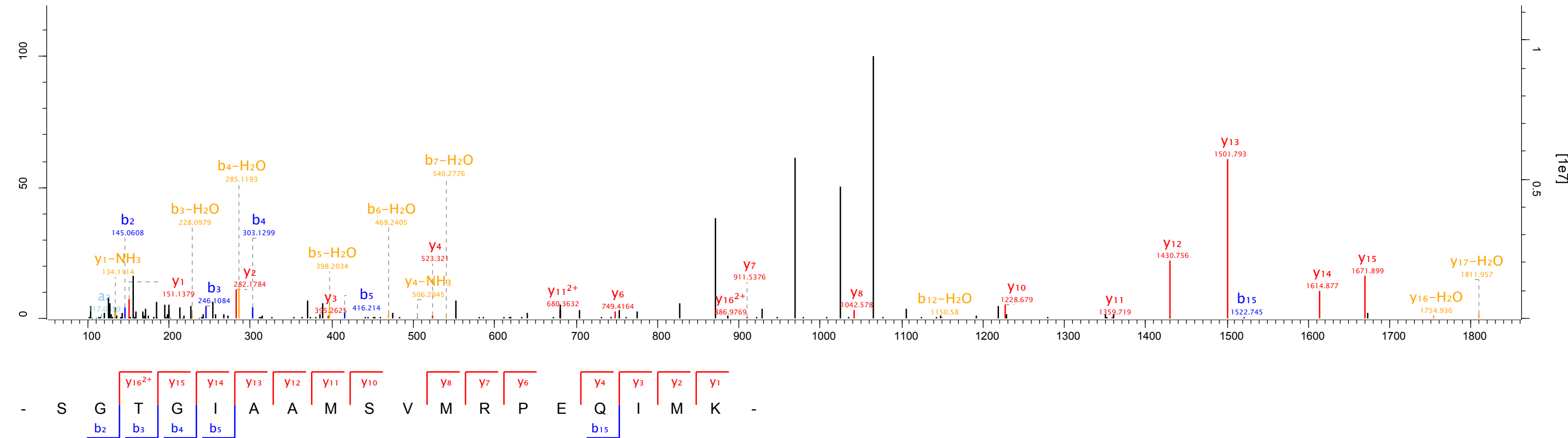




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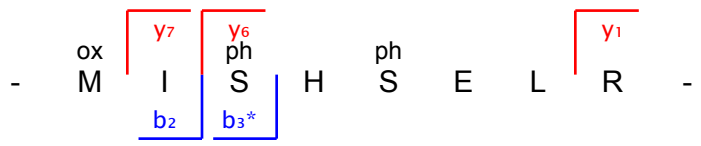
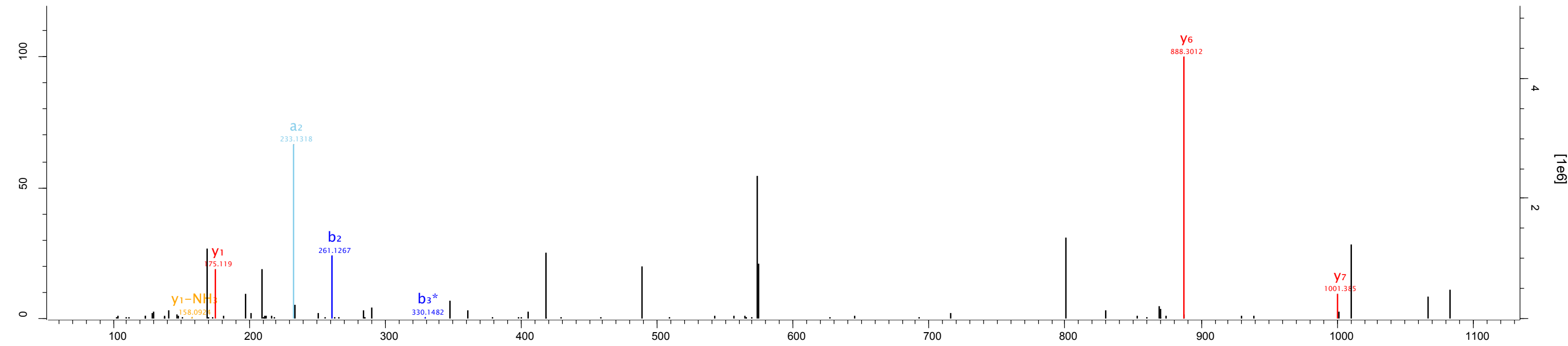
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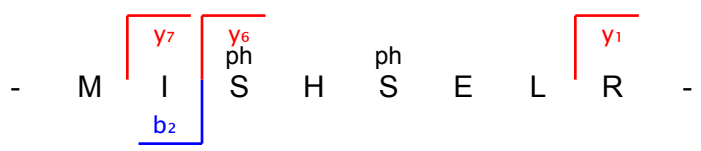
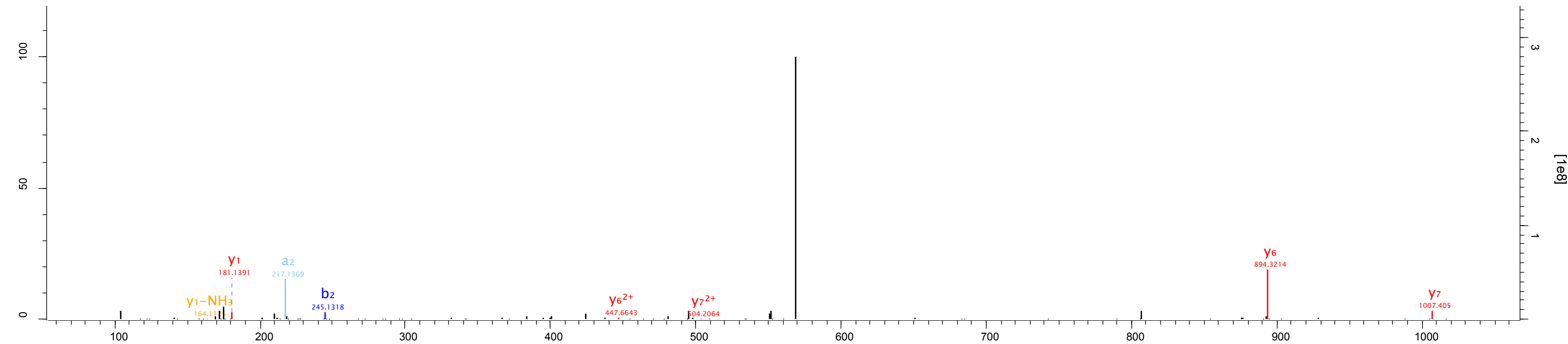
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20180707_MaS_A375SR_ML_proteome_2_22

Scan 6724 Method FTMS; HCD Score 46.43 m/z 574.71 Gene names PSPHP1

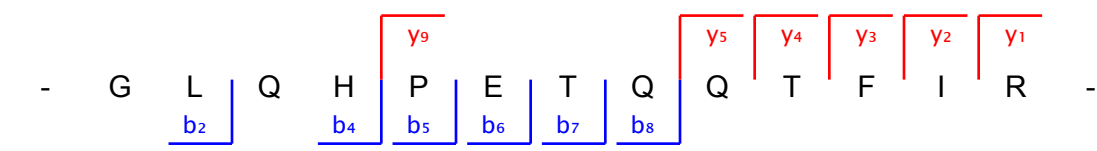
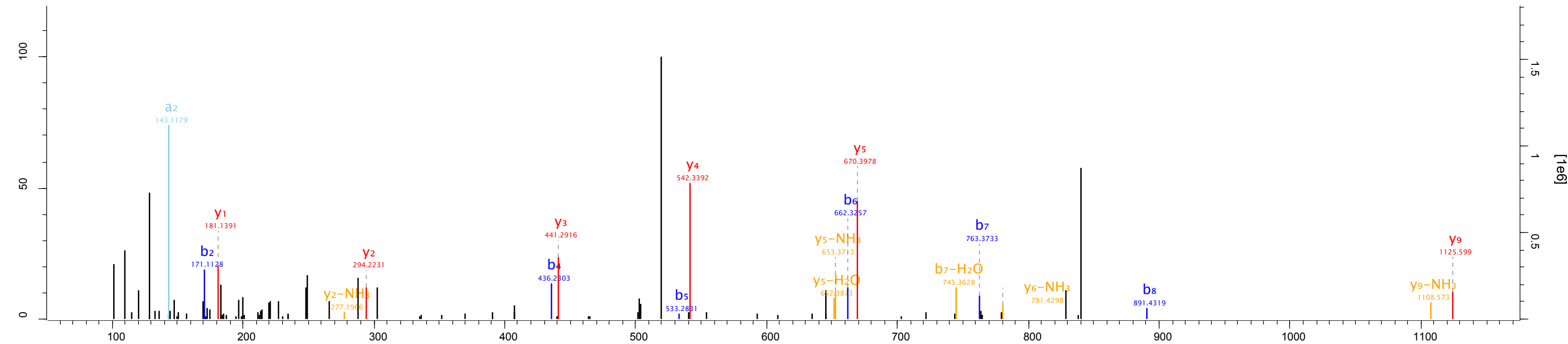


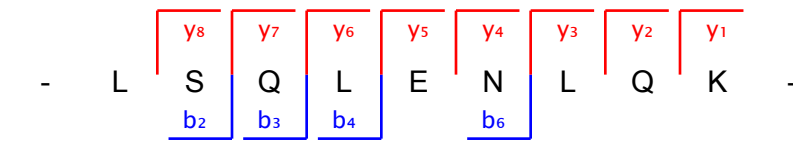
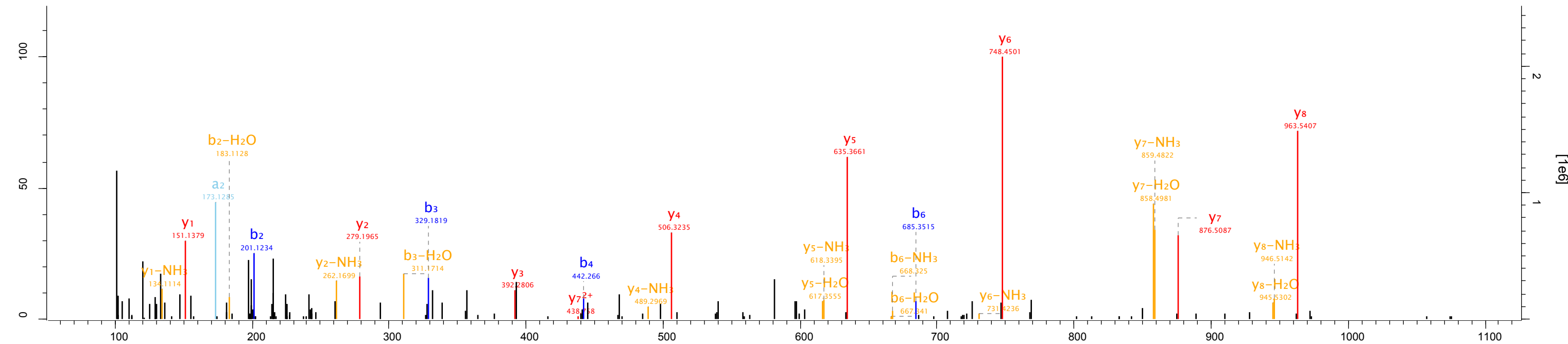
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Scan 9224 Method FTMS; HCD Score 48.76 m/z 569.73 Gene names PSPHP1

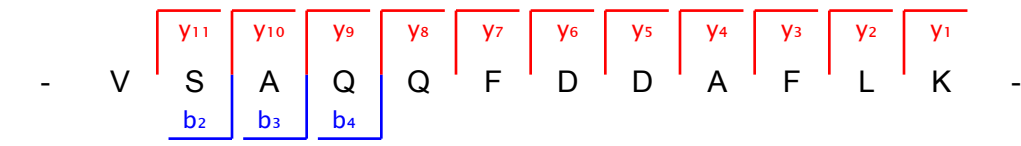
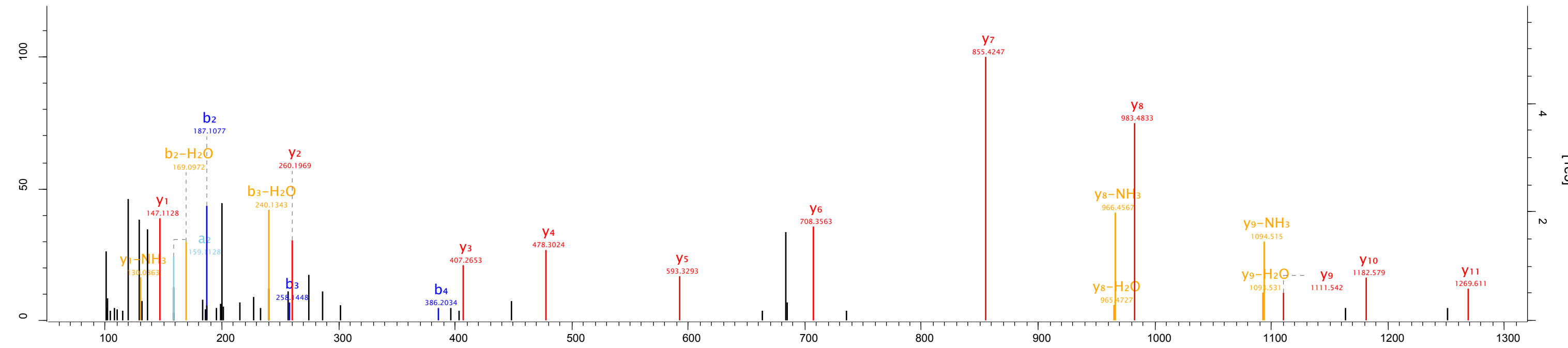


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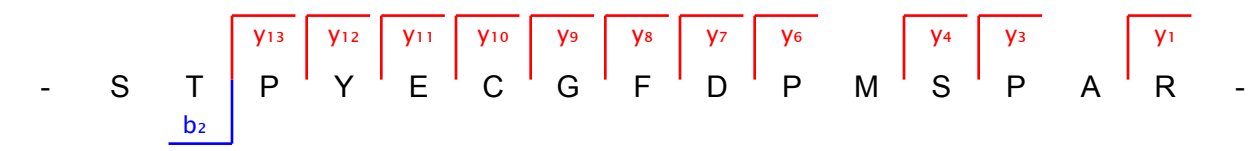
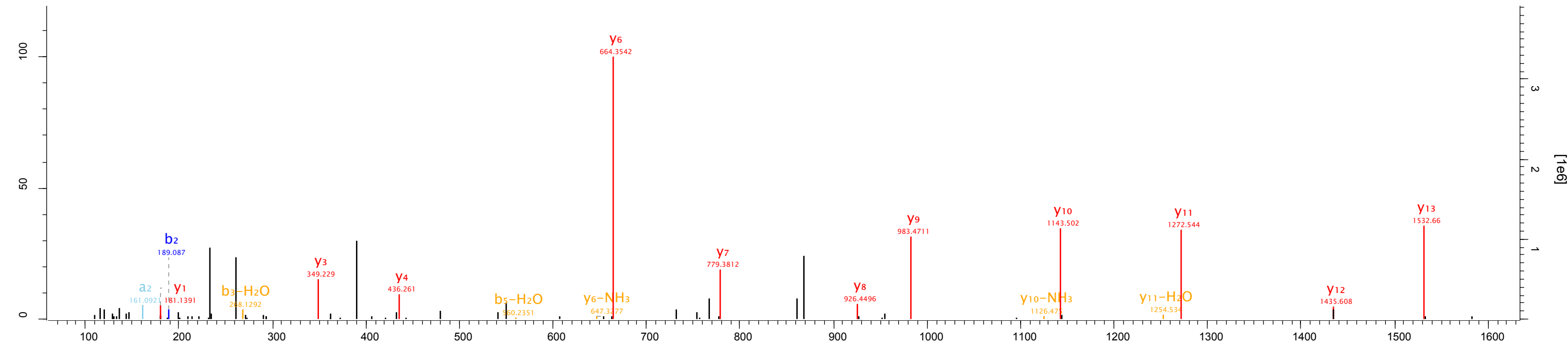




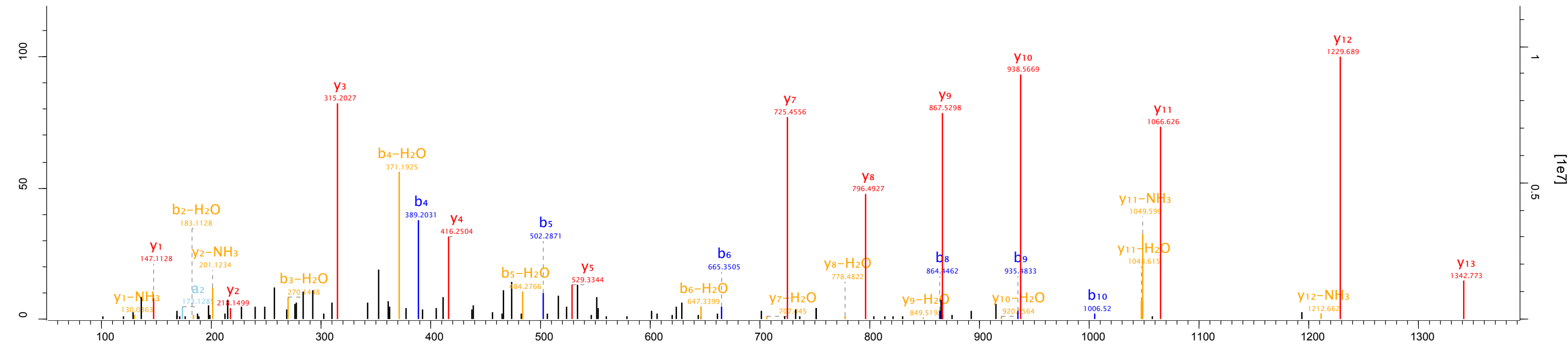
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 Scan: 24064 Method: FTMS; HCD Score: 104.24 m/z: 684.84 Gene names: PIGN



Raw file 20180707_MaS_A375SR_ML_proteome_2_28 Scan 19554 Method FTMS; HCD Score 72.9 m/z 861.37 Gene names MT-ND3



Raw file 20180707_MaS_A375SR_ML_proteome_2_28 Scan 22954 Method FTMS; HCD Score 93.43 m/z 865.99 Gene names KRTCAP2

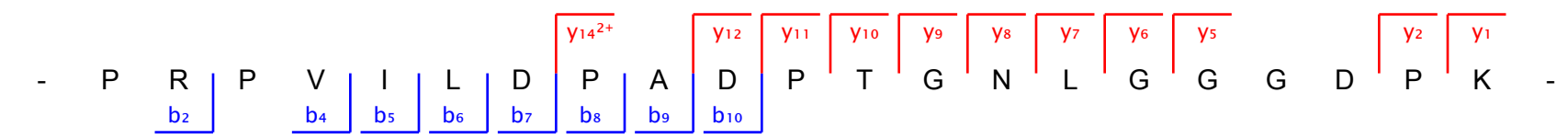
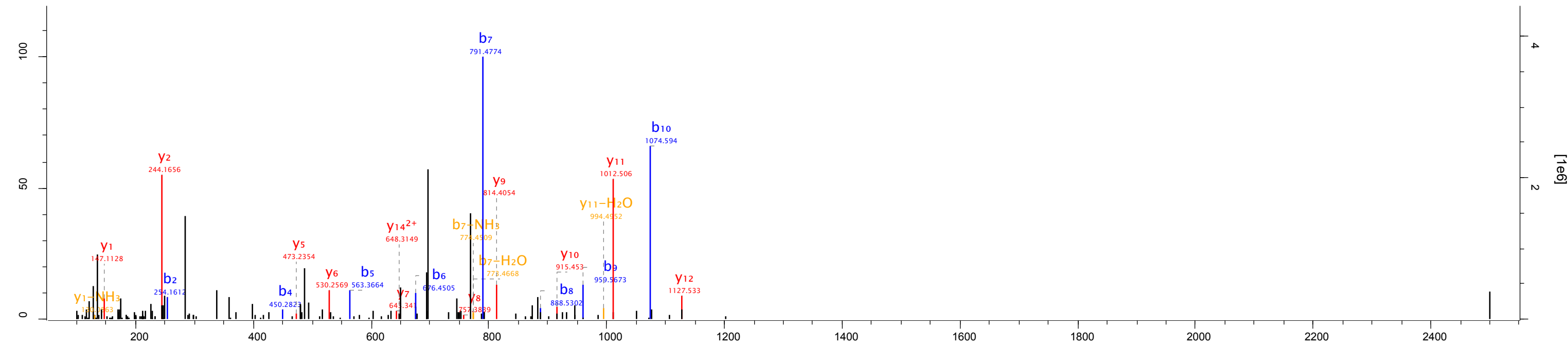


- I S S T L Y Q A A A P V L T P A K -

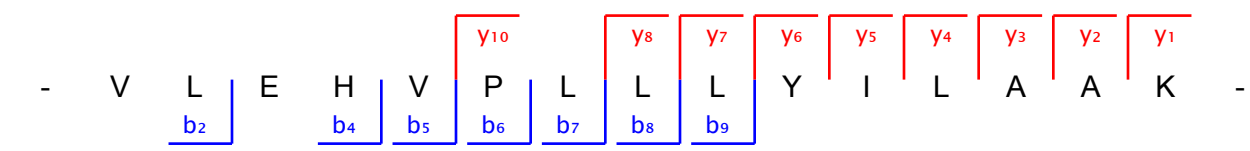
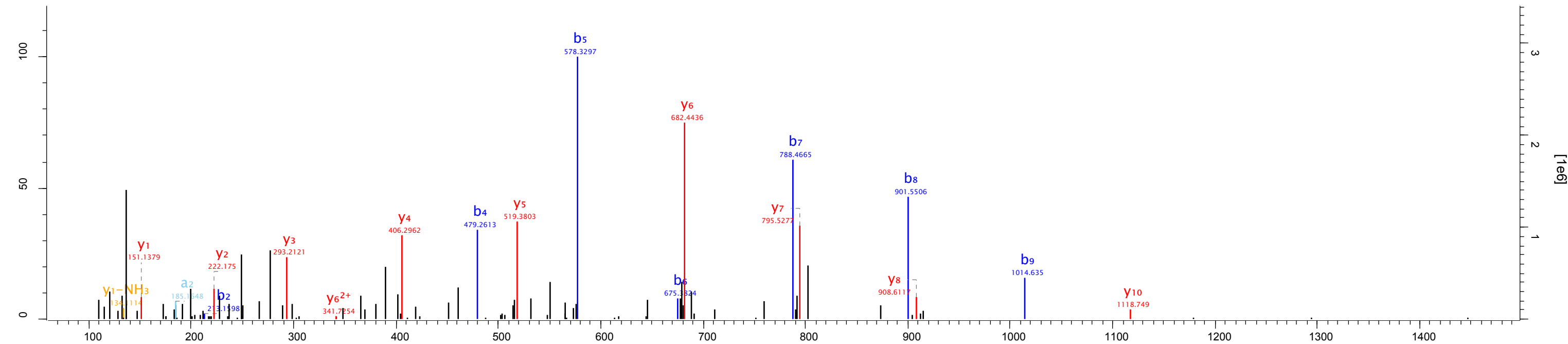
Fragmentation mapping (b and y ions):

- b ions (blue boxes):** a2 (S), b4 (T), b5 (L), b6 (Y), b8 (A), b9 (A), b10 (A)
- y ions (red boxes):** y1 (K), y2 (A), y3 (P), y4 (T), y5 (L), y7 (P), y8 (A), y9 (A), y10 (A), y11 (Q), y12 (Y), y13 (L)

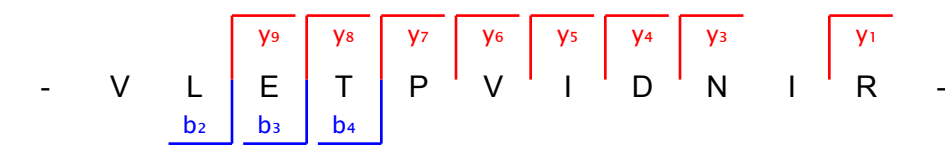
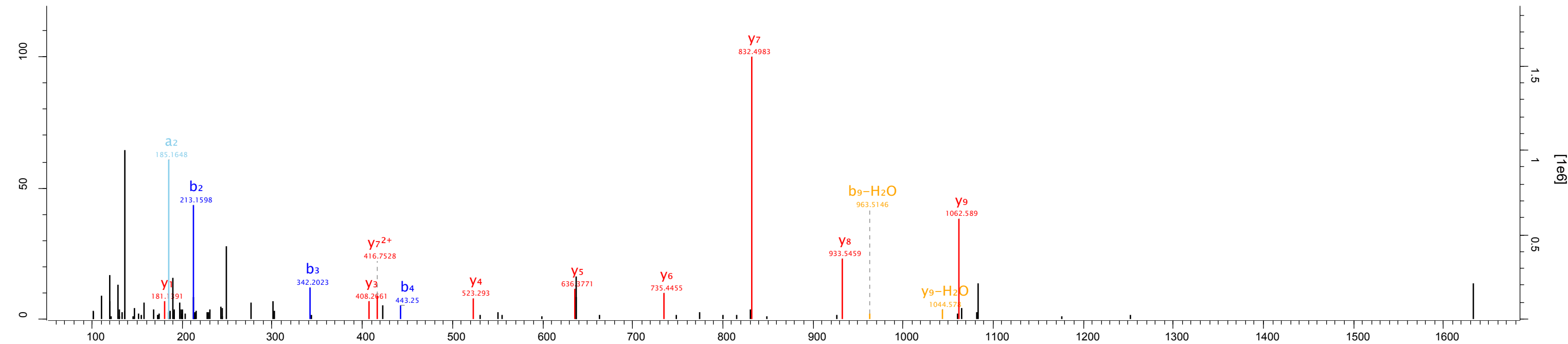
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 Scan: 19444 Method: FTMS; HCD Score: 49.66 m/z: 696.04 Gene names: OAS1



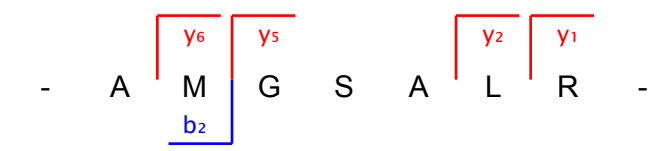
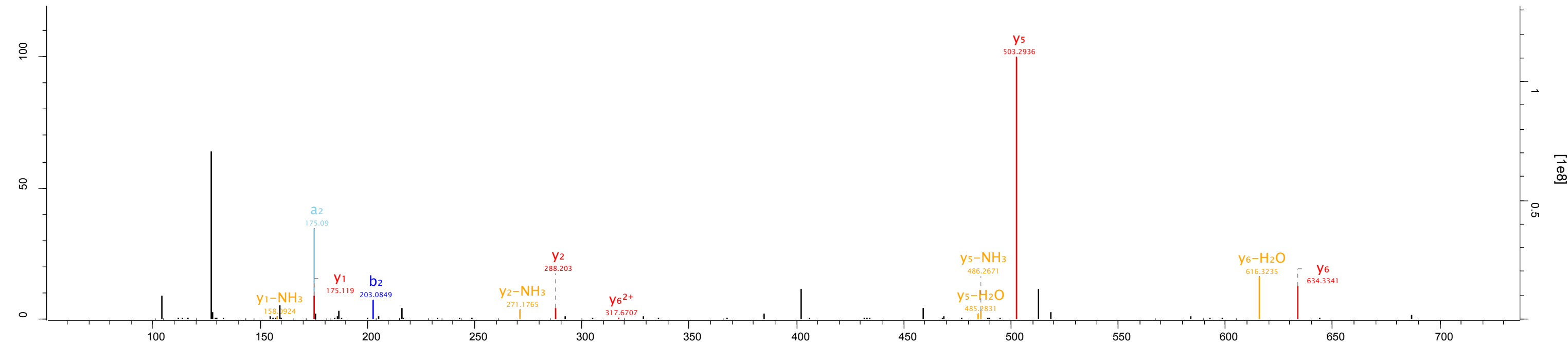
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 Scan 29394 Method FTMS; HCD Score 69.92 m/z 566.03 Gene names SMIM11



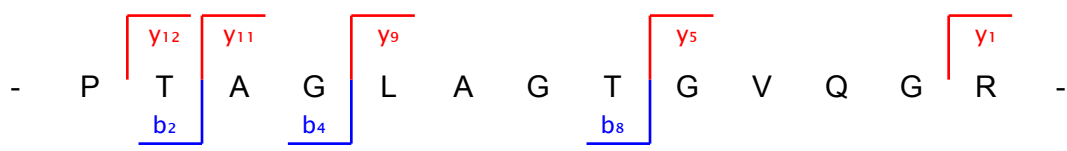
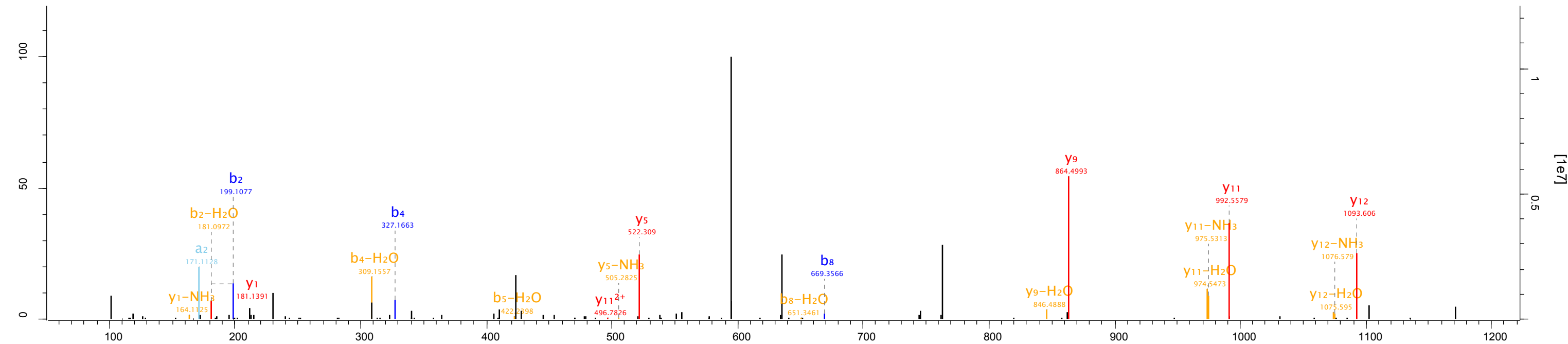
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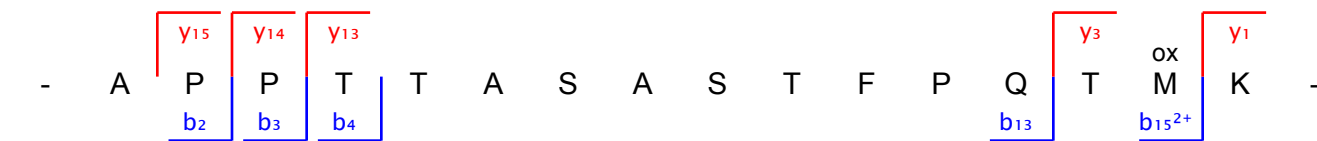
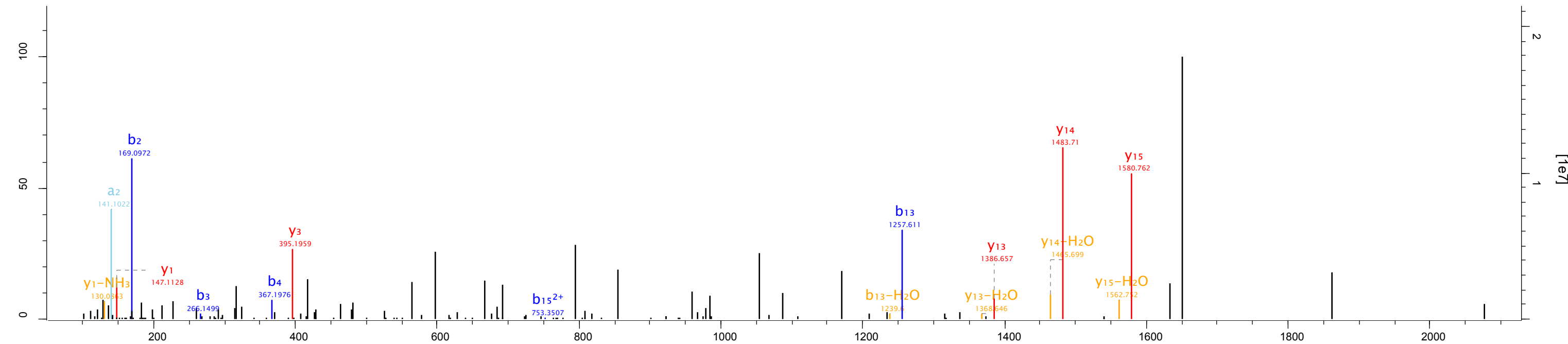


Raw file
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Scan 6424 Method FTMS; HCD Score 84.36 m/z 353.19

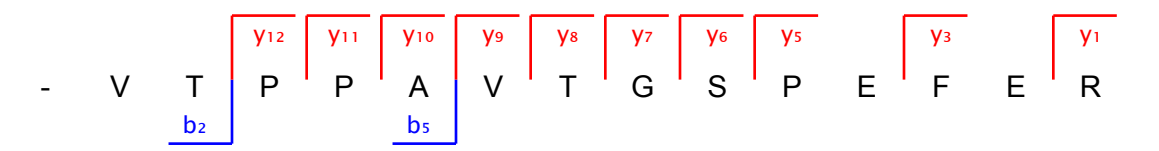
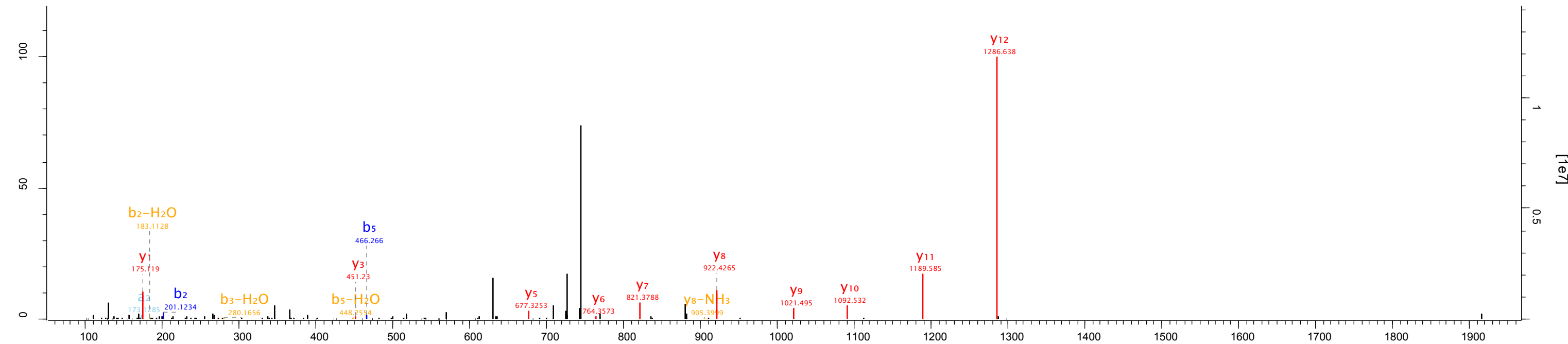


Raw file 20180707_MaS_A375SR_ML_proteome_2_30
 Scan 8374 Method FTMS; HCD Score 99.75 m/z 595.83



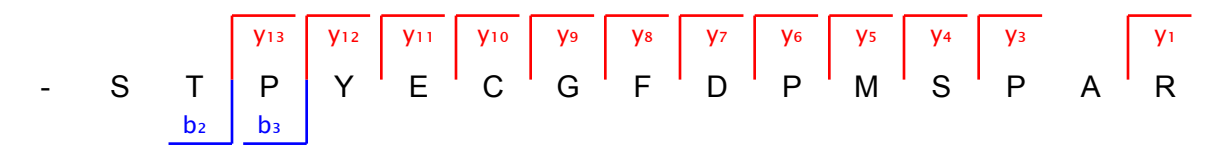
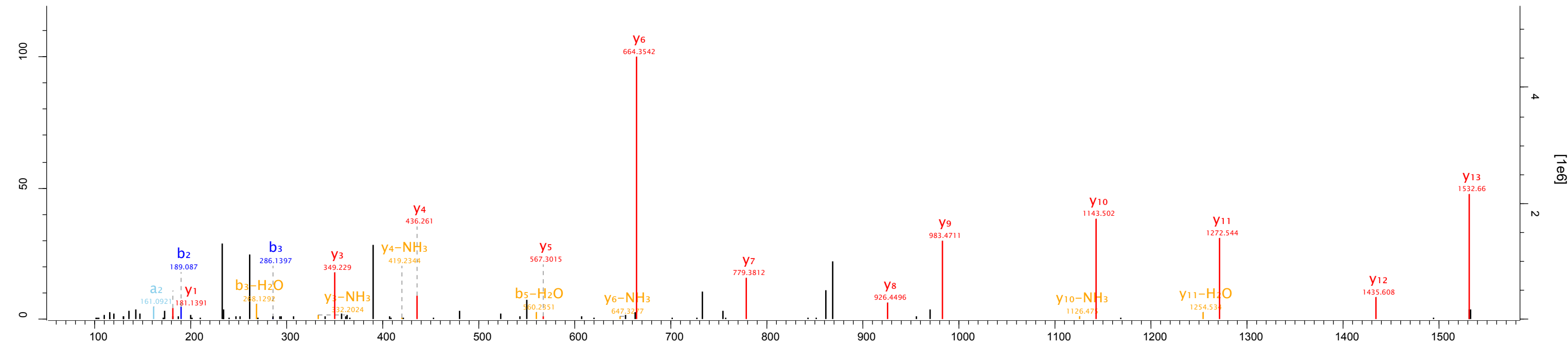


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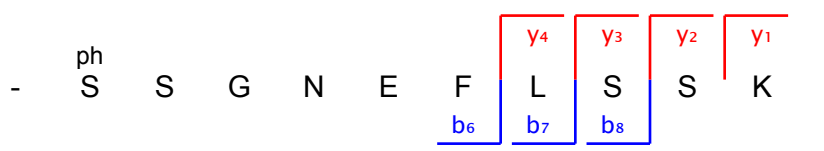
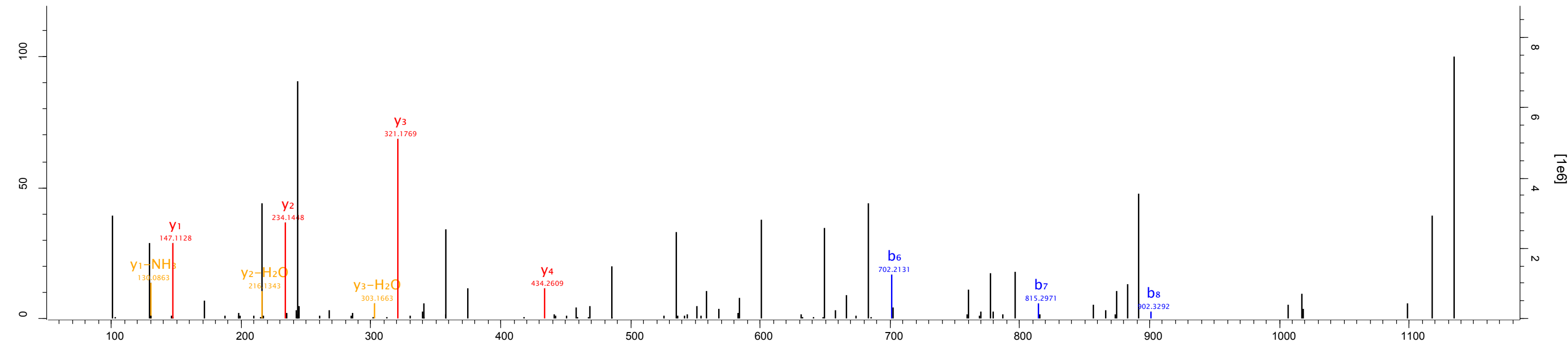


Raw file
20180707_MaS_A375SR_ML_proteome_22

Scan: 19254
Method: FTMS; HCD
Score: 87.52
m/z: 861.38
Gene names: MT-ND3

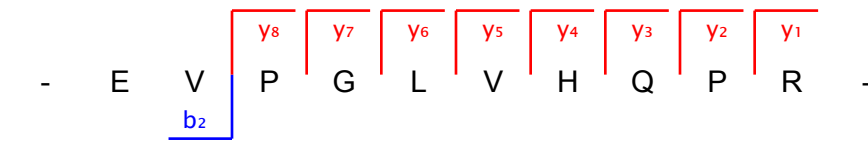
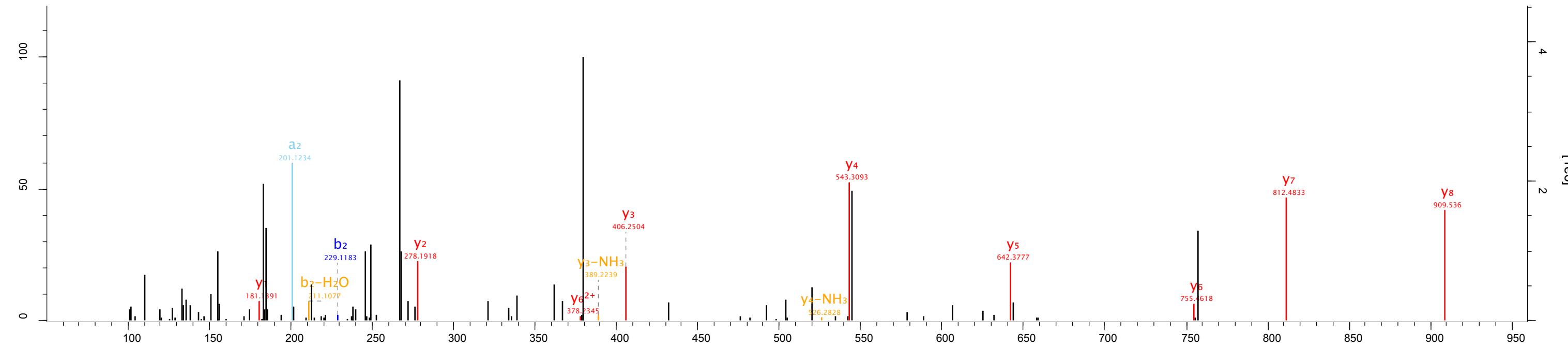


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 Scan: 3384 Method: FTMS; HCD Score: 66.19 m/z: 568.24 Gene names: MAP3K19

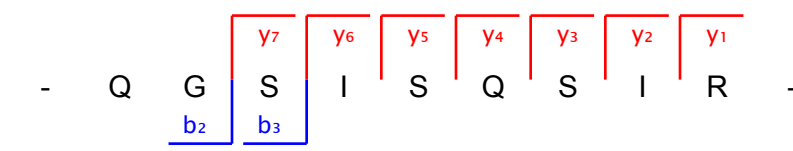
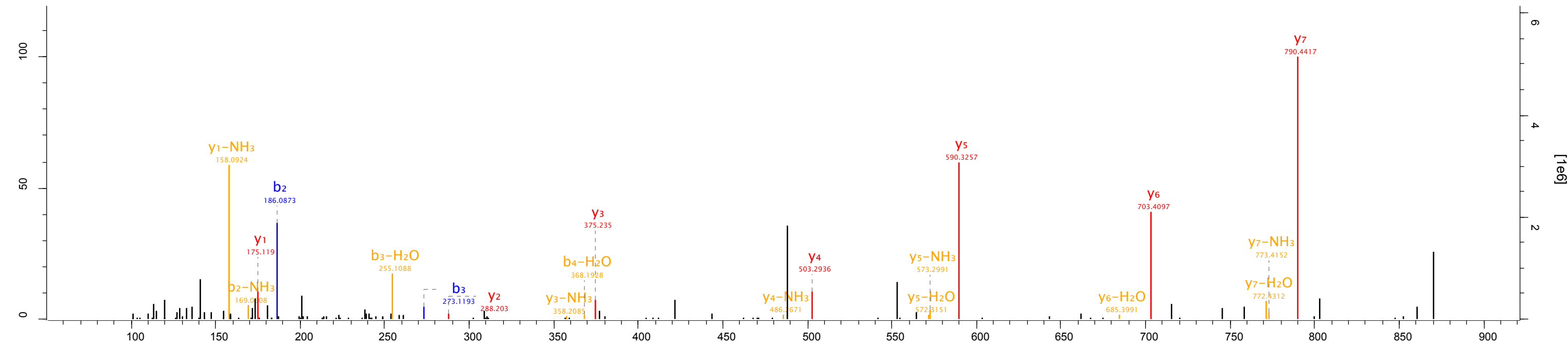


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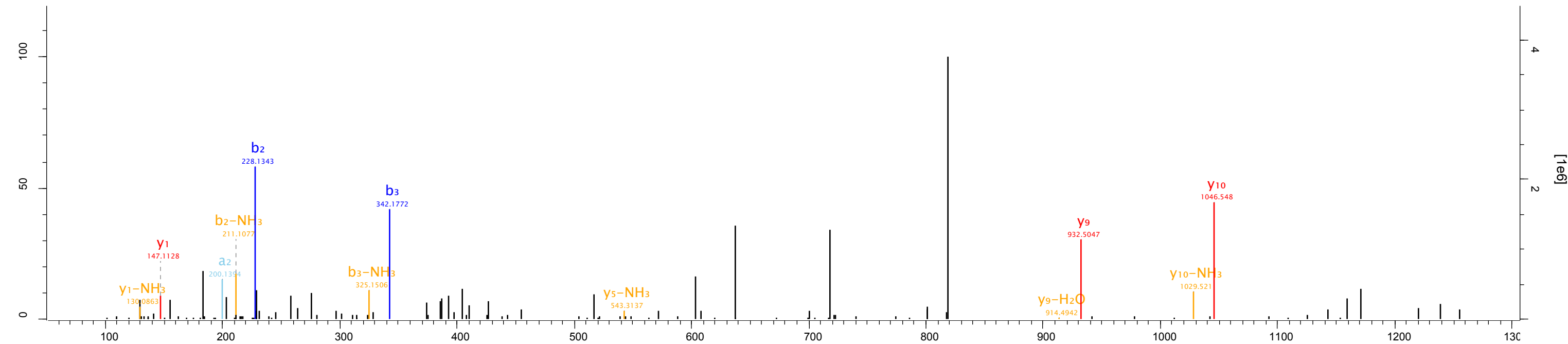
Scan 9724 Method FTMS; HCD Score 40.39 m/z 379.89 Gene names C1orf21



Raw file 20180707_MaS_A375SR_ML_proteome_25 Scan 9574 Method FTMS; HCD Score 111.06 m/z 488.26

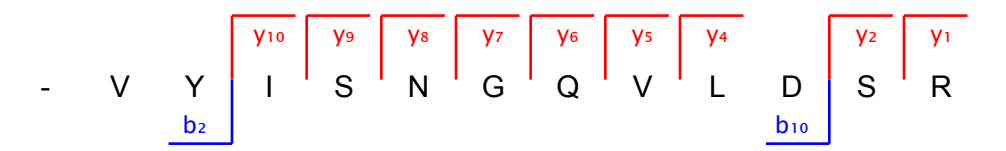
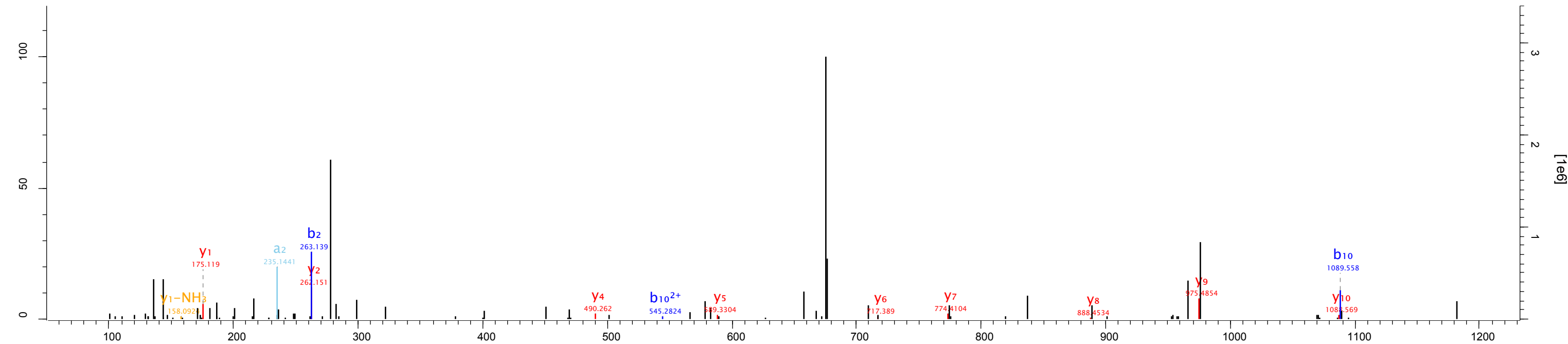


Raw file 20180707_MaS_A375SR_ML_proteome_27 Scan 12694 Method FTMS; HCD Score 54.26 m/z 637.34

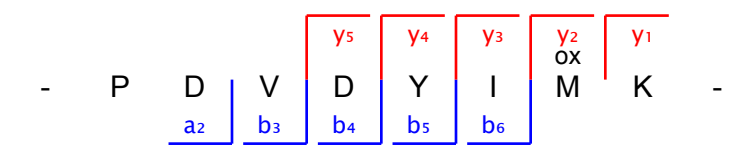
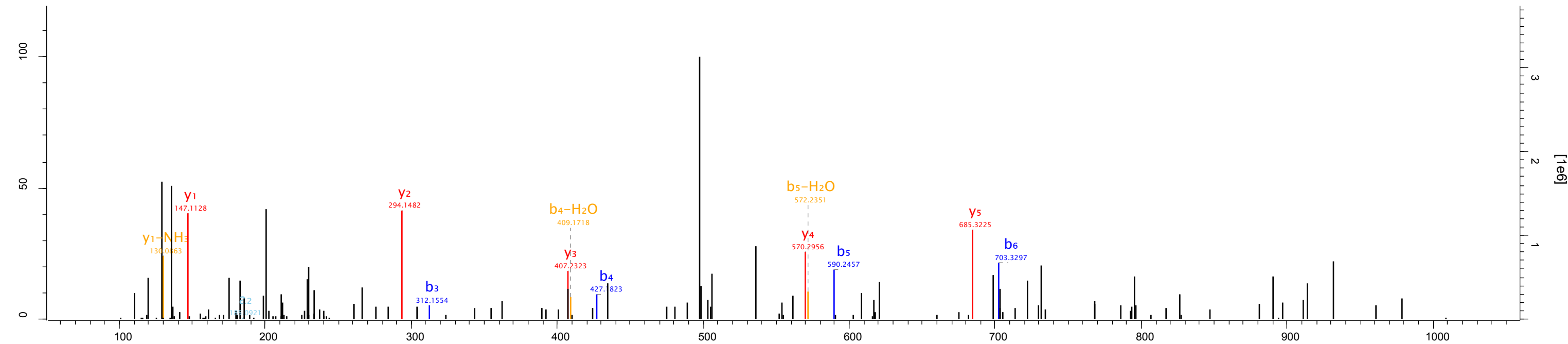


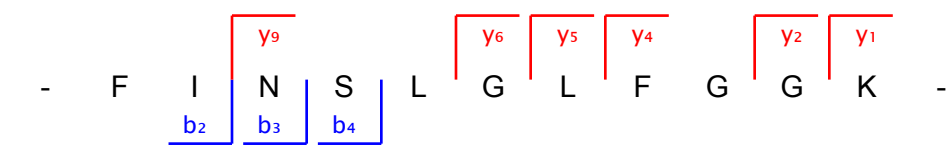
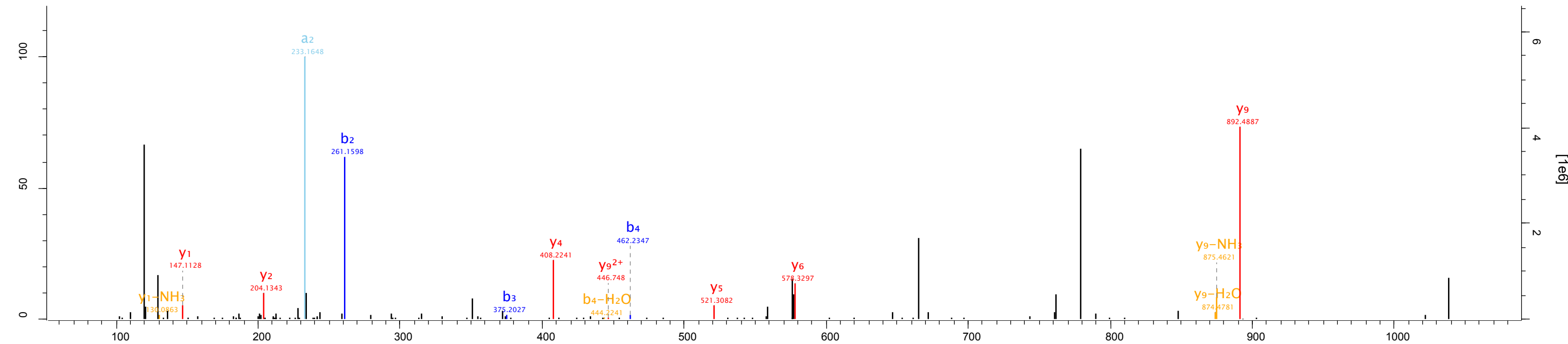
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Scan Method Score m/z Gene names
14434 FTMS; HCD 36.63 676.81 SELK

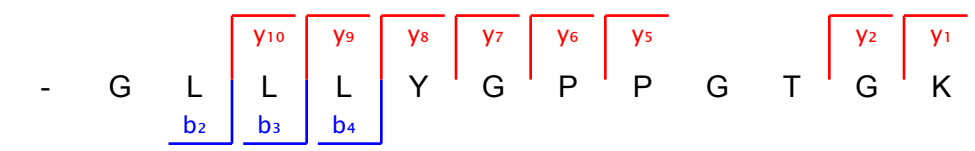
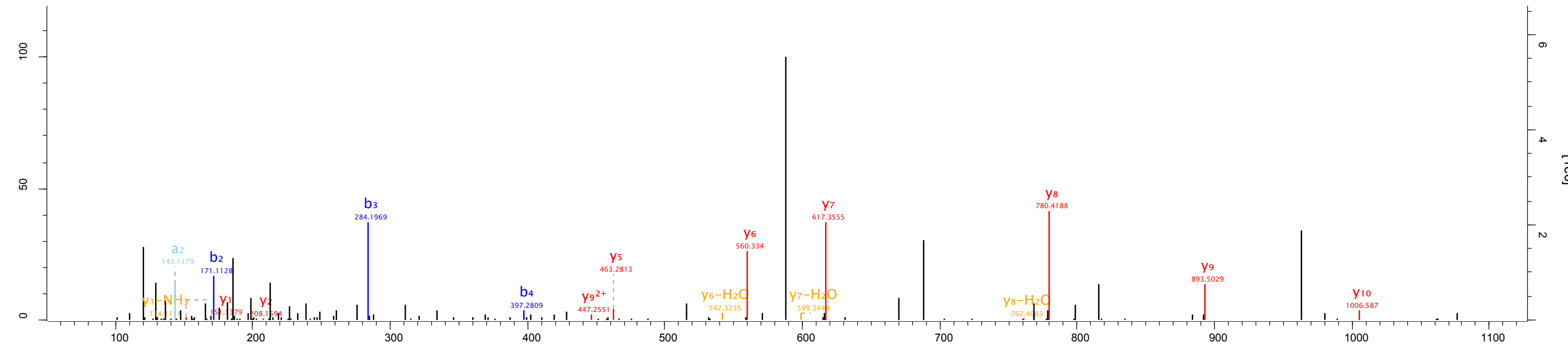


Raw file 20180707_MaS_A375SR_ML_proteome_27 Scan 20534 Method FTMS; HCD Score 73.25 m/z 498.74

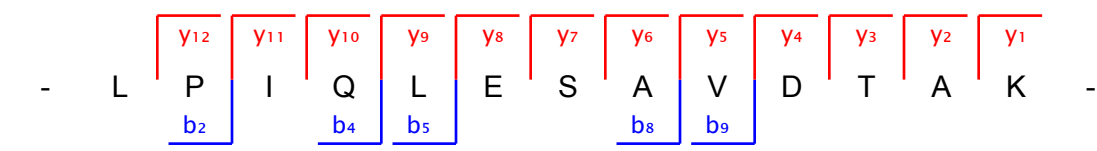
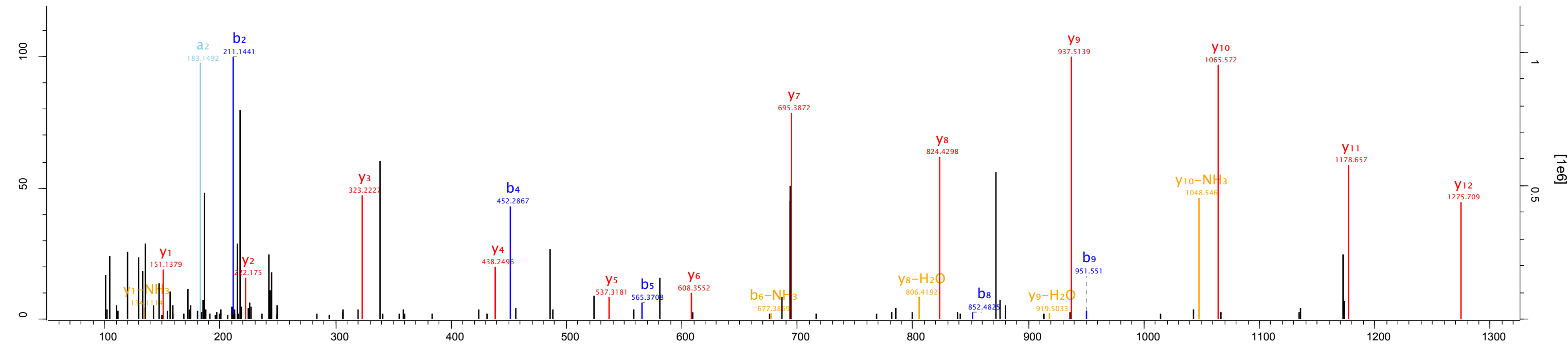


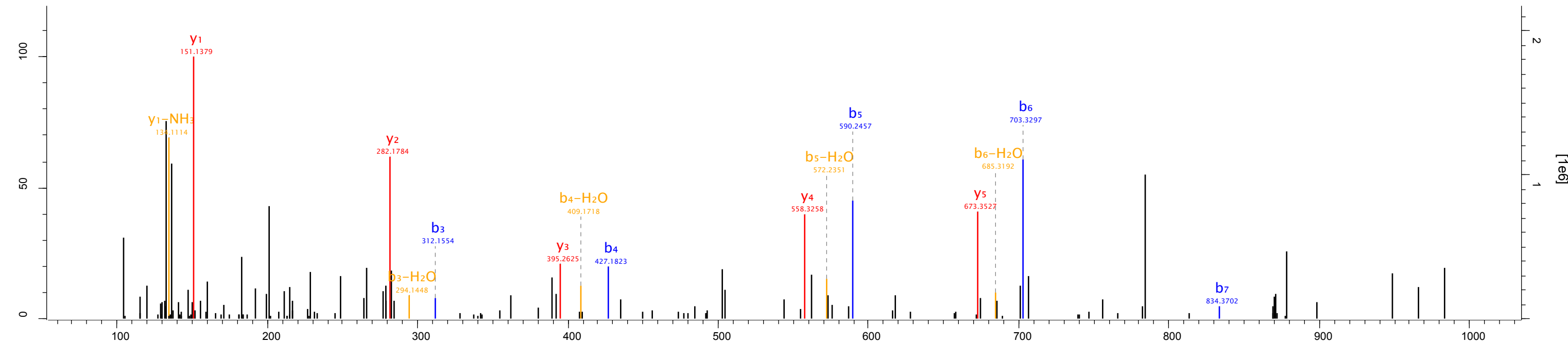


Raw file 20180707_MaS_A375SR_ML_proteome_29 Scan 21404 Method FTMS; HCD Score 55.04 m/z 588.85 Gene names KATNAL2



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 Scan: 21954 Method: FTMS; HCD Score: 86.5 m/z: 694.9 Gene names: CHRM3



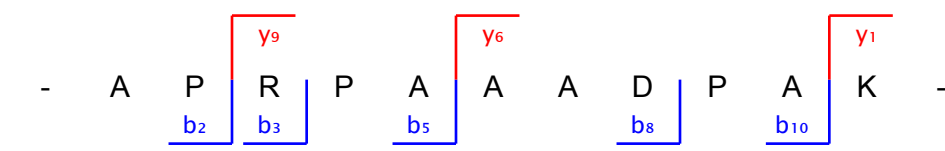
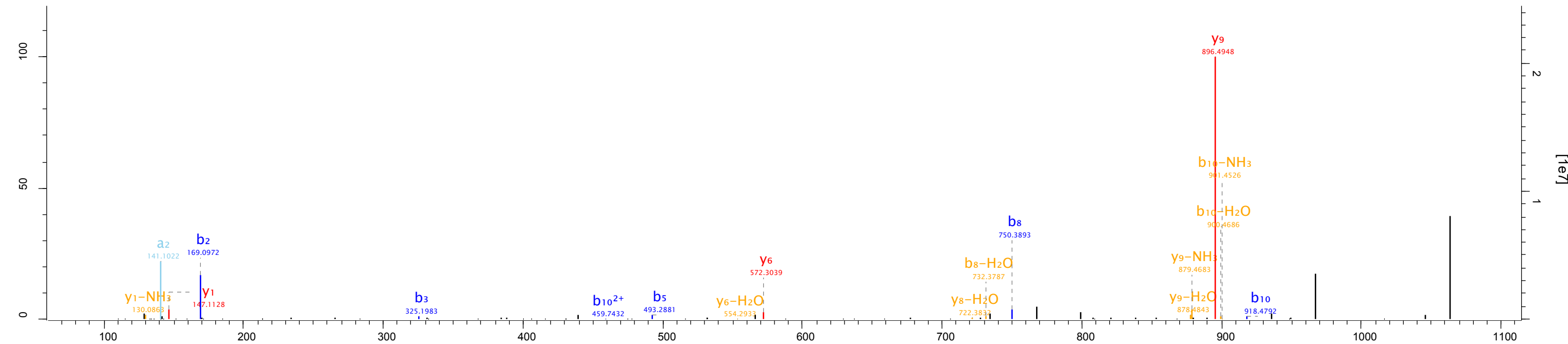


- P D V D Y I M K -

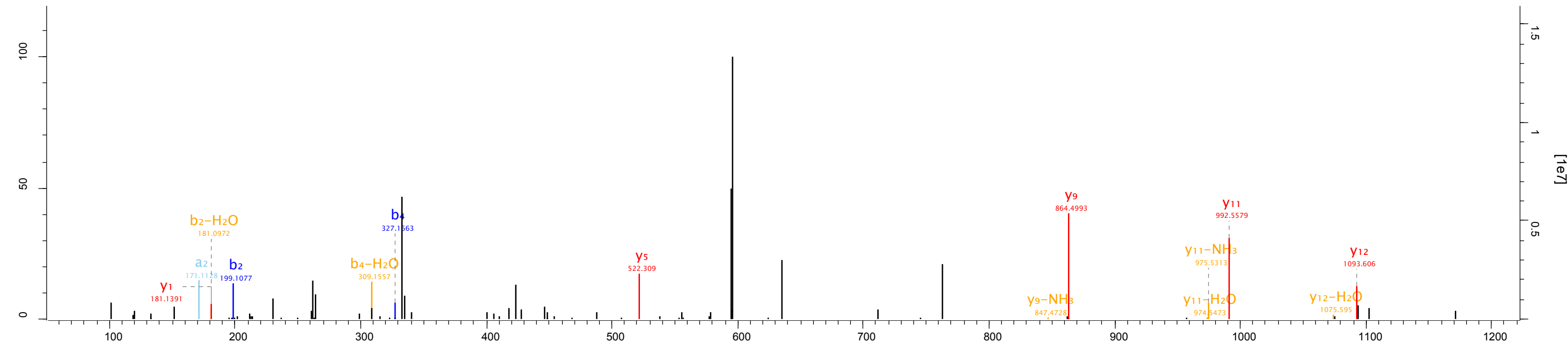
b3 b4 b5 b6 b7

y5 y4 y3 y2 y1

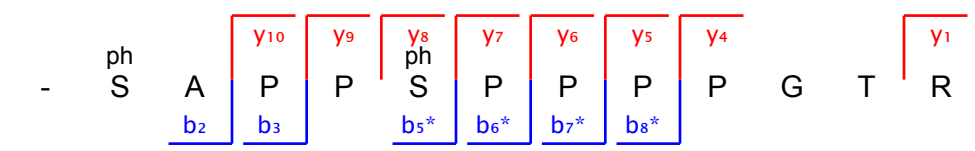
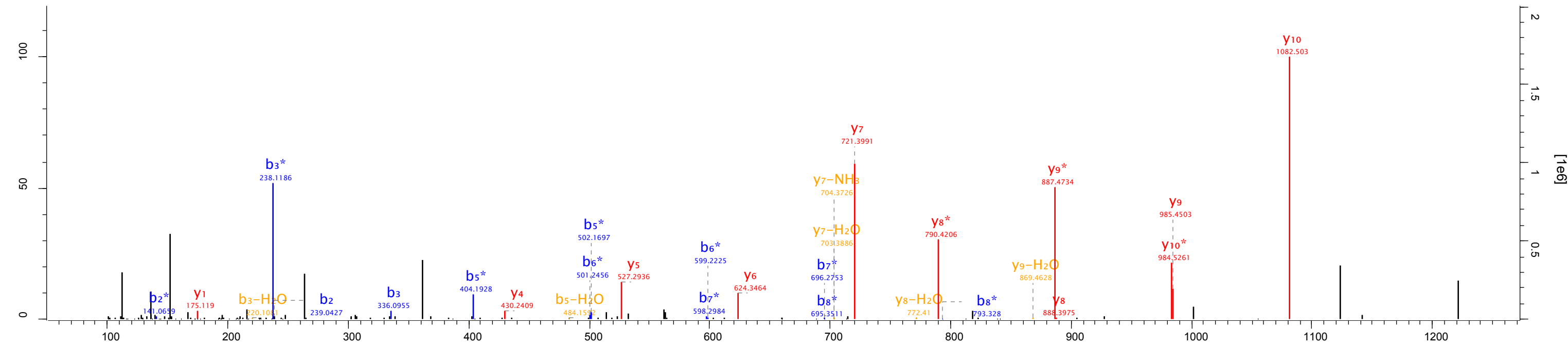
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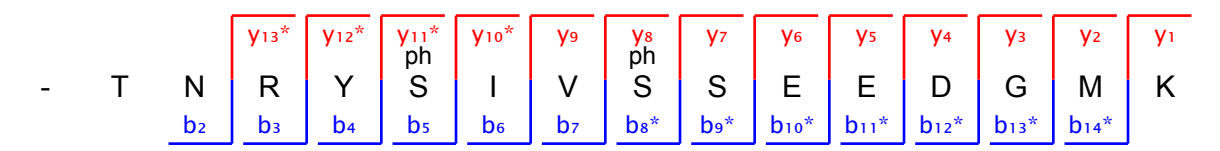
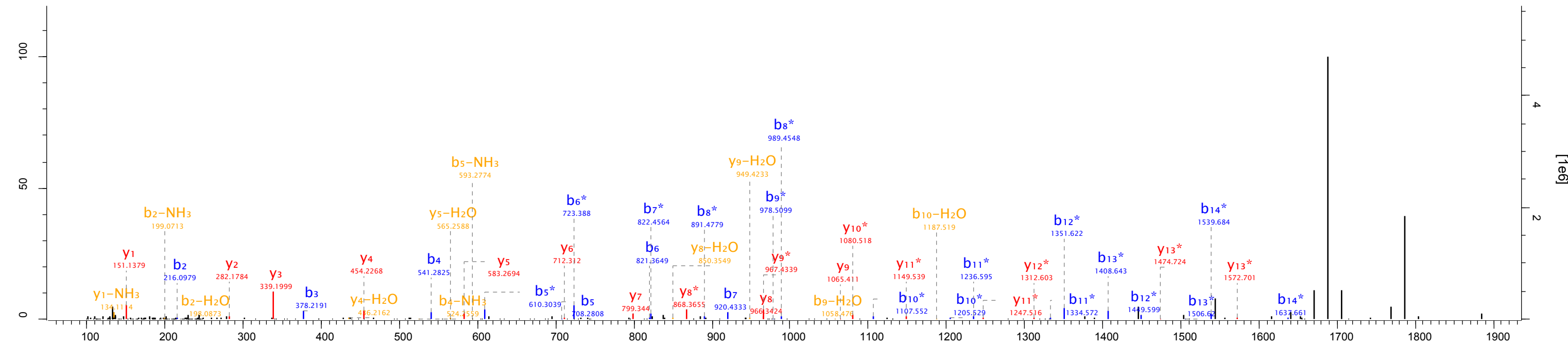
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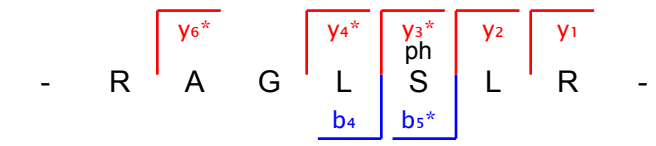
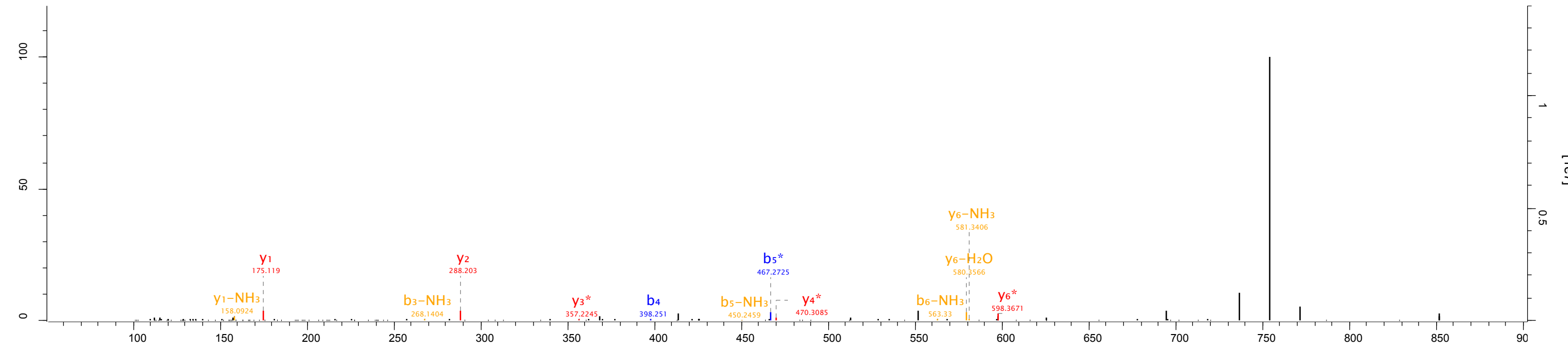
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 Scan: 6635 Method: FTMS; HCD Score: 83.89 m/z: 660.77 Gene names: GPSM3



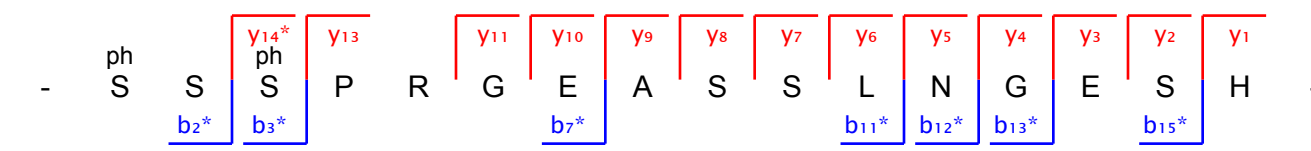
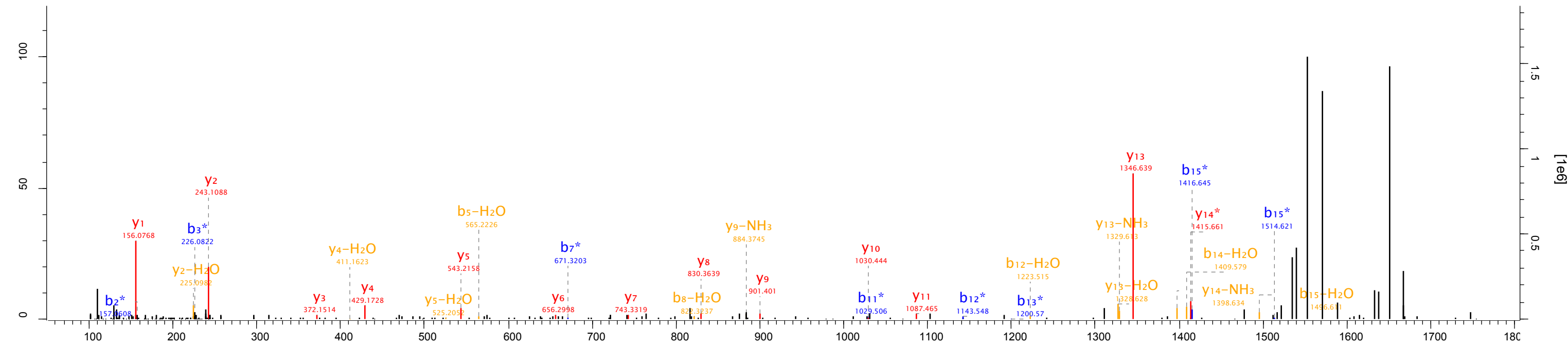
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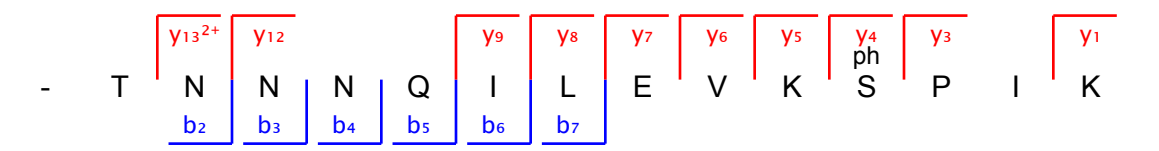
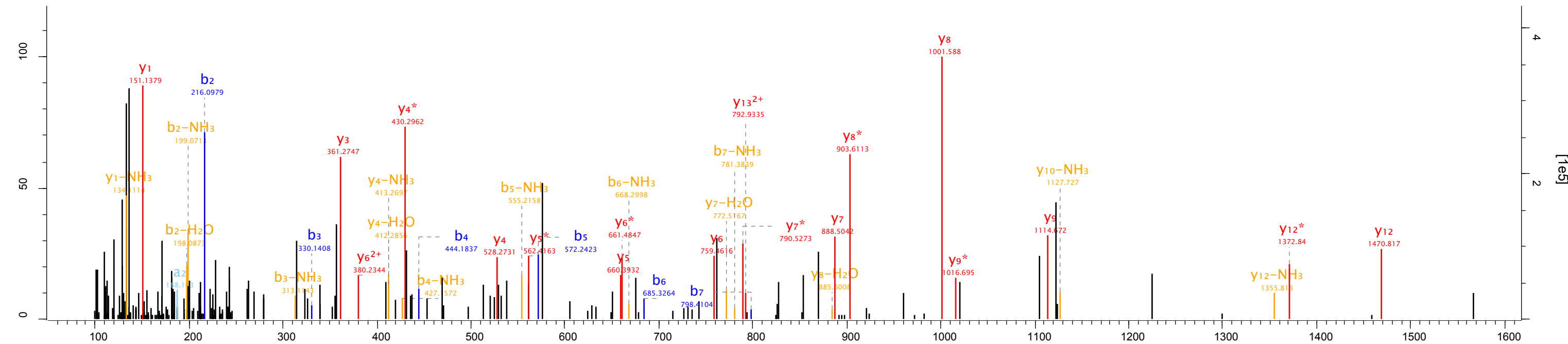
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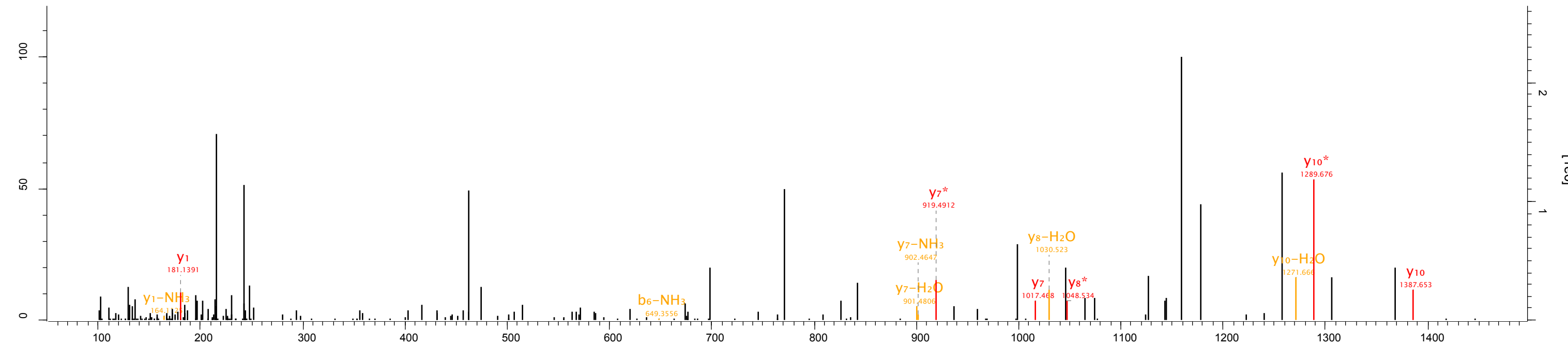
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 Scan: 8195 Method: FTMS; HCD Score: 75.06 m/z: 884.84 Gene names: YAF2



Raw file 20150812_A375SR_Phospho_BR1_04 Scan 13615 Method FTMS; HCD Score 124.98 m/z 562.64 Gene names MLLT3



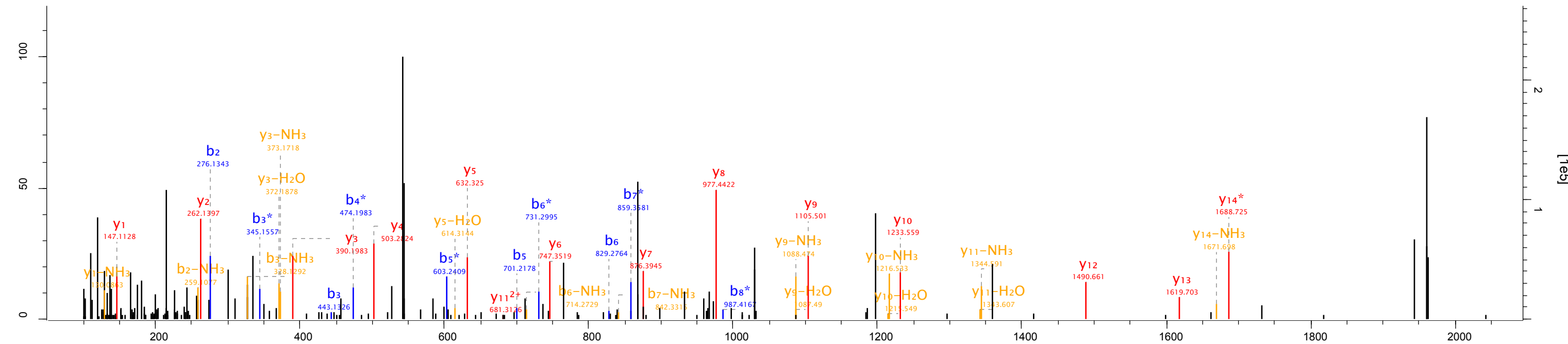
Raw file 20150812_A375SR_Phospho_BR1_04 Scan 8735 Method FTMS; HCD Score 44.51 m/z 500.92



- L L Q E I S S N R I R -

Fragmentation mapping: y10 (L), y8* (E), y7 (I), y1 (R)

Raw file 20150812_A375SR_Phospho_BR1_05 Scan 12155 Method FTMS; HCD Score 100.76 m/z 1031.42

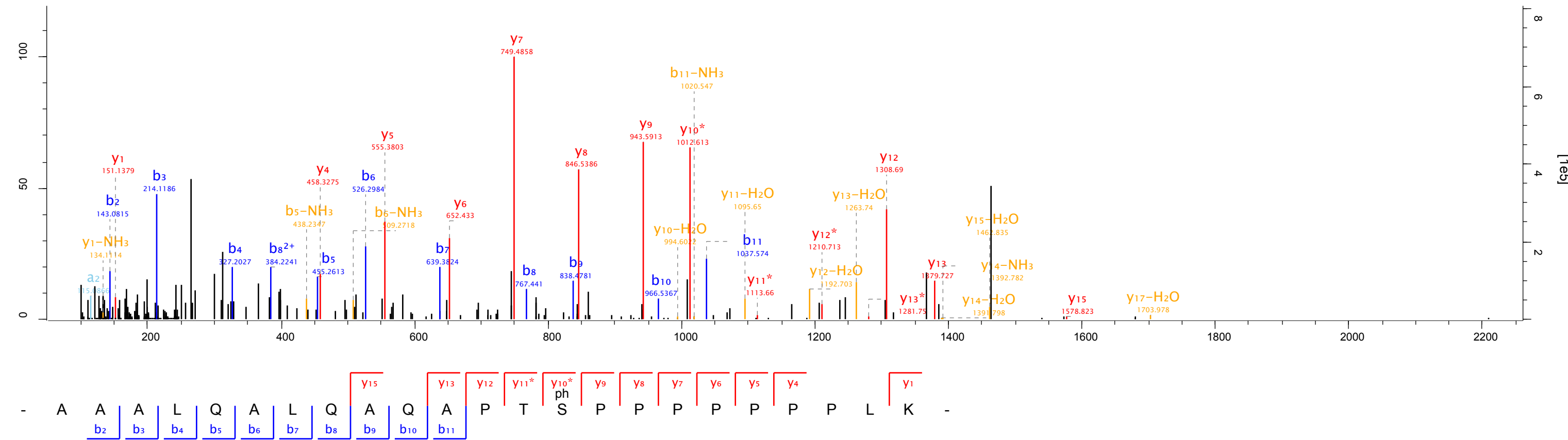


- F Q **Q** **S** **E** **E** **Q** **Q** **Q** T E D E L Q D K -

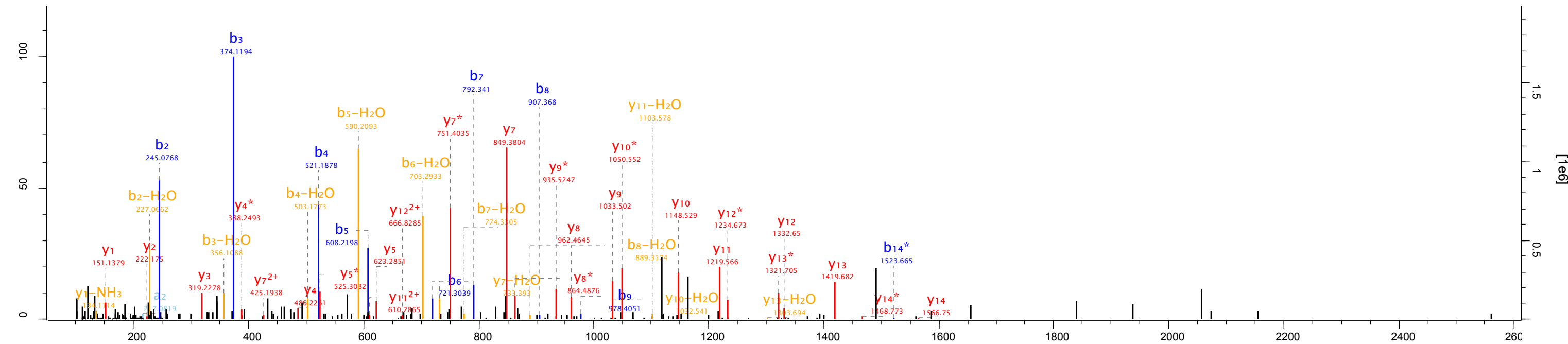
Fragmentation mapping (b-ions in blue, y-ions in red):

- b2: Q
- b3: **Q**
- b4*: **S**
- b5: **E**
- b6: **Q**
- b7*: **Q**
- b8*: **Q**
- y1: K
- y2: D
- y3: Q
- y4: L
- y5: E
- y6: D
- y7: E
- y8: T
- y9: **Q**
- y10: **Q**
- y11: **Q**
- y12: **E**
- y13: **E**
- y14: **S**
- y14*: **Q**

Raw file 20150812_A375SR_Phospho_BR1_05 Scan 21145 Method FTMS; HCD Score 90.06 m/z 782.76 Gene names ZNF579

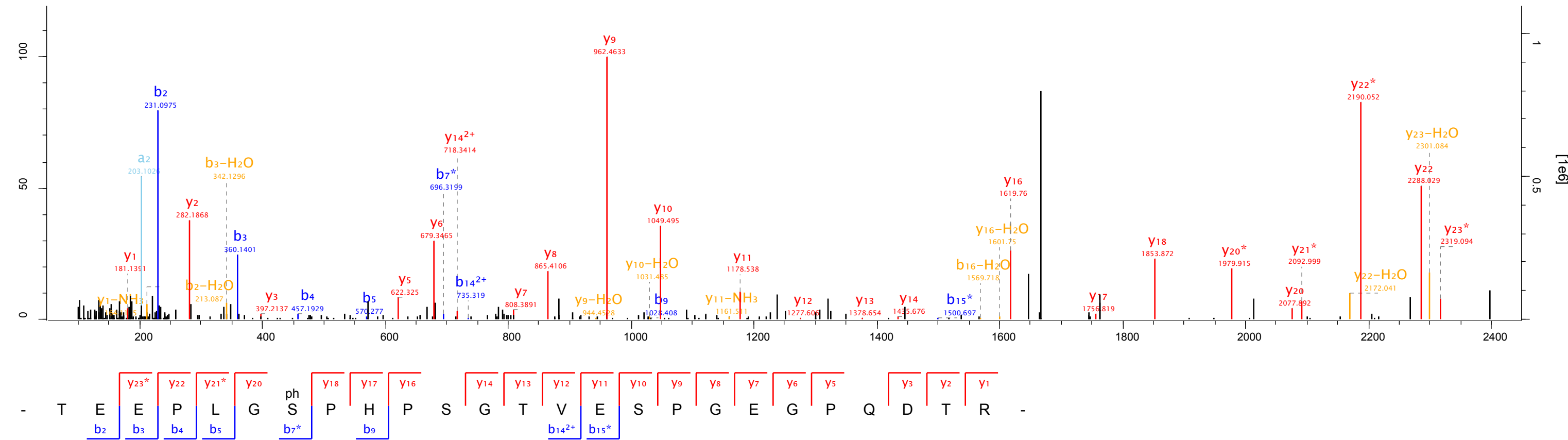


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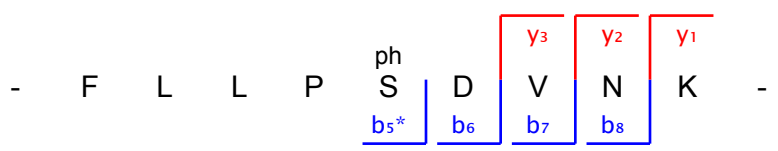
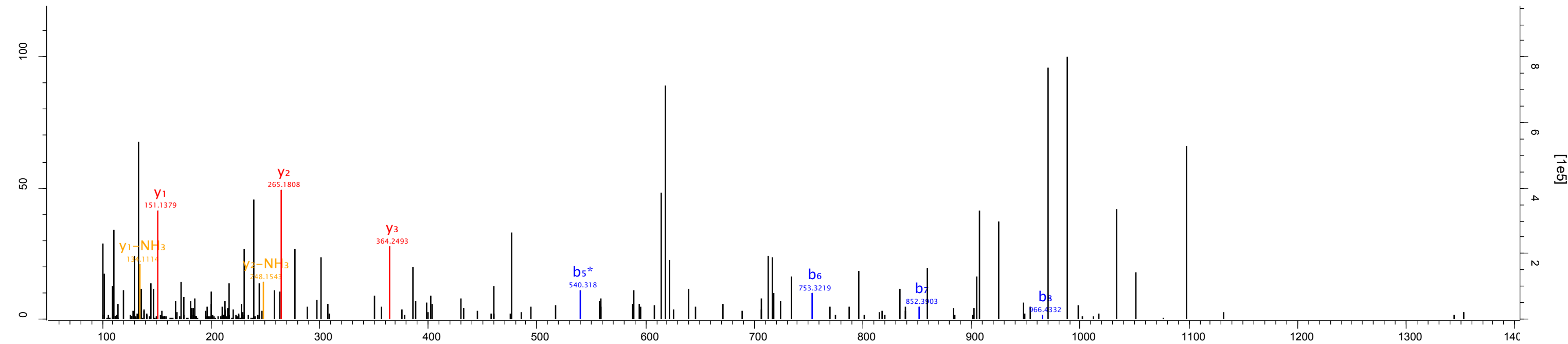


ac
 - S D E F S L A D A L P E H S P A K -
 b2 b3 b4 b5 b6 b7 b8 b9 b14*

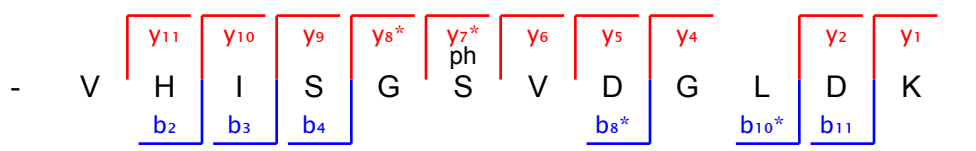
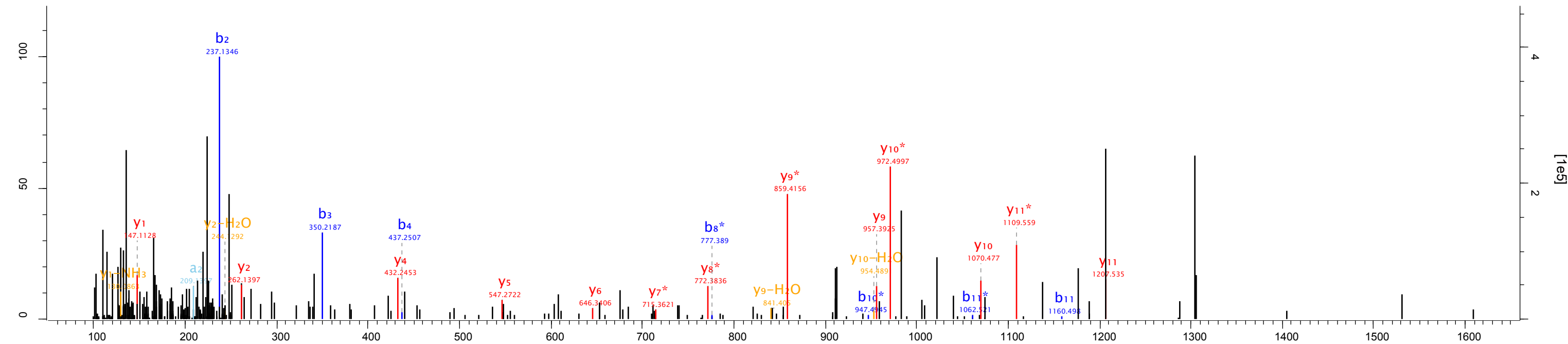
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 20150812_A375SR_Phospho_BR1_06 12655 FTMS; HCD 109.77 883.4 ZNF446



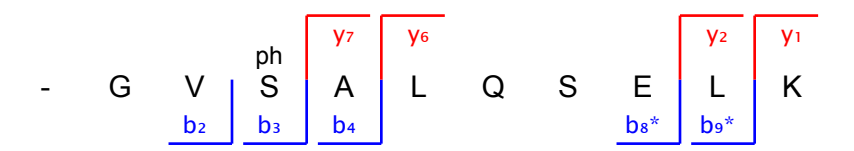
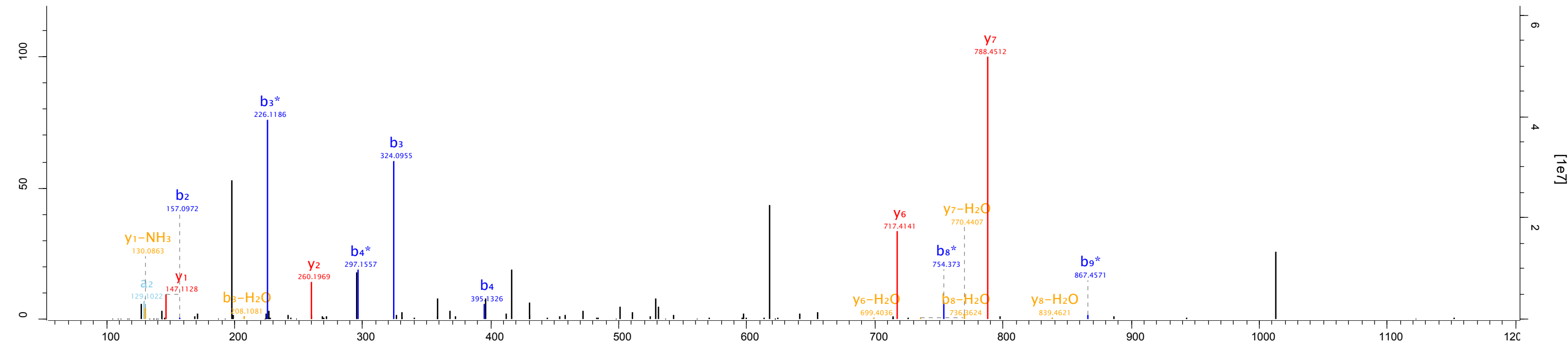
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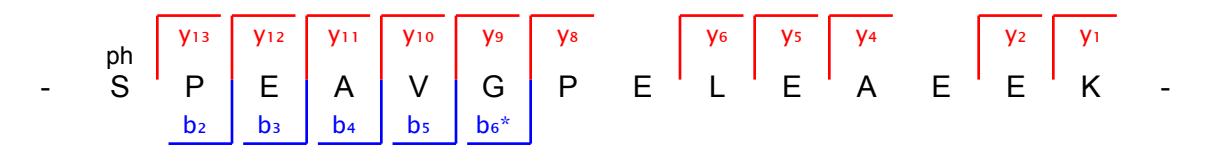
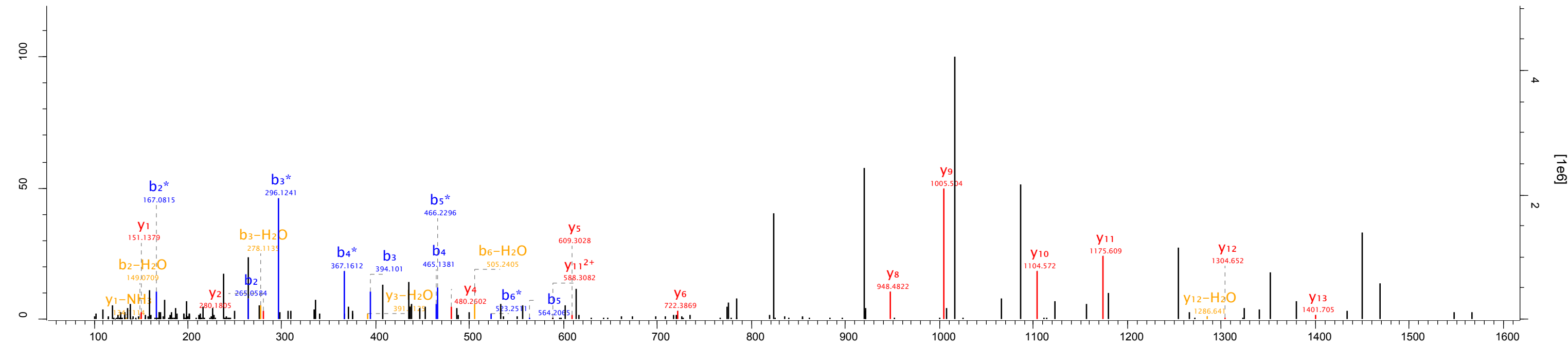
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 Scan: 12635 Method: FTMS; HCD Score: 50.13 m/z: 653.81 Gene names: PHACTR2



Raw file 20150812_A375SR_Phospho_BR1_07 Scan 13725 Method FTMS; HCD Score 62.34 m/z 556.27

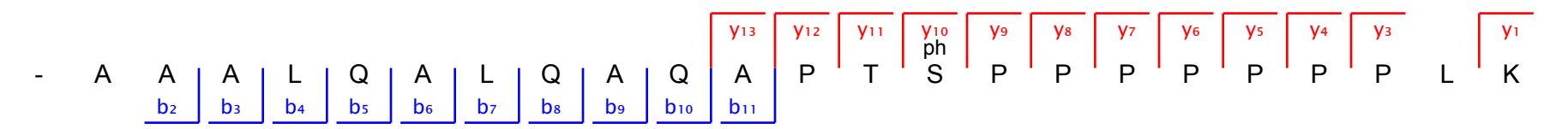
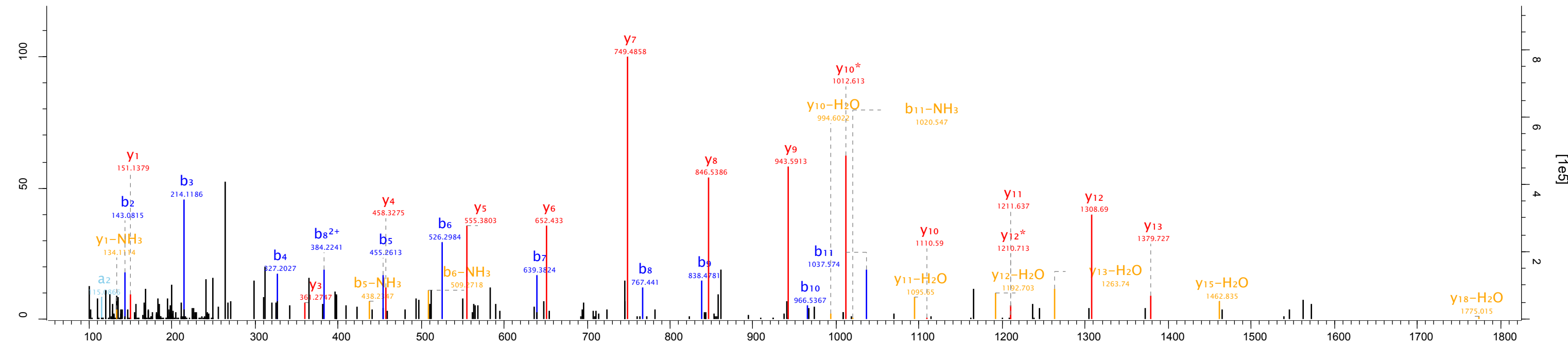


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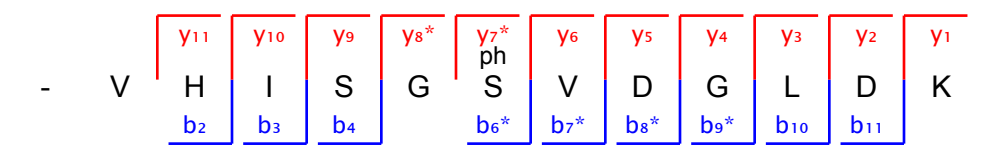
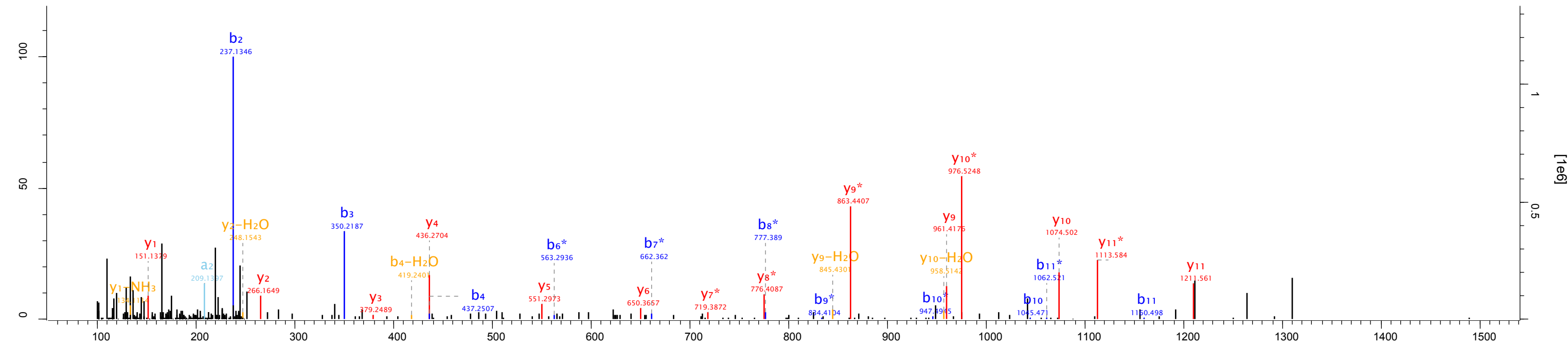


Raw file
20150812_A375SR_Phospho_BR1_07

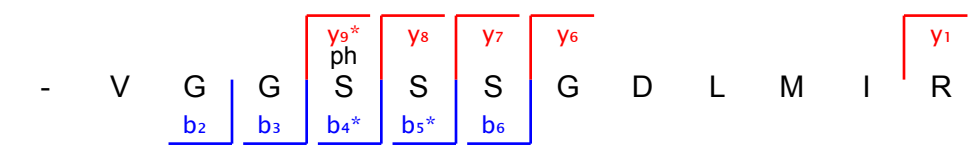
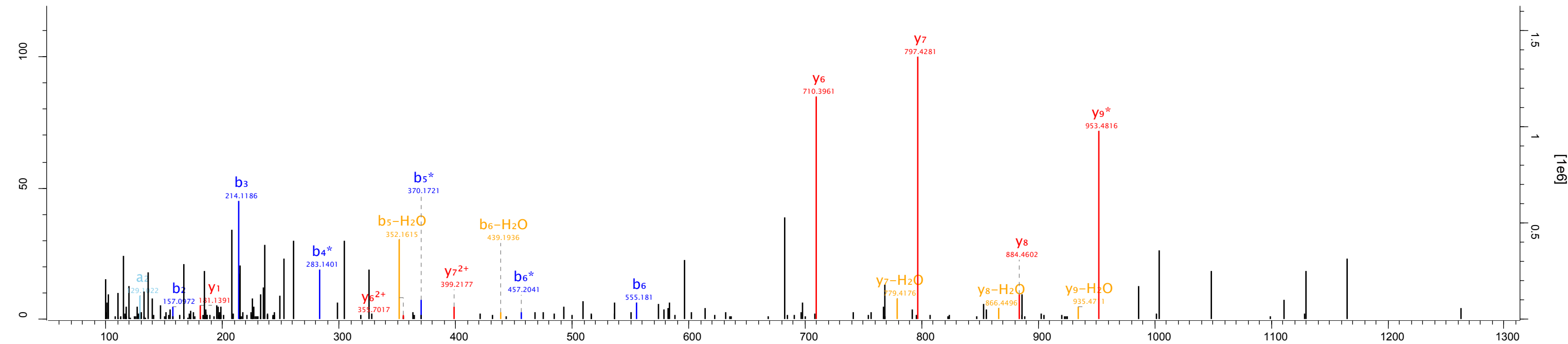
Scan 21625 Method FTMS; HCD Score 88.57 m/z 782.76 Gene names ZNF579



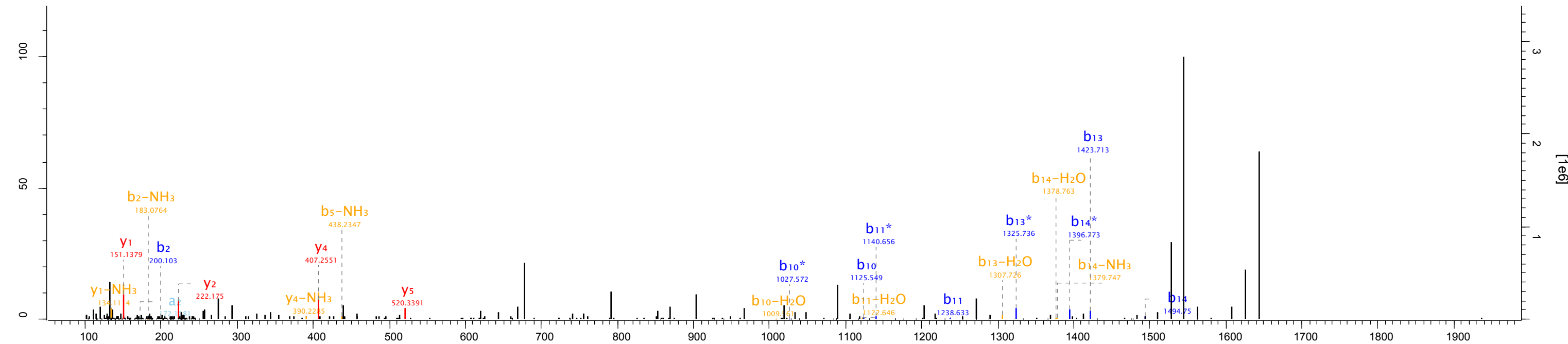
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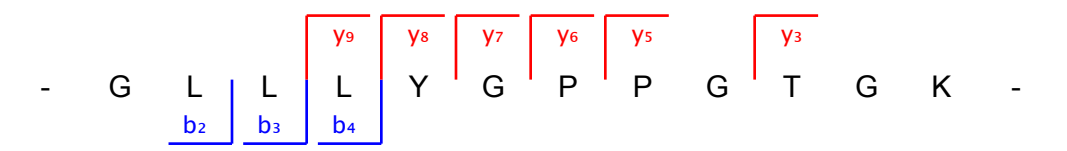
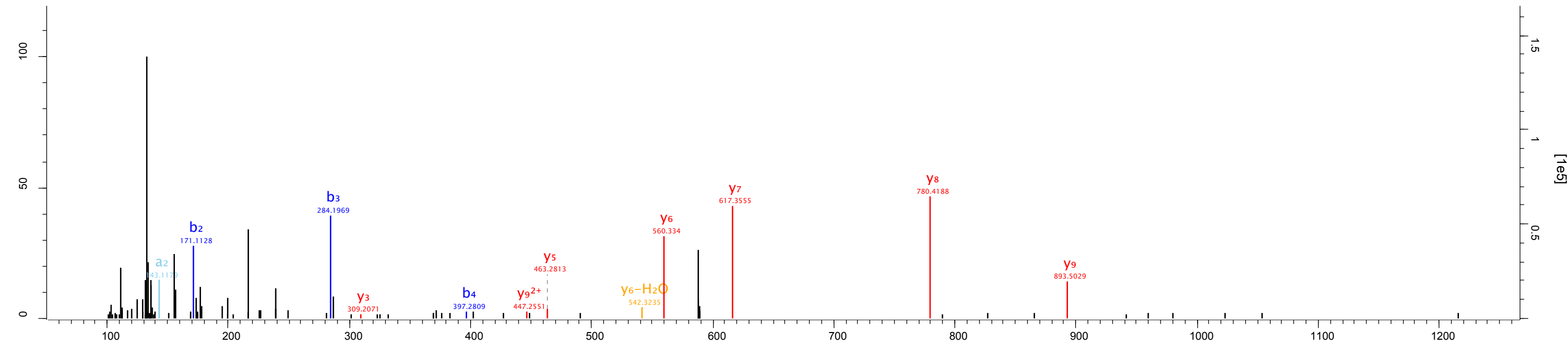
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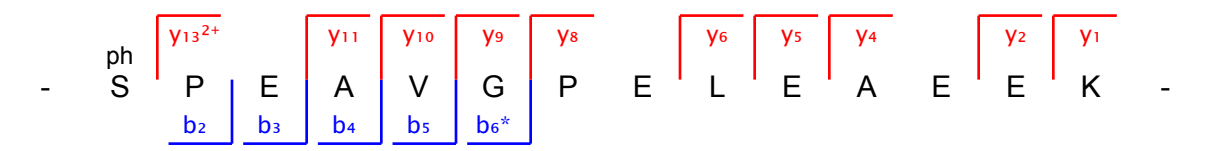
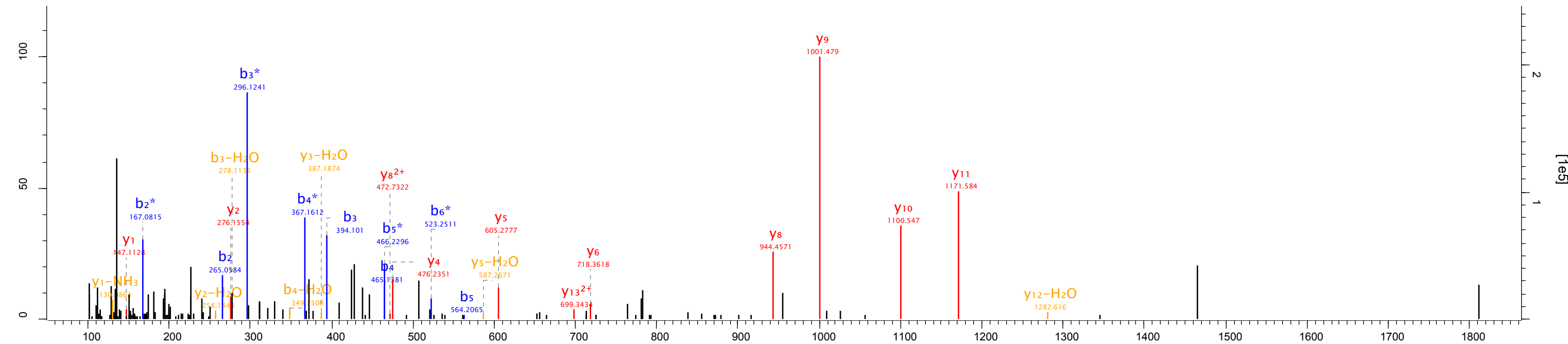
Raw file 20150812_A375SR_Phospho_BR1_10 Scan 20295 Method FTMS; HCD Score 45.99 m/z 823.45



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 Scan: 12895 Method: FTMS; HCD Score: 49.45 m/z: 588.85 Gene names: KATNAL2



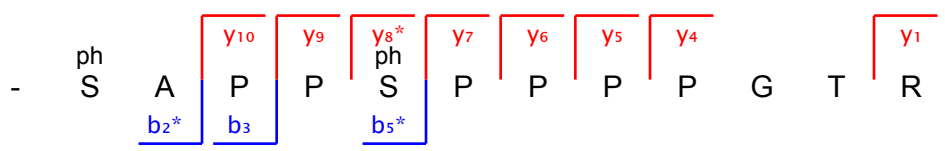
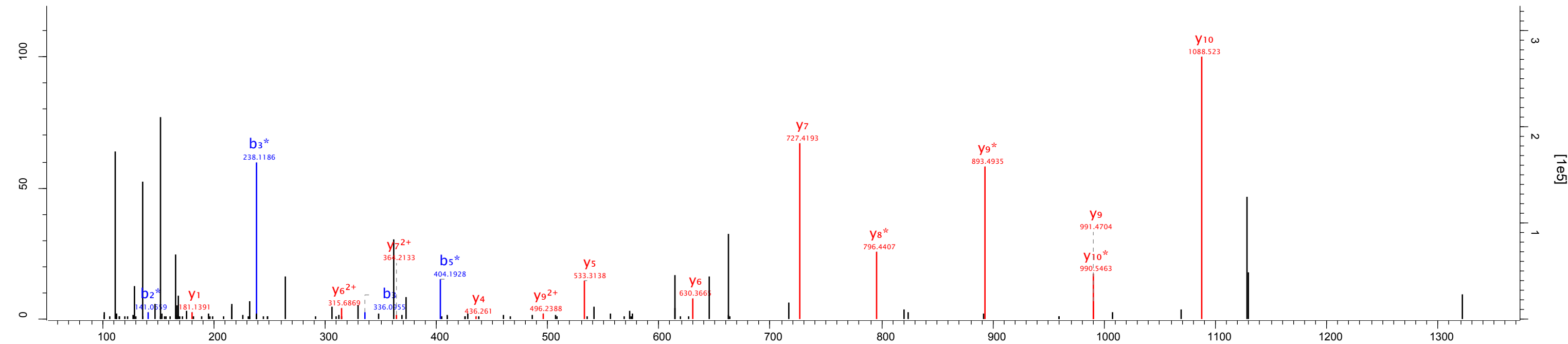
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 Method: FTMS; HCD
 Score: 62.44
 m/z: 782.84
 Gene names: PWWP2A



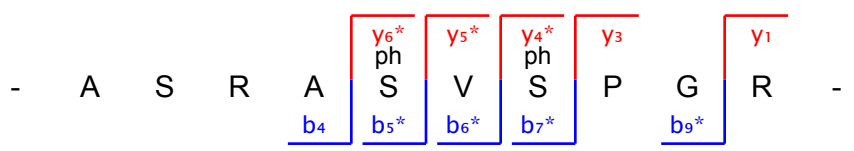
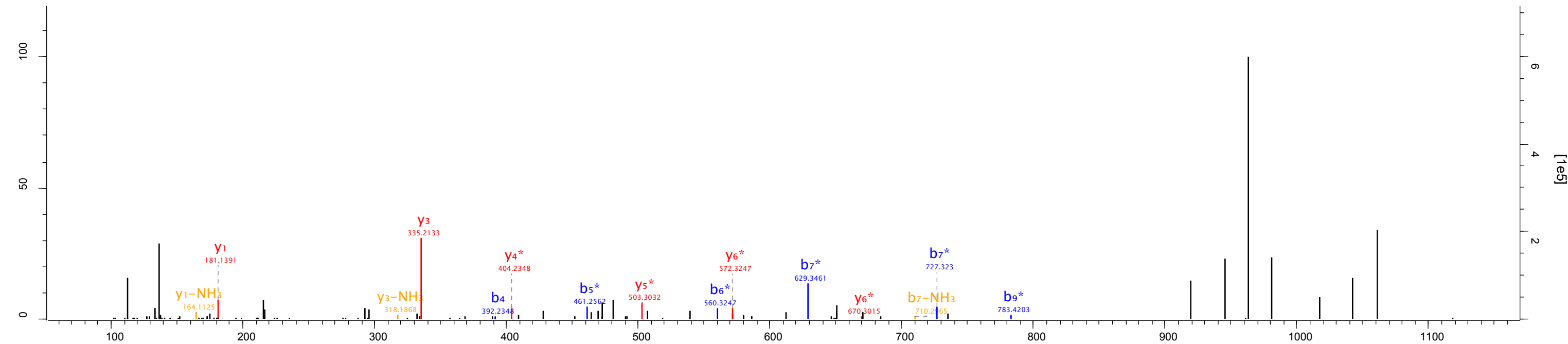
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20150814_A375SR_Phospho_BR2_02

Scan	Method	Score	m/z	Gene names
6165	FTMS; HCD	48.91	663.78	GPSM3



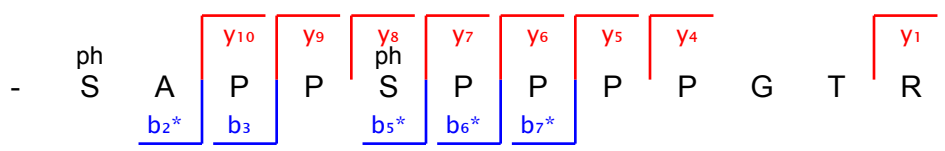
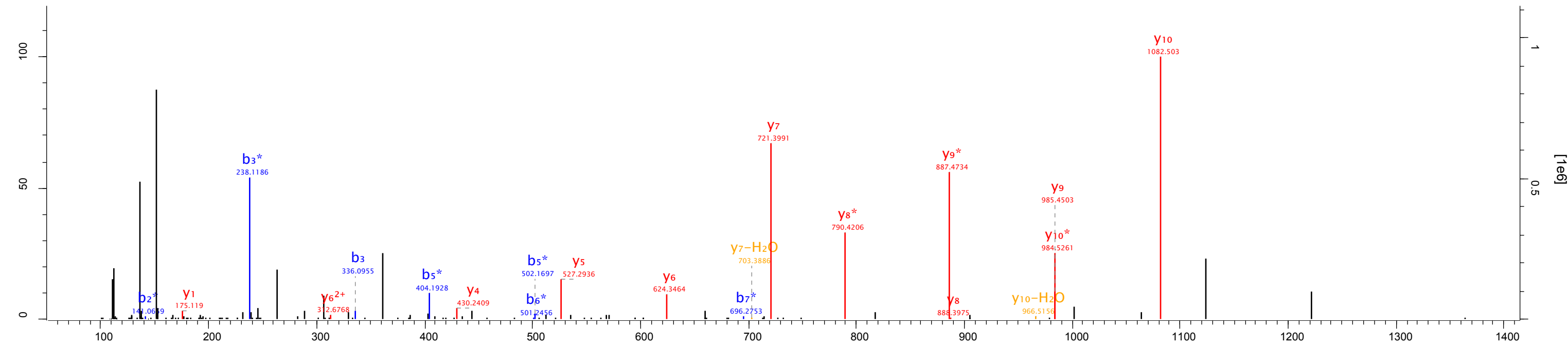
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 Scan: 6325 Method: FTMS; HCD Score: 51.64 m/z: 580.26 Gene names: OTOP3



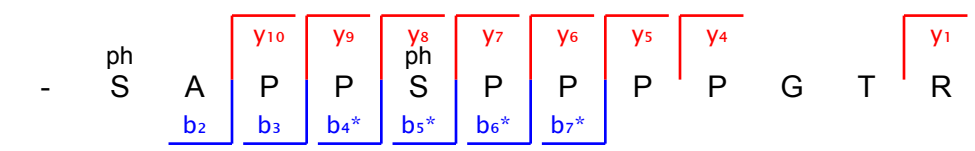
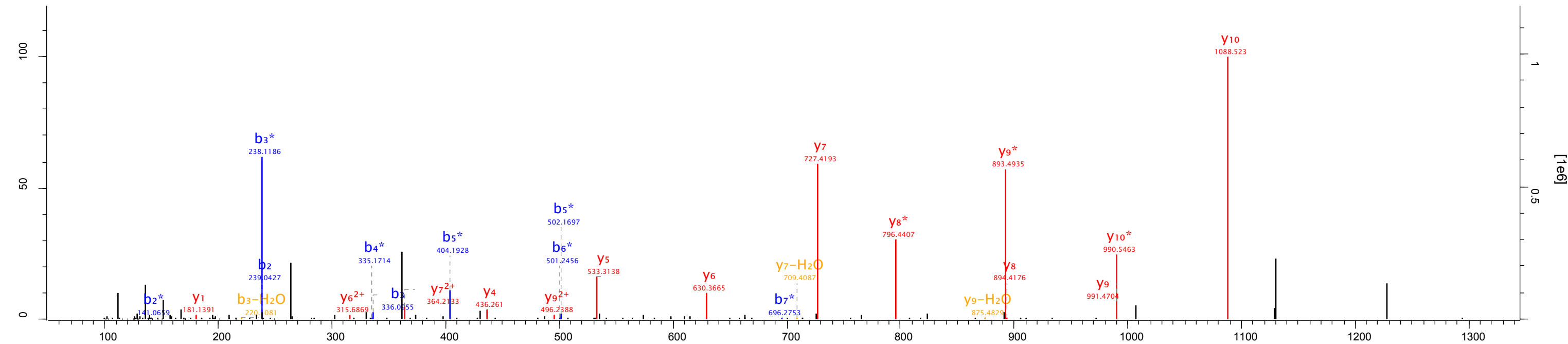
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20150814_A375SR_Phospho_BR2_02

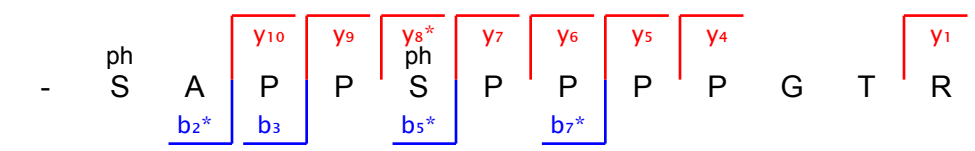
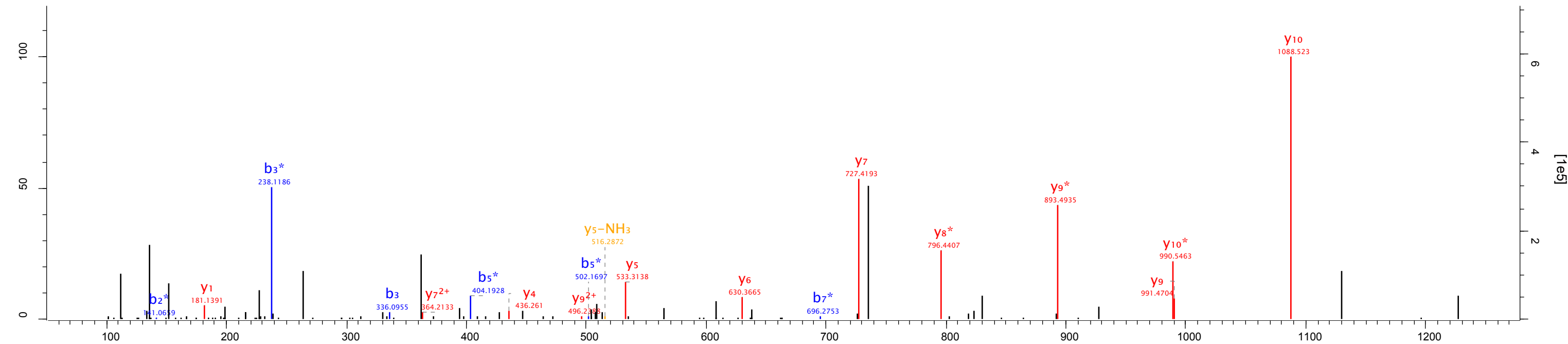
Scan 6335 Method FTMS; HCD Score 62.66 m/z 660.77 Gene names GPSM3



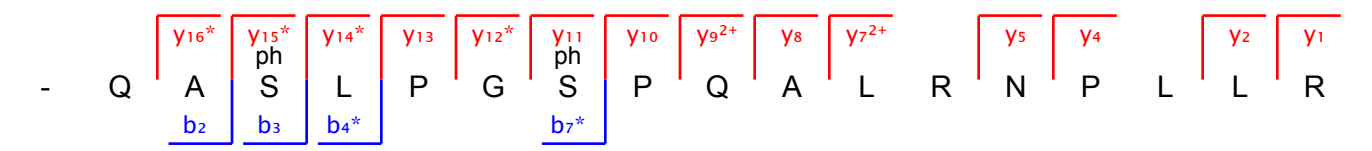
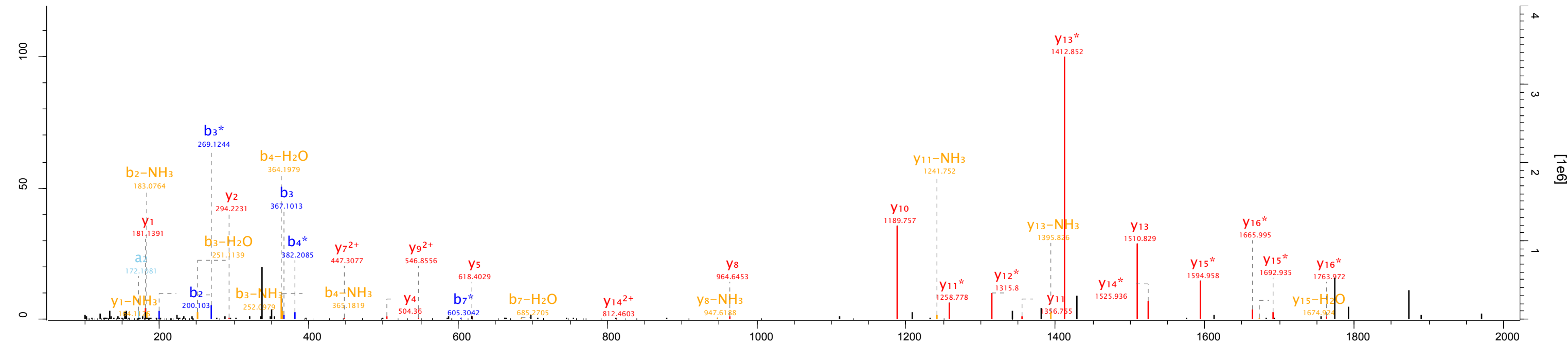
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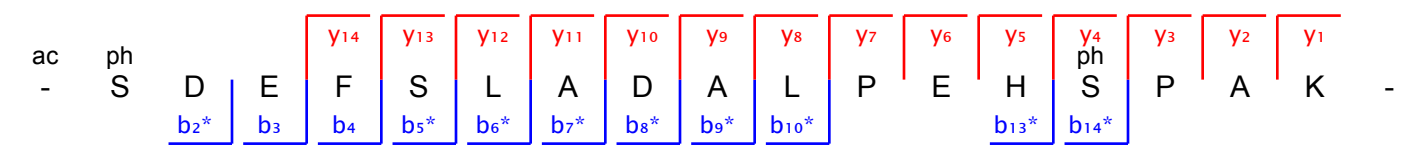
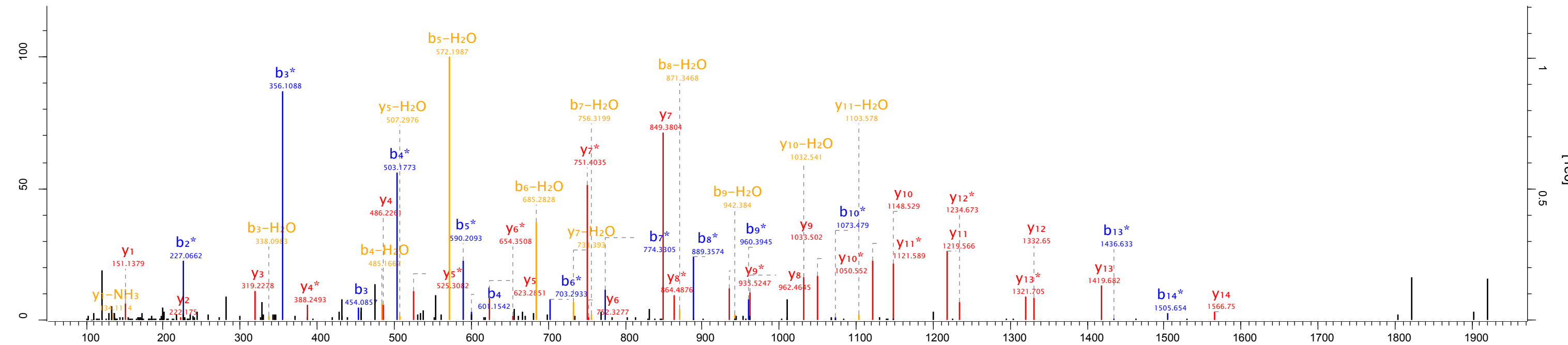
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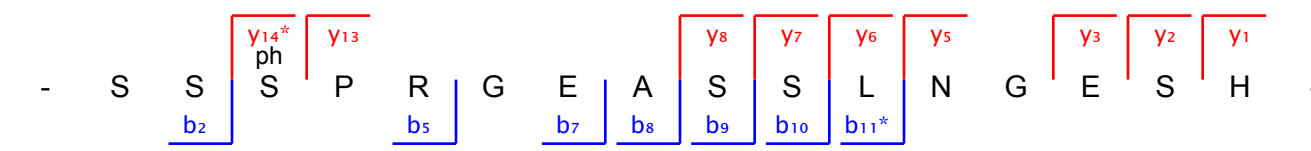
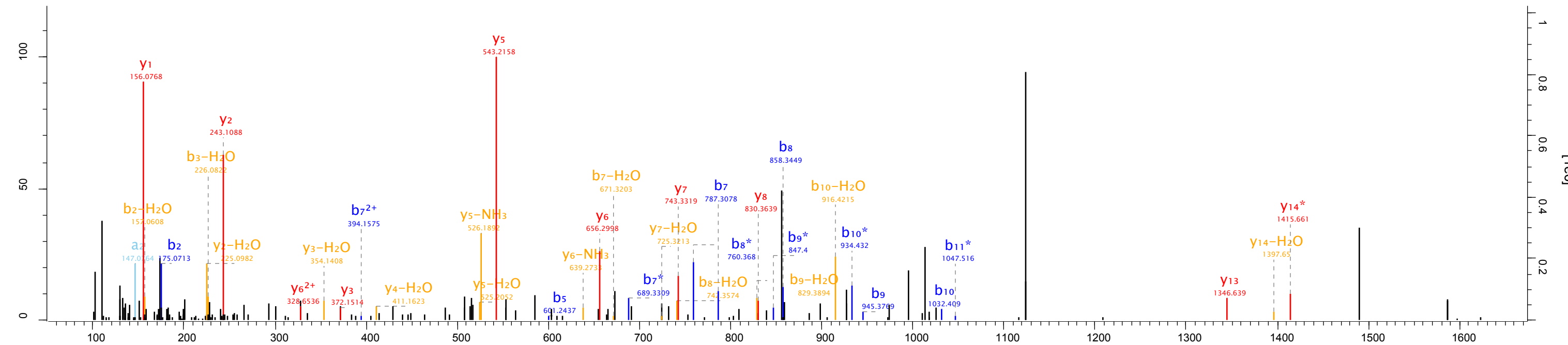
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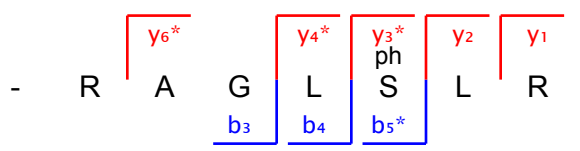
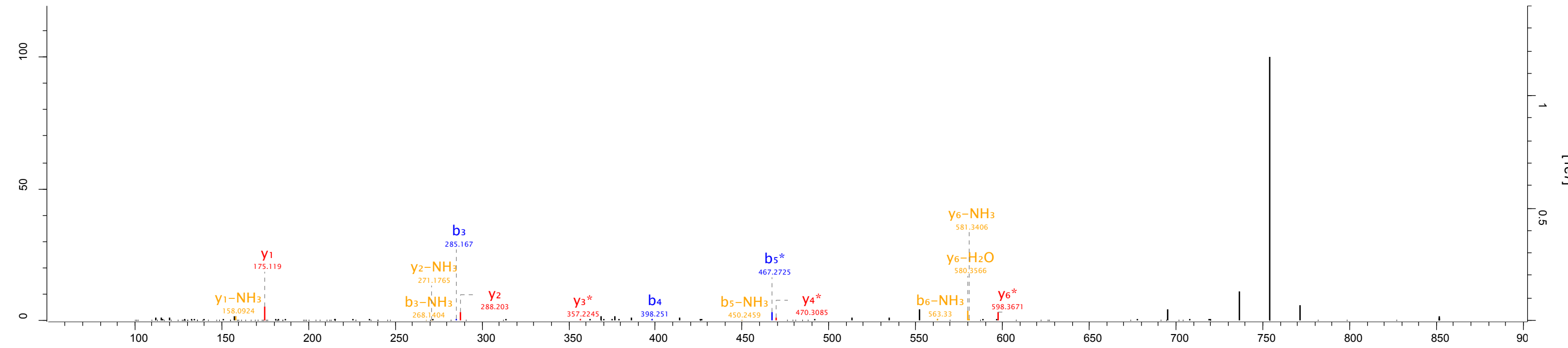
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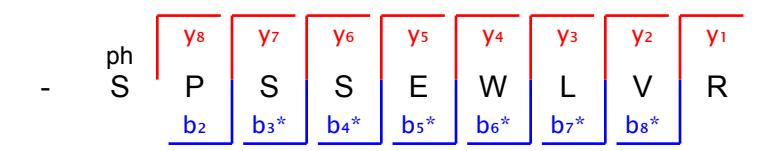
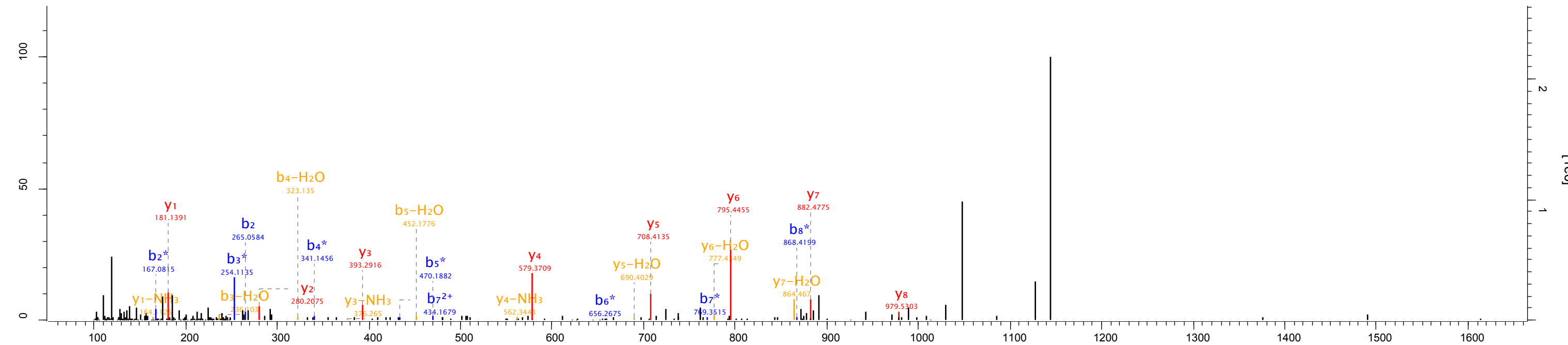
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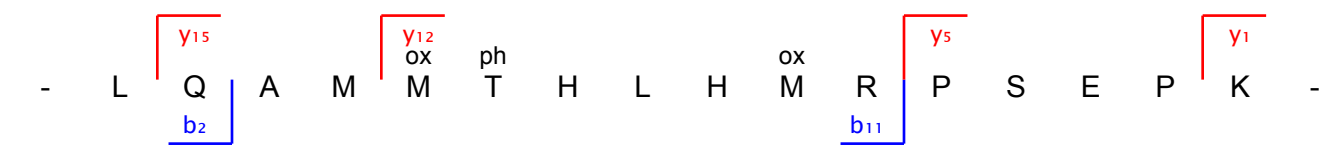
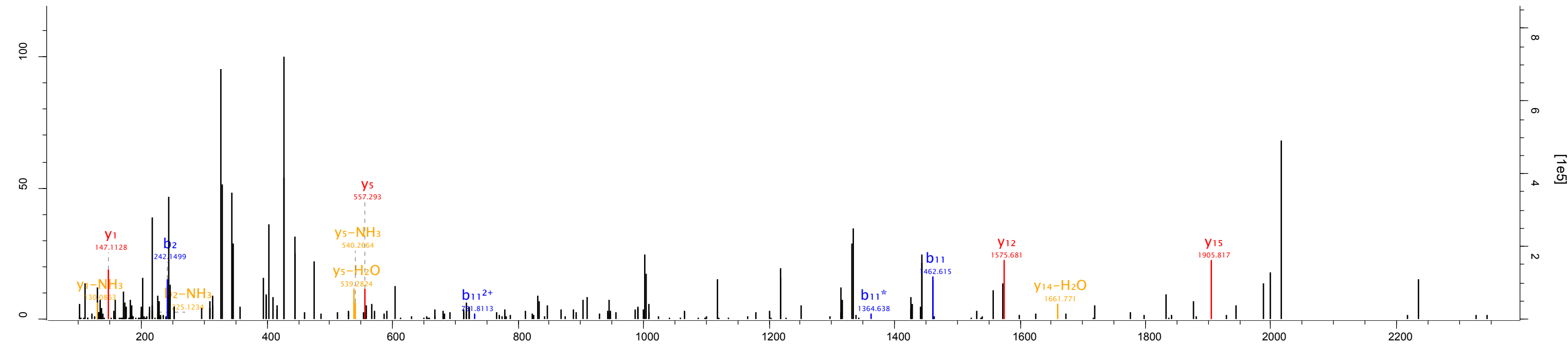
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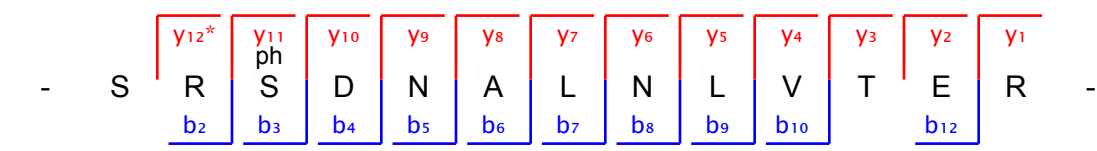
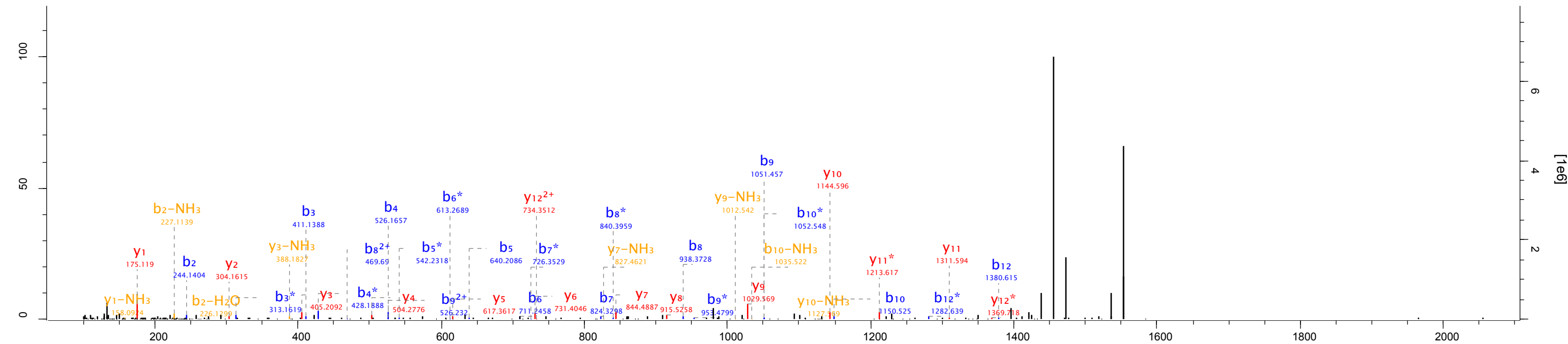
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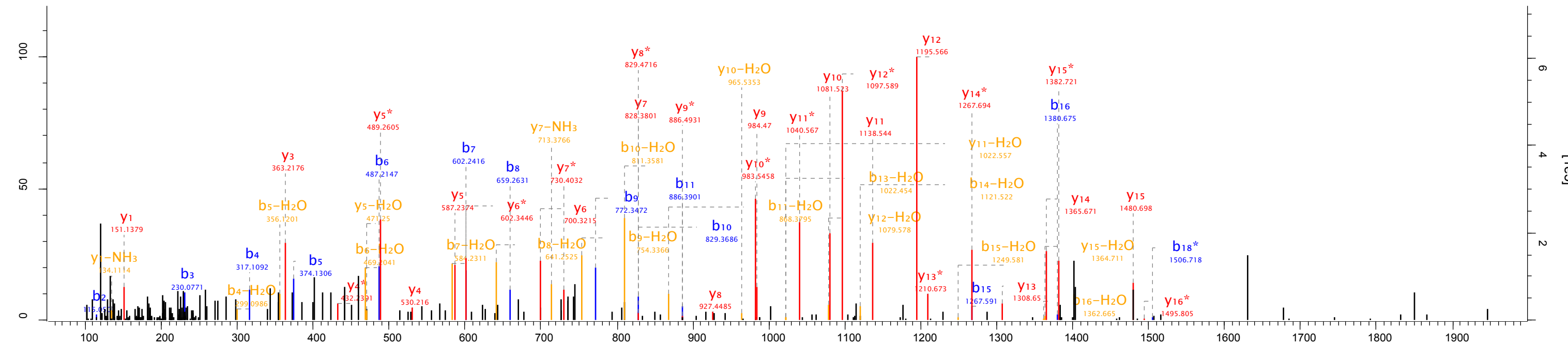


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Raw file Scan Method Score m/z Gene names
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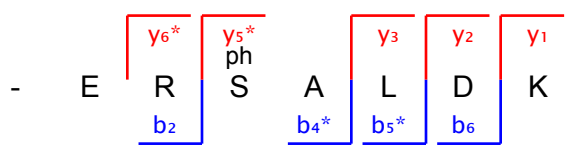
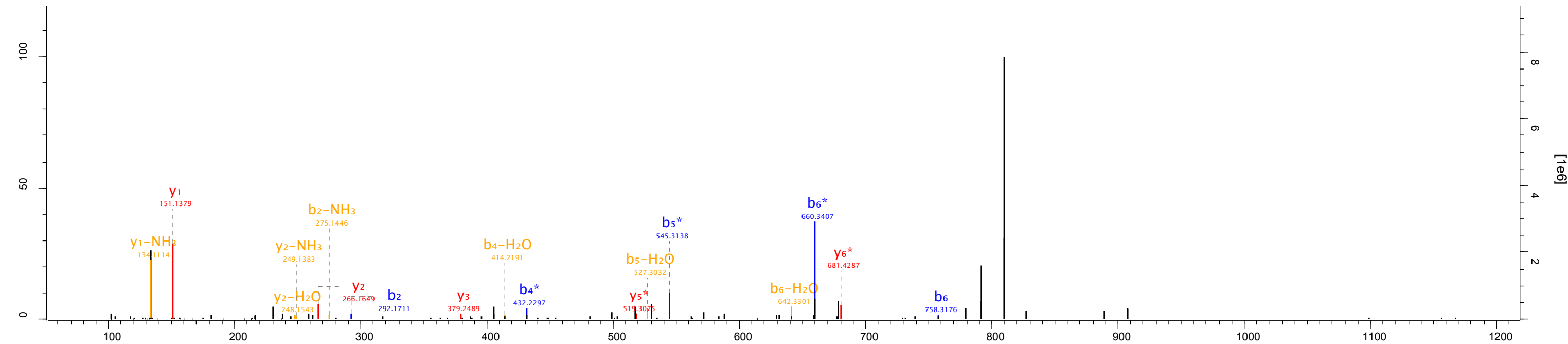




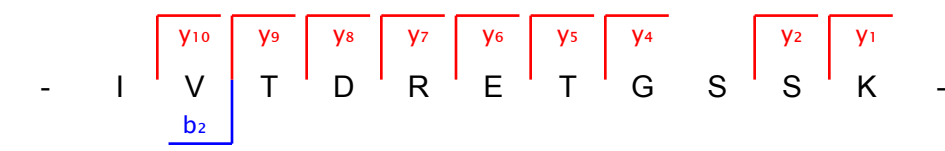
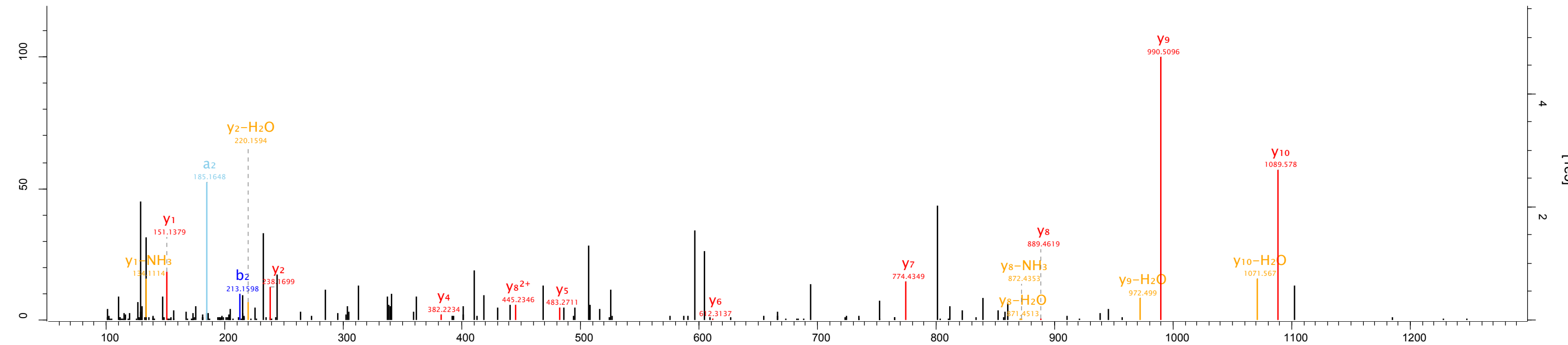
- G G D S G L D G L G G P G V Q L G S P D K -

b₂
b₃
b₄
b₅
y₁₆*
y₁₅
y₁₄
y₁₃
y₁₂
y₁₁
y₁₀
y₉
y₈
y₇
y₆
y₅
y₄
y₃
b₁₅
b₁₆
b₁₈*

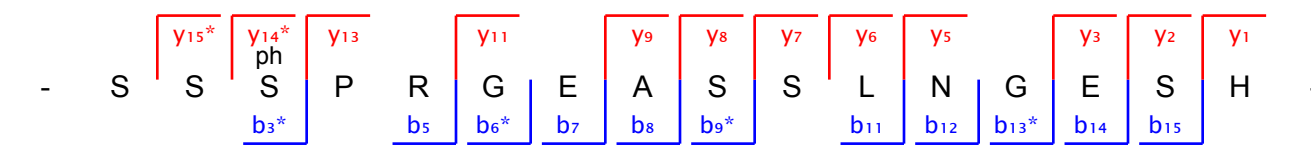
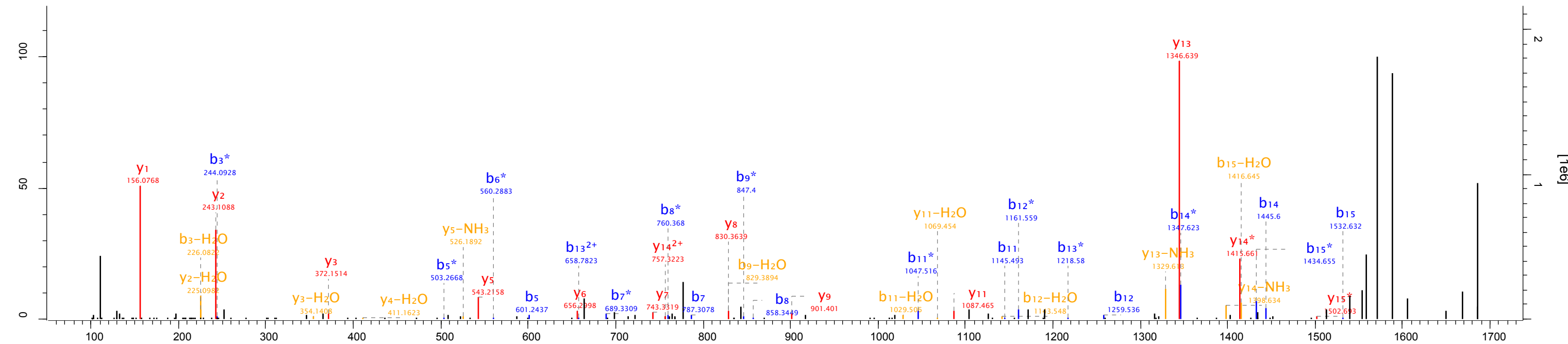
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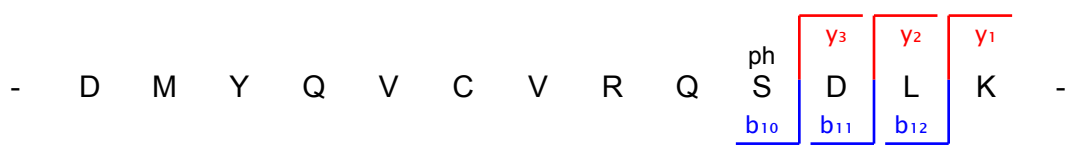
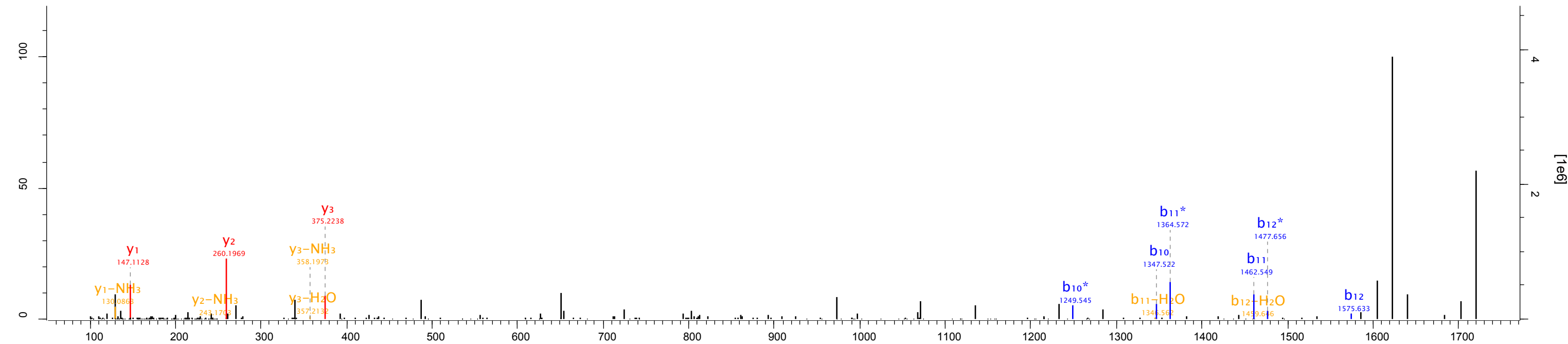
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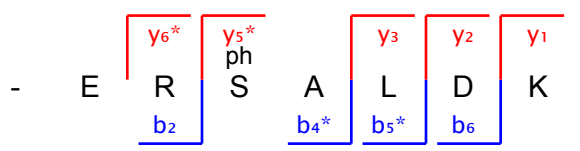
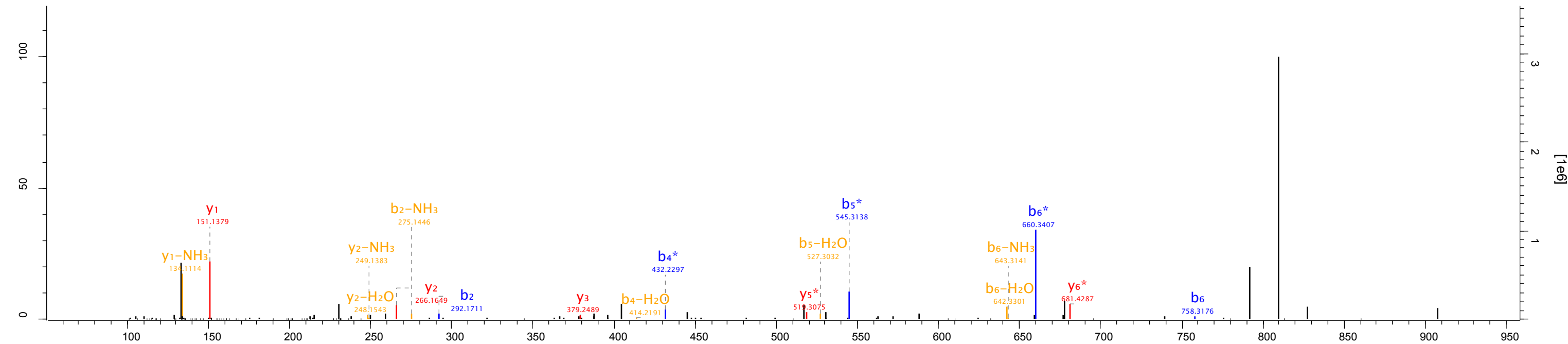
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 Scan: 6015 Method: FTMS; HCD Score: 159.22 m/z: 844.36 Gene names: YAF2



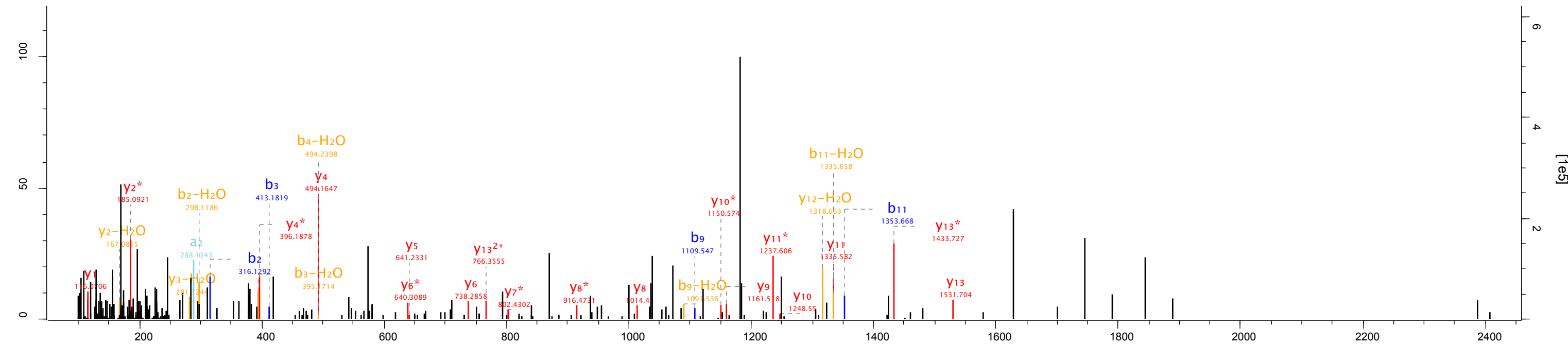
Raw file 20150814_A375SR_Phospho_BR2_06 Scan 17685 Method FTMS; HCD Score 40.19 m/z 861.87



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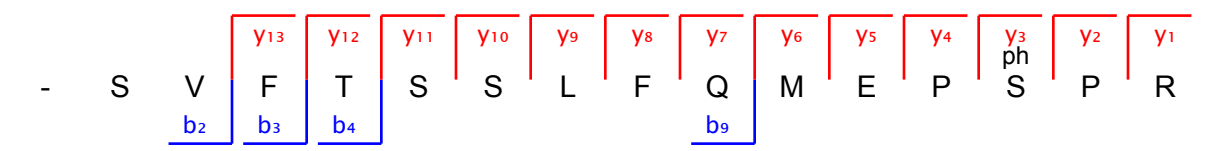
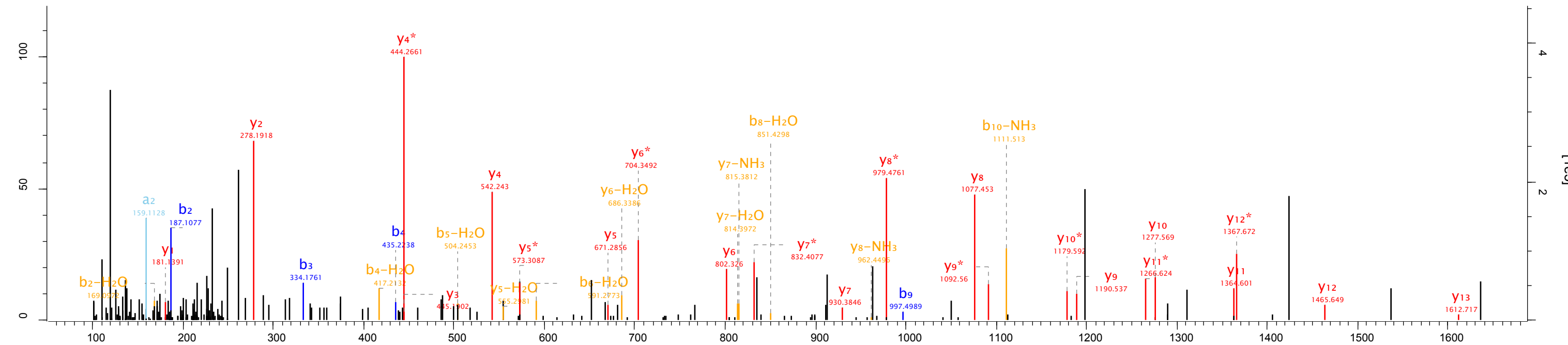


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 Scan: 24955 Method: FTMS; HCD Score: 72.59 m/z: 923.91 Gene names: MSANTD3

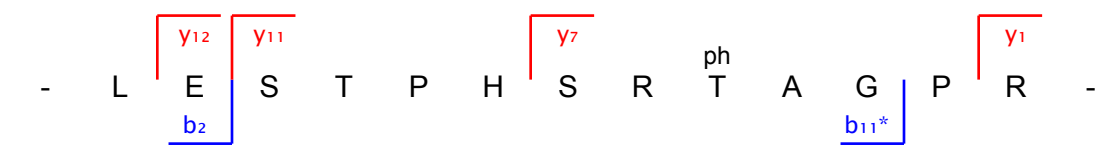
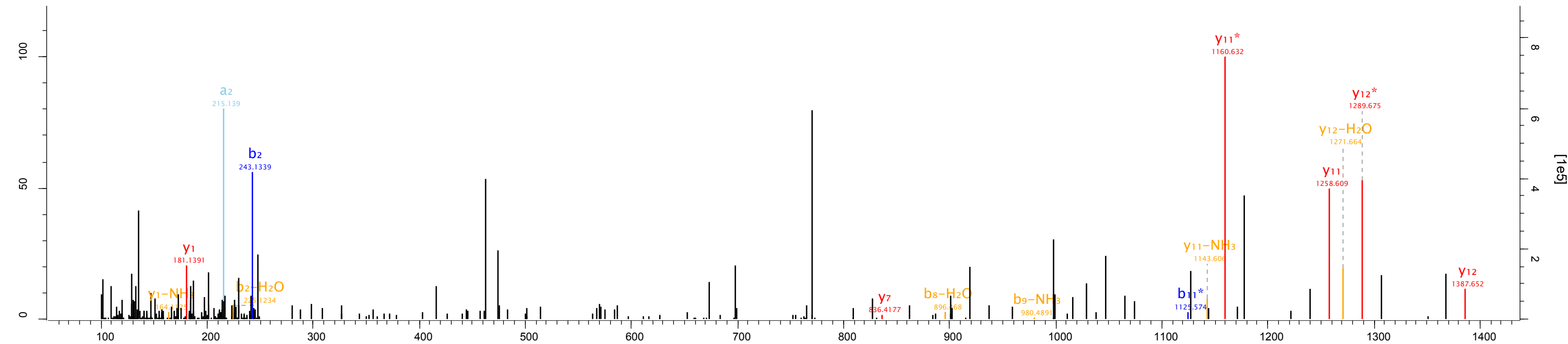


- E W P V S S F N R P F P N S P -
 b₂ b₃ b₉ b₁₁ y₁₃ y₁₁ y₁₀ y₉ y₈ y₇* y₆ y₅ y₄ y₂* y_{ph} y₁

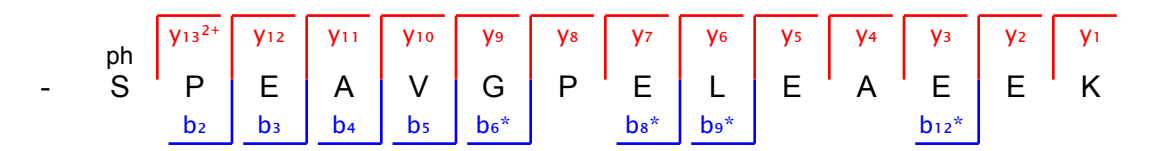
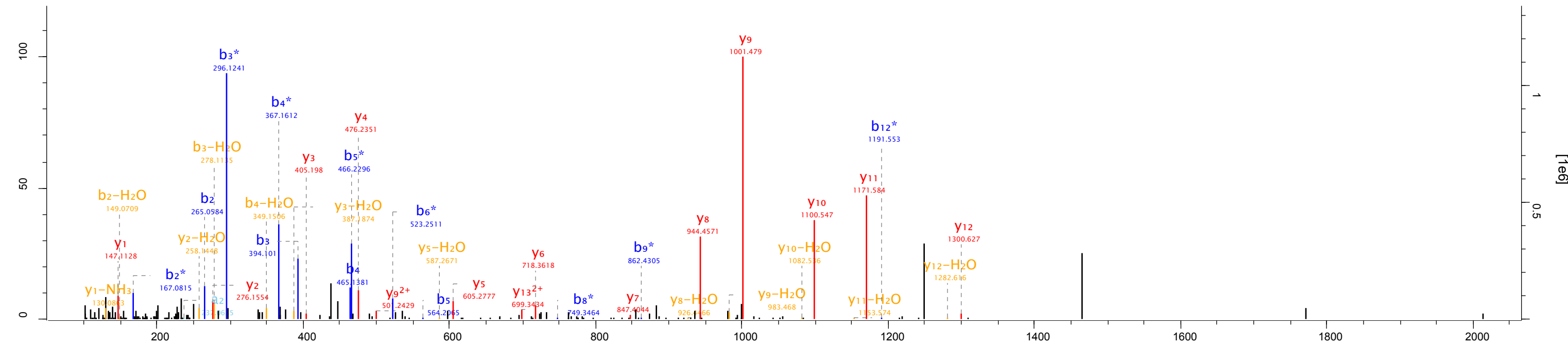
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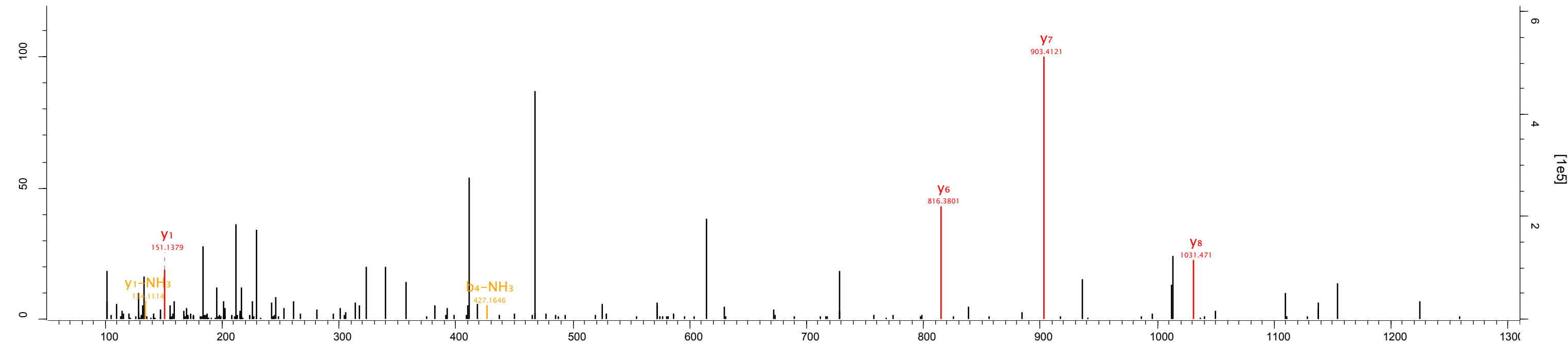
Raw file 20150814_A375SR_Phospho_BR2_06 Scan 8865 Method FTMS; HCD Score 41.54 m/z 500.92



Raw file 20150814_A375SR_Phospho_BR2_07 Scan 13385 Method FTMS; HCD Score 135.69 m/z 782.84 Gene names PWWP2A



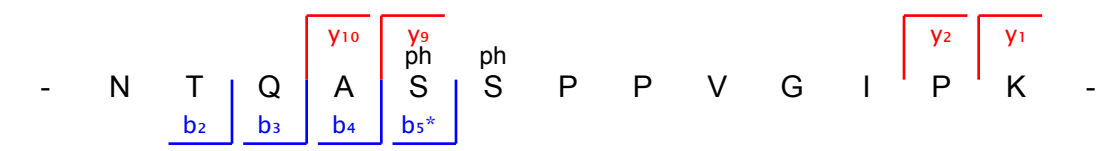
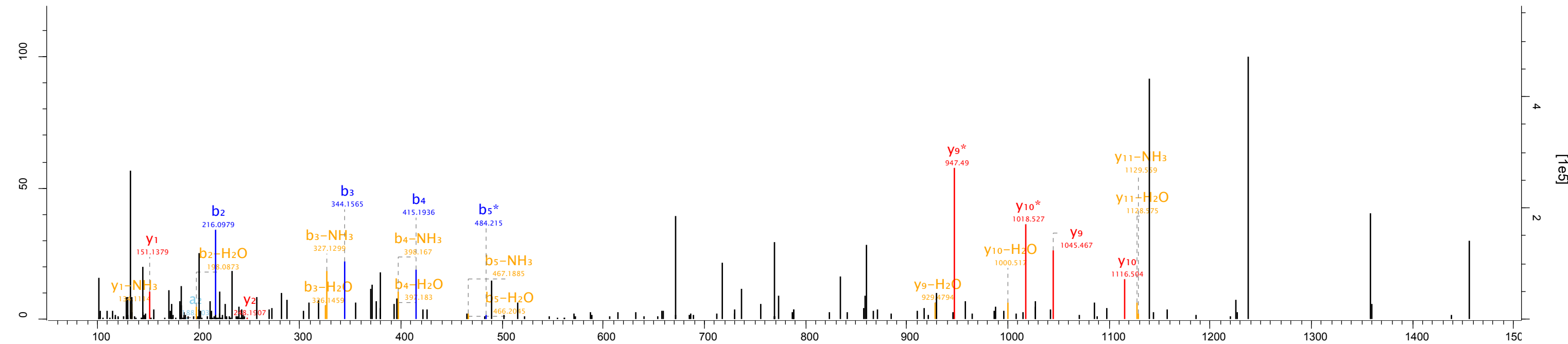
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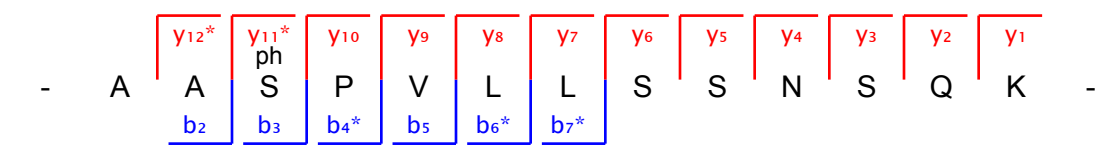
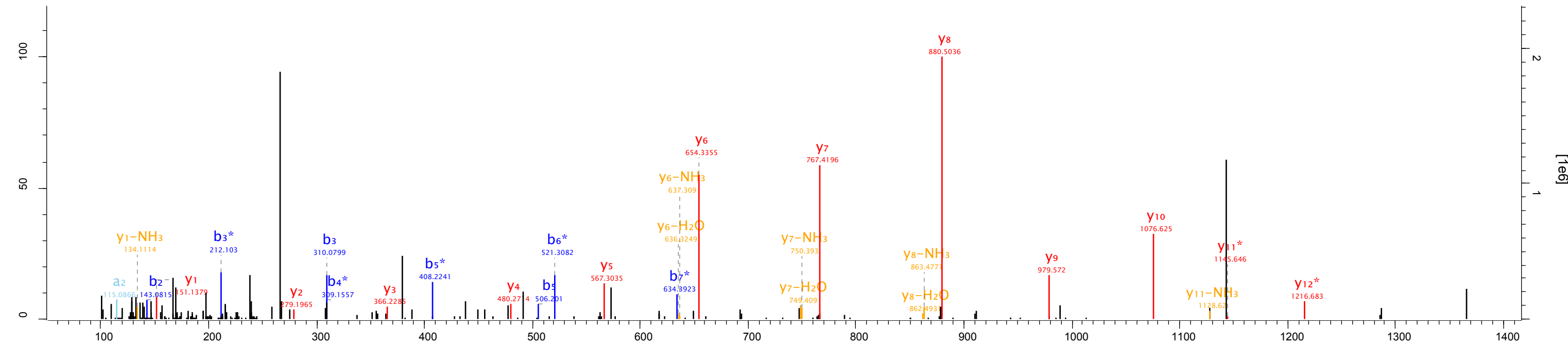
- P M Q S Q L E S Q K -

Annotations above the sequence: y₈ above Q, y₇ above S, y₆ above Q, and y₁ above K.

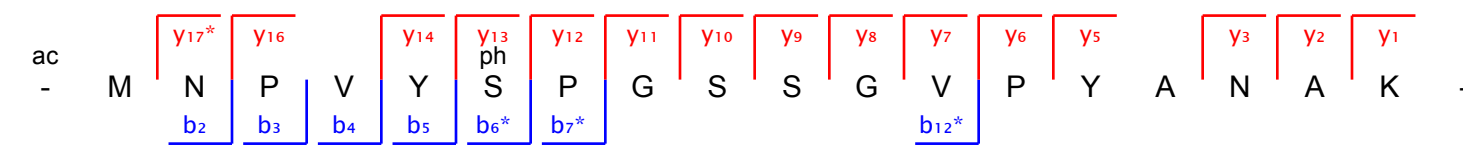
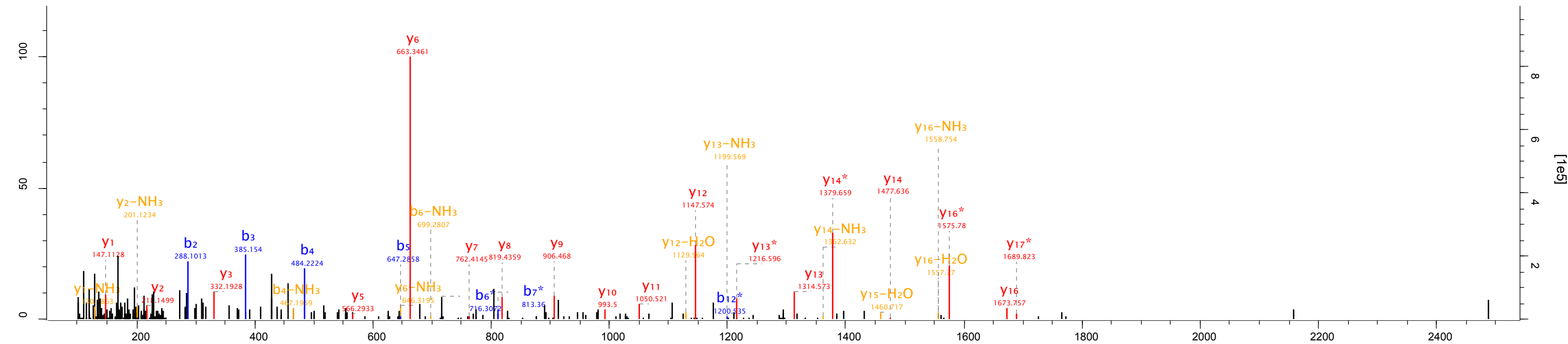
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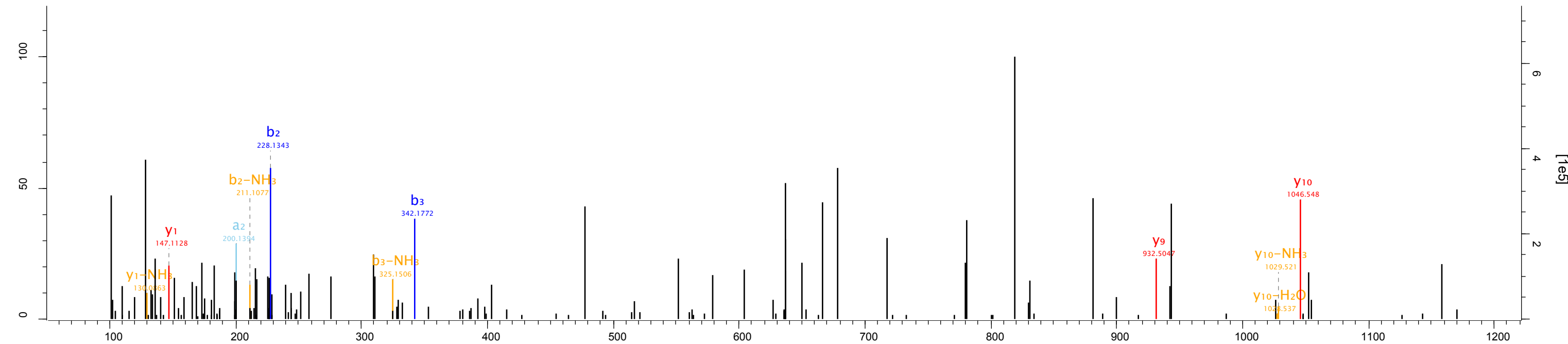
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 Scan: 11405 Method: FTMS; HCD Score: 98.51 m/z: 693.35 Gene names: ELK3



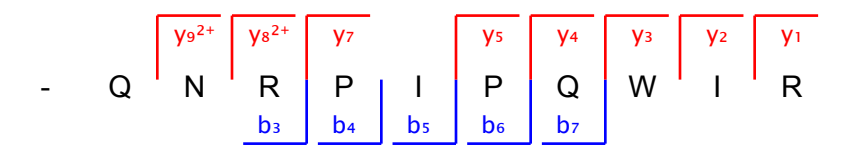
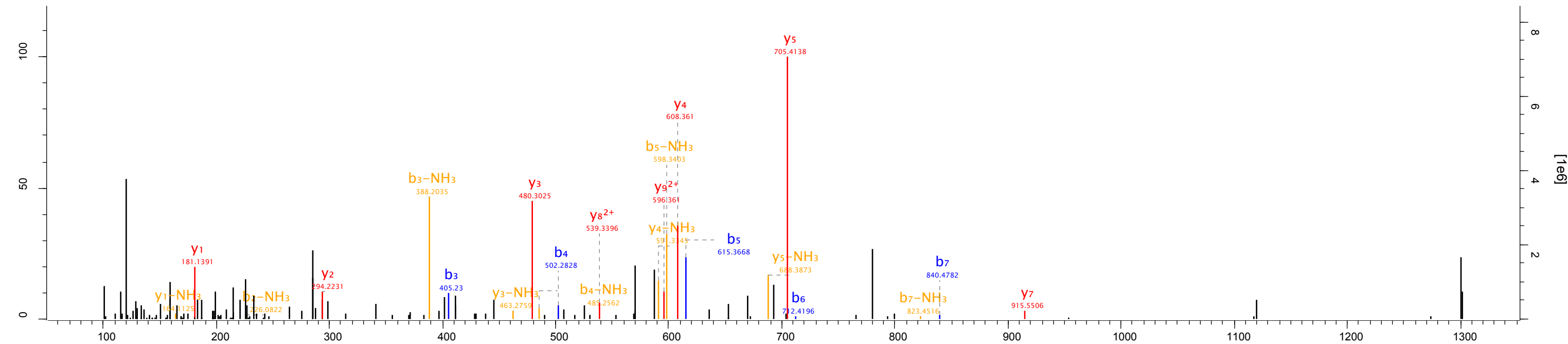
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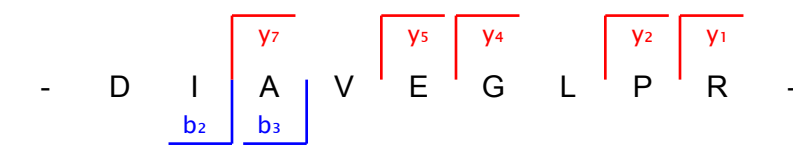
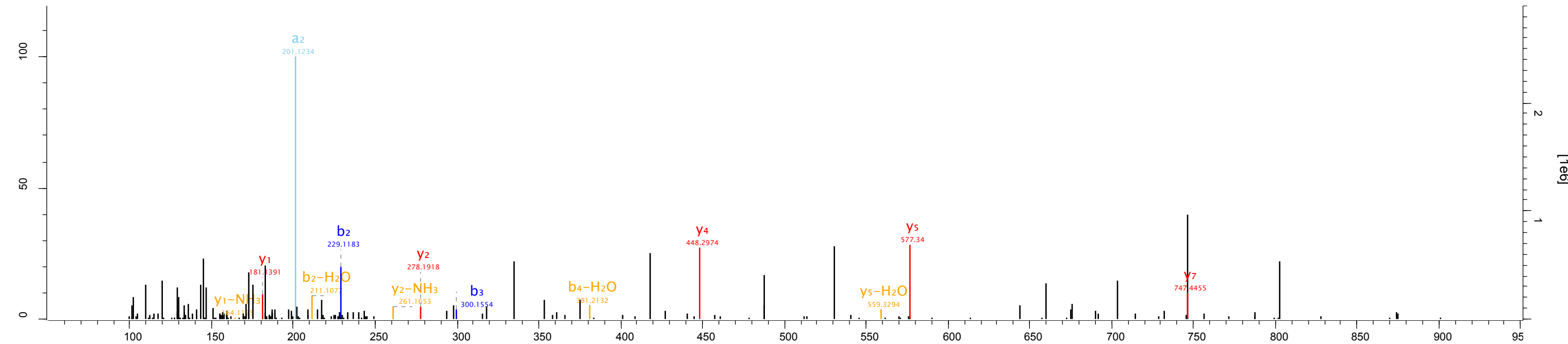
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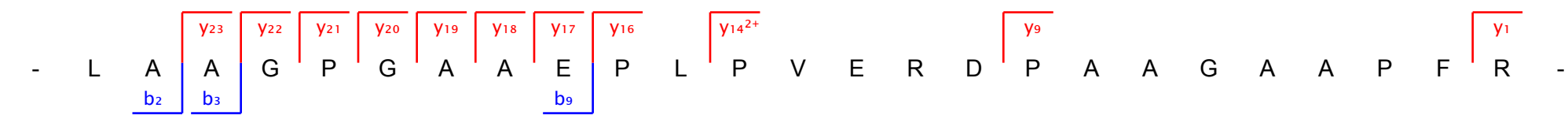
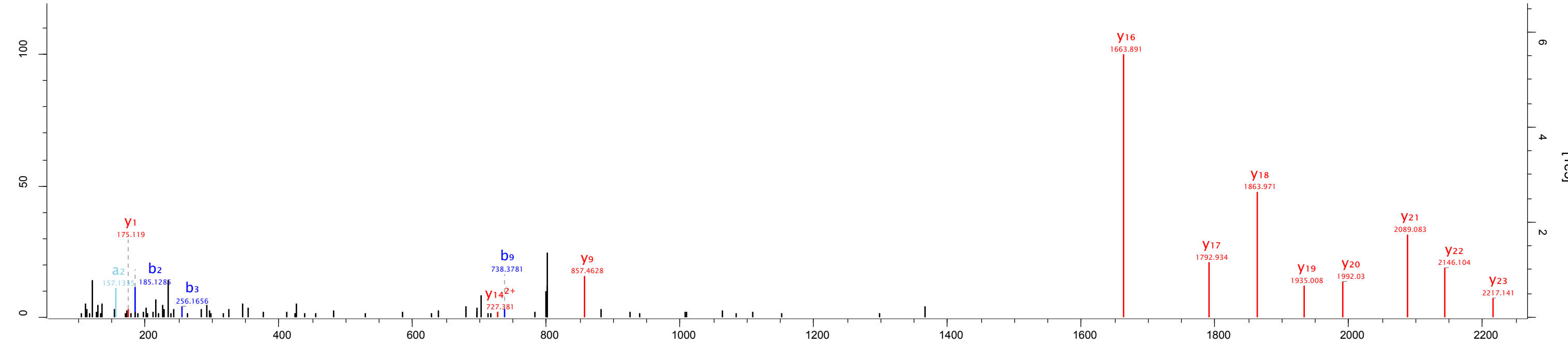
Raw file 20150818_A375SR-Proteome_BR2 Scan 37155 Method FTMS; HCD Score 39.01 m/z 488.28



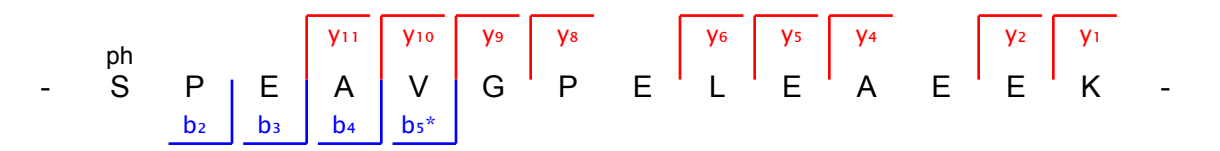
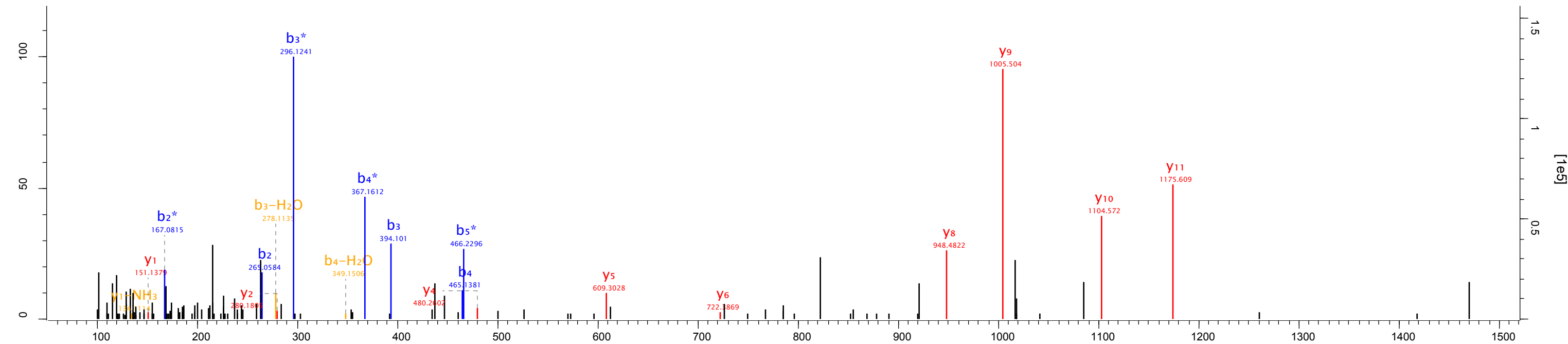
Raw file

20150818_A375SR-Proteome_BR2

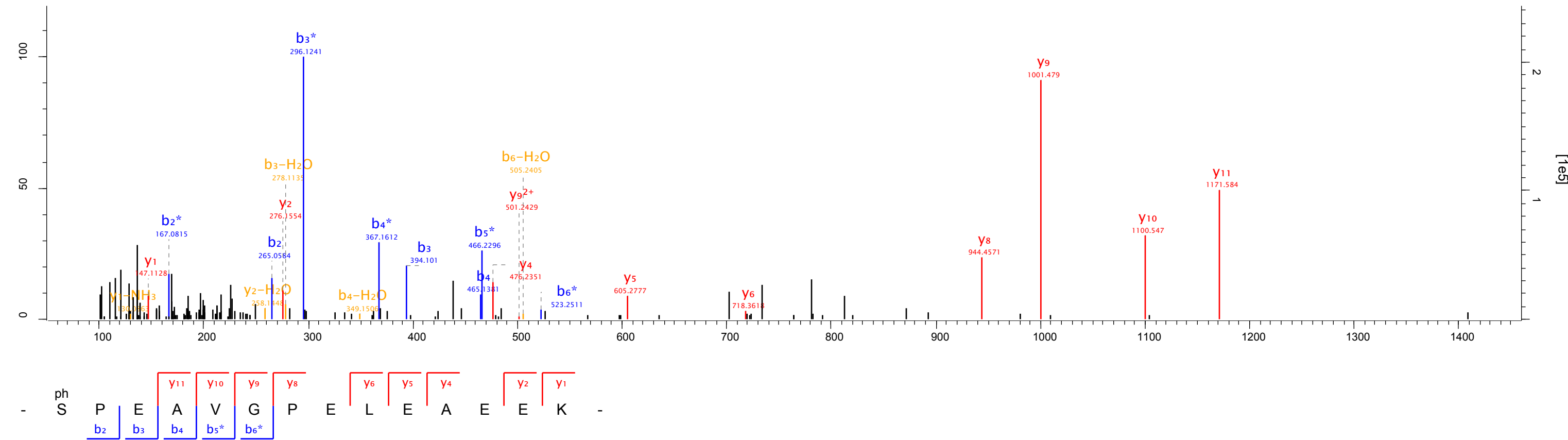
Scan	Method	Score	m/z	Gene names
63525	FTMS; HCD	29.86	801.43	ZNF511



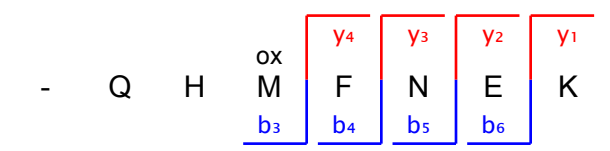
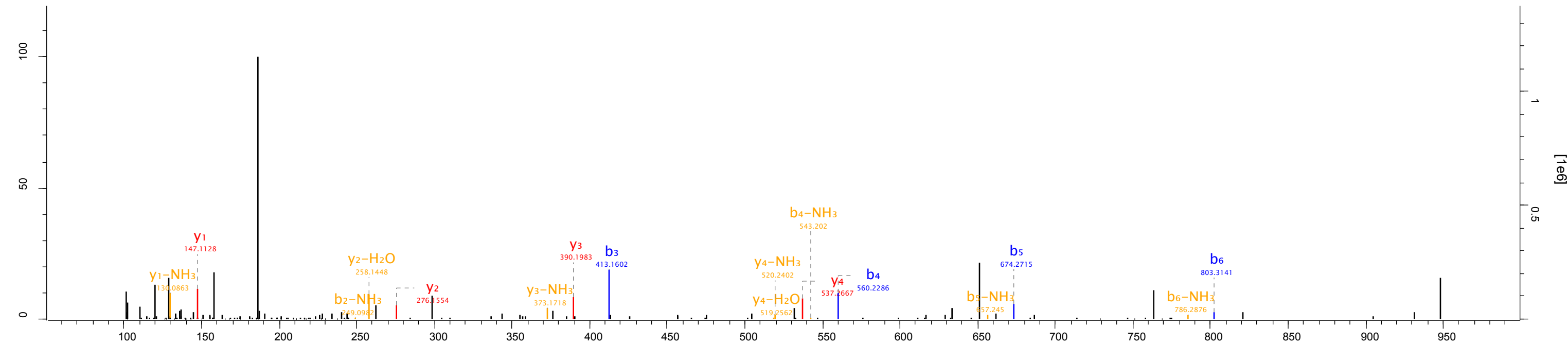
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 Scan: 12785 Method: FTMS; HCD Score: 62.94 m/z: 785.36 Gene names: PWWP2A



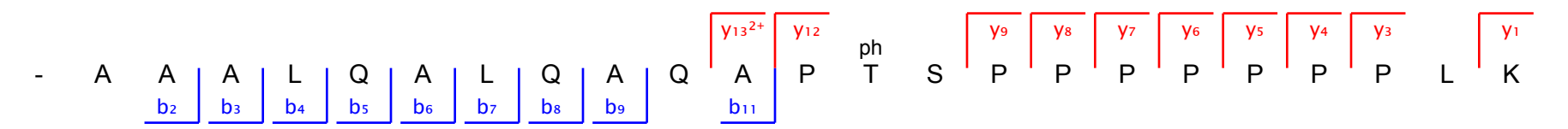
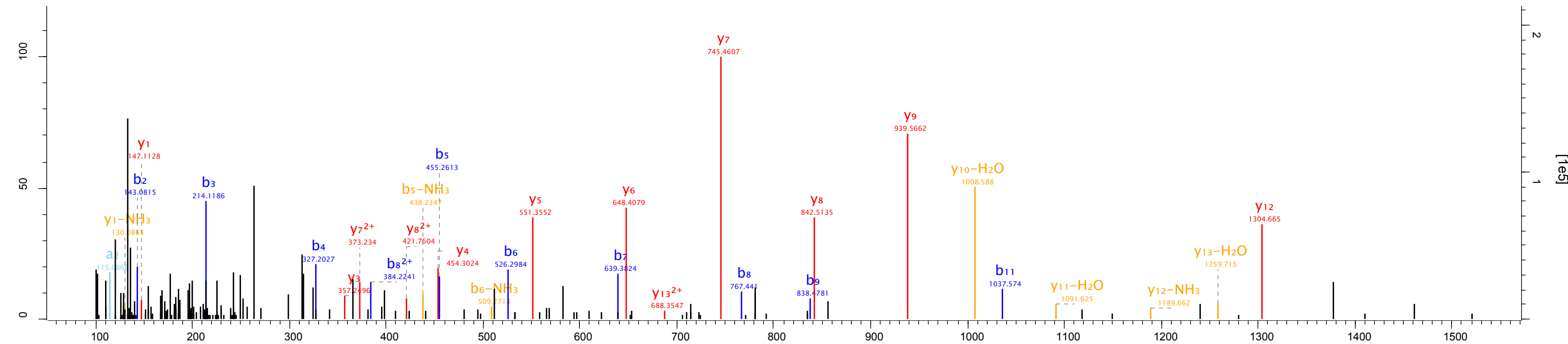
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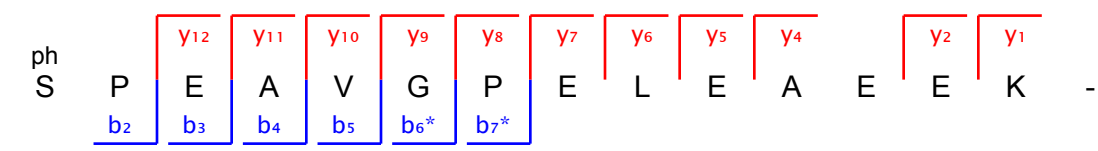
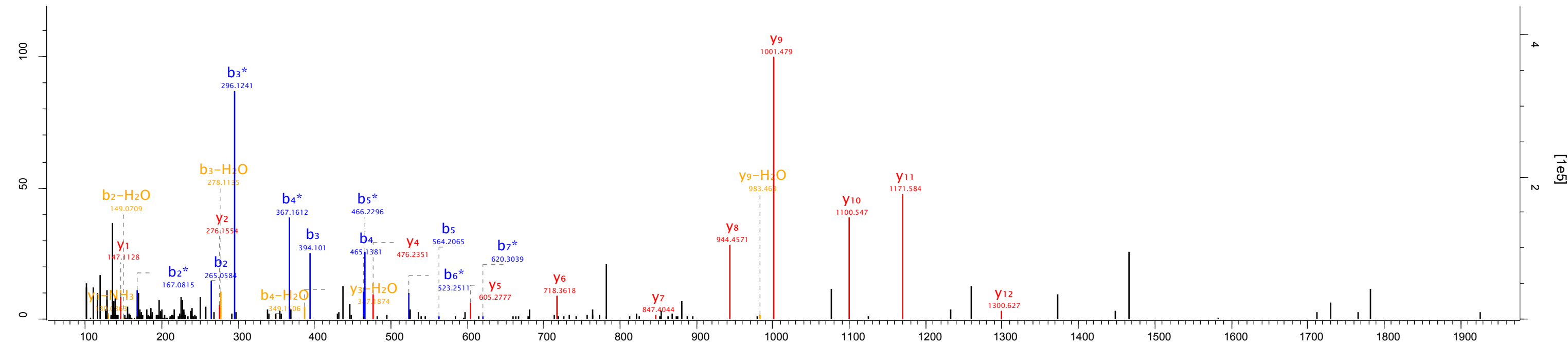
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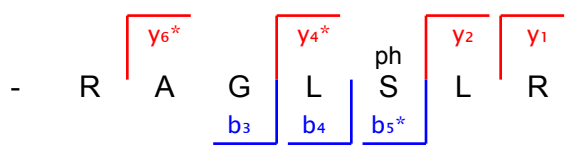
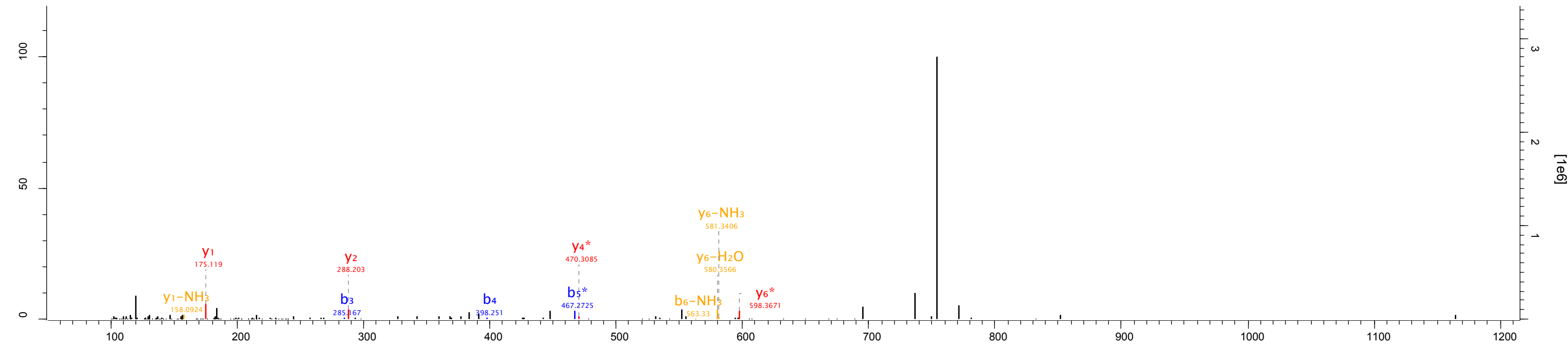
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 Scan: 21465 Method: FTMS; HCD Score: 75.21 m/z: 781.42 Gene names: ZNF579



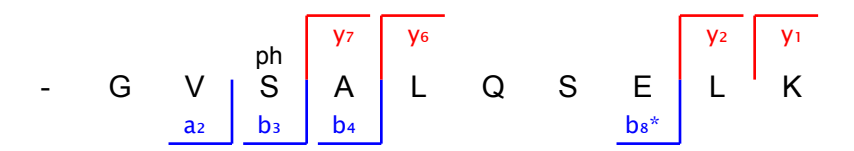
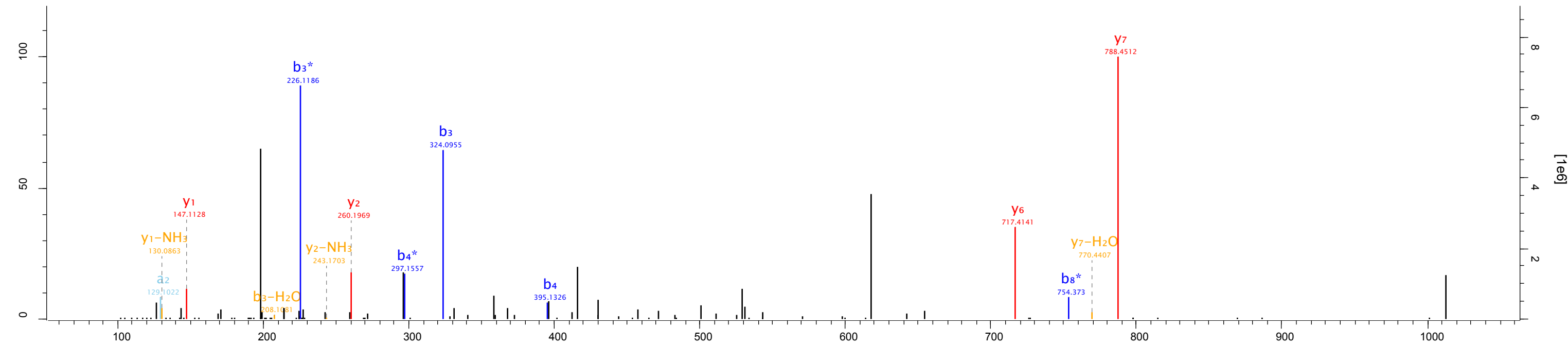
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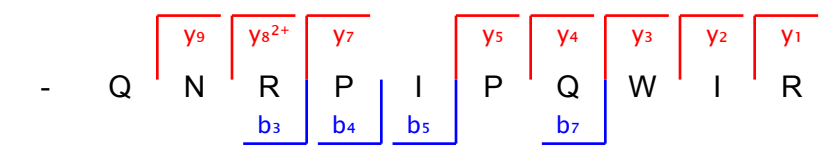
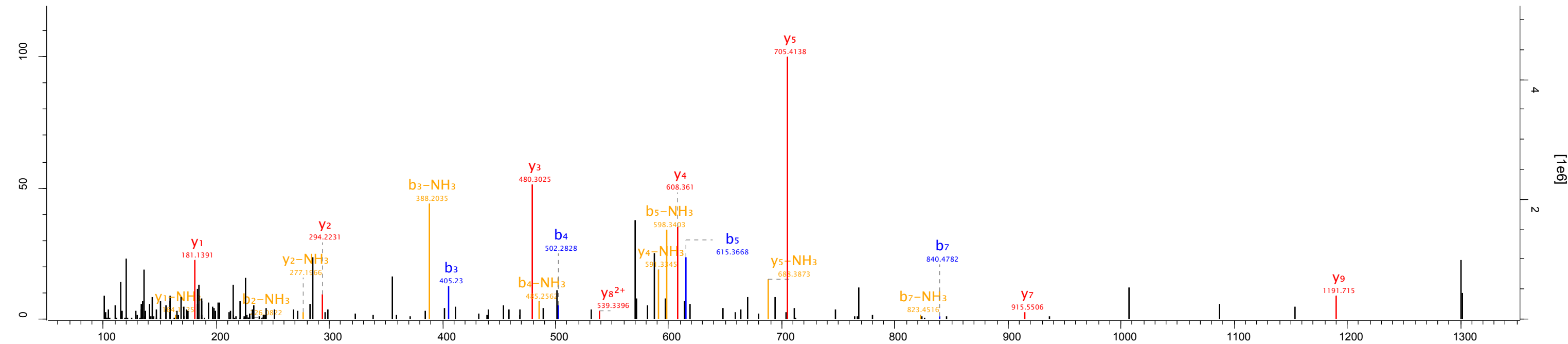
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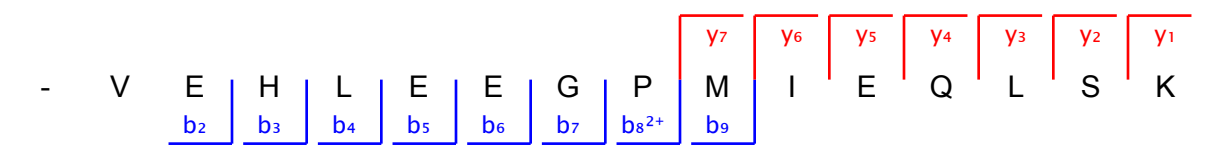
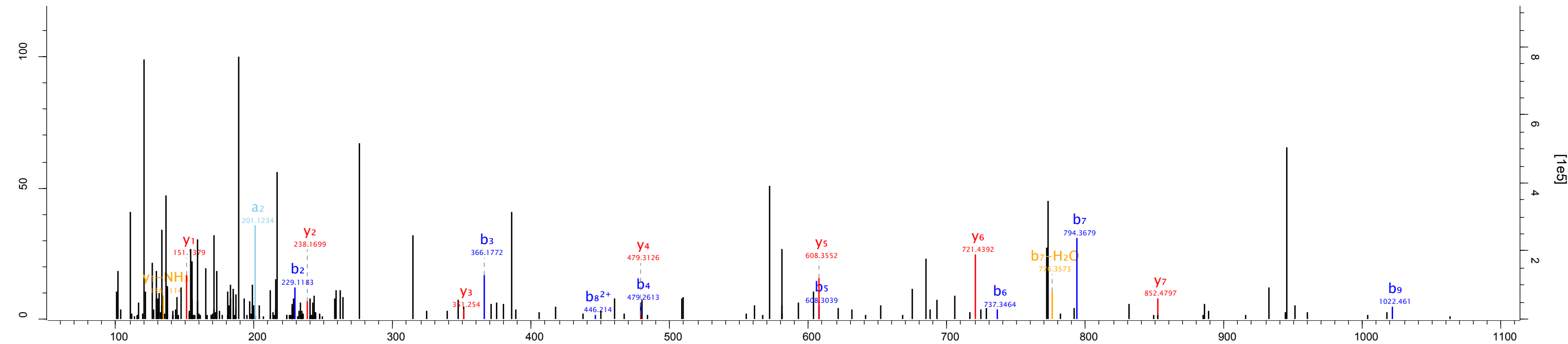
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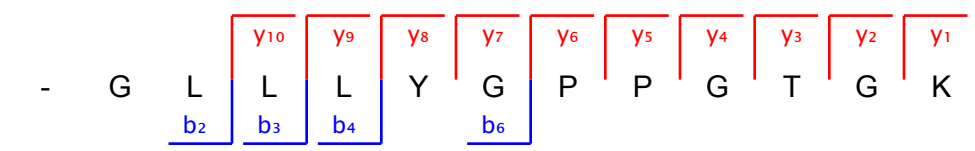
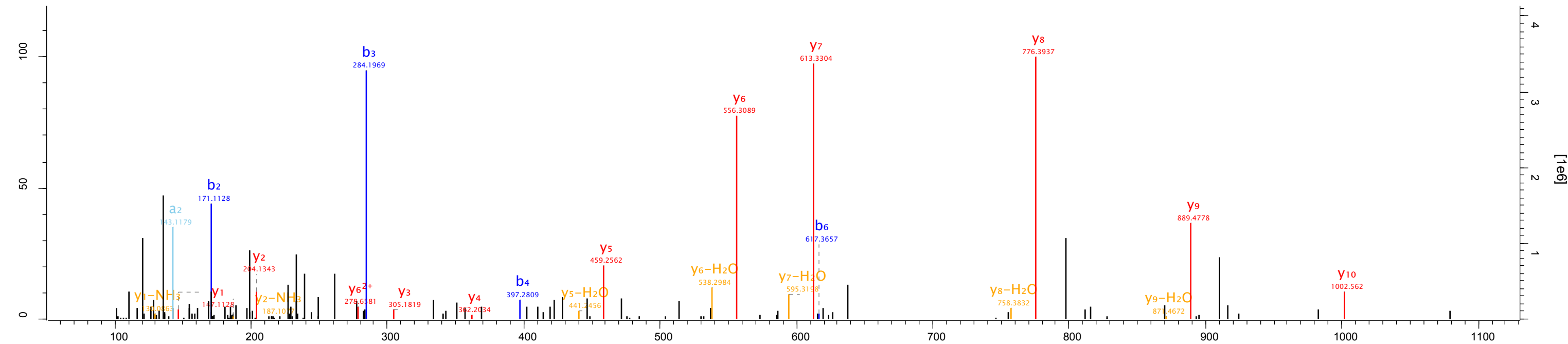
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 Scan: 44925 Method: FTMS; HCD Score: 111.46 m/z: 440.6 Gene names: RPL39P5;RPL39



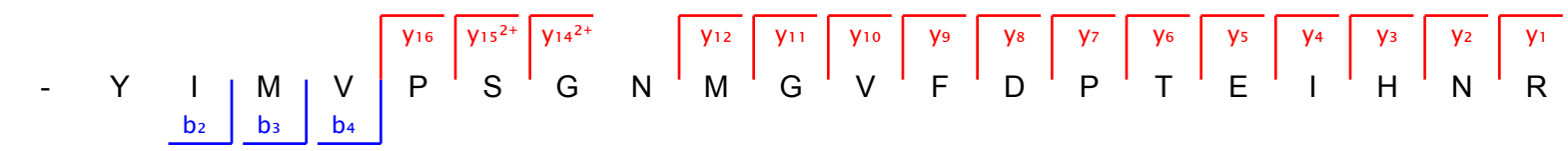
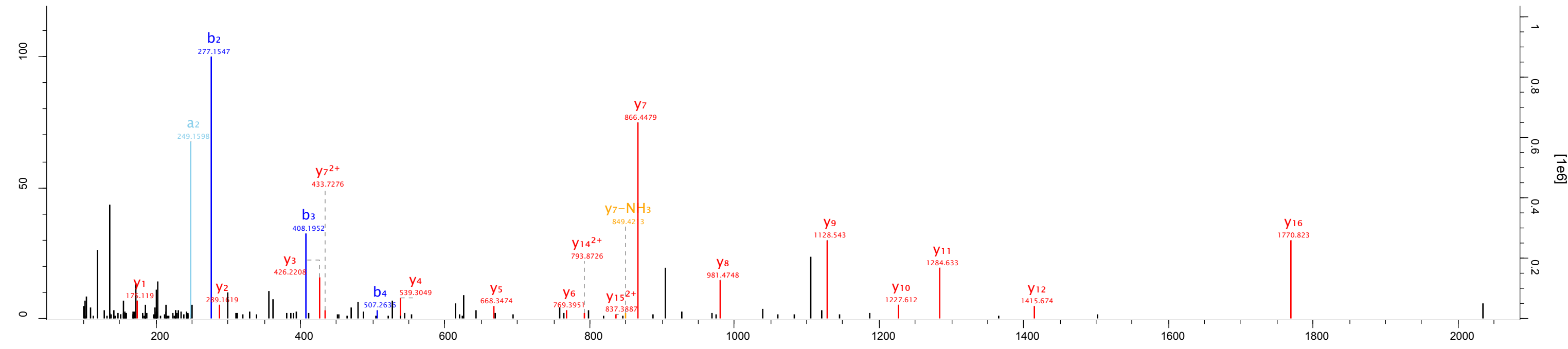
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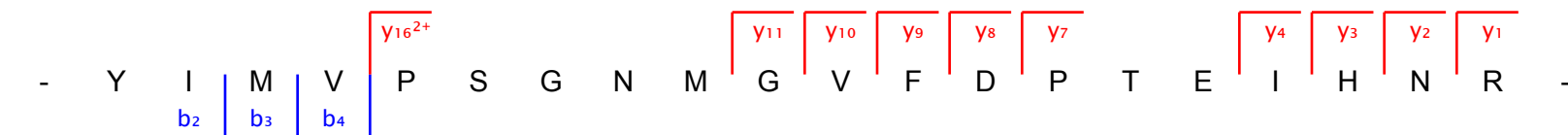
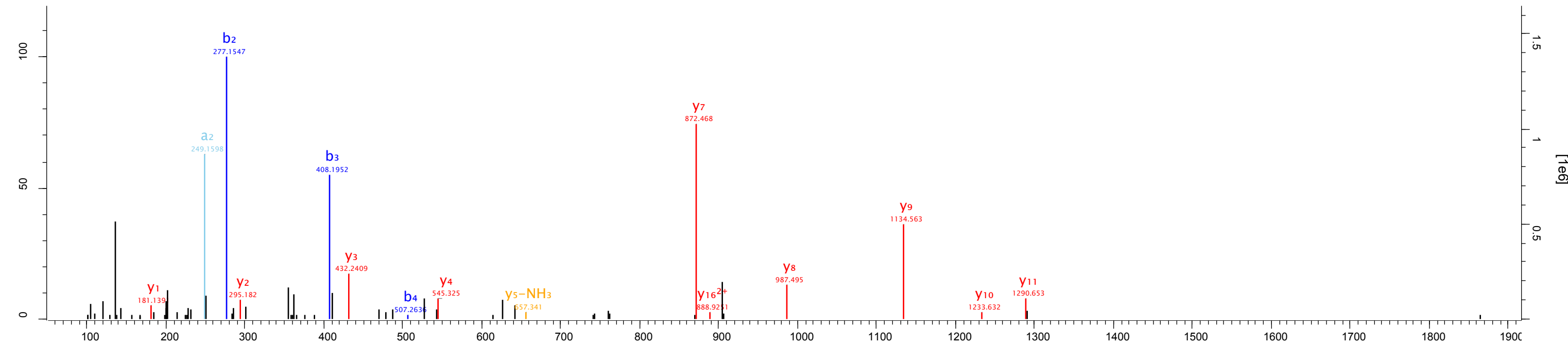


Raw file: 20150822_A375SR-Proteome_BR3
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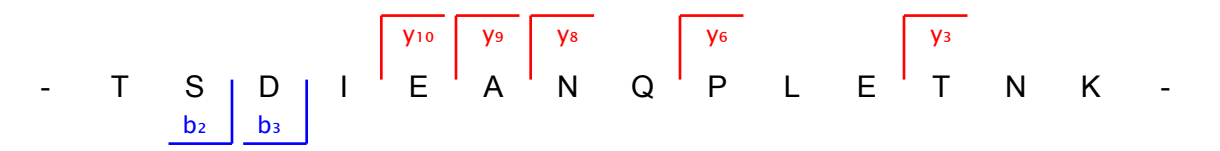
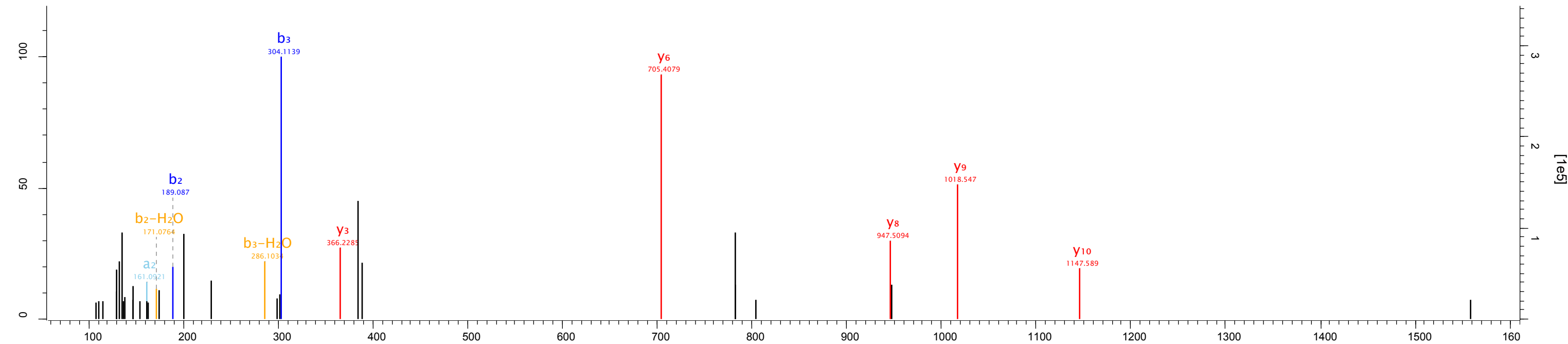


Raw file: 20150822_A375SR-Proteome_BR3
 Scan: 90205 Method: FTMS; HCD Score: 66.78 m/z: 759.7 Gene names: CNIH4



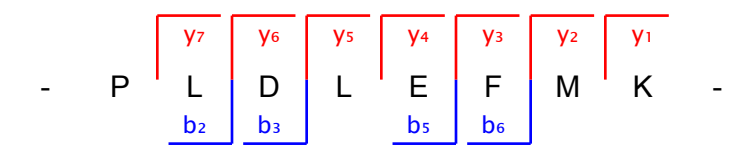
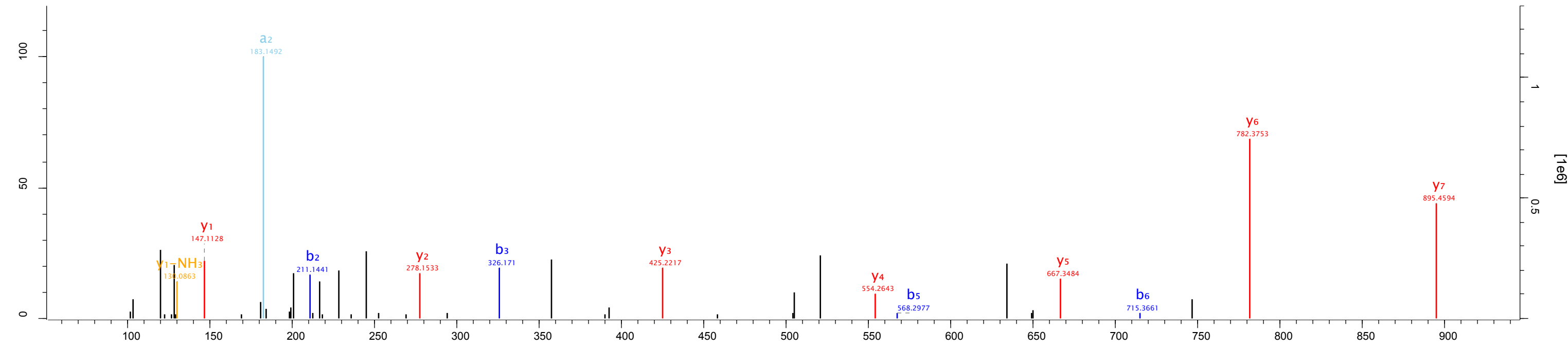


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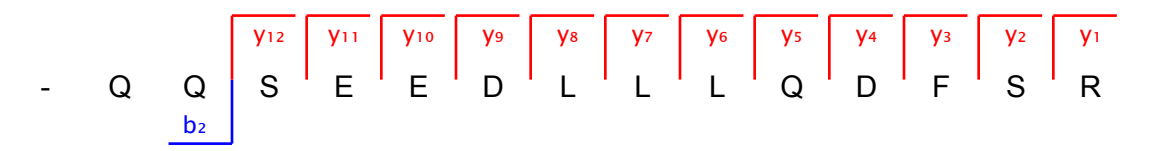
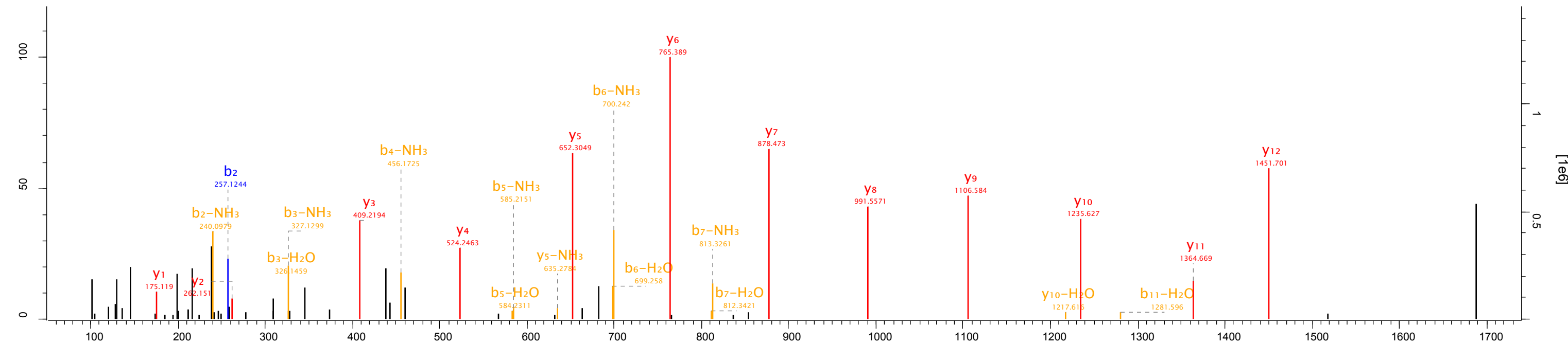
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20180707_MaS_A375SR_LM_proteome_06

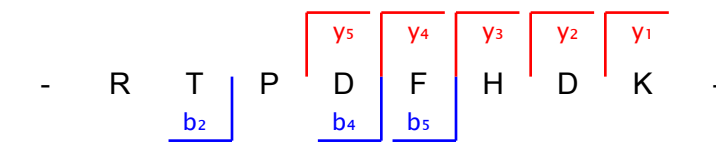
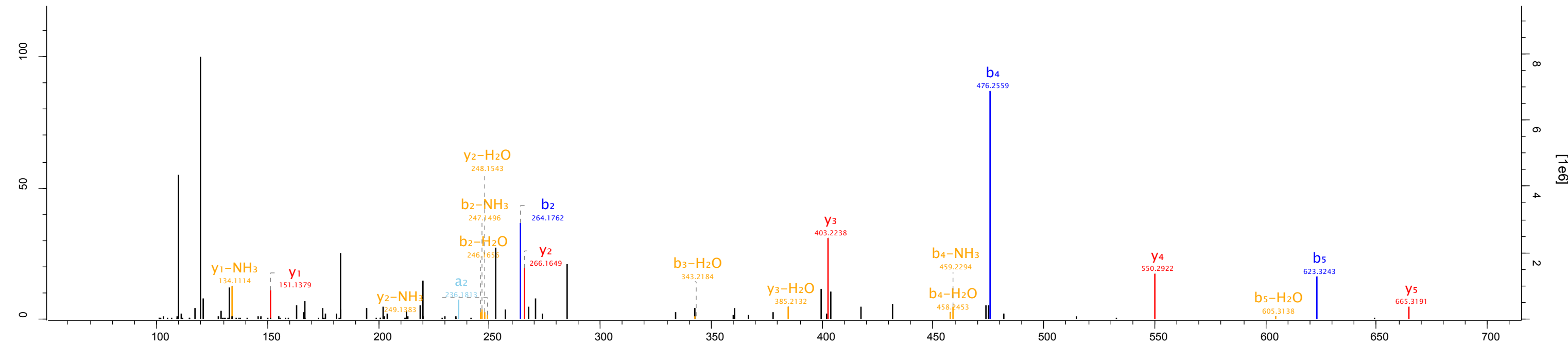
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Method: FTMS; HCD
Score: 70.26
m/z: 496.76
Gene names: SEPT3



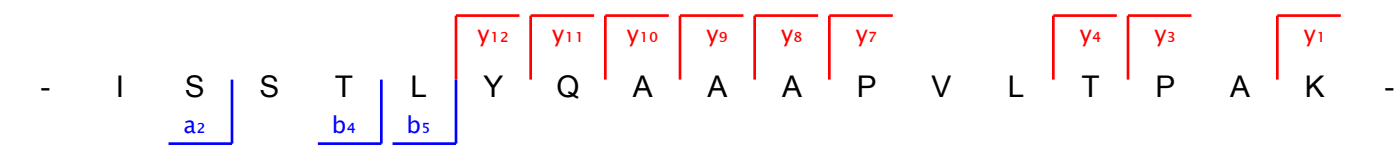
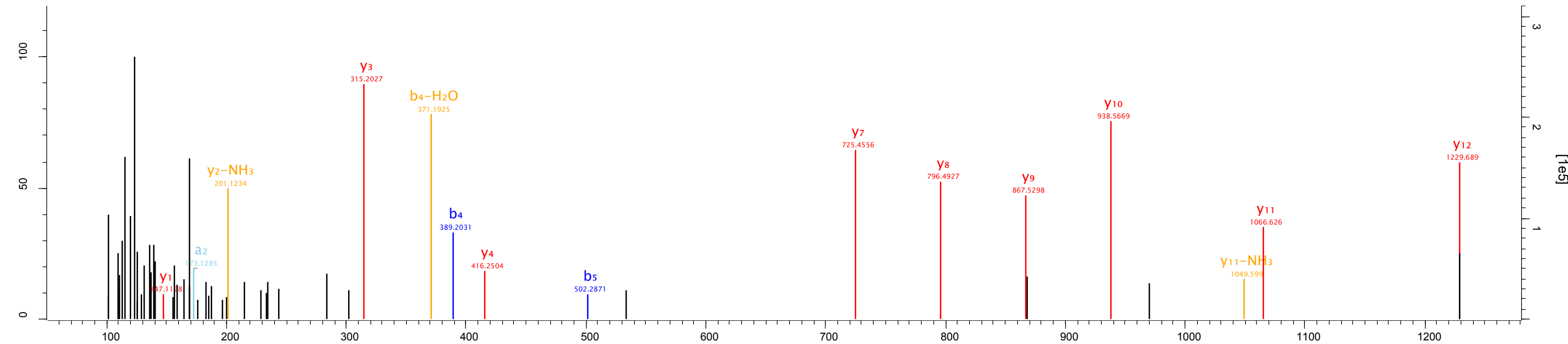
Raw file
20180707_MaS_A375SR_LM_proteome_07

Scan 26915 Method FTMS; HCD Score 61.44 m/z 854.41 Gene names SSR3

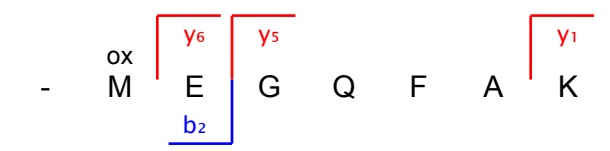
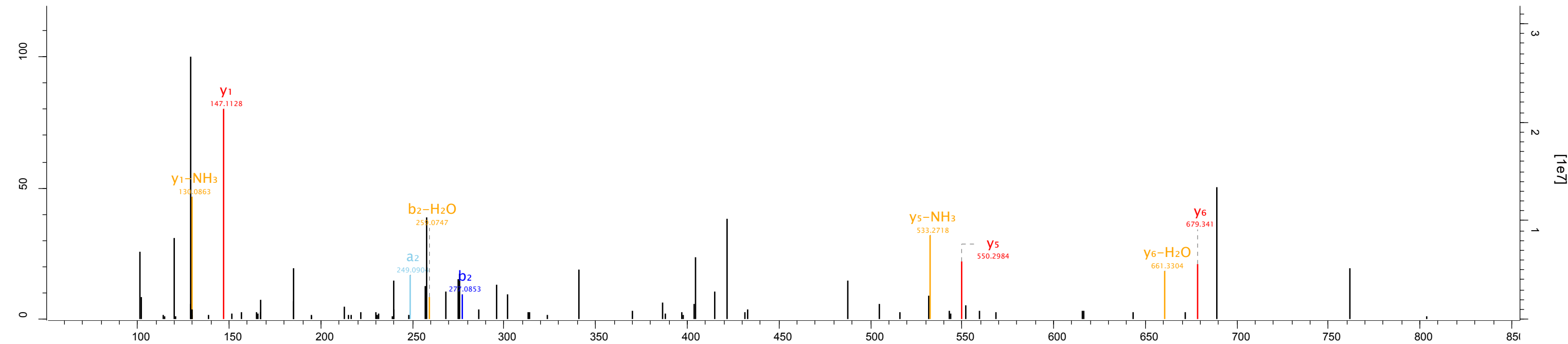




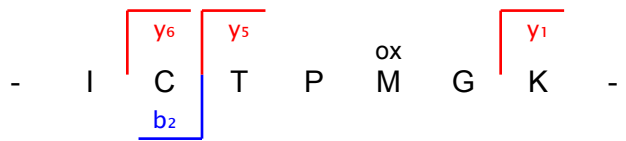
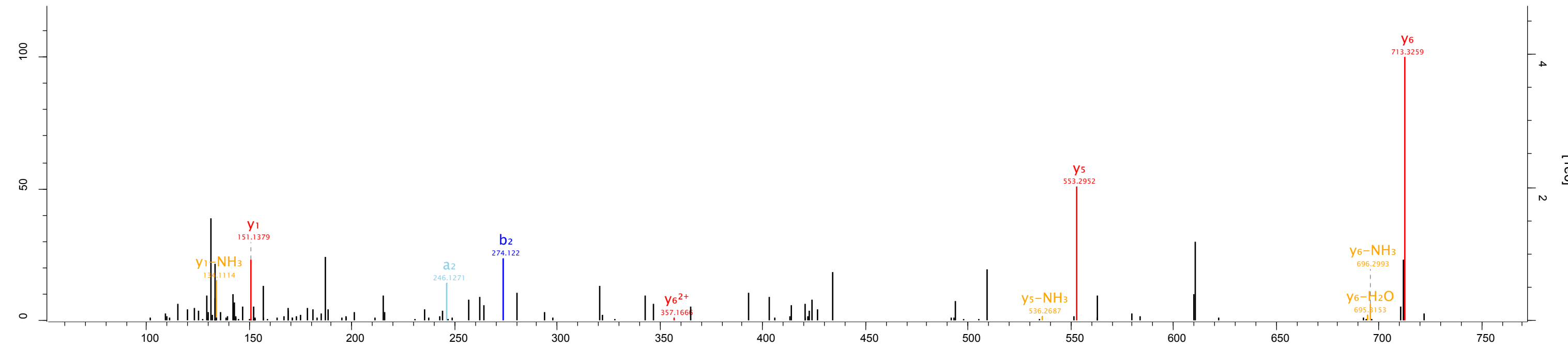
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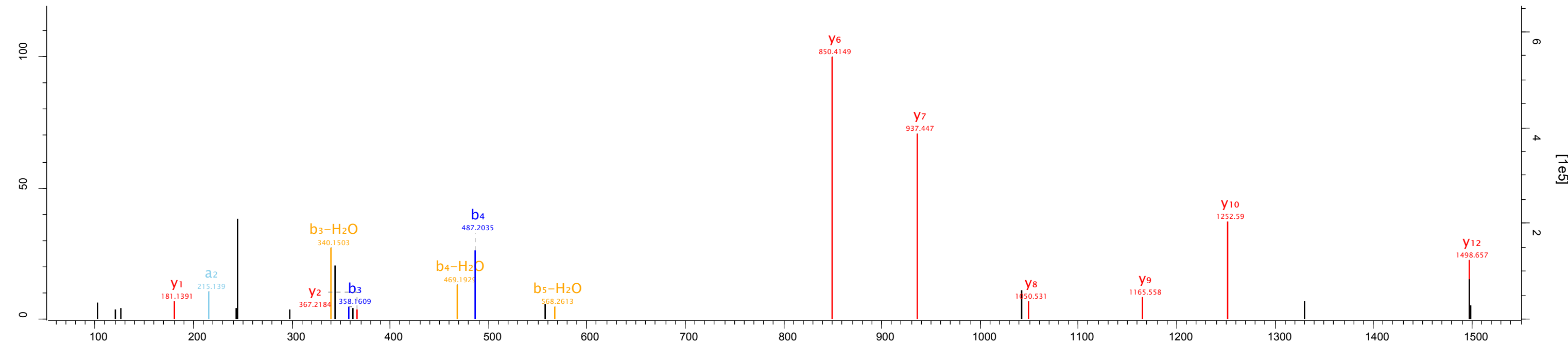
Raw file 20180707_MaS_A375SR_LM_proteome_10 Scan 3855 Method FTMS; HCD Score 52.68 m/z 413.69



Raw file 20180707_MaS_A375SR_LM_proteome_14 Scan 7045 Method FTMS; HCD Score 62.72 m/z 413.71 Gene names PROK2



Raw file
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 Scan 26405 Method FTMS; HCD Score 54.28 m/z 1042.97 Gene names RNF121



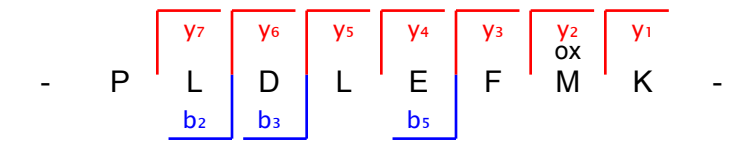
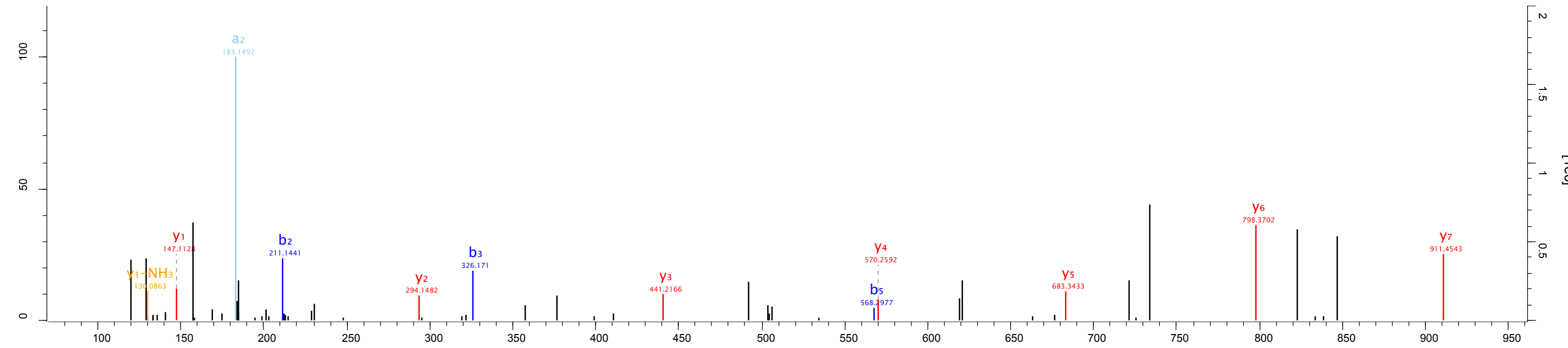
- E L D E V D M S D L S P E E Q W R -

Fragmentation mapping (b-ions in blue, y-ions in red):

- b₂ (L), b₃ (D), b₄ (E)
- y₁₂ (D), y₁₀ (S), y₉ (D), y₈ (L), y₇ (S), y₆ (P), y₂ (W), y₁ (R)

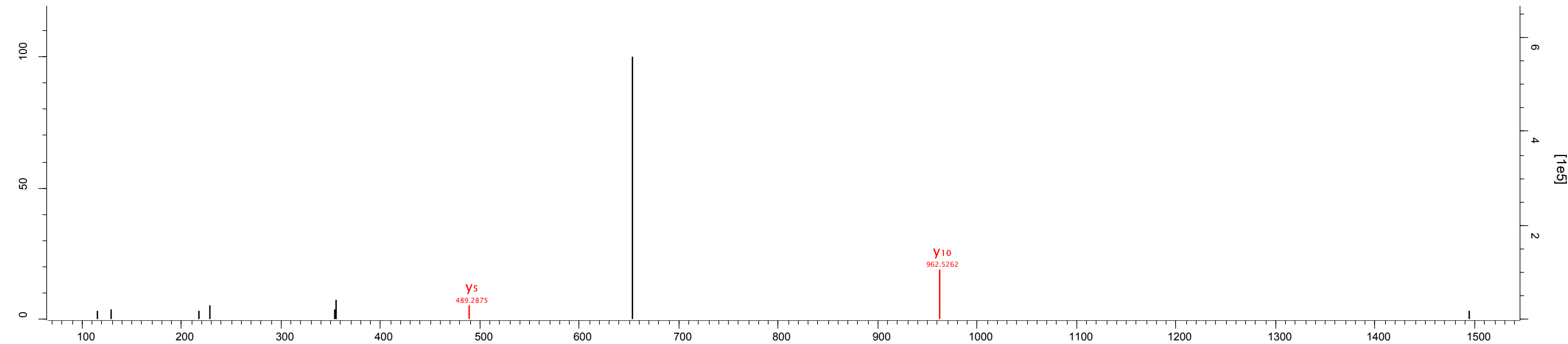
Raw file
20180707_MaS_A375SR_LM_proteome_22

Scan 20225 Method FTMS; HCD Score 57.86 m/z 504.76 Gene names SEPT3



Raw file
20180707_MaS_A375SR_LM_proteome_22

Scan	Method	Score	m/z	Gene names
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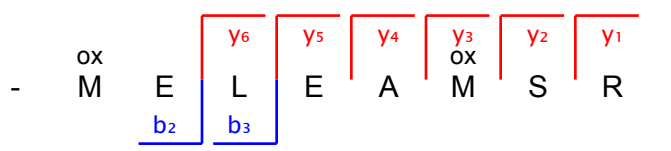
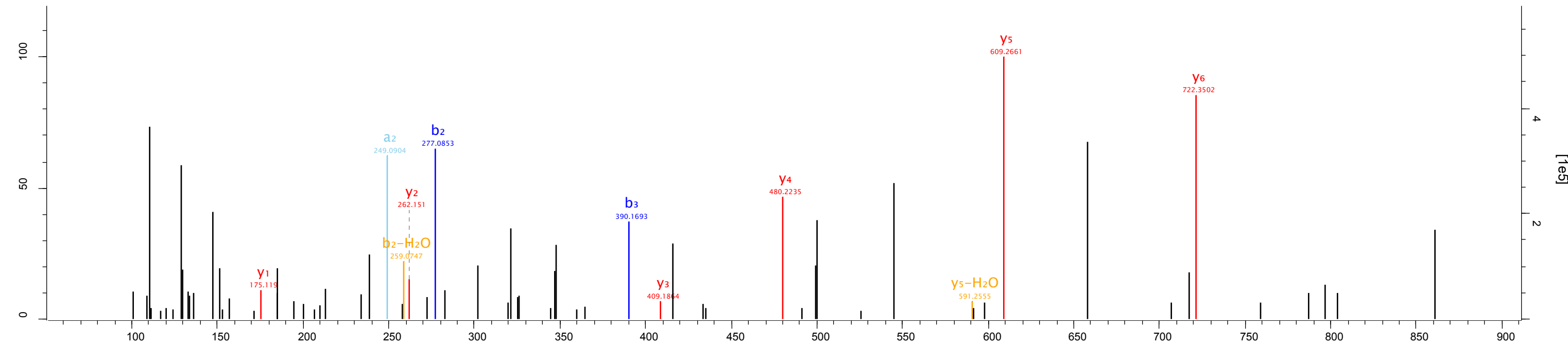


- G G V D T A A A P A G G A P P A H A P G P G R -

Red brackets above the sequence indicate the peptide fragments corresponding to the labeled peaks: y10 (A P P A H A) and y5 (P G P G R).

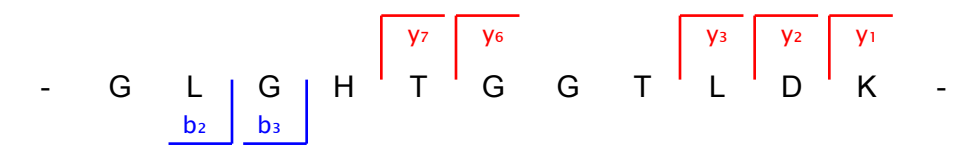
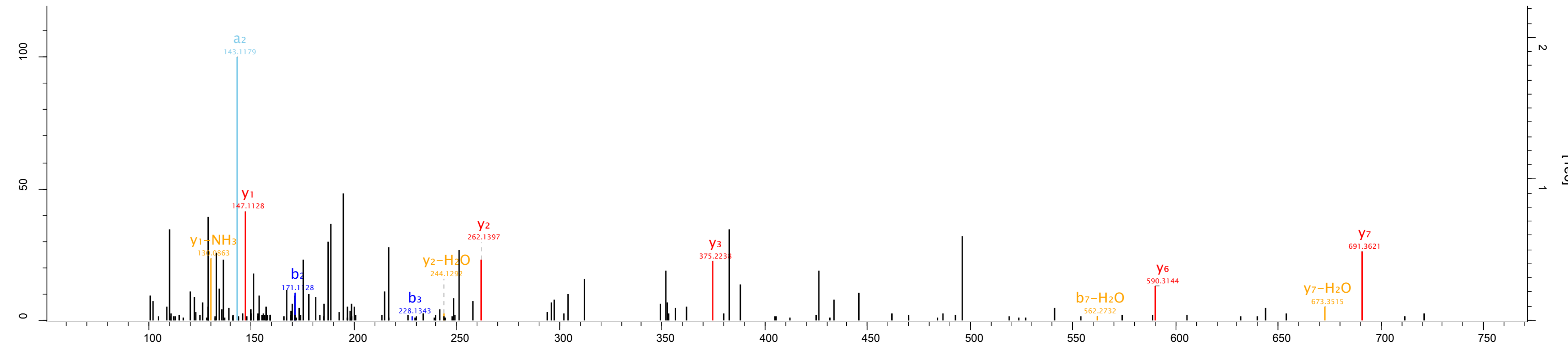
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20180707_MaS_A375SR_LM_proteome_27

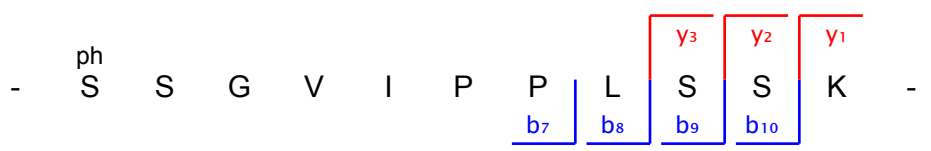
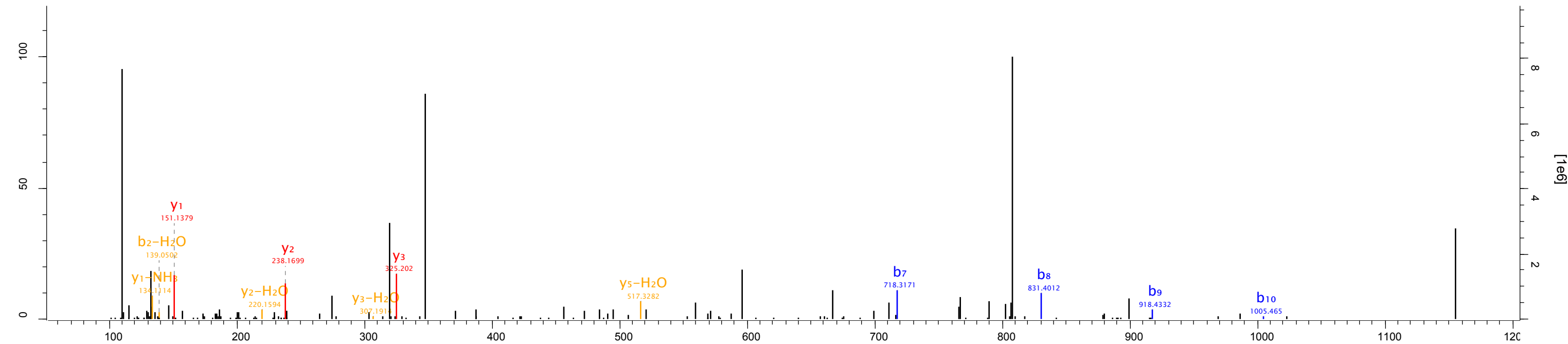
Scan	Method	Score	m/z	Gene names
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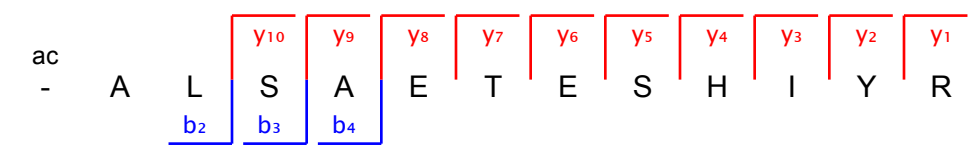
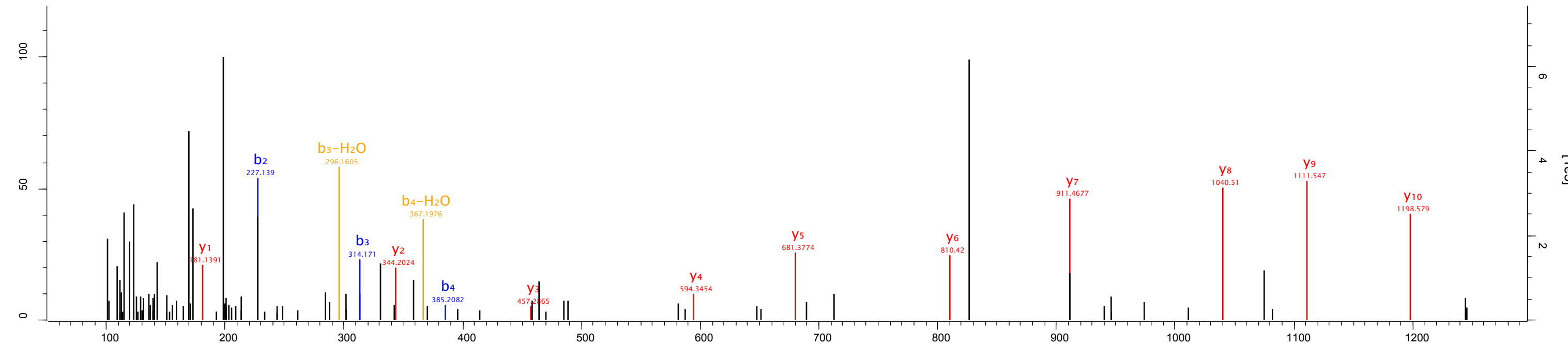
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Scan Method Score m/z Gene names
4295 FTMS; HCD 30.89 352.18 TYMP



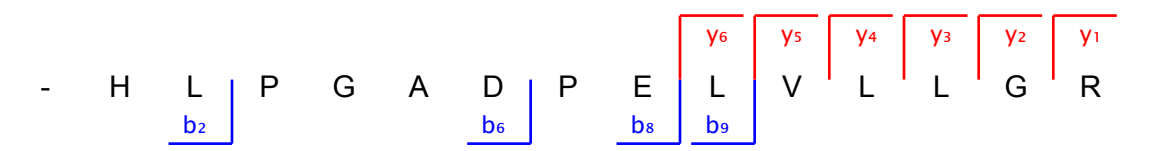
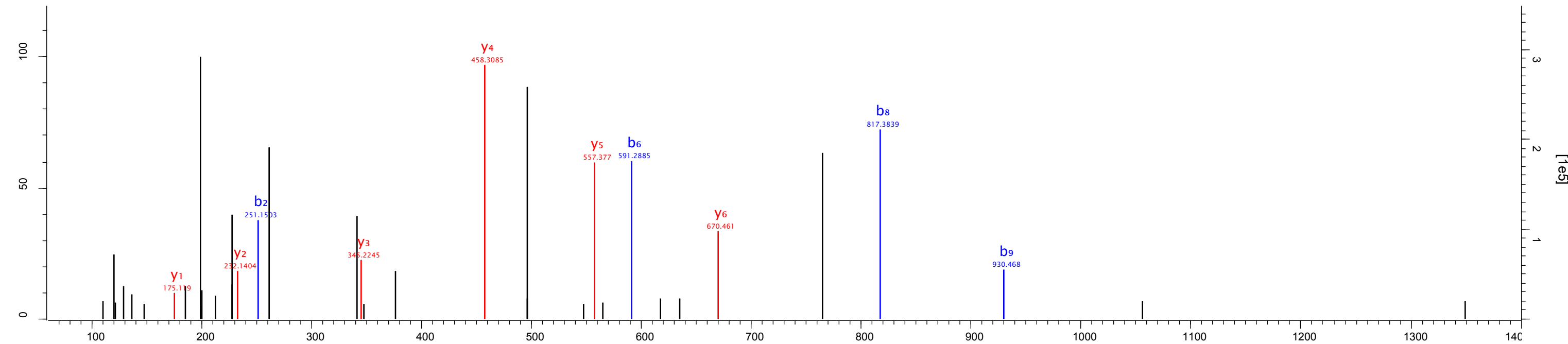


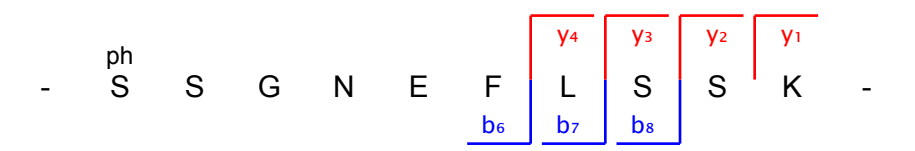
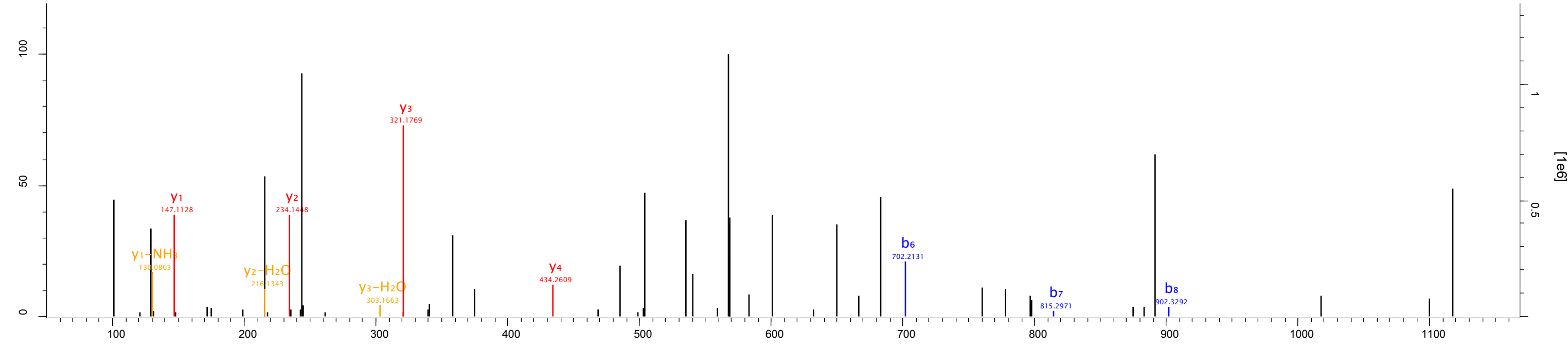
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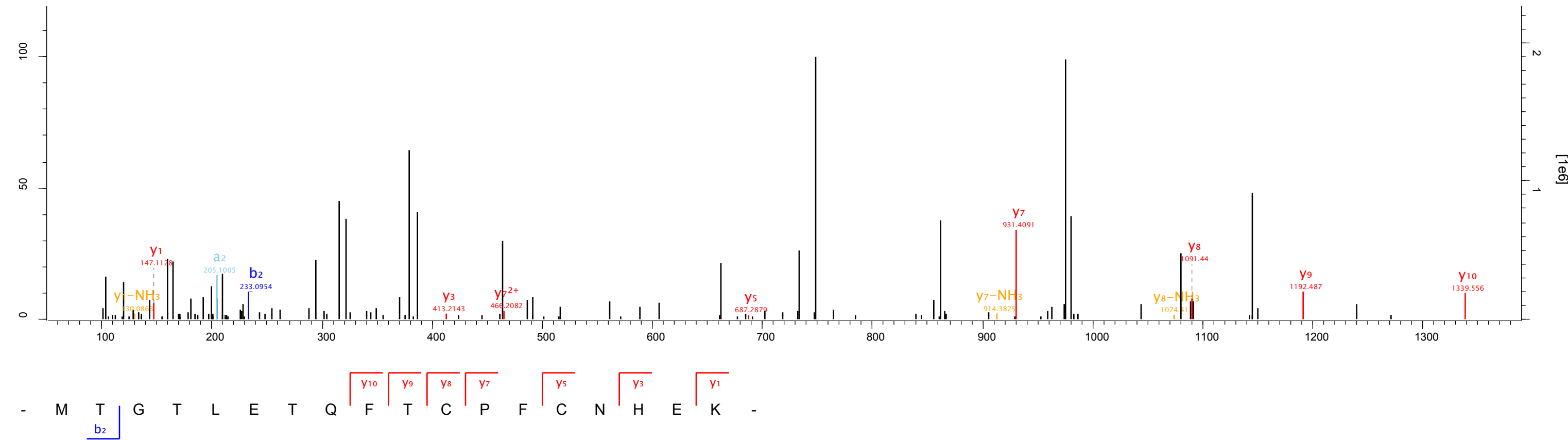


Raw file
20180707_MaS_A375SR_ML_proteome_03

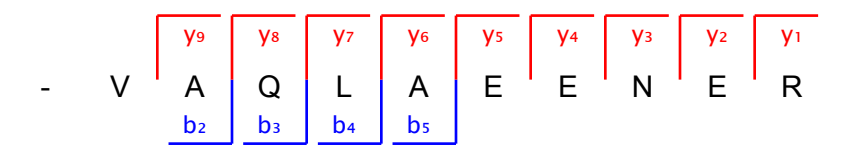
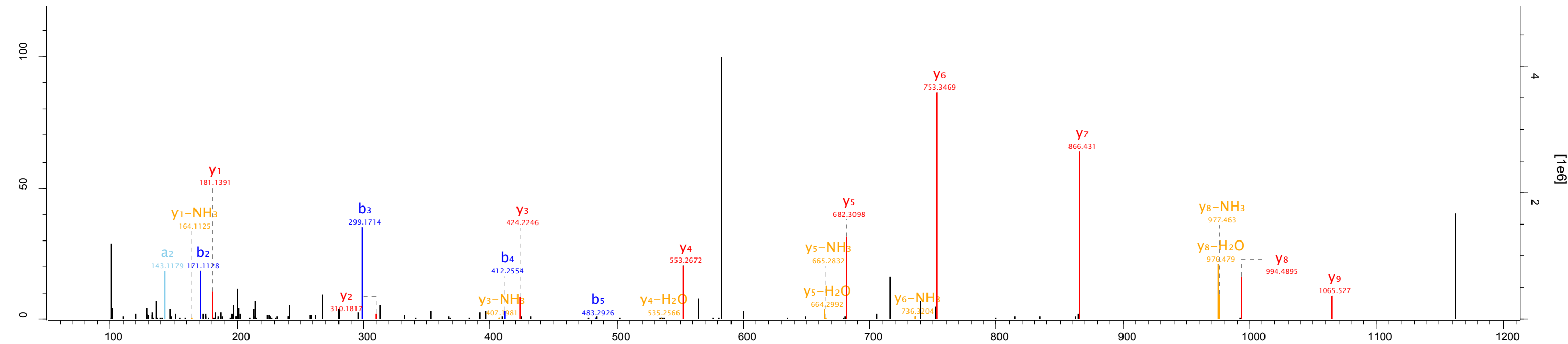
Scan 21265 Method FTMS; HCD Score 31 m/z 496.29 Gene names SELM



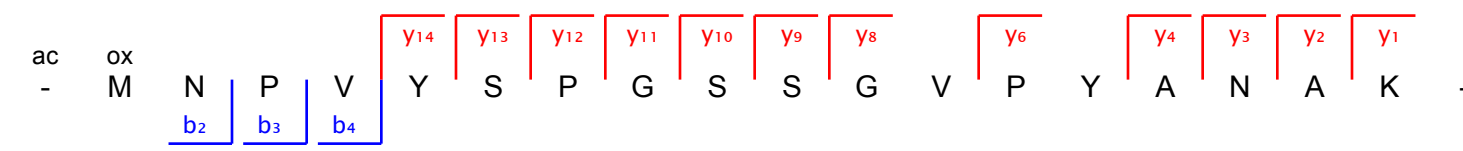
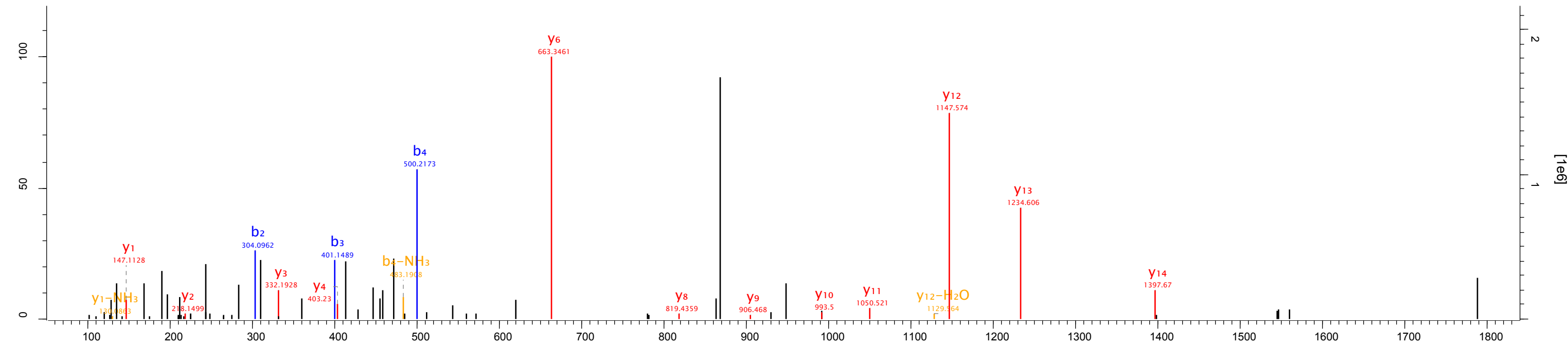




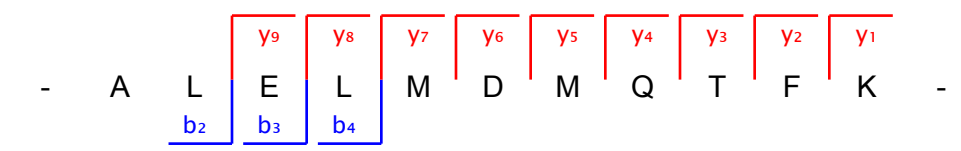
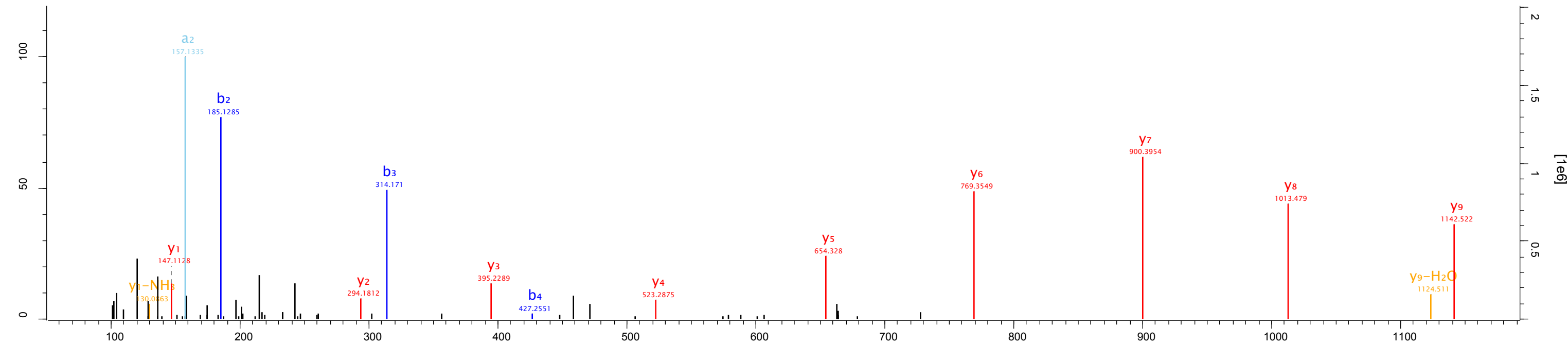
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 Scan: 7715 Method: FTMS; HCD Score: 91.7 m/z: 582.8 Gene names: DDIT3



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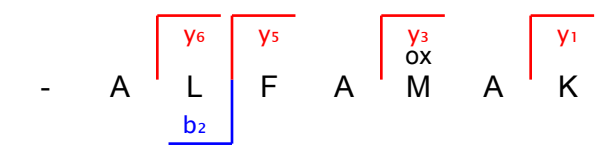
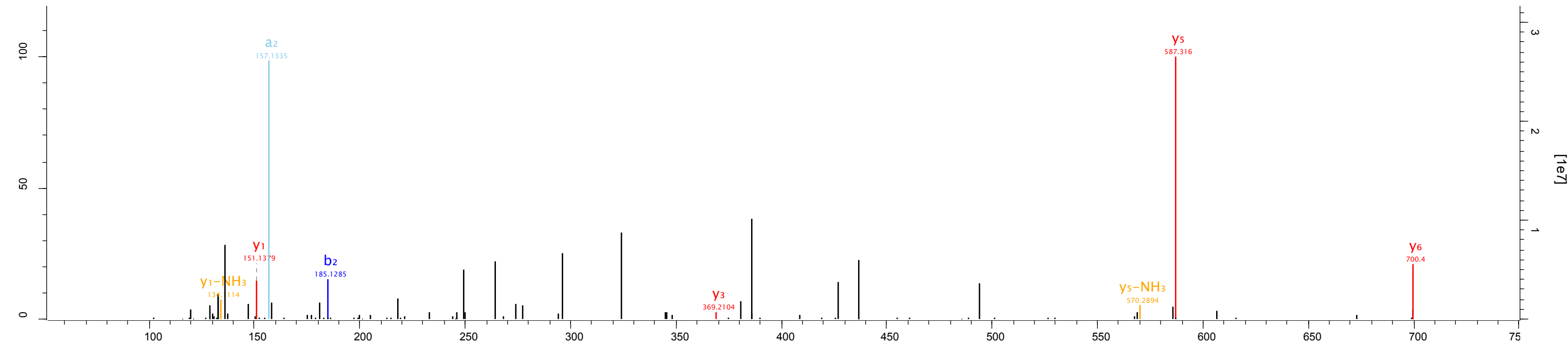


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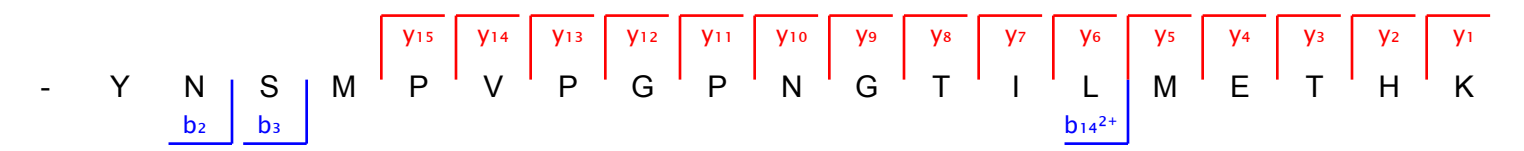
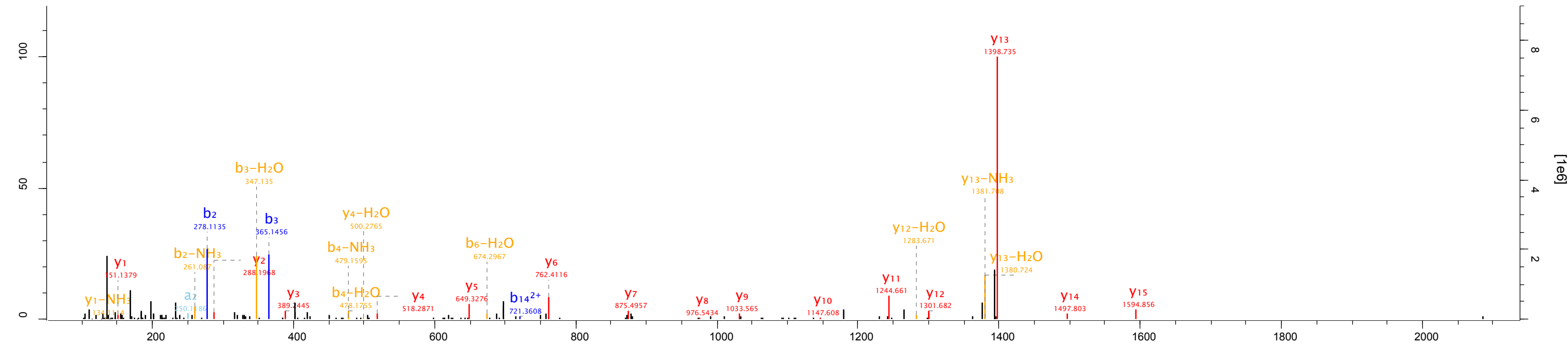


Raw file
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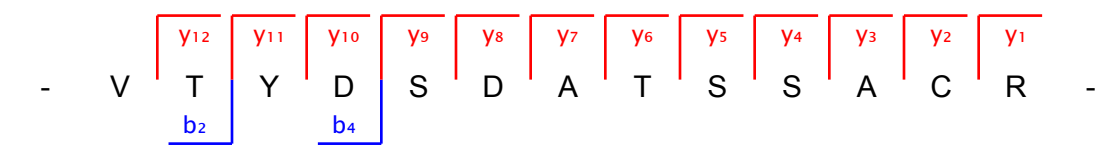
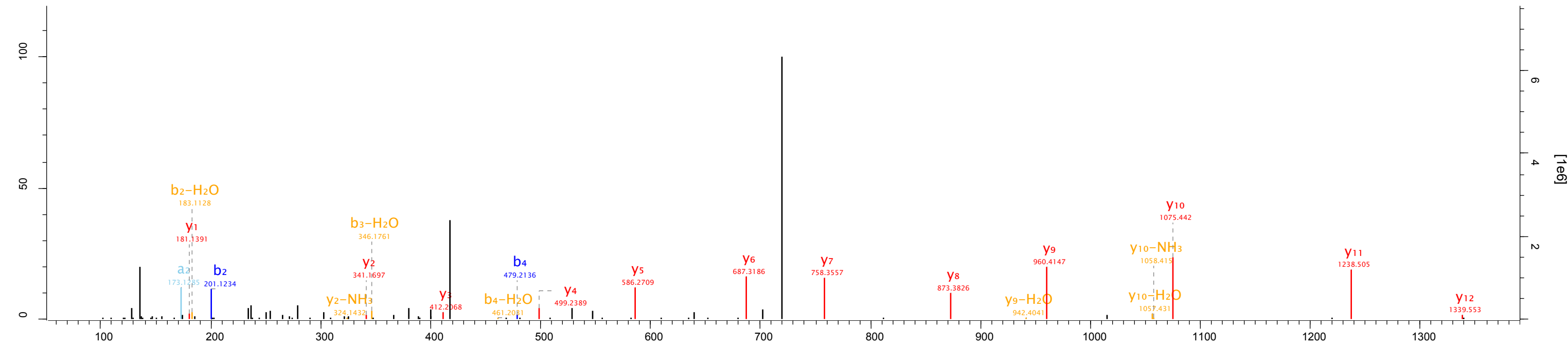
Scan: 12515
Method: FTMS; HCD
Score: 48.76
m/z: 386.22
Gene names: RASD1



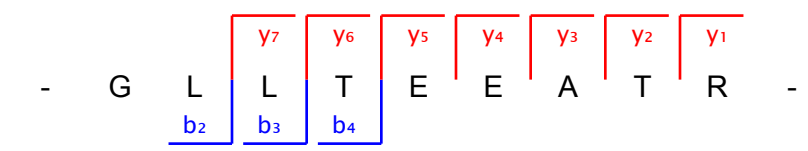
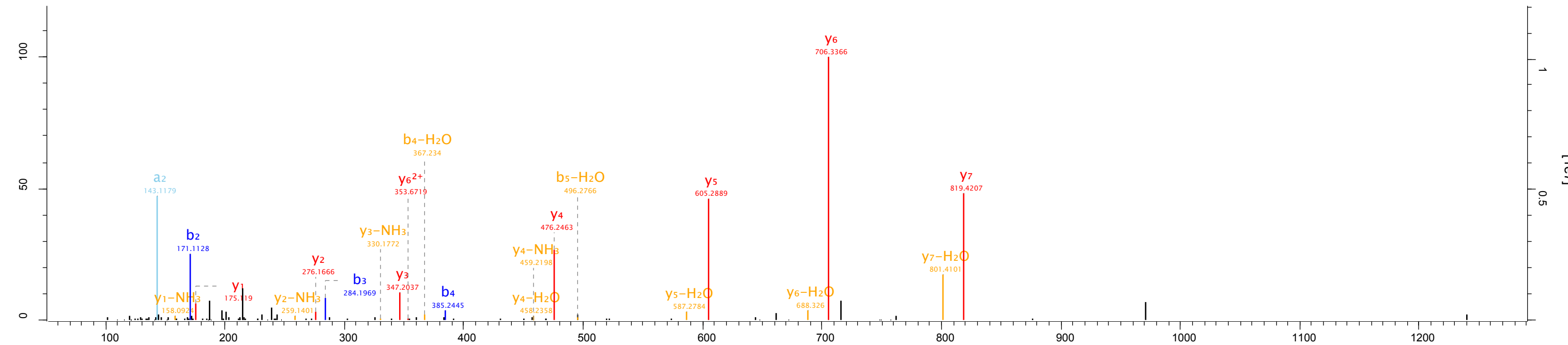
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 Scan: 21875 Method: FTMS; HCD Score: 82.77 m/z: 697.35 Gene names: SLC31A1



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 Scan: 6755 Method: FTMS; HCD Score: 88.09 m/z: 720.32 Gene names: LEPROT

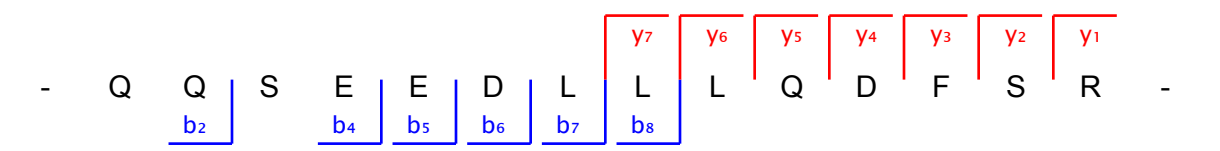
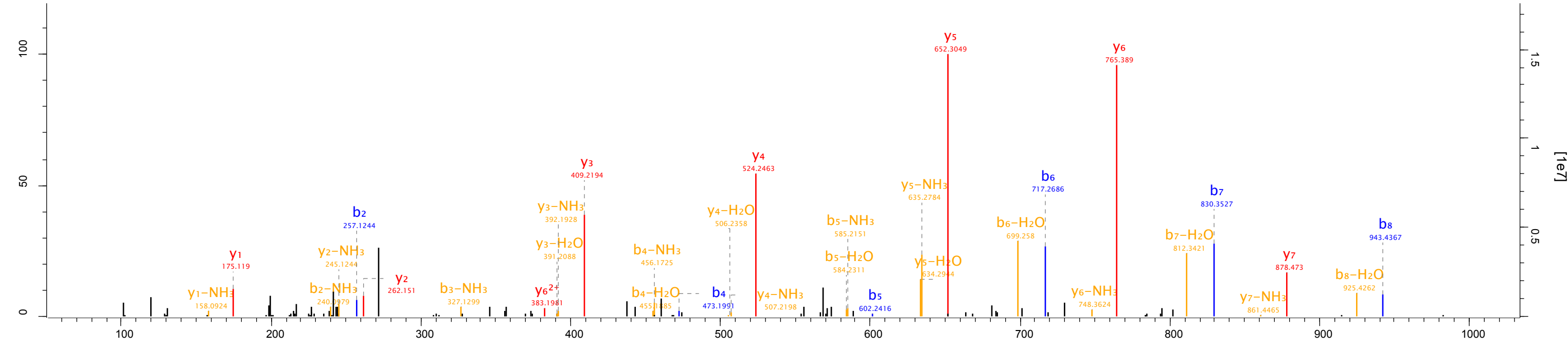


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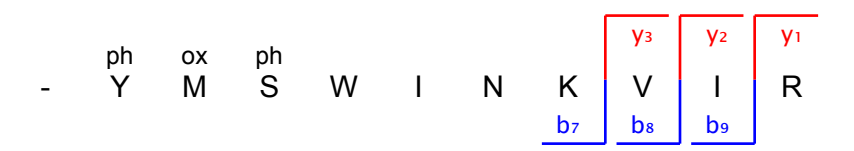
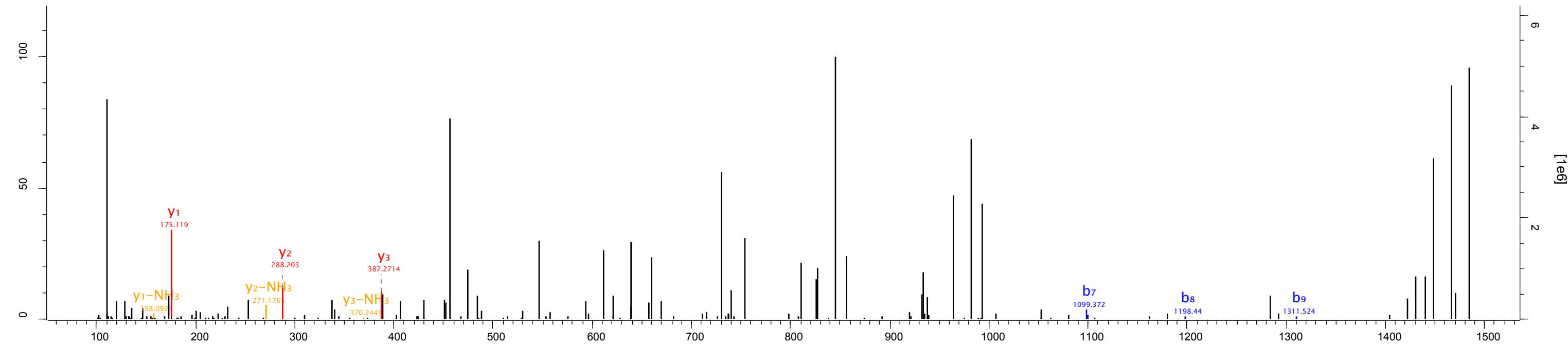


20180707_MaS_A375SR_ML_proteome_09

26635 FTMS; HCD 130.19 569.94 SSR3

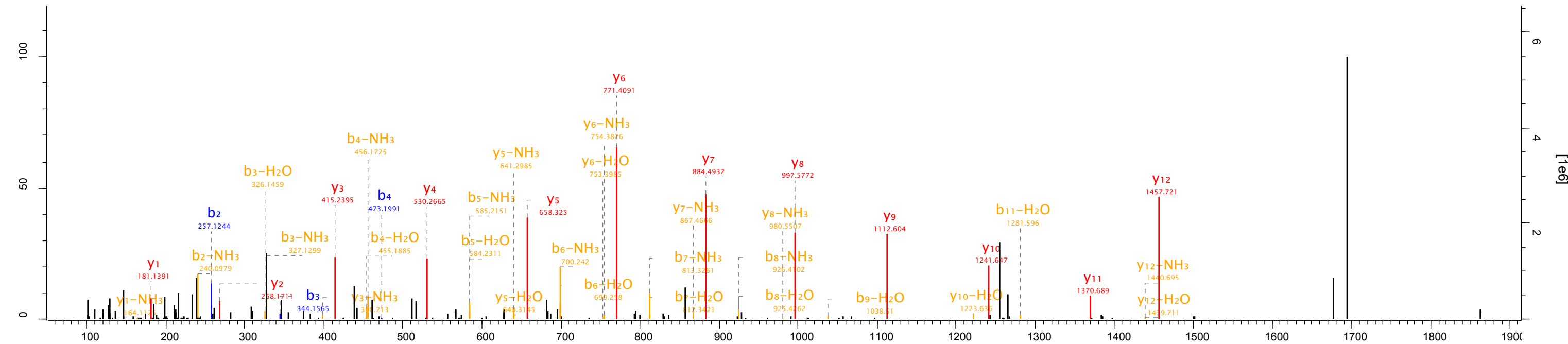


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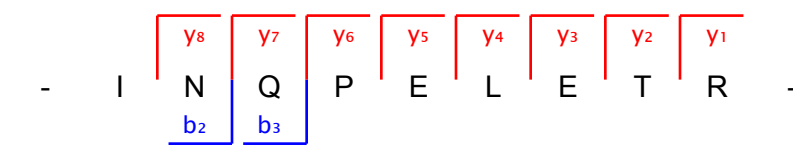
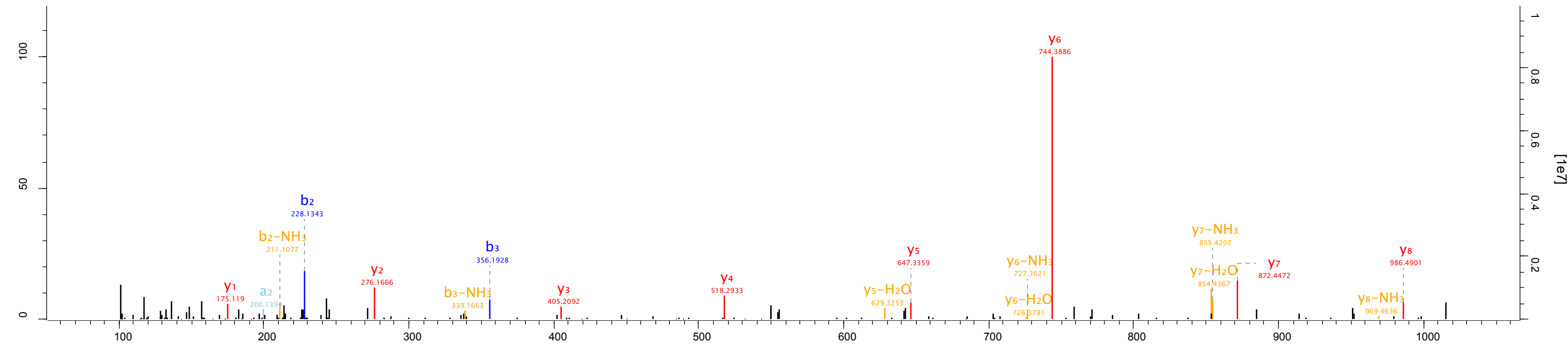
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Scan 27885 Method FTMS; HCD Score 105.58 m/z 857.92 Gene names SSR3



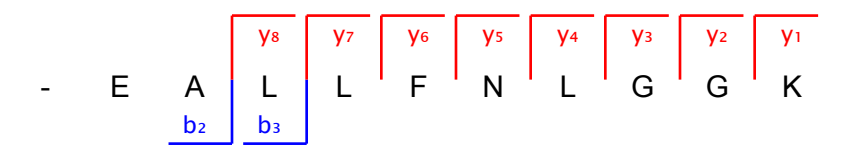
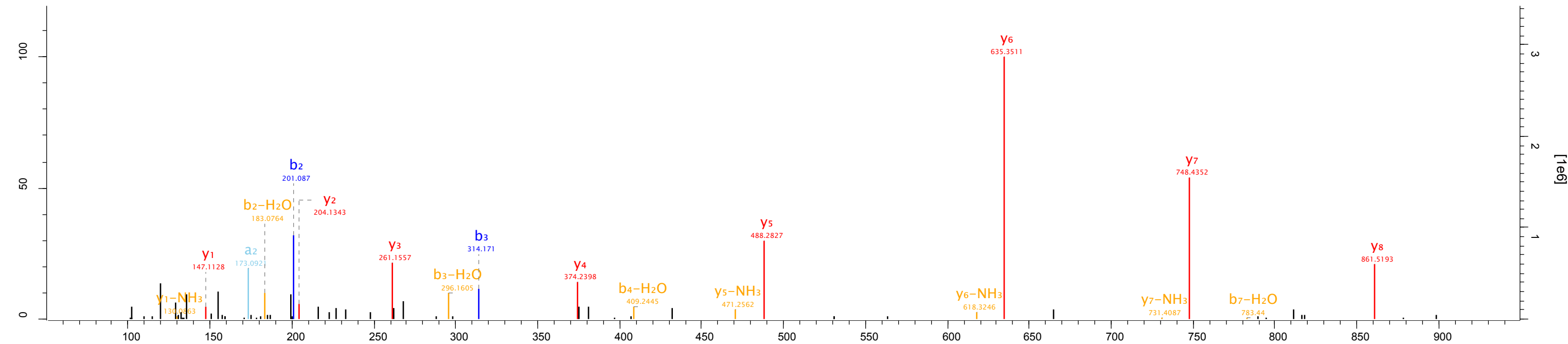
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b2 b3 b4

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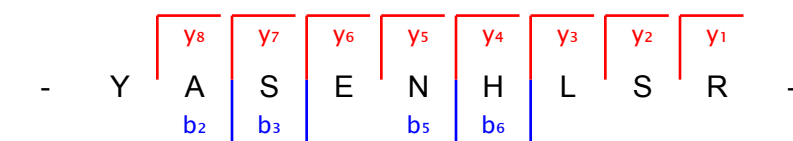
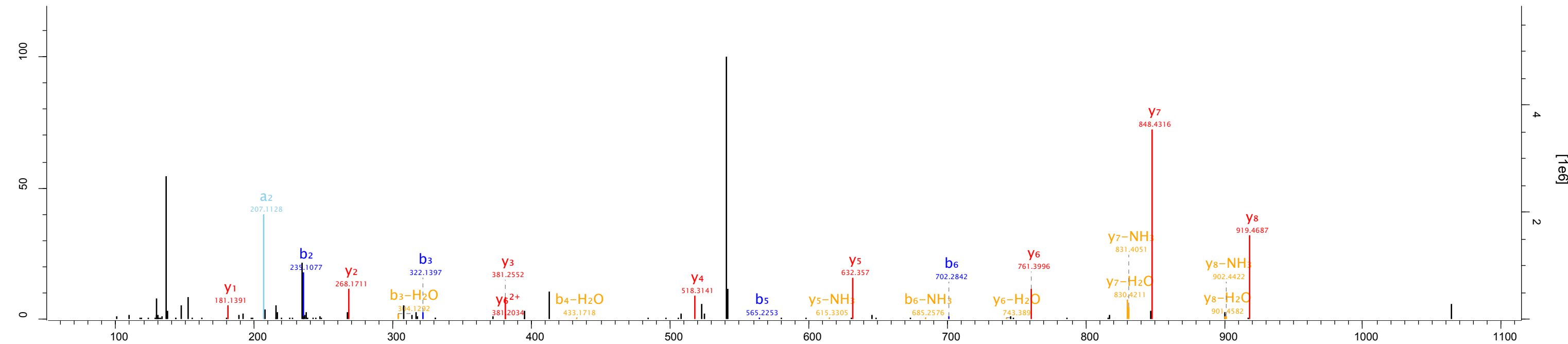
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20180707_MaS_A375SR_ML_proteome_11

Scan 27985 Method FTMS; HCD Score 90.91 m/z 531.3 Gene names CYB561

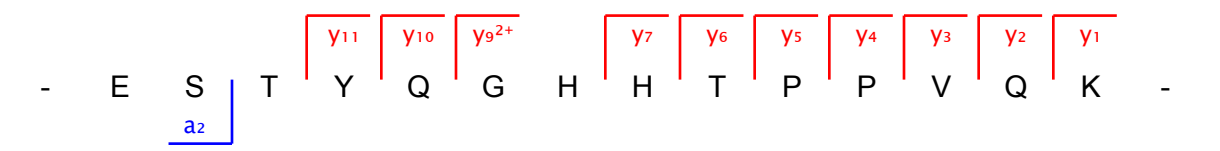
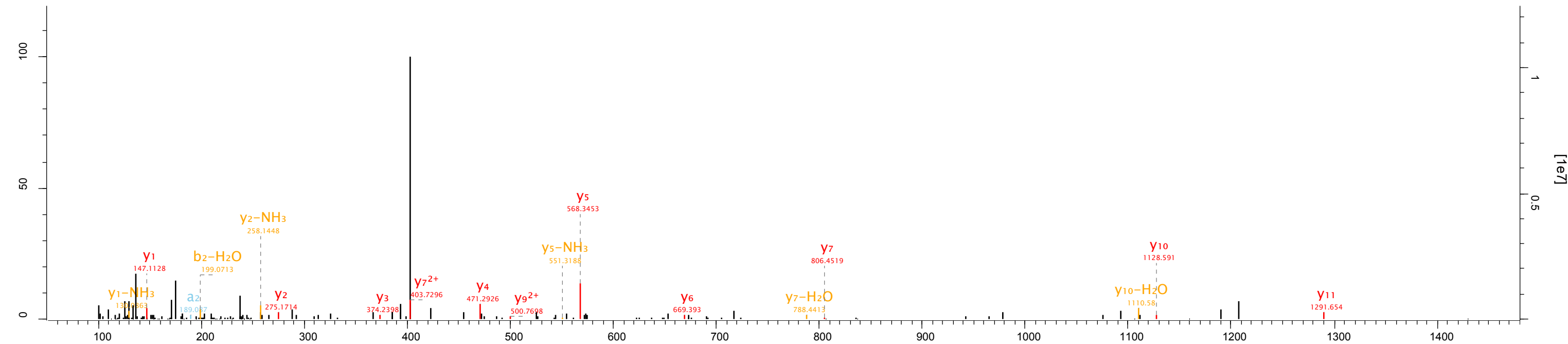


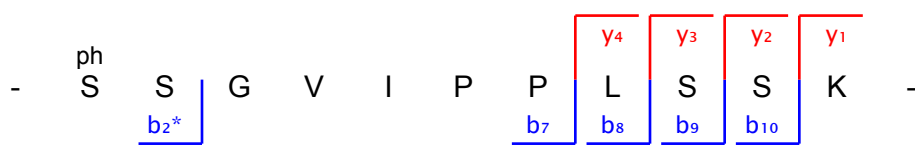
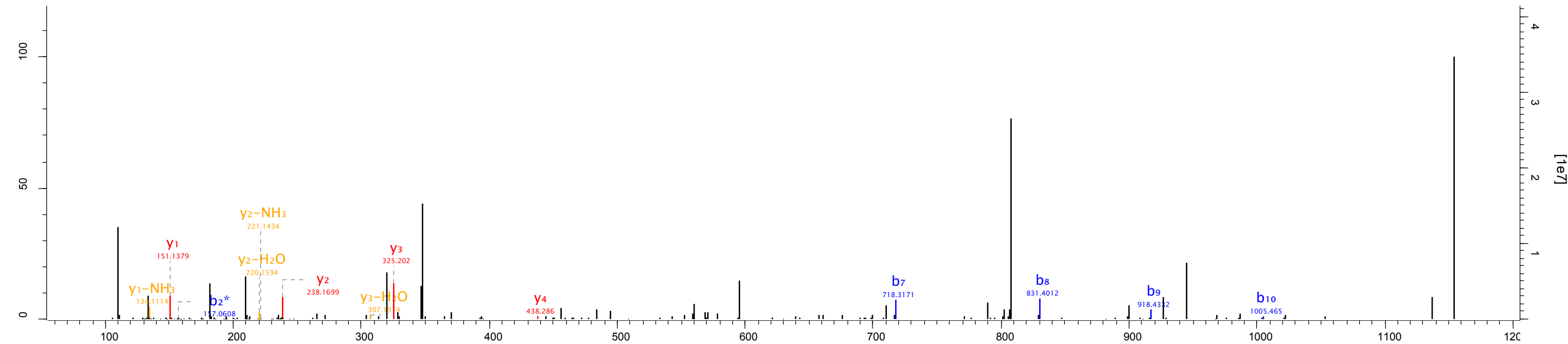
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20180707_MaS_A375SR_ML_proteome_11

Scan 3165 Method FTMS; HCD Score 110.53 m/z 541.77 Gene names TM4SF1

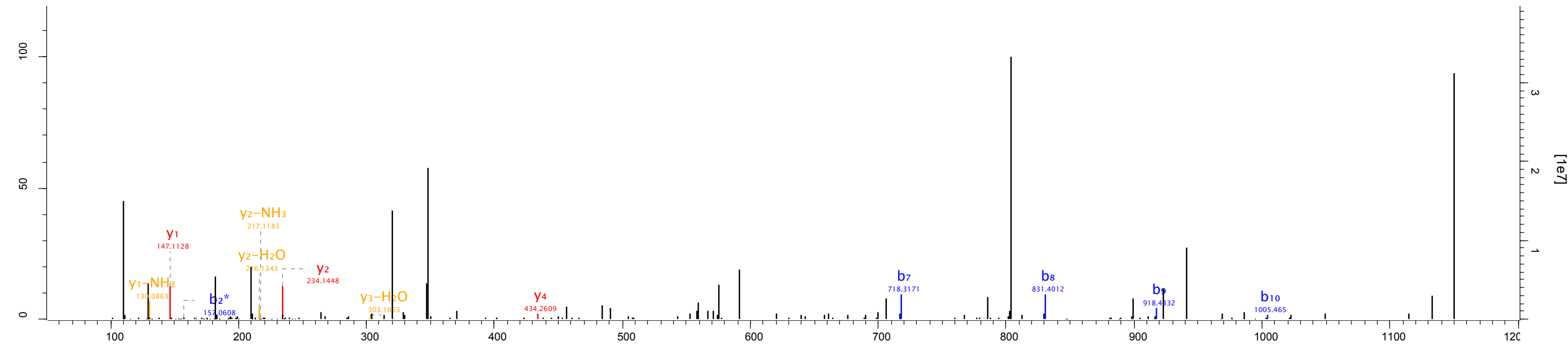


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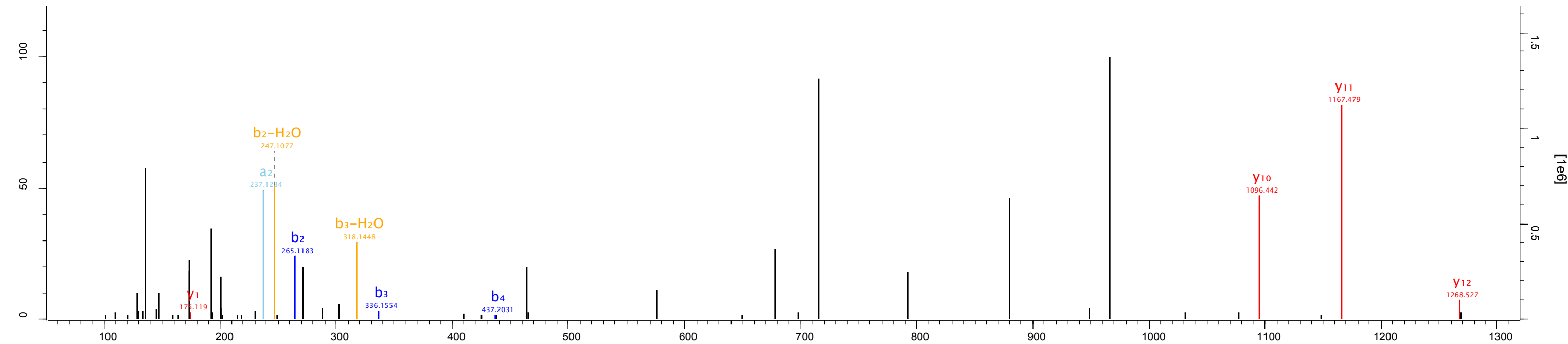




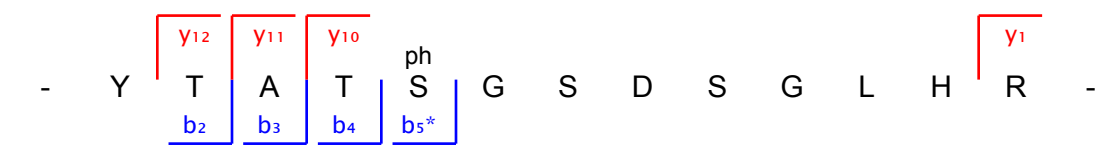
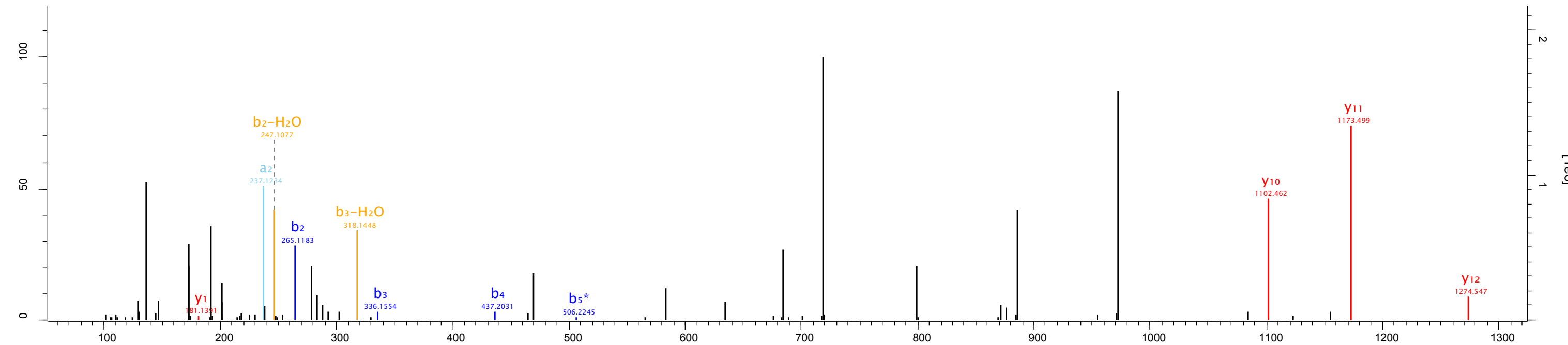
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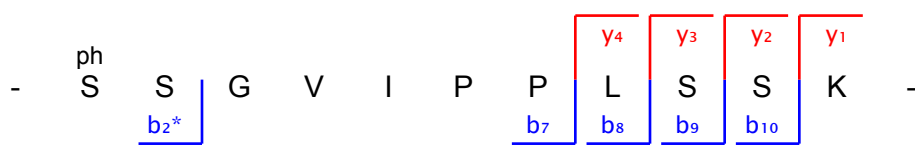
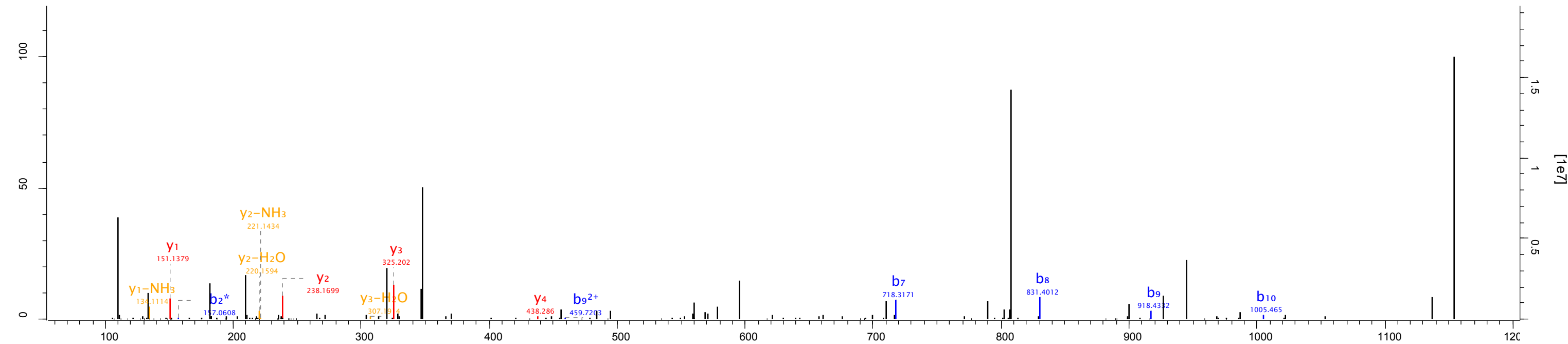


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 Scan: 11445 Method: FTMS; HCD Score: 47.71 m/z: 716.3



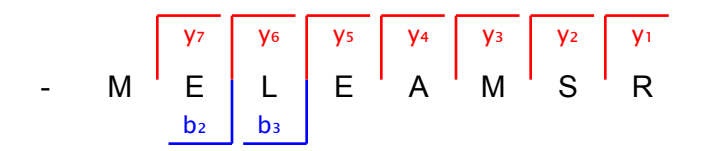
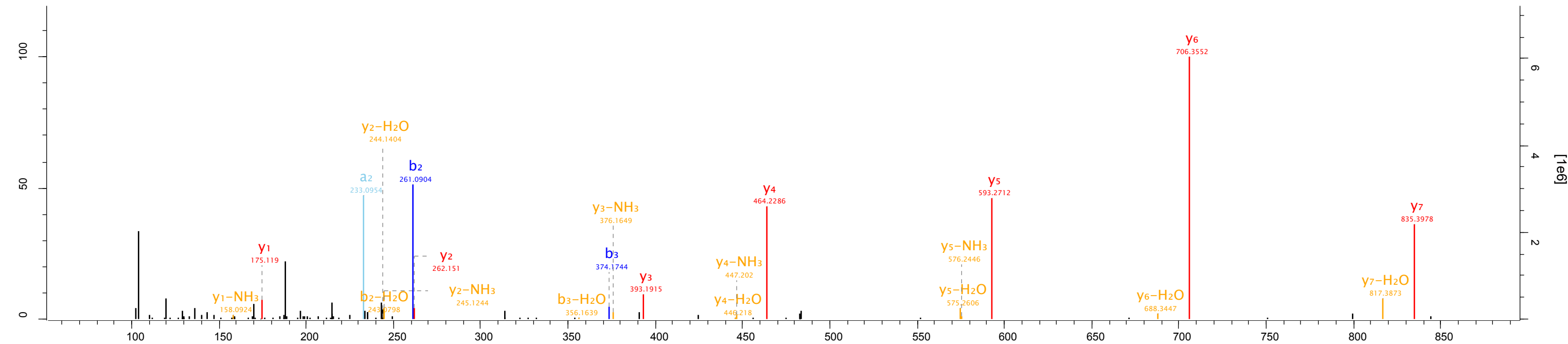
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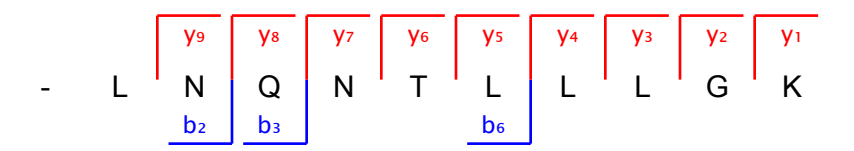
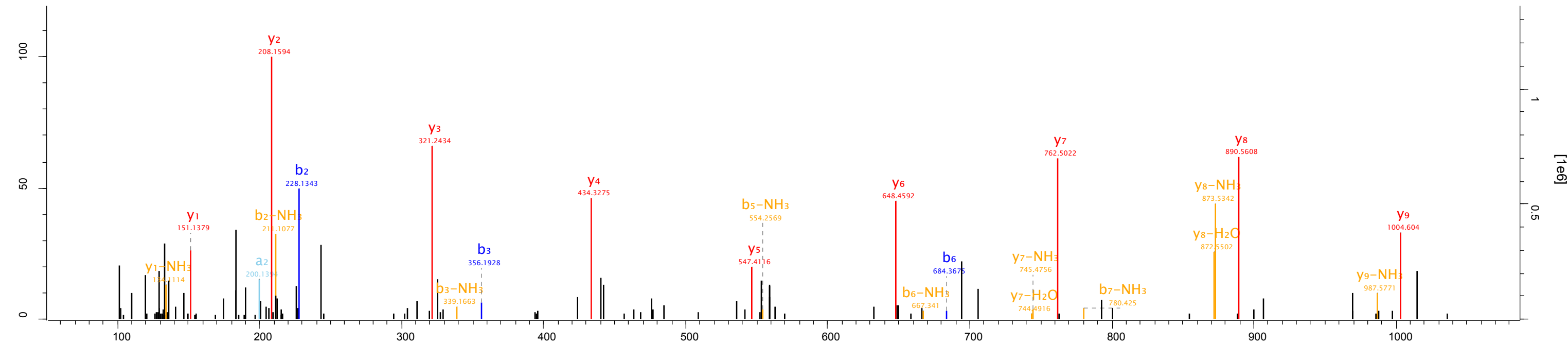
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20180707_MaS_A375SR_ML_proteome_13

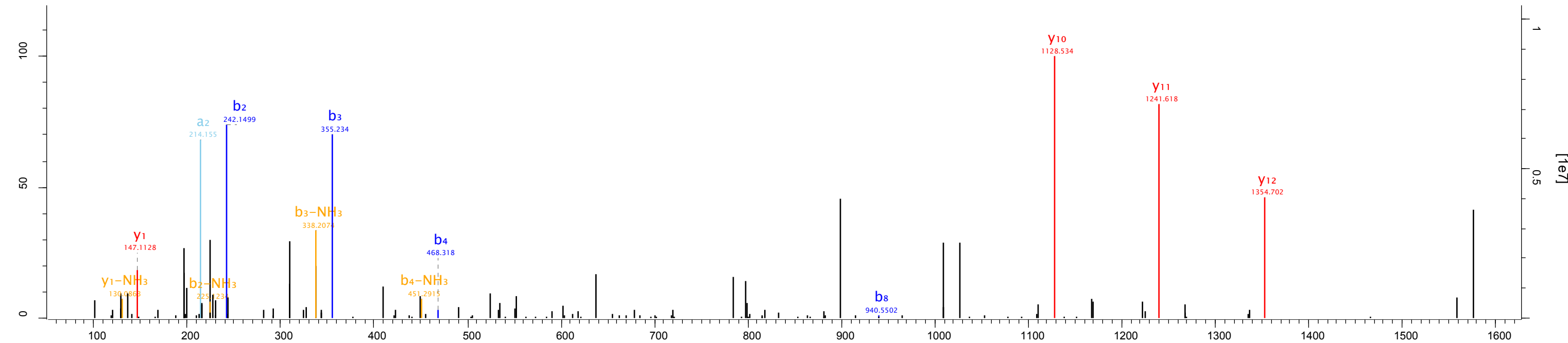
Scan 14085 Method FTMS; HCD Score 122.19 m/z 483.72 Gene names TMEM258



Raw file
20180707_MaS_A375SR_ML_proteome_14

Scan 17765 Method FTMS; HCD Score 107.95 m/z 559.35 Gene names NAT9

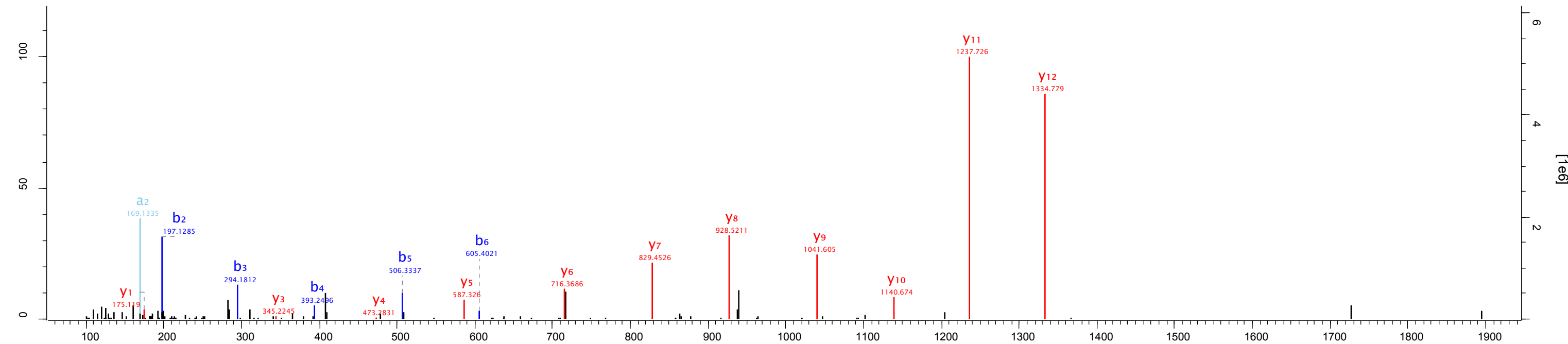




- L Q L L F D L P A L T G S K -

Fragmentation mapping:

- Q: b2
- L: b3
- L: b4
- P: b8
- T: ph
- S: y1
- K: y1
- F: y10
- L: y11
- L: y12



- V P P V I V L E N Q G L R -

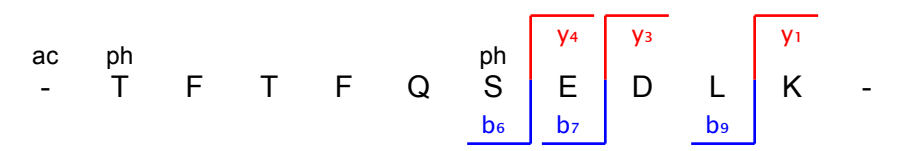
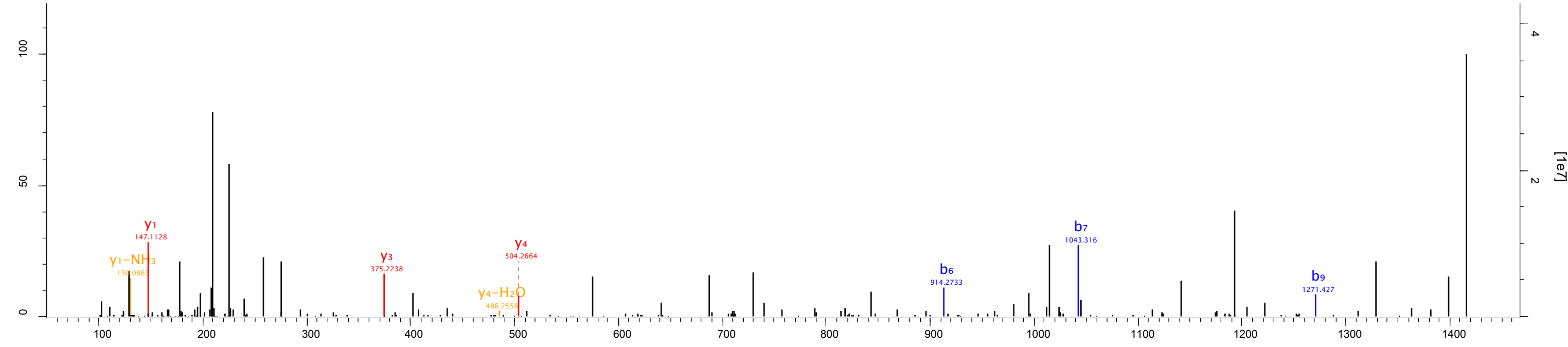
Fragmentation mapping (b and y ions):

- b2: P
- b3: P
- b4: V
- b5: I
- b6: V
- y1: R
- y3: Q
- y4: G
- y5: N
- y6: E
- y7: L
- y8: V
- y9: I
- y10: V
- y11: P
- y12: P

Raw file

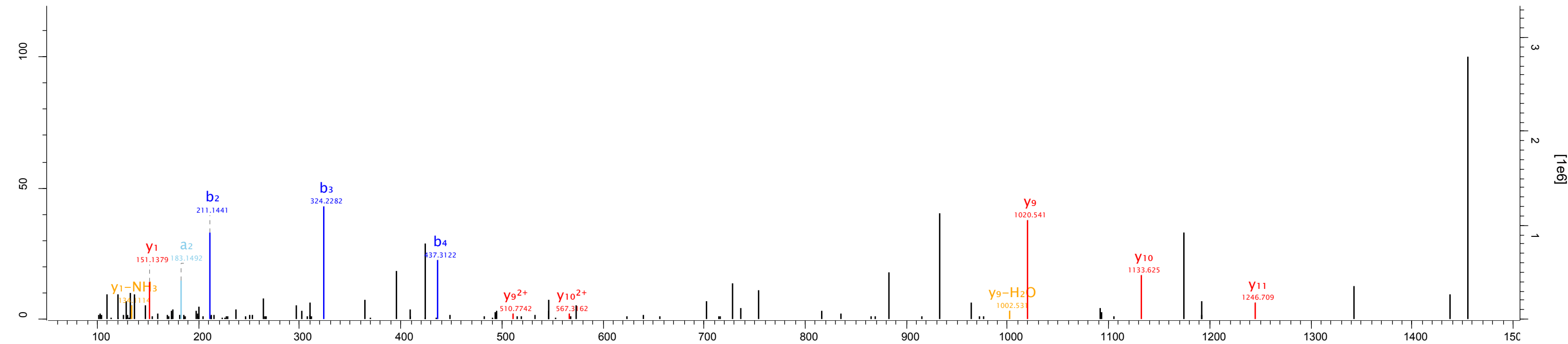
20180707_MaS_A375SR_ML_proteome_15

Scan 8015 Method FTMS; HCD Score 61.59 m/z 709.27 Gene names ZNF704

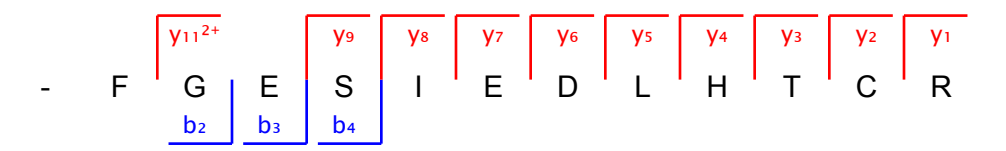
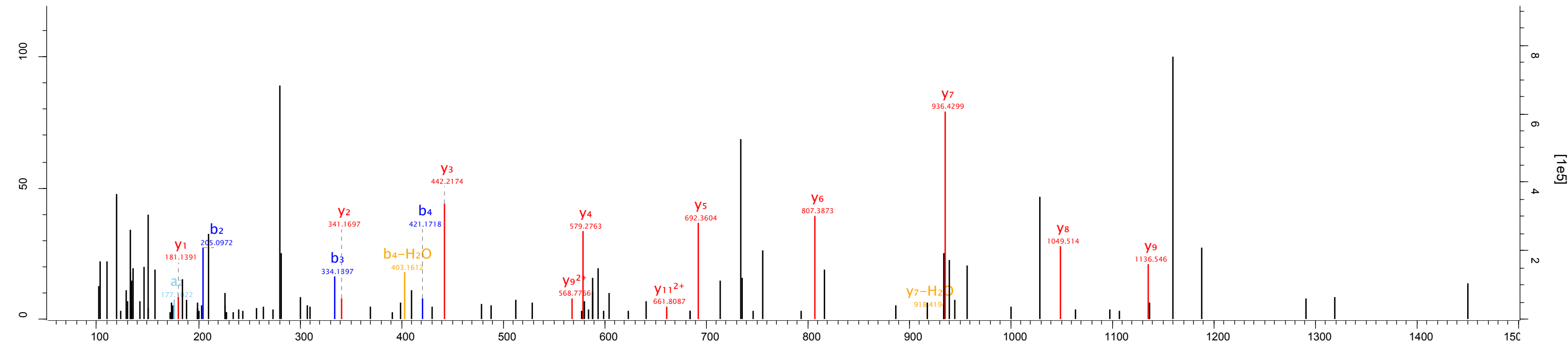


Raw file
20180707_MaS_A375SR_ML_proteome_17

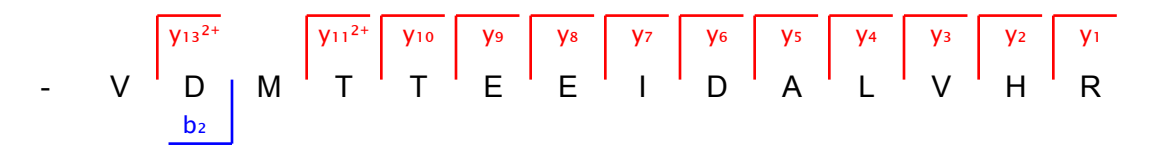
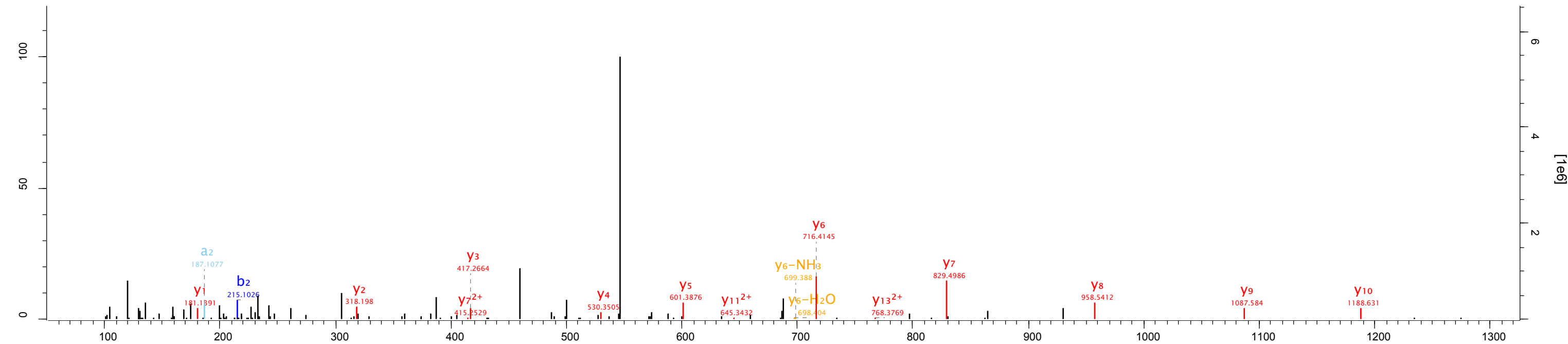
Scan 25815 Method FTMS; HCD Score 50.35 m/z 728.93 Gene names IL1R1



Raw file: 20180707_MaS_A375SR_ML_proteome_18
 Scan: 14795 Method: FTMS; HCD Score: 70.09 m/z: 735.34 Gene names: PIGX

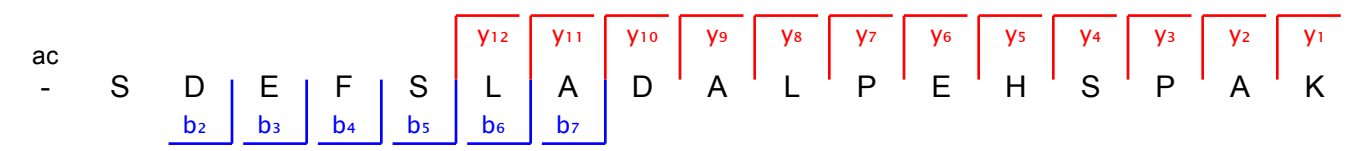
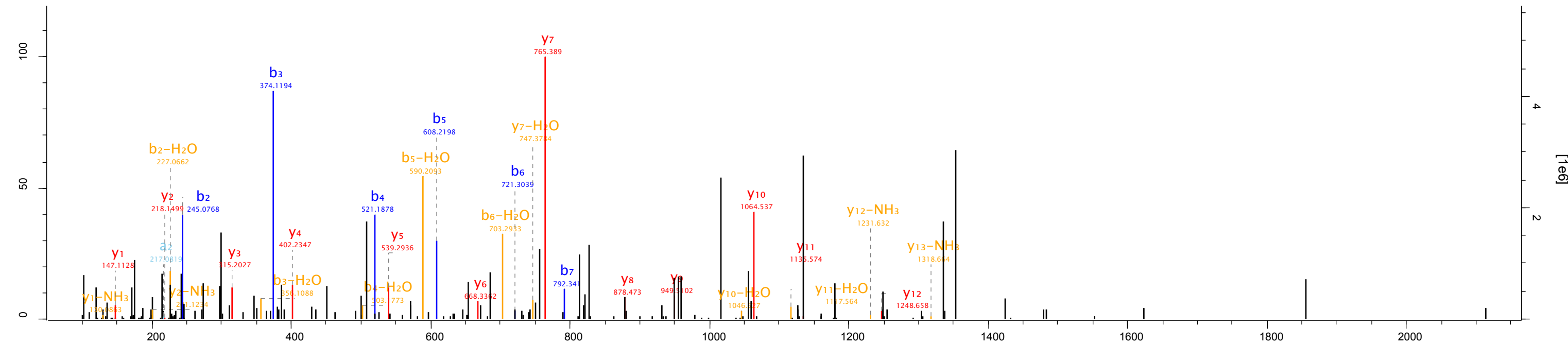


Raw file: 20180707_MaS_A375SR_ML_proteome_18
 Scan: 24505 Method: FTMS; HCD Score: 47.77 m/z: 545.61 Gene names: METAP1D



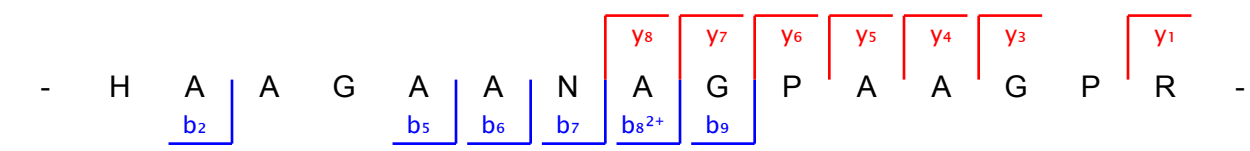
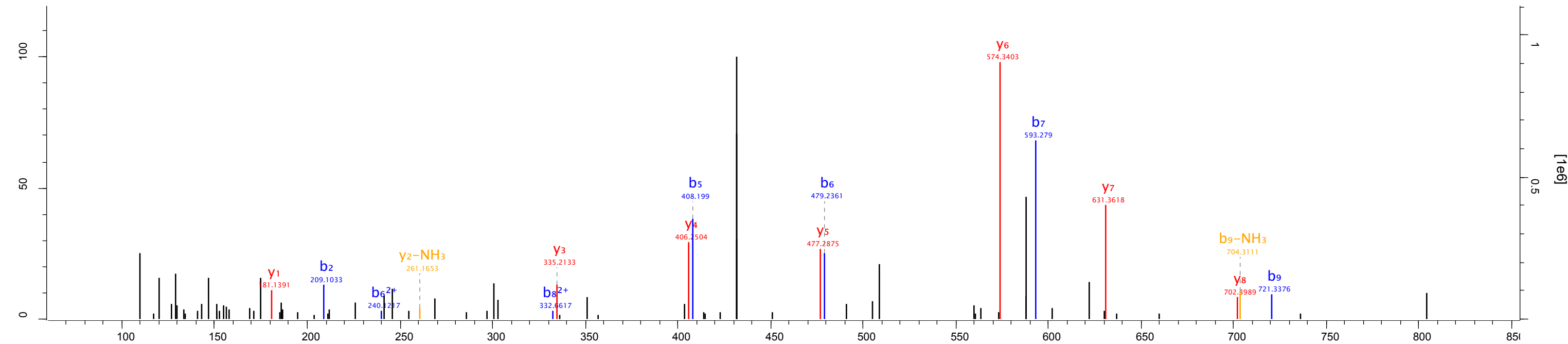
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20180707_MaS_A375SR_ML_proteome_18

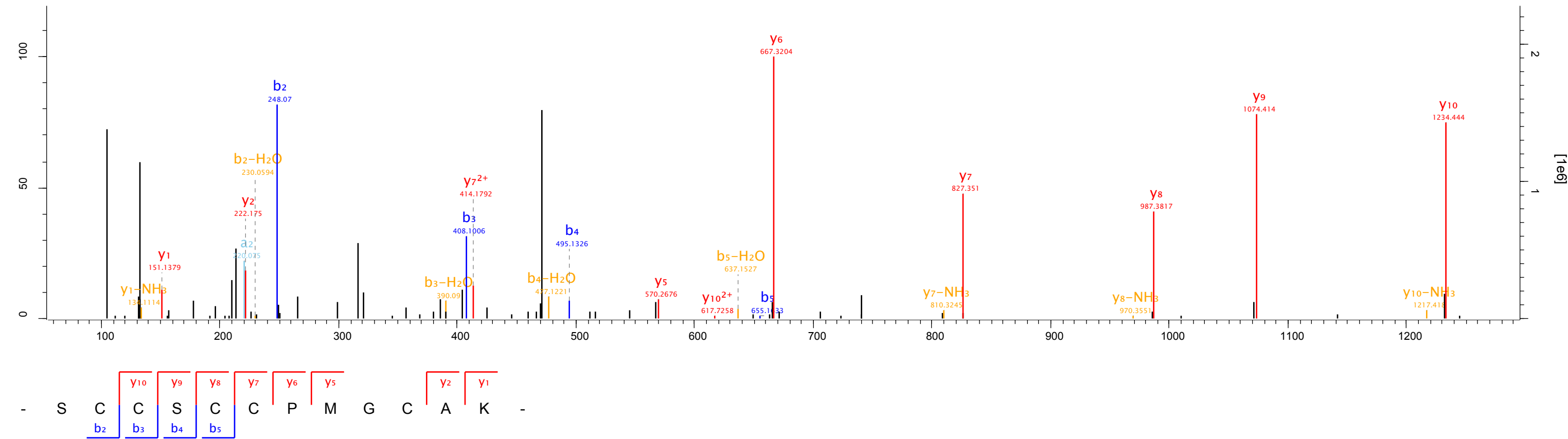
Scan 26405 Method FTMS; HCD Score 90.71 m/z 929.45 Gene names MAPK1IP1L

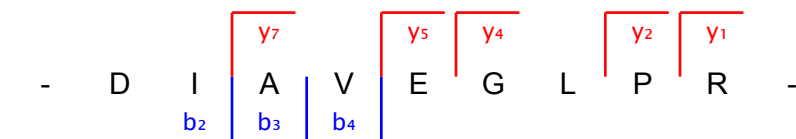
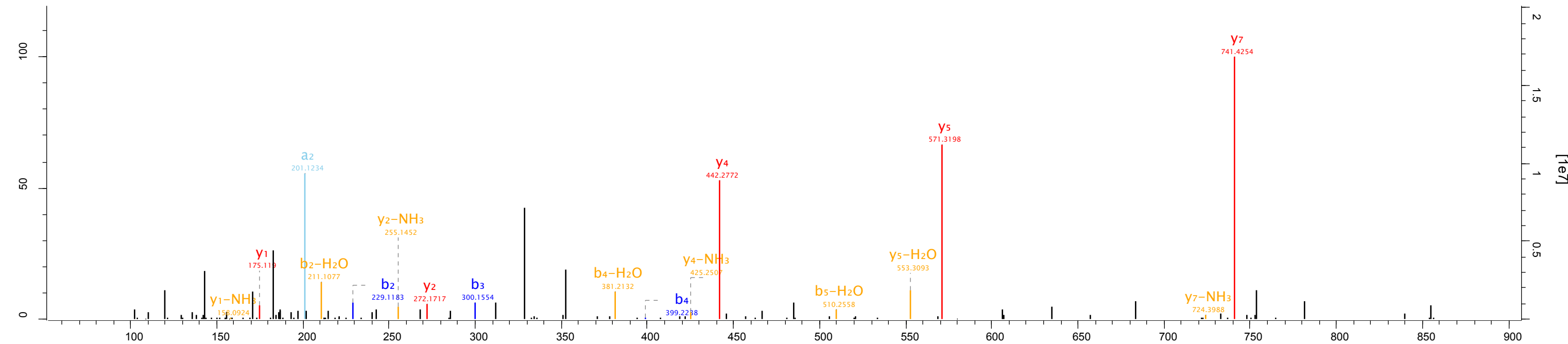


Raw file
20180707_MaS_A375SR_ML_proteome_18

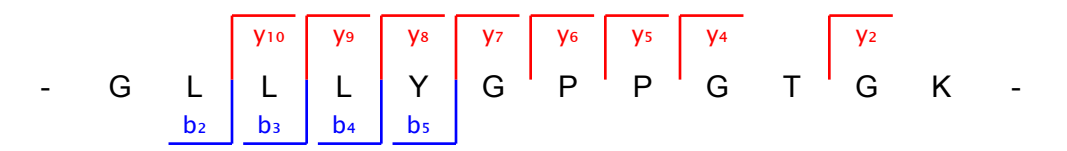
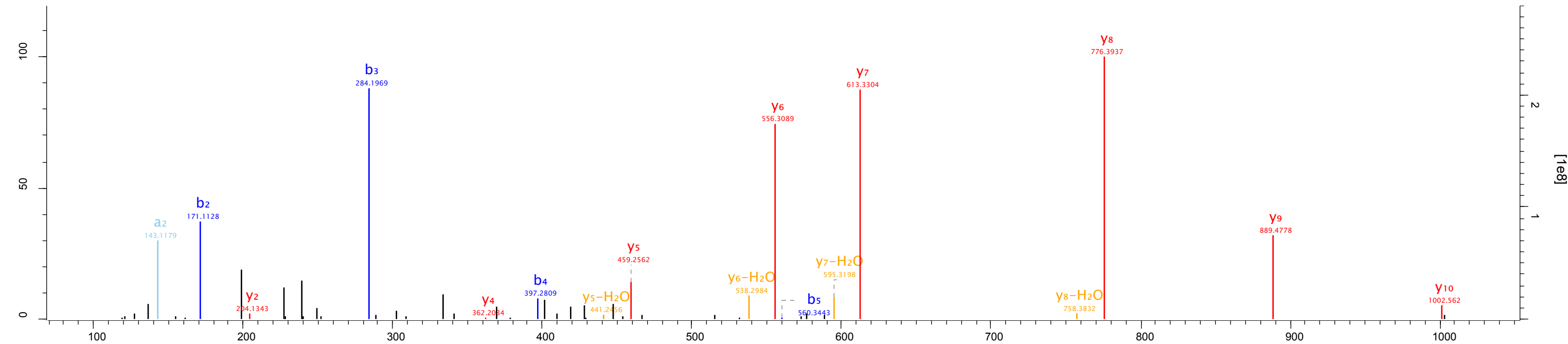
Scan 2815 Method FTMS; HCD Score 40.75 m/z 432.23 Gene names FAM89B



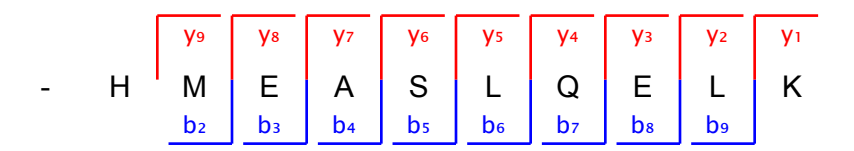
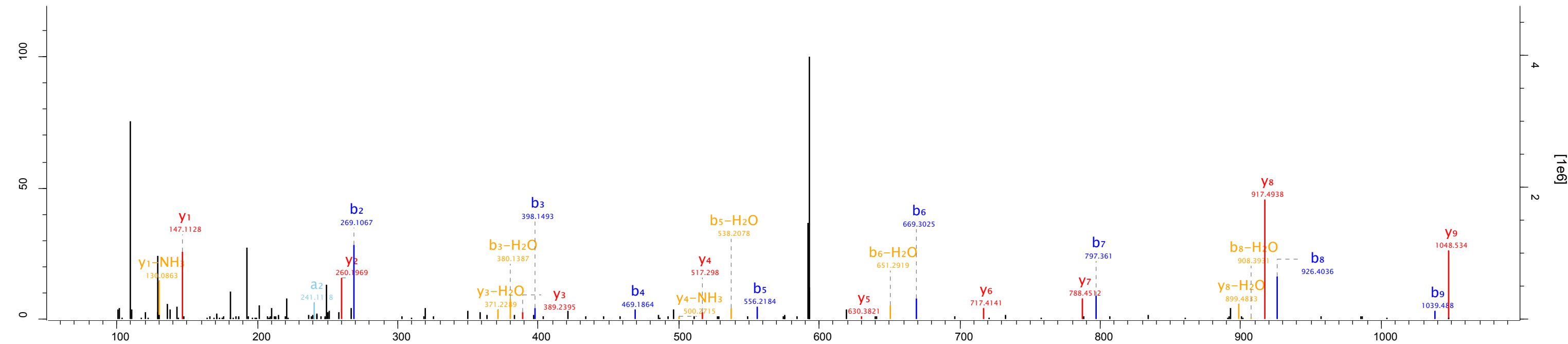




Raw file
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 Scan 21375 Method FTMS; HCD Score 73.44 m/z 586.84 Gene names KATNAL2

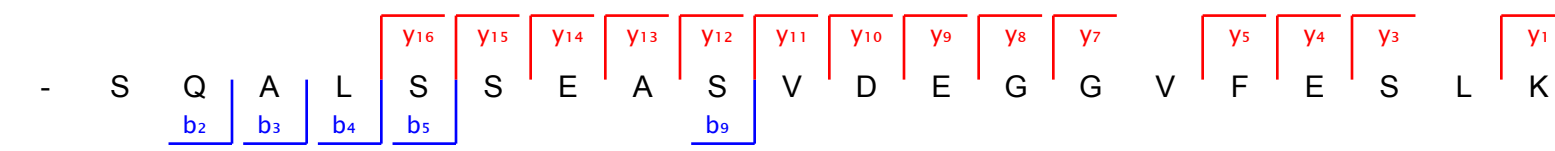
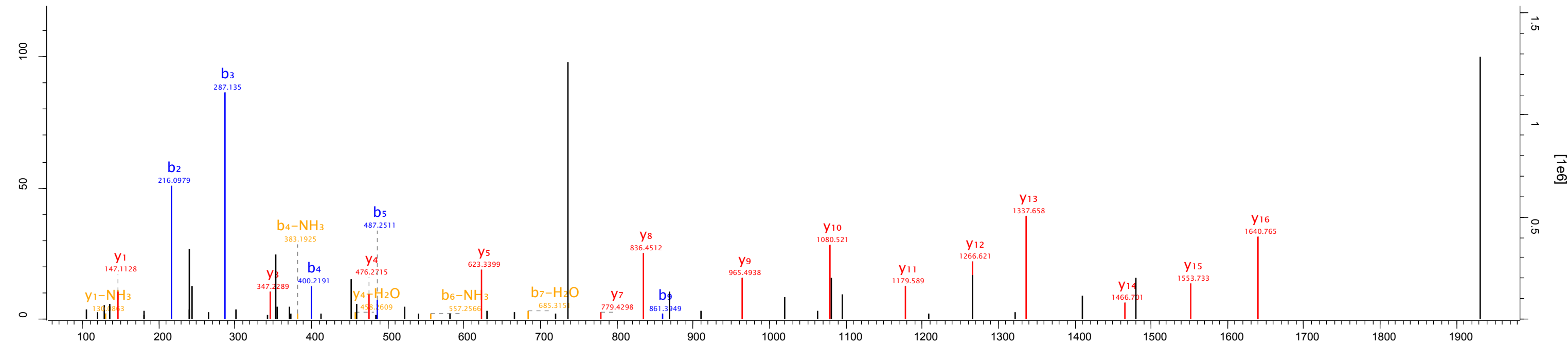


Raw file: 20180707_MaS_A375SR_ML_proteome_2_01
 Scan: 11765 Method: FTMS; HCD Score: 136.96 m/z: 593.3 Gene names: IGFBP5

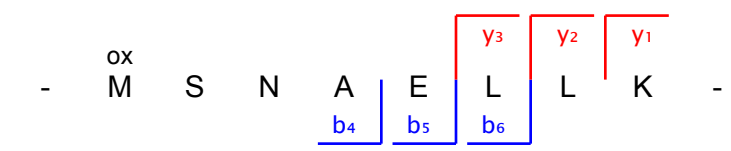
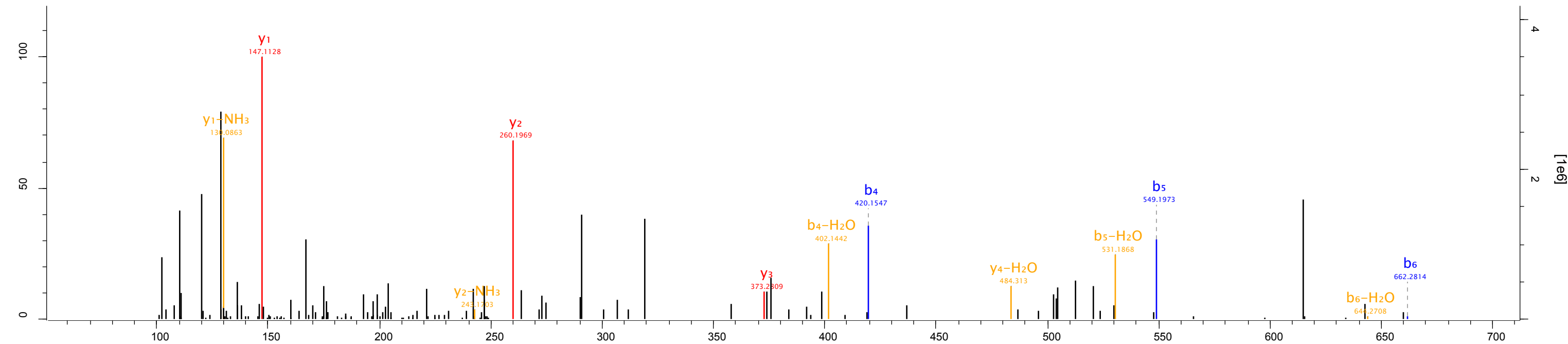


Raw file
20180707_MaS_A375SR_ML_proteome_2_01

Scan 23605 Method FTMS; HCD Score 68.42 m/z 1020.99 Gene names RNFT2

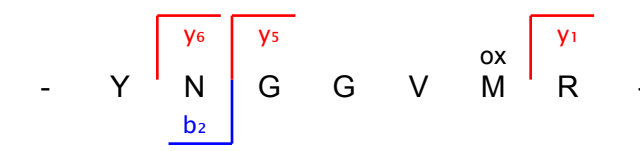
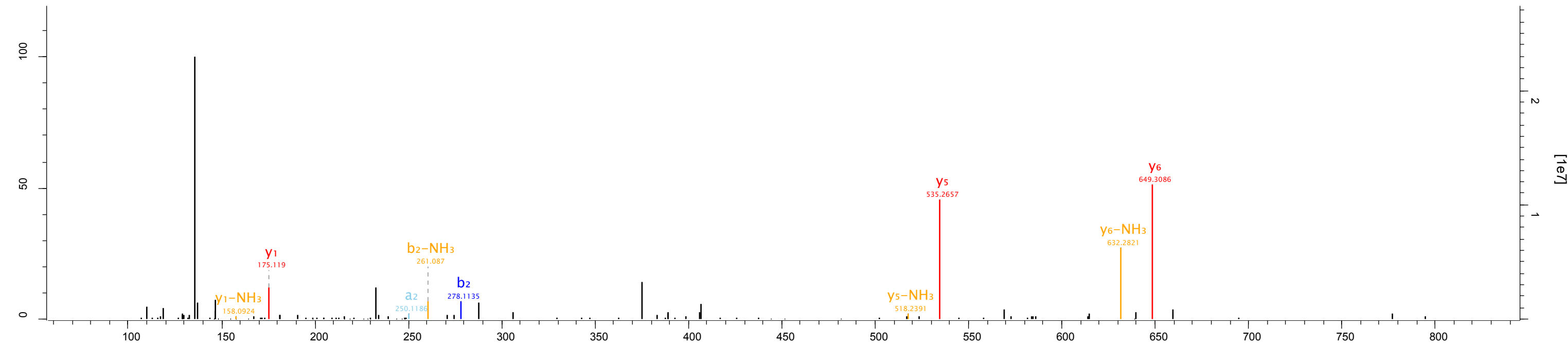


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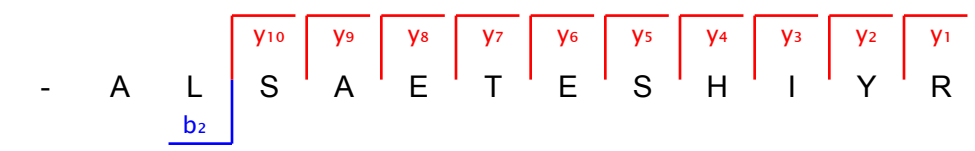
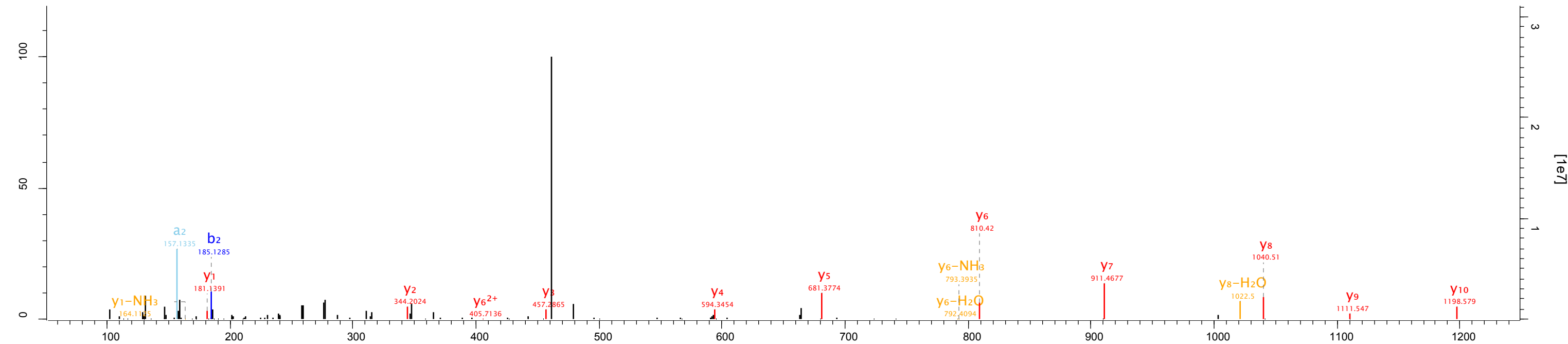


Raw file
20180707_MaS_A375SR_ML_proteome_2_01

Scan	Method	Score	m/z	Gene names
5135	FTMS; HCD	54.53	406.69	KCNN2

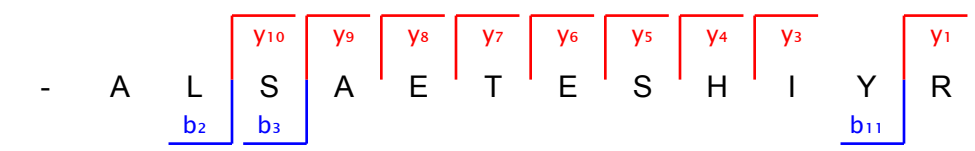
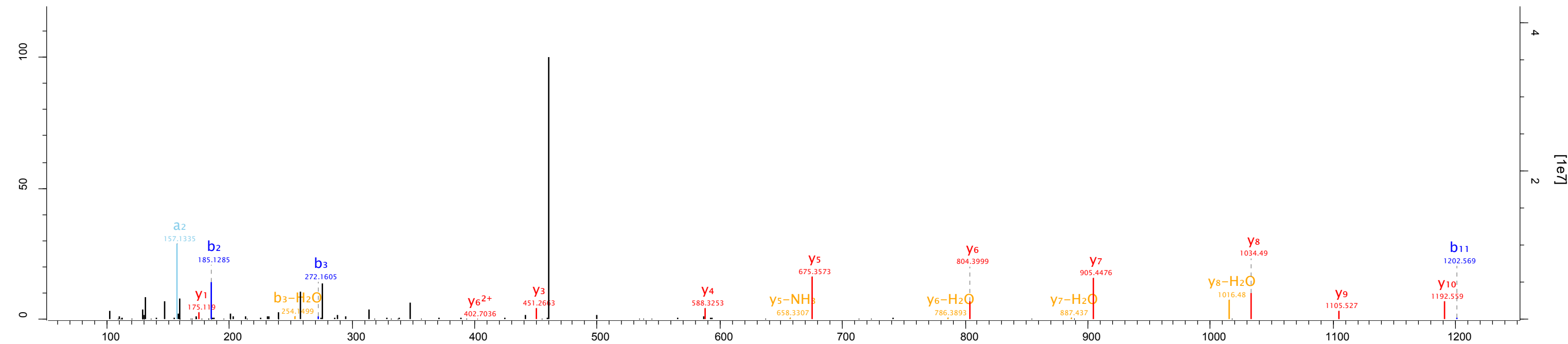


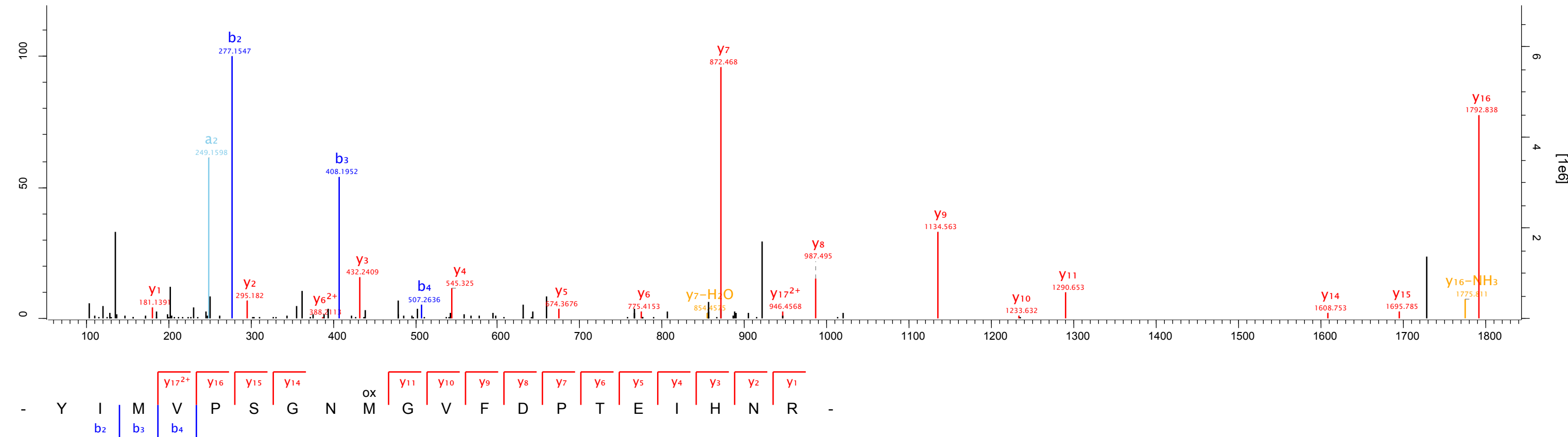
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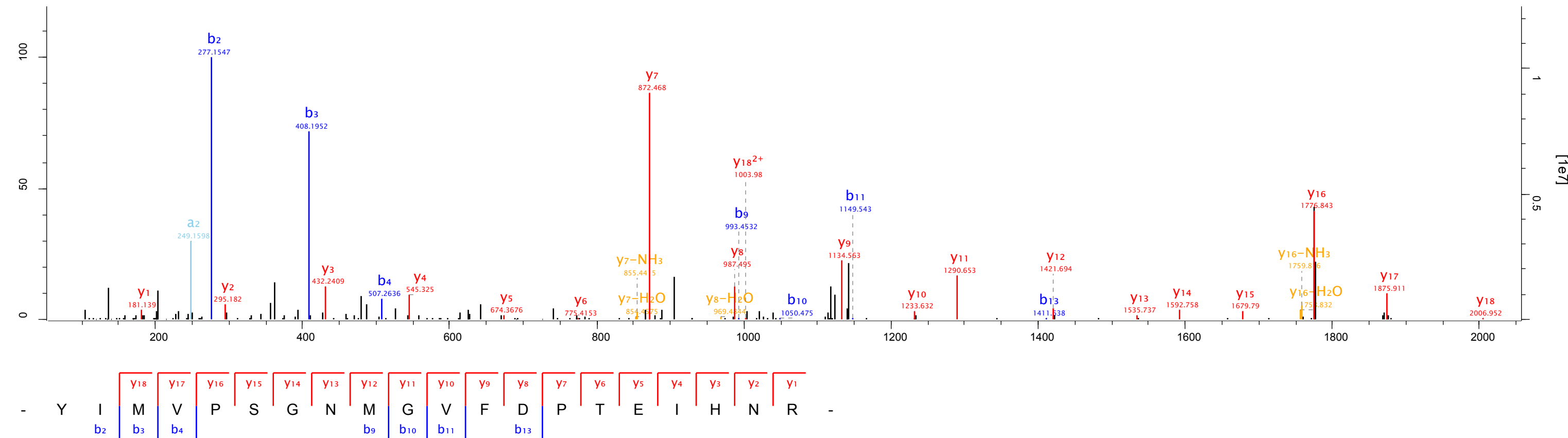


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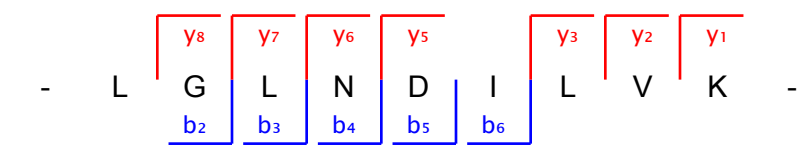
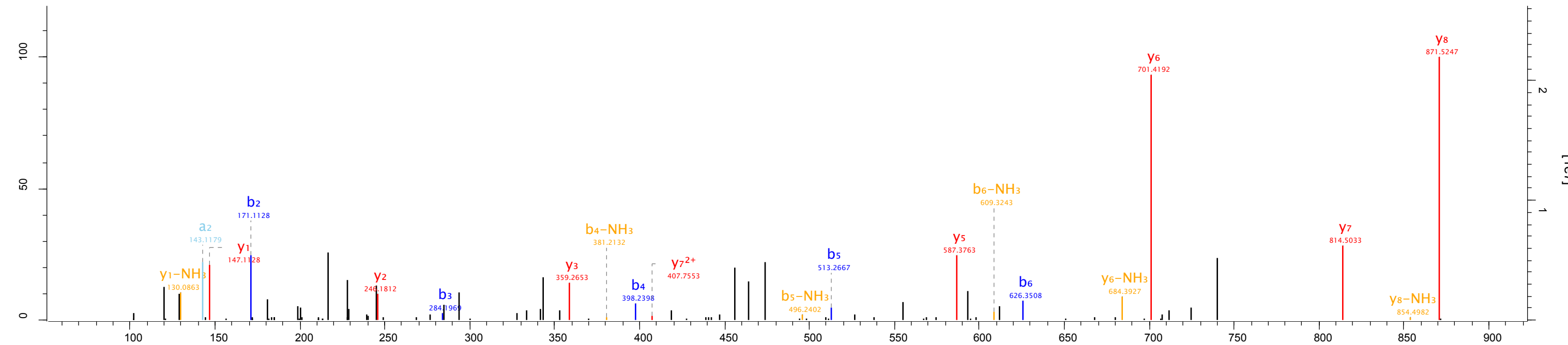
Scan 9685 Method FTMS; HCD Score 90.61 m/z 459.56 Gene names CYB561D2



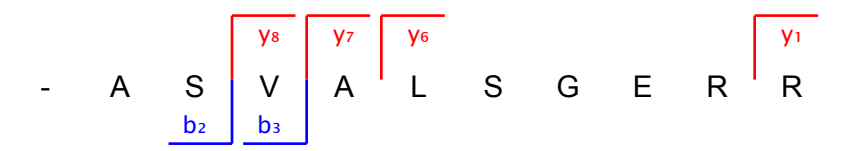
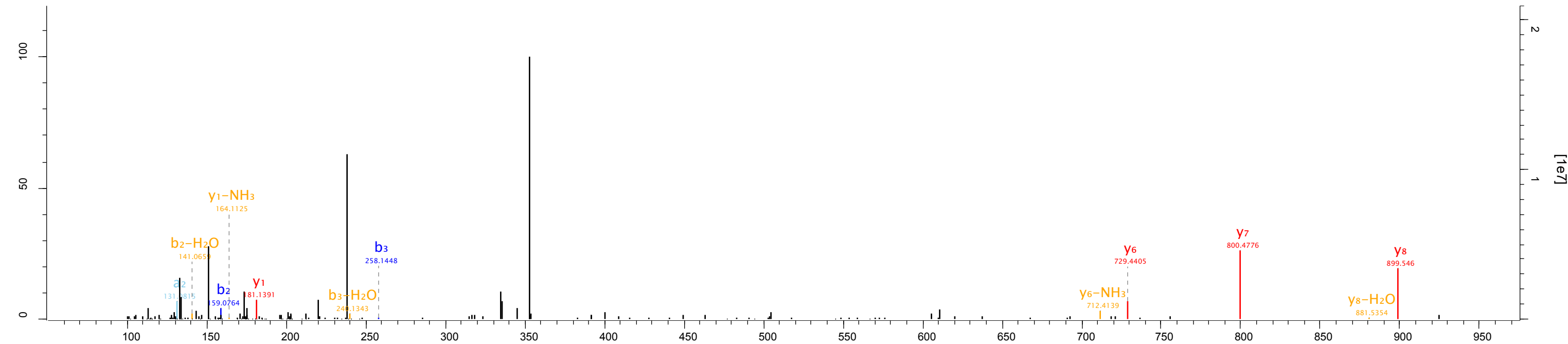




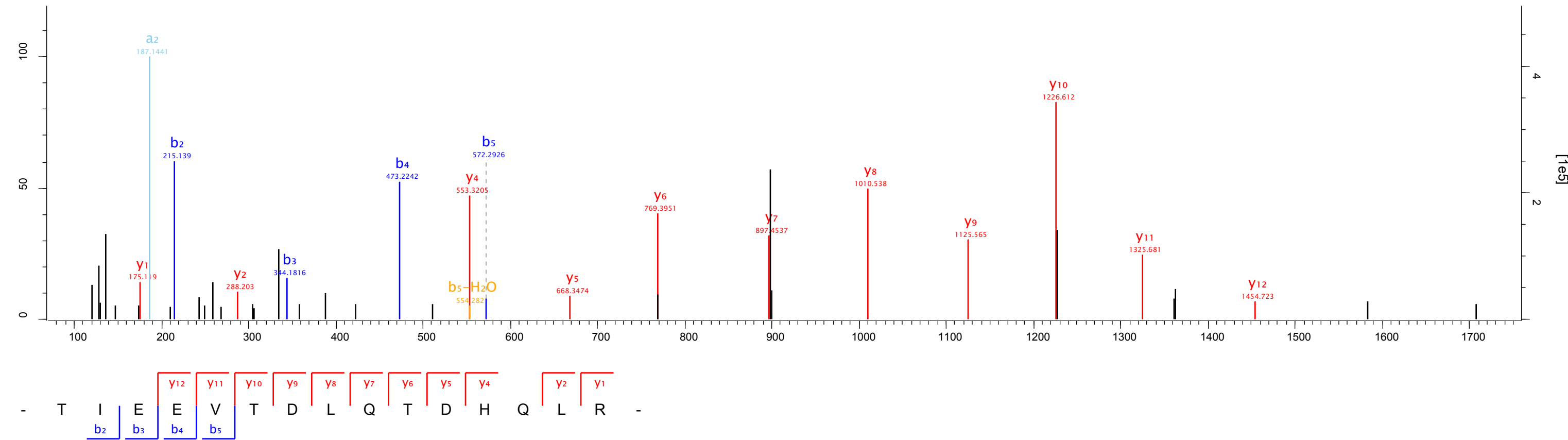
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 Scan 26465 Method FTMS; HCD Score 110.88 m/z 492.81 Gene names STON2



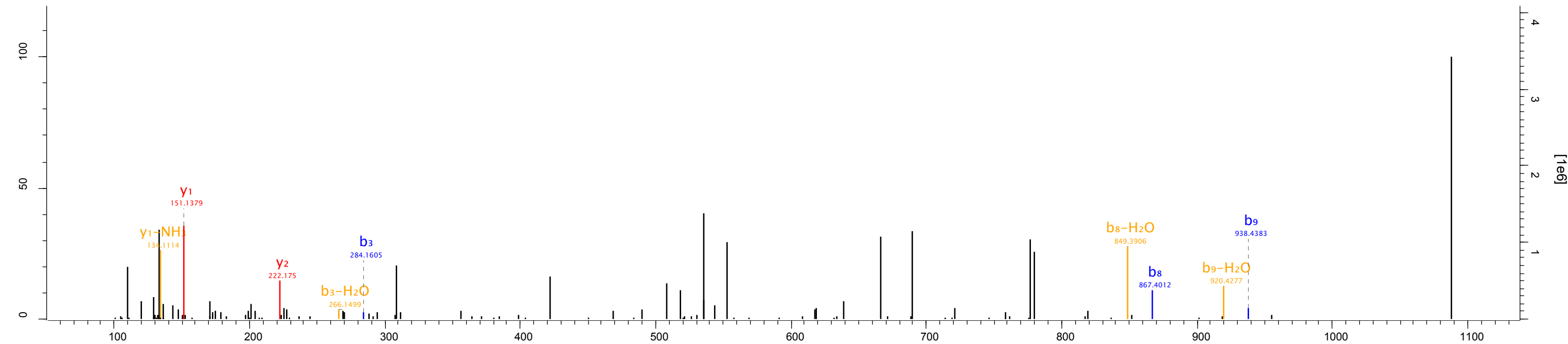
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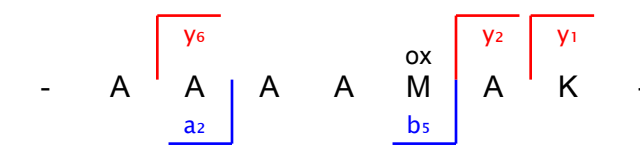
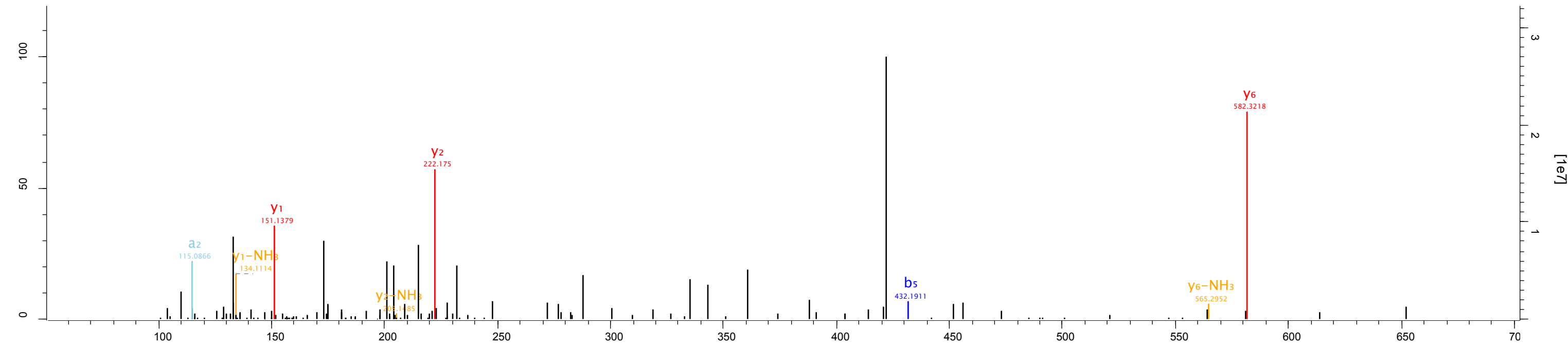
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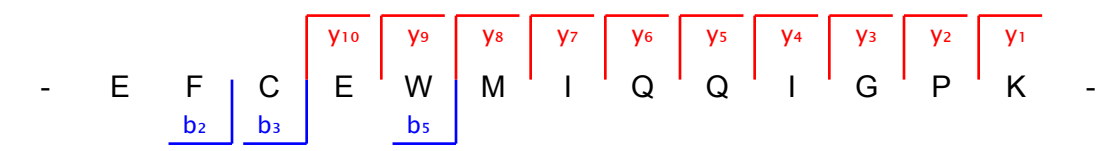
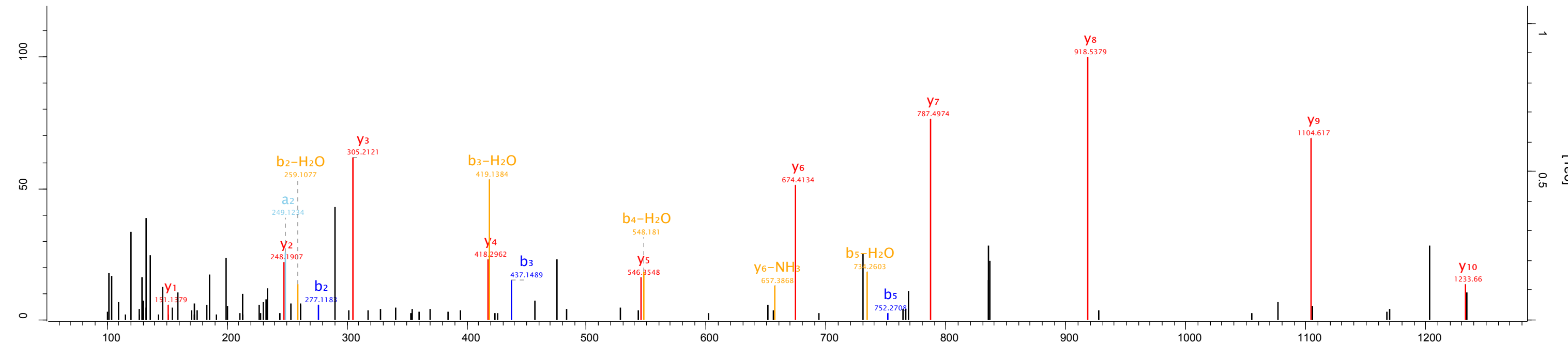
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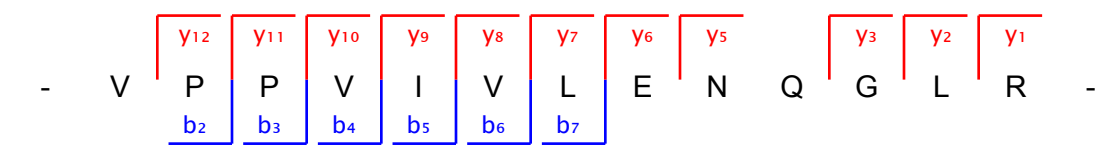
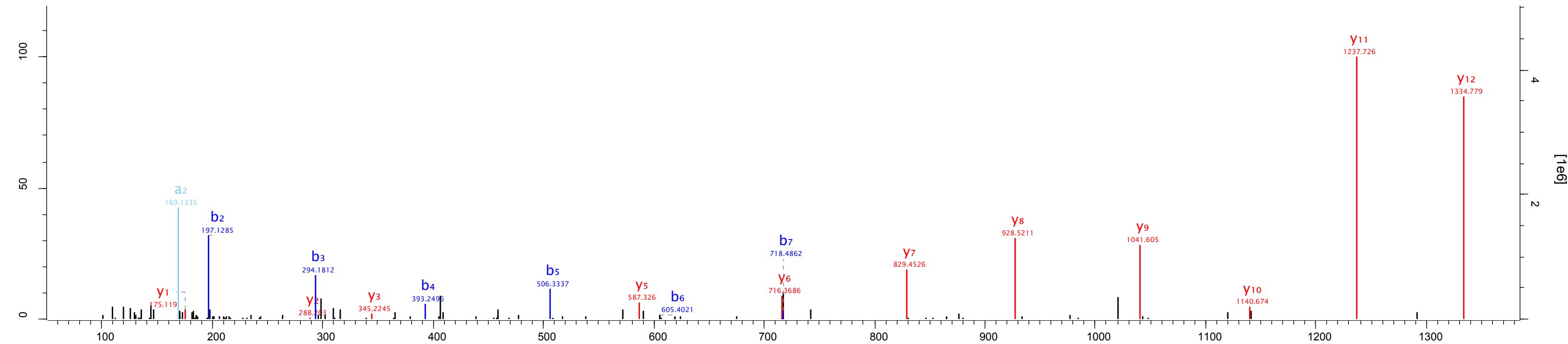
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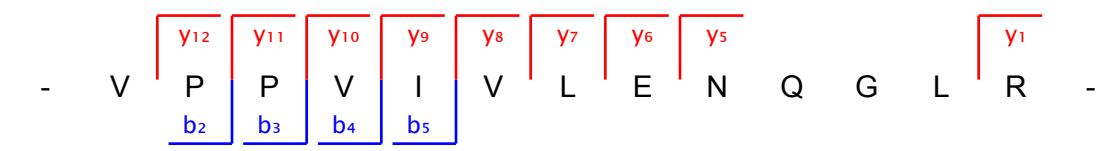
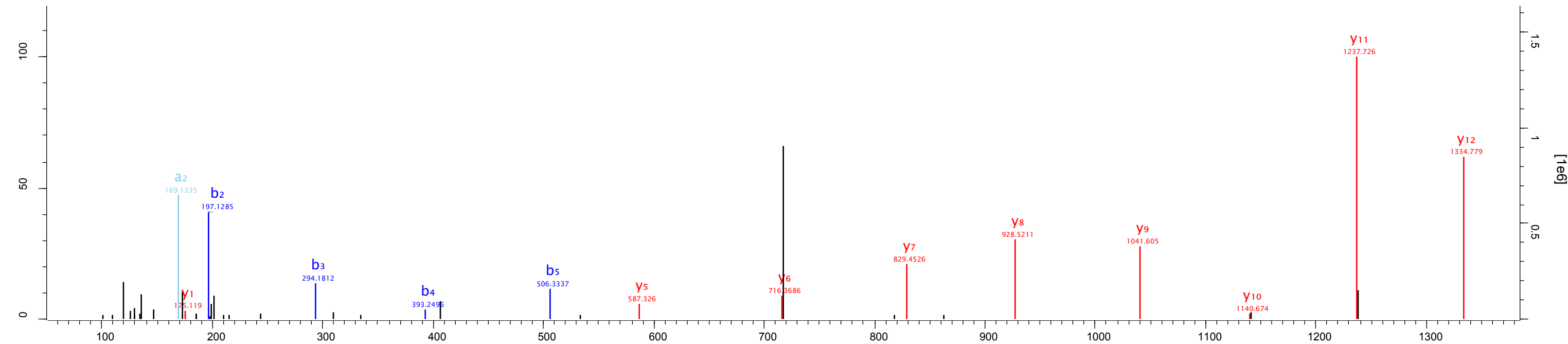
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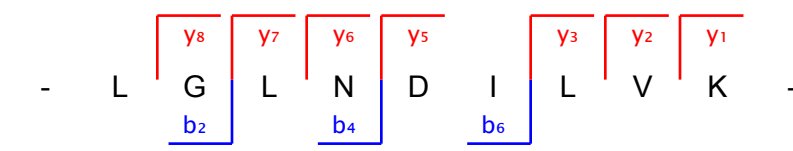
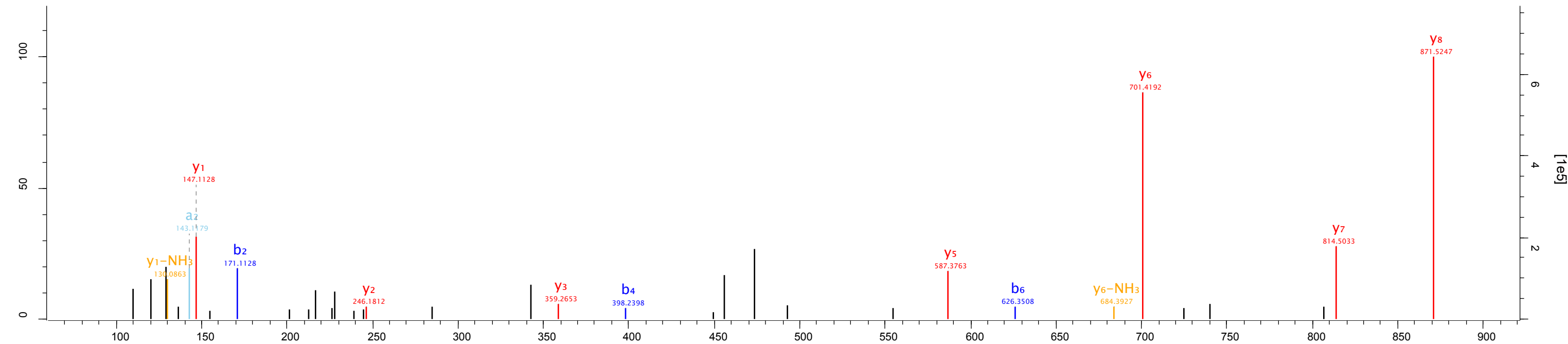
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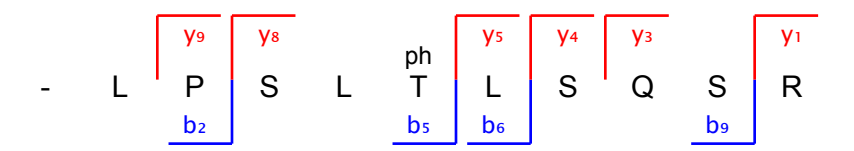
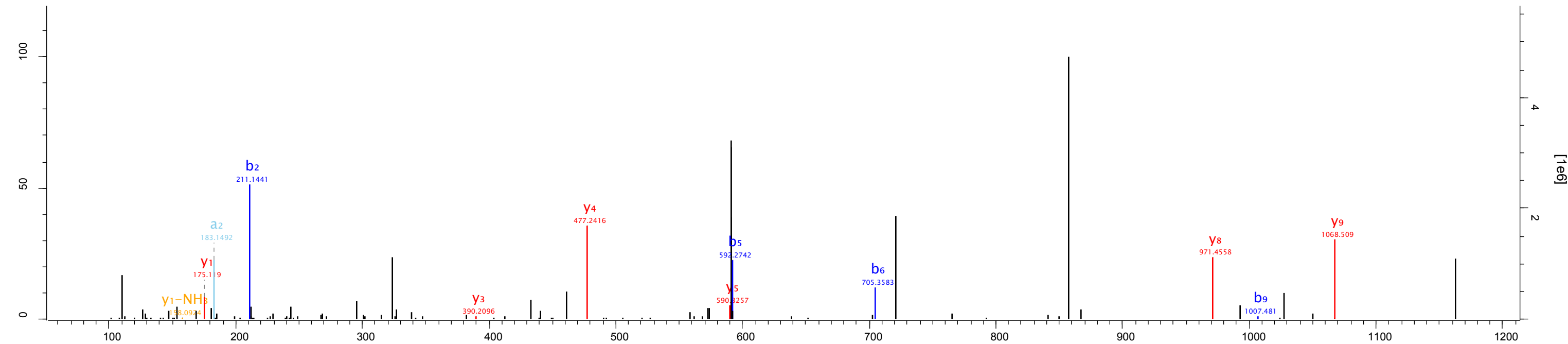
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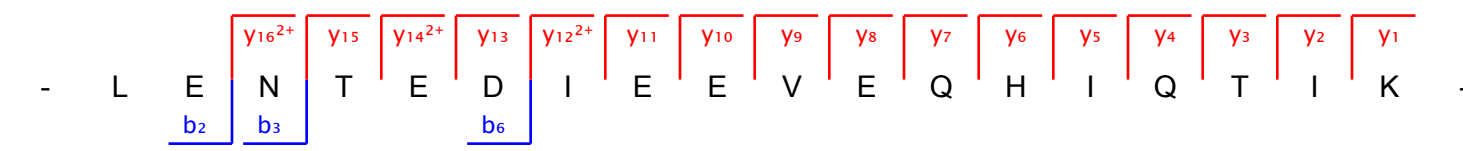
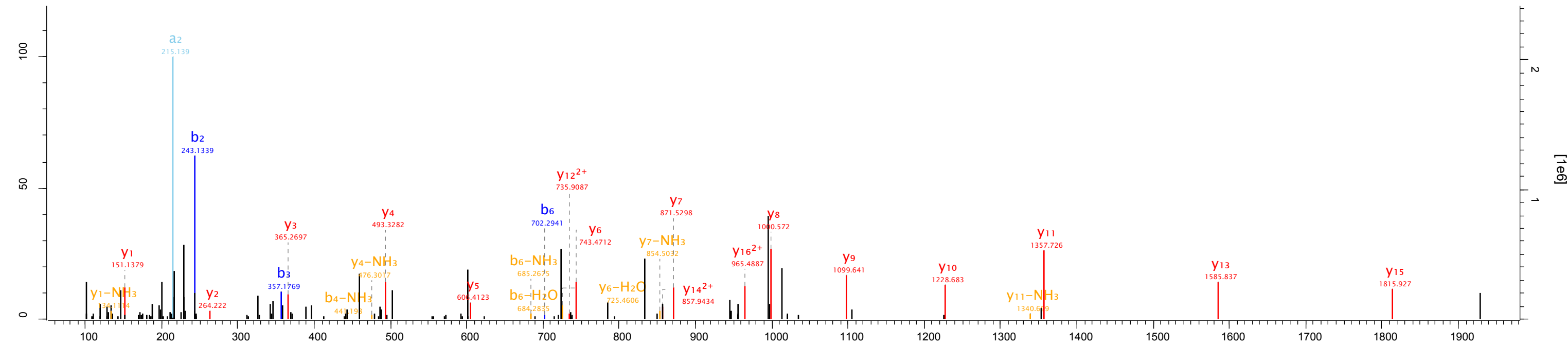
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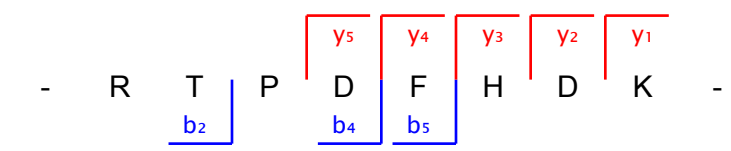
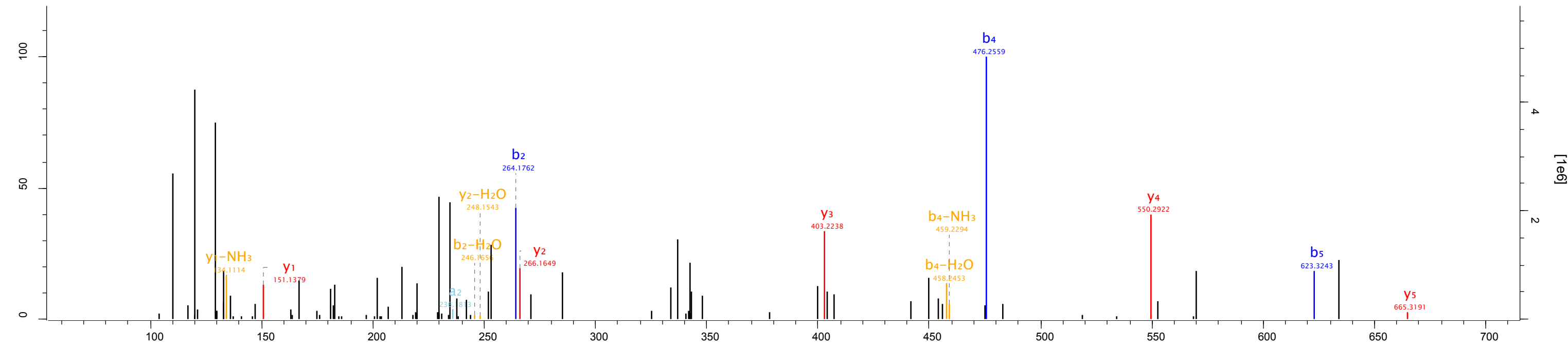
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Raw file: 20180707_MaS_A375SR_ML_proteome_2_07
 Scan: 23445 Method: FTMS; HCD Score: 81.85 m/z: 724.7 Gene names: LMBRD1

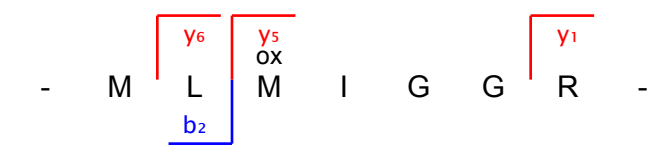
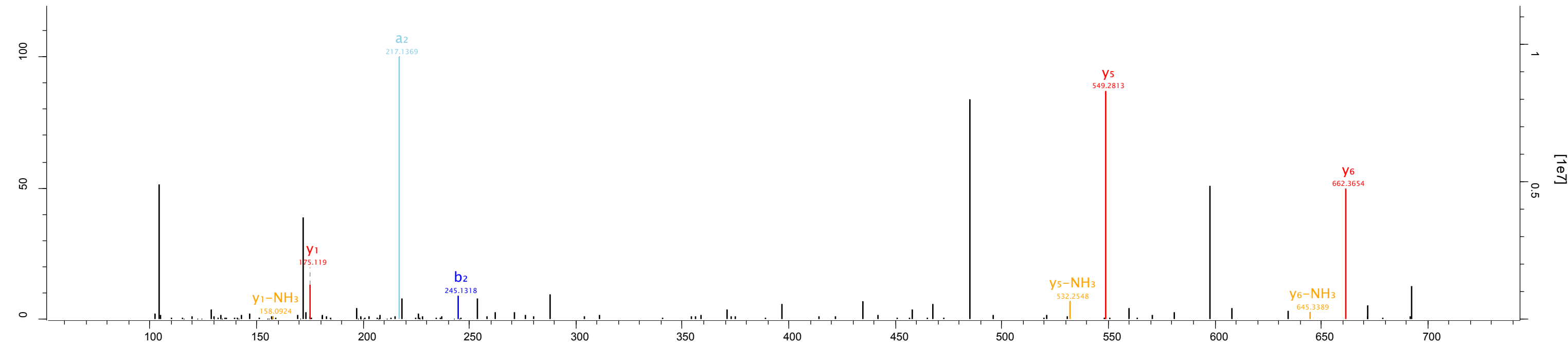


Raw file 20180707_MaS_A375SR_ML_proteome_2_08 Scan 3195 Method FTMS; HCD Score 45.02 m/z 342.52 Gene names COX7B

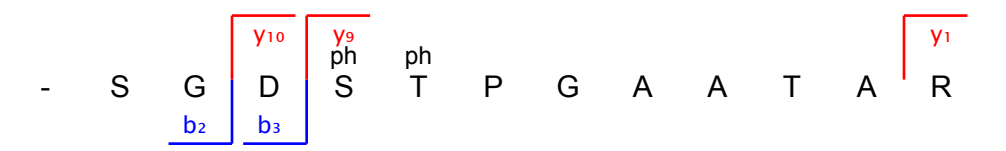
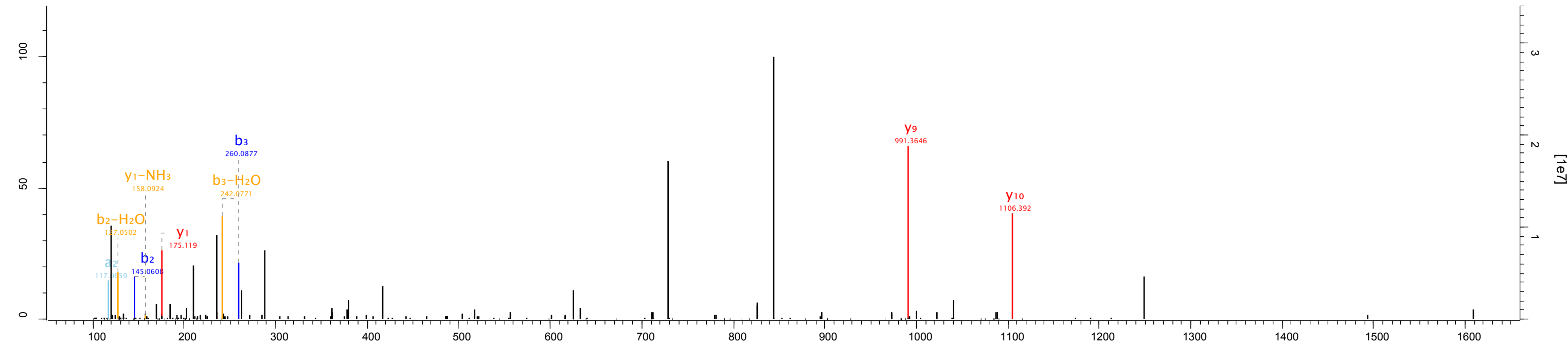


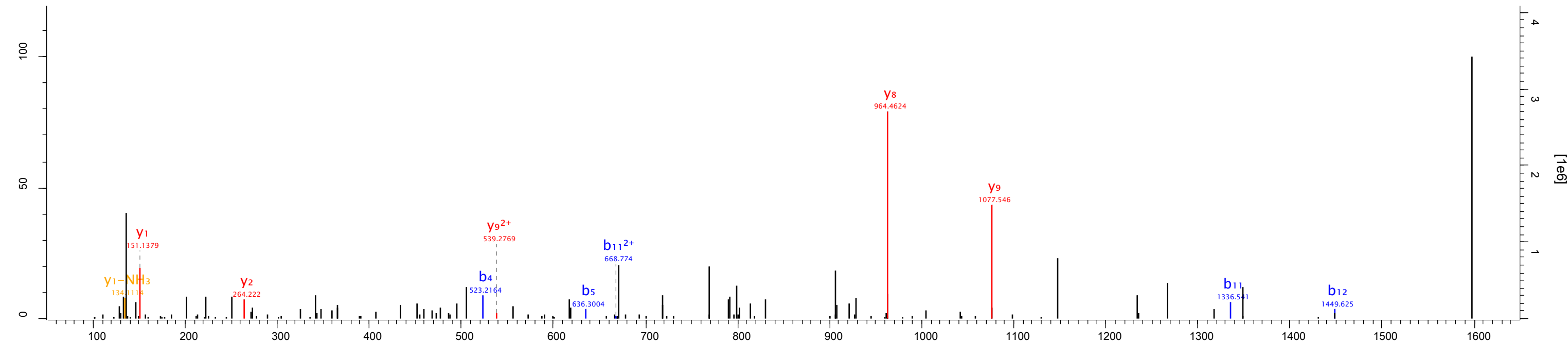
Raw file
20180707_MaS_A375SR_ML_proteome_2_08

Scan	Method	Score	m/z
9395	FTMS; HCD	44.97	397.21



Raw file
 20180707_MaS_A375SR_ML_proteome_2_09
 Scan 14975 Method FTMS; HCD Score 54.78 m/z 625.73



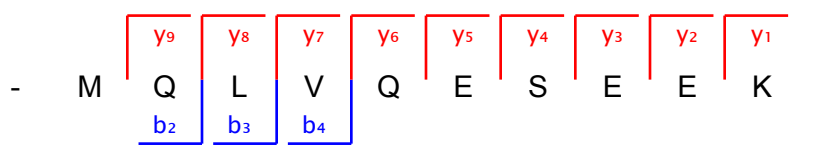
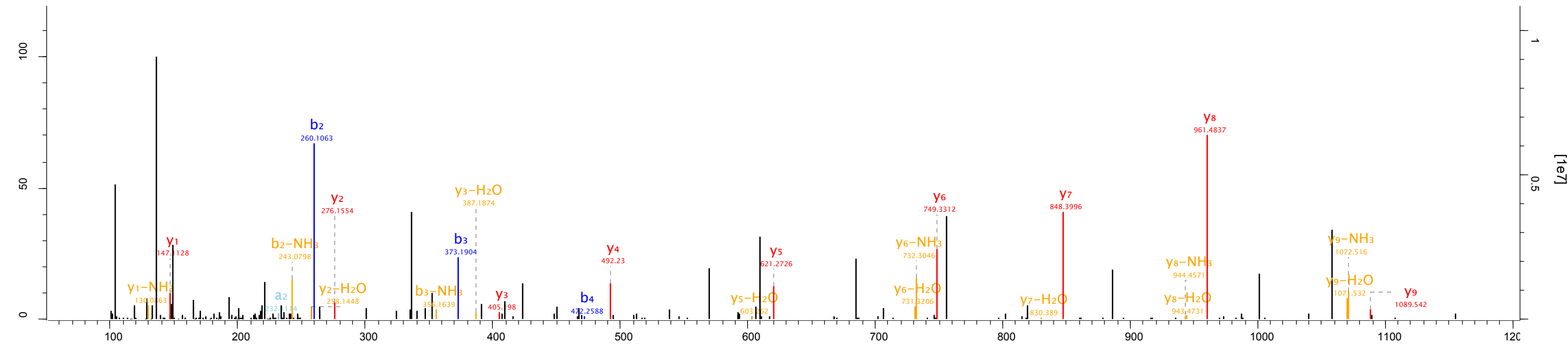


- ph S L I E L P H ph S A P M L K -

Fragmentation labels (b and y ions) are shown below the corresponding amino acids:

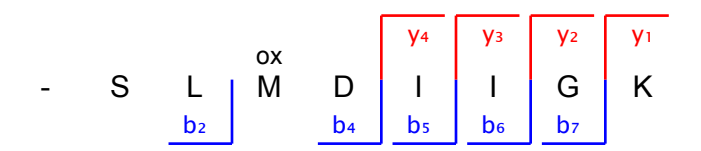
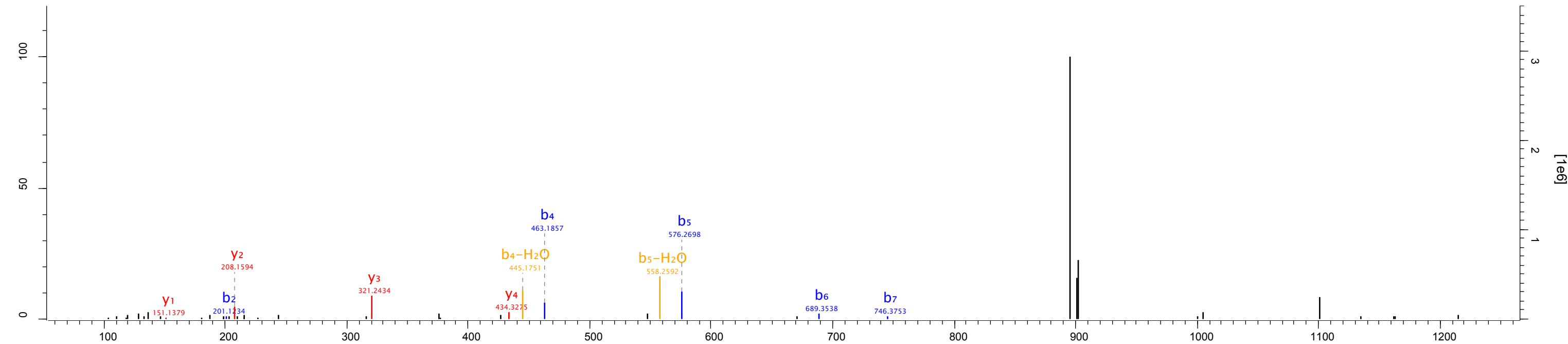
- b₄ (under E)
- b₅ (under L)
- b₁₁ (under M)
- b₁₂ (under L)
- y₉ (above E)
- y₈ (above P)
- y₂ (above L)
- y₁ (above K)

Raw file: 20180707_MaS_A375SR_ML_proteome_2_11
 Scan: 10705 Method: FTMS; HCD Score: 112.95 m/z: 610.79



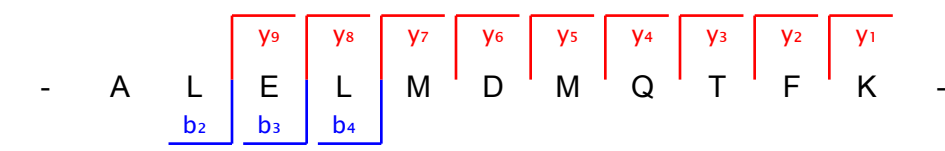
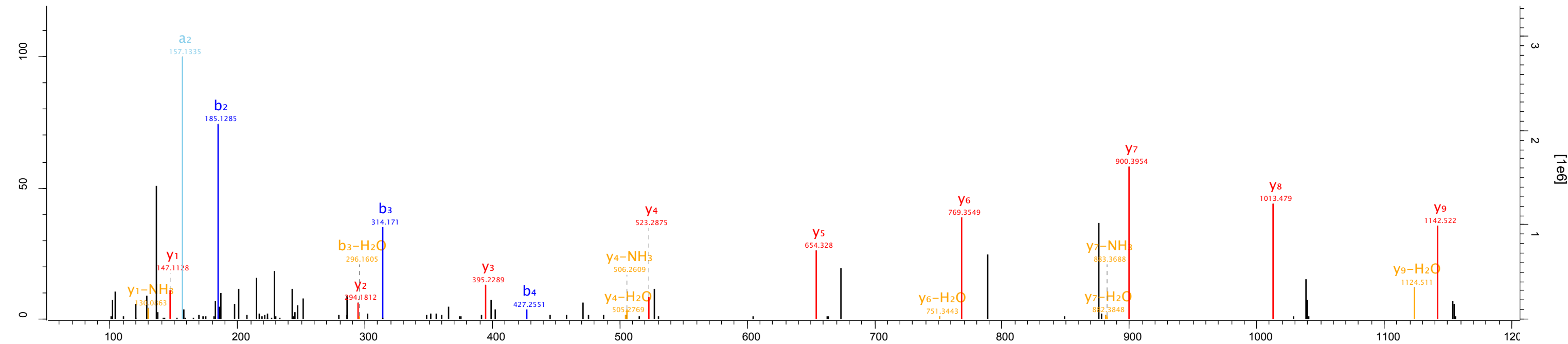
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20180707_MaS_A375SR_ML_proteome_2_11

Scan 23585 Method FTMS; HCD Score 68.91 m/z 896.5 Gene names MYO16



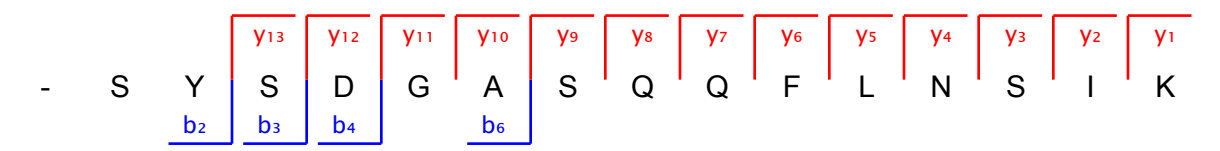
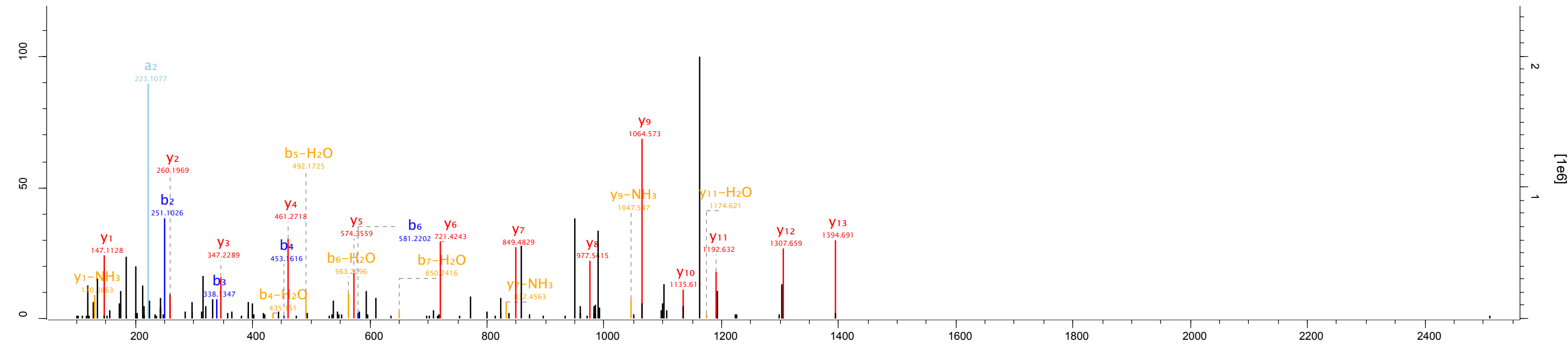
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20180707_MaS_A375SR_ML_proteome_2_11

Scan 27835 Method FTMS; HCD Score 101.39 m/z 663.83 Gene names ANKRD30A



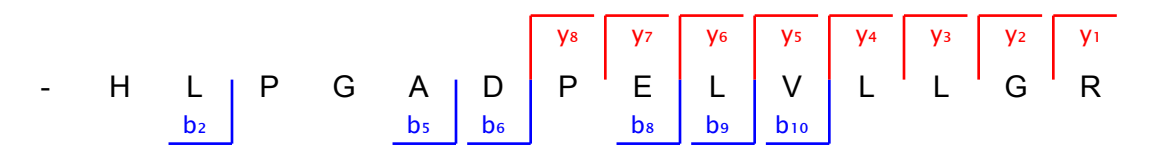
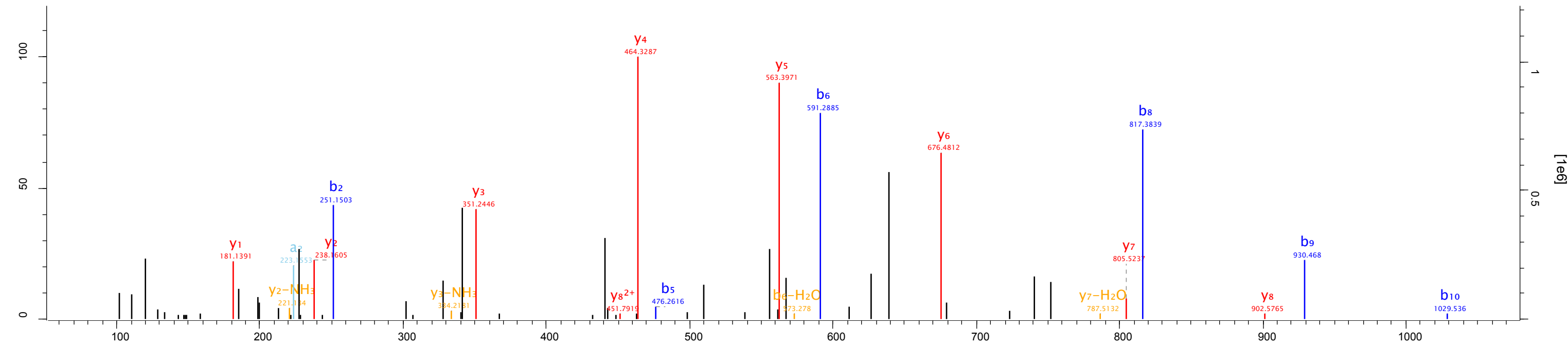
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20180707_MaS_A375SR_ML_proteome_2_13

Scan: 21505
Method: FTMS; HCD
Score: 96.49
m/z: 823.4
Gene names: UBXN2A



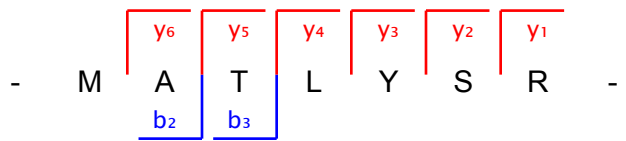
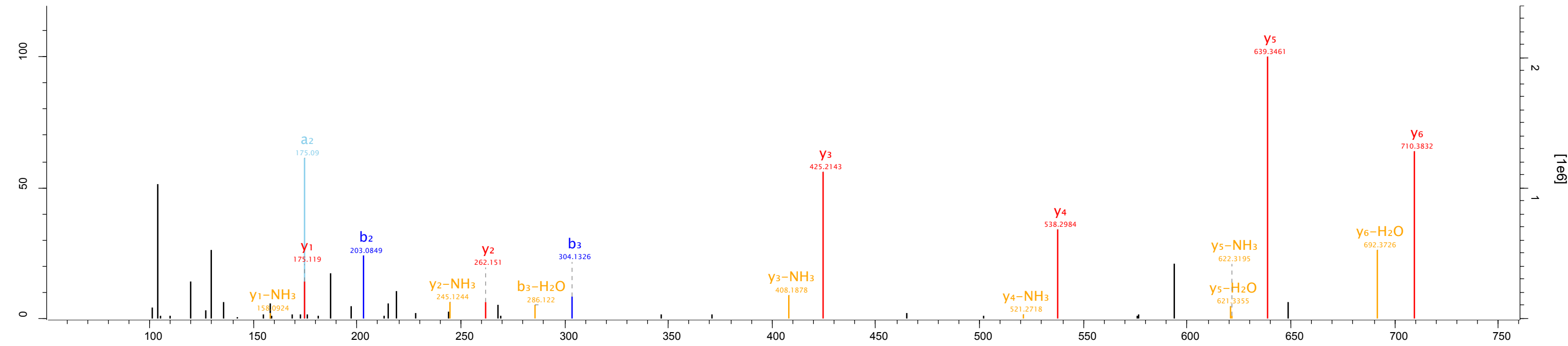
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20180707_MaS_A375SR_ML_proteome_2_13

Scan 24635 Method FTMS; HCD Score 94.12 m/z 498.29 Gene names SELM

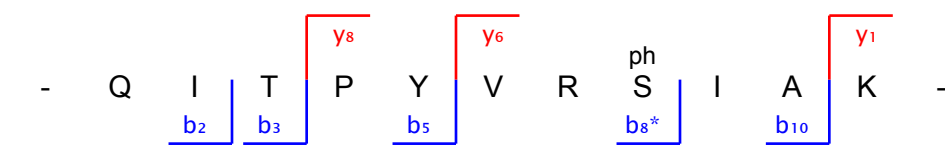
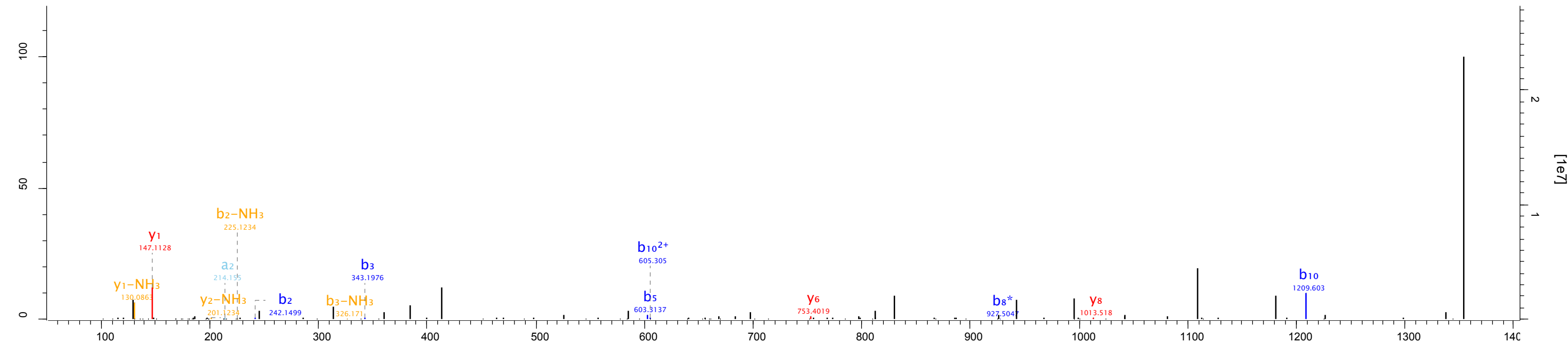


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20180707_MaS_A375SR_ML_proteome_2_14

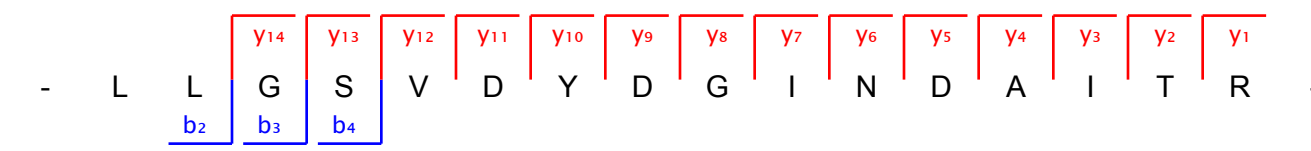
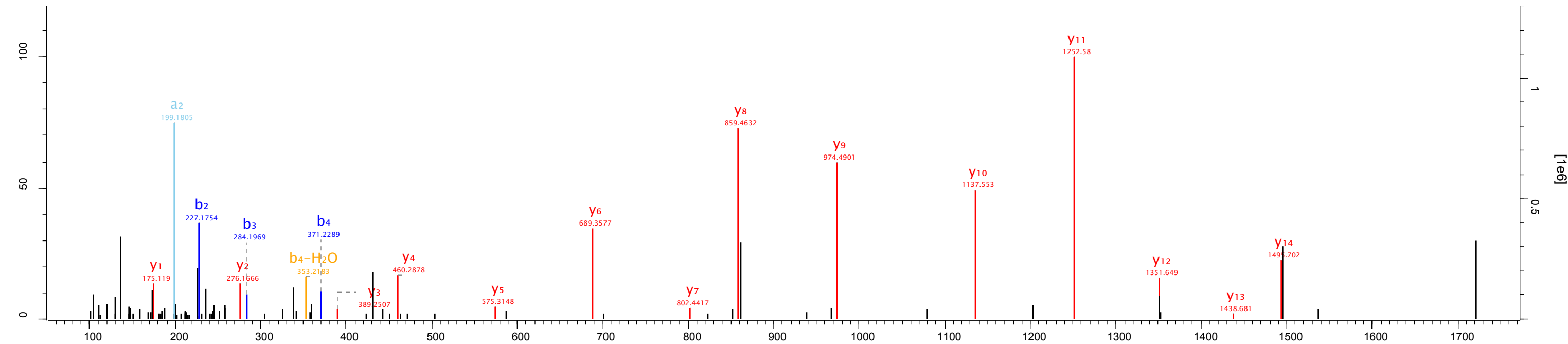
Scan 10605 Method FTMS; HCD Score 130.77 m/z 421.22 Gene names PTGDS



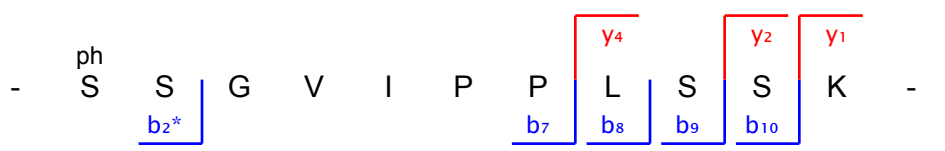
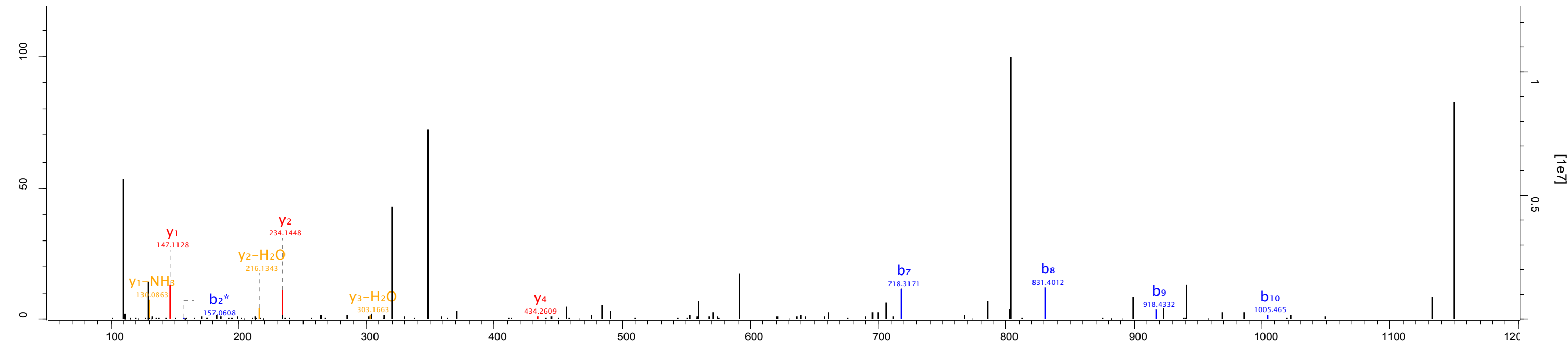
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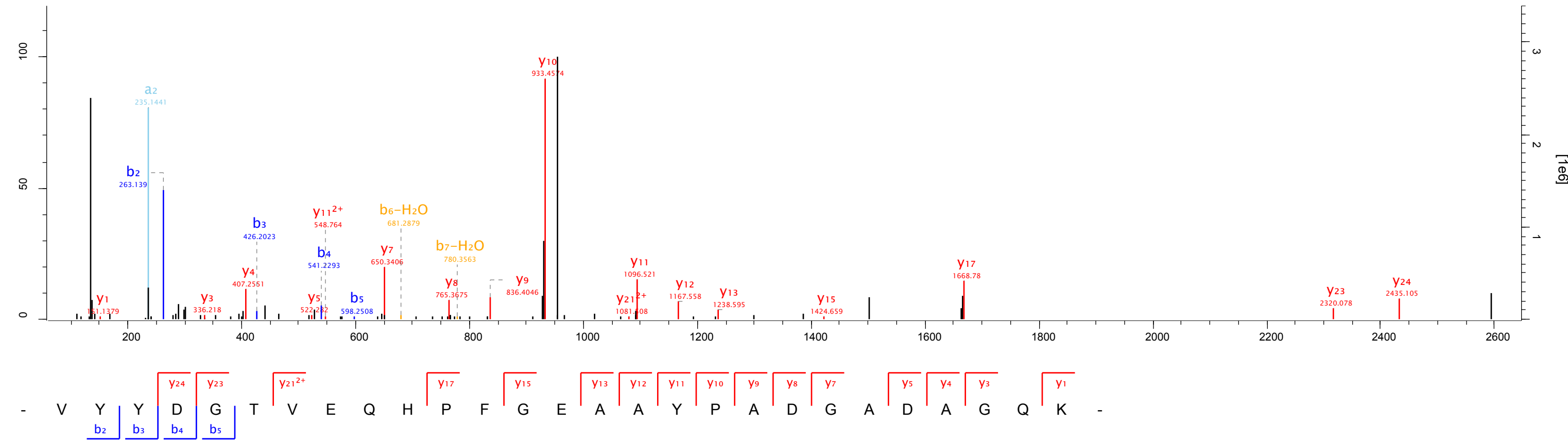


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 20180707_MaS_A375SR_ML_proteome_2_16
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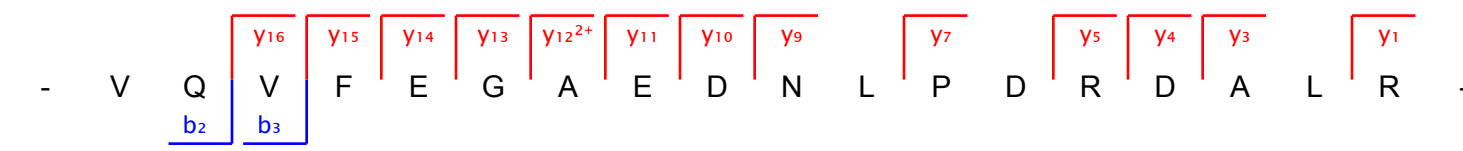
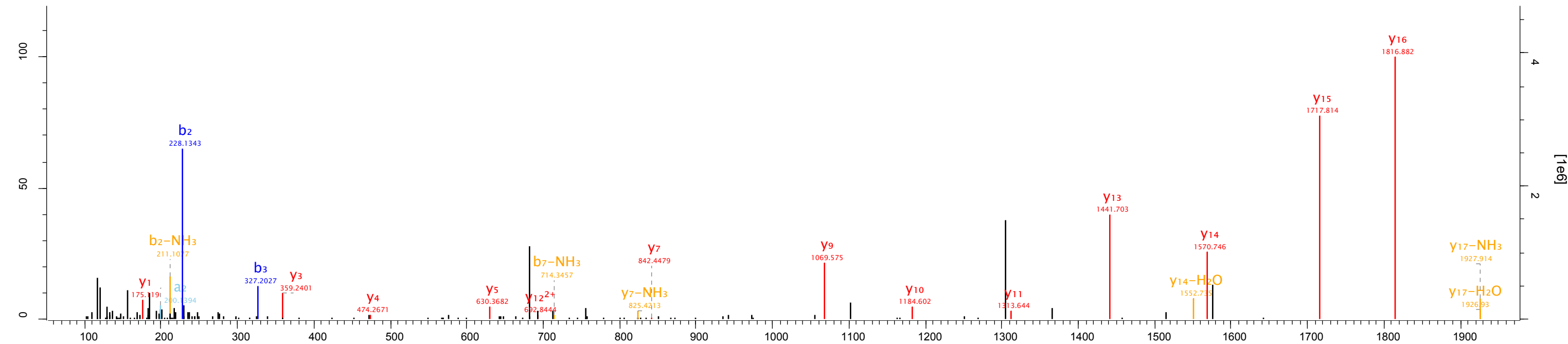


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20180707_MaS_A375SR_ML_proteome_2_17

Scan 18995 Method FTMS; HCD Score 44.6 m/z 954.44 Gene names C6orf120

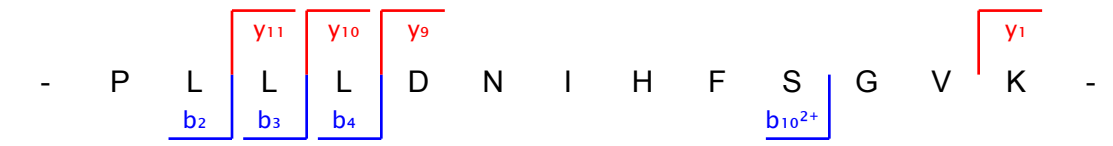
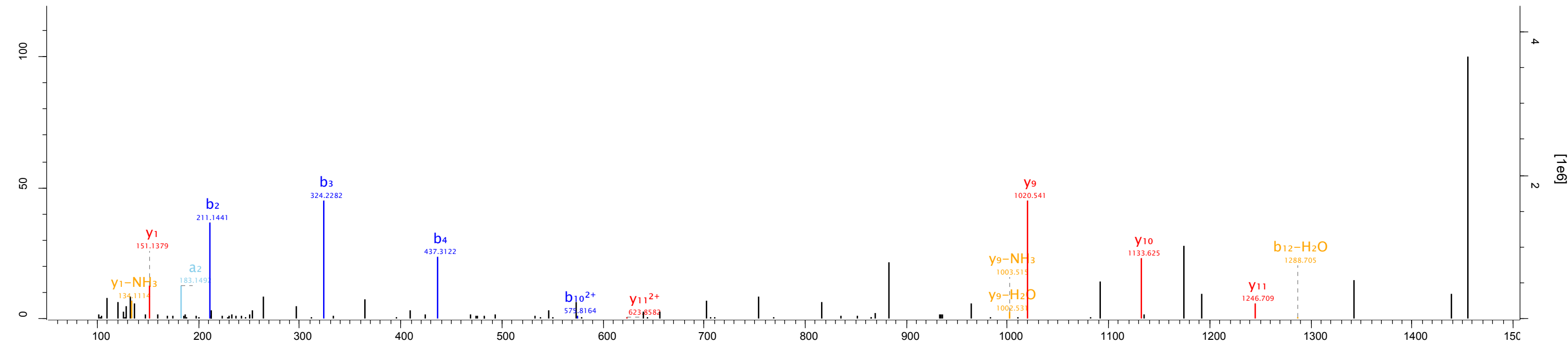


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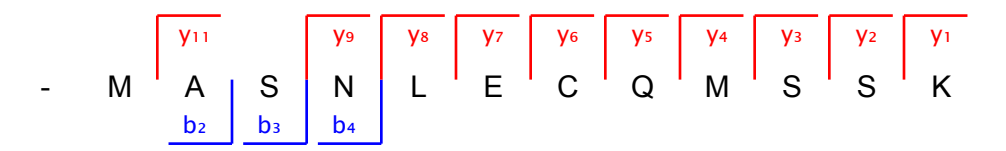
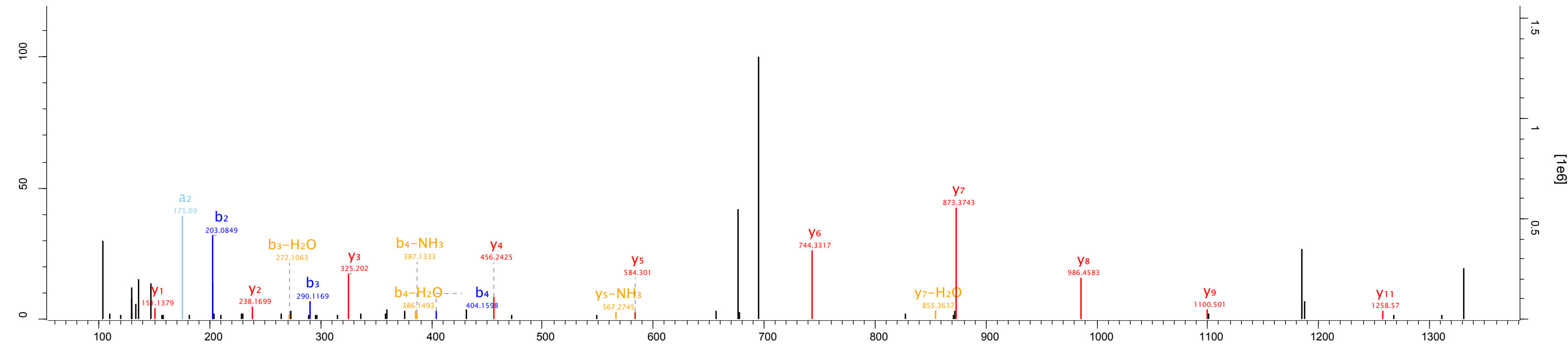
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Scan 25965 Method FTMS; HCD Score 67.08 m/z 729.43 Gene names IL1R1

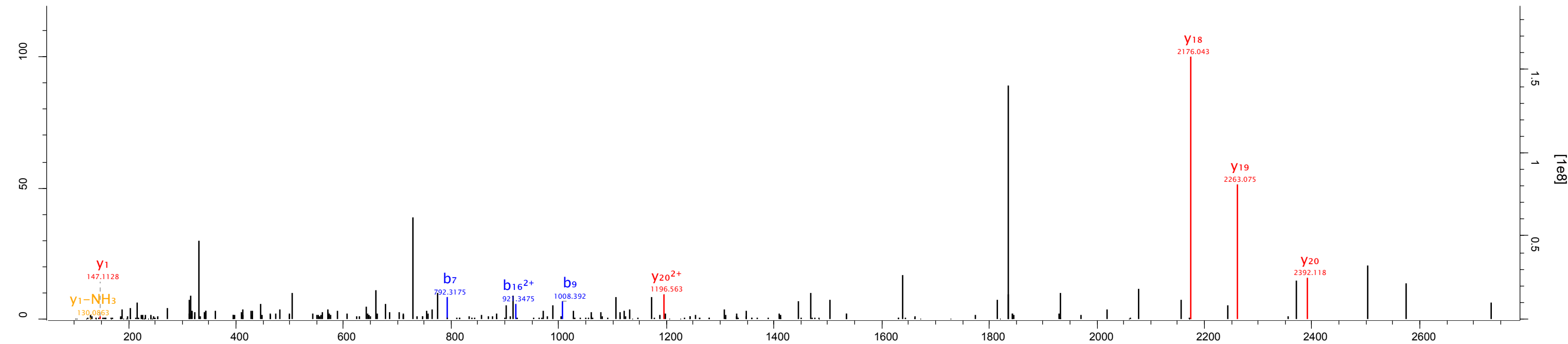


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Scan 10805 Method FTMS; HCD Score 84.36 m/z 695.31 Gene names KIAA1549L



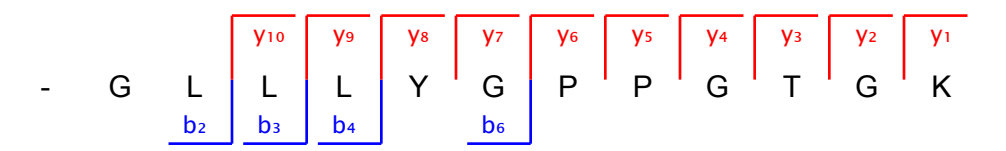
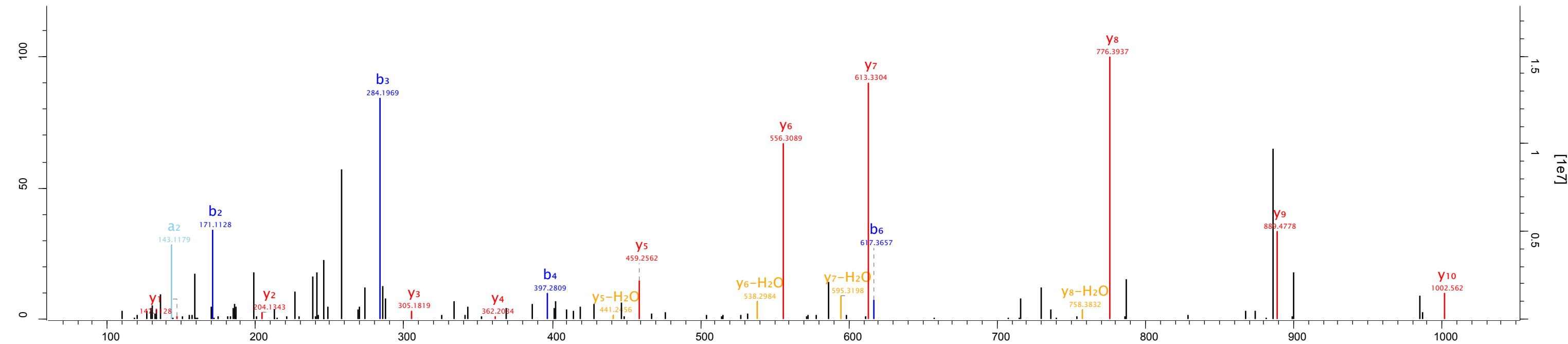
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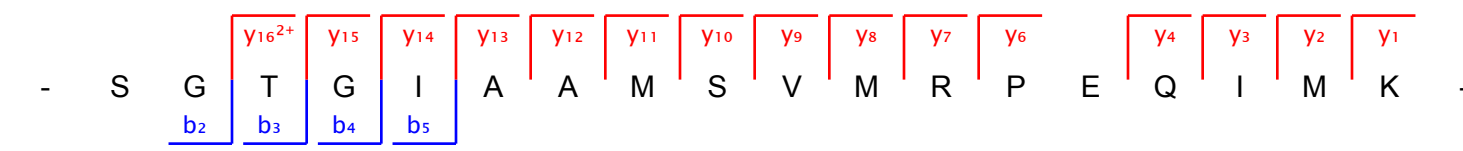
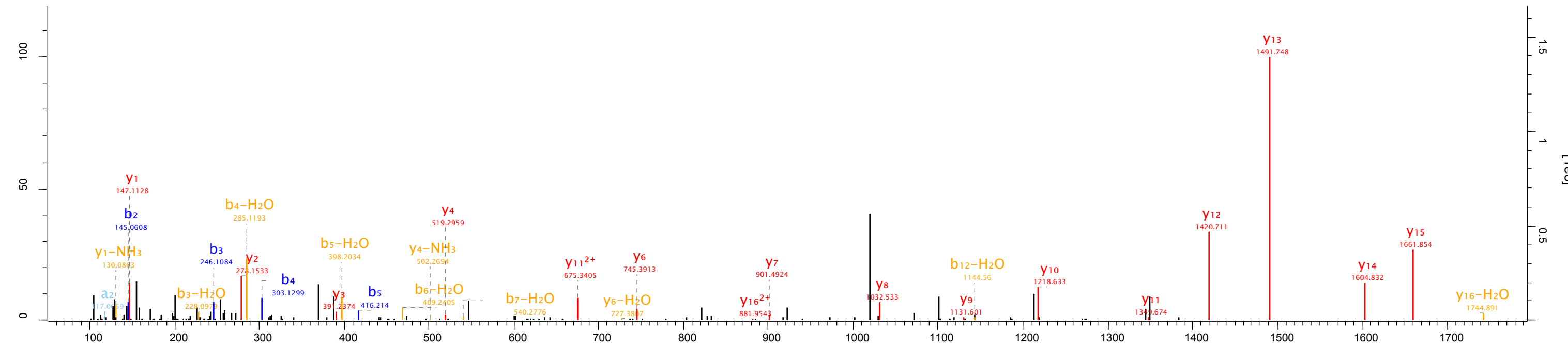
- L P P ph S S T E E S E E S S H A L F D H K L Q V L T N K -

Fragmentation mapping:
 - Blue brackets below 'E' (residue 7) and 'S' (residue 11) are labeled b7 and b9 respectively.
 - A blue bracket below 'L' (residue 14) is labeled b16²⁺.
 - Red brackets above 'E' (residue 7), 'S' (residue 11), and 'E' (residue 15) are labeled y20, y19, and y18 respectively.
 - A red bracket above 'K' (residue 23) is labeled y1.

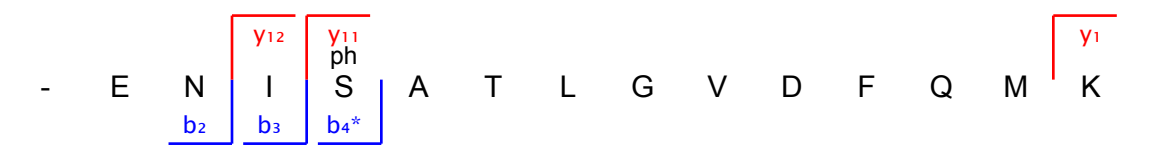
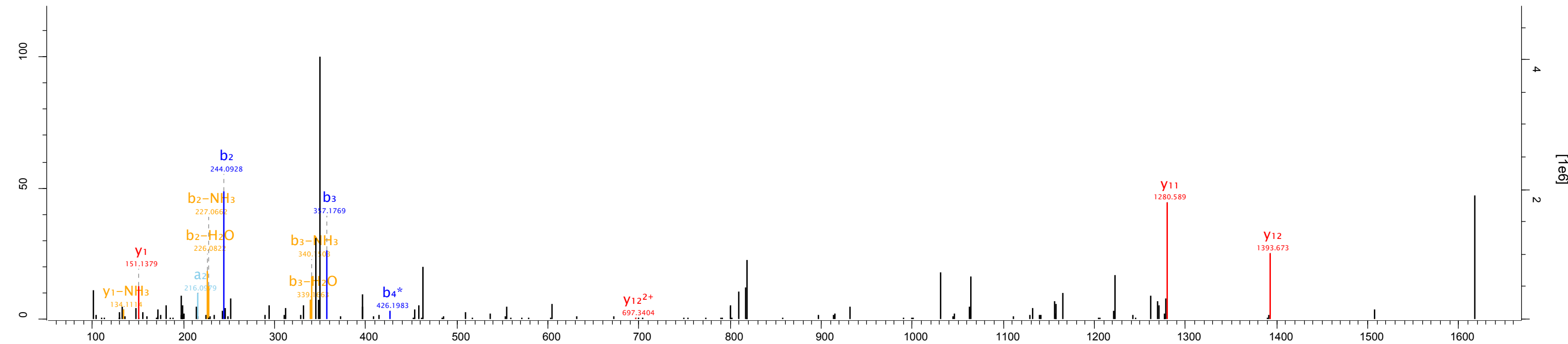
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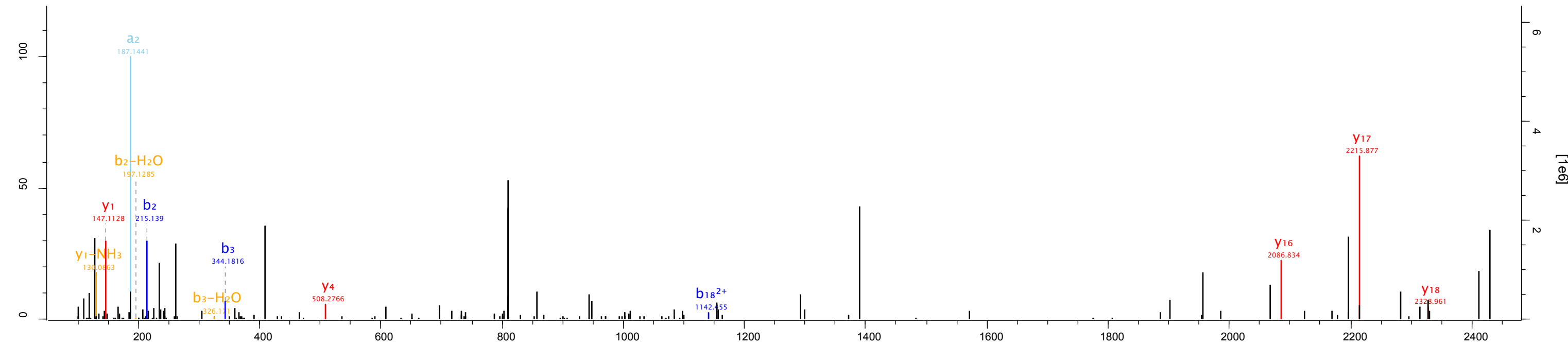


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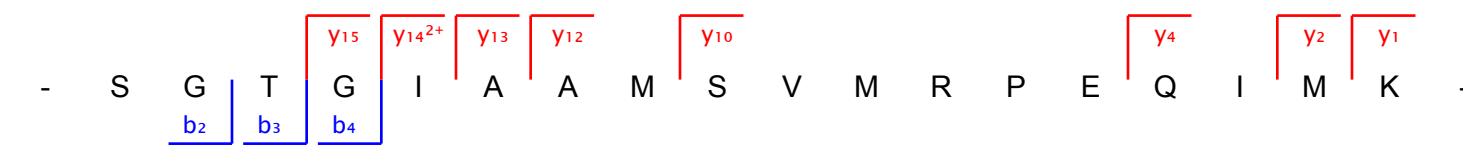
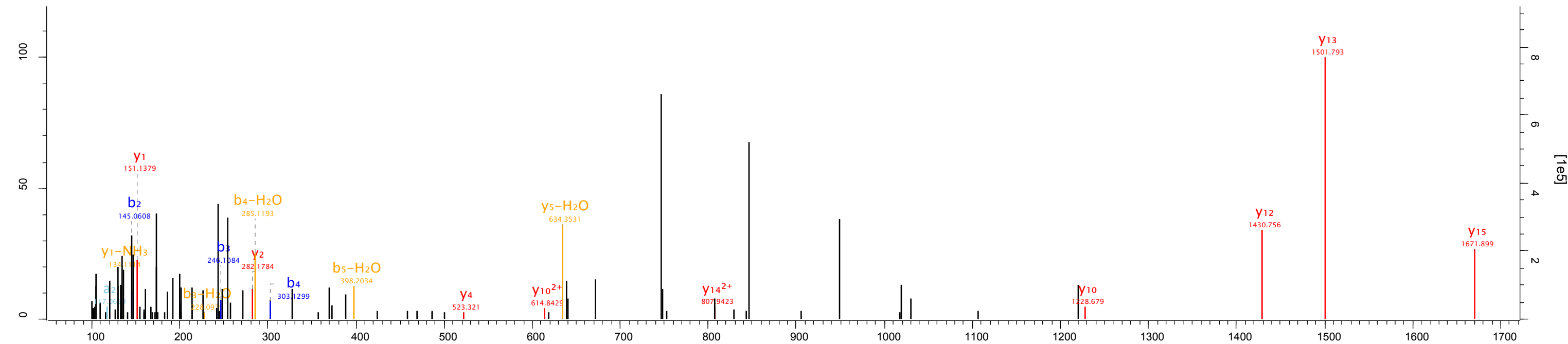
- T I E F ph T L P ph T V T N T V G K P T Y K -

Fragmentation labels (b-ions in blue, y-ions in red) are shown below the corresponding amino acids:

- b_2 (under I)
- b_3 (under E)
- y_{18} (above I)
- y_{17} (above E)
- y_{16} (above F)
- y_4 (above P)
- b_{18}^{2+} (under Y)
- y_1 (above K)

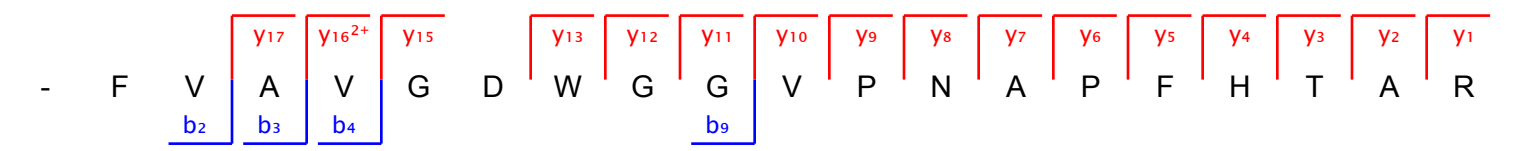
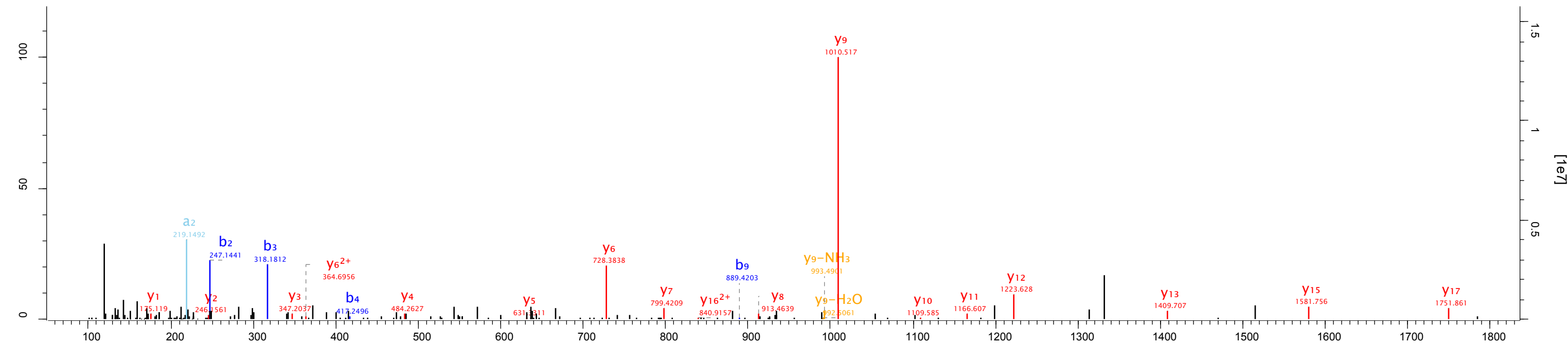
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Scan 23735 Method FTMS; HCD Score 25.16 m/z 639.67 Gene names ATP6V0C

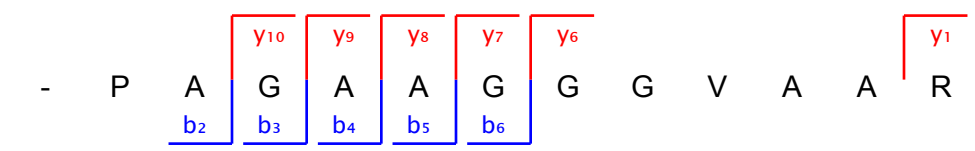
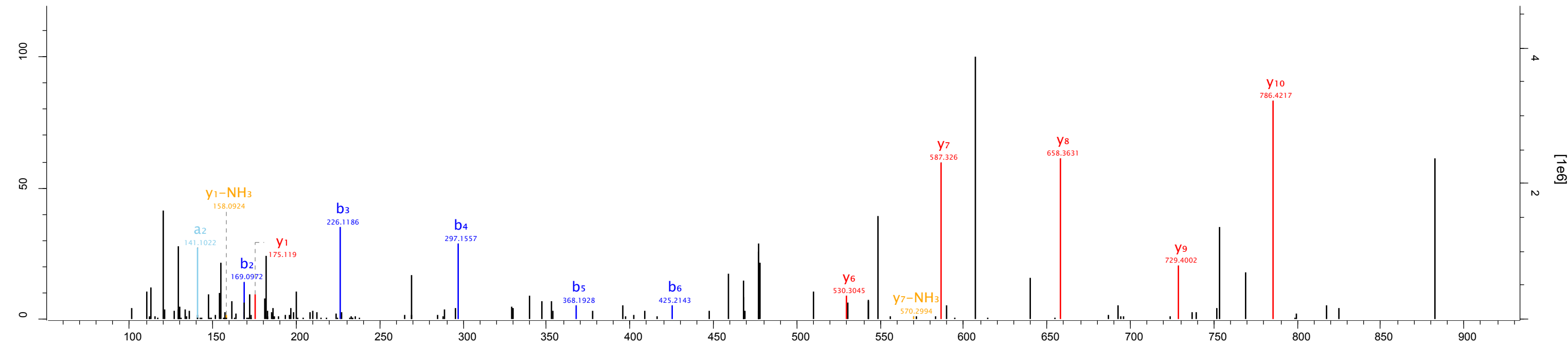


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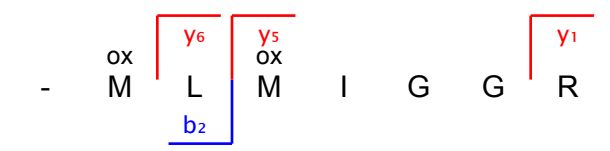
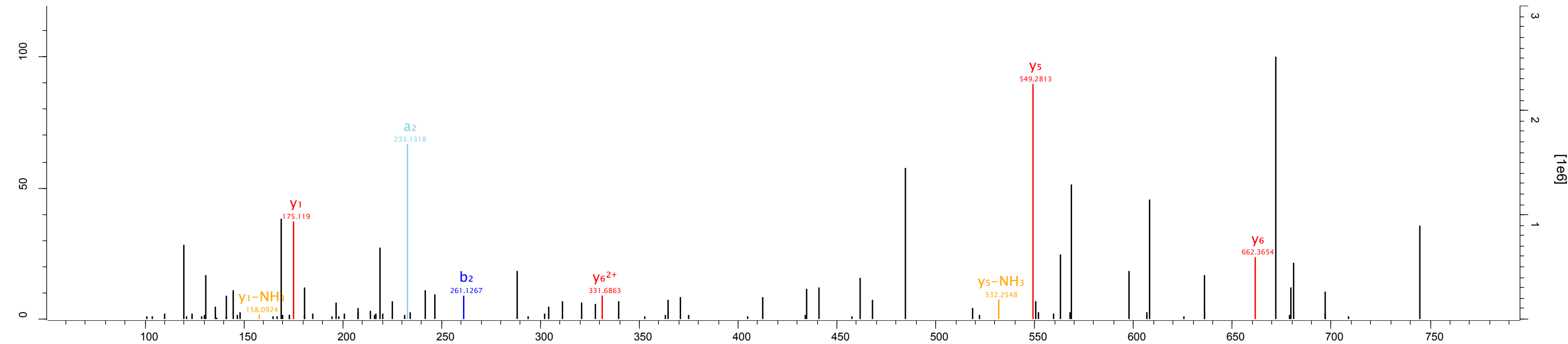
Scan 24285 Method FTMS; HCD Score 54.83 m/z 667.01 Gene names ACP5



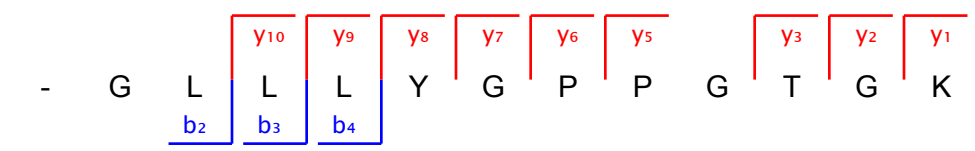
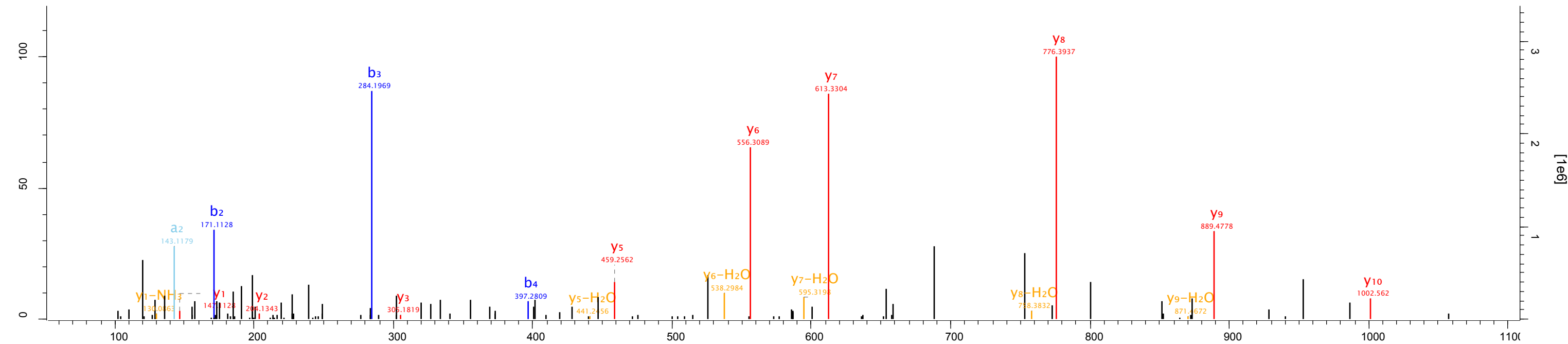
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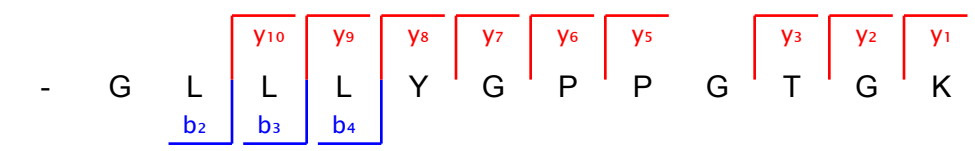
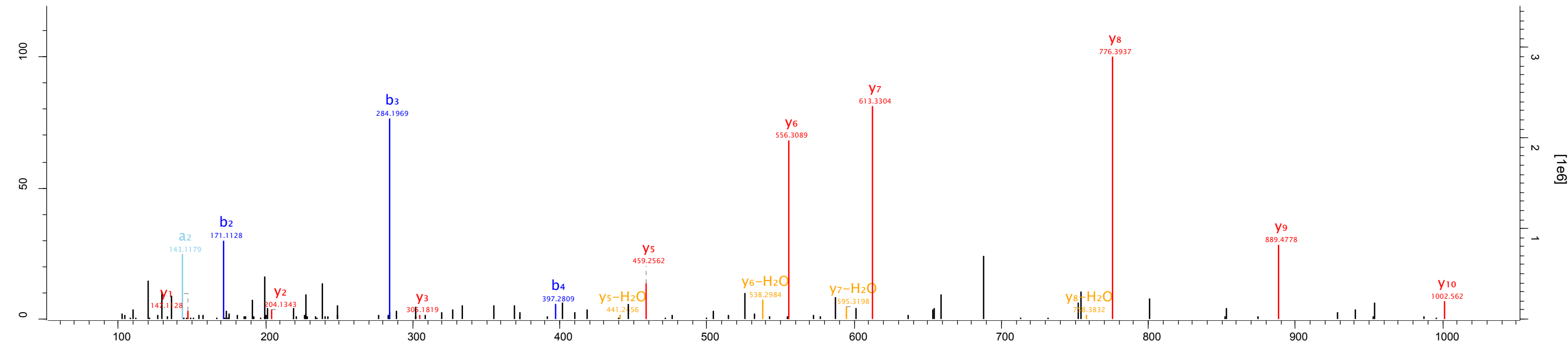
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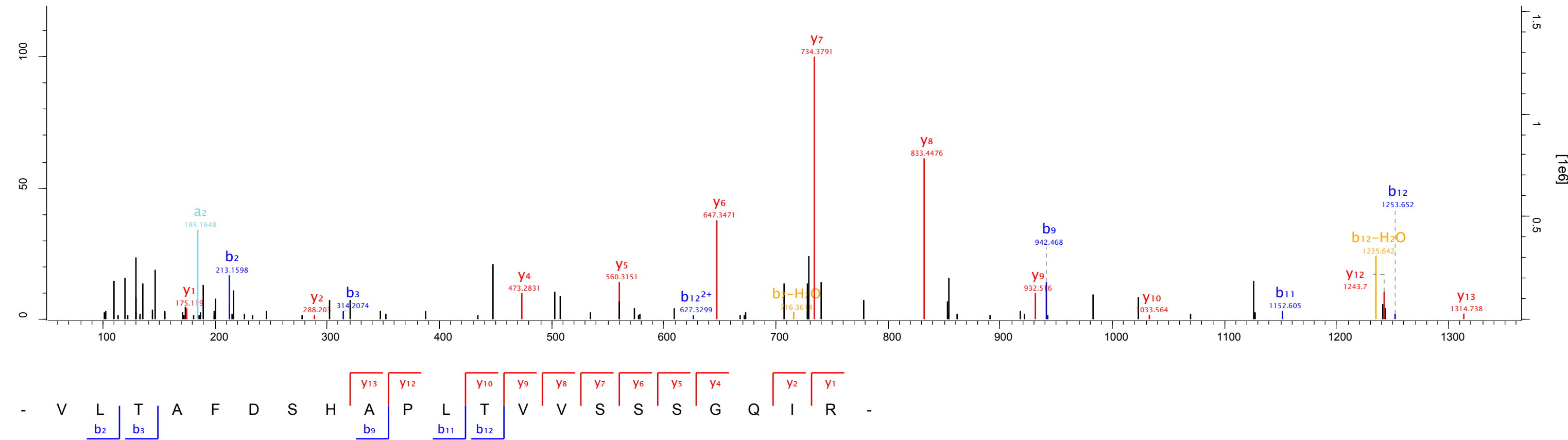


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 Scan: 22475 Method: FTMS; HCD Score: 63.09 m/z: 586.84 Gene names: KATNAL2



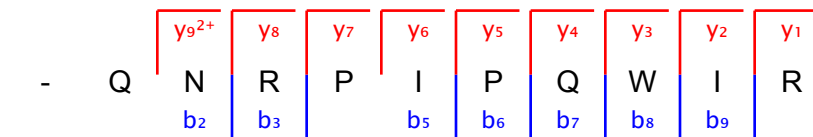
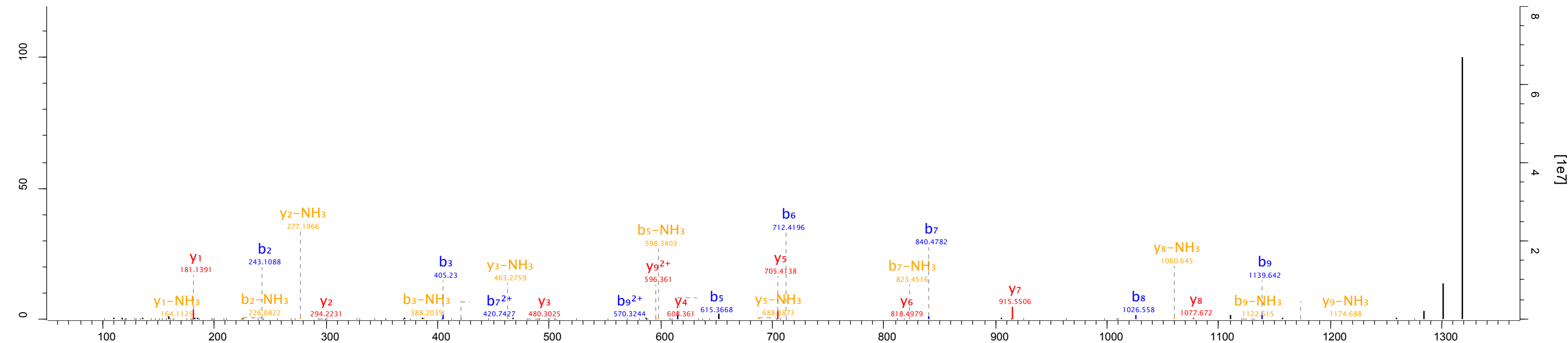
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 Scan 22485 Method FTMS; HCD Score 63.09 m/z 587.33 Gene names KATNAL2





Raw file
20180707_MaS_A375SR_ML_proteome_2_23

Scan 16705 Method FTMS; HCD Score 199.46 m/z 660.39 Gene names RPL39P5;RPL39



20180707_MaS_A375SR_ML_proteome_2_24

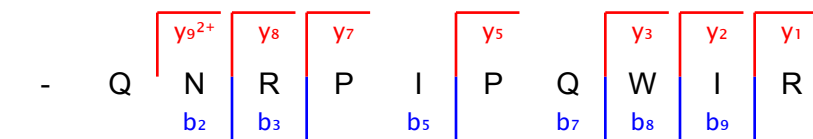
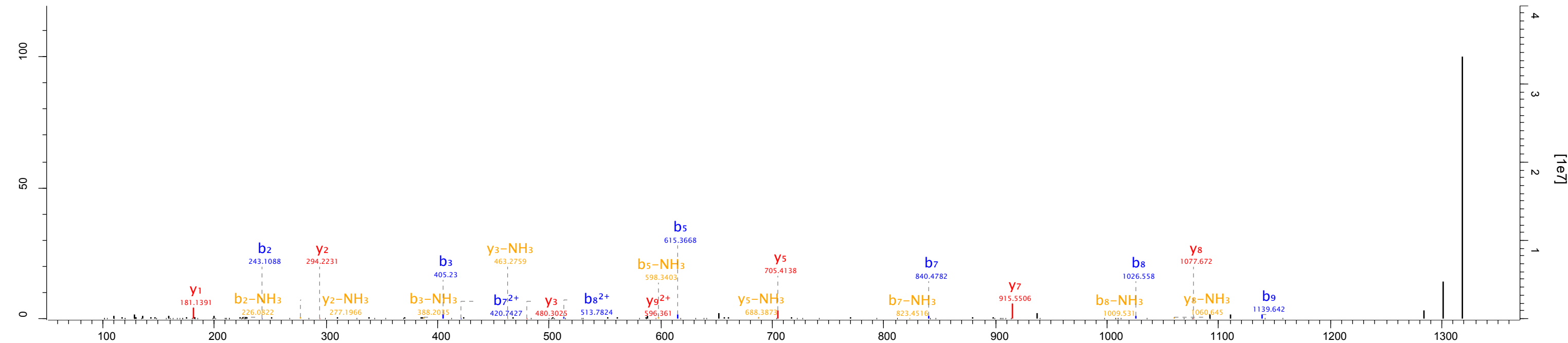
15625

FTMS; HCD

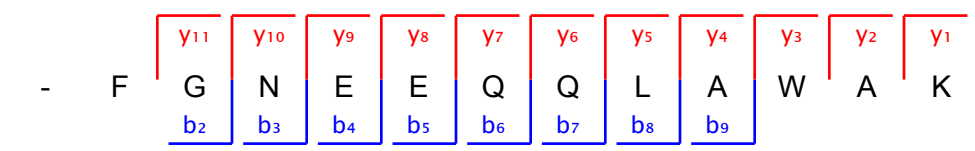
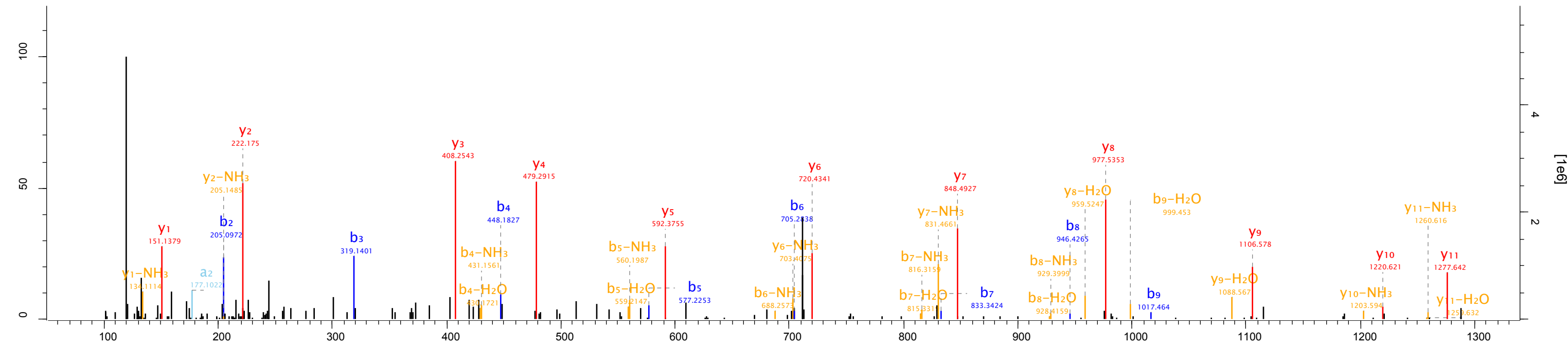
121.64

660.39

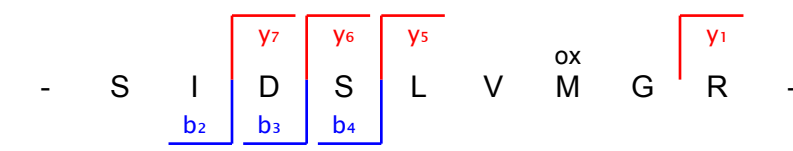
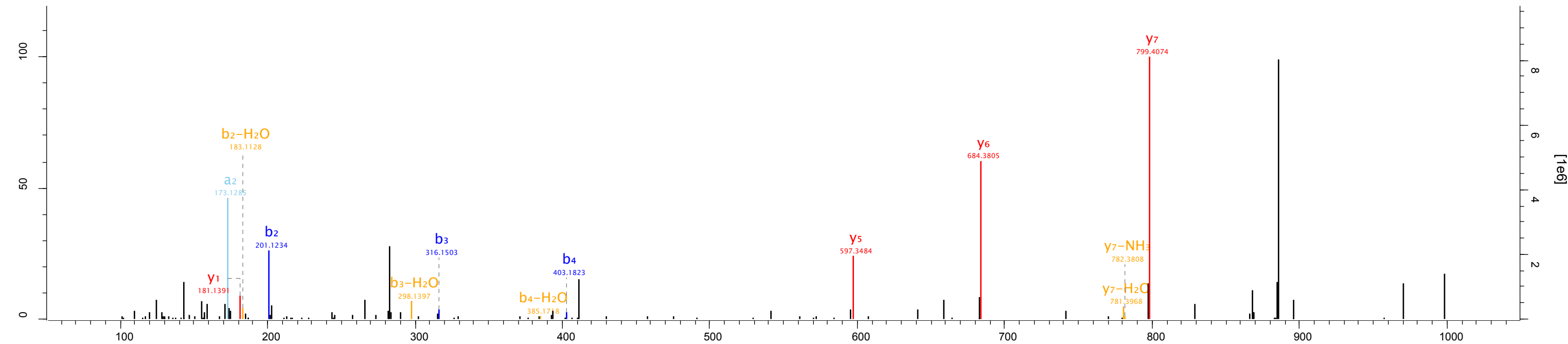
RPL39P5;RPL39

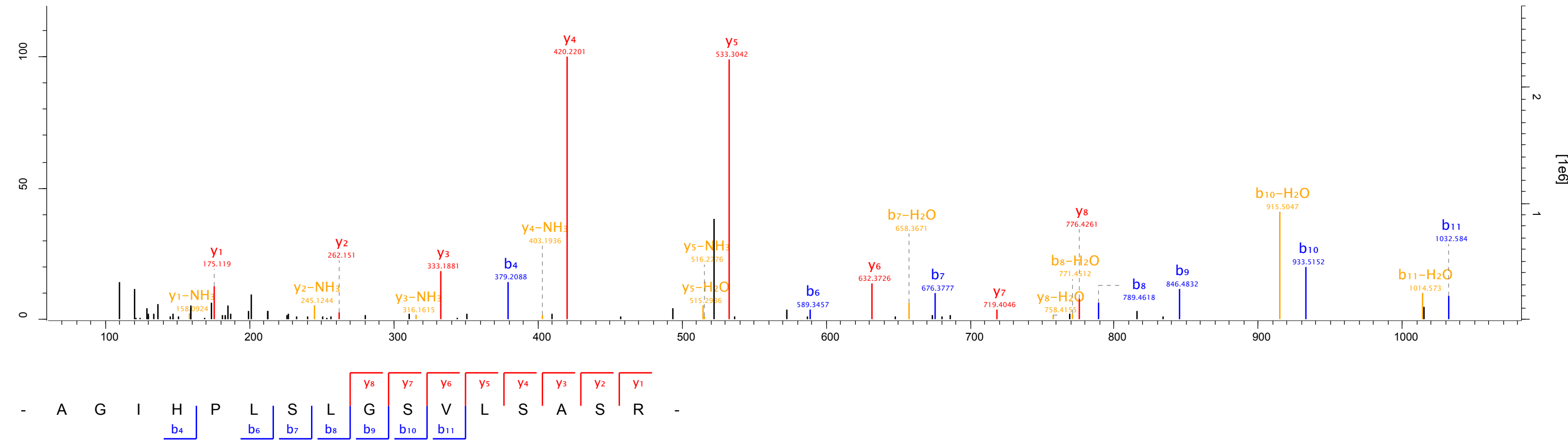


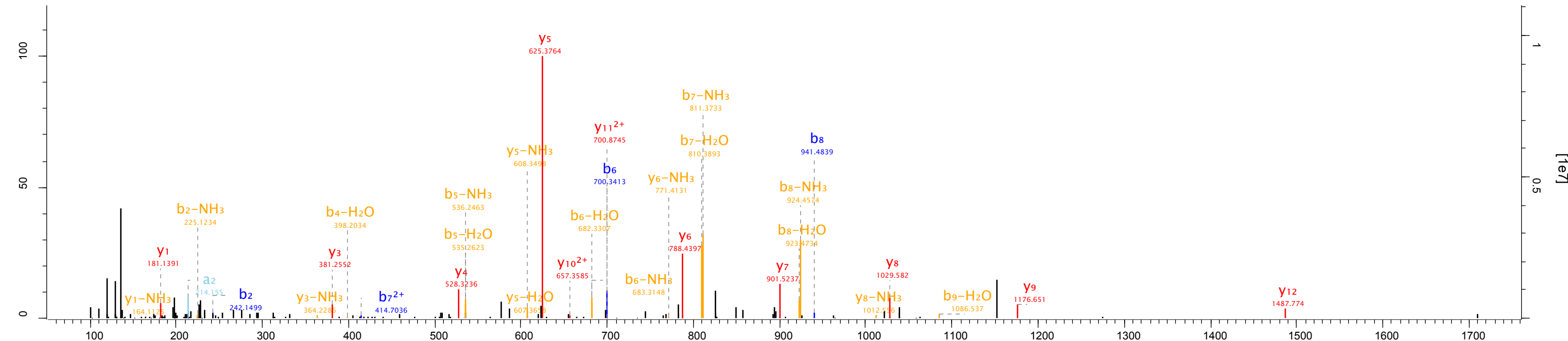
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 Scan: 17875 Method: FTMS; HCD Score: 220.81 m/z: 712.86 Gene names: SPATA22



Raw file 20180707_MaS_A375SR_ML_proteome_2_25 Scan 12125 Method FTMS; HCD Score 66.69 m/z 500.26







- Q L S S H F Q I Y P F S L R -

b₂ b₆ b_{7²⁺} b₈

y₁₂ y_{11²⁺} y_{10²⁺} y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₁

Raw file

20180707_MaS_A375SR_ML_proteome_2_26

Scan

13015

Method

FTMS; HCD

Score

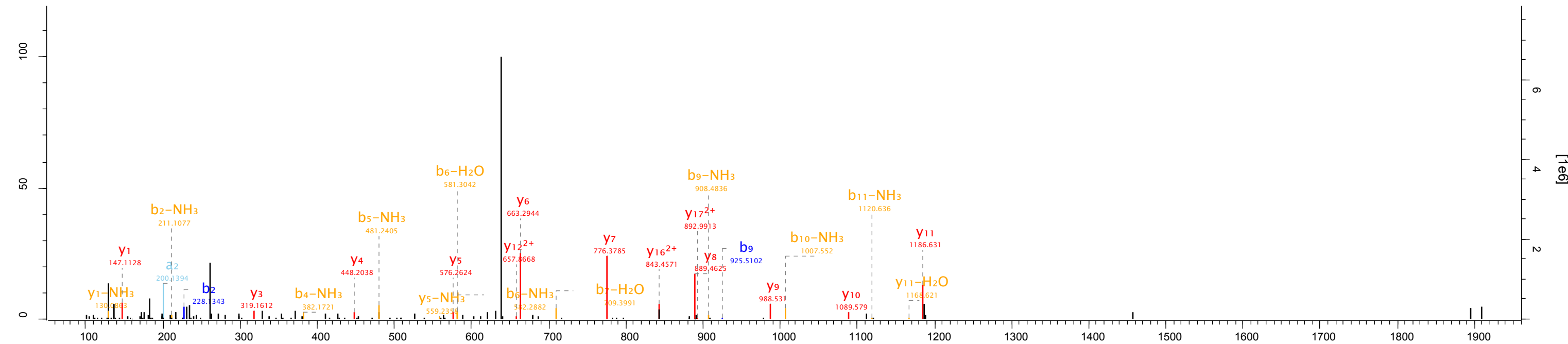
47.68

m/z

638.35

Gene names

FABP7

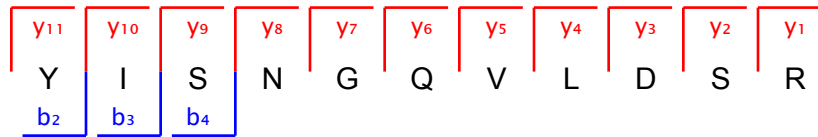
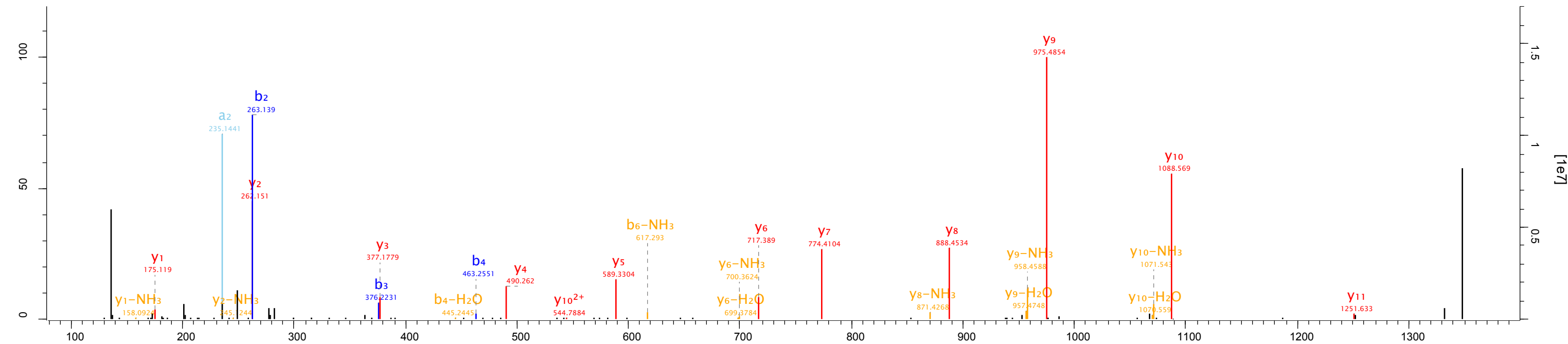


- Q V G N V T K P T V I I S Q E G D K -

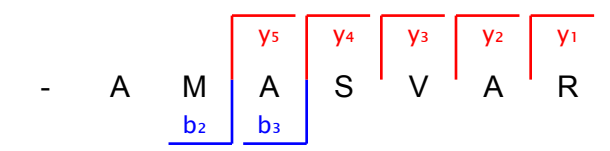
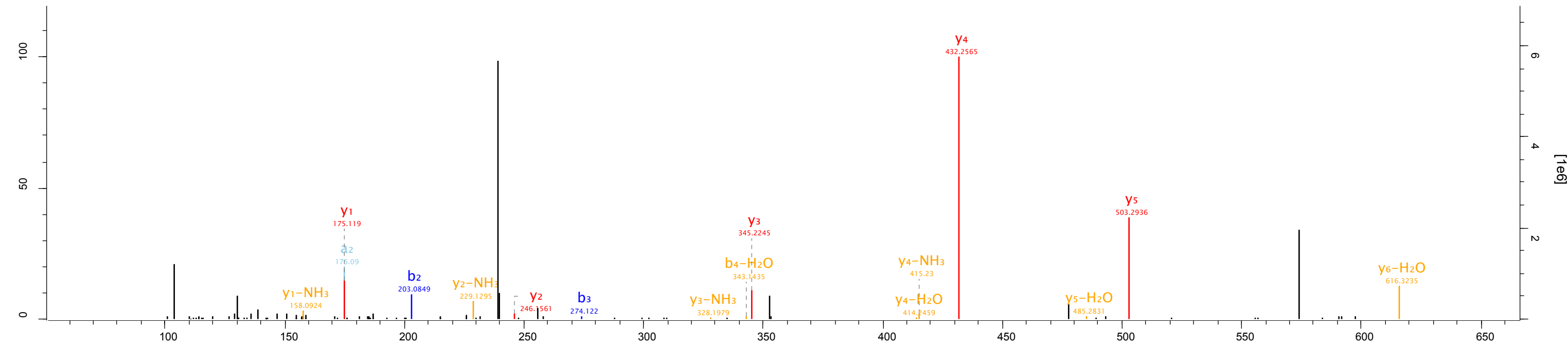
b₂ b₉

Raw file
20180707_MaS_A375SR_ML_proteome_2_27

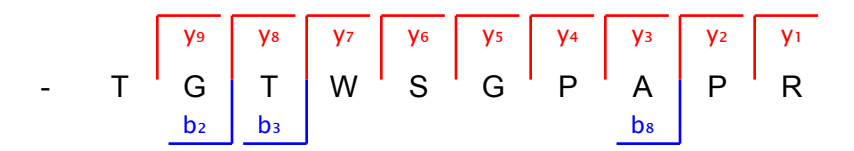
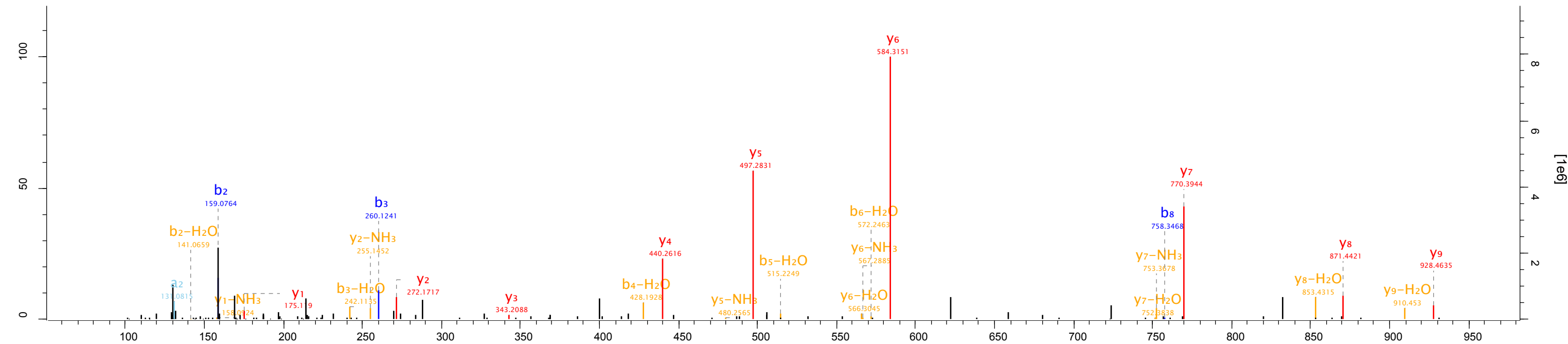
Scan 14485 Method FTMS; HCD Score 151.26 m/z 675.85 Gene names SELK



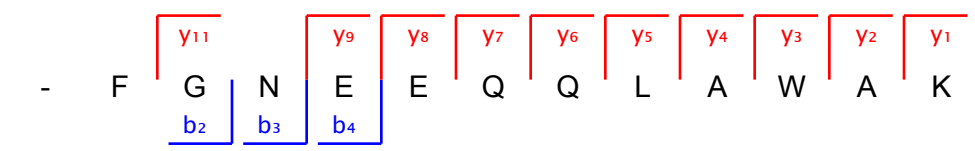
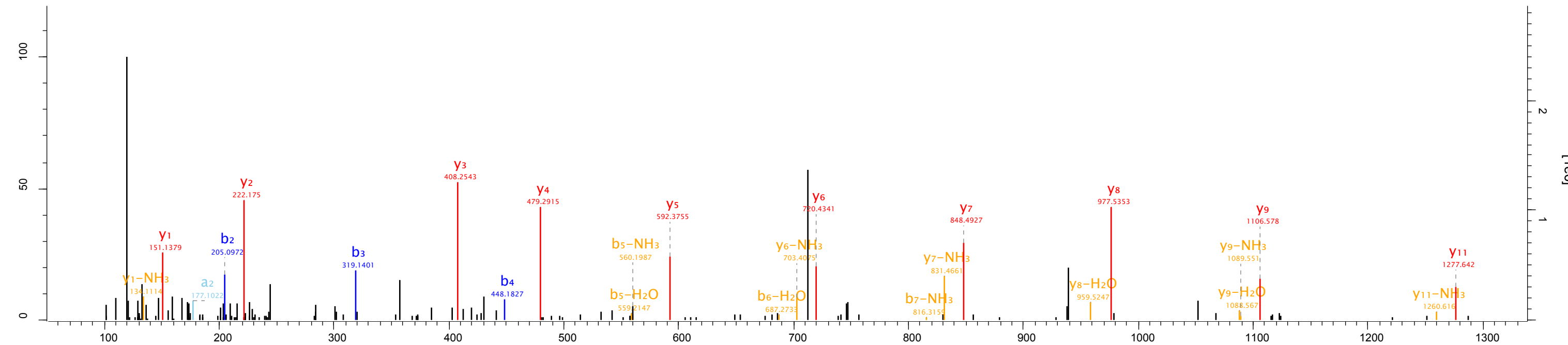
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 Scan 6235 Method FTMS; HCD Score 107.74 m/z 353.19 Gene names ART4



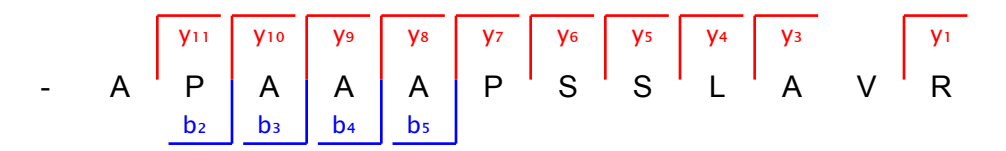
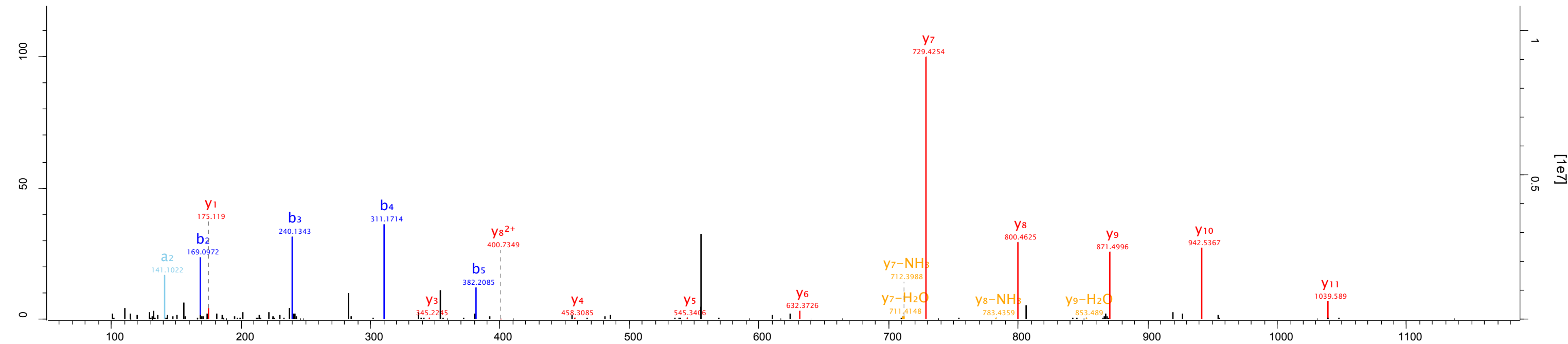
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Raw file 20180707_MaS_A375SR_ML_proteome_2_28 Scan 17665 Method FTMS; HCD Score 135.99 m/z 713.36 Gene names SPATA22

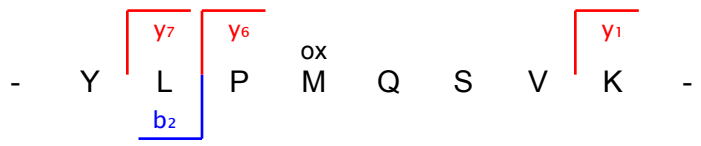
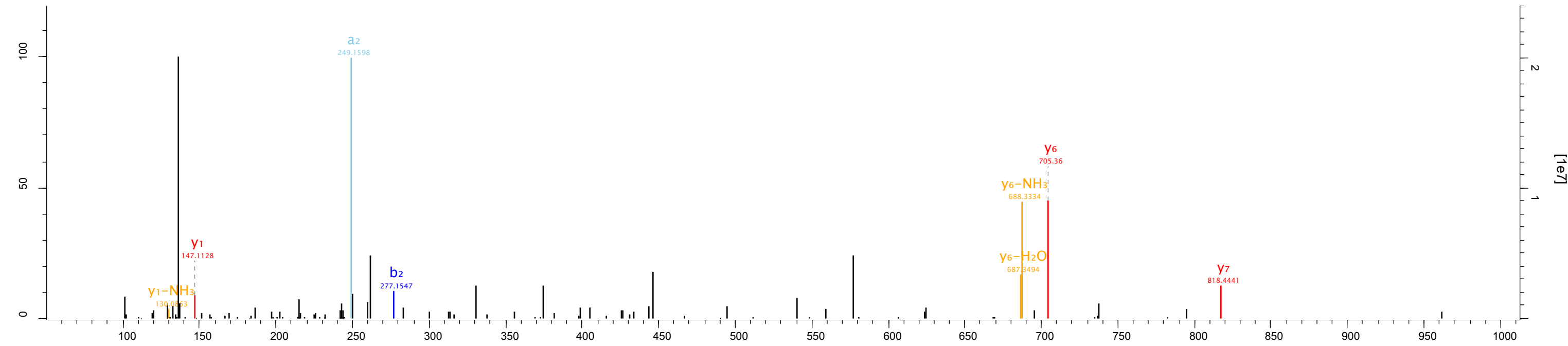


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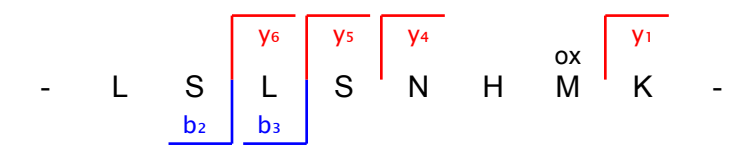
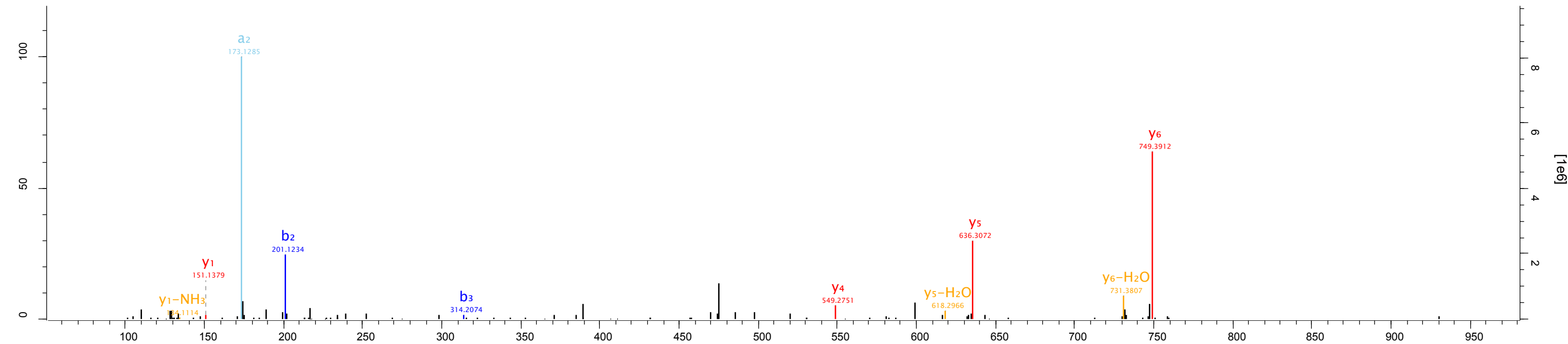


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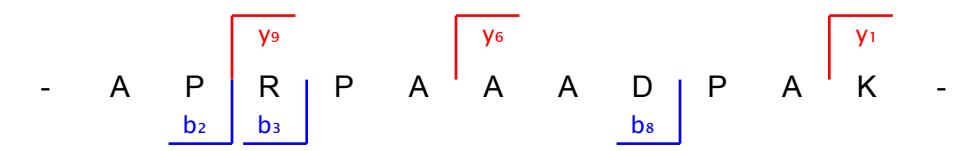
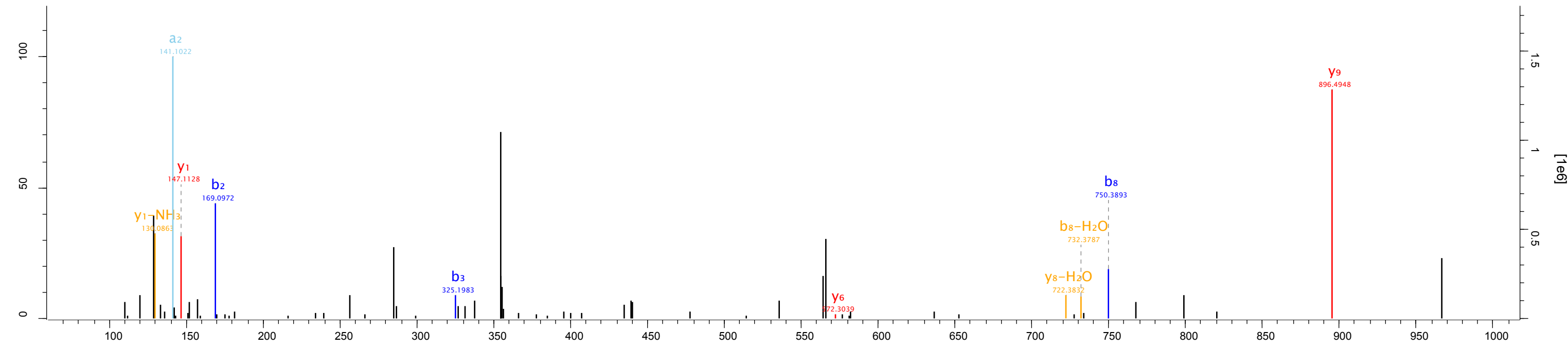
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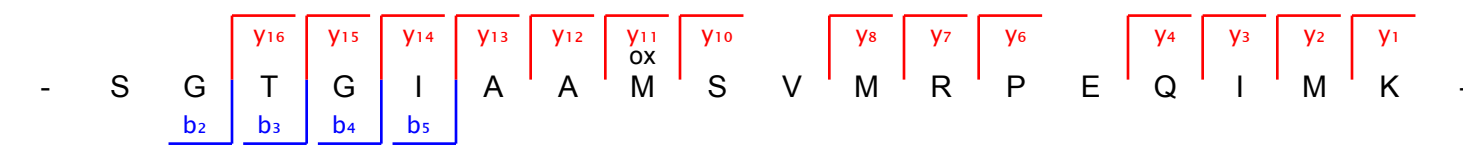
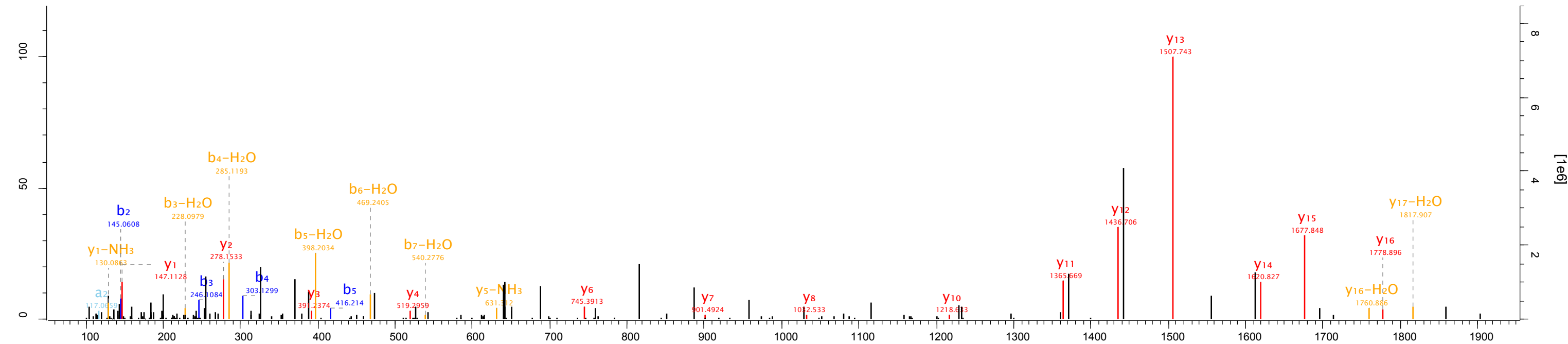
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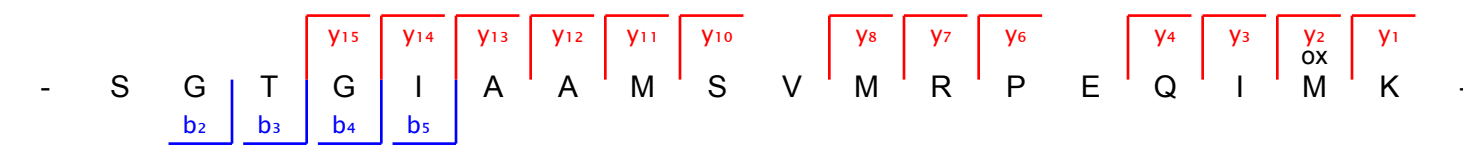
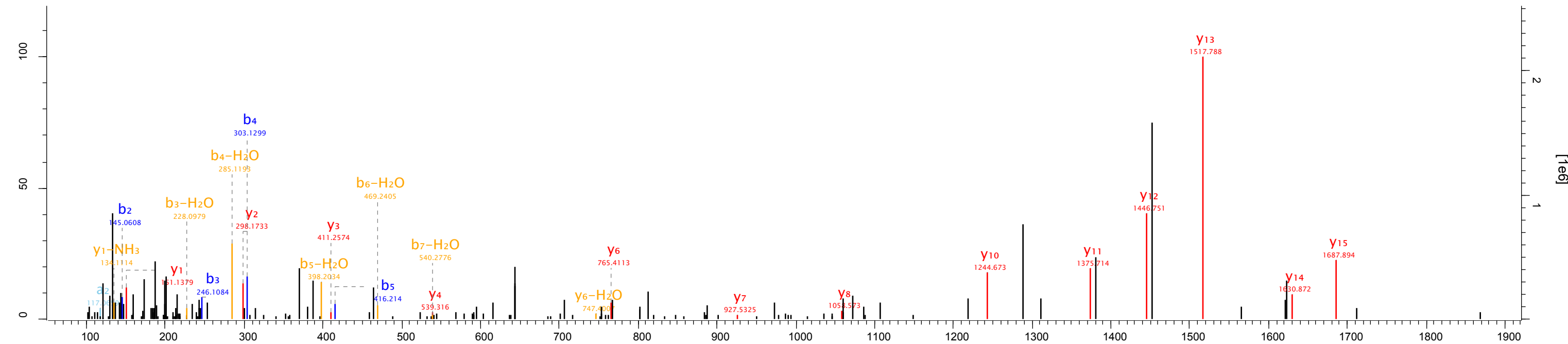
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 Scan 4055 Method FTMS; HCD Score 34.77 m/z 355.53



Raw file 20180707_MaS_A375SR_ML_proteome_20 Scan 18725 Method FTMS; HCD Score 81.51 m/z 641.99 Gene names ATP6V0C

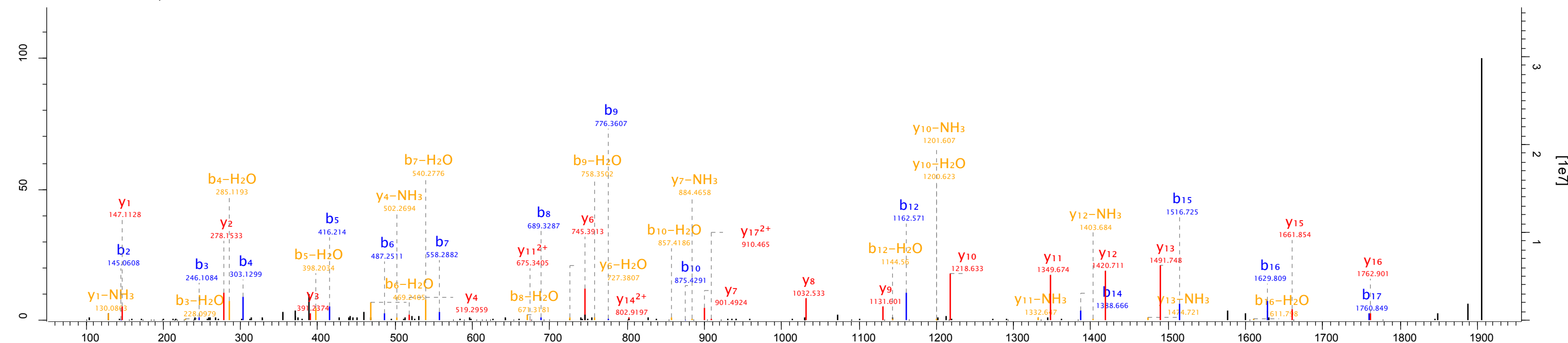


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Scan 23705 Method FTMS; HCD Score 216.34 m/z 954.48 Gene names ATP6V0C

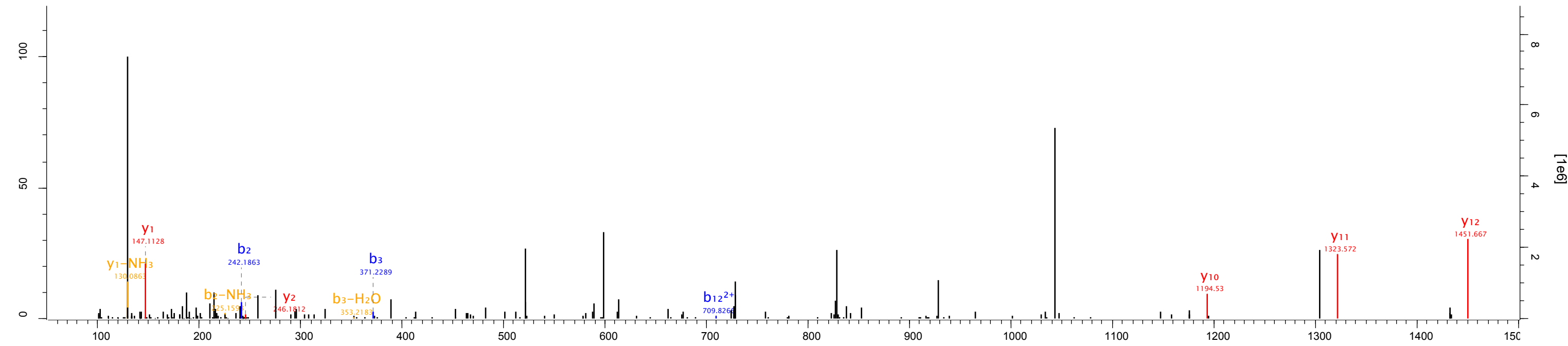


- S G T G I A A M S V M R P E Q I M K -

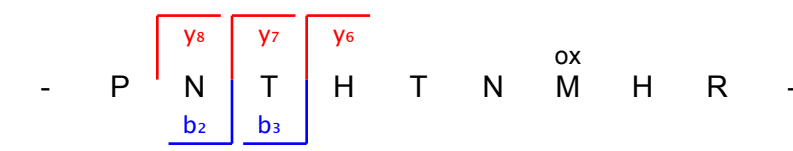
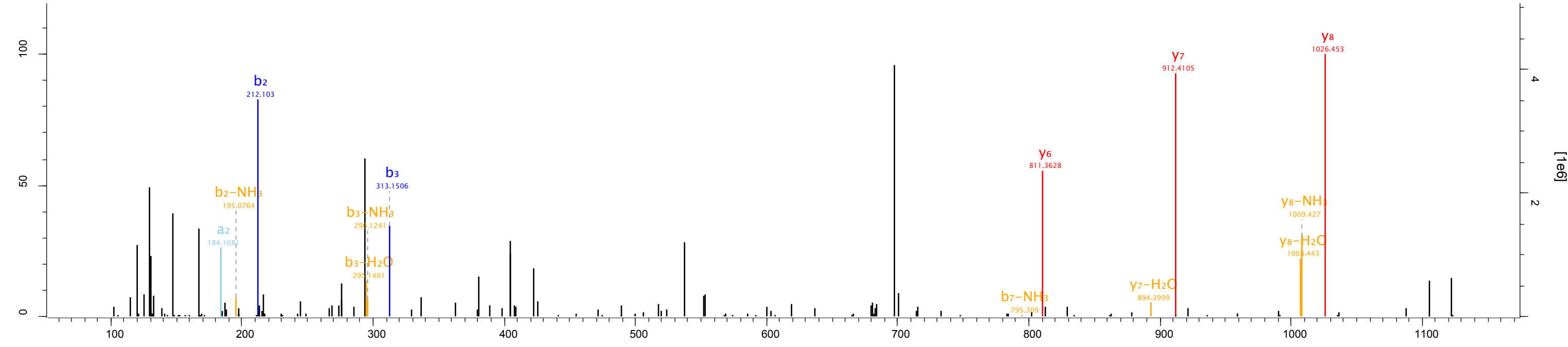
y17 ²⁺	y16	y15	y14 ²⁺	y13	y12	y11	y10	y9	y8	y7	y6	y4	y3	y2	y1
b2	b3	b4	b5	b6	b7	b8	b9	b10	b12	b14	b15	b16	b17		

Raw file
20180707_MaS_A375SR_ML_proteome_20

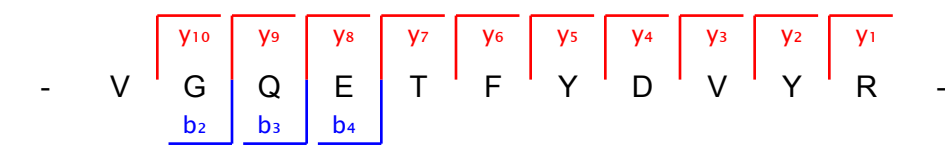
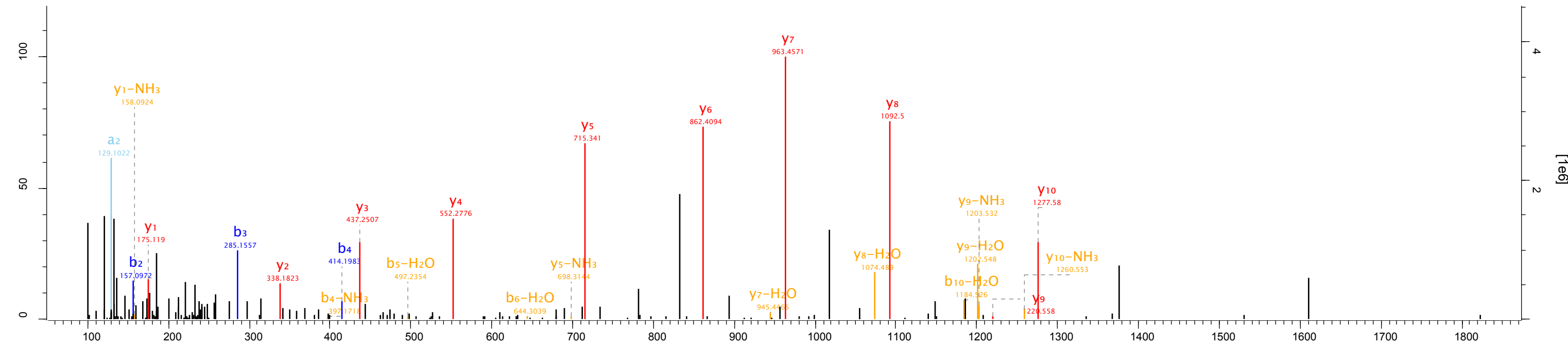
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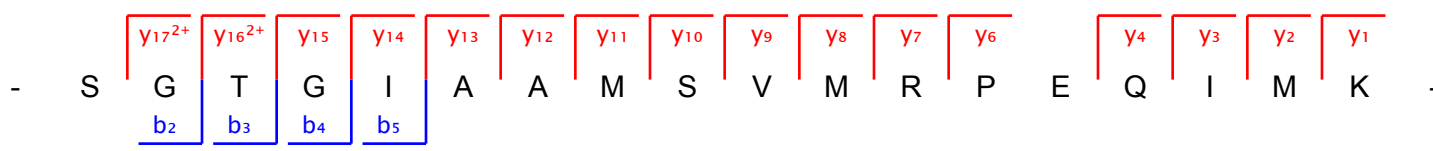
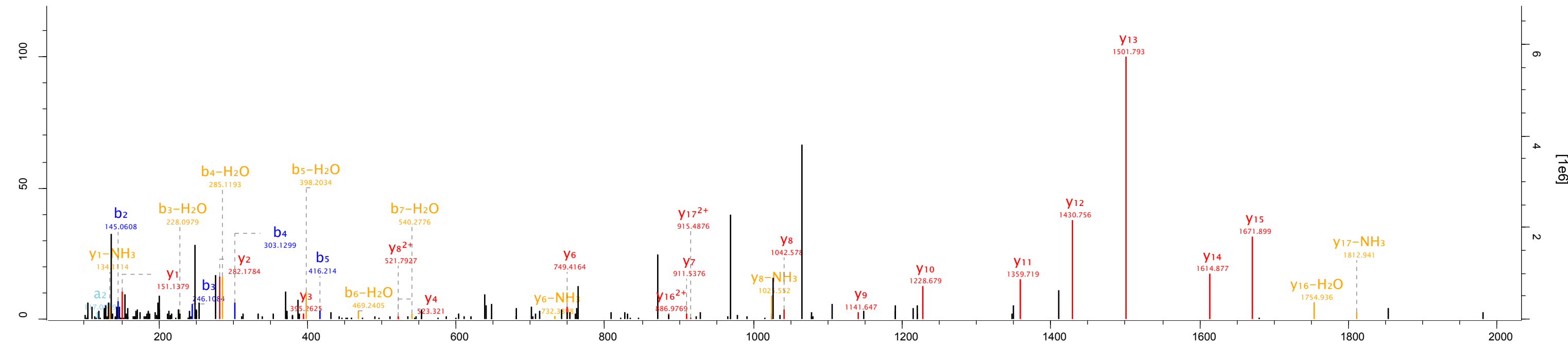
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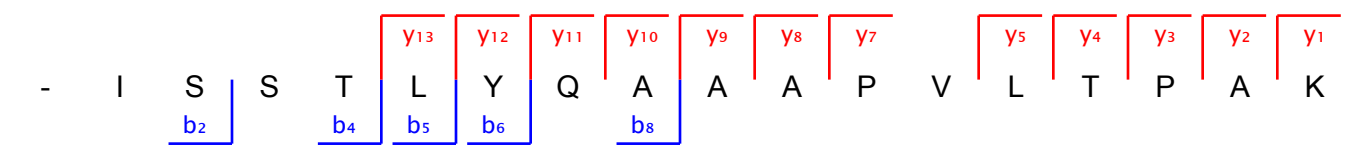
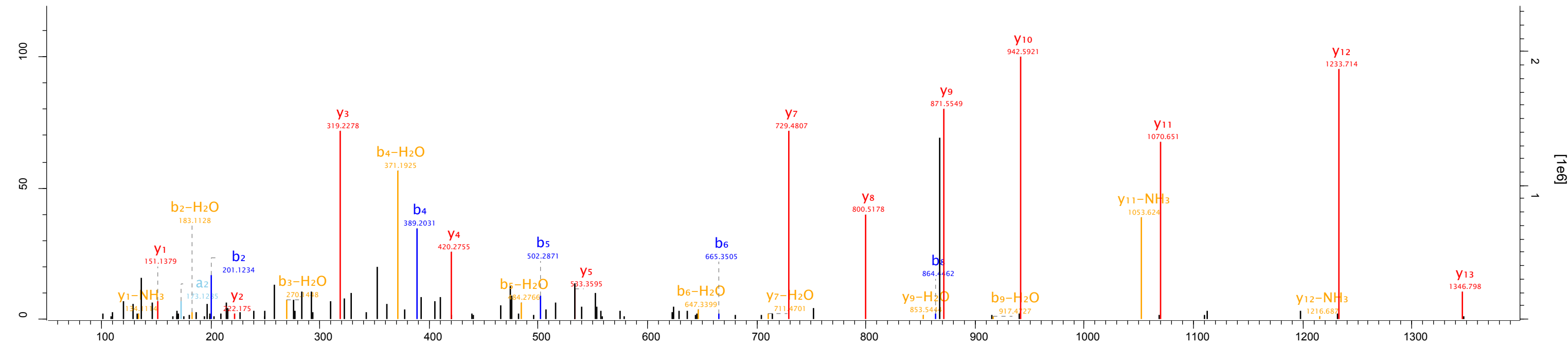
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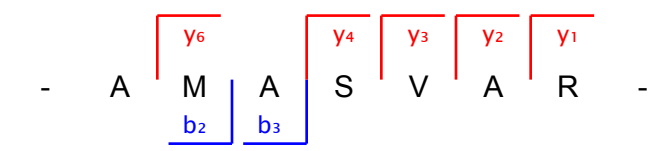
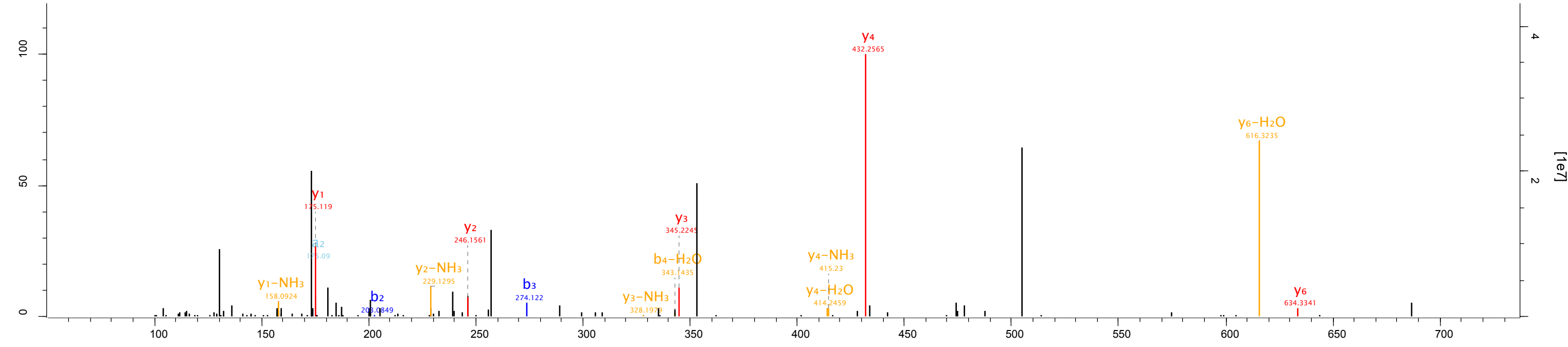
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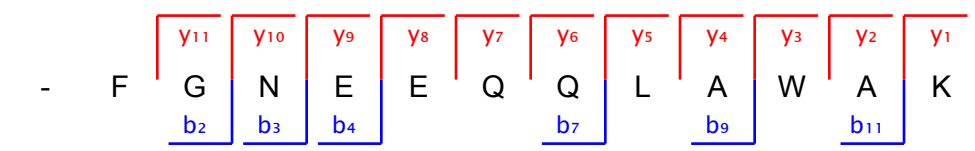
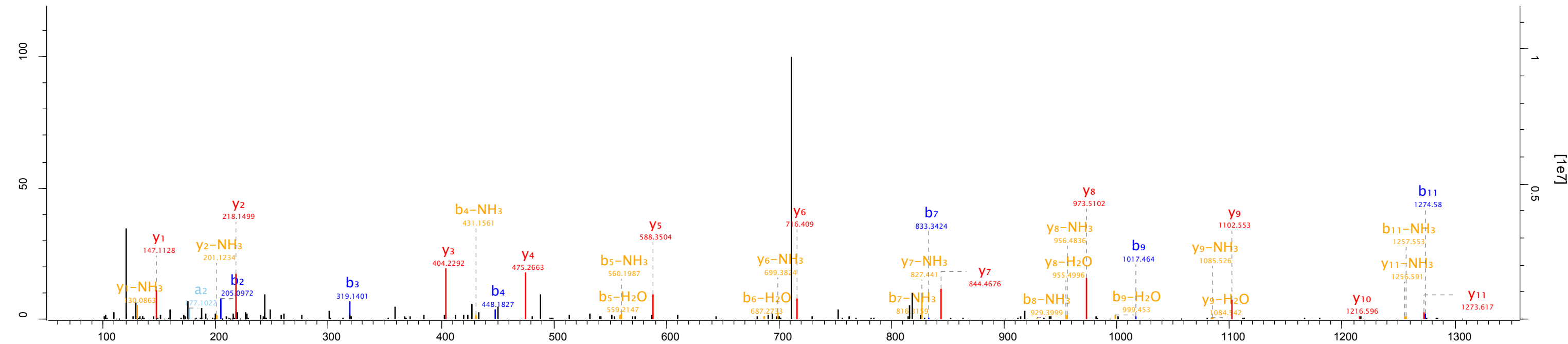
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20180707_MaS_A375SR_ML_proteome_22

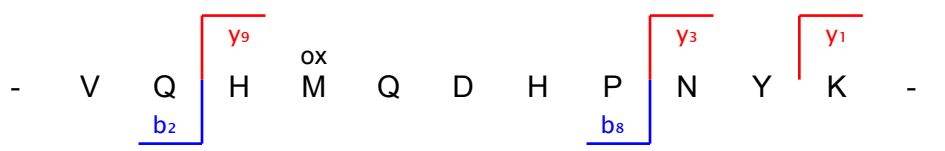
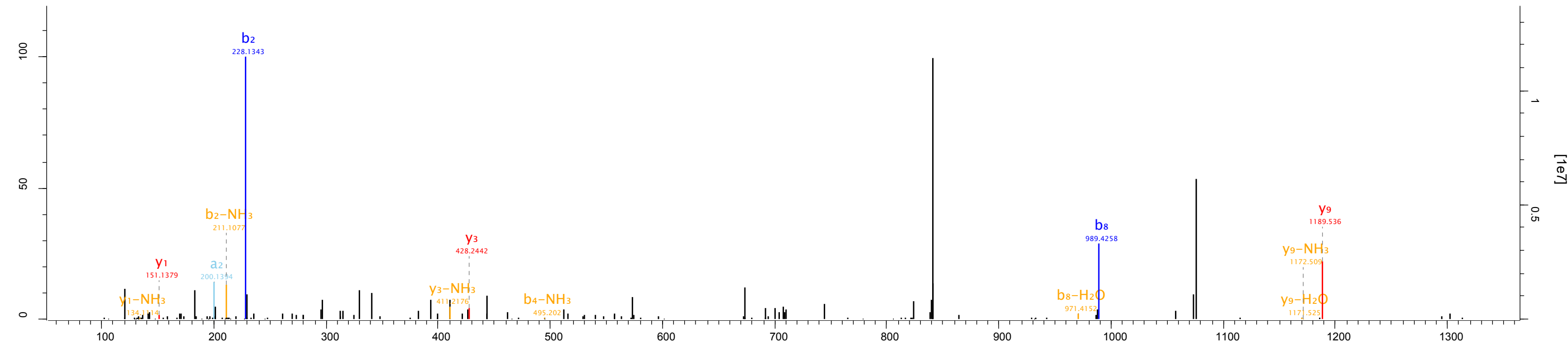
Scan	Method	Score	m/z	Gene names
6205	FTMS; HCD	92.19	353.19	ART4



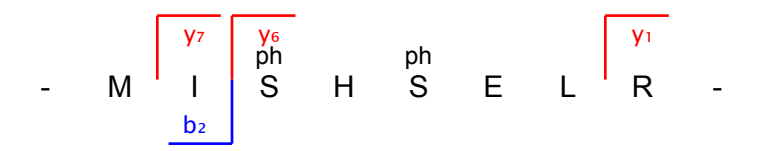
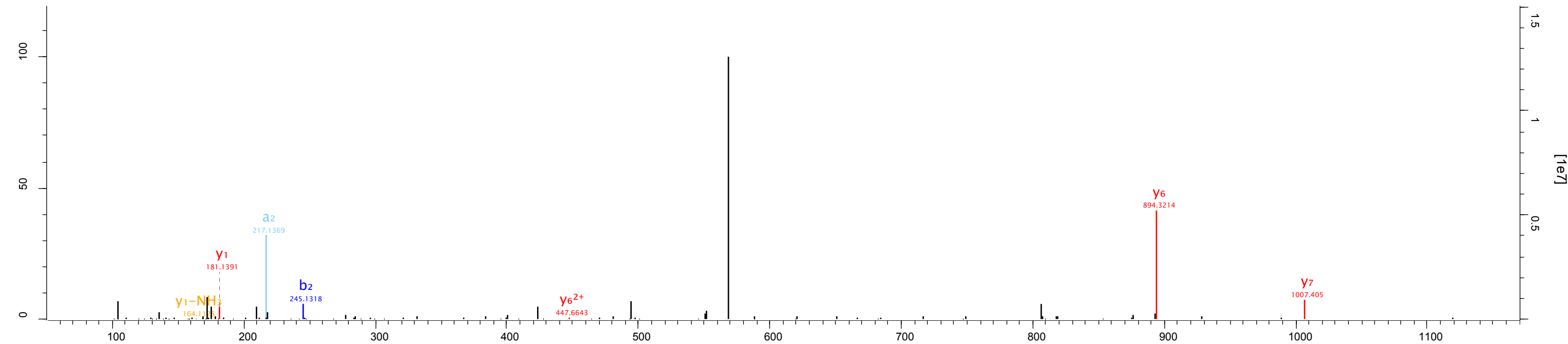
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 Scan: 17675 Method: FTMS; HCD Score: 160.16 m/z: 711.35 Gene names: SPATA22



Raw file 20180707_MaS_A375SR_ML_proteome_23 Scan 24005 Method FTMS; HCD Score 43.3 m/z 708.83 Gene names SOX17

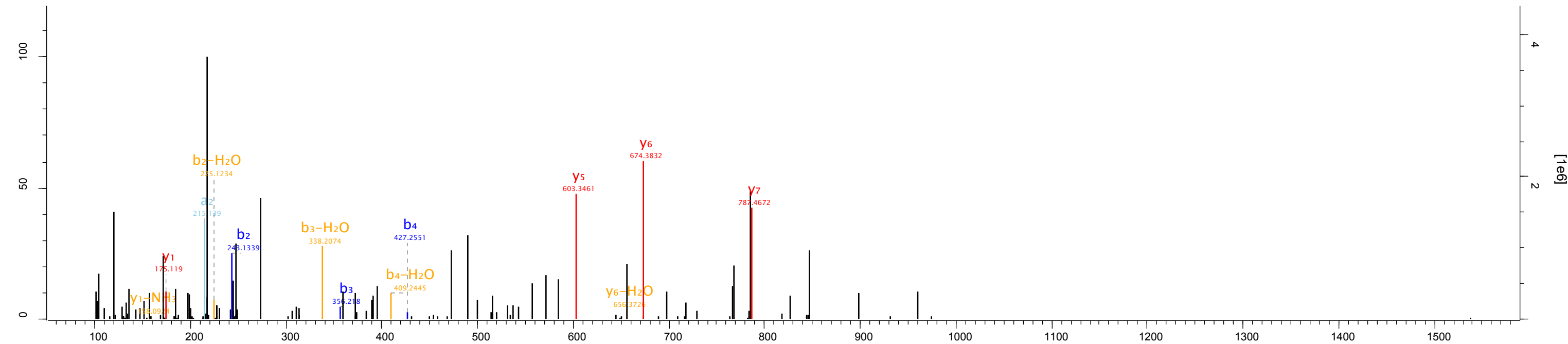


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 Scan: 8145 Method: FTMS; HCD Score: 54.2 m/z: 569.73 Gene names: PSPHP1



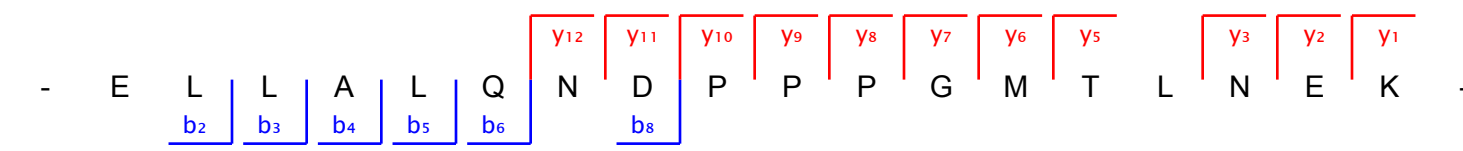
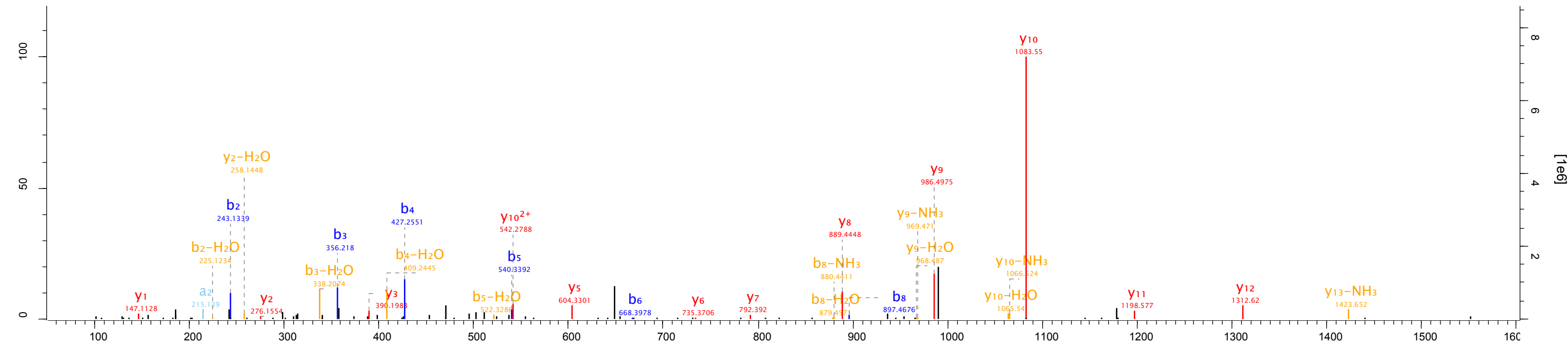
Raw file
20180707_MaS_A375SR_ML_proteome_24

Scan 23235 Method FTMS; HCD Score 49.44 m/z 515.3

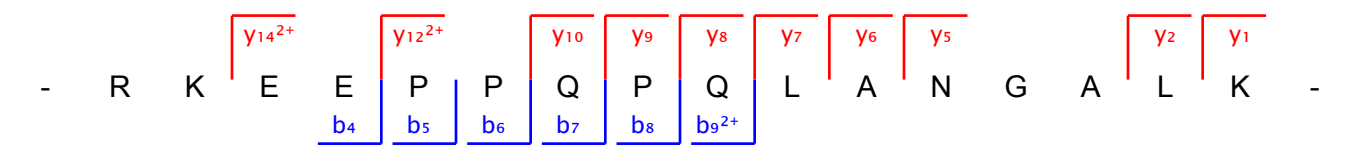
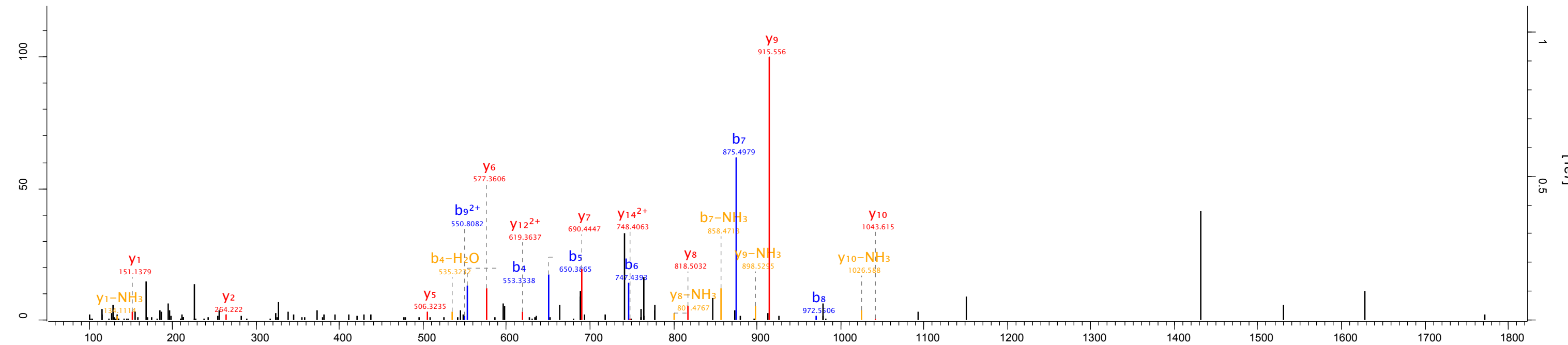


- L E I A E V S L R -
b2 b3 b4 y1 y6 y5

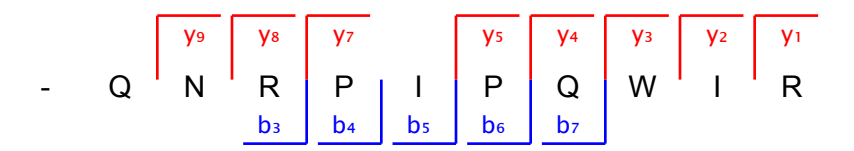
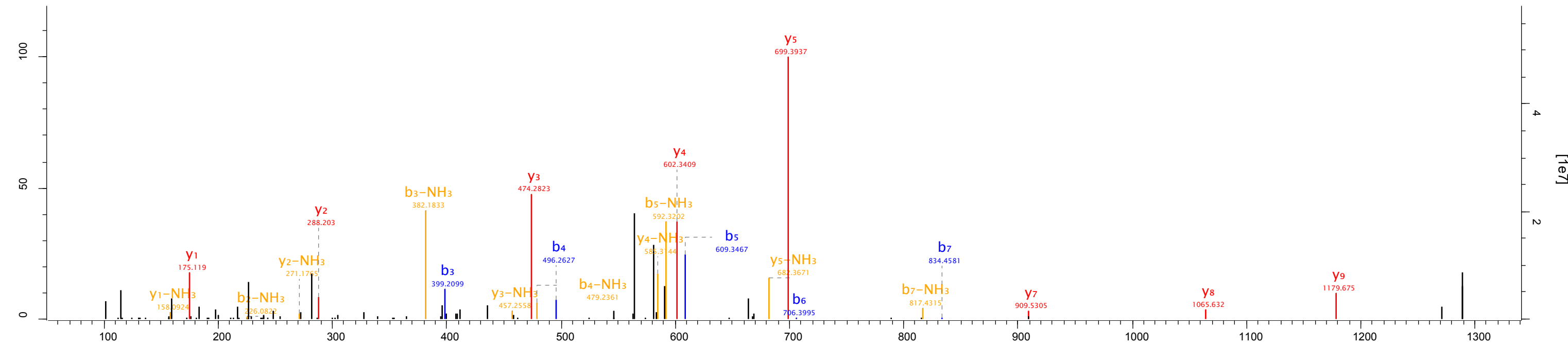
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 Scan: 24945 Method: FTMS; HCD Score: 122.46 m/z: 991.01 Gene names: UBE2W

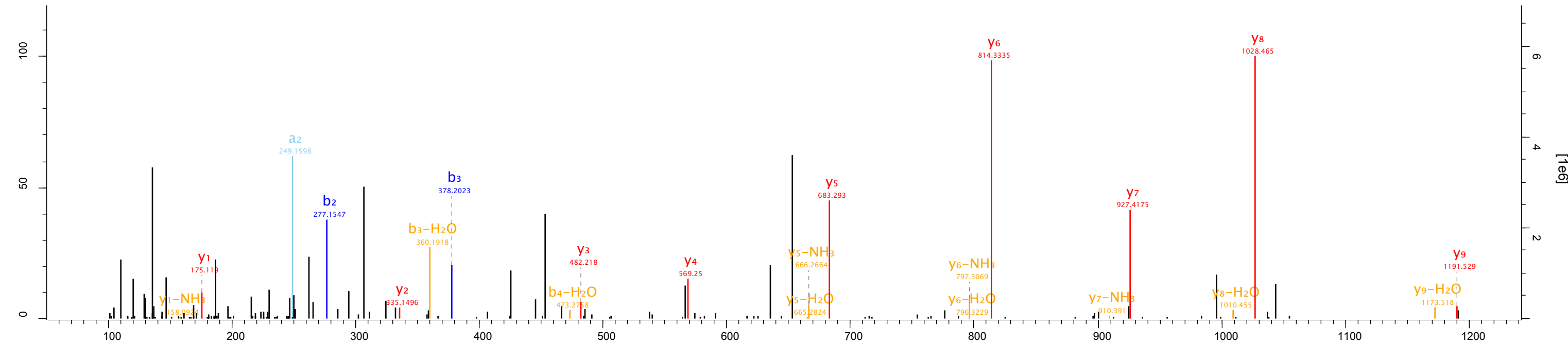


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 Scan: 9455 Method: FTMS; HCD Score: 63.68 m/z: 597.35 Gene names: C20orf24



Raw file 20180707_MaS_A375SR_ML_proteome_25 Scan 16545 Method FTMS; HCD Score 140.83 m/z 436.58 Gene names RPL39P5;RPL39



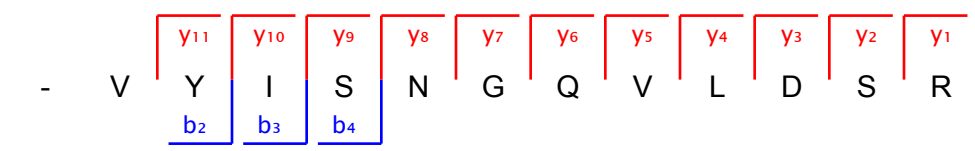
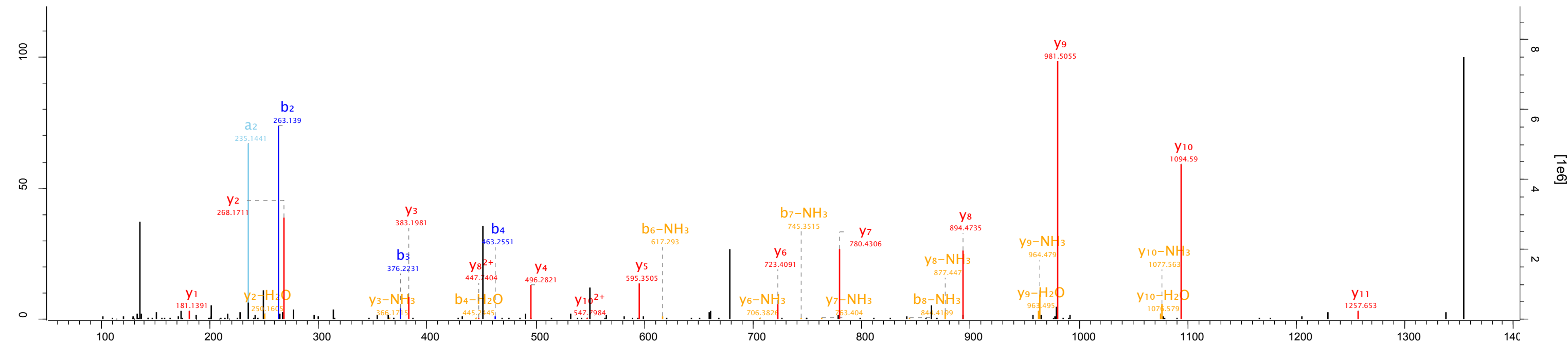


- L Y T I M N S F C R -

b2 b3

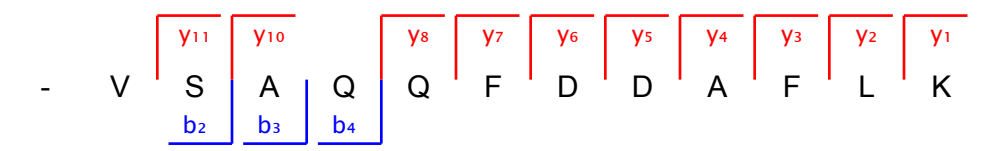
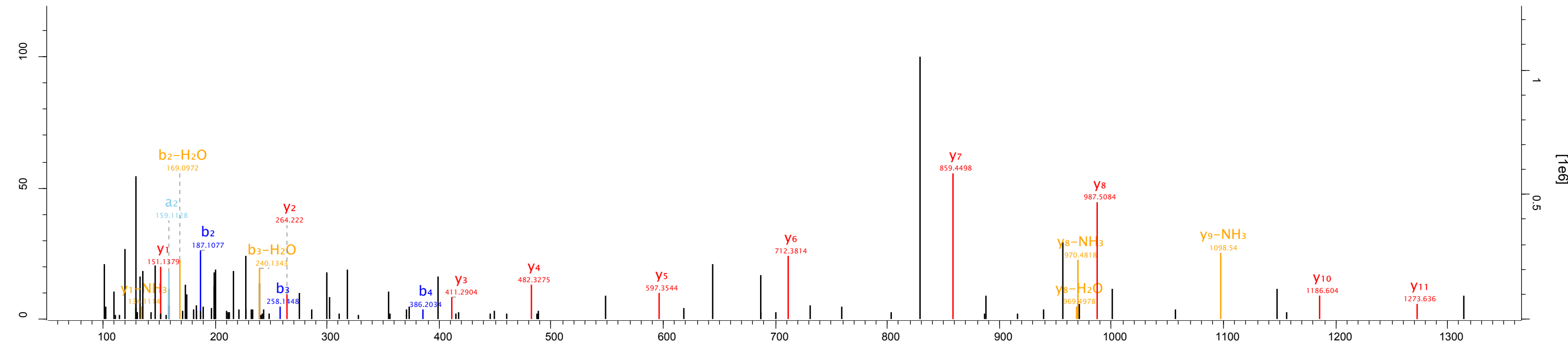
Raw file
20180707_MaS_A375SR_ML_proteome_27

Scan 14455 Method FTMS; HCD Score 124.21 m/z 678.86 Gene names SELK

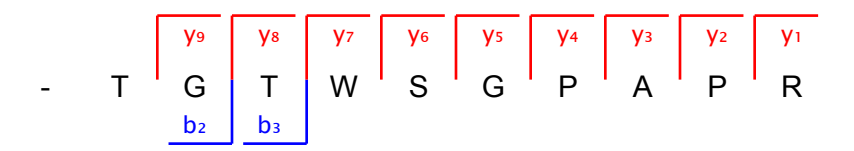
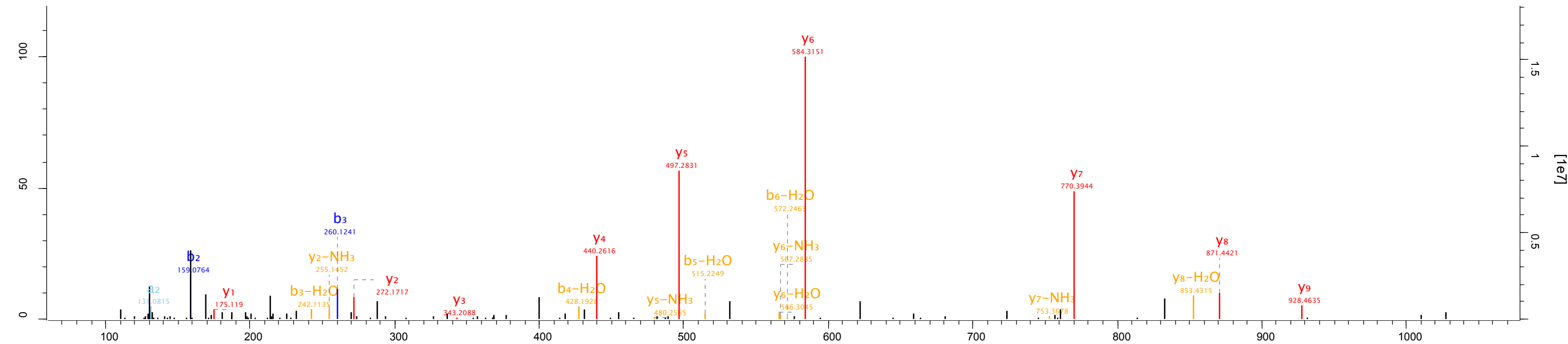


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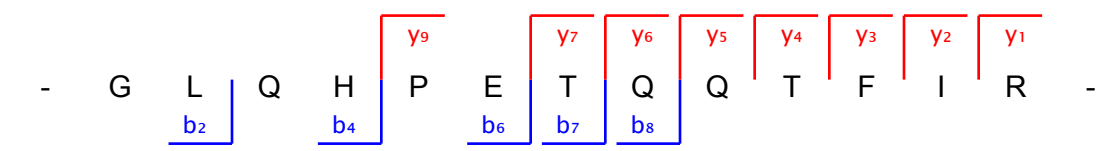
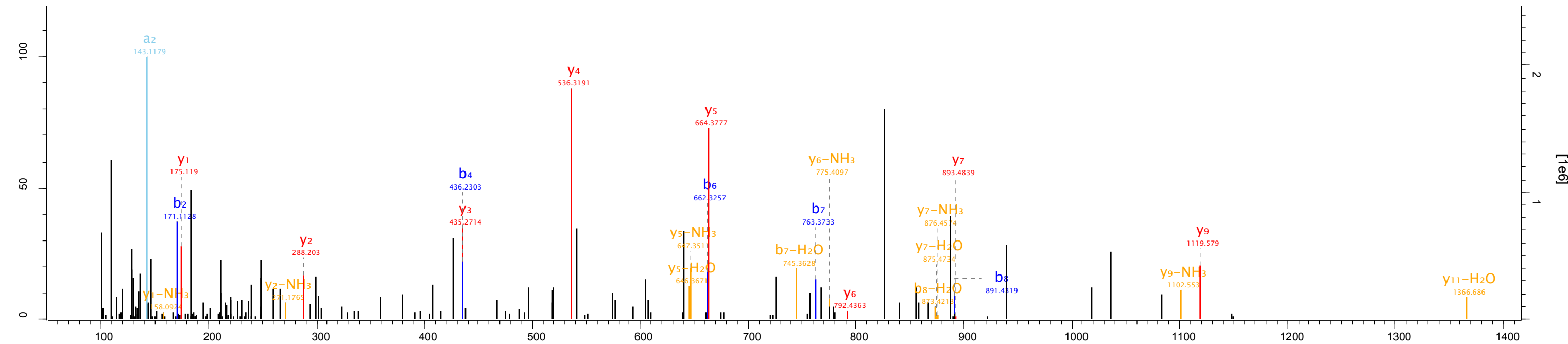
Scan Method Score m/z Gene names
24075 FTMS; HCD 68 687.36 PIGN



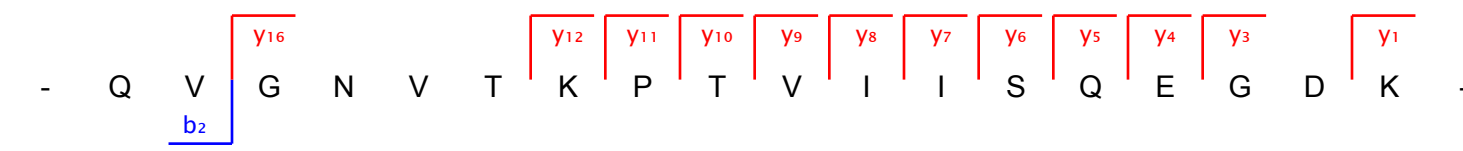
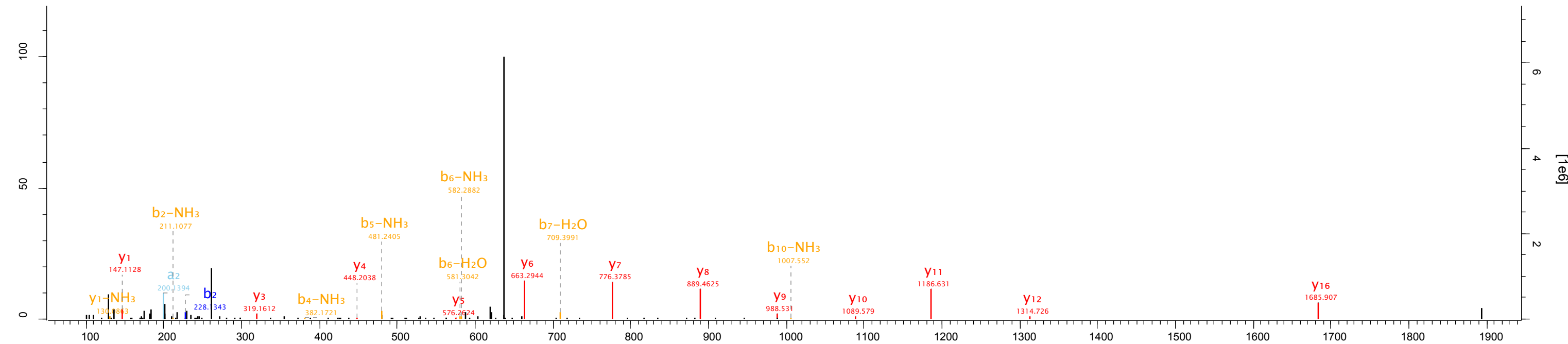
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 Scan: 9385 Method: FTMS; HCD Score: 101.97 m/z: 515.26 Gene names: CR2



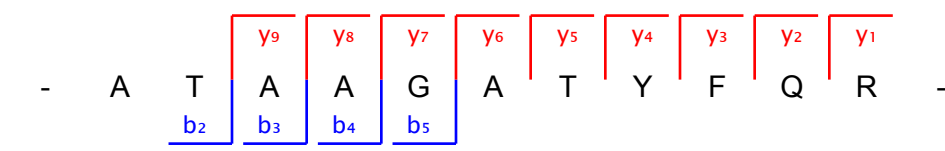
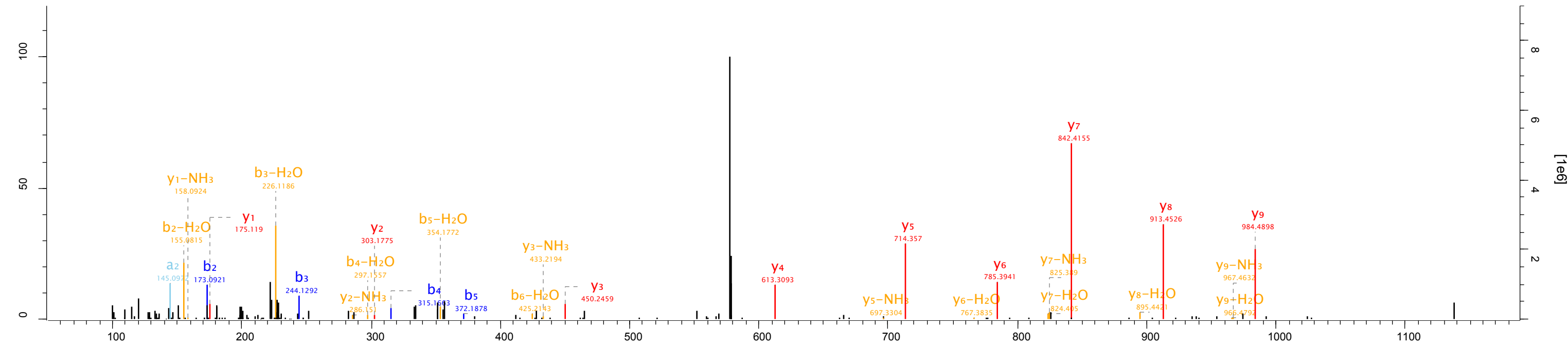
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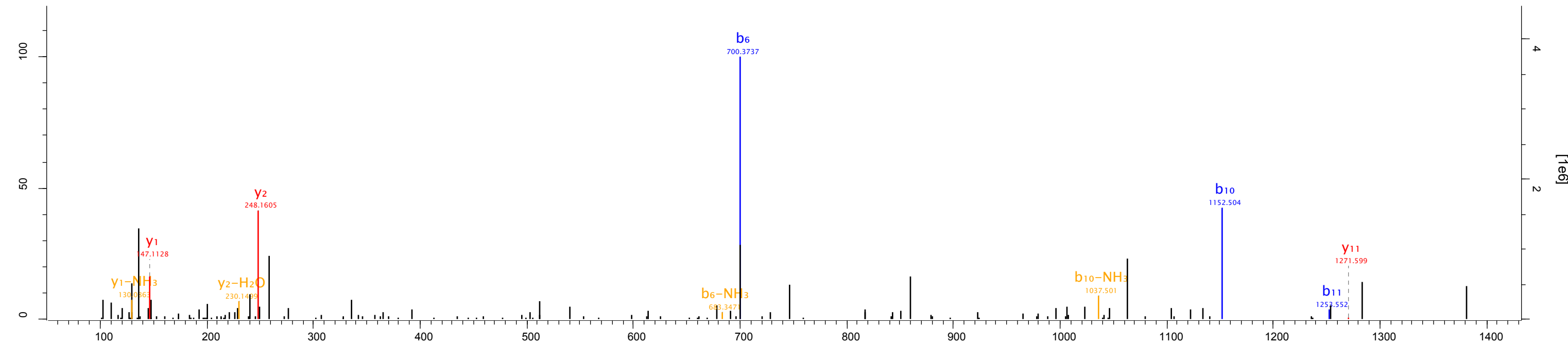


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 Scan: 12825 Method: FTMS; HCD Score: 39.9 m/z: 638.35 Gene names: FABP7



Raw file: 20180707_MaS_A375SR_ML_proteome_29
 Scan: 11765 Method: FTMS; HCD Score: 130.01 m/z: 578.79 Gene names: TMEM254

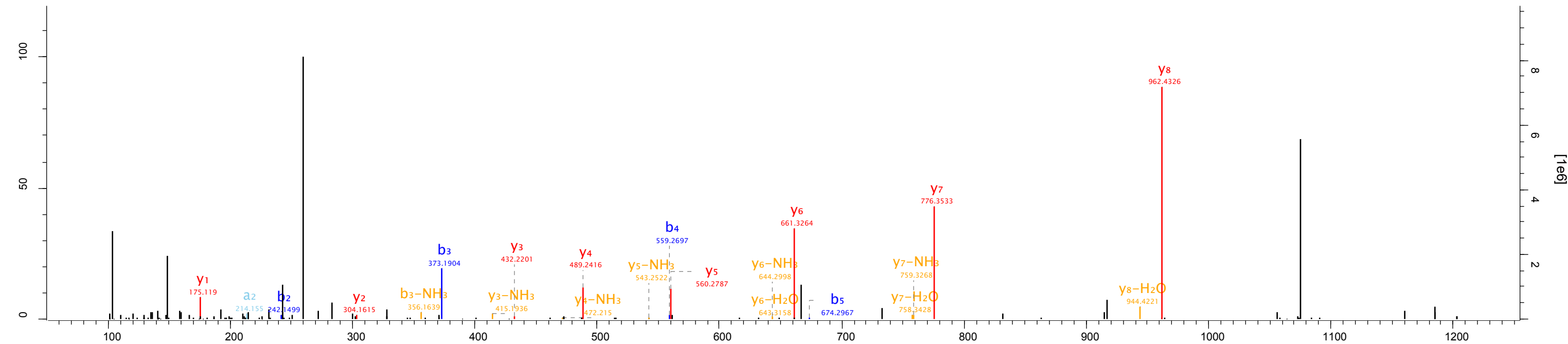




- Q Q S R L S ph S S T P T K -

Fragmentation sites are indicated by brackets below the sequence:

- y_{11} (red bracket above Q)
- b_6 (blue bracket below S)
- b_{10} (blue bracket below P)
- b_{11} (blue bracket below T)
- y_2 (red bracket above T)
- y_1 (red bracket above K)

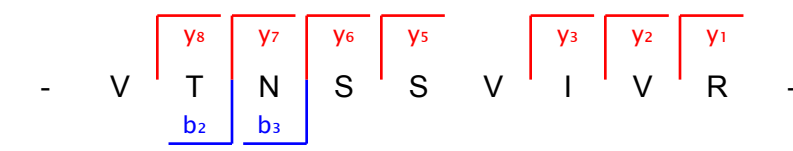
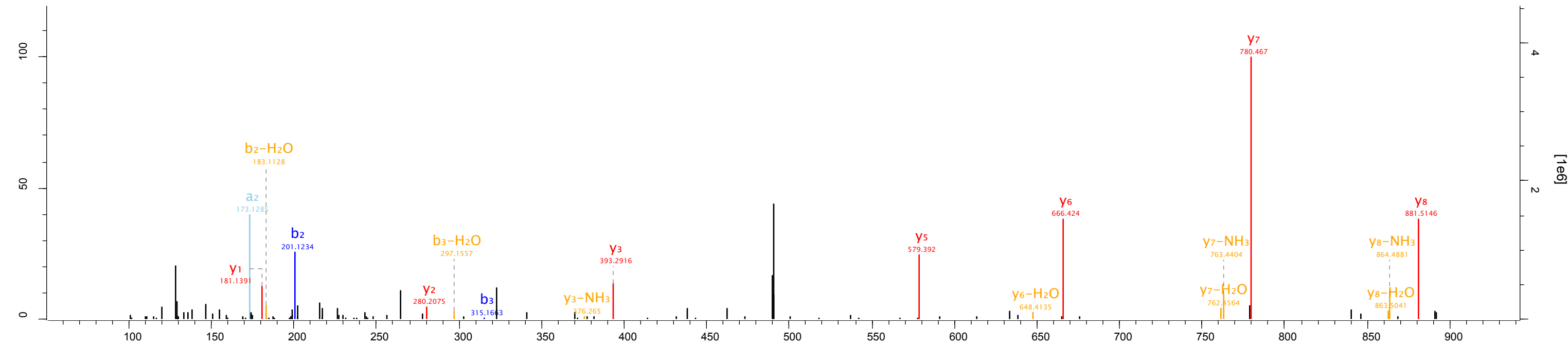


- L Q M W D T A G Q E R -

Fragmentation sites are indicated by boxes below the sequence:

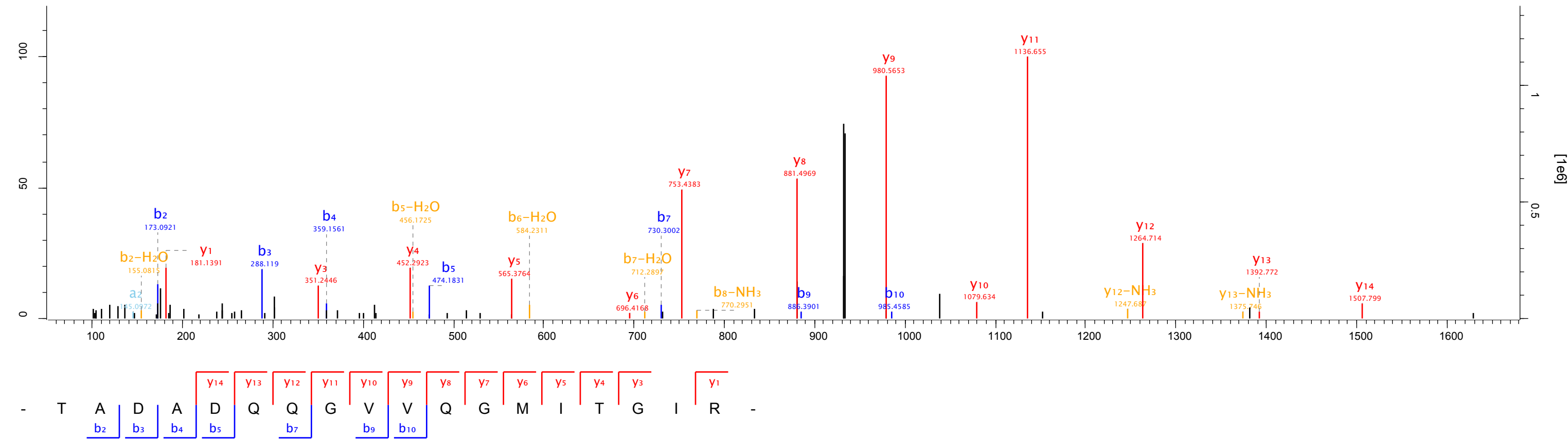
- Q (b₂)
- M (b₃)
- W (b₄)
- D (b₅)
- W (y₈)
- D (y₇)
- T (y₆)
- A (y₅)
- G (y₄)
- Q (y₃)
- E (y₂)
- R (y₁)

Raw file 20180707_MaS_A375SR_ML_proteome_29 Scan 8125 Method FTMS; HCD Score 102.62 m/z 490.8 Gene names FBXO27

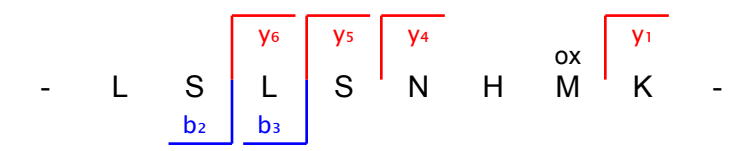
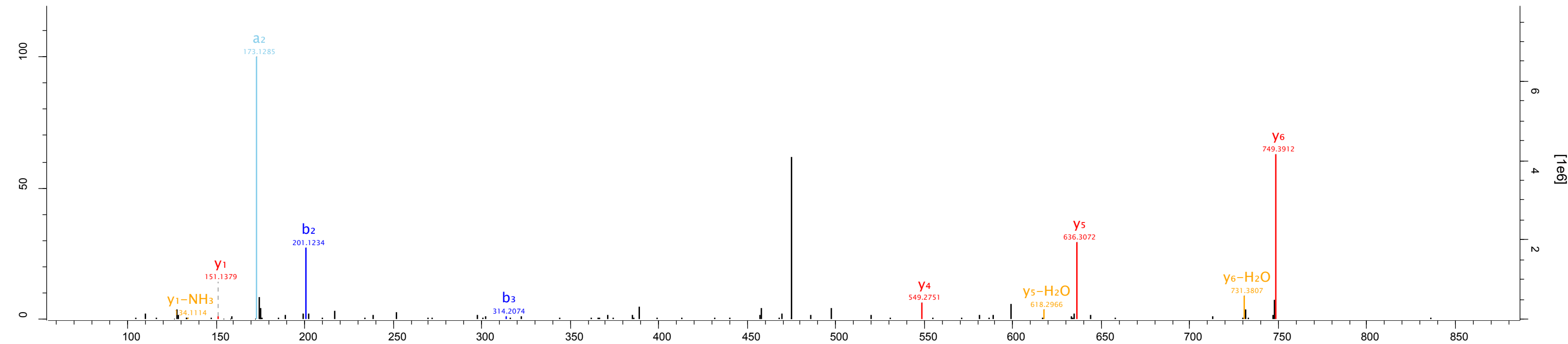


Raw file
20180707_MaS_A375SR_ML_proteome_30

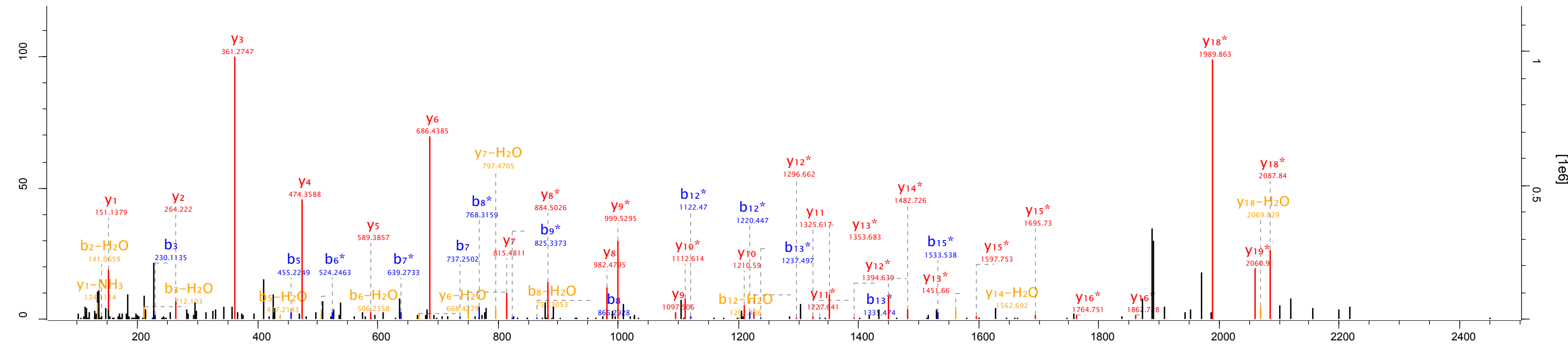
Scan: 23335
Method: FTMS; HCD
Score: 92.47
m/z: 933.48
Gene names: HIAT1



Raw file 20180707_MaS_A375SR_ML_proteome_30 Scan 5555 Method FTMS; HCD Score 45.68 m/z 475.26



Raw file: 20150812_A375SR_Phospho_BR1_02
 Scan: 20426 Method: FTMS; HCD Score: 124.99 m/z: 1208.47 Gene names: PAX3

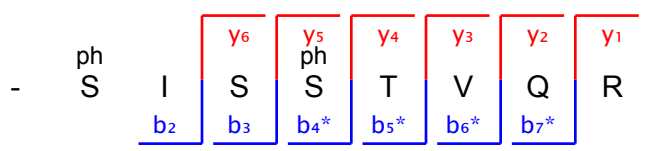
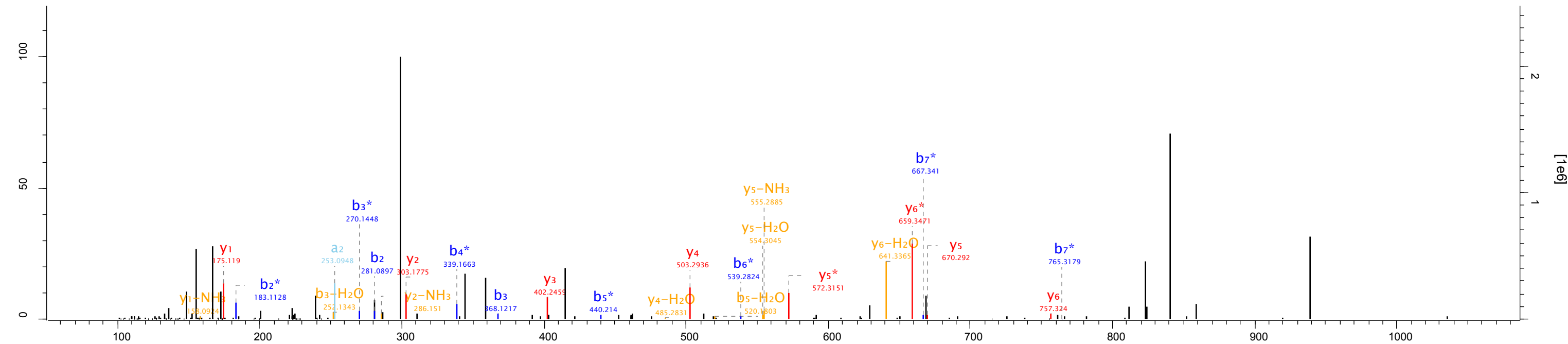


Sequence: - A S A P Q S D I D S E P D L P L K -

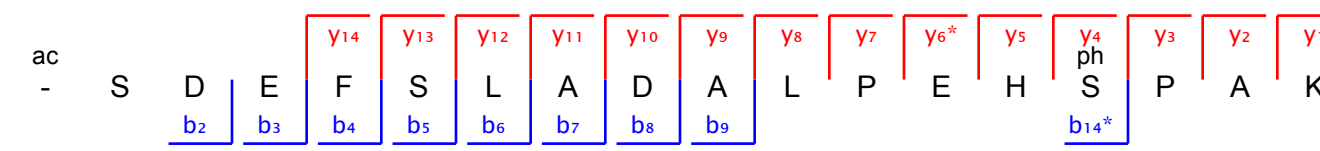
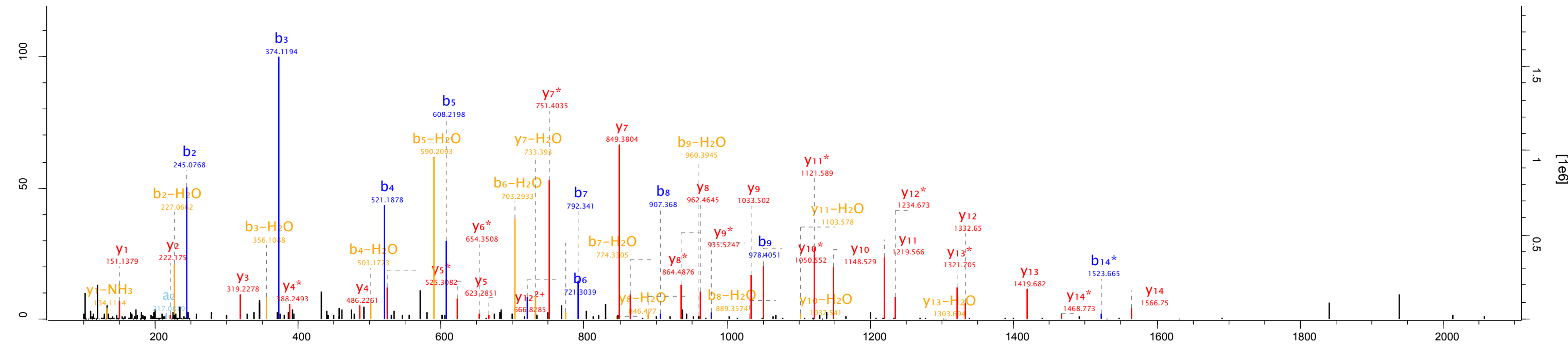
Fragmentation sites (b ions): b3, b5, b6*, b7, b8, b9*, b12*, b13*, b15*

Fragmentation sites (y ions): y1, y2, y3, y4, y5, y6, y7, y8, y9, y10, y11, y12*, y13*, y14*, y15*, y16*, y18*, y19*

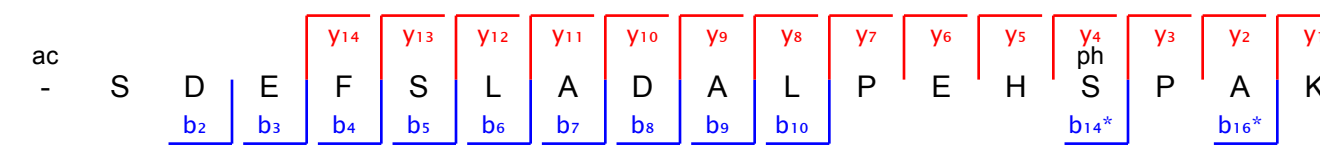
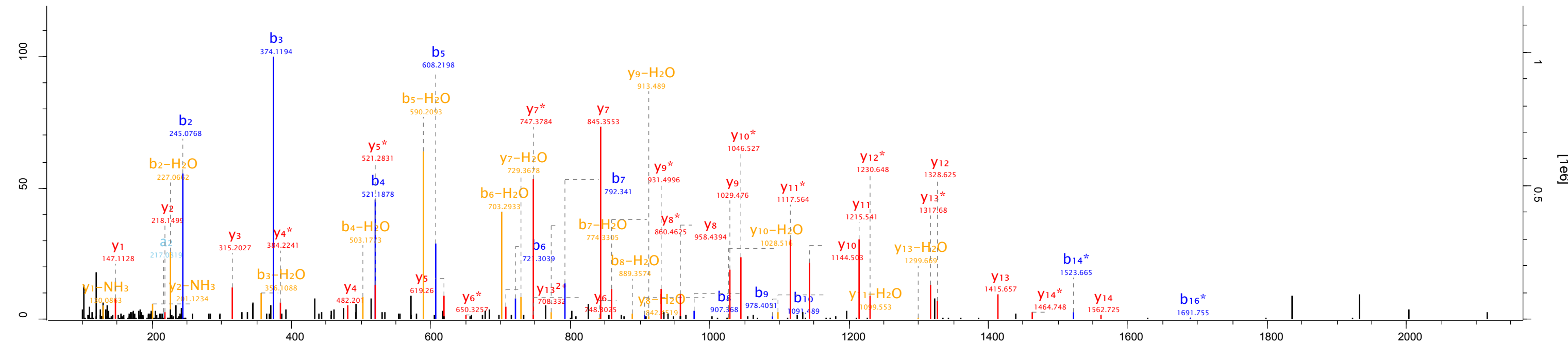
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 Scan: 8446 Method: FTMS; HCD Score: 91.04 m/z: 519.21 Gene names: RHBDF2



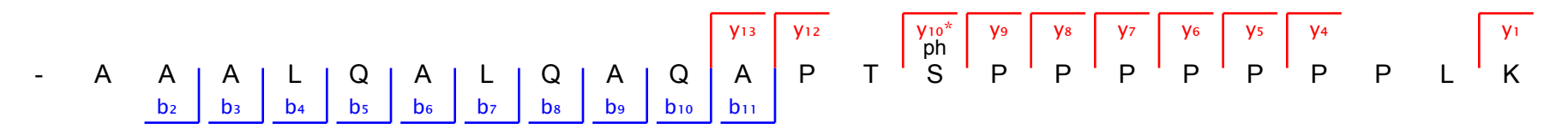
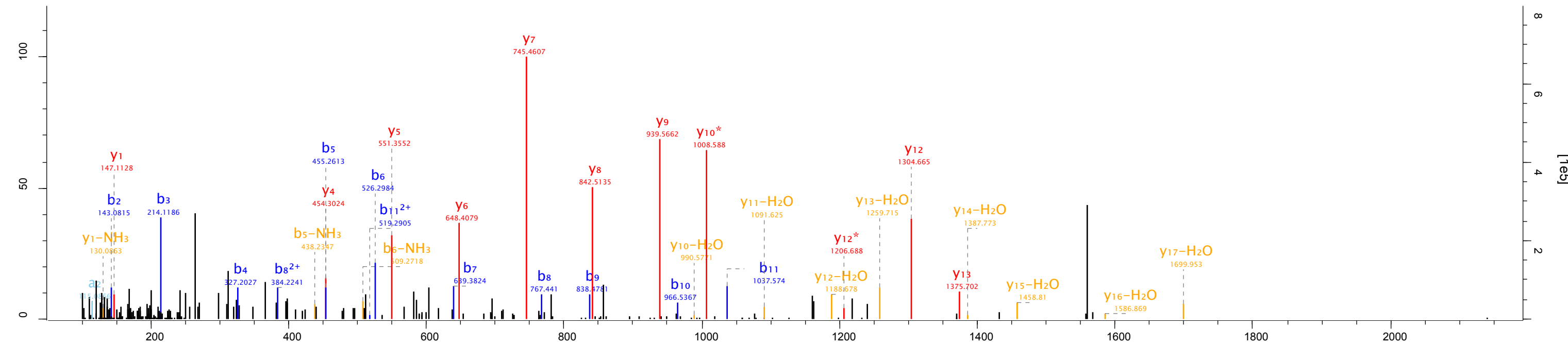
Raw file
 20150812_A375SR_Phospho_BR1_03
 Scan 24836 Method FTMS; HCD Score 258.37 m/z 970.94 Gene names MAPK11P1L



Raw file 20150812_A375SR_Phospho_BR1_03 Scan 24846 Method FTMS; HCD Score 257.37 m/z 968.42 Gene names MAPK11P1L

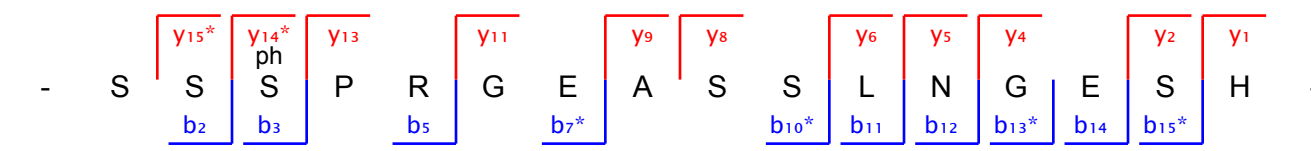
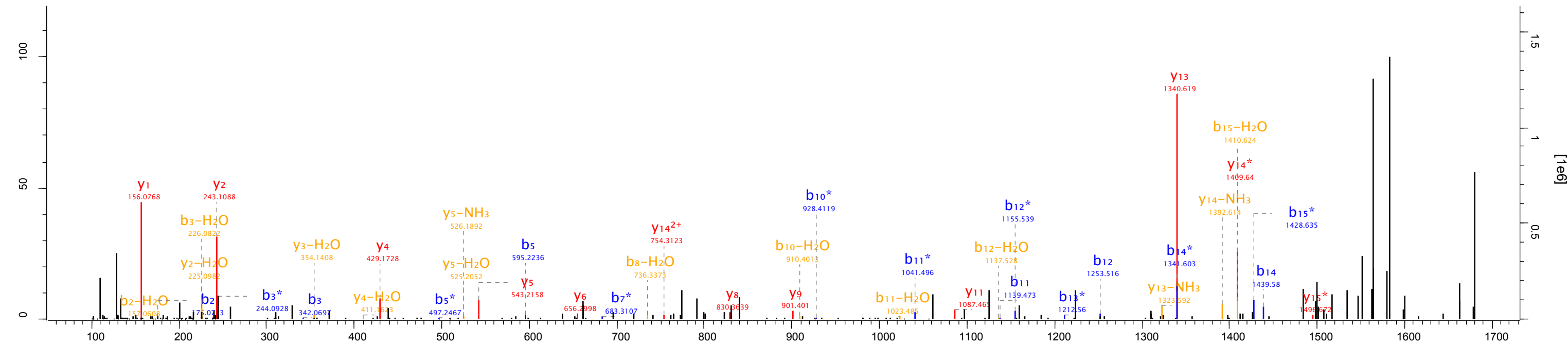


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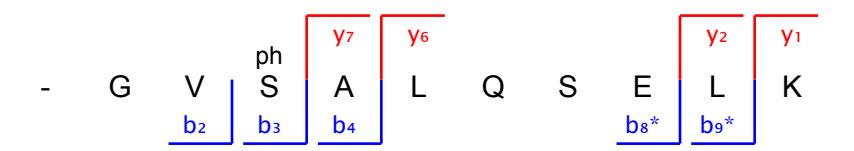
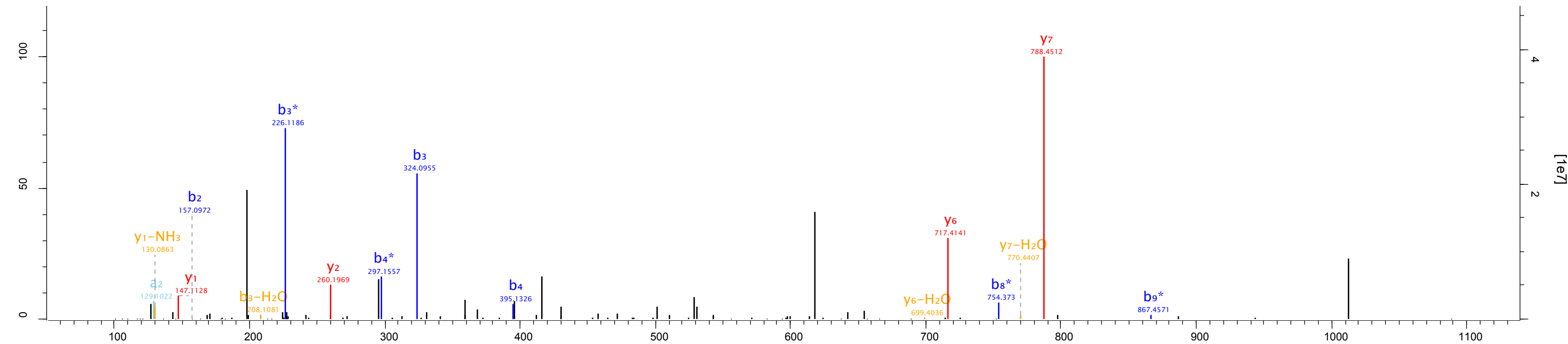


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20150812_A375SR_Phospho_BR1_04

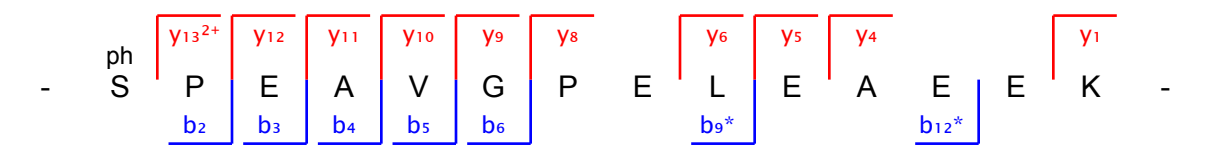
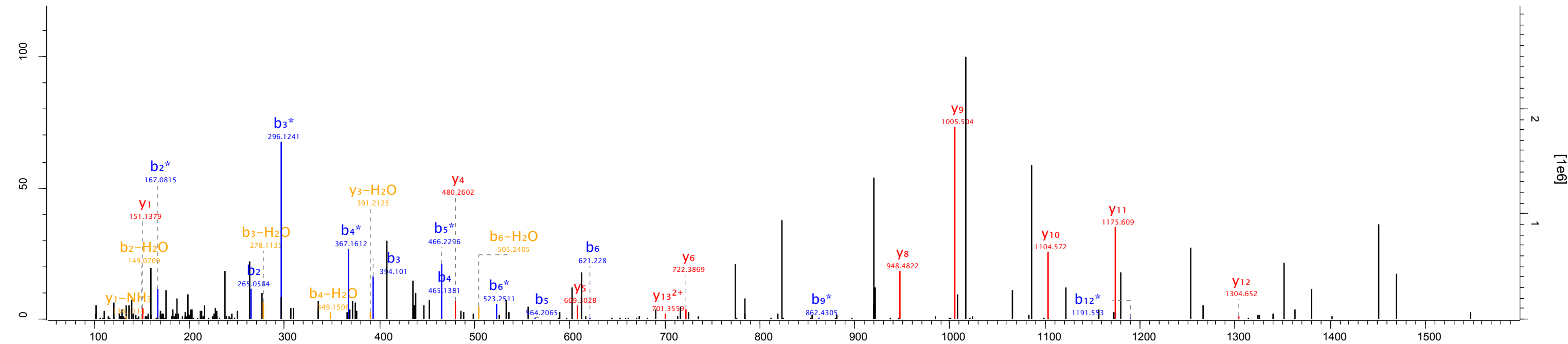
Scan 6106 Method FTMS; HCD Score 102.65 m/z 841.35 Gene names YAF2



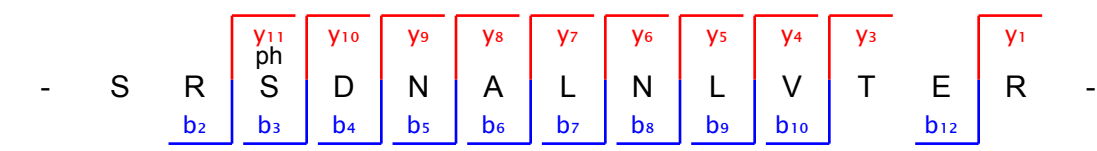
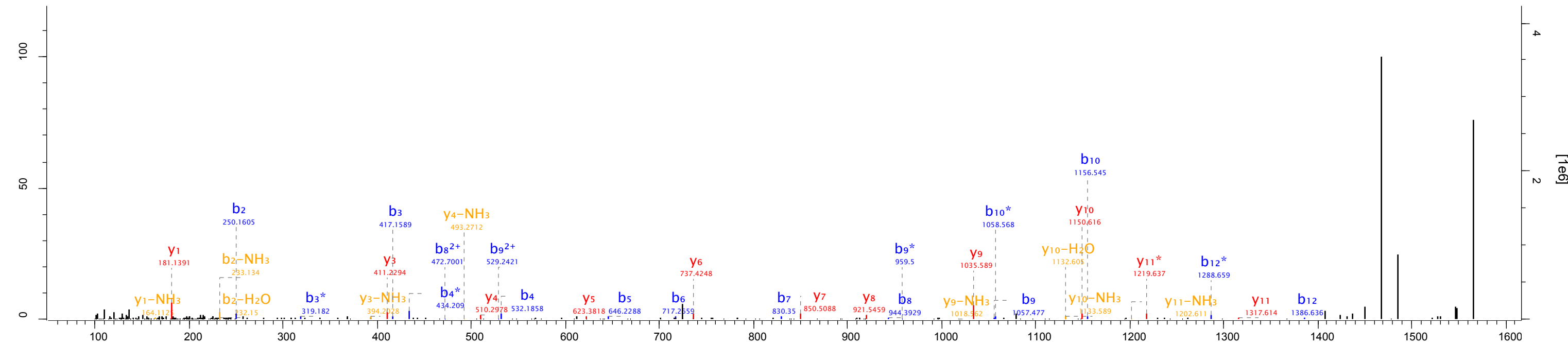
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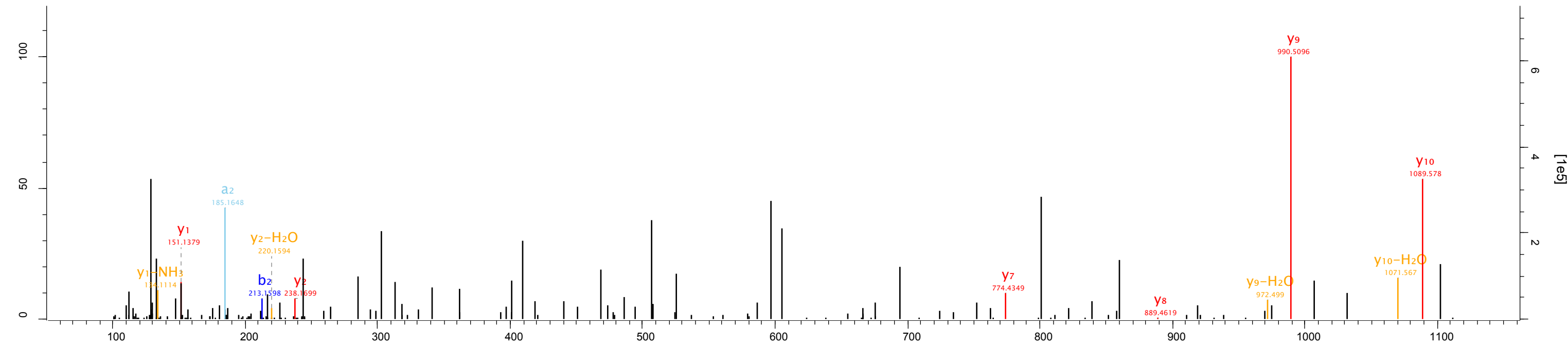
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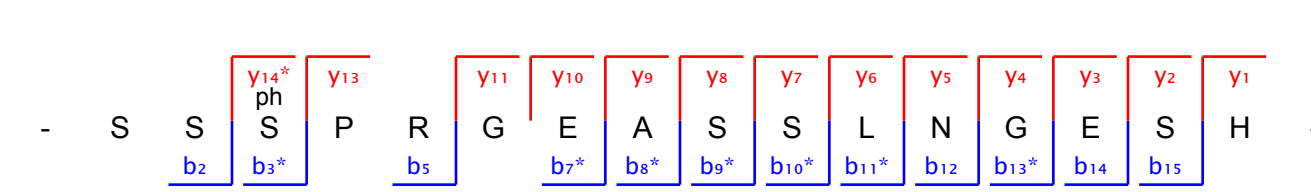
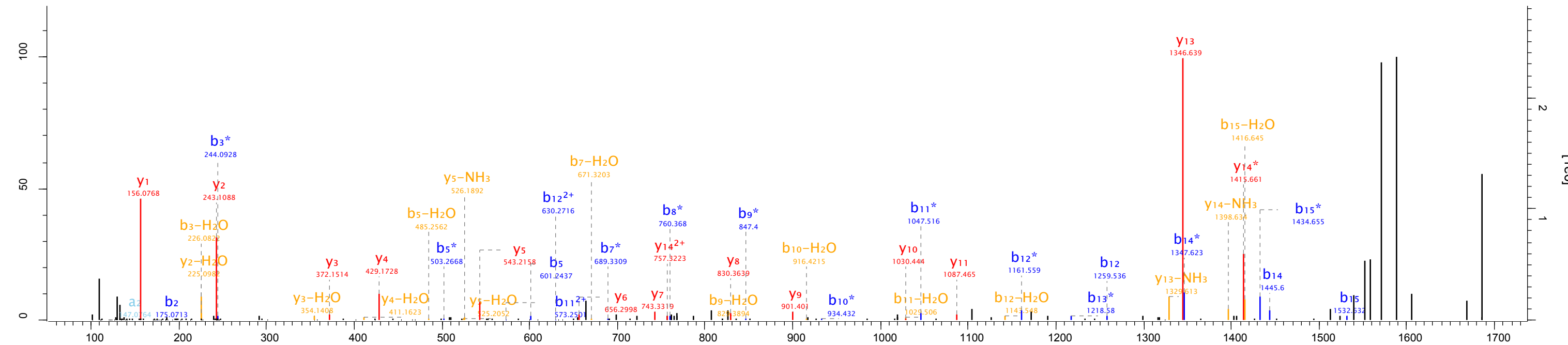
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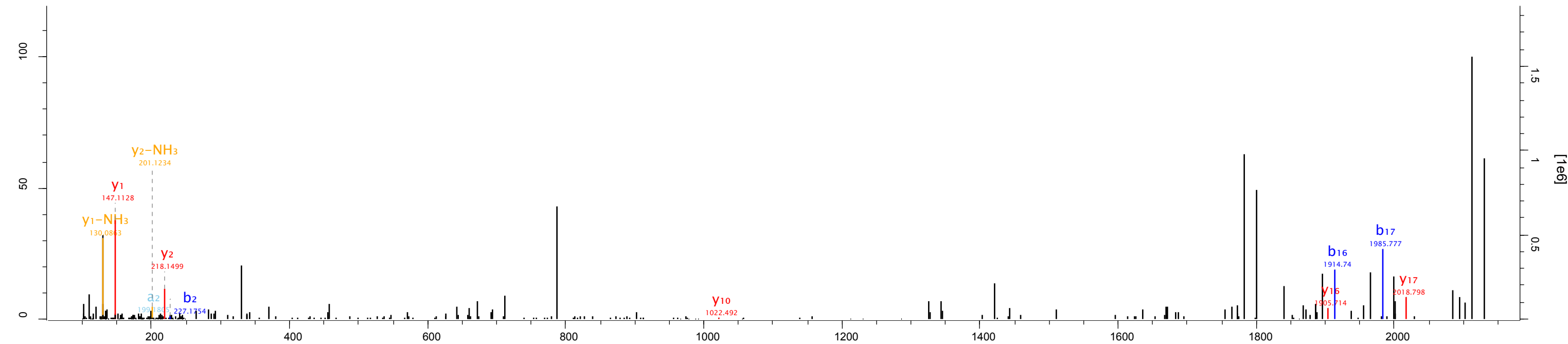
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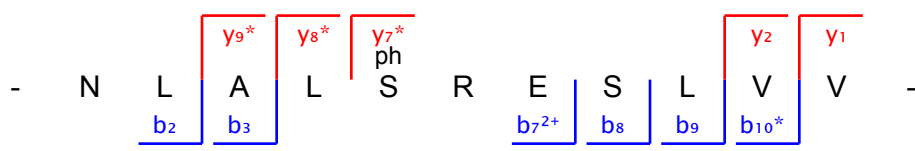
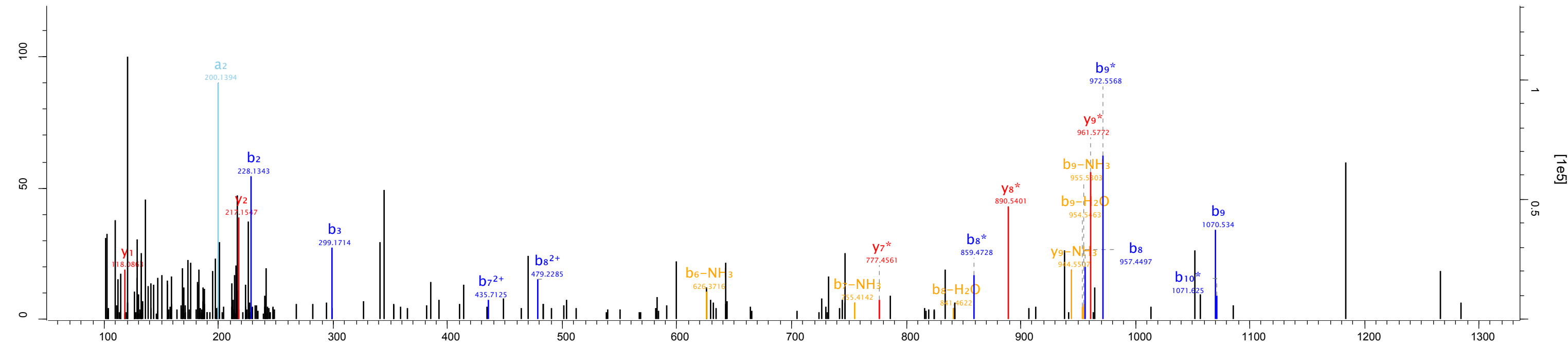
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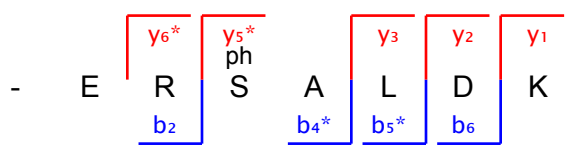
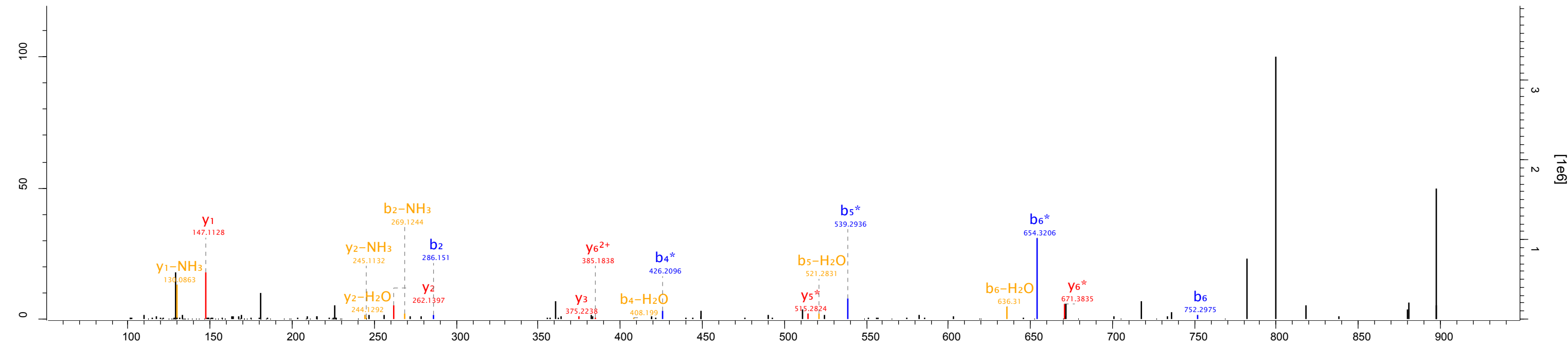
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 Scan 16406 Method FTMS; HCD Score 47.55 m/z 711.63 Gene names LINC00614



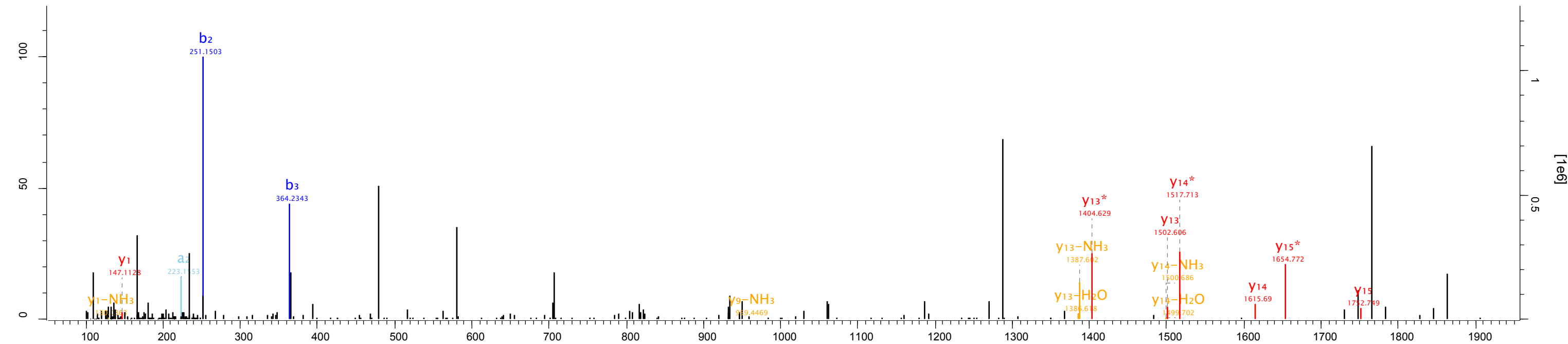
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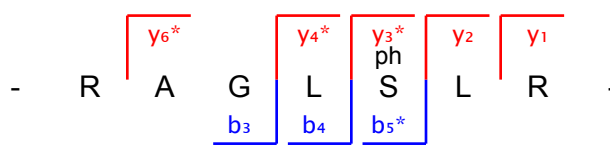
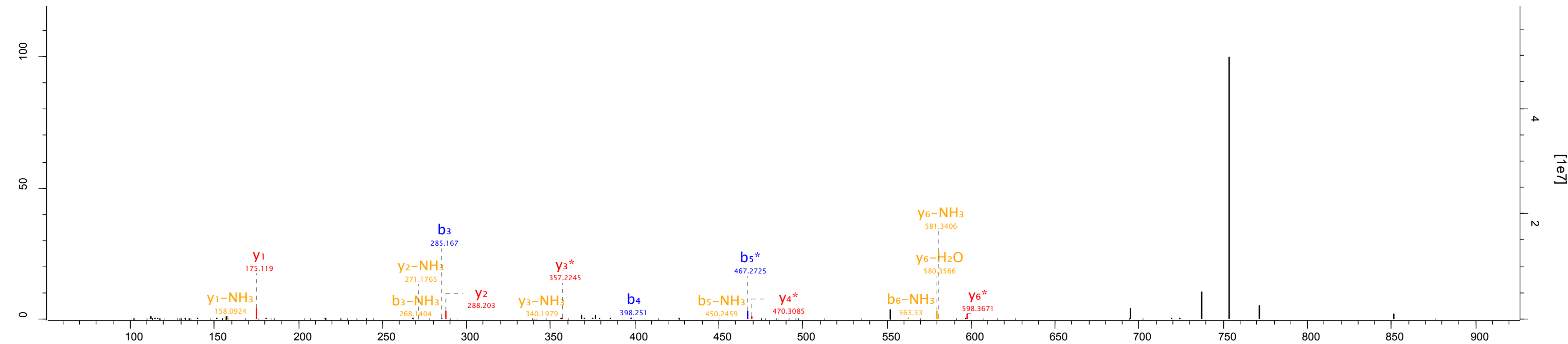
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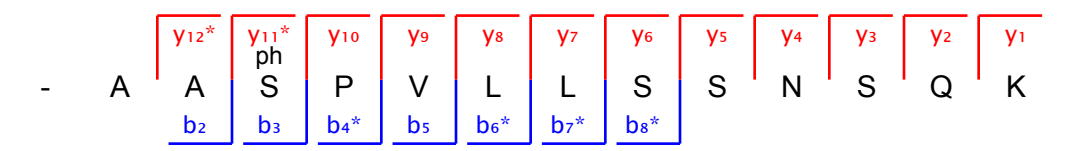
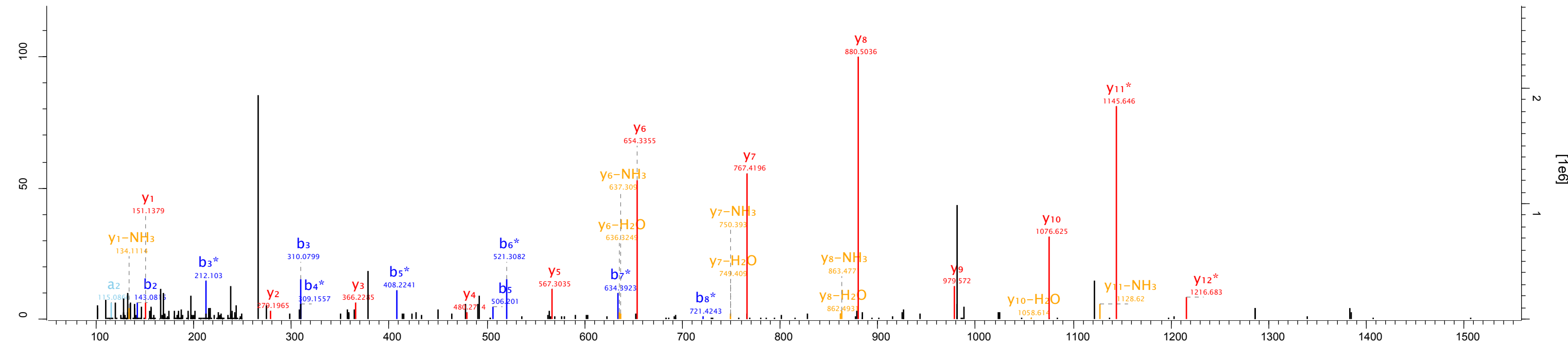
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 Scan 13056 Method FTMS; HCD Score 56.12 m/z 933.93 Gene names CPM



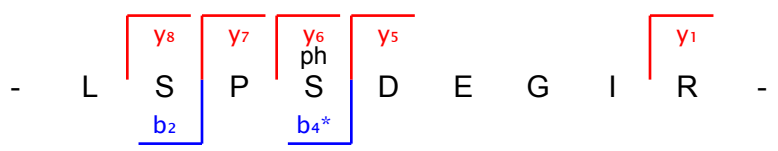
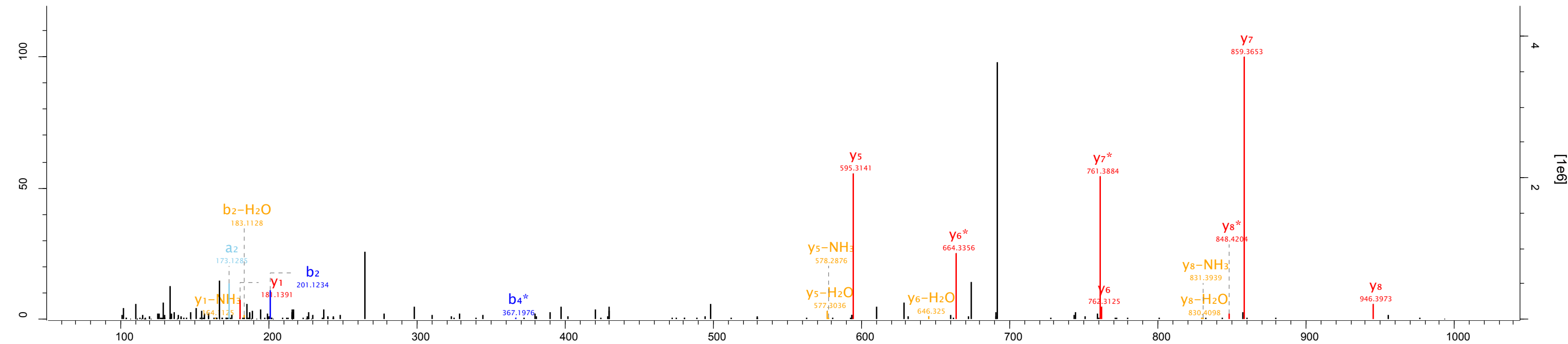
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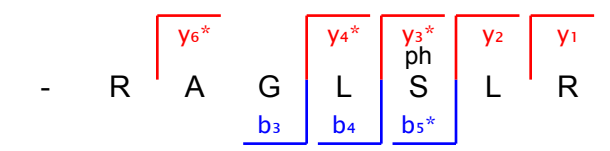
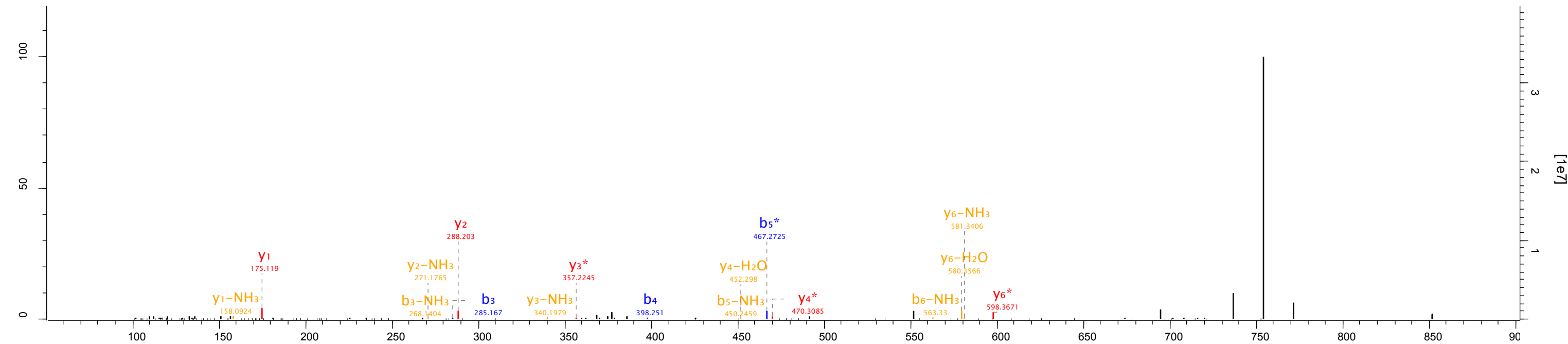
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 Scan: 10716 Method: FTMS; HCD Score: 107.73 m/z: 693.35 Gene names: ELK3



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 Scan: 4746 Method: FTMS; HCD Score: 50.27 m/z: 530.25

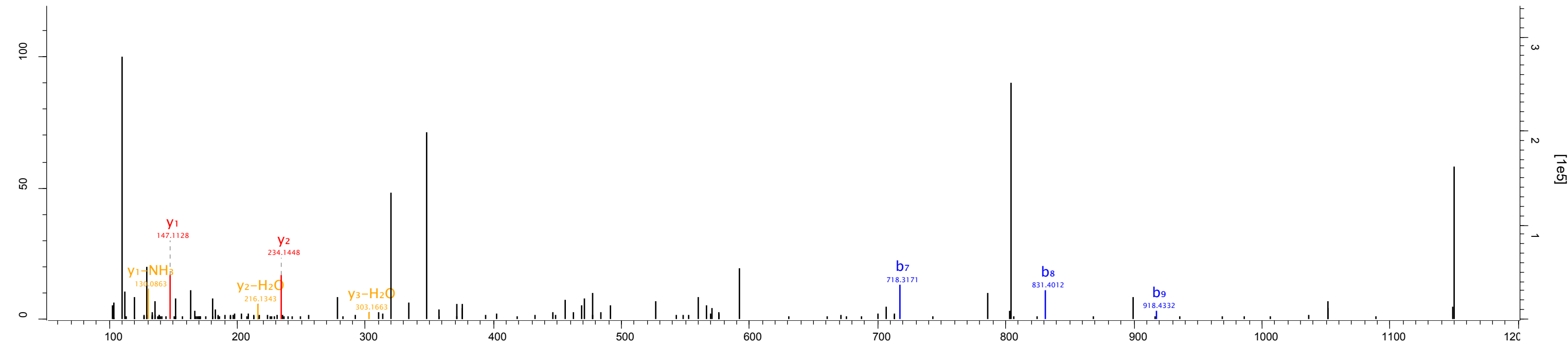


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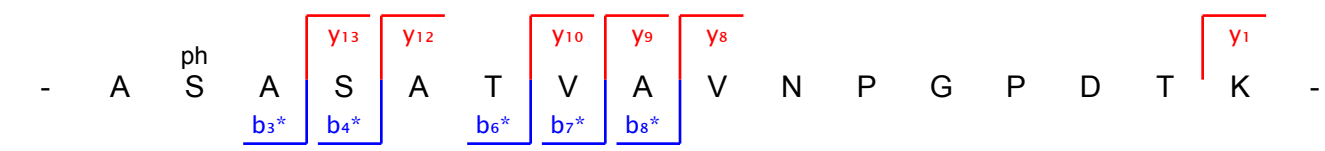
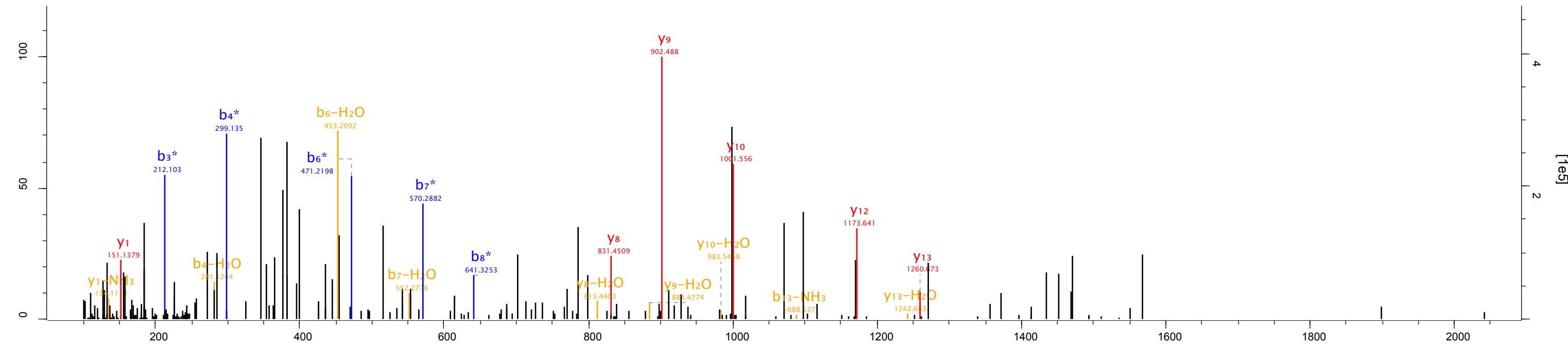
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Scan 7076 Method FTMS; HCD Score 42.72 m/z 576.29

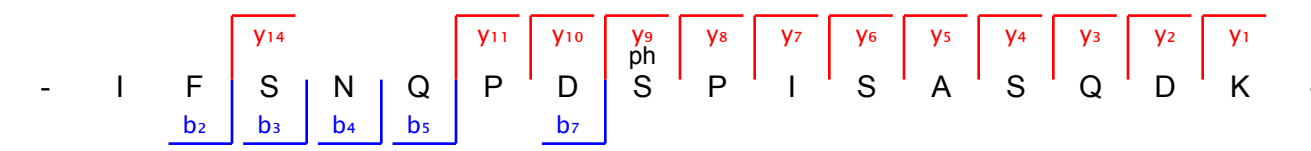
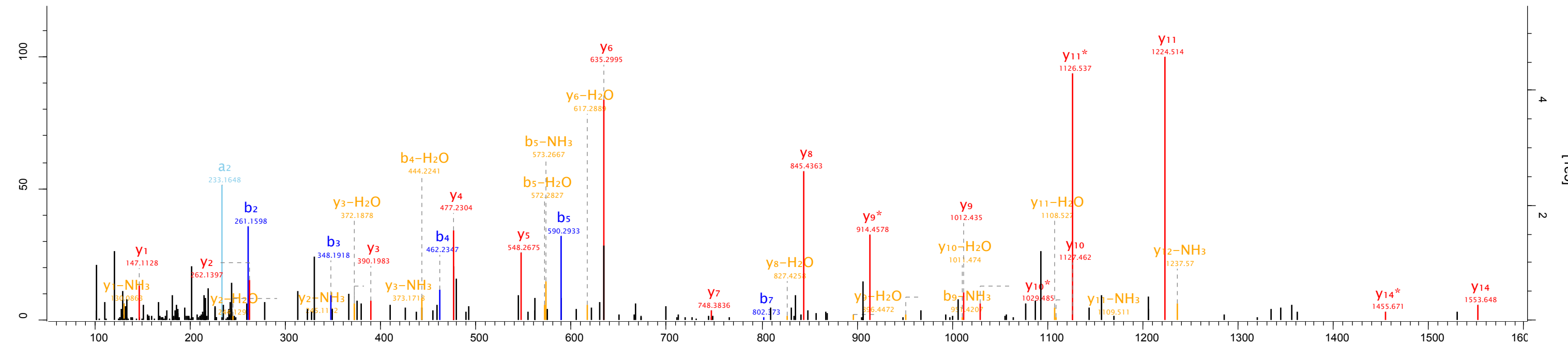


- ph
S S G V I P P L S S K -
b7 b8 b9 y2 y1

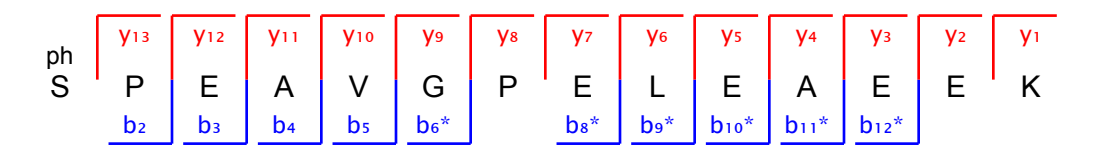
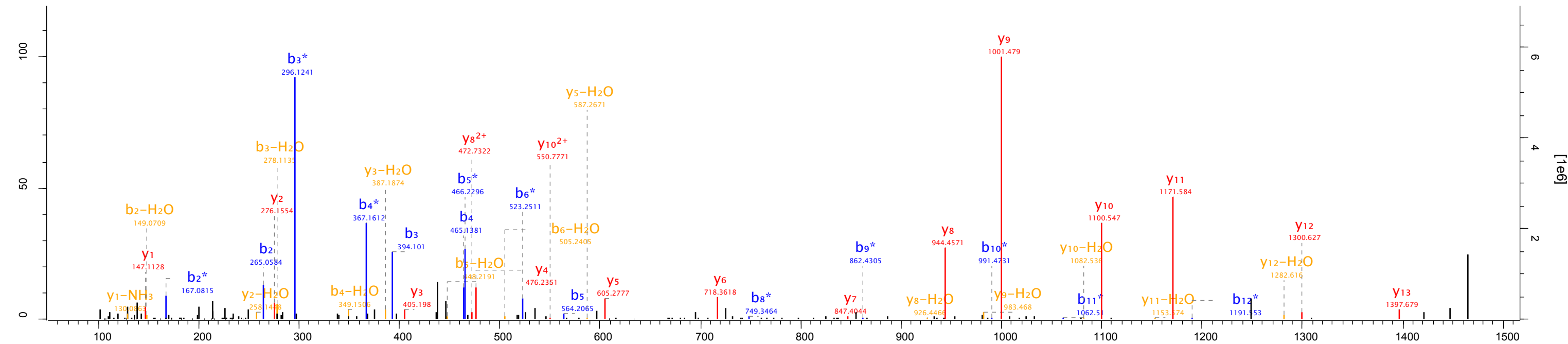
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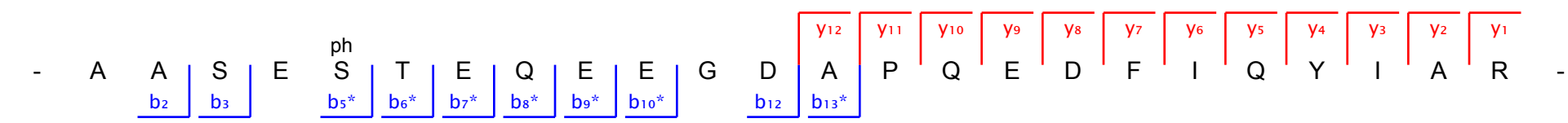
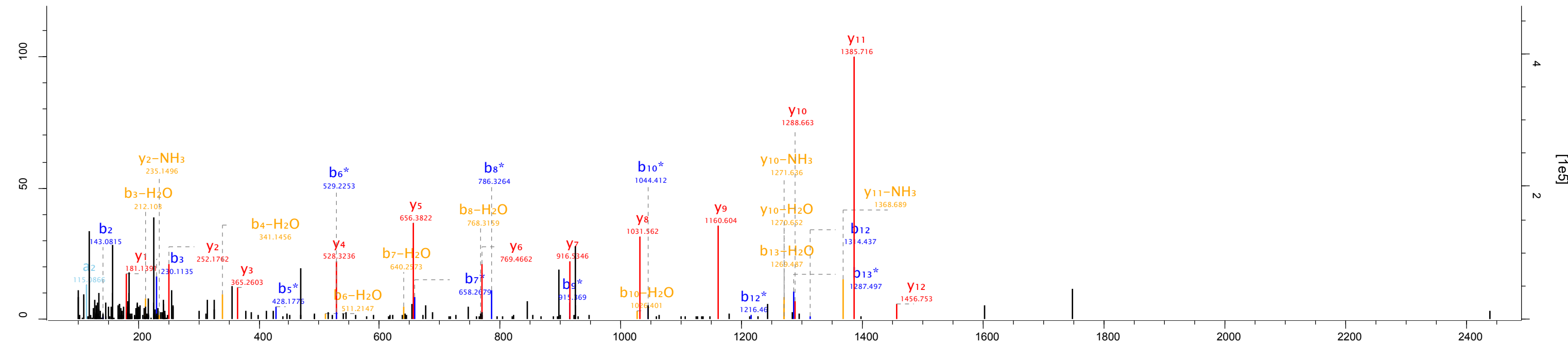
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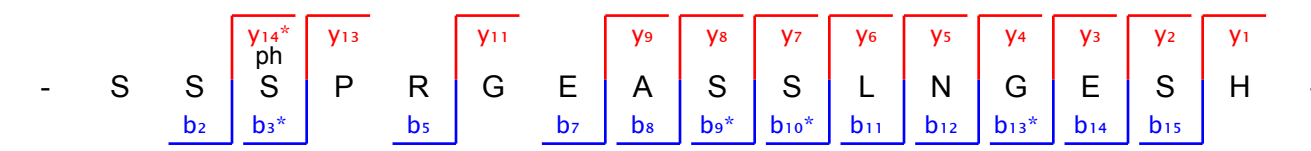
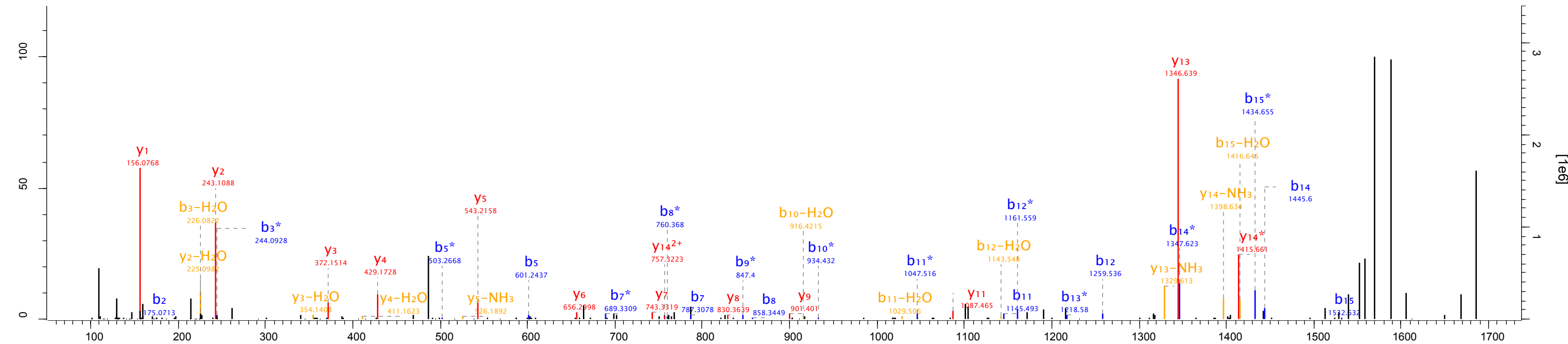
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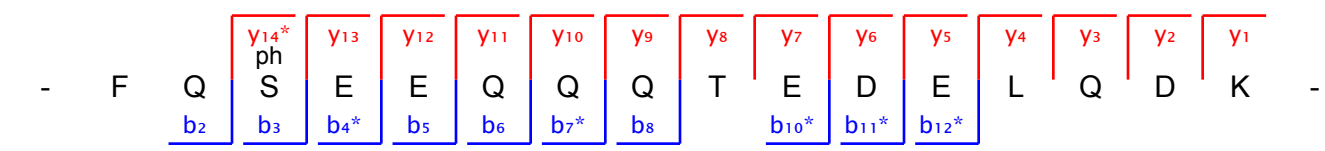
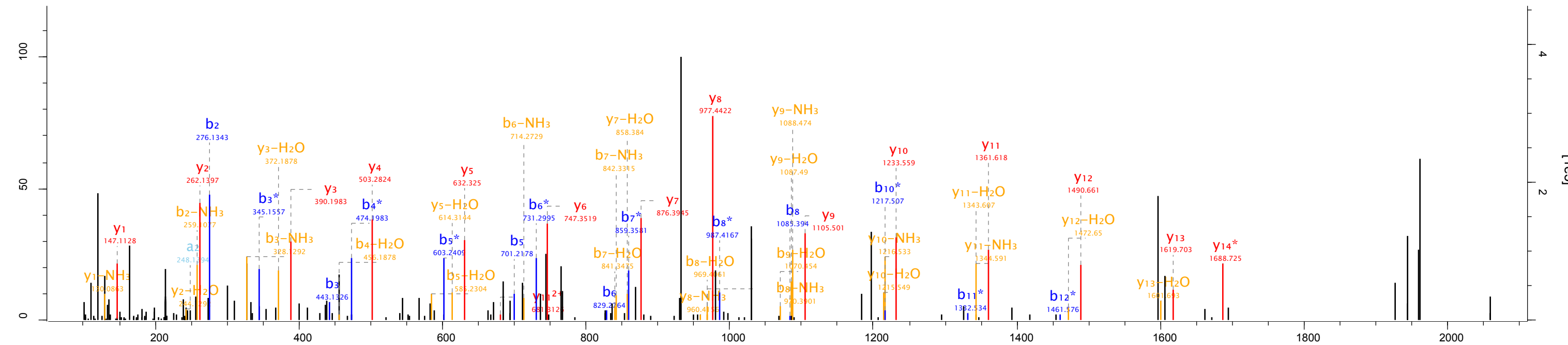
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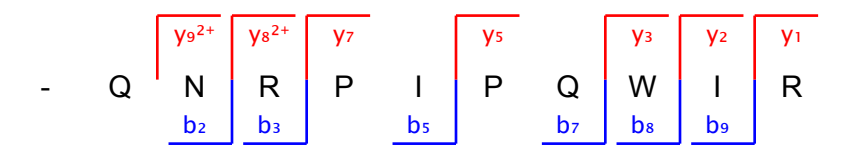
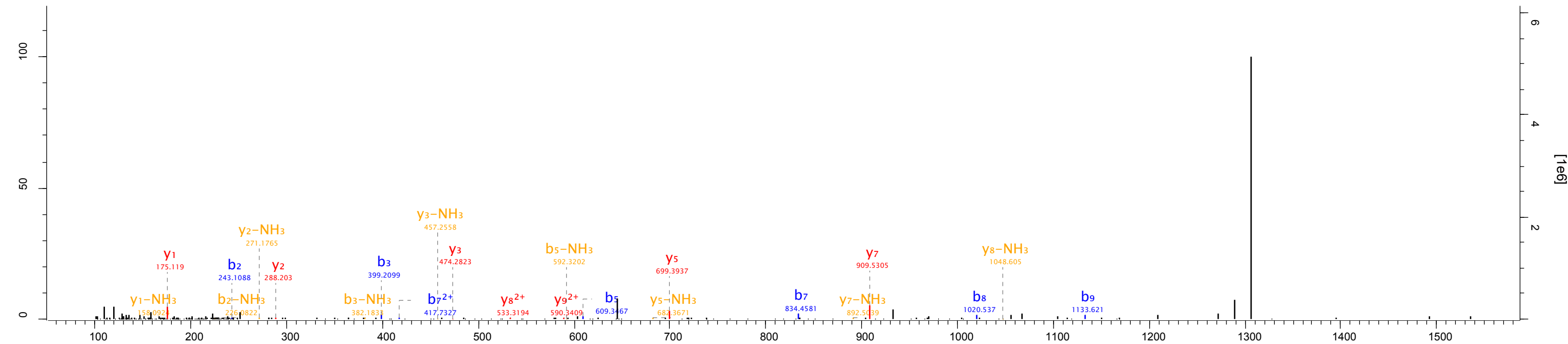
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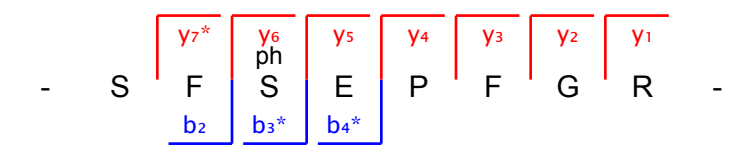
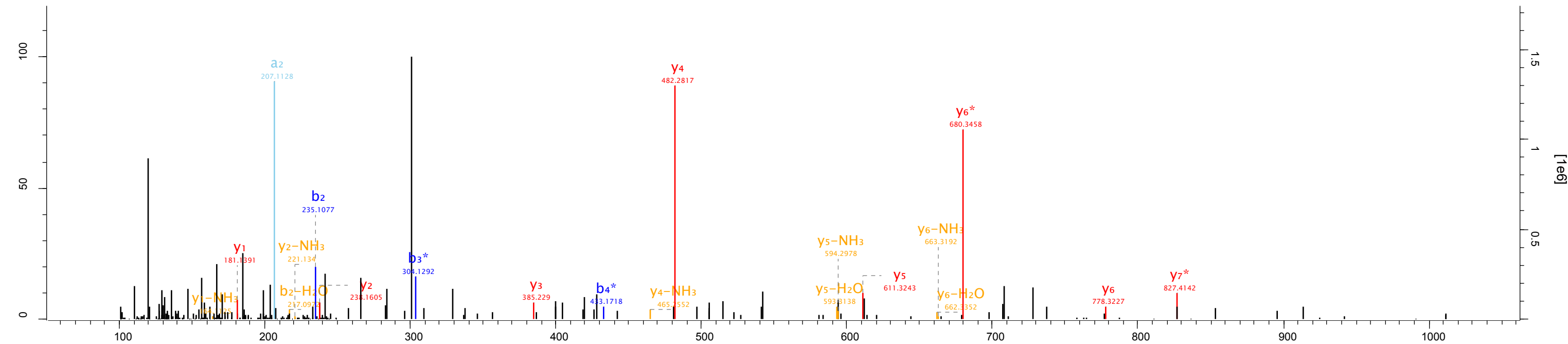
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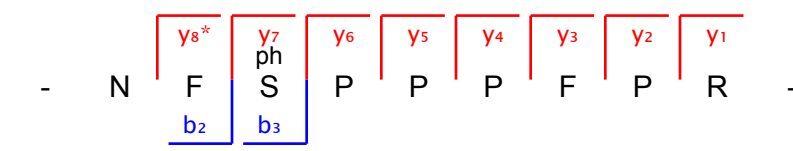
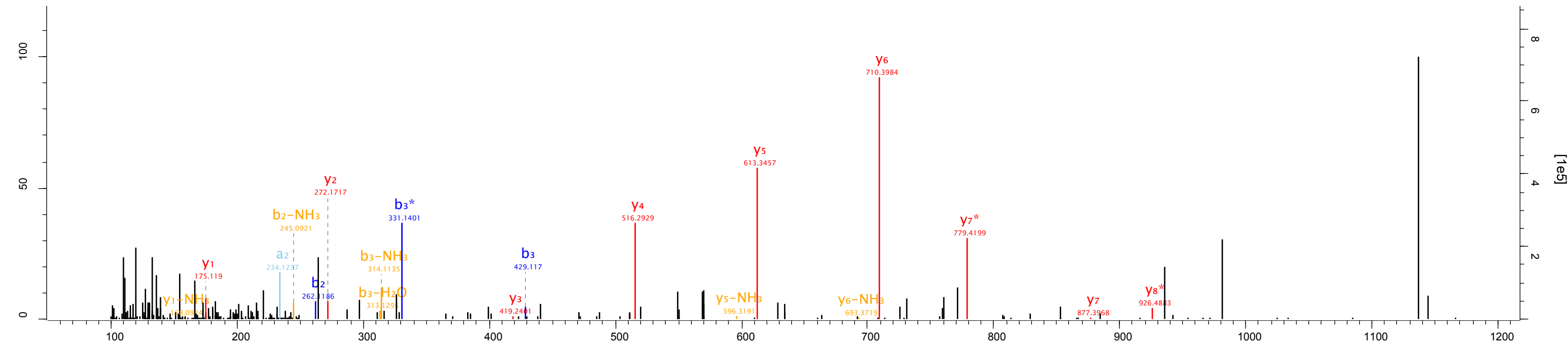
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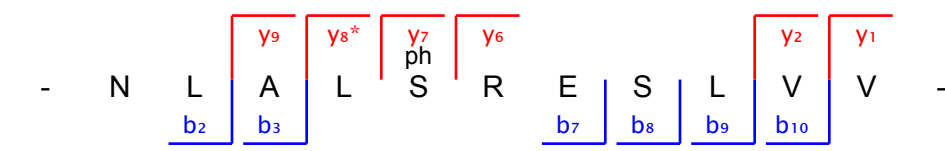
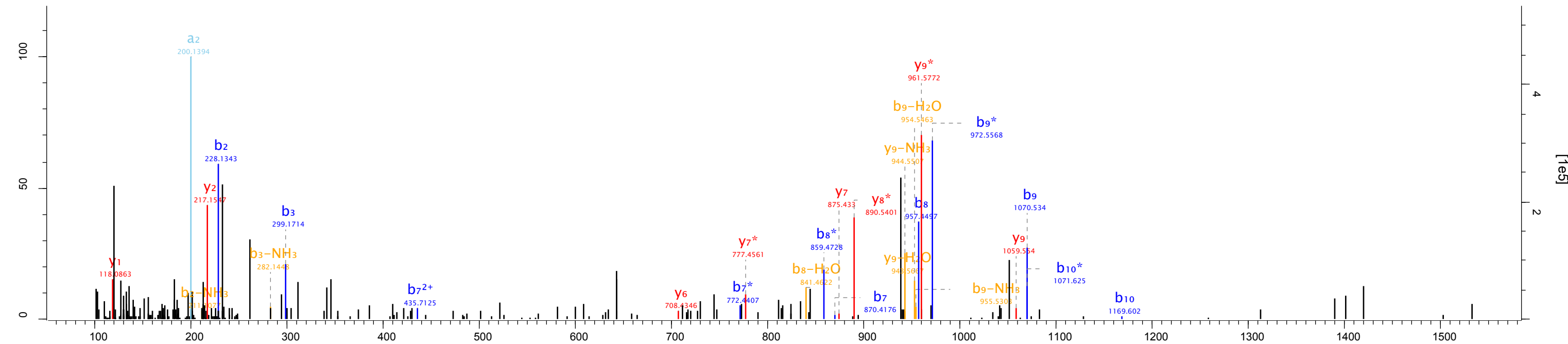
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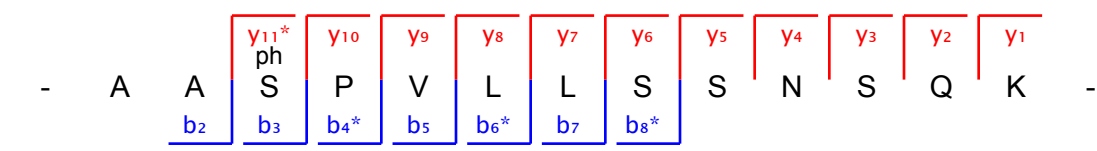
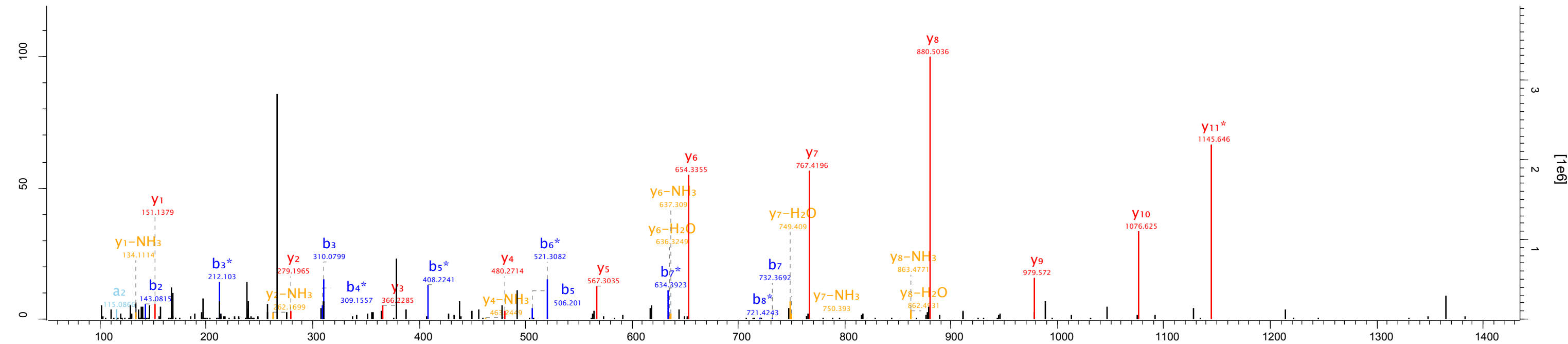
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 Scan: 19516 Method: FTMS; HCD Score: 55.98 m/z: 569.76 Gene names: CCDC125



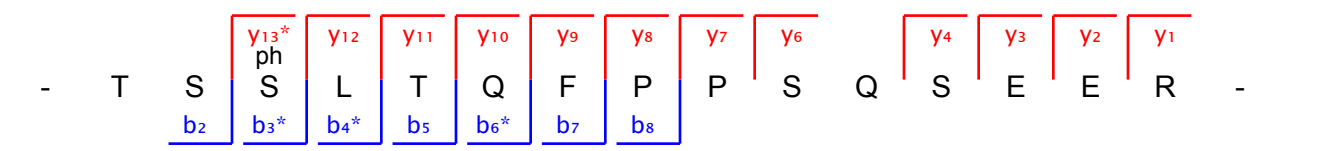
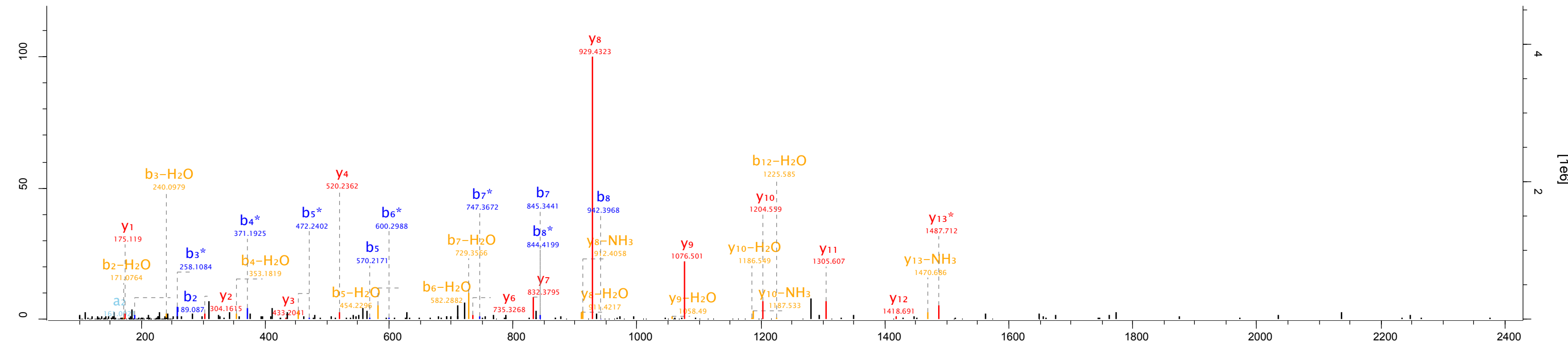
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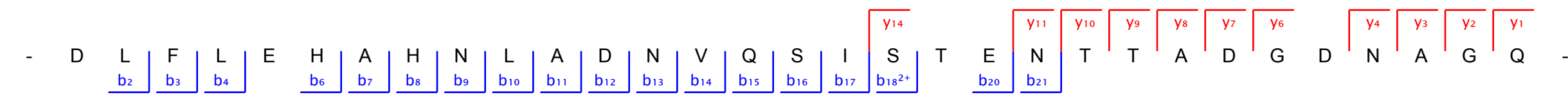
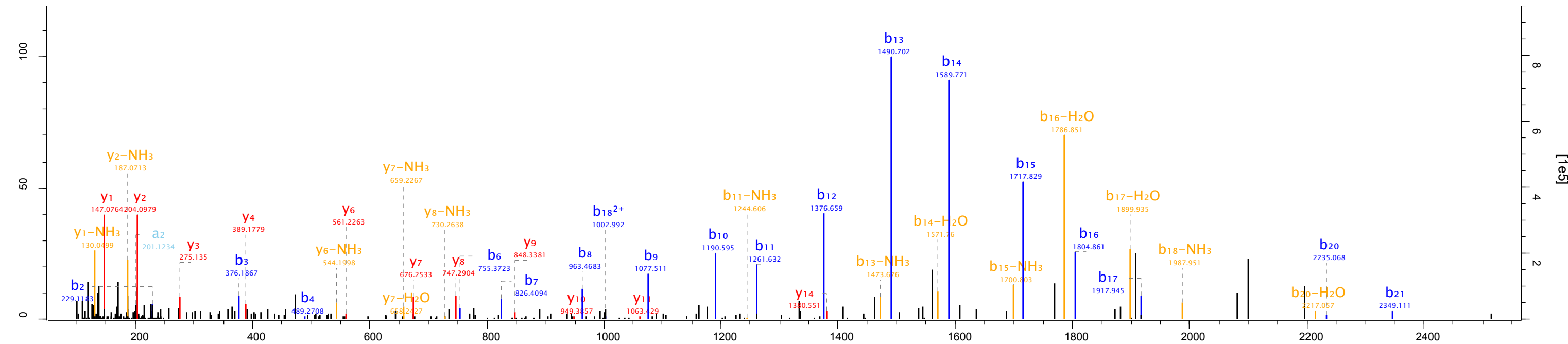
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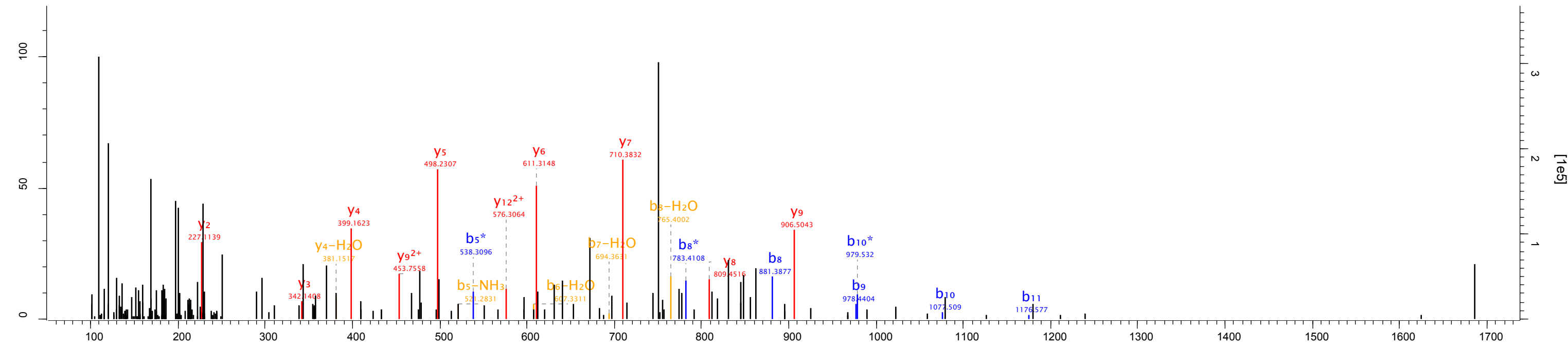
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 Scan: 15216 Method: FTMS; HCD Score: 109.5 m/z: 887.89 Gene names: RANBP3;ZNF8



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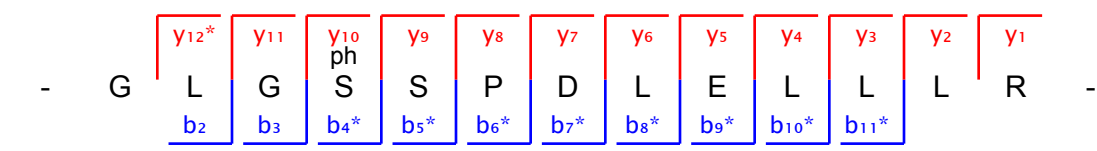
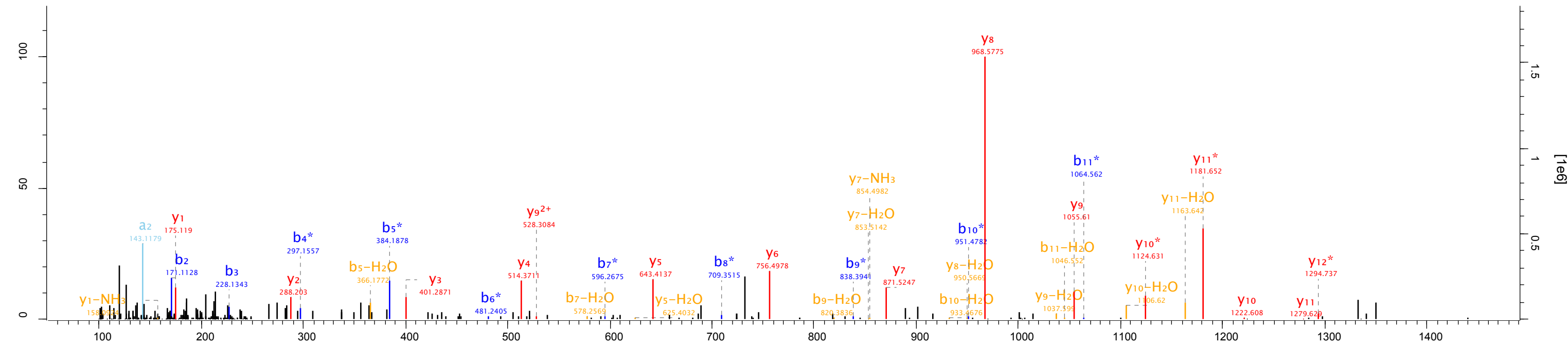
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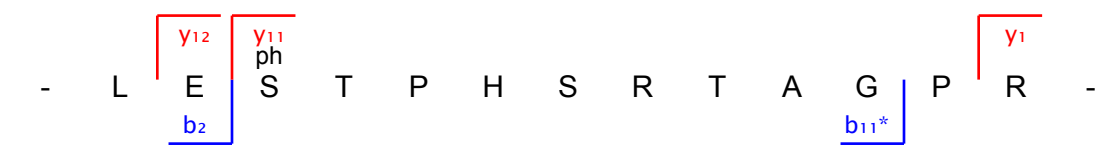
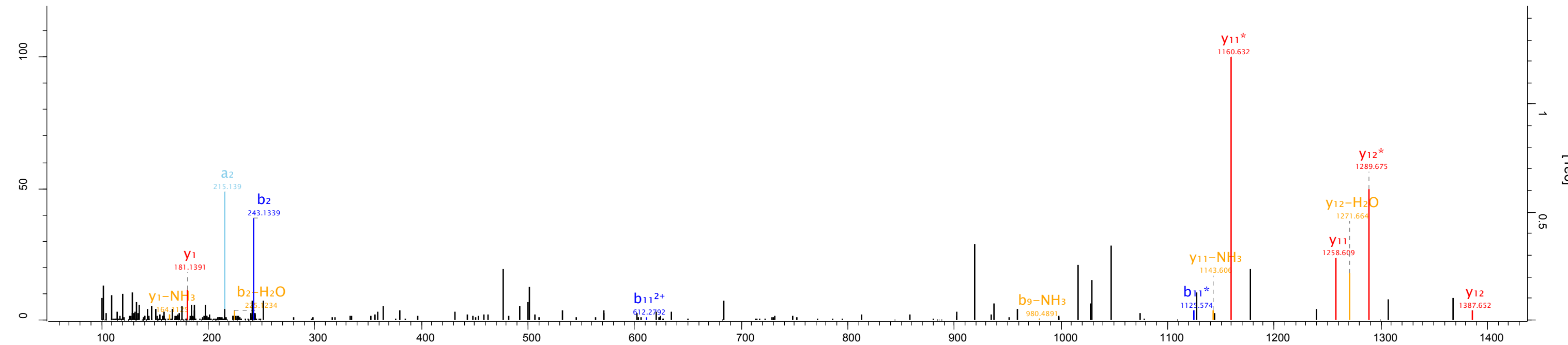
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b₅*
y₁₂²⁺
b₈
y₉
b₉
y₈
b₁₀
y₇
b₁₁
y₆
y₅
y₄
y₃
y₂

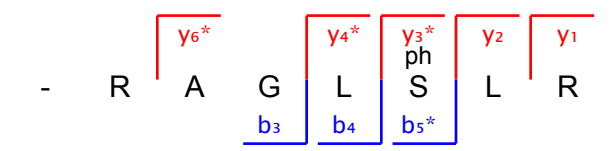
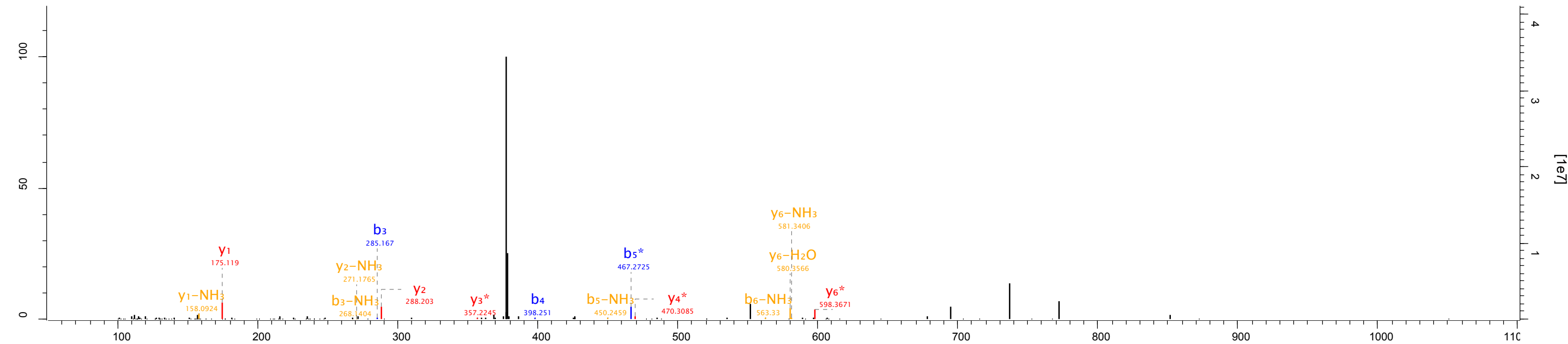
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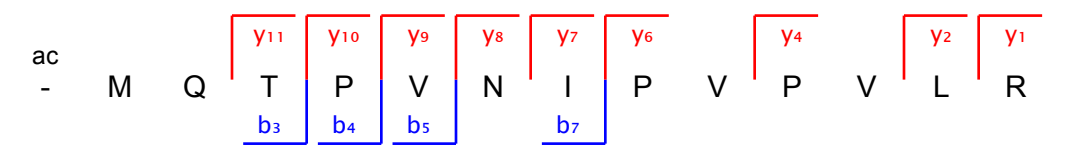
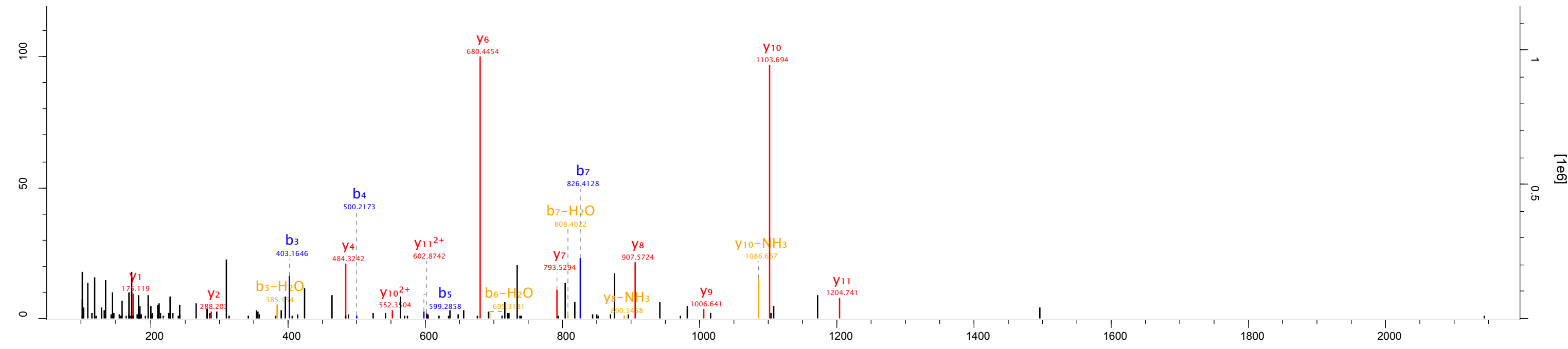
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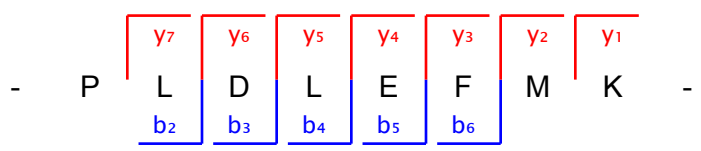
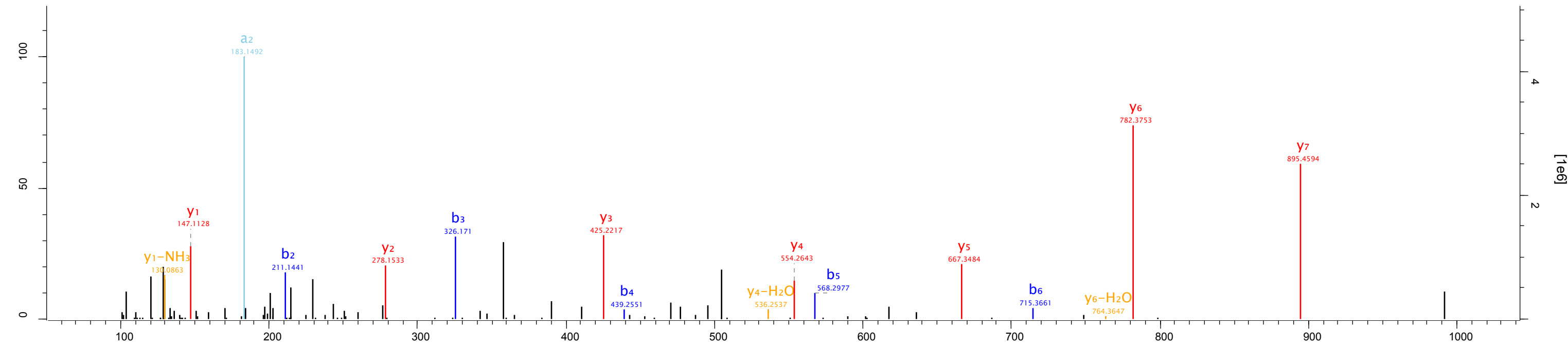
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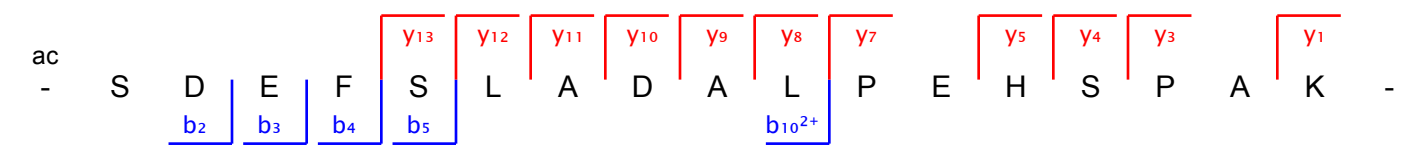
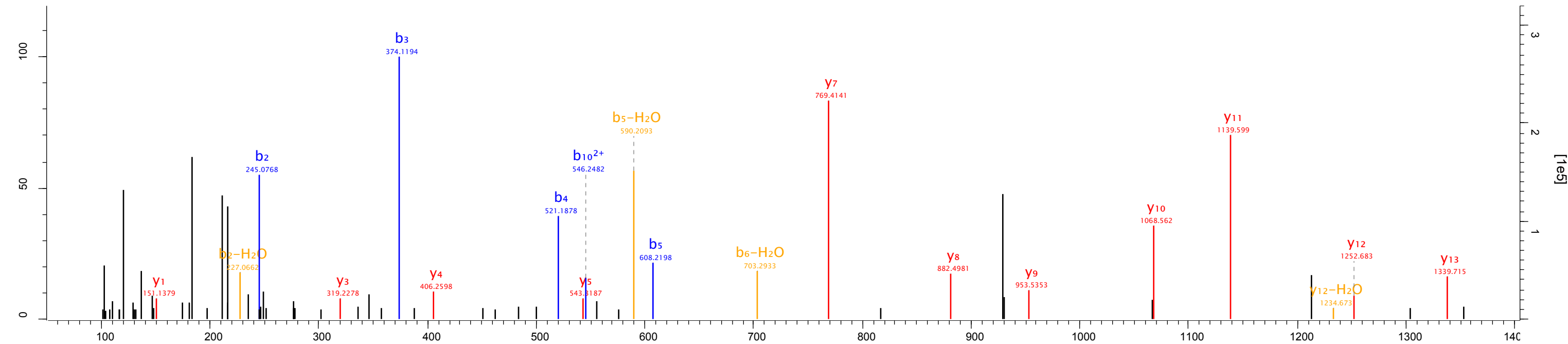
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 Method: FTMS; HCD
 Score: 74.99
 m/z: 753.43
 Gene names: GEMIN7



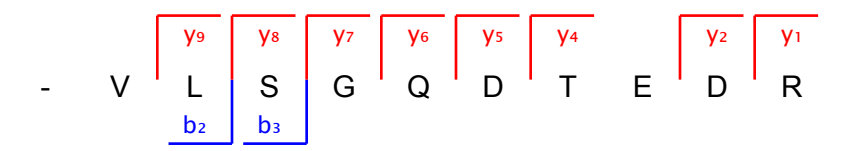
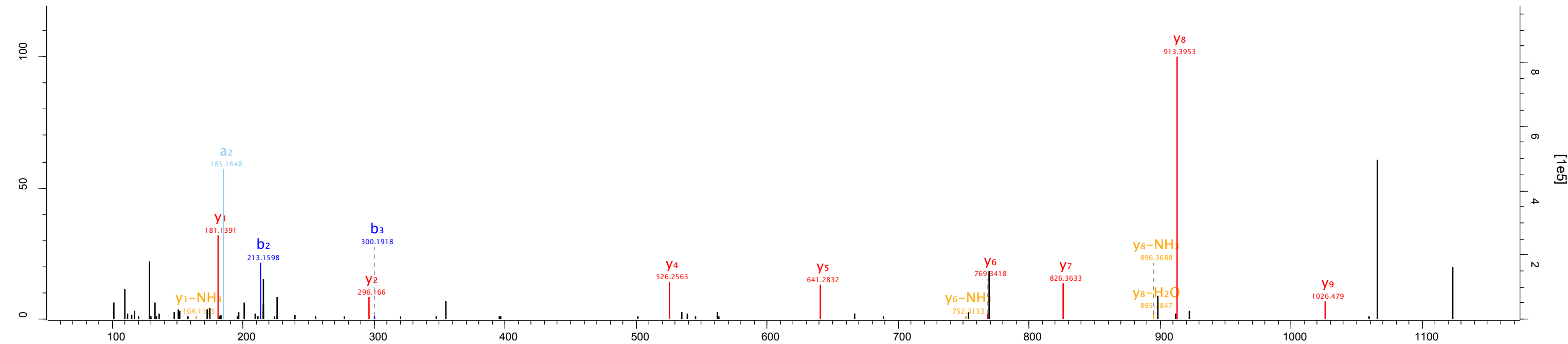
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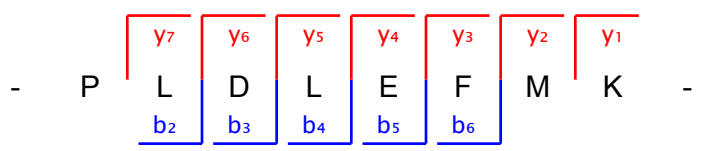
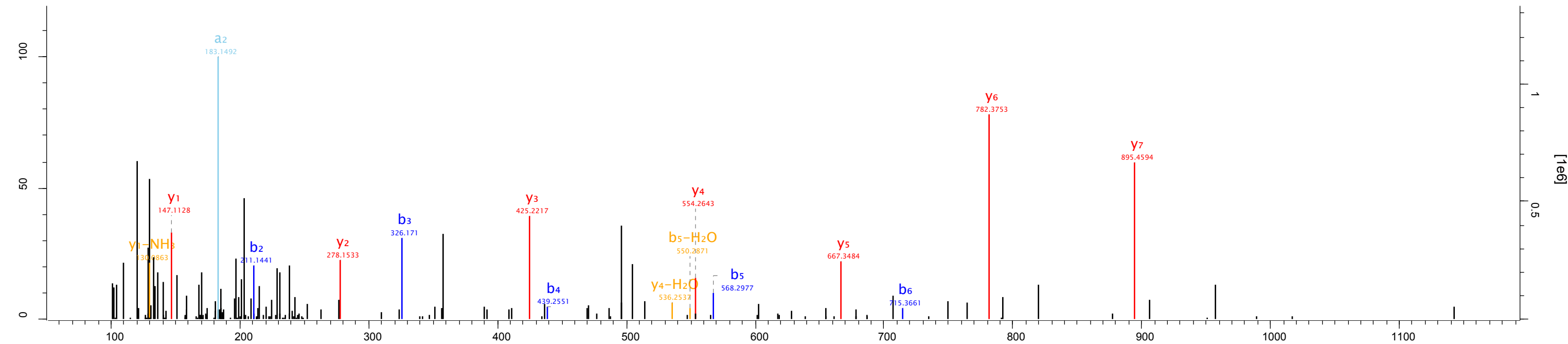
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 Scan: 79686 Method: FTMS; HCD Score: 79.84 m/z: 930.95 Gene names: MAPK1IP1L



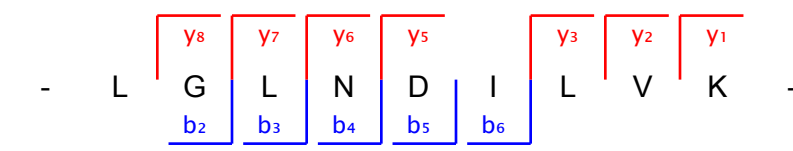
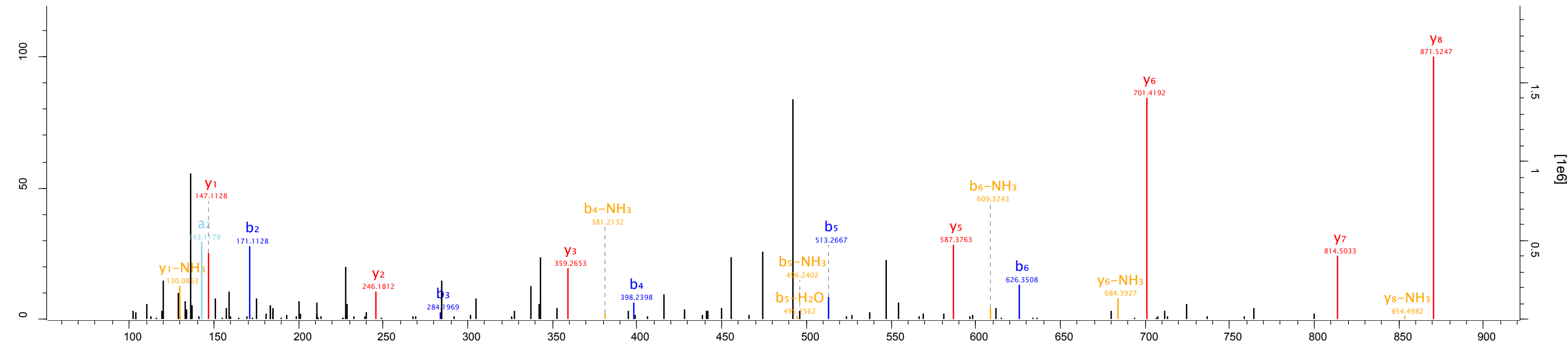
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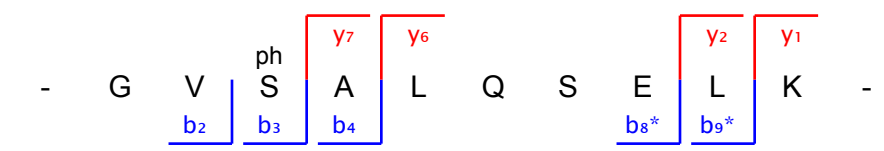
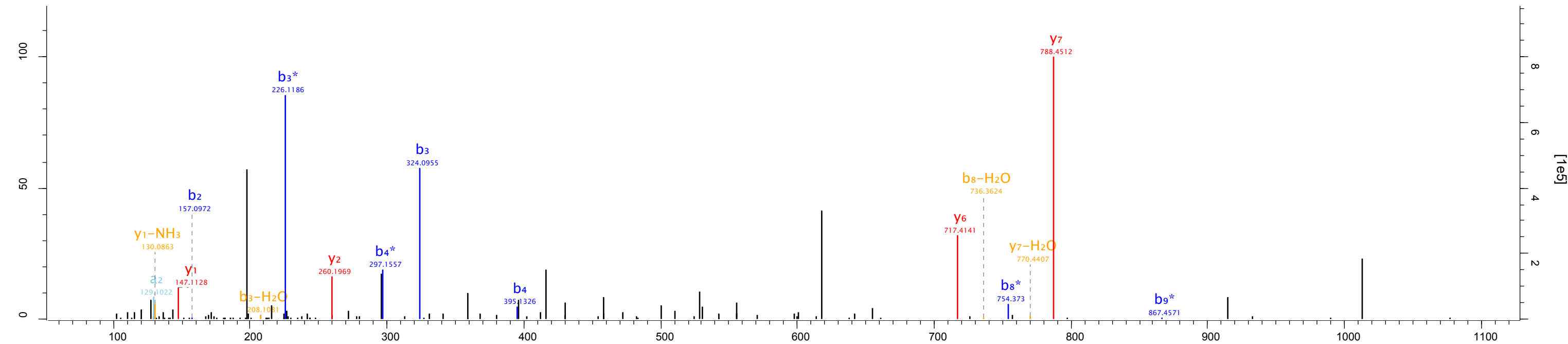


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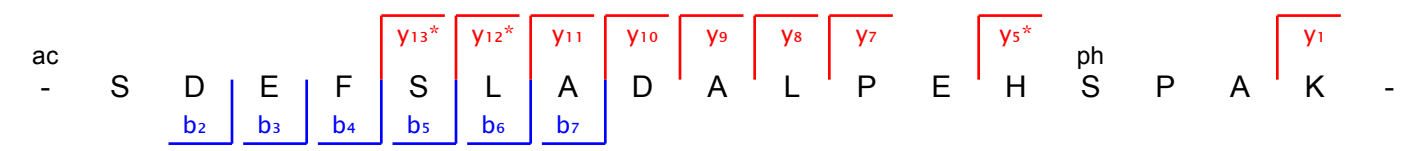
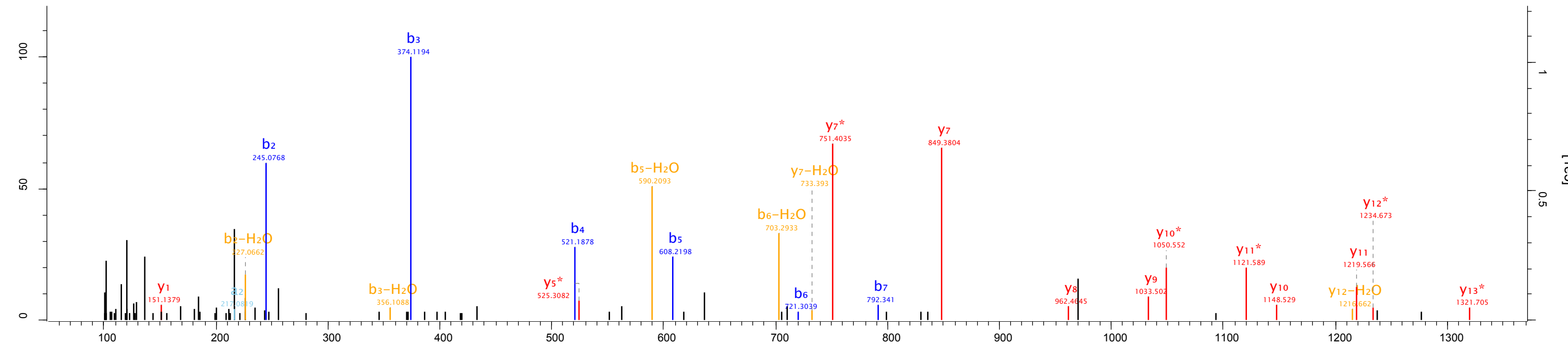


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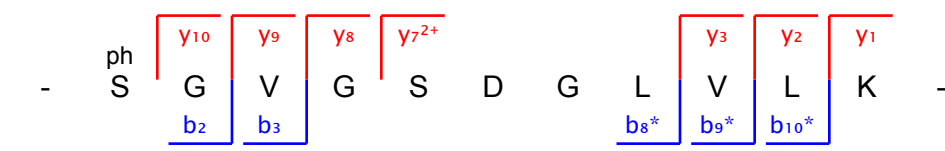
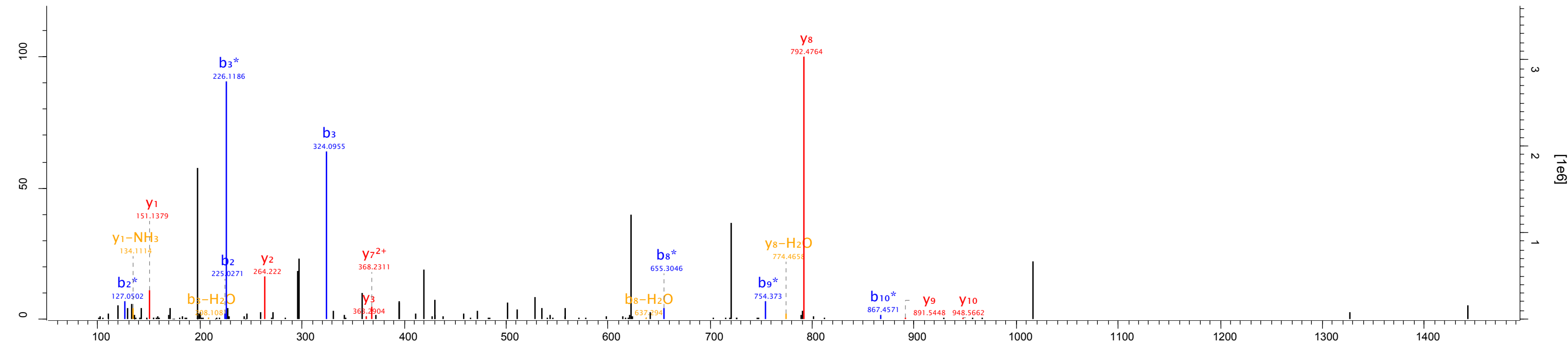




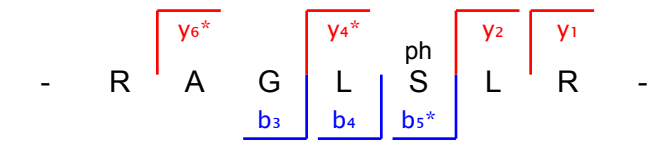
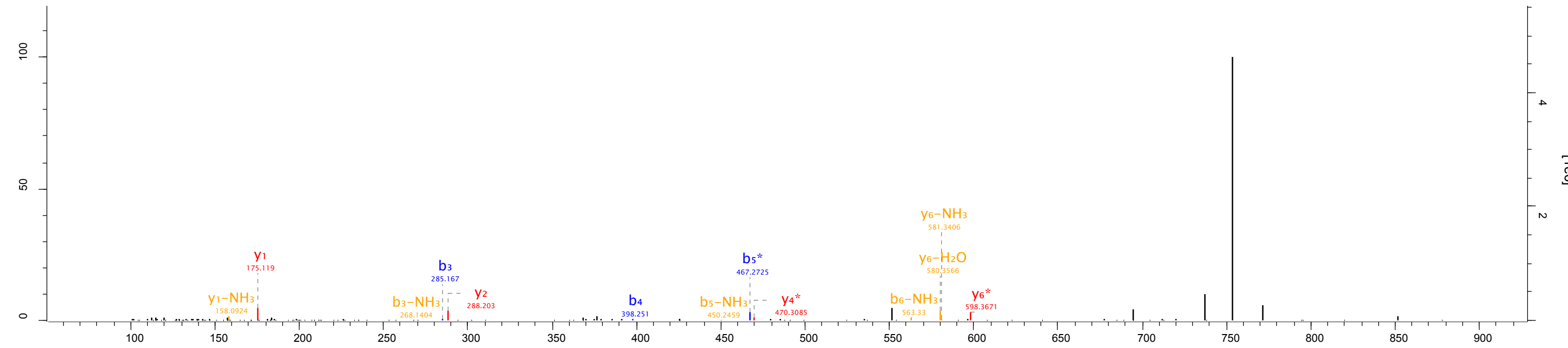
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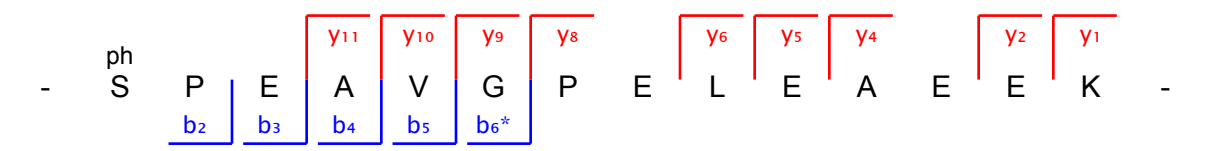
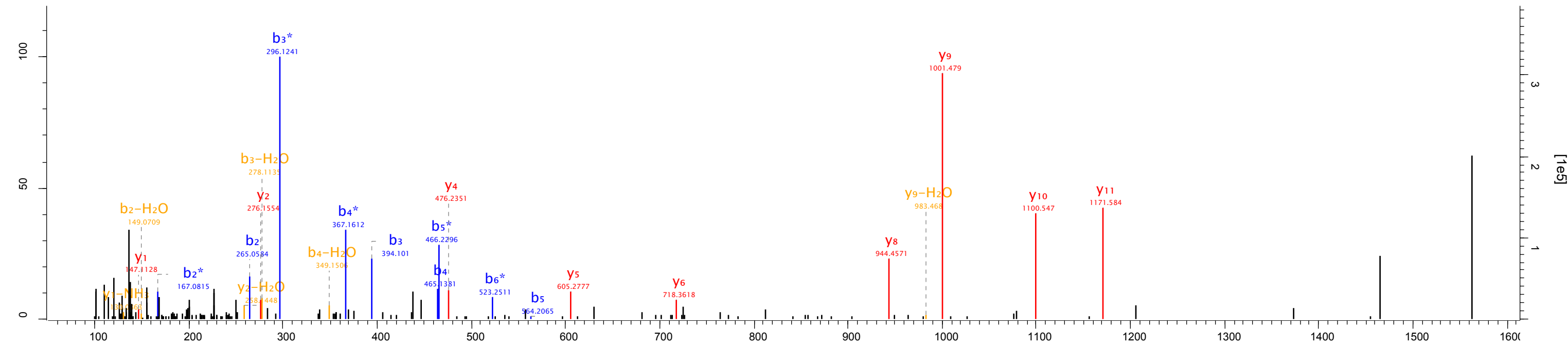
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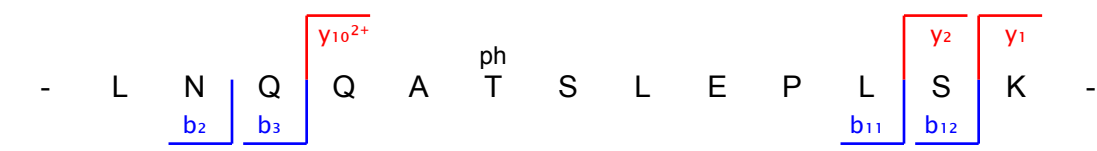
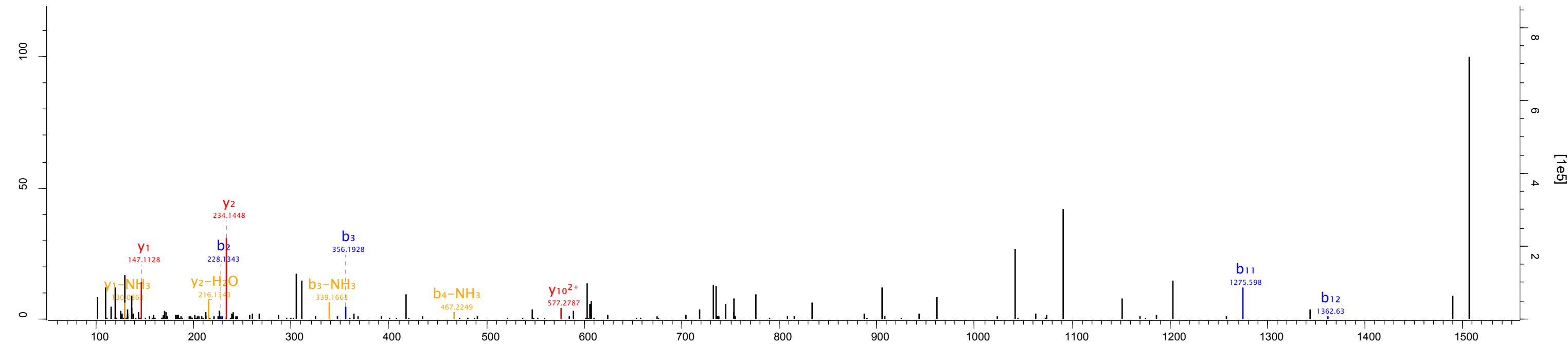
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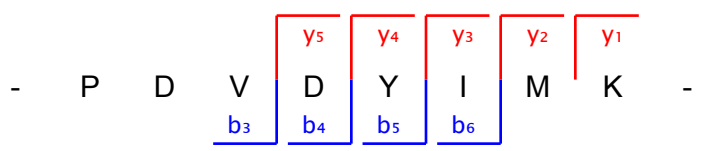
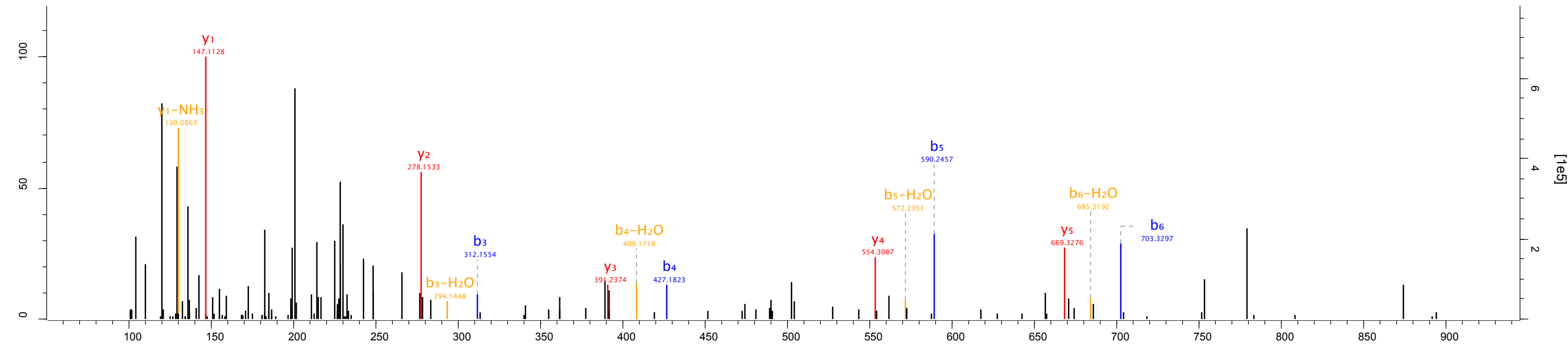
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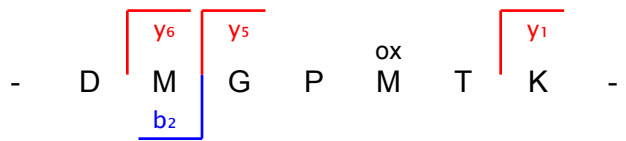
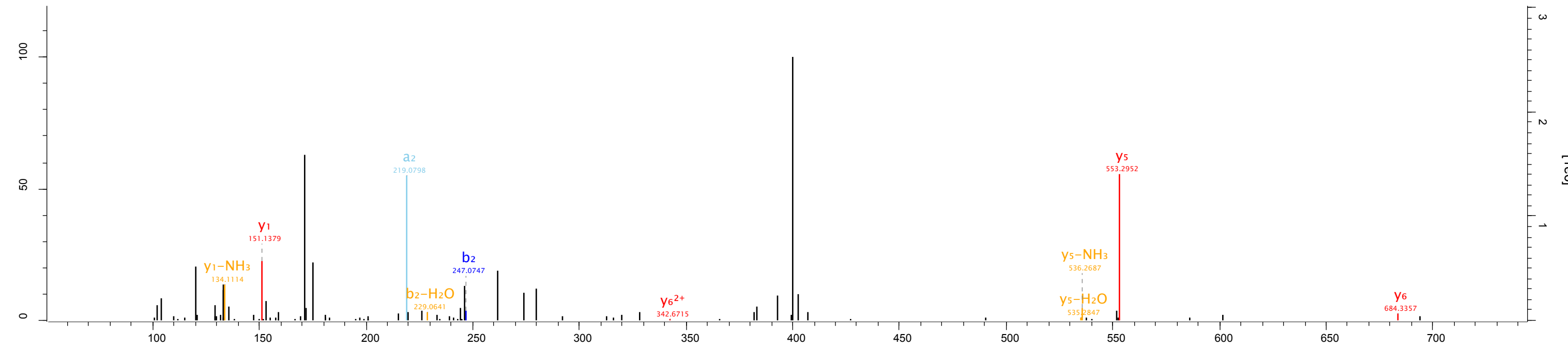


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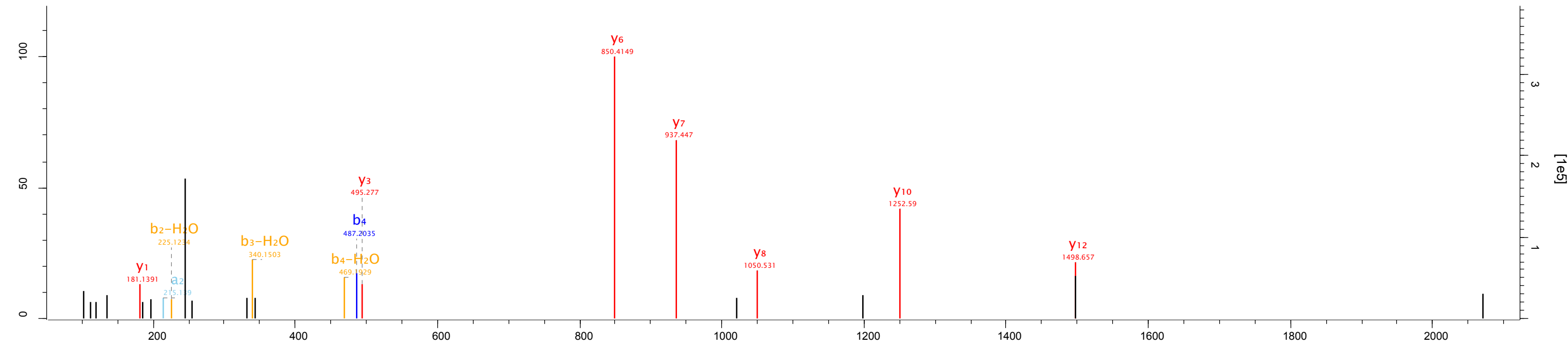
Raw file
20180707_MaS_A375SR_LM_proteome_02

Scan 9366 Method FTMS; HCD Score 45.88 m/z 400.18



Raw file
20180707_MaS_A375SR_LM_proteome_03

Scan 26386 Method FTMS; HCD Score 34.93 m/z 1042.46 Gene names RNF121

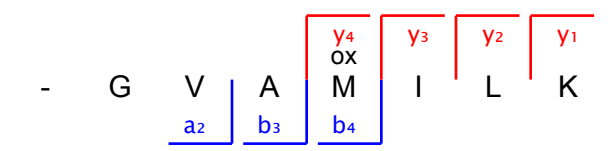
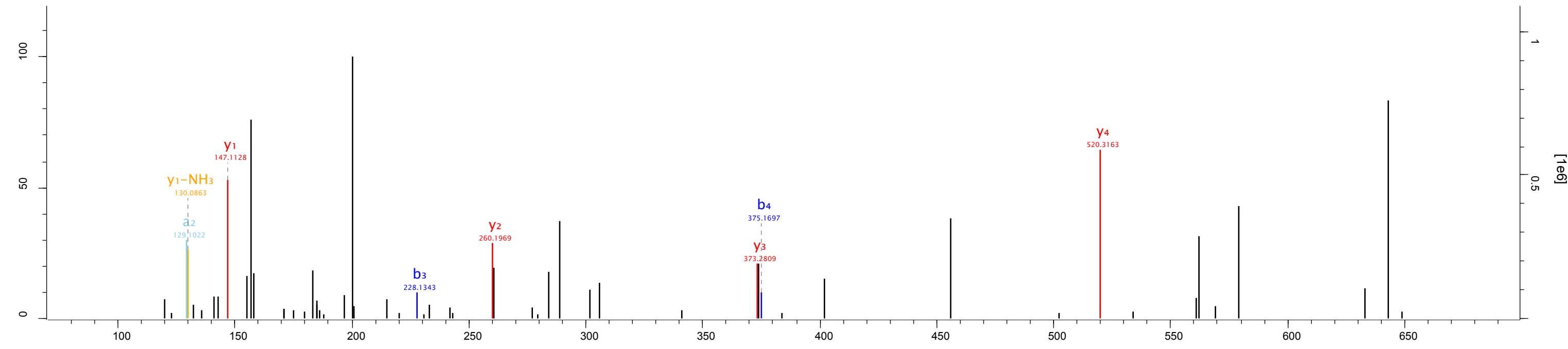


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a2 b4 y12 y10 y8 y7 y6 y3 y1

[1e5]

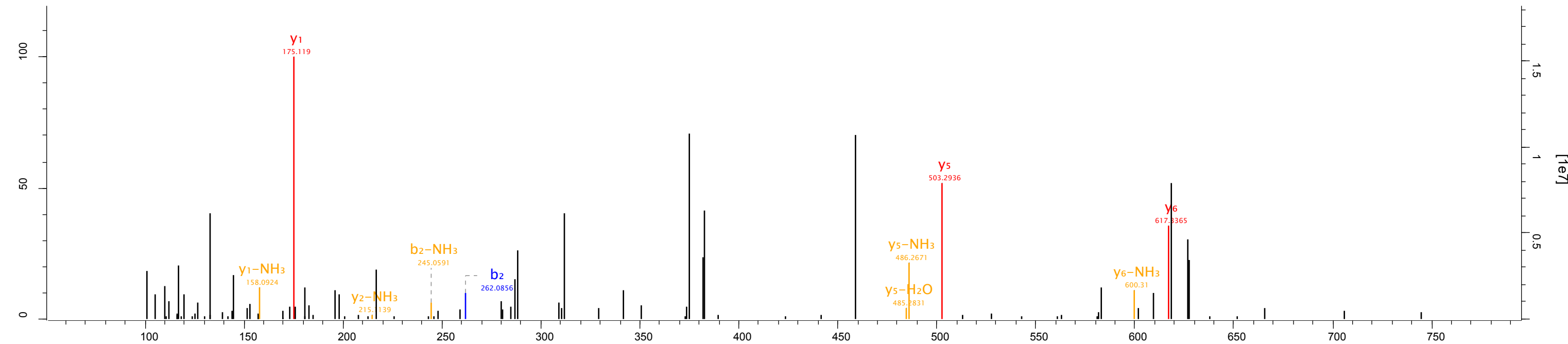
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20180707_MaS_A375SR_LM_proteome_04

Scan	Method	Score	m/z
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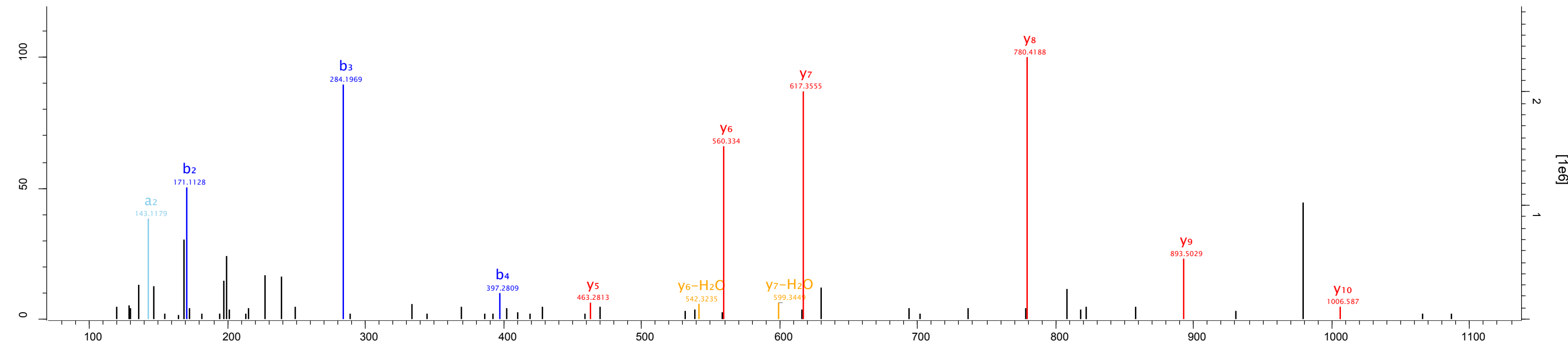
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20180707_MaS_A375SR_LM_proteome_05

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Raw file
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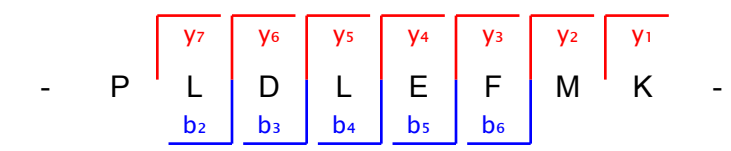
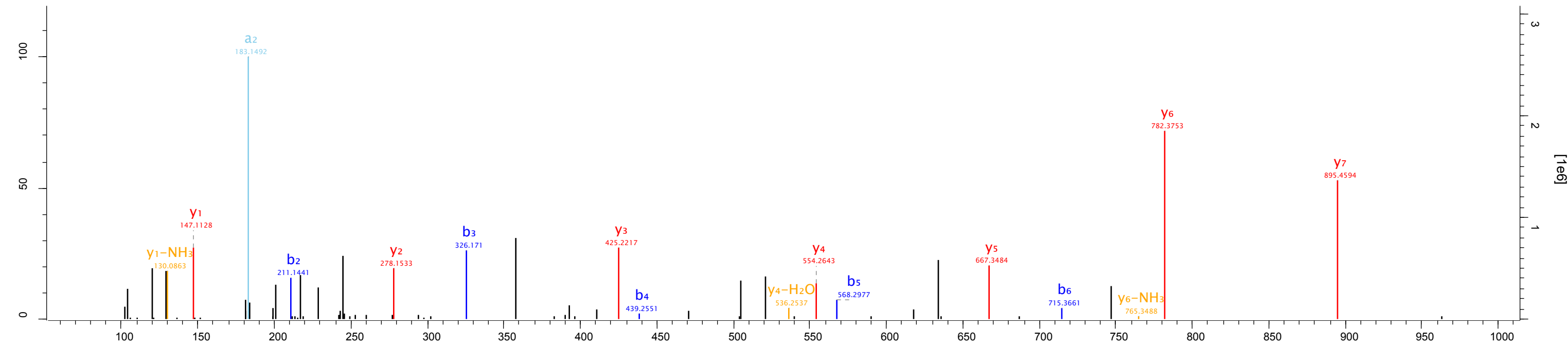
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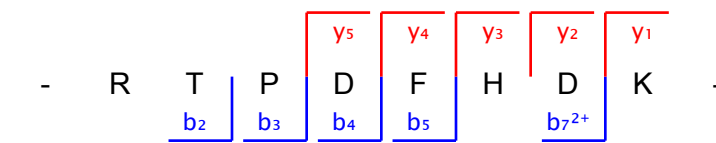
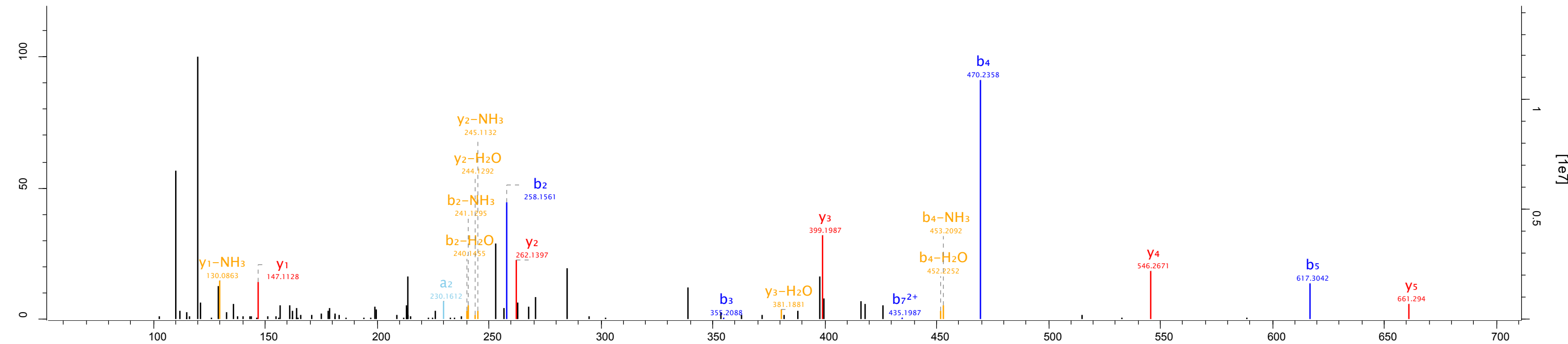


- G L L L Y G P P G T G K -
b2 b3 b4 y10 y9 y8 y7 y6 y5

Raw file
20180707_MaS_A375SR_LM_proteome_07

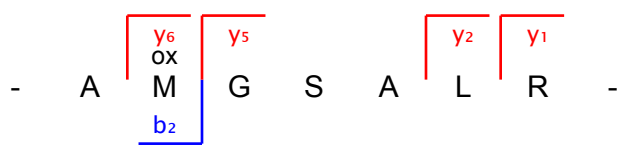
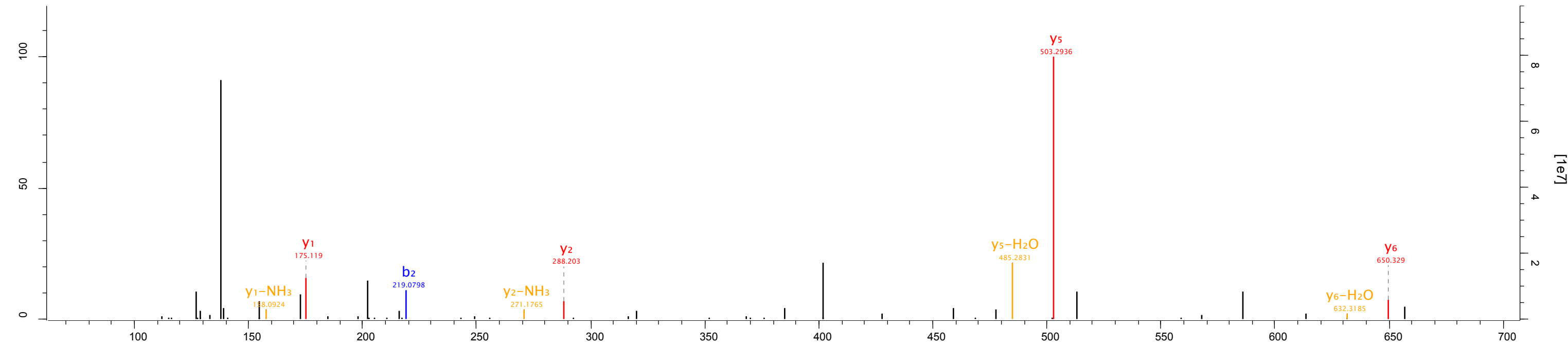
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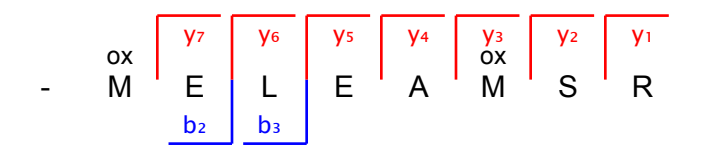
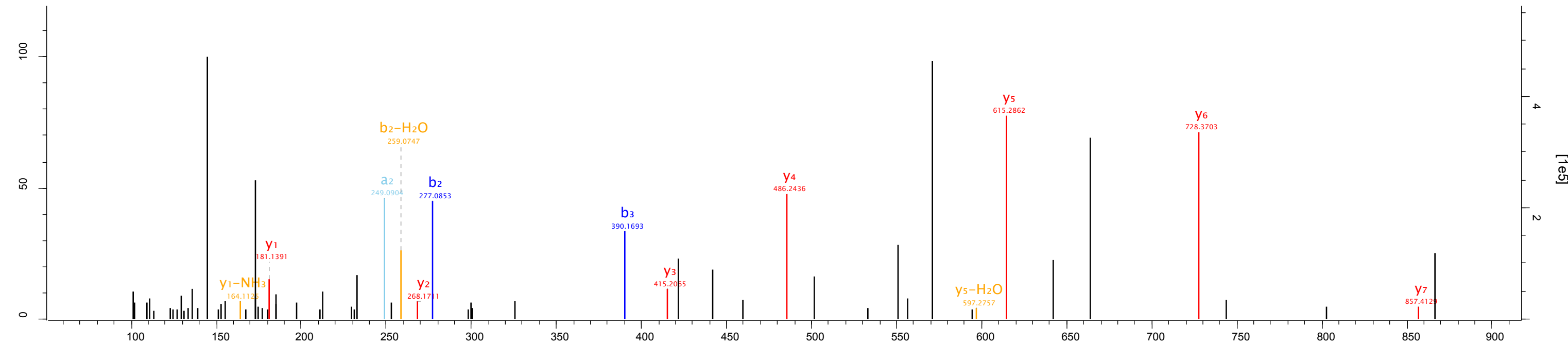
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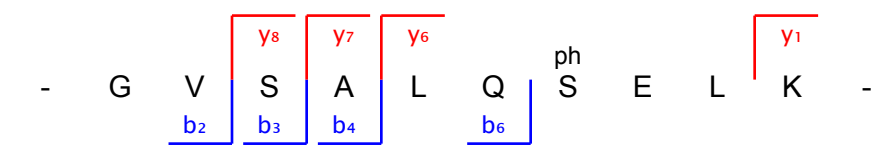
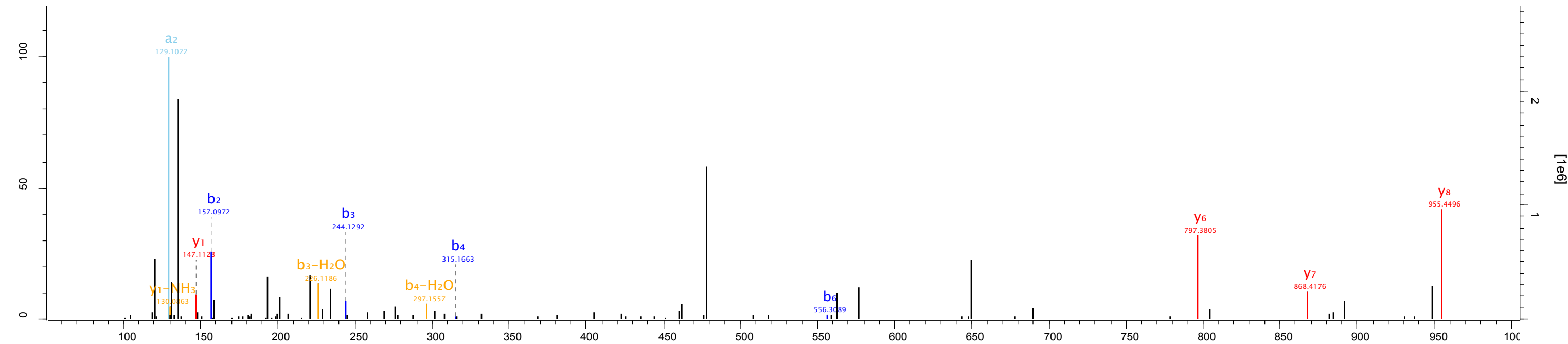
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Scan Method Score m/z Gene names
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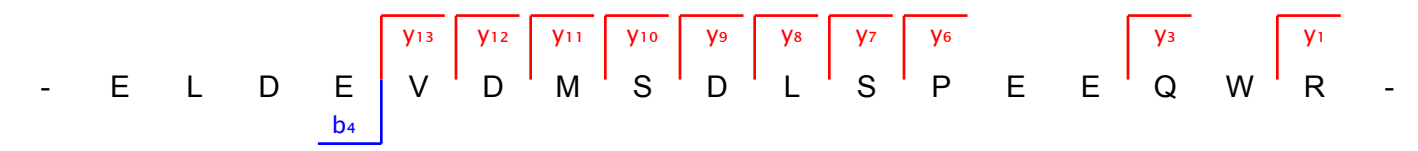
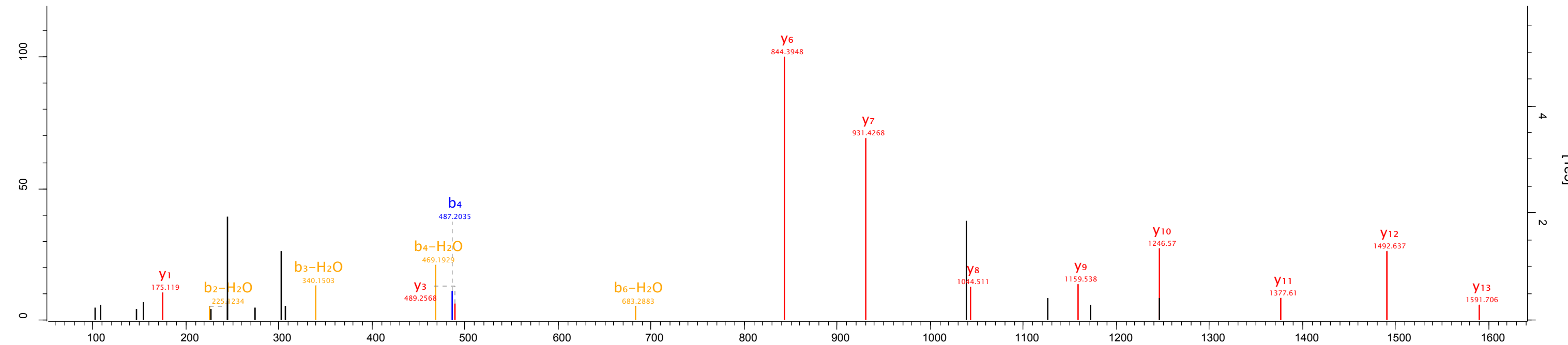


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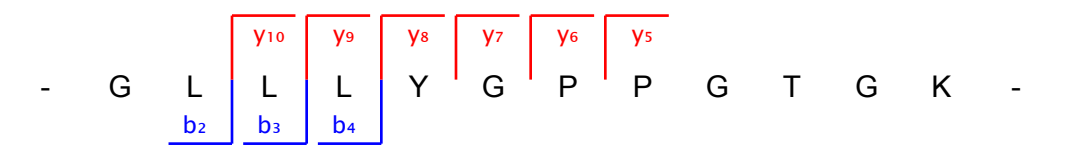
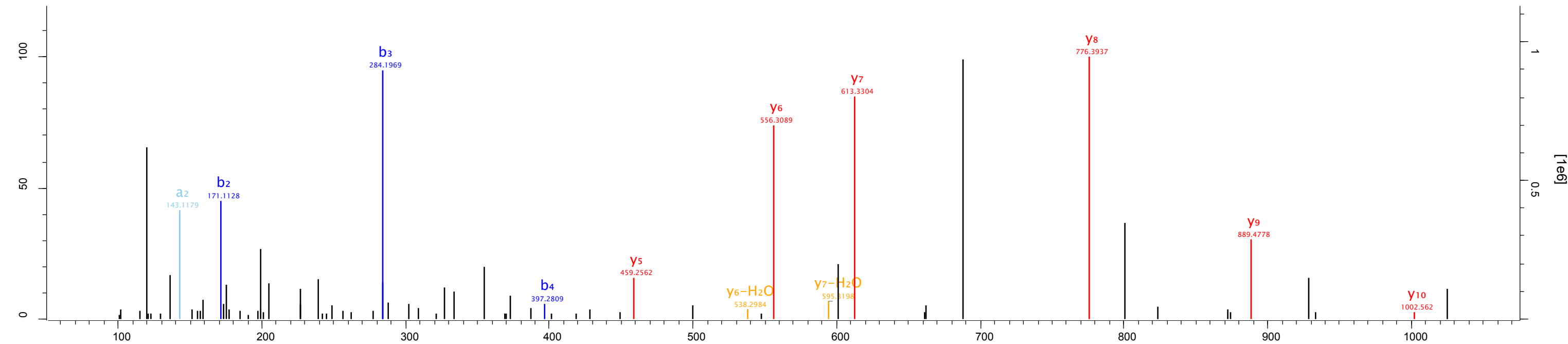
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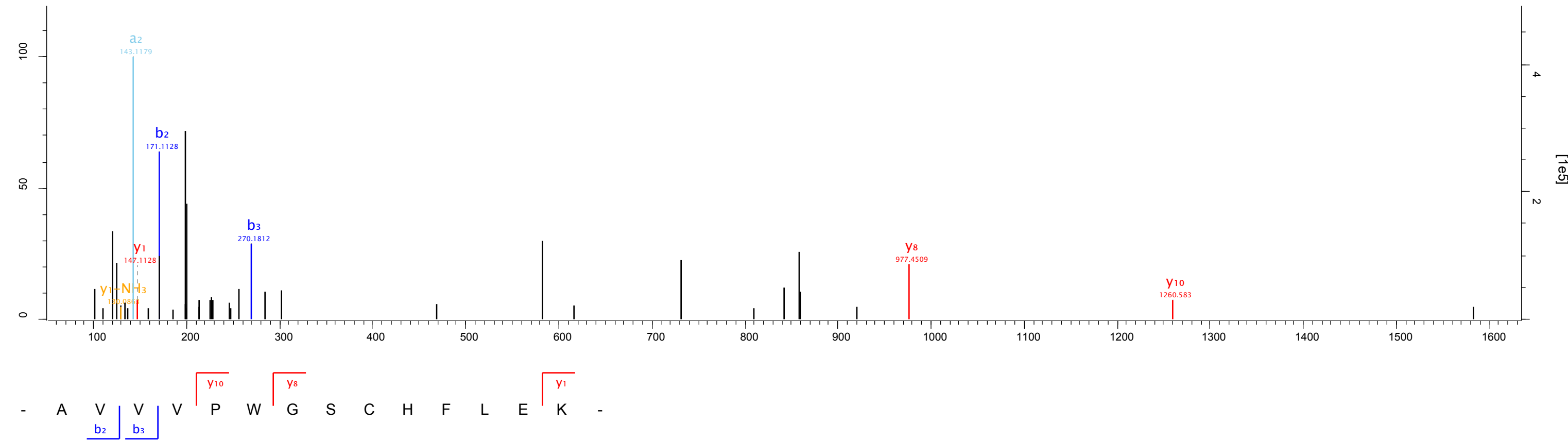


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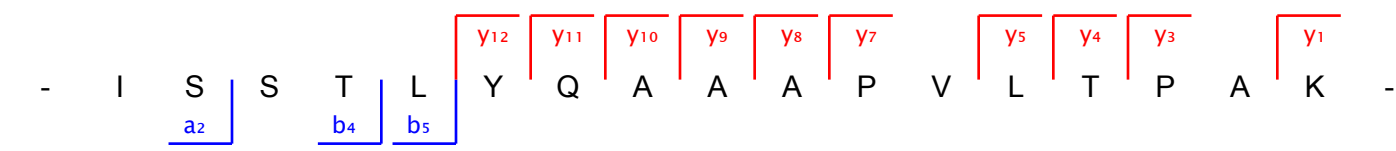
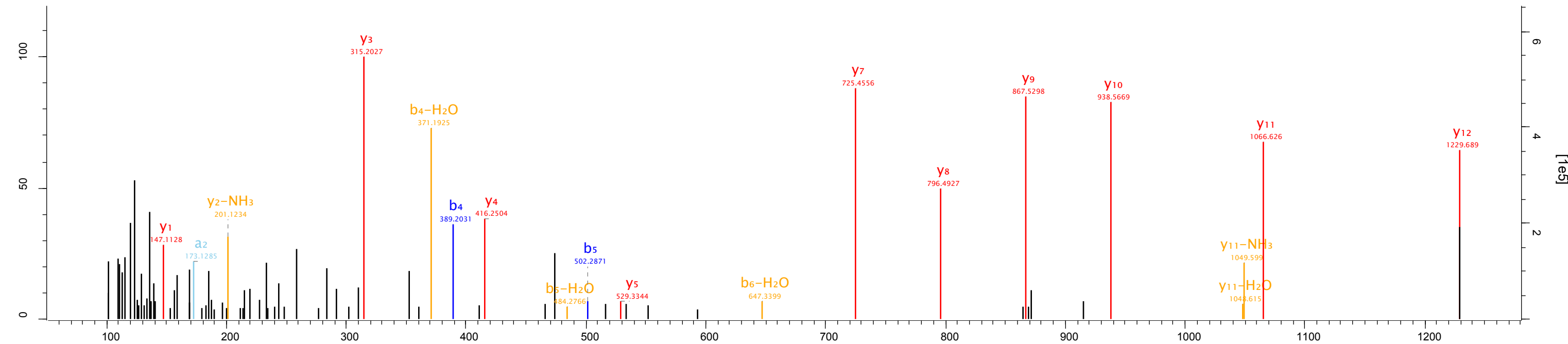


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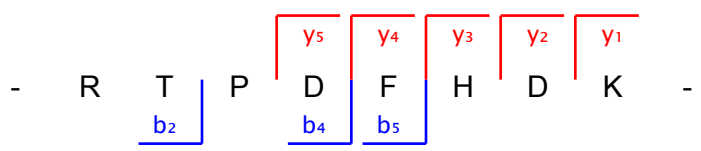
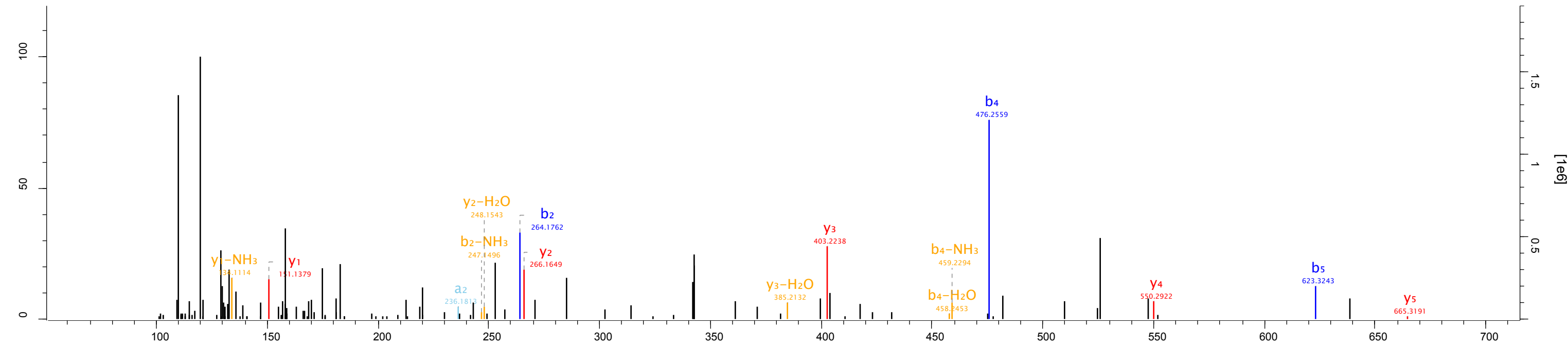




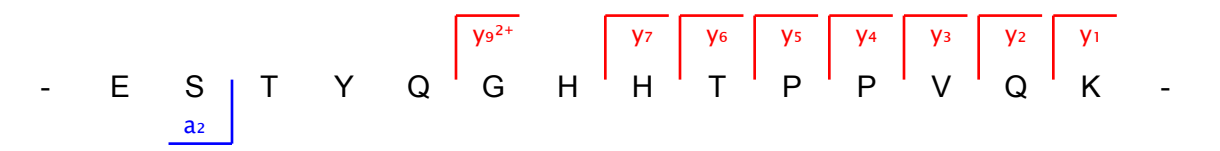
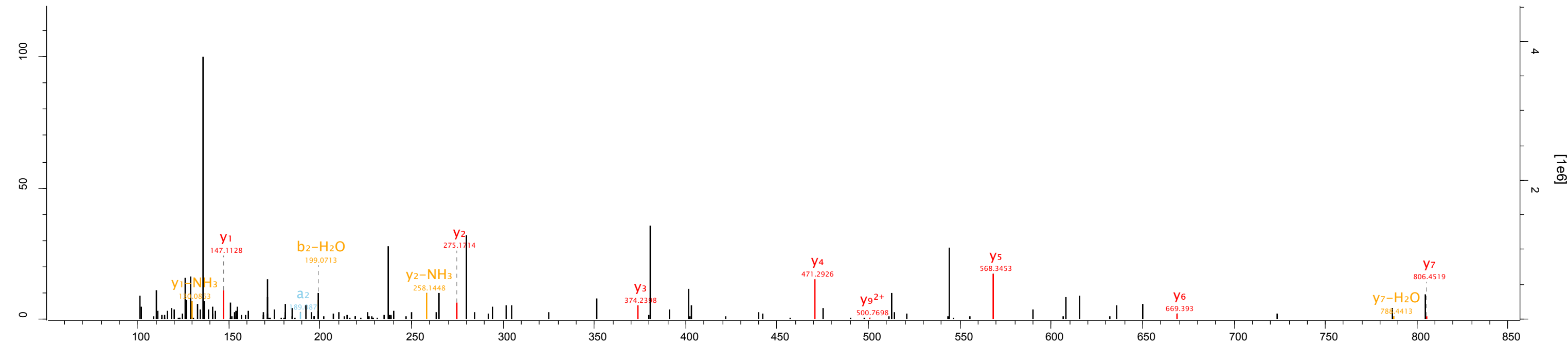
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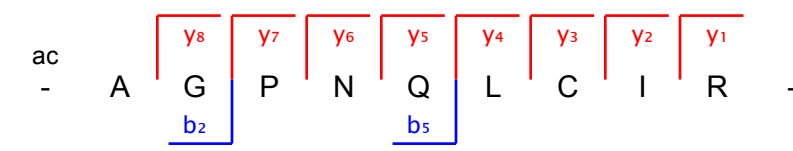
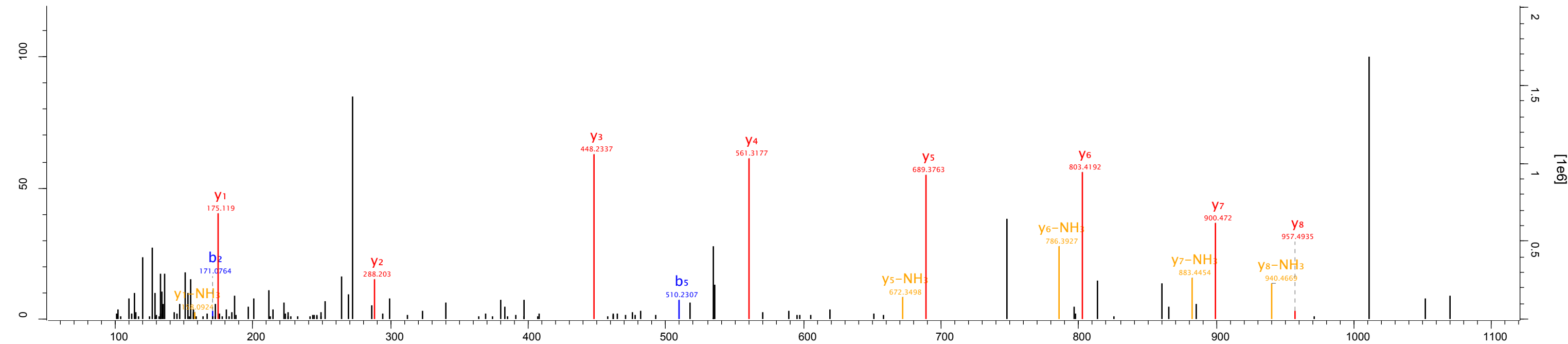
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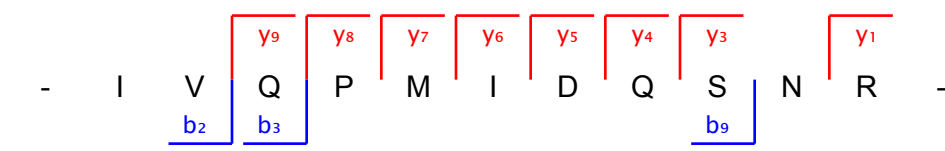
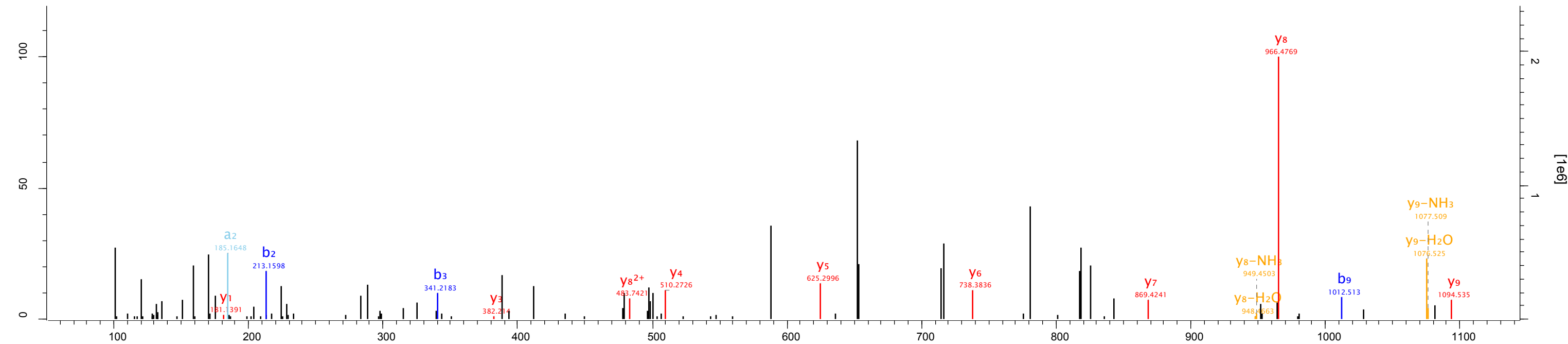
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 Scan: 3716 Method: FTMS; HCD Score: 25.12 m/z: 402.95 Gene names: MT-CO3



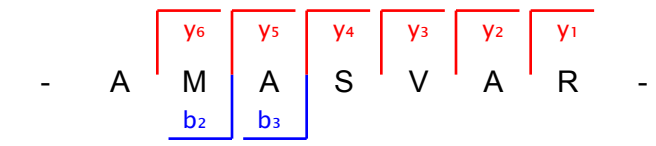
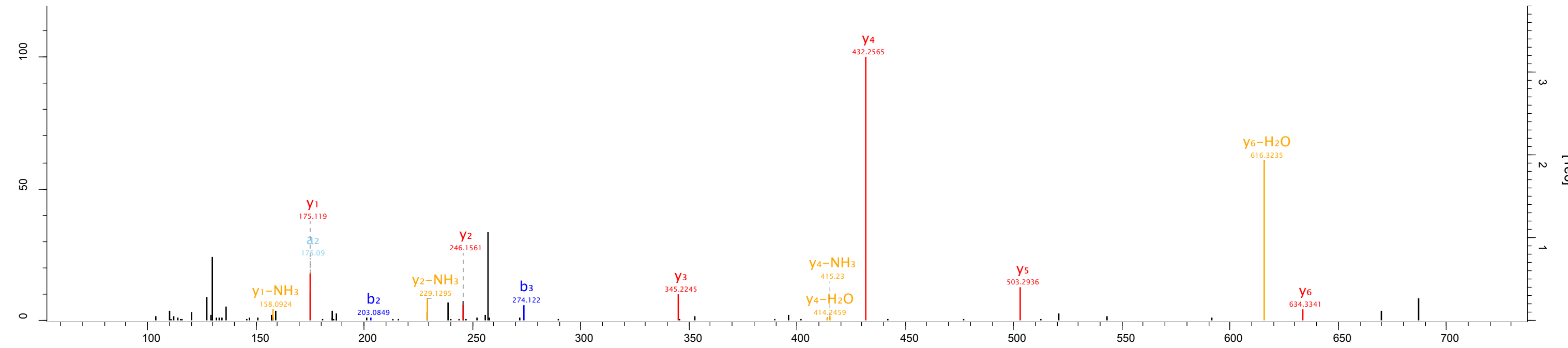
Raw file: 20180707_MaS_A375SR_ML_proteome_01
 Scan: 16706 Method: FTMS; HCD Score: 101.54 m/z: 535.77 Gene names: SAMD8



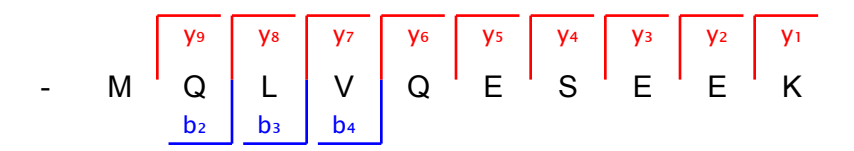
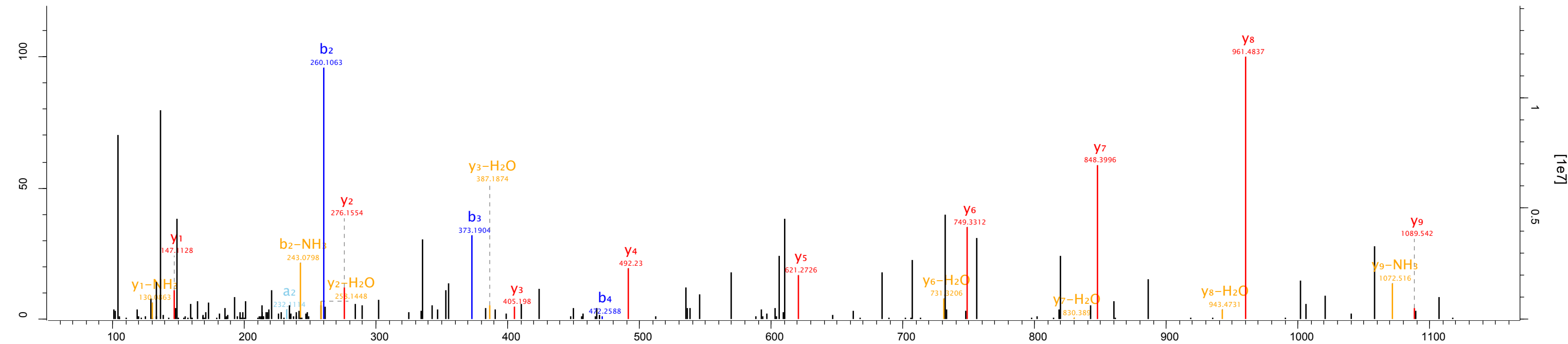
Raw file: 20180707_MaS_A375SR_ML_proteome_02
 Scan: 10916 Method: FTMS; HCD Score: 72.34 m/z: 653.85 Gene names: MEIS2;MEIS3;MEIS1;MEIS3P1



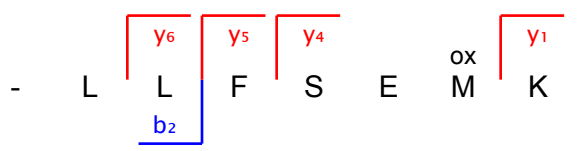
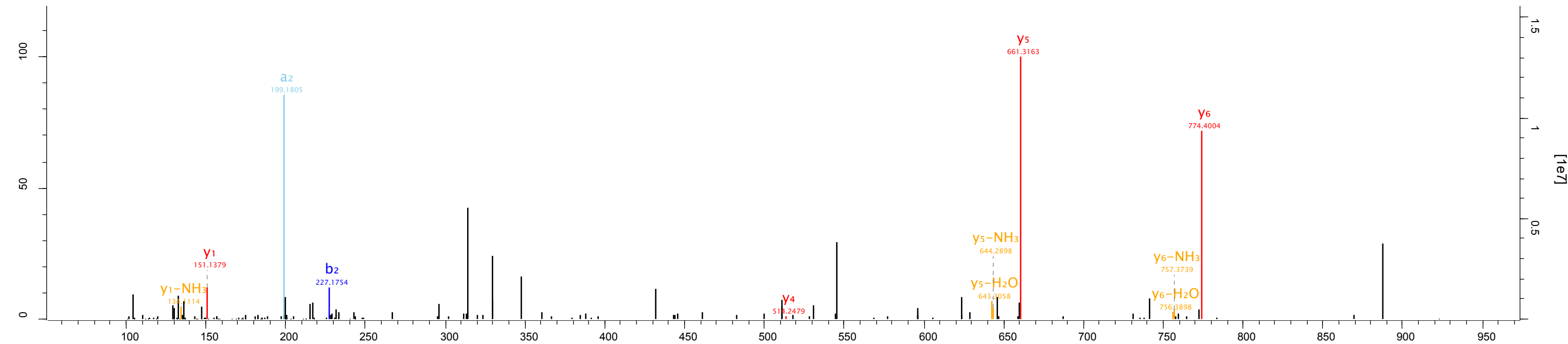
Raw file: 20180707_MaS_A375SR_ML_proteome_02
 Scan: 5556 Method: FTMS; HCD Score: 92.47 m/z: 353.19 Gene names: ART4



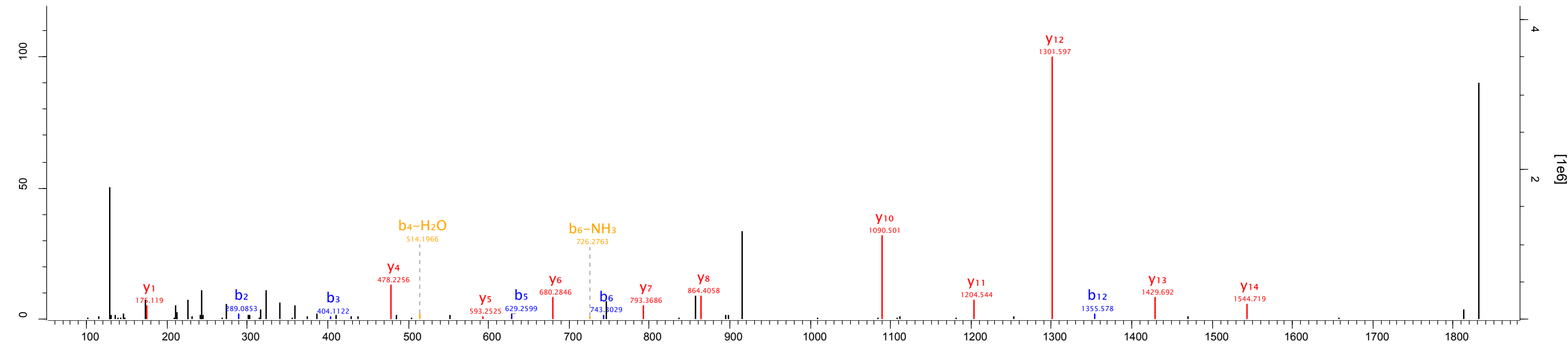
Raw file: 20180707_MaS_A375SR_ML_proteome_04
 Scan: 10556 Method: FTMS; HCD Score: 74.96 m/z: 610.79



Raw file: 20180707_MaS_A375SR_ML_proteome_04
 Scan: 12236 Method: FTMS; HCD Score: 60.79 m/z: 444.24 Gene names: C1orf234



Raw file: 20180707_MaS_A375SR_ML_proteome_04
 Scan: 14926 Method: FTMS; HCD Score: 62.94 m/z: 916.9 Gene names: ADPRM

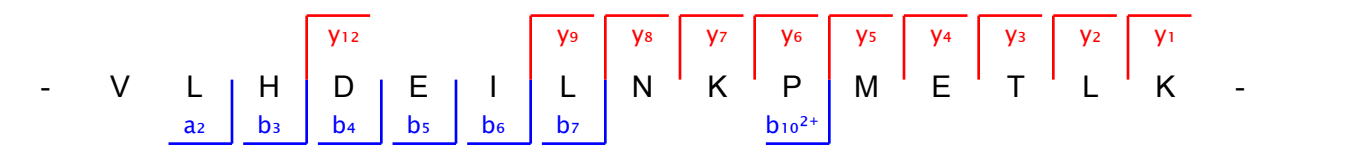
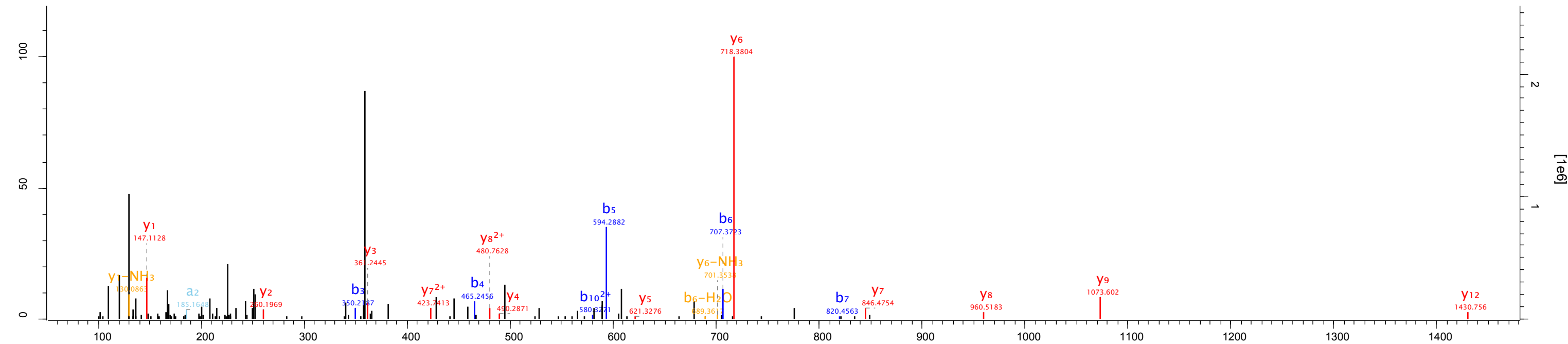


ac - M D D K P N P E A L S D S S E R -

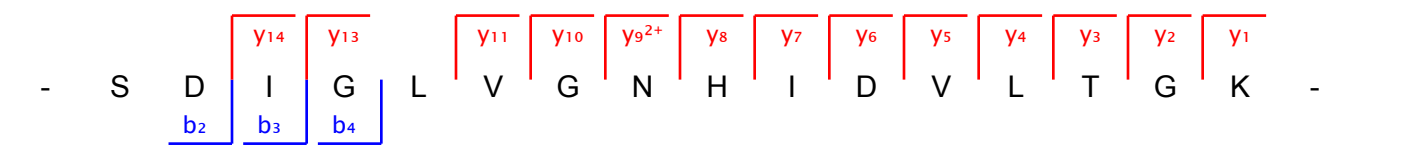
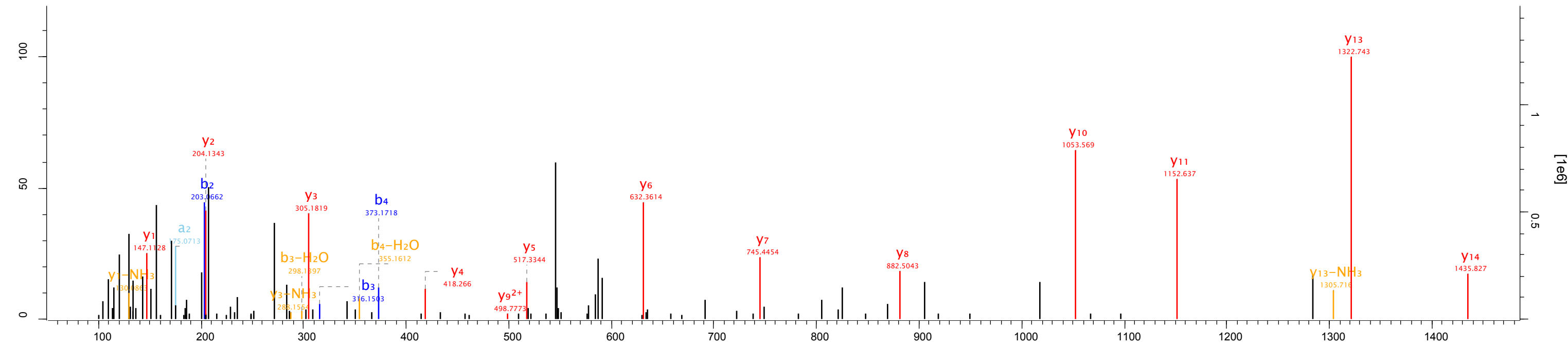
Fragmentation mapping (b and y ions):

- b2: M-D
- b3: D-D
- b5: P-P
- b6: N-P
- b12: D-S
- y1: E-R
- y4: S-S
- y5: D-S
- y6: S-S
- y7: L-S
- y8: A-S
- y10: P-E
- y11: N-E
- y12: P-E
- y13: D-E
- y14: D-E

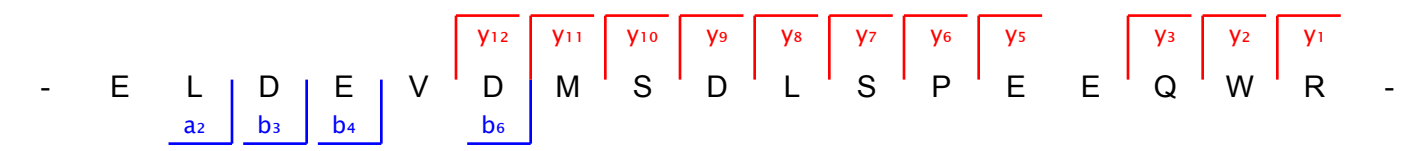
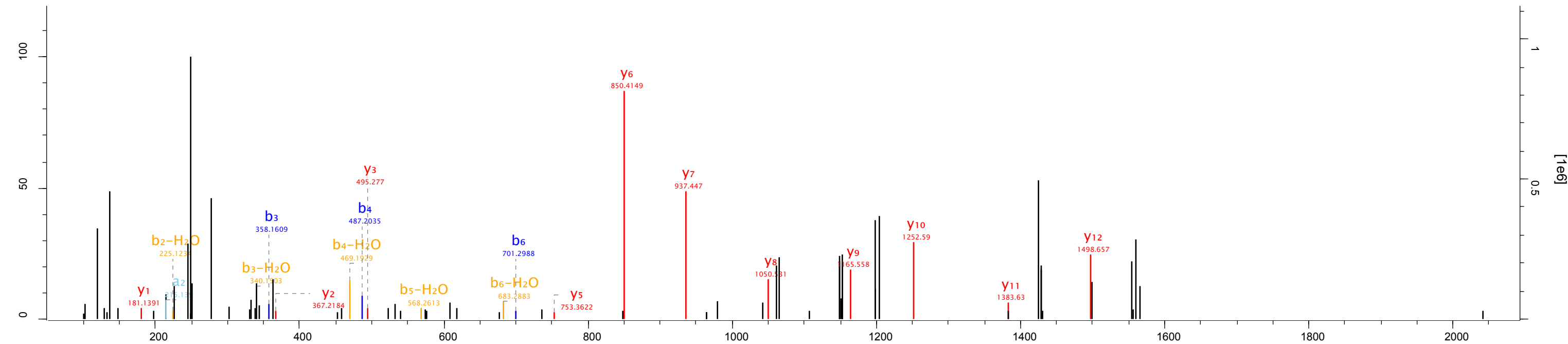
Raw file: 20180707_MaS_A375SR_ML_proteome_06
 Scan: 17326 Method: FTMS; HCD Score: 63.95 m/z: 445.75 Gene names: SLC35A3

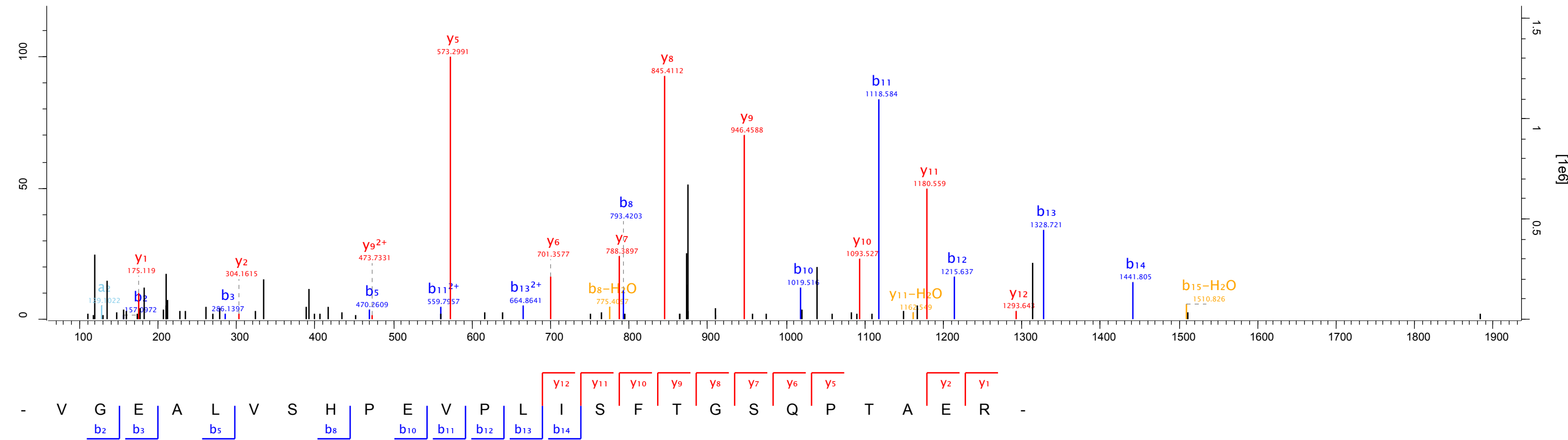


Raw file: 20180707_MaS_A375SR_ML_proteome_06
 Scan: 22916 Method: FTMS; HCD Score: 84.41 m/z: 546.97 Gene names: EDEM2



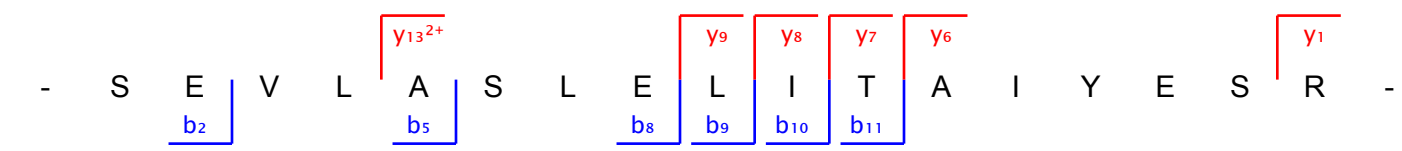
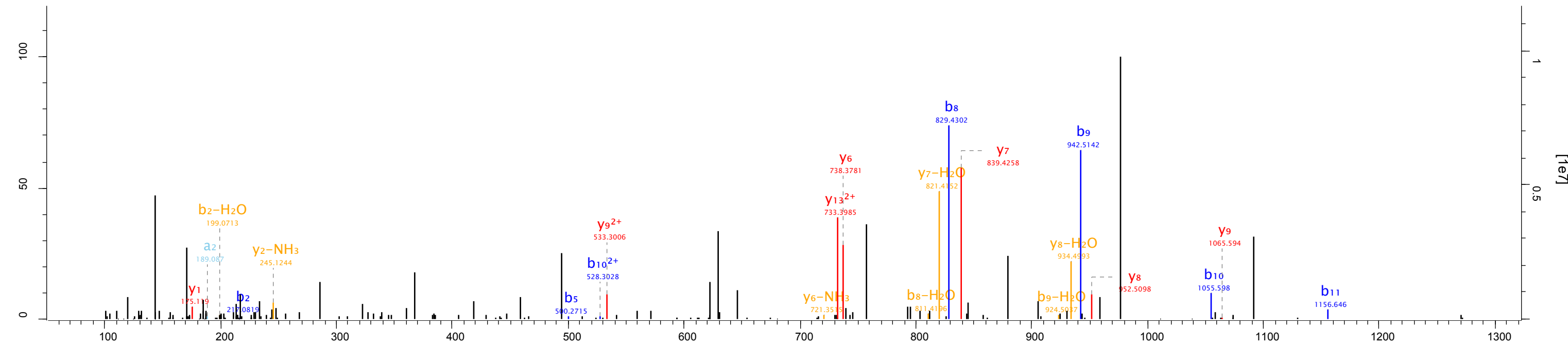
Raw file: 20180707_MaS_A375SR_ML_proteome_06
 Scan: 26436 Method: FTMS; HCD Score: 43.95 m/z: 1042.46 Gene names: RNF121





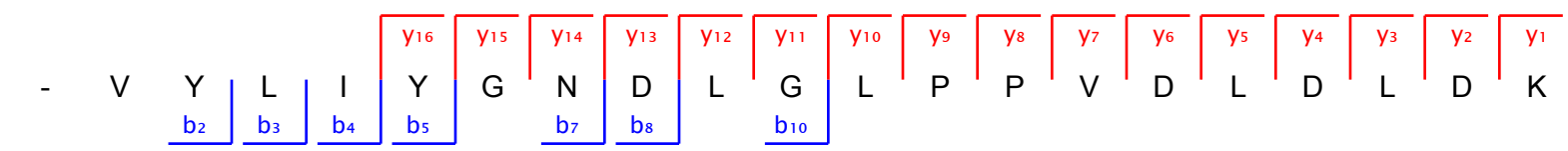
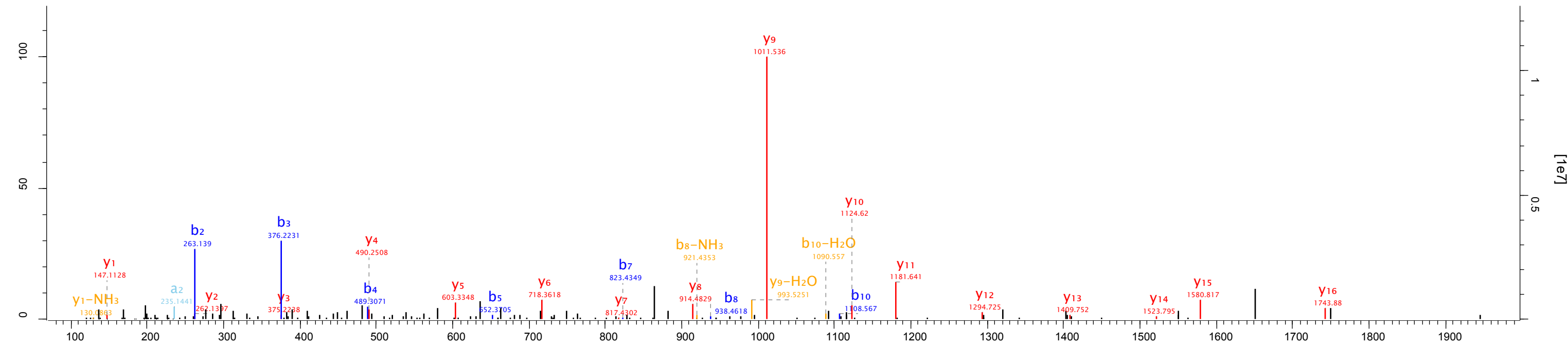
Raw file
20180707_MaS_A375SR_ML_proteome_08

Scan 28406 Method FTMS; HCD Score 40.49 m/z 632.01



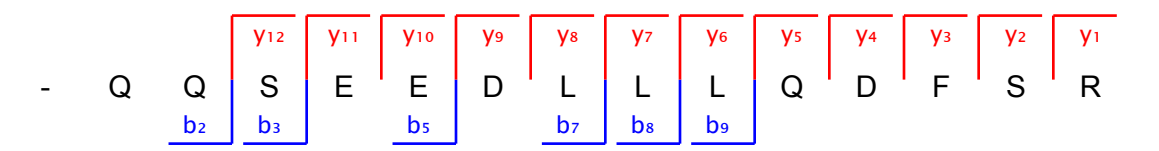
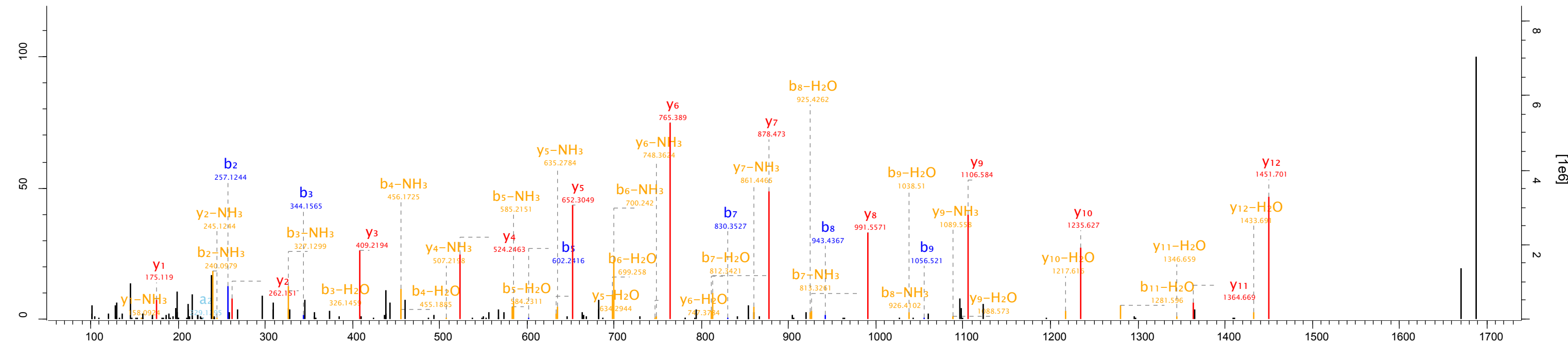
Raw file
20180707_MaS_A375SR_ML_proteome_08

Scan 29056 Method FTMS; HCD Score 75.06 m/z 1117.1 Gene names GPLD1



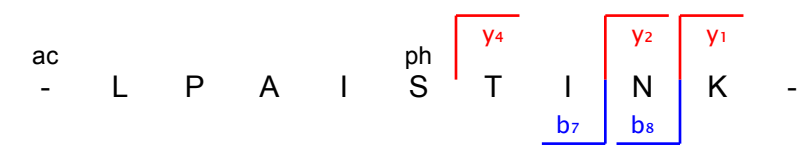
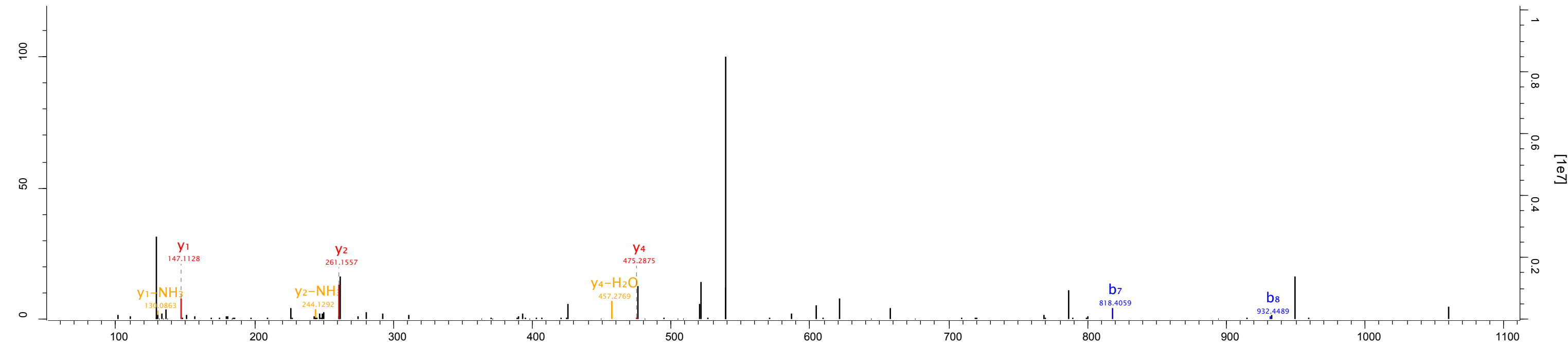
Raw file
20180707_MaS_A375SR_ML_proteome_09

Scan Method Score m/z Gene names
26576 FTMS; HCD 164.57 854.41 SSR3

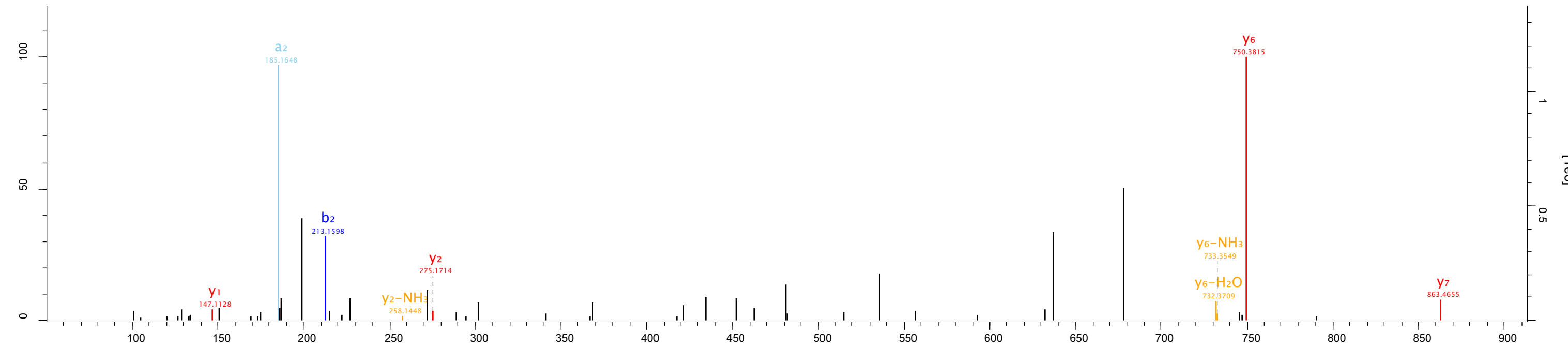


Raw file
20180707_MaS_A375SR_ML_proteome_09

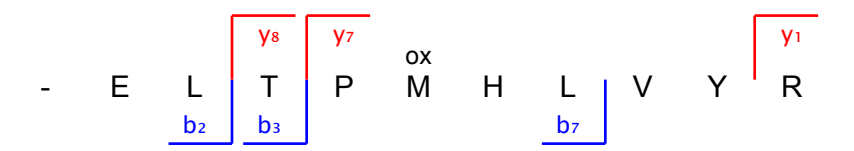
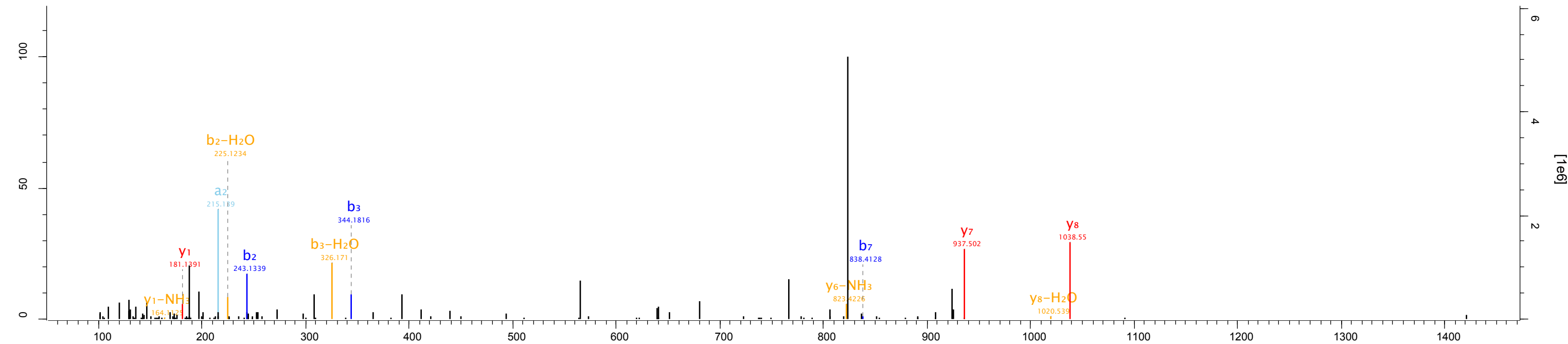
Scan 2856 Method FTMS; HCD Score 51.07 m/z 539.78



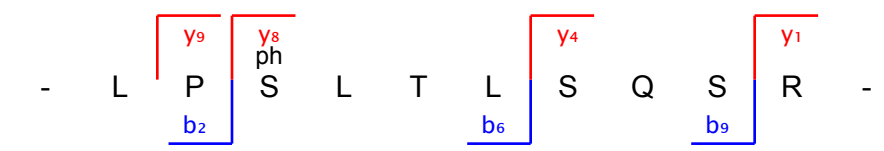
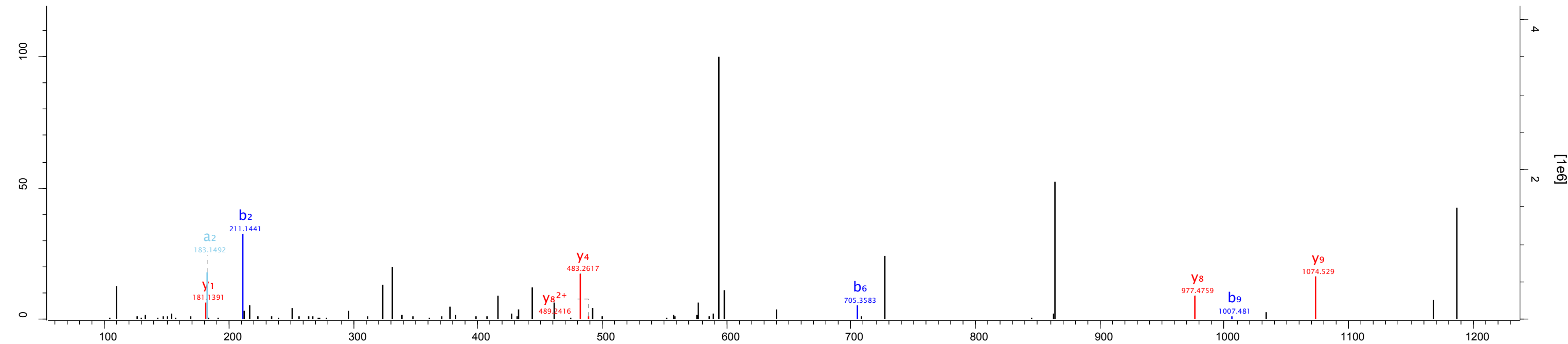
Raw file: 20180707_MaS_A375SR_ML_proteome_09
 Scan: 7976 Method: FTMS; HCD Score: 45.08 m/z: 481.77 Gene names: CAPN6

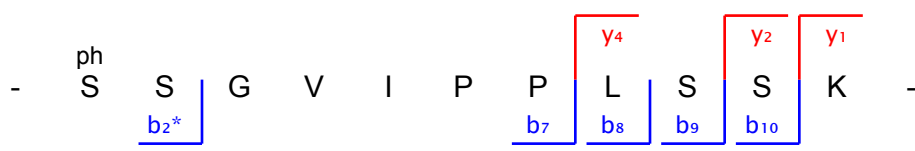
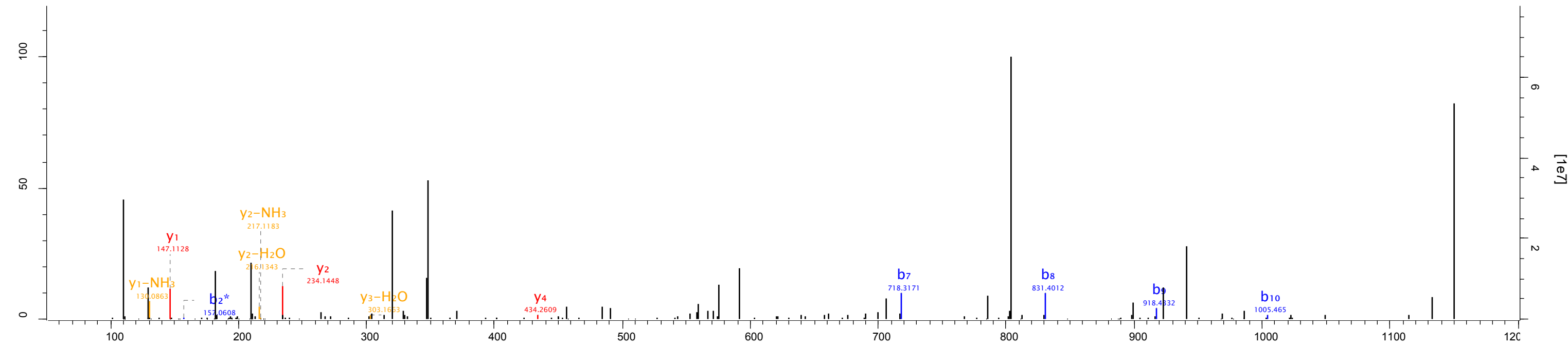


Raw file 20180707_MaS_A375SR_ML_proteome_10 Scan 17526 Method FTMS; HCD Score 48.09 m/z 640.84



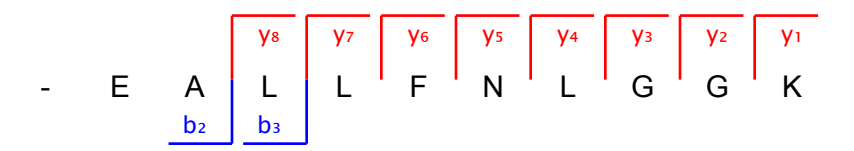
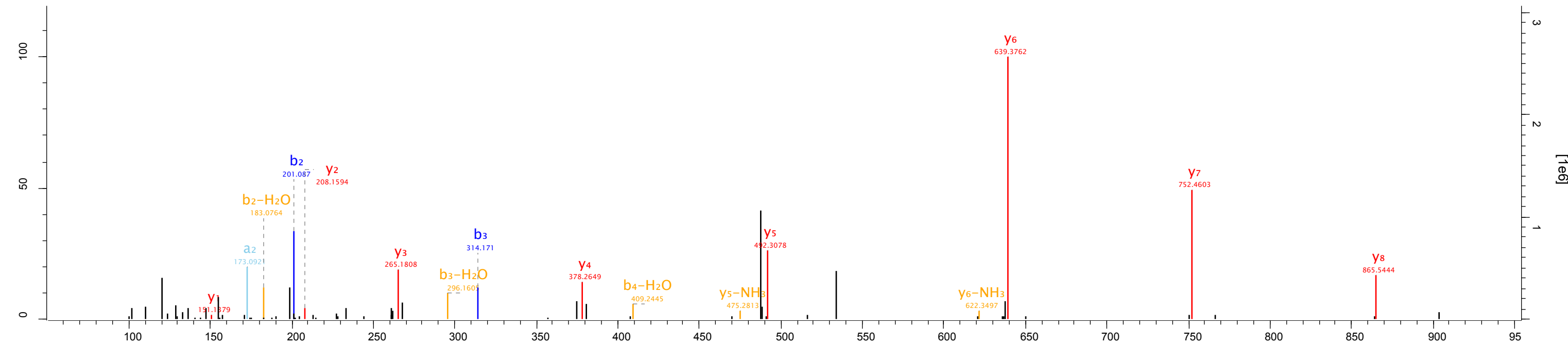
Raw file 20180707_MaS_A375SR_ML_proteome_10 Scan 7576 Method FTMS; HCD Score 41.4 m/z 594.31



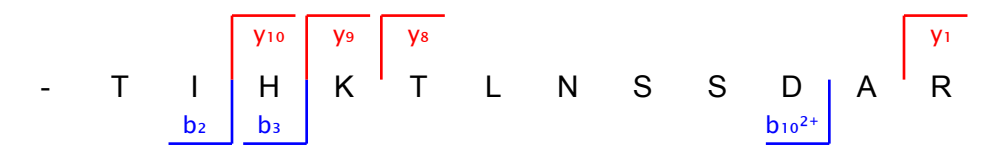
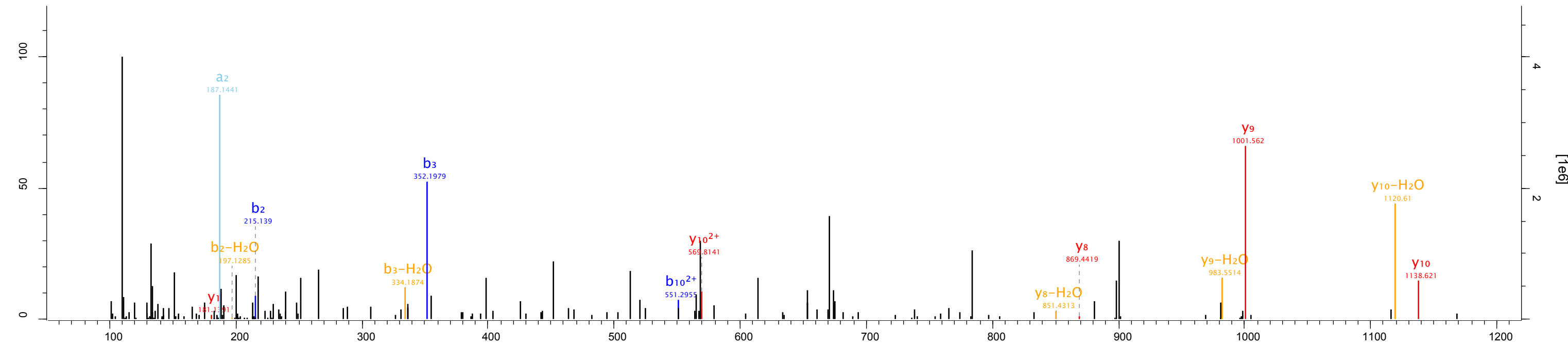


Raw file
20180707_MaS_A375SR_ML_proteome_12

Scan: 27476
Method: FTMS; HCD
Score: 90.91
m/z: 533.32
Gene names: CYB561

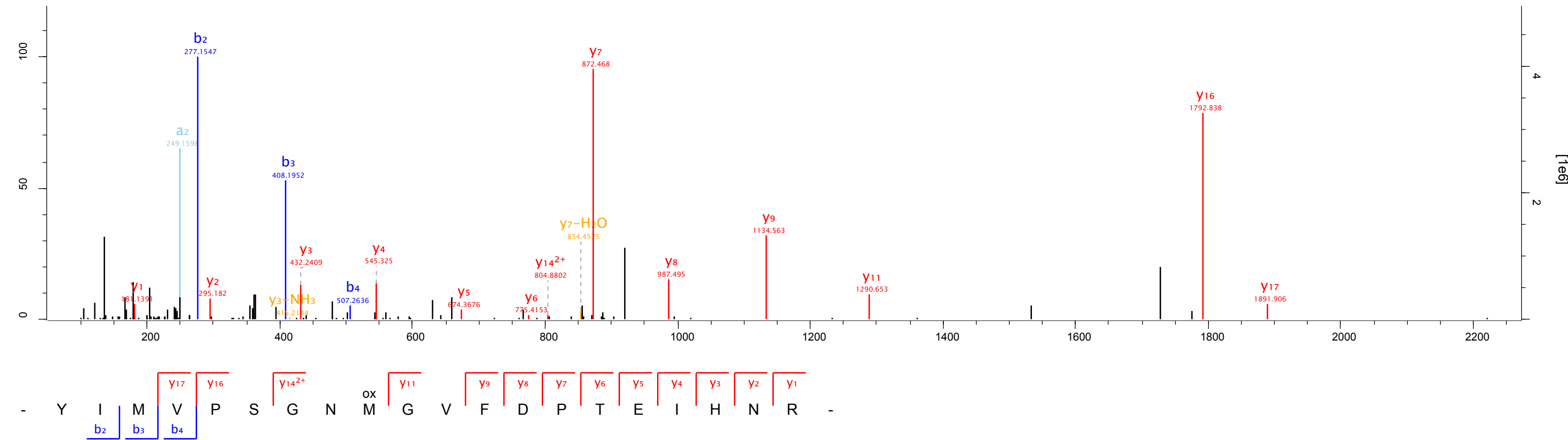


Raw file 20180707_MaS_A375SR_ML_proteome_12 Scan 6026 Method FTMS; HCD Score 52.25 m/z 451.59



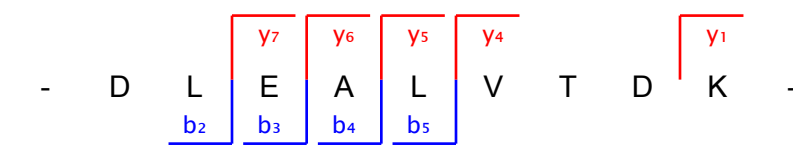
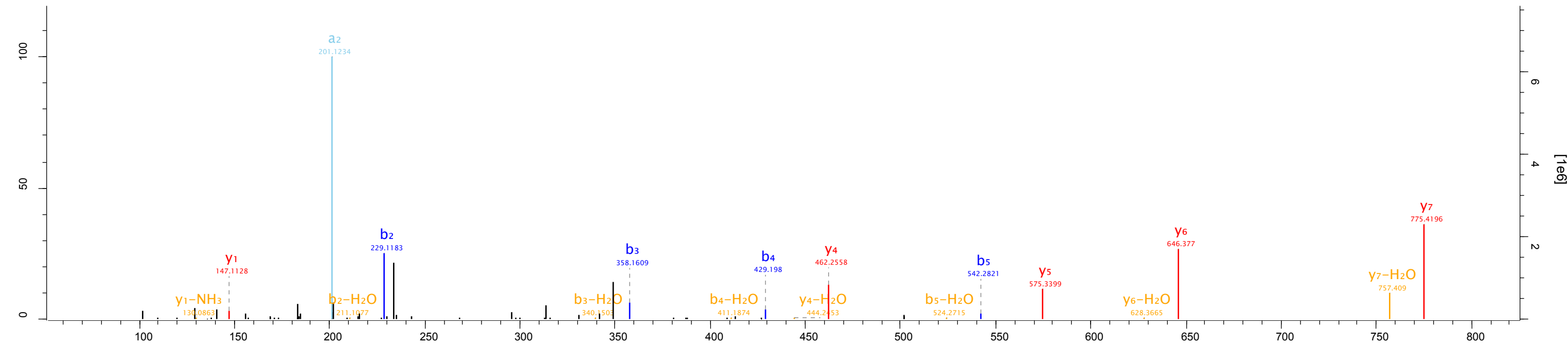
Raw file
20180707_MaS_A375SR_ML_proteome_13

Scan 23726 Method FTMS; HCD Score 65.42 m/z 767.7 Gene names CNIH4

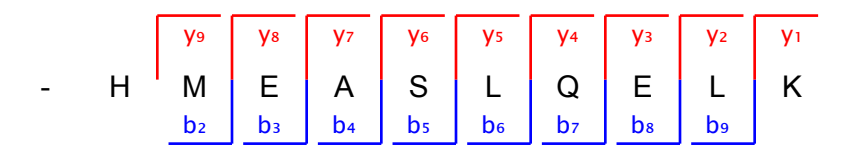
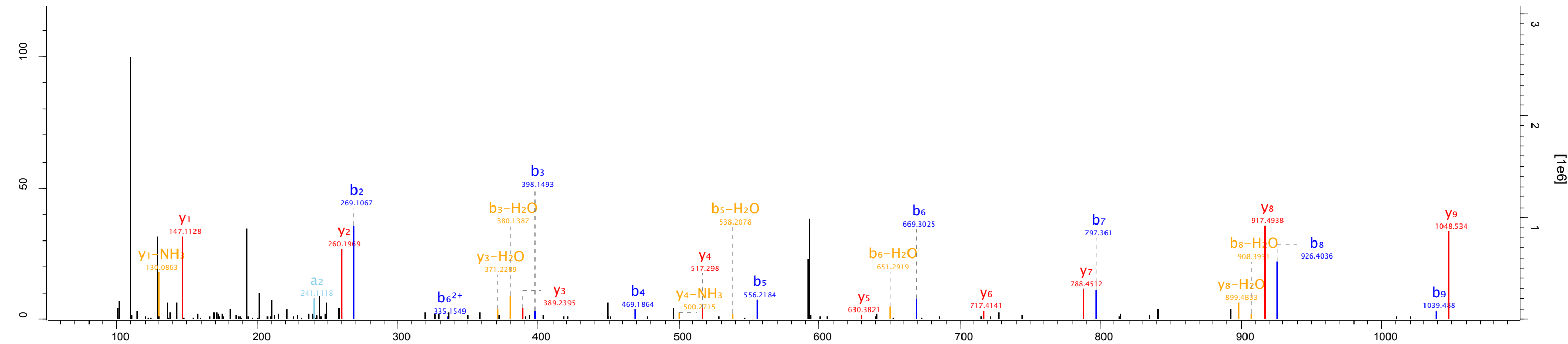


Raw file
20180707_MaS_A375SR_ML_proteome_13

Scan 26116 Method FTMS; HCD Score 84 m/z 502.27 Gene names PGM5

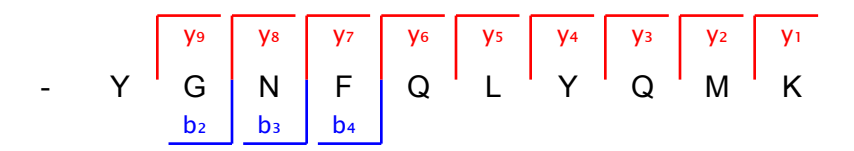
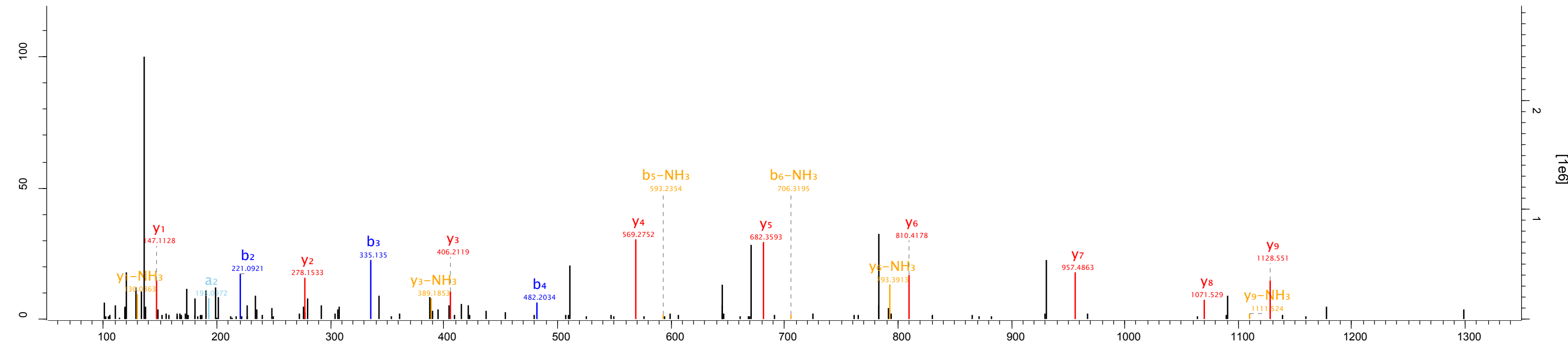


Raw file 20180707_MaS_A375SR_ML_proteome_14 Scan 11806 Method FTMS; HCD Score 165.63 m/z 593.3 Gene names IGFBP5



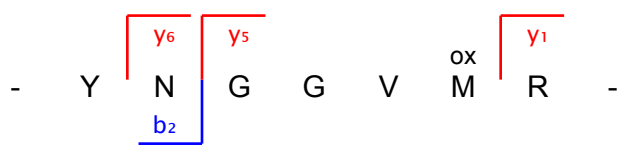
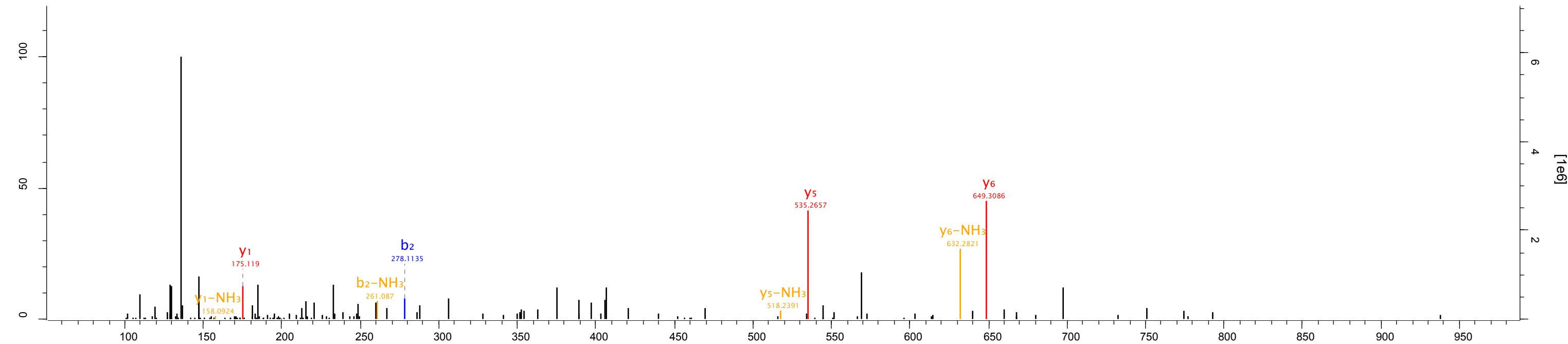
Raw file
20180707_MaS_A375SR_ML_proteome_14

Scan 21046 Method FTMS; HCD Score 101.65 m/z 646.31 Gene names IFIT2



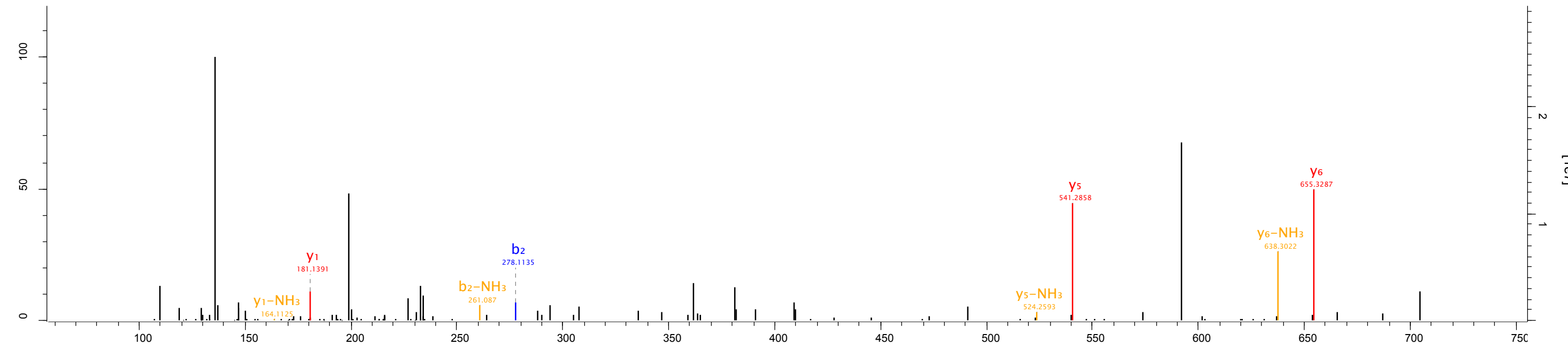
Raw file
20180707_MaS_A375SR_ML_proteome_14

Scan 5186 Method FTMS; HCD Score 43.07 m/z 406.69 Gene names KCNN2



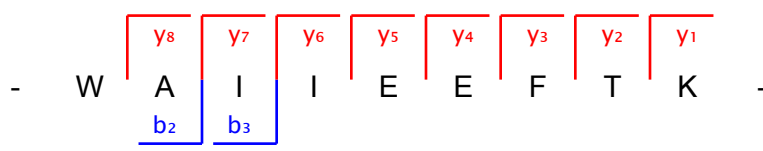
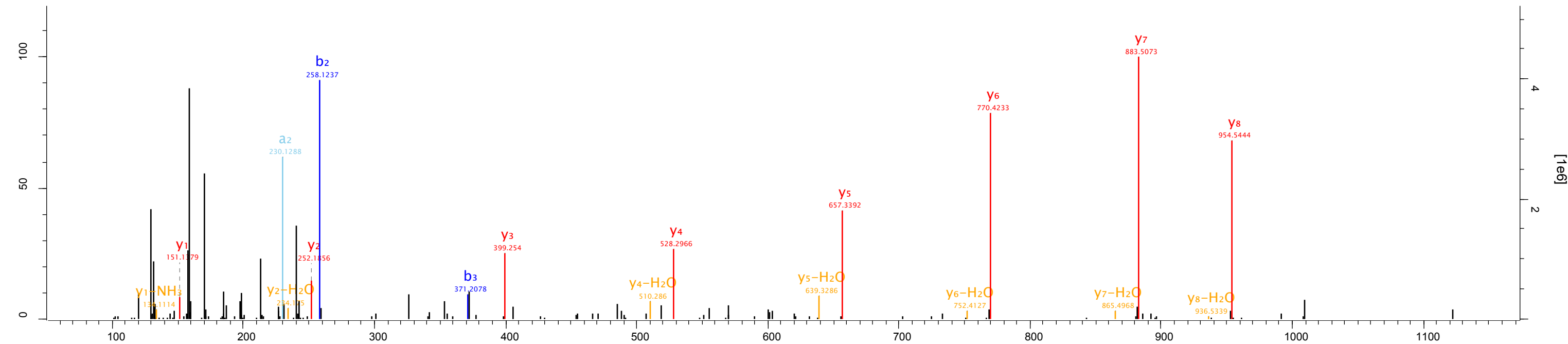
Raw file
20180707_MaS_A375SR_ML_proteome_14

Scan 5216 Method FTMS; HCD Score 48.17 m/z 409.7 Gene names KCNN2

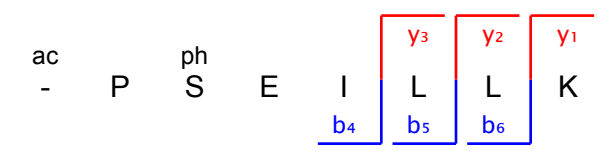
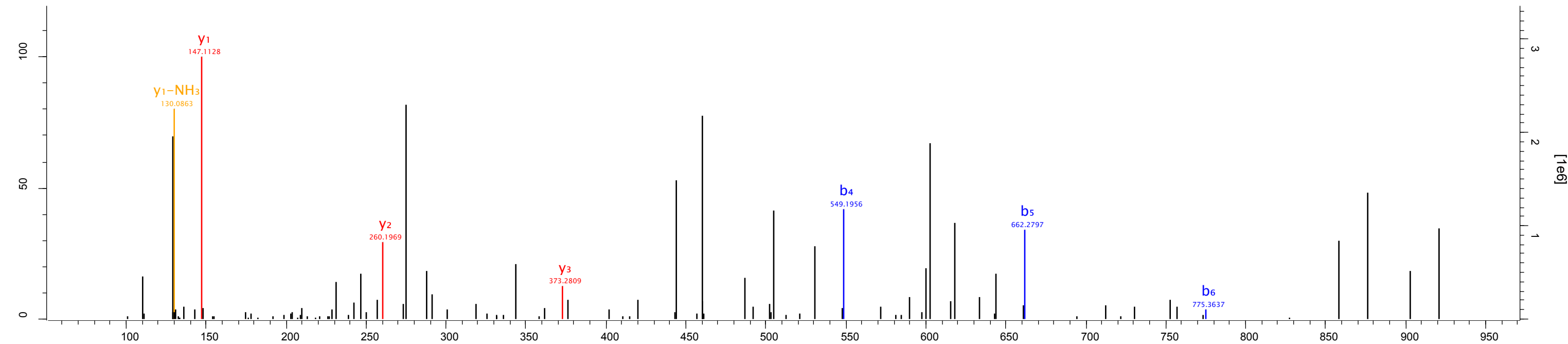


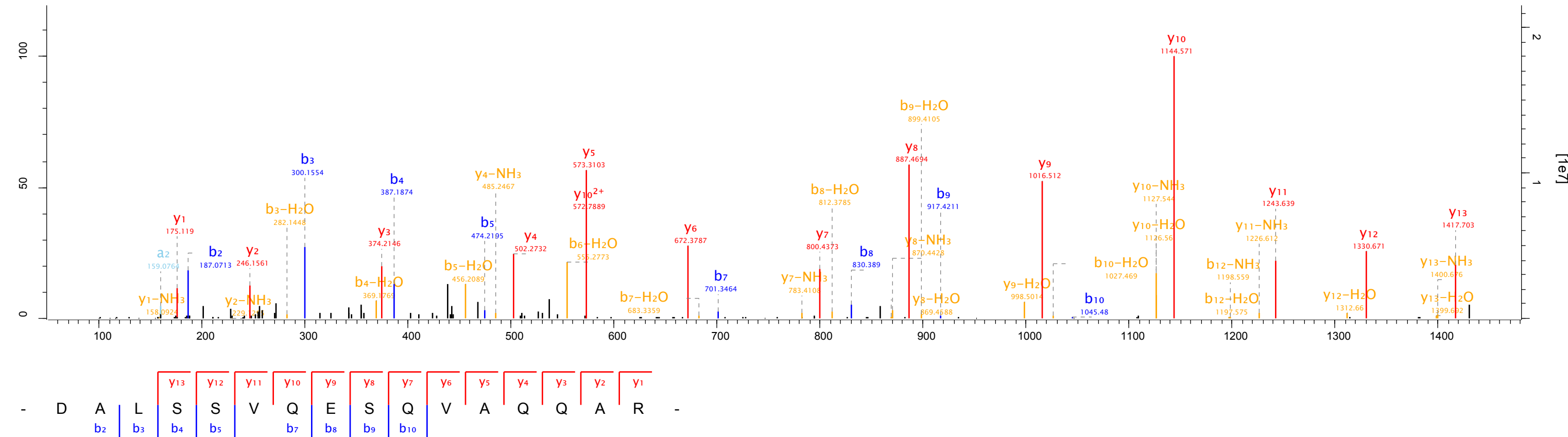
Raw file
20180707_MaS_A375SR_ML_proteome_15

Scan: 28486
Method: FTMS; HCD
Score: 89.05
m/z: 570.81
Gene names: MT-ND2



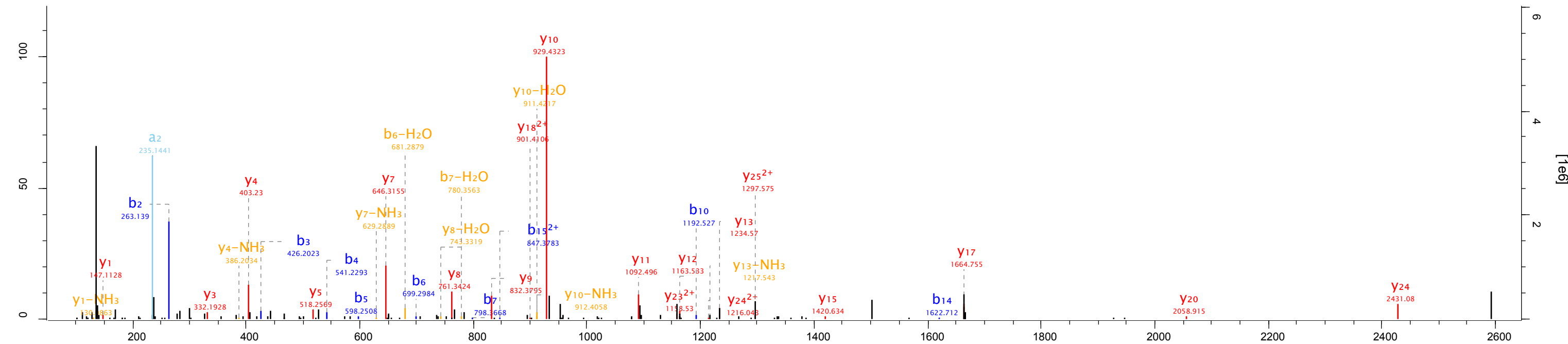
Raw file 20180707_MaS_A375SR_ML_proteome_15 Scan 5256 Method FTMS; HCD Score 79.45 m/z 461.24





Raw file
20180707_MaS_A375SR_ML_proteome_17

Scan 18726 Method FTMS; HCD Score 85.8 m/z 953.43 Gene names C6orf120



- V Y Y D G T V E Q H P F G E A A Y P A D G A D A G Q K -

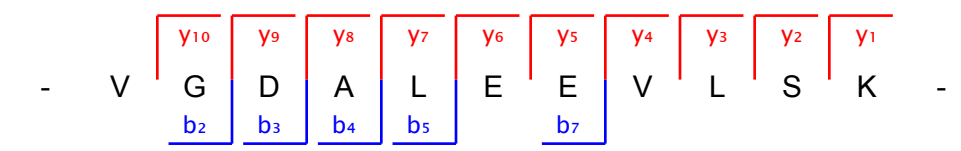
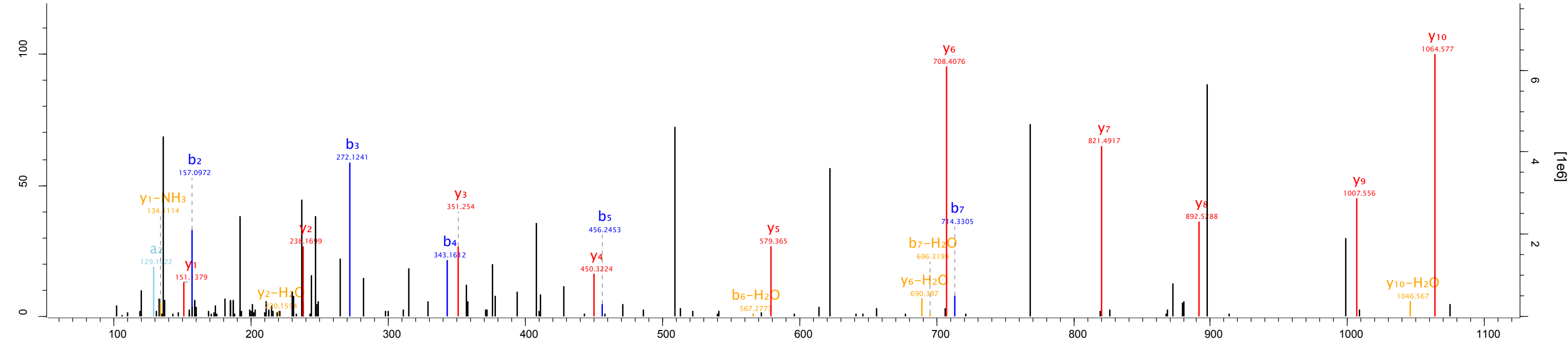
Fragmentation scheme (b and y ions) shown below the sequence:

- b2: Y
- b3: Y
- b4: D
- b5: G
- b6: T
- b7: V
- b10: H
- b14: E
- b15²⁺: EA
- y1: K
- y3: G
- y4: A
- y5: D
- y7: G
- y8: D
- y9: A
- y10: P
- y11: Y
- y12: A
- y13: A
- y15: G
- y17: P
- y18²⁺: H
- y20: E
- y23²⁺: G
- y24: D
- y25²⁺: Y

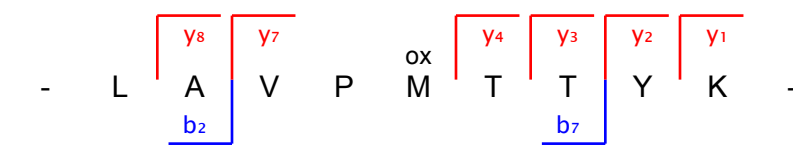
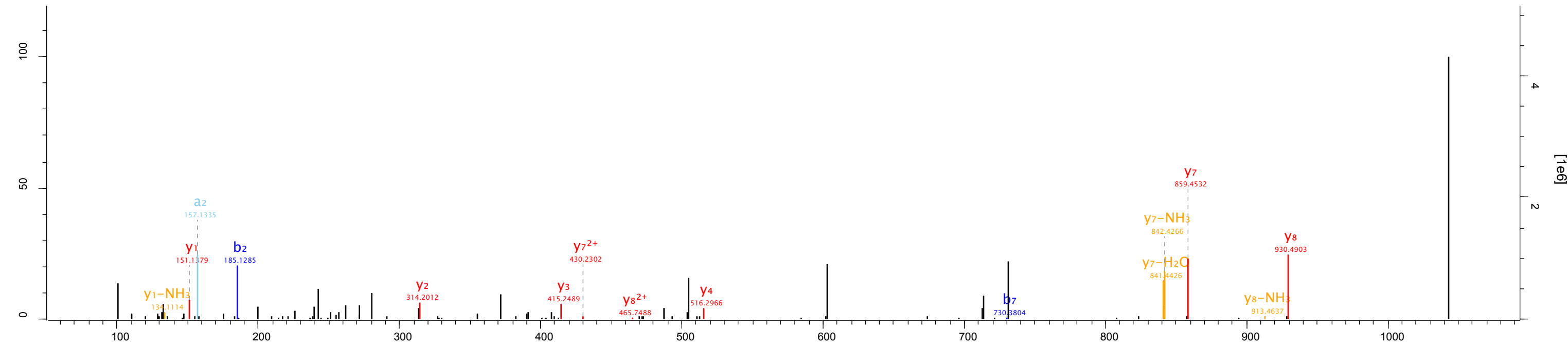
Raw file

20180707_MaS_A375SR_ML_proteome_17

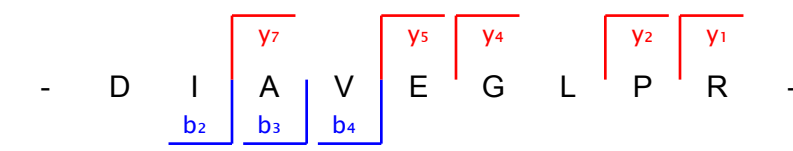
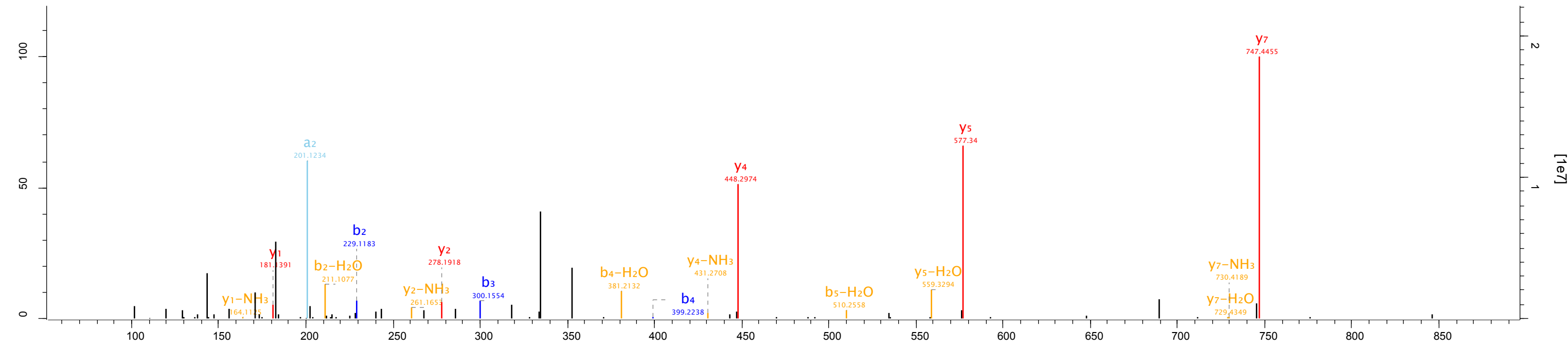
Scan	Method	Score	m/z	Gene names
24456	FTMS; HCD	108.56	582.33	GADD45A



Raw file 20180707_MaS_A375SR_ML_proteome_17 Scan 3956 Method FTMS; HCD Score 64.71 m/z 522.29

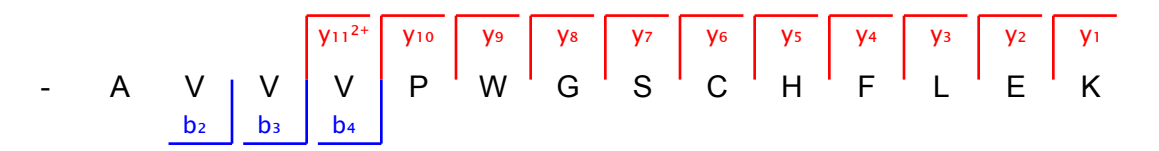
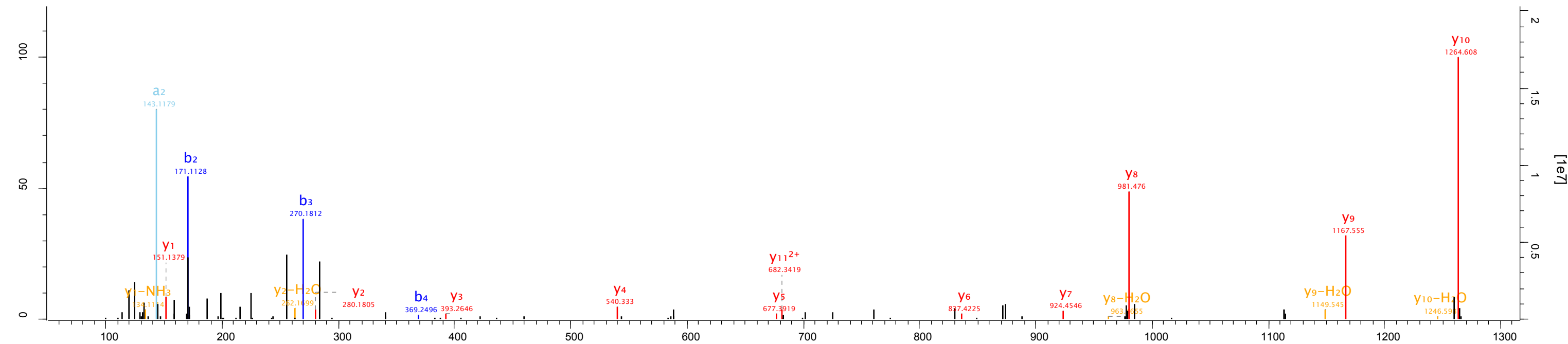


Raw file 20180707_MaS_A375SR_ML_proteome_18 Scan 17466 Method FTMS; HCD Score 100.02 m/z 488.28

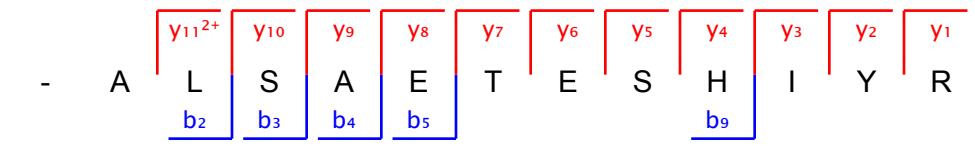
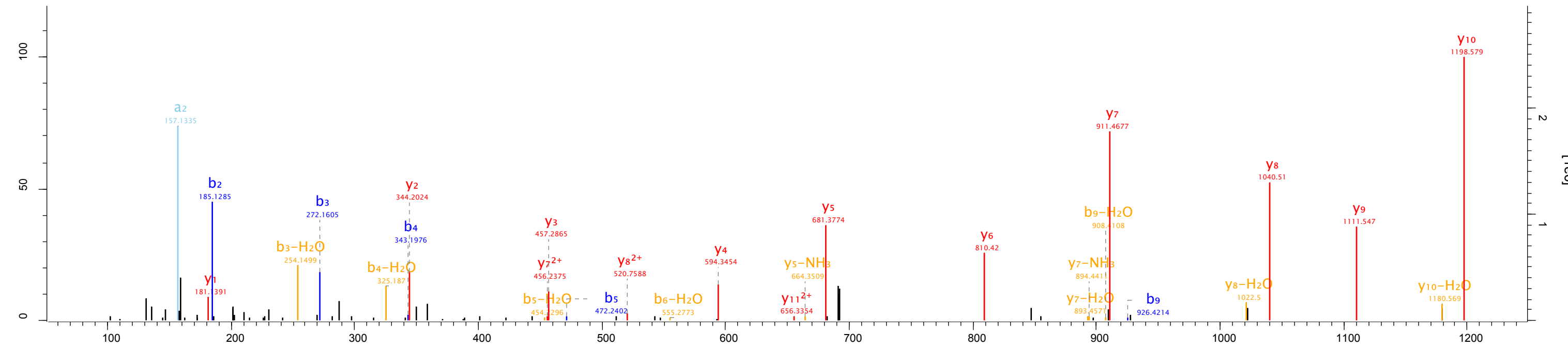


Raw file
20180707_MaS_A375SR_ML_proteome_19

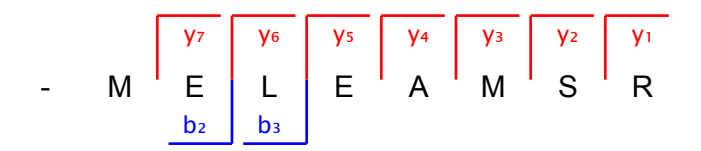
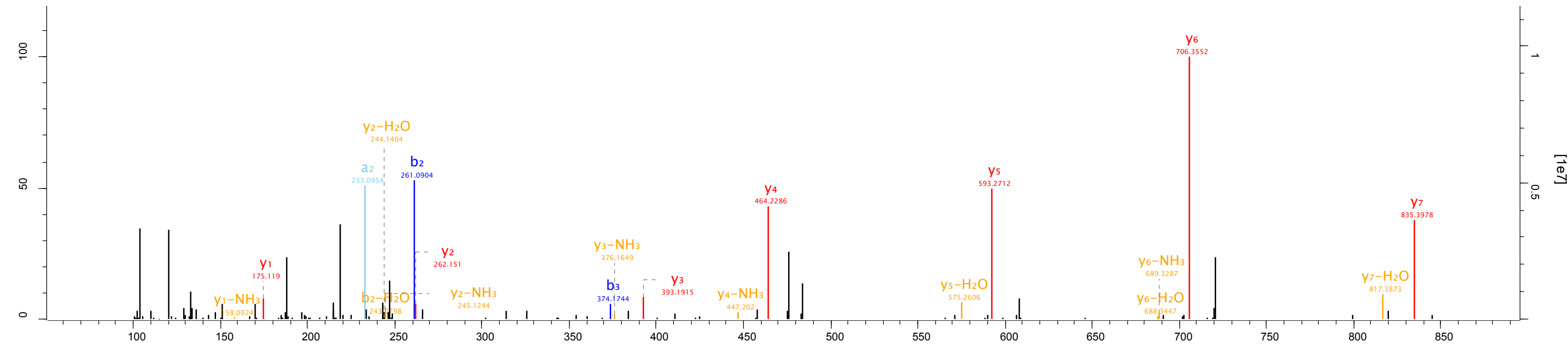
Scan 24736 Method FTMS; HCD Score 77.2 m/z 544.96 Gene names SPPL2A



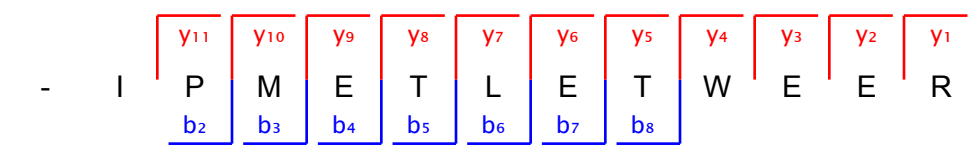
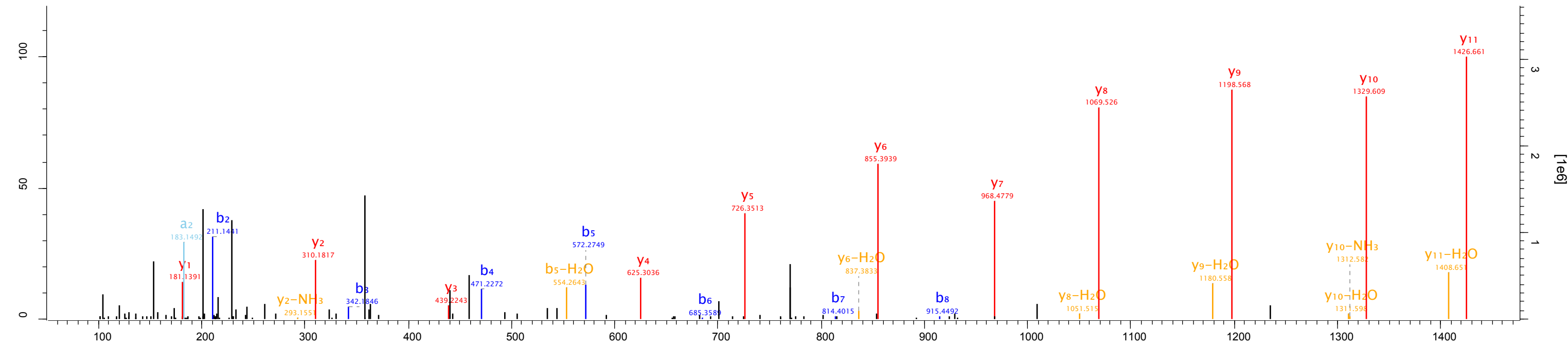
Raw file: 20180707_MaS_A375SR_ML_proteome_2_01
 Scan: 9676 Method: FTMS; HCD Score: 142.19 m/z: 691.86 Gene names: CYB561D2



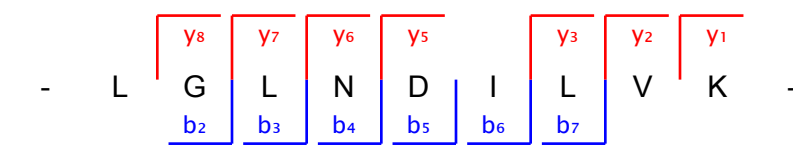
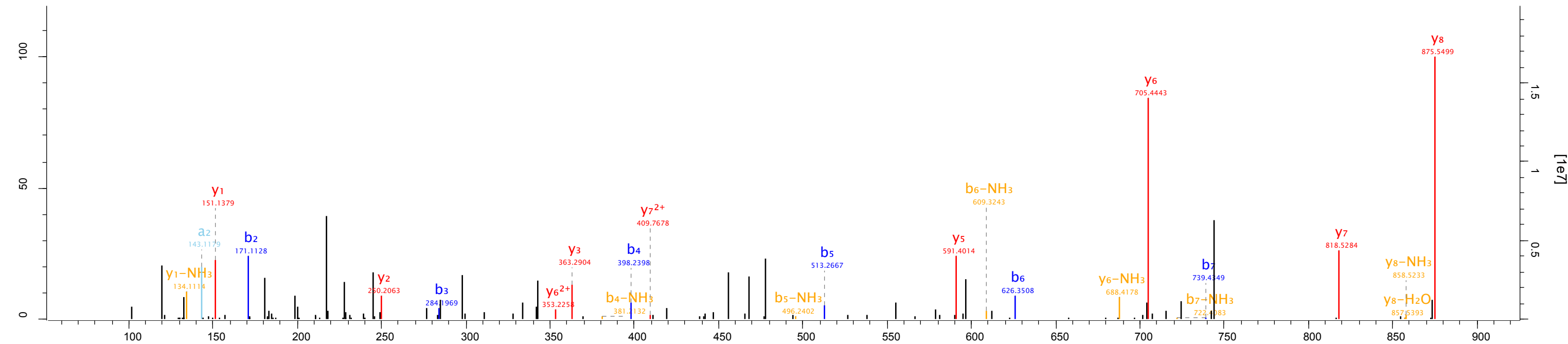
Raw file: 20180707_MaS_A375SR_ML_proteome_2_02
 Scan: 13976 Method: FTMS; HCD Score: 99.14 m/z: 483.72 Gene names: TMEM258



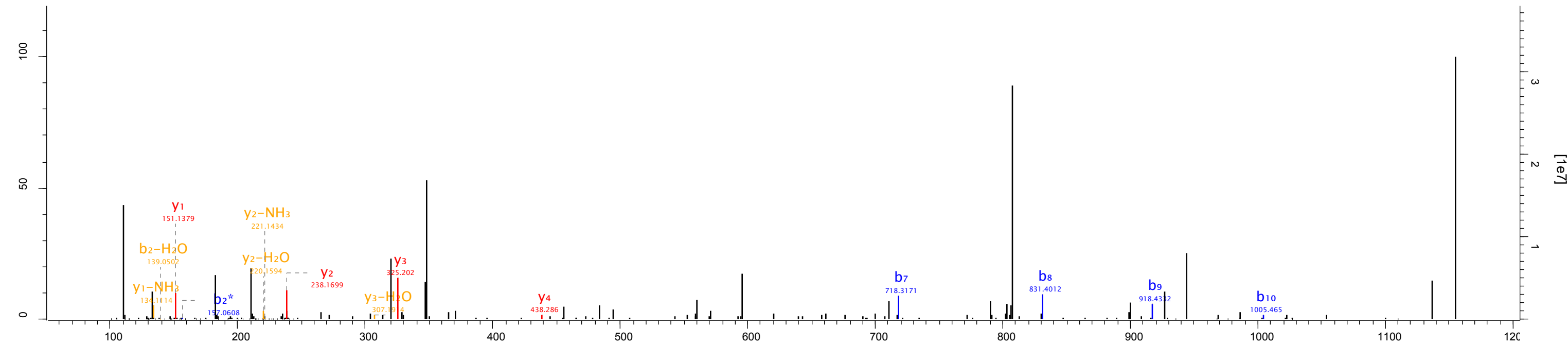
Raw file: 20180707_MaS_A375SR_ML_proteome_2_03
 Scan: 25796 Method: FTMS; HCD Score: 164.11 m/z: 770.38 Gene names: R3HDM4



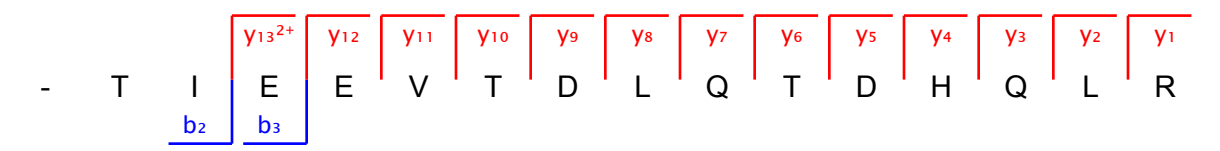
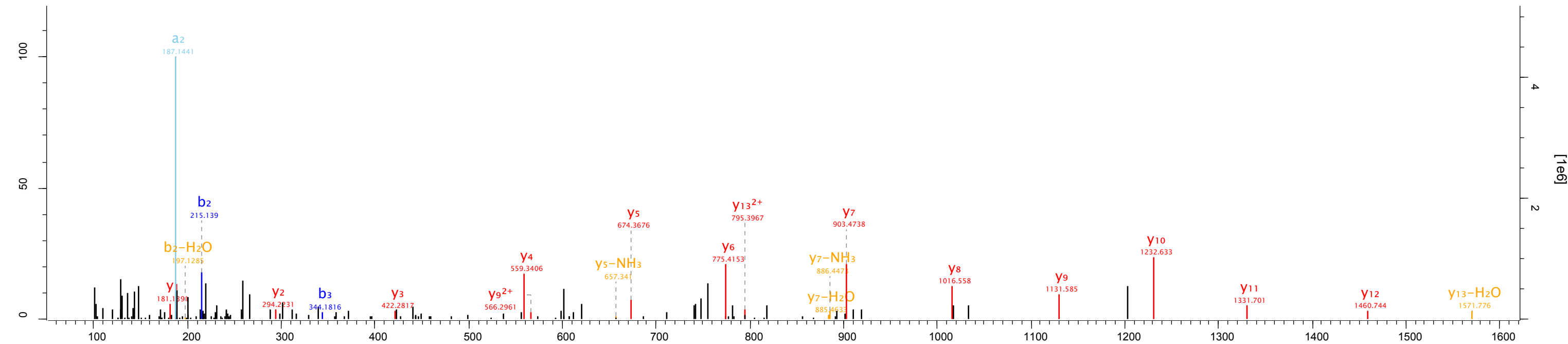
Raw file: 20180707_MaS_A375SR_ML_proteome_2_03
 Scan: 26466 Method: FTMS; HCD Score: 114.86 m/z: 494.82 Gene names: STON2



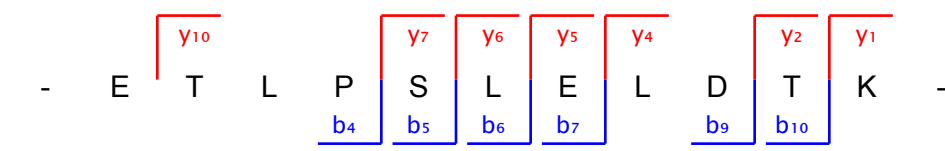
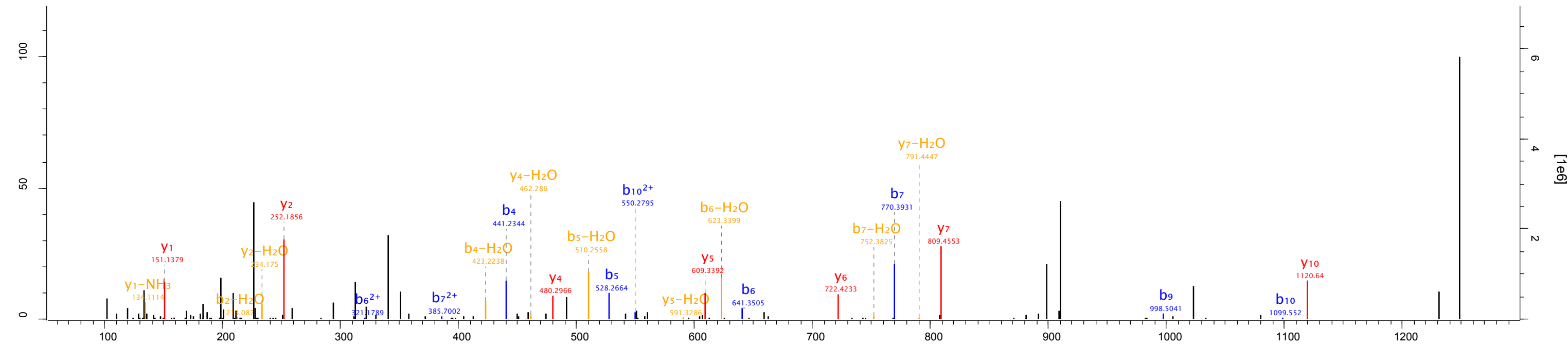
Raw file 20180707_MaS_A375SR_ML_proteome_2_03 Scan 4156 Method FTMS; HCD Score 63.62 m/z 578.3



Raw file 20180707_MaS_A375SR_ML_proteome_2_04 Scan 16476 Method FTMS; HCD Score 64.04 m/z 602.31 Gene names C8orf37

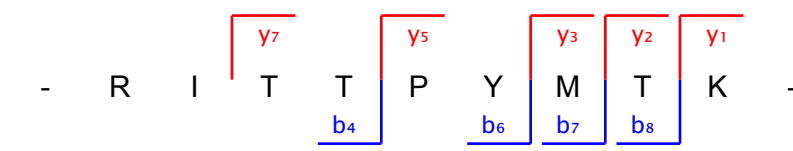
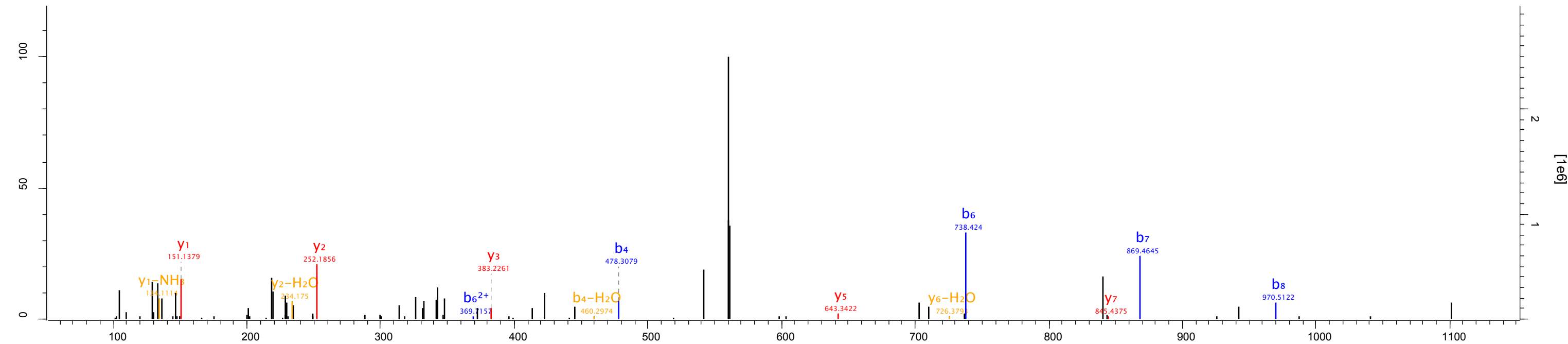


Raw file 20180707_MaS_A375SR_ML_proteome_2_04 Scan 23466 Method FTMS; HCD Score 127.83 m/z 625.35

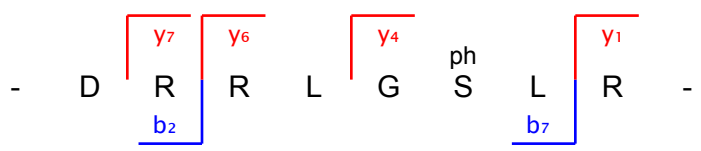
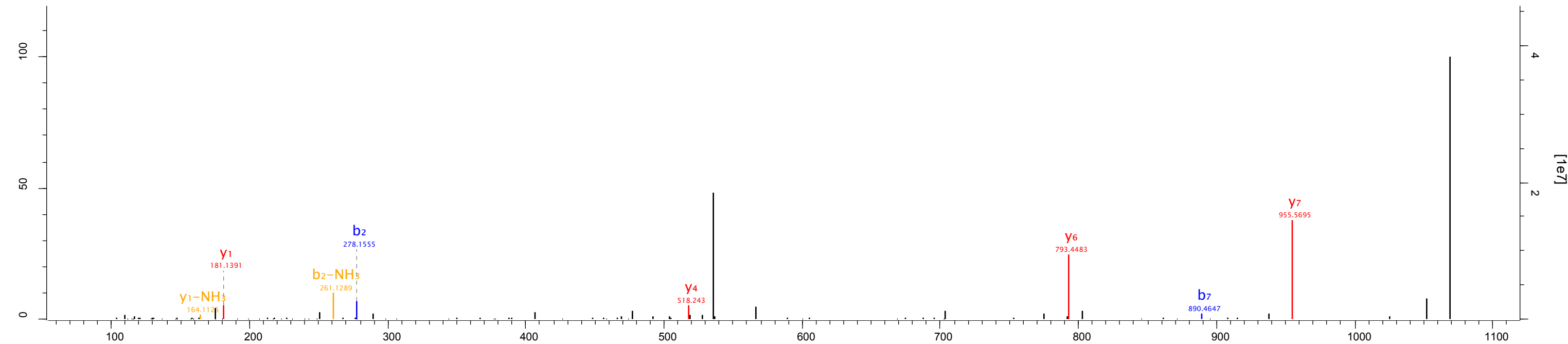


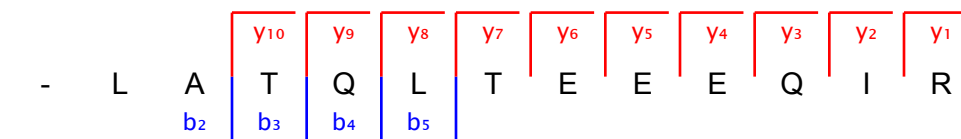
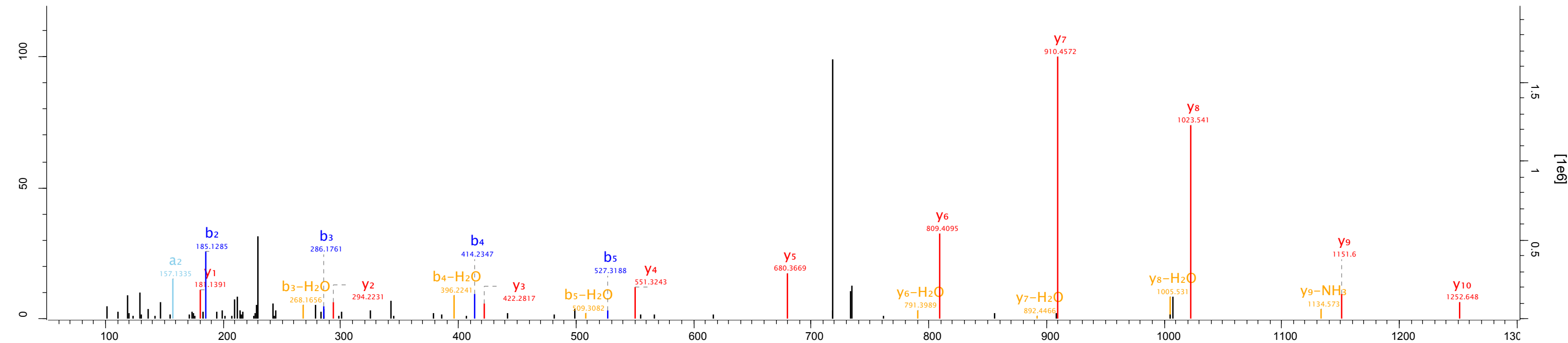
Raw file
20180707_MaS_A375SR_ML_proteome_2_05

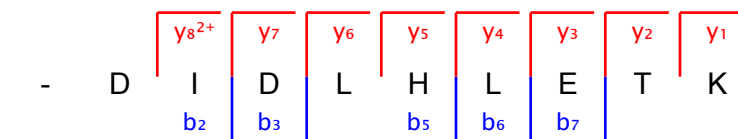
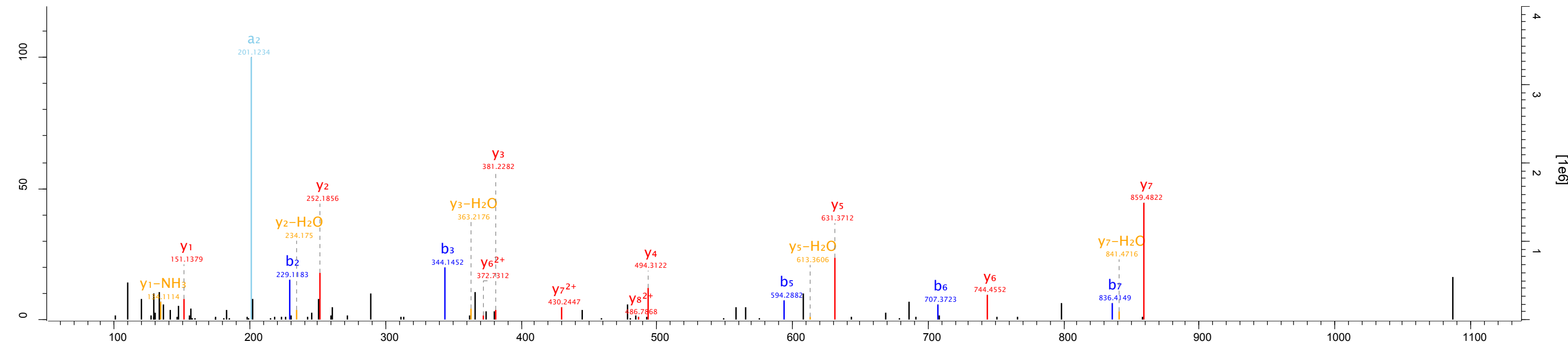
Scan 8906 Method FTMS; HCD Score 49 m/z 560.83 Gene names POLR2F



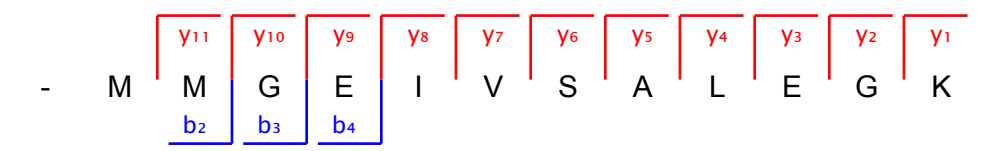
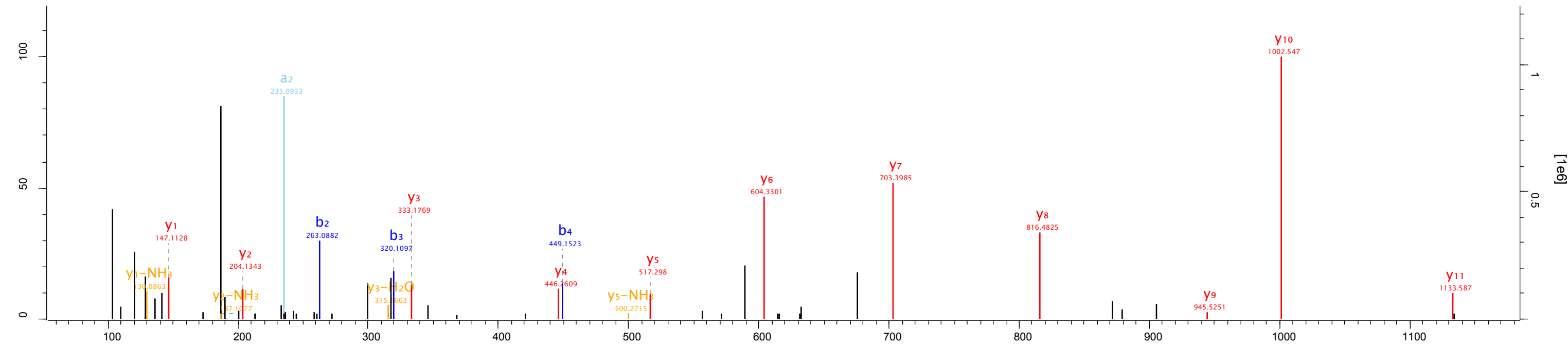
Raw file 20180707_MaS_A375SR_ML_proteome_2_06 Scan 4666 Method FTMS; HCD Score 69.82 m/z 535.8





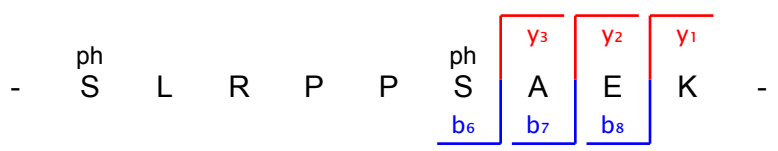
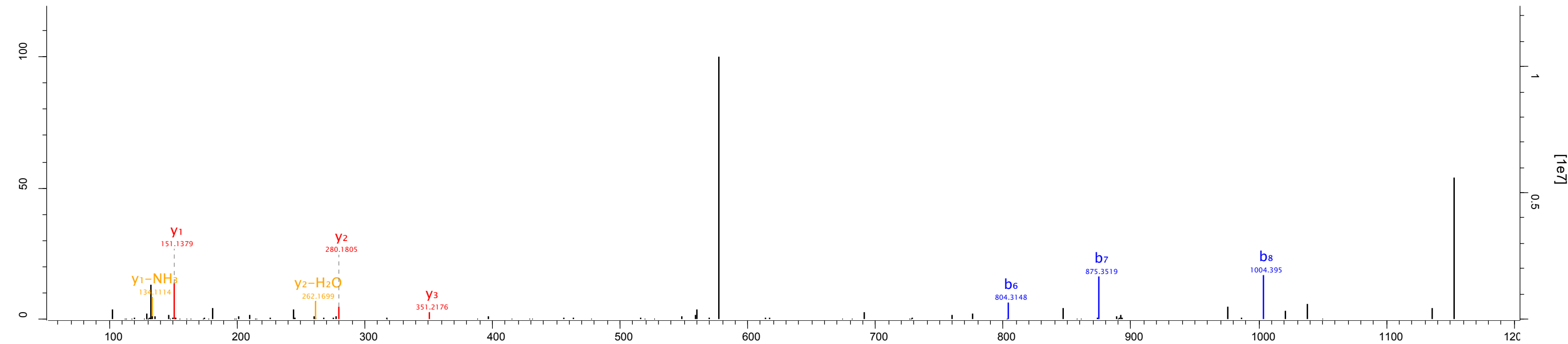


Raw file 20180707_MaS_A375SR_ML_proteome_2_08 Scan 27176 Method FTMS; HCD Score 81.57 m/z 632.82 Gene names CCNF



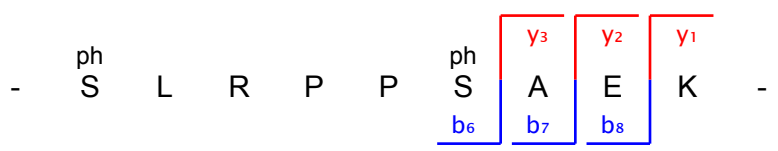
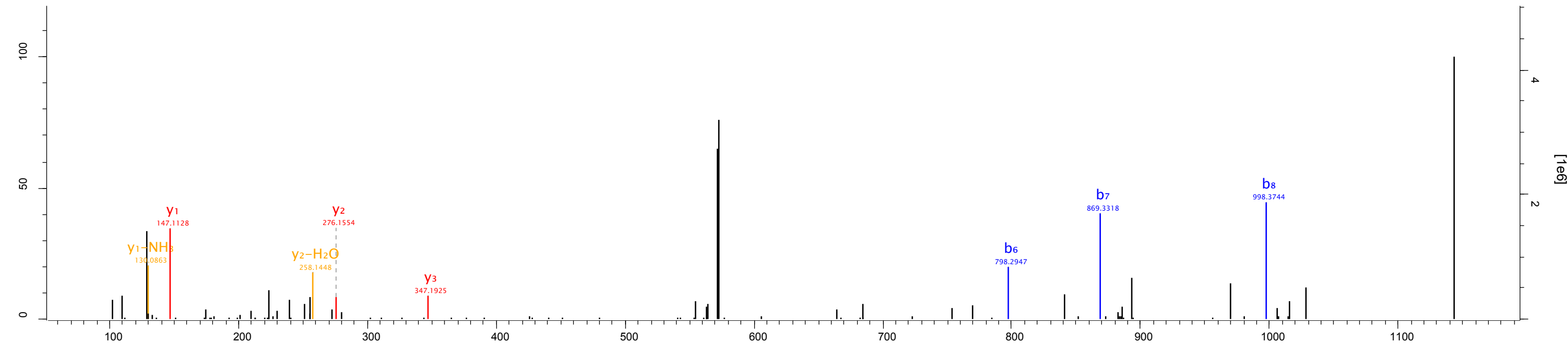
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20180707_MaS_A375SR_ML_proteome_2_08

Scan 5646 Method FTMS; HCD Score 46 m/z 577.77

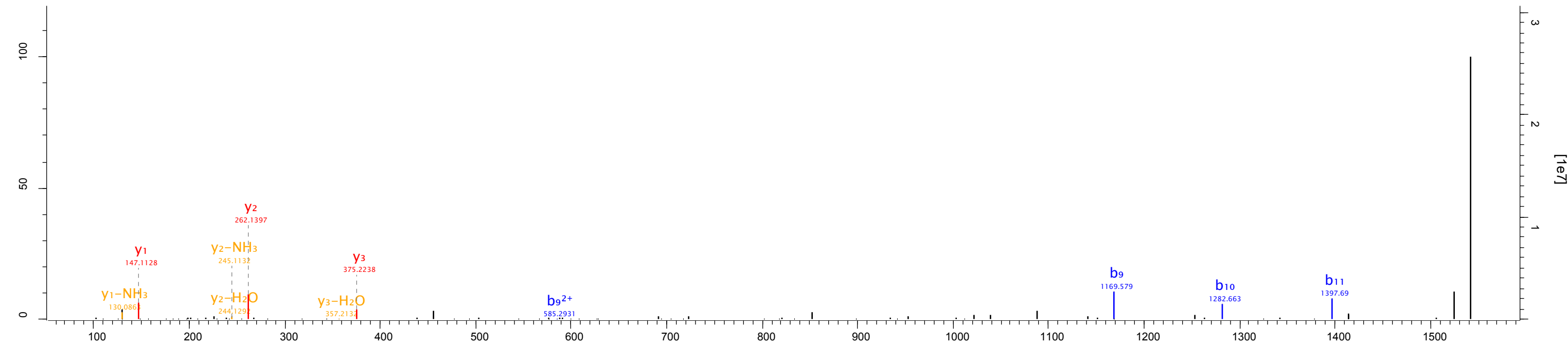


Raw file
20180707_MaS_A375SR_ML_proteome_2_08

Scan 5656 Method FTMS; HCD Score 53.76 m/z 572.74

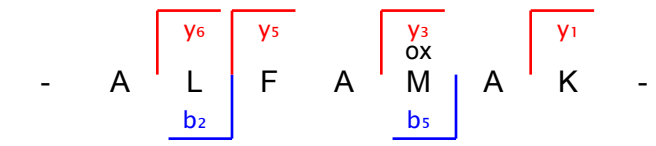
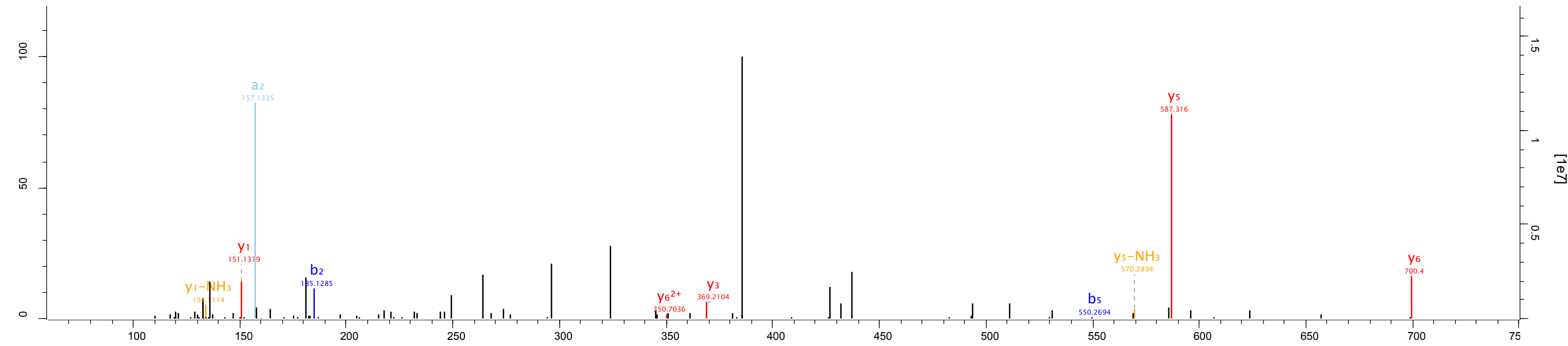


Raw file 20180707_MaS_A375SR_ML_proteome_2_09 Scan 11276 Method FTMS; HCD Score 78.34 m/z 772.4 Gene names VAV1

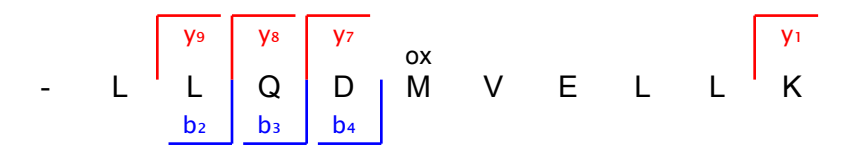
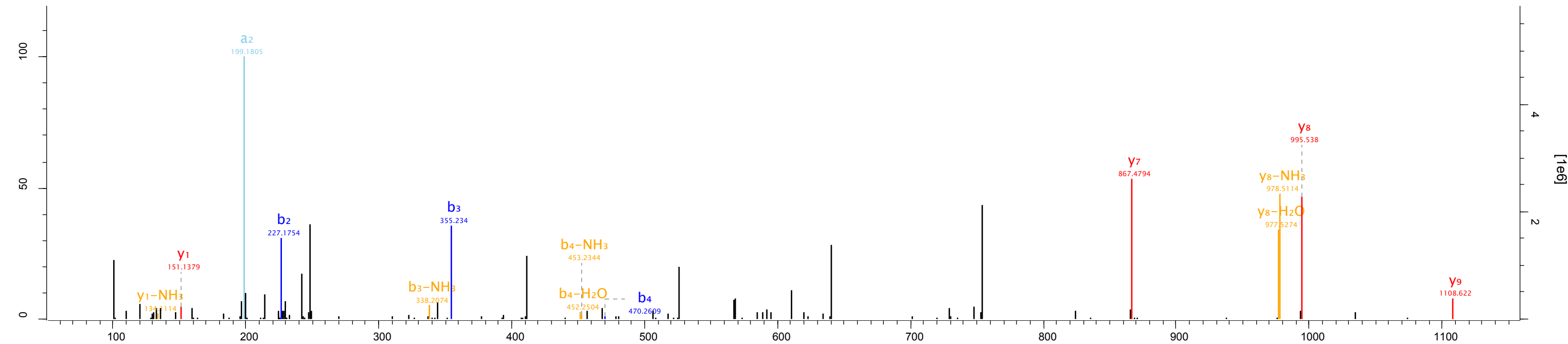


Raw file
20180707_MaS_A375SR_ML_proteome_2_09

Scan 12506 Method FTMS; HCD Score 53.1 m/z 386.22 Gene names RASD1

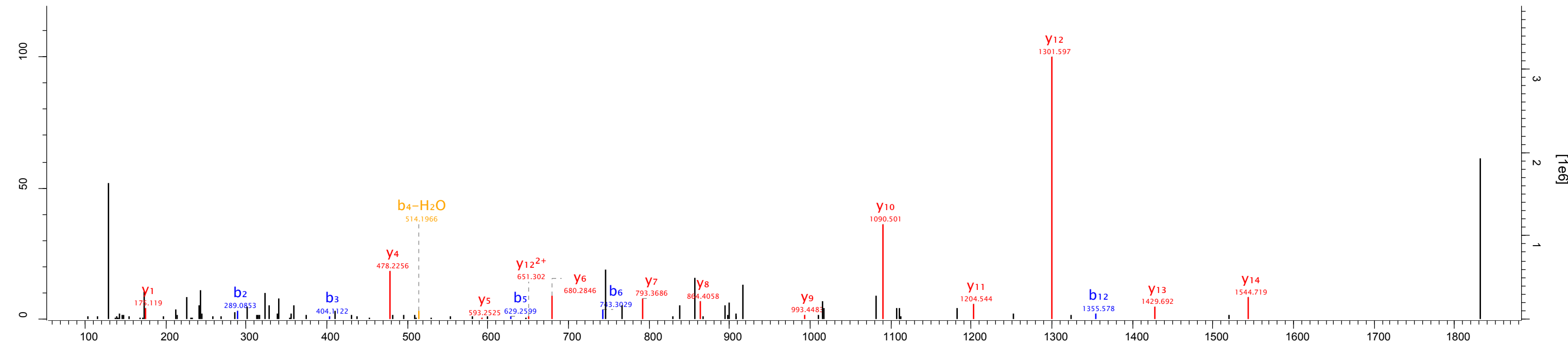


Raw file 20180707_MaS_A375SR_ML_proteome_2_10 Scan 25226 Method FTMS; HCD Score 52.73 m/z 611.36



20180707_MaS_A375SR_ML_proteome_2_11

15176 FTMS; HCD 54.1 916.9 ADPRM



ac

- M D D K P N P E A L S D S S E R -

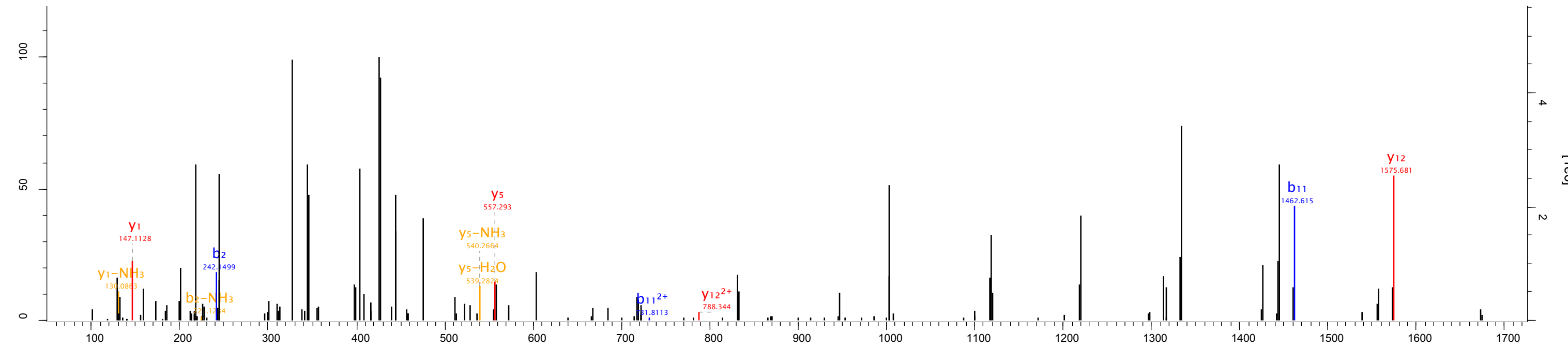
Fragmentation mapping (b and y ions) is shown below the sequence:

- b₂ (under D)
- b₃ (under D)
- b₅ (under P)
- b₆ (under N)
- b₁₂ (under D)
- y₁ (above R)
- y₄ (above S)
- y₅ (above D)
- y₆ (above S)
- y₇ (above L)
- y₈ (above A)
- y₉ (above E)
- y₁₀ (above P)
- y₁₁ (above N)
- y₁₂ (above P)
- y₁₃ (above K)
- y₁₄ (above D)

Raw file

20180707_MaS_A375SR_ML_proteome_2_11

Scan 15736 Method FTMS; HCD Score 53.38 m/z 1009.96 Gene names FOXP2



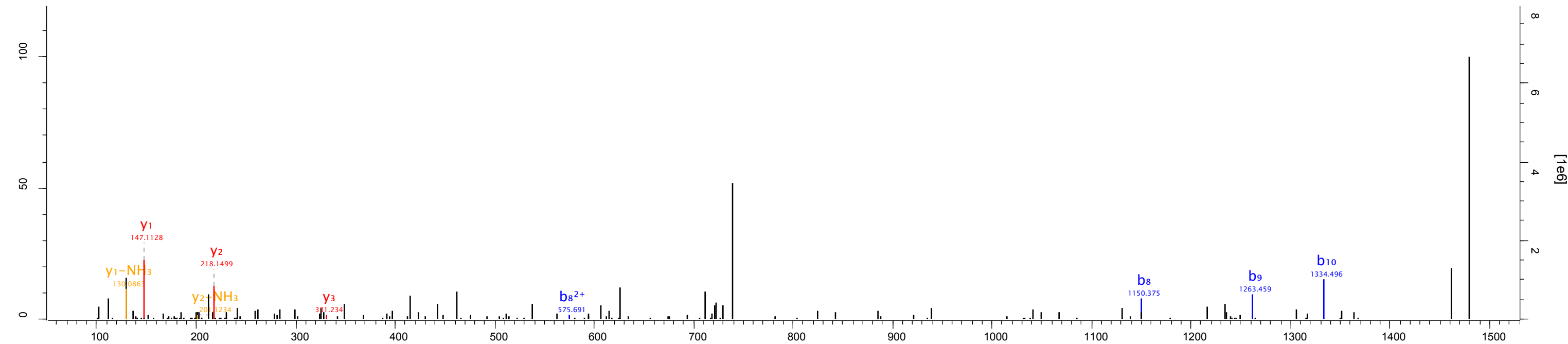
- L Q A M M T H L H M R P S E P K -

Fragmentation labels: b2 (under Q), y12 ox (above M), y5 (above P), y1 (above K)

Raw file

20180707_MaS_A375SR_ML_proteome_2_12

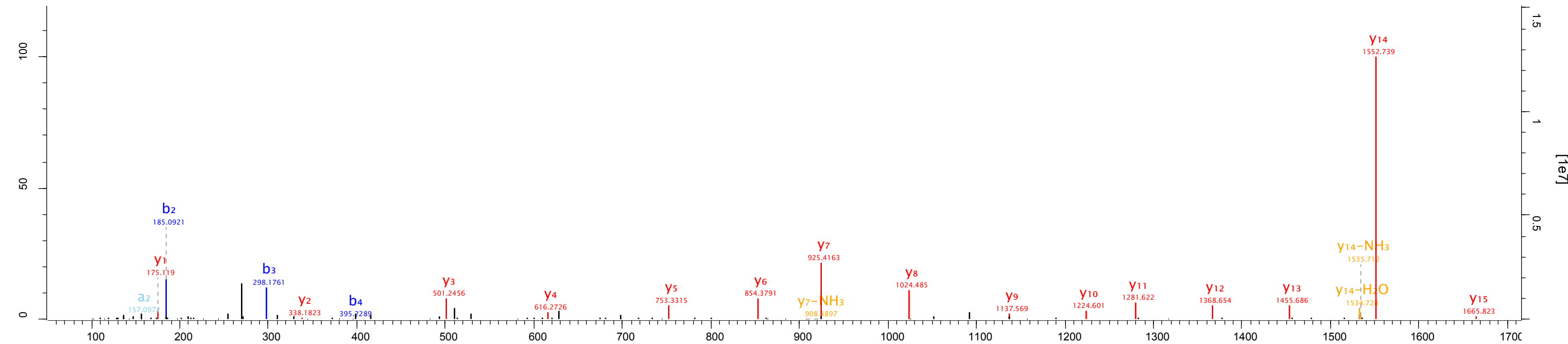
Scan	Method	Score	m/z	Gene names
11646	FTMS; HCD	41.82	740.81	DNAJB13



ac - ox M E ph T ph S R G R N L A K -

Fragmentation mapping:
 - Red boxes above the sequence: y3 (L), y2 (A), y1 (K)
 - Blue boxes below the sequence: b8 (N), b9 (L), b10 (A)

Raw file 20180707_MaS_A375SR_ML_proteome_2_12 Scan 25666 Method FTMS; HCD Score 94.2 m/z 925.96 Gene names PDPDF

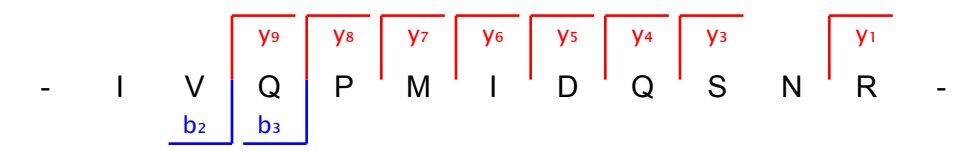
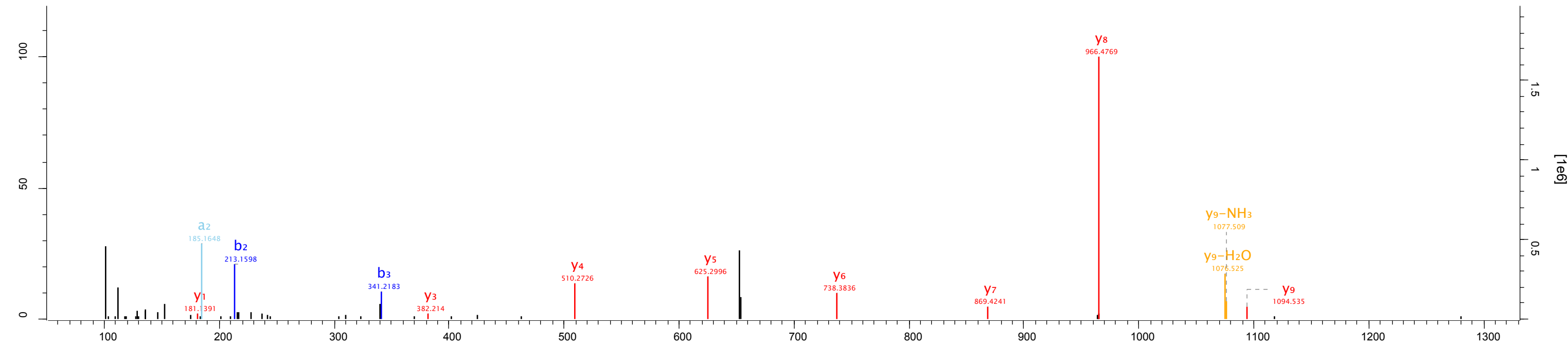


ac - A A I P S S G S L V A T H D Y Y R -

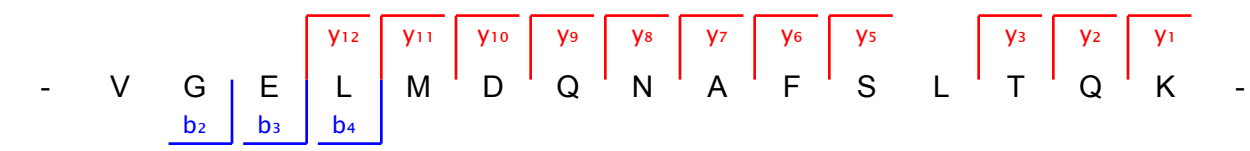
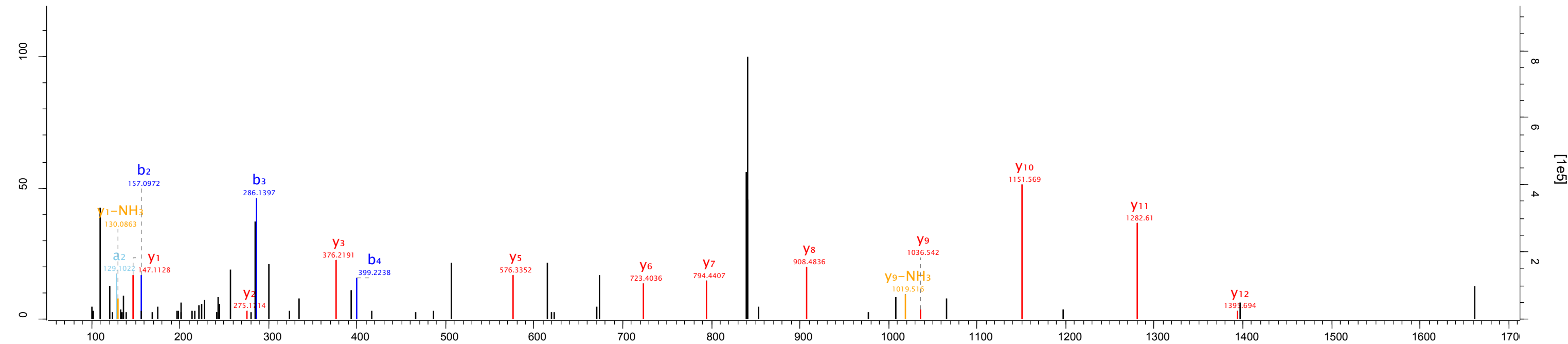
Fragmentation scheme showing b and y ions for the peptide sequence: A A I P S S G S L V A T H D Y Y R -

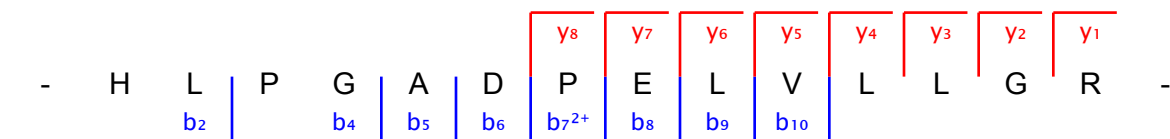
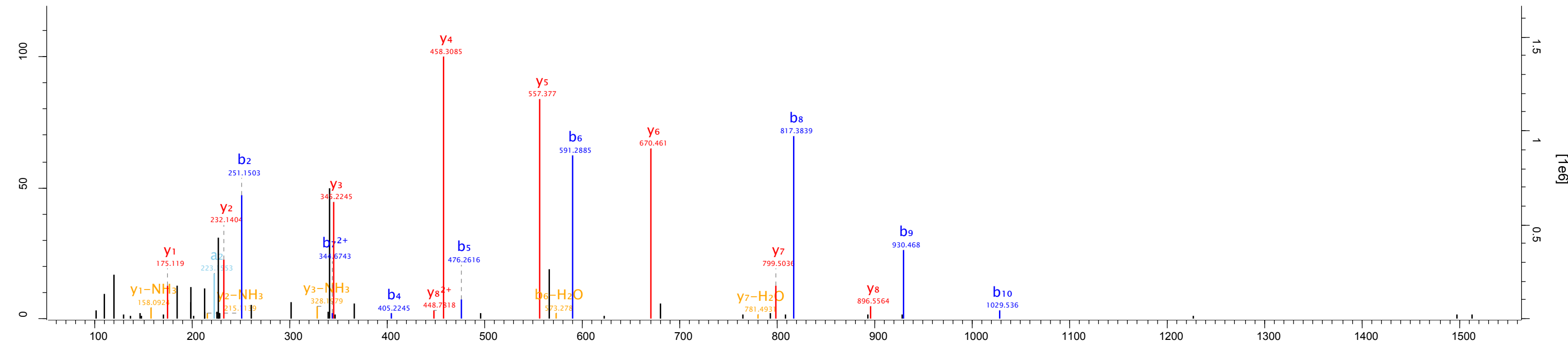
Red boxes indicate y ions (y1 to y15) above the amino acids. Blue boxes indicate b ions (b2, b3, b4) below the amino acids.

Raw file: 20180707_MaS_A375SR_ML_proteome_2_13
 Scan: 13406 Method: FTMS; HCD Score: 67.38 m/z: 653.85 Gene names: MEIS2;MEIS3;MEIS1;MEIS3P1



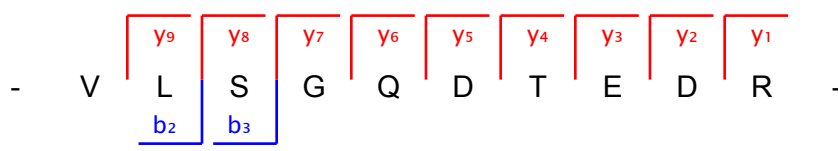
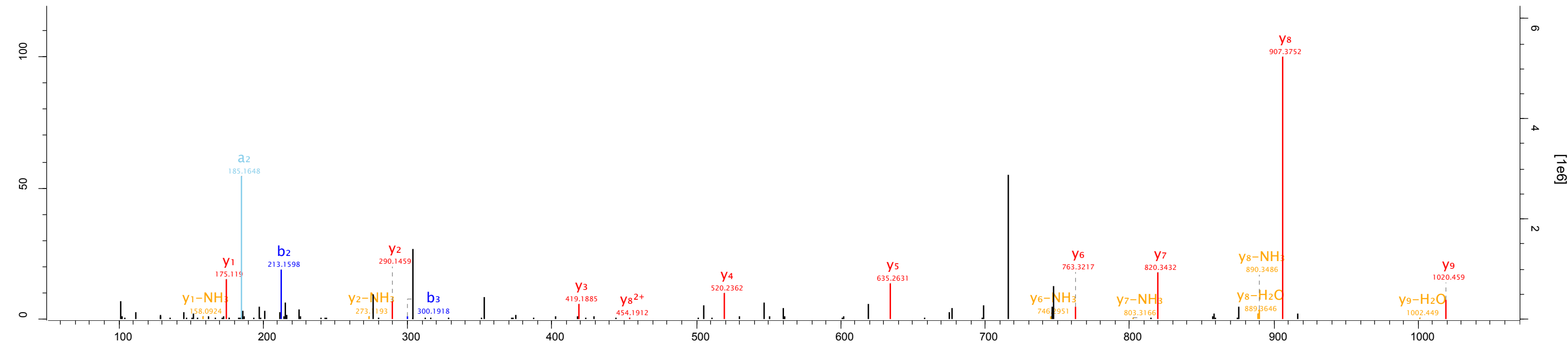
Raw file 20180707_MaS_A375SR_ML_proteome_2_13
 Scan 23426 Method FTMS; HCD Score 59.67 m/z 840.92 Gene names GTF2H5





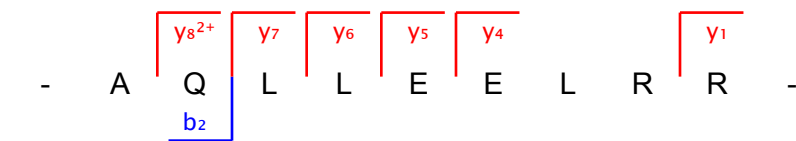
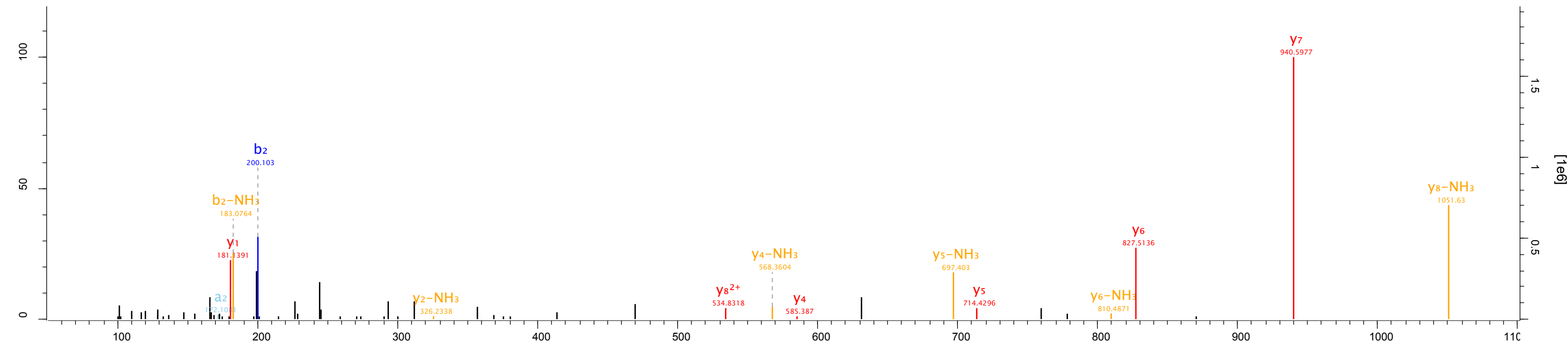
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20180707_MaS_A375SR_ML_proteome_2_14

Scan 4836 Method FTMS; HCD Score 79.66 m/z 560.27 Gene names SFT2D2

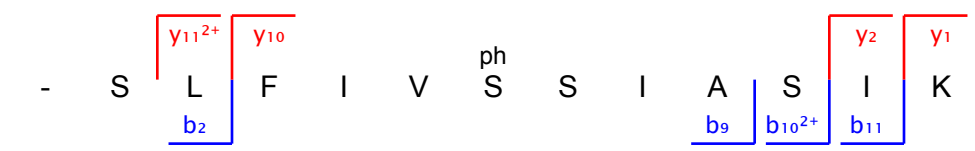
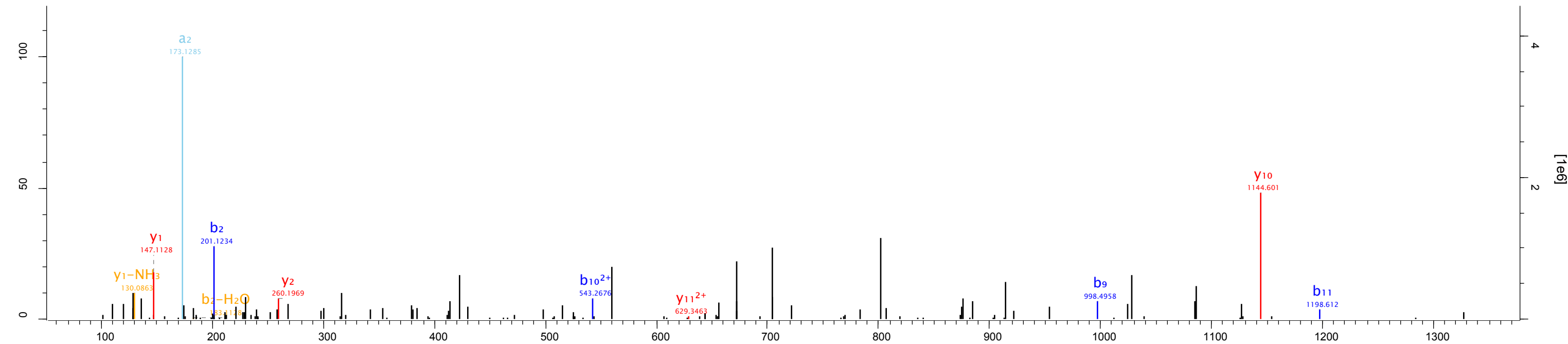


Raw file
20180707_MaS_A375SR_ML_proteome_2_15

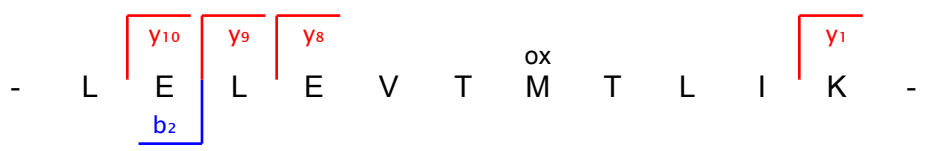
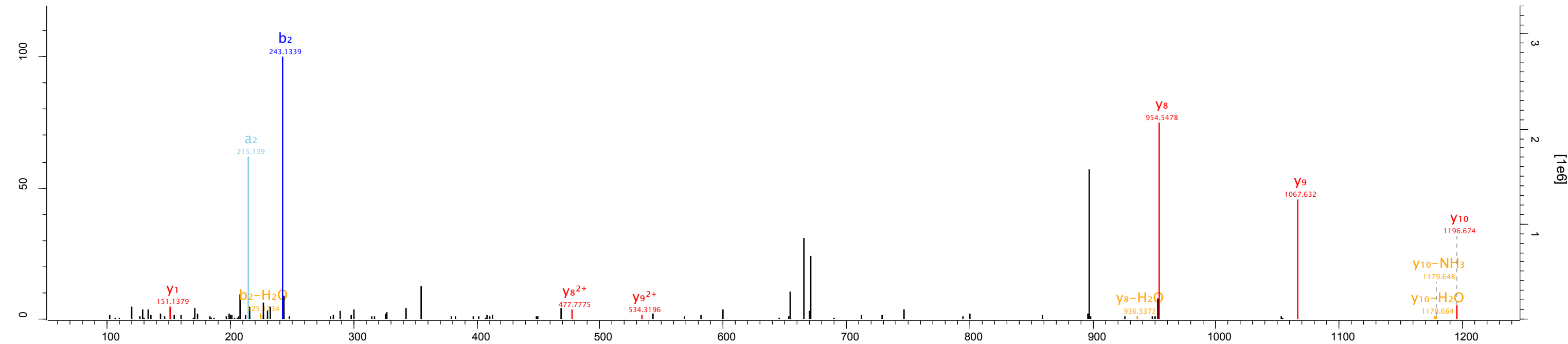
Scan 16696 Method FTMS; HCD Score 66.27 m/z 380.57 Gene names PNKD

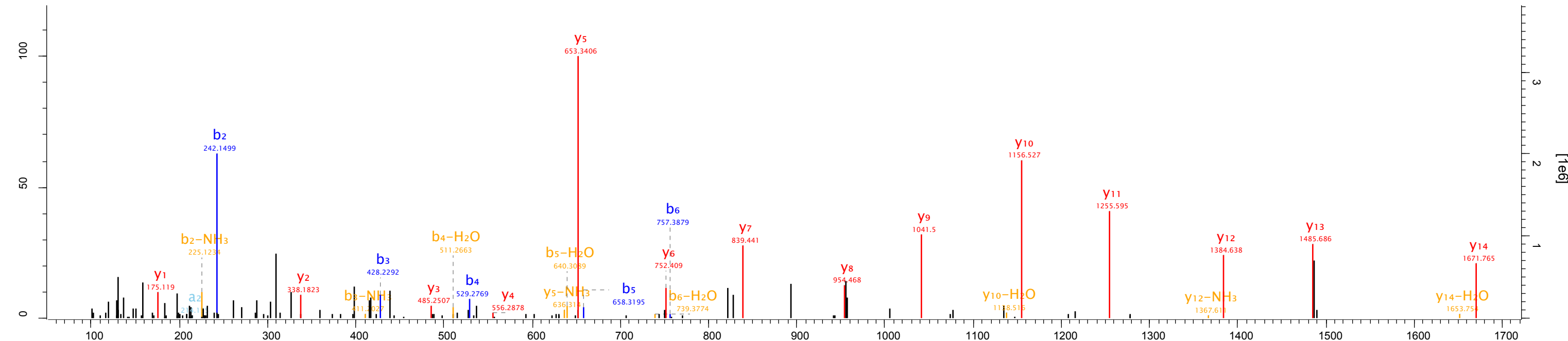


Raw file 20180707_MaS_A375SR_ML_proteome_2_15 Scan 21706 Method FTMS; HCD Score 54.78 m/z 672.86



Raw file 20180707_MaS_A375SR_ML_proteome_2_15 Scan 26716 Method FTMS; HCD Score 57.53 m/z 655.38



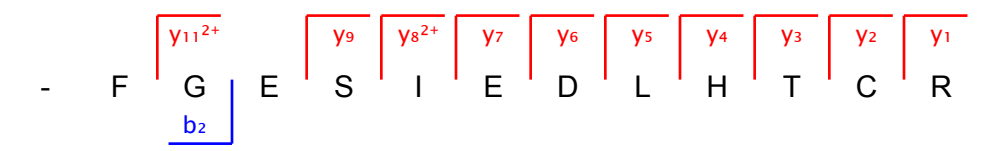
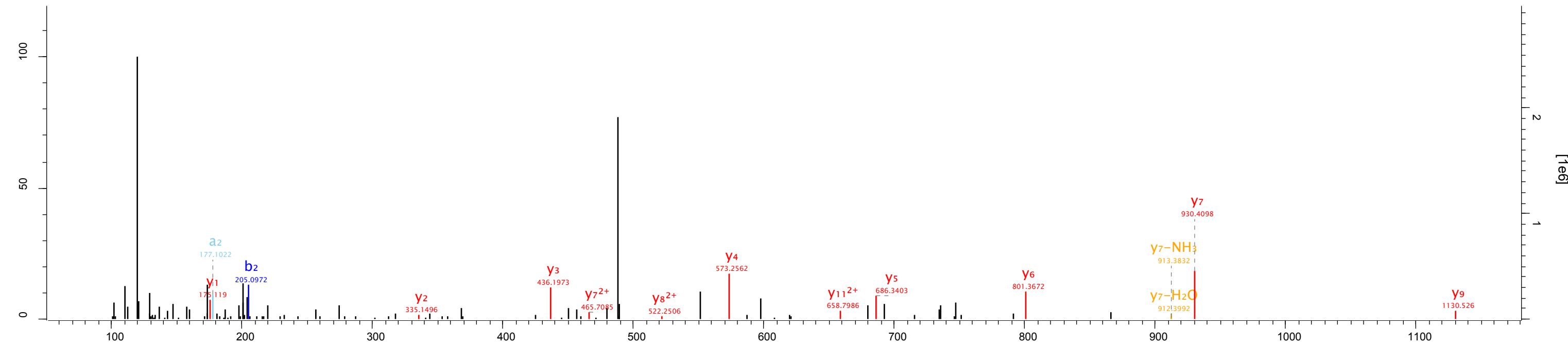


- L Q W T E V D S D S V P A F Y R -

Fragmentation sites are indicated by boxes below the amino acid sequence:

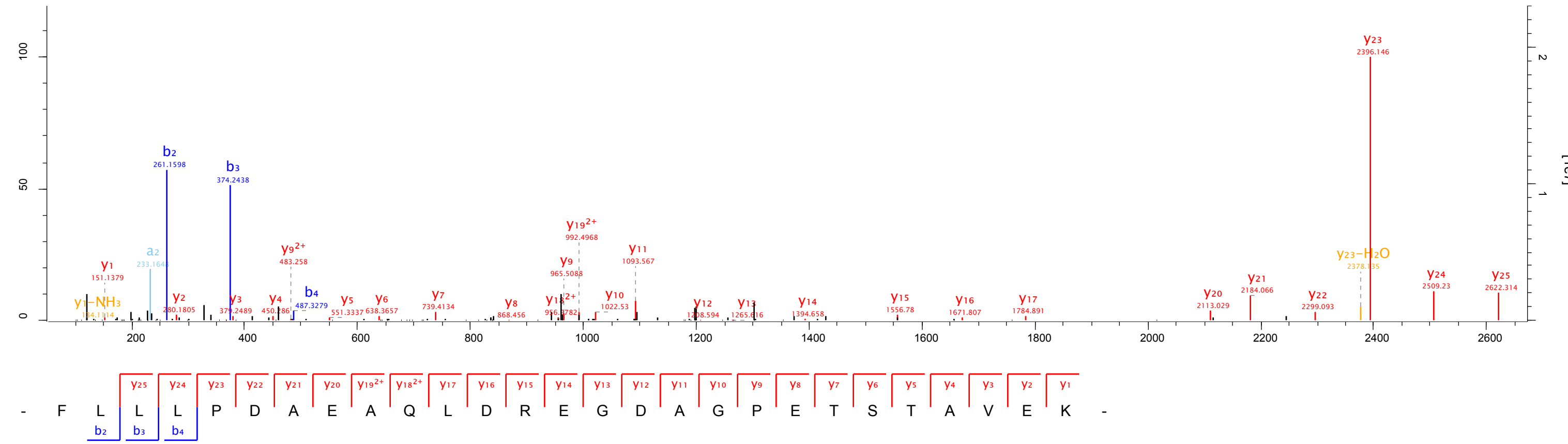
- Red boxes (y ions): W, T, E, V, D, S, D, S, V, P, A, F, Y, R
- Blue boxes (b ions): Q, W, T, E, V

Raw file 20180707_MaS_A375SR_ML_proteome_2_16 Scan 15036 Method FTMS; HCD Score 55.04 m/z 488.56 Gene names PIGX



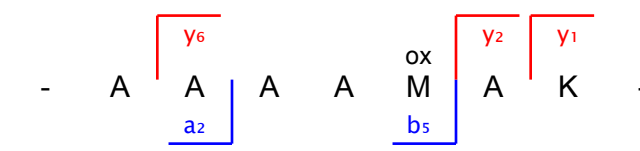
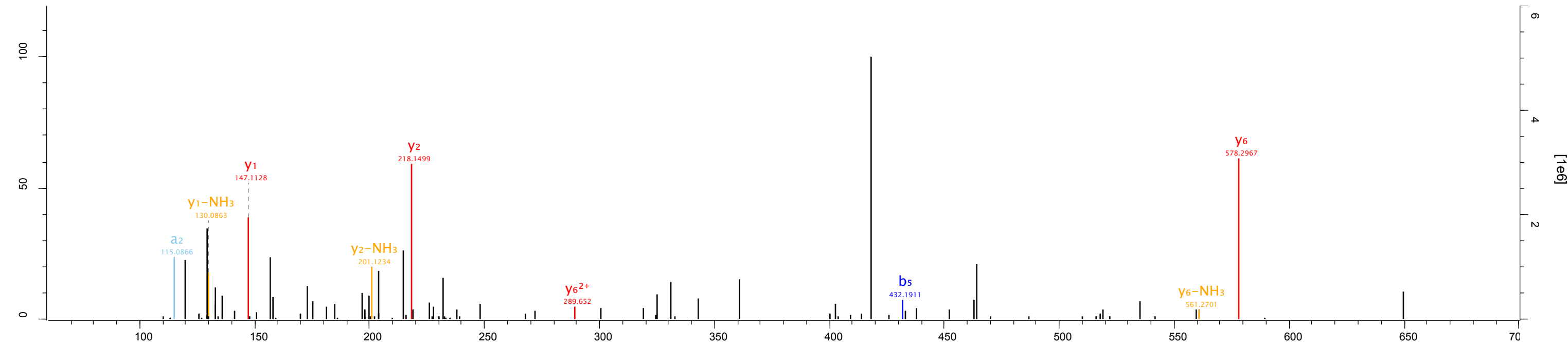
Raw file
20180707_MaS_A375SR_ML_proteome_2_16

Scan: 27616
Method: FTMS; HCD
Score: 88.71
m/z: 961.83
Gene names: TMEM128



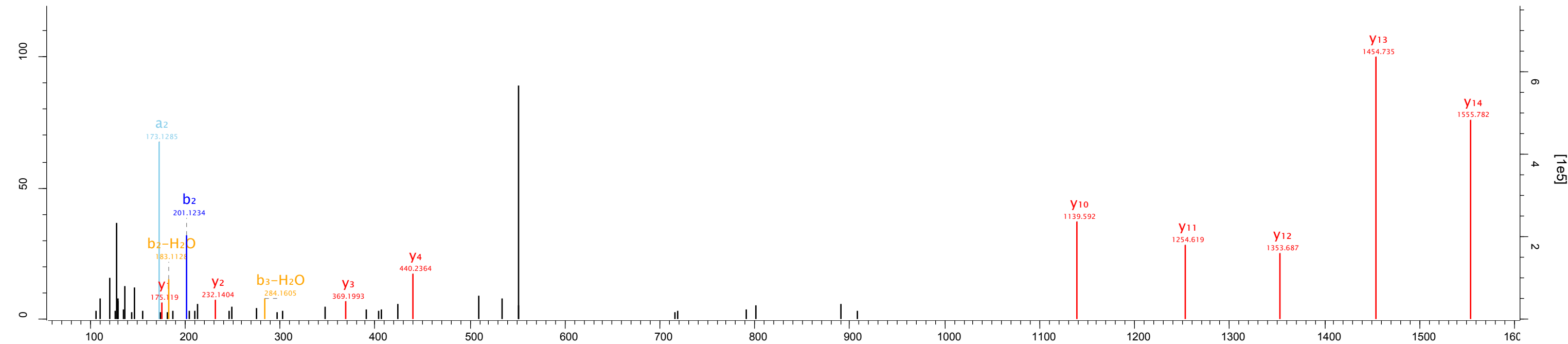
Raw file
20180707_MaS_A375SR_ML_proteome_2_16

Scan 2796 Method FTMS; HCD Score 57.45 m/z 325.17

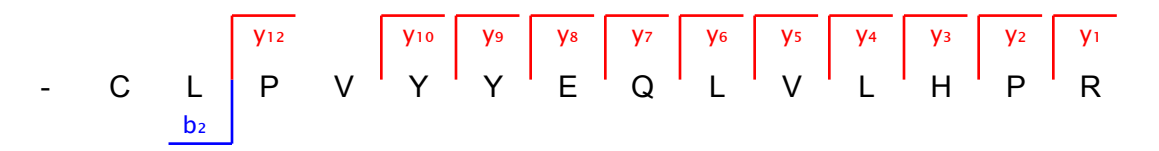
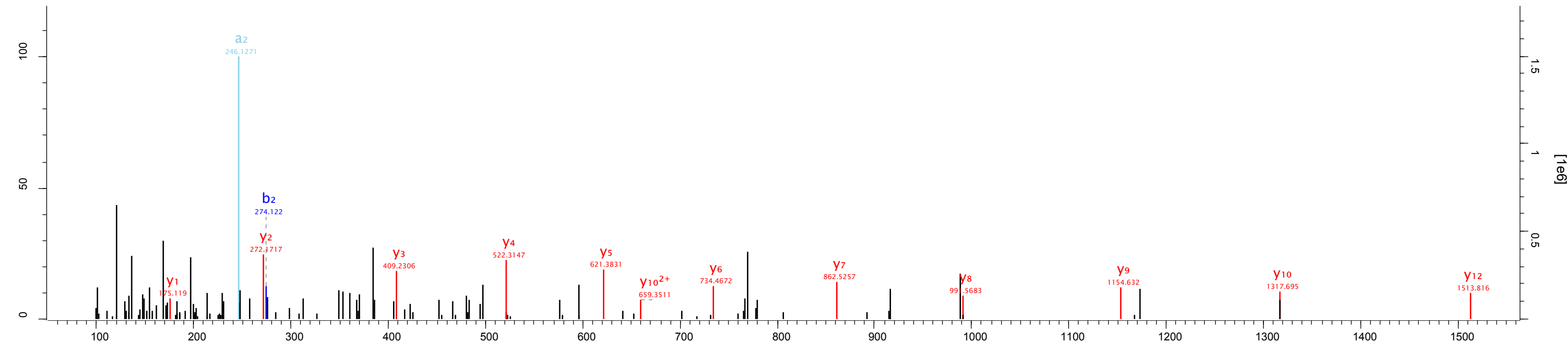


Raw file
20180707_MaS_A375SR_ML_proteome_2_17

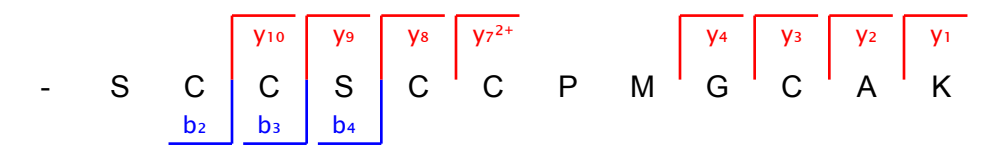
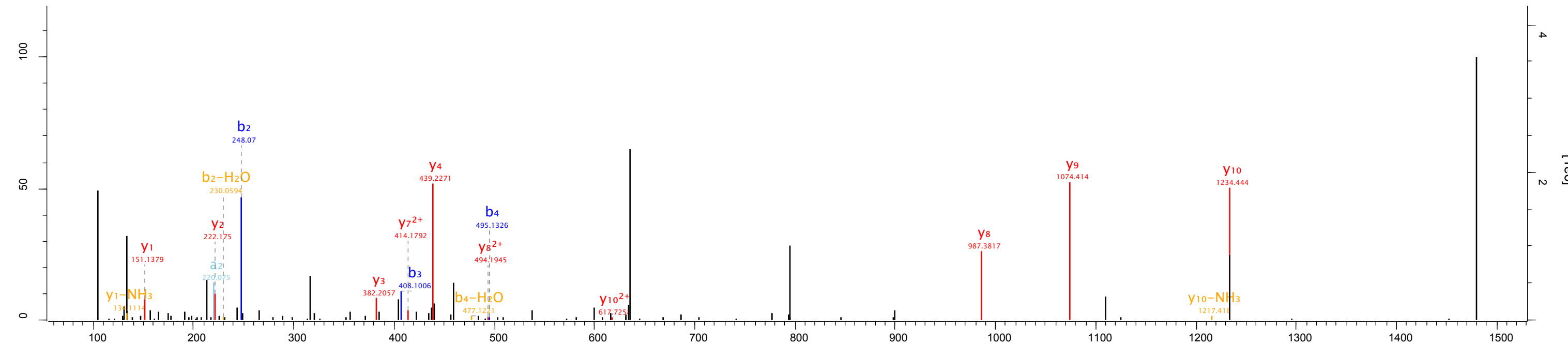
Scan 10316 Method FTMS; HCD Score 38.38 m/z 552.29 Gene names LSM10



Raw file 20180707_MaS_A375SR_ML_proteome_2_17
 Scan 27536 Method FTMS; HCD Score 65.04 m/z 596.32 Gene names TPST2

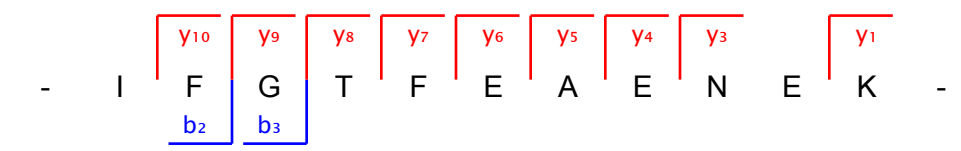
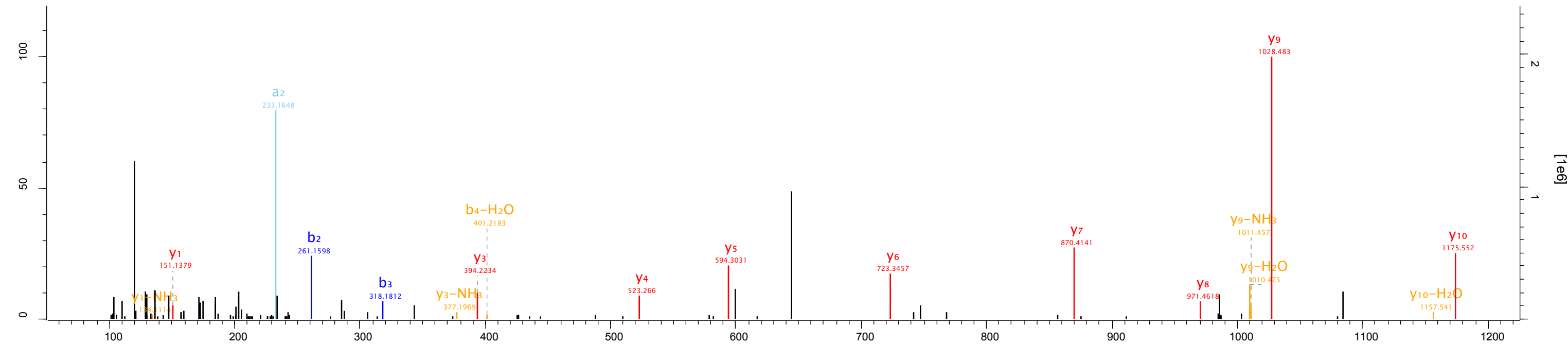


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 Scan 6156 Method FTMS; HCD Score 58.17 m/z 741.26 Gene names MT1L



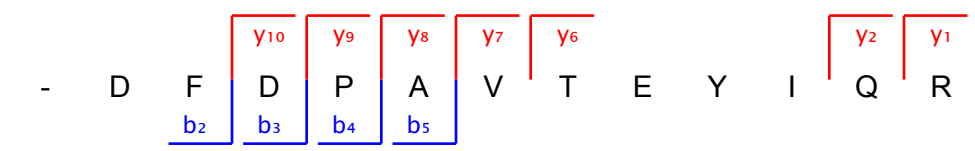
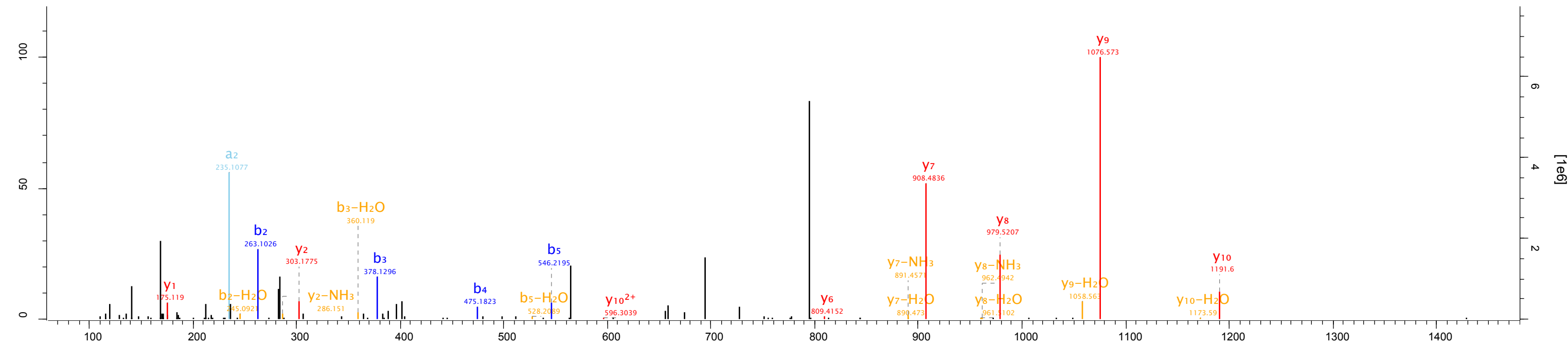
Raw file
20180707_MaS_A375SR_ML_proteome_2_18

Scan 18356 Method FTMS; HCD Score 85.81 m/z 644.82 Gene names AGMO

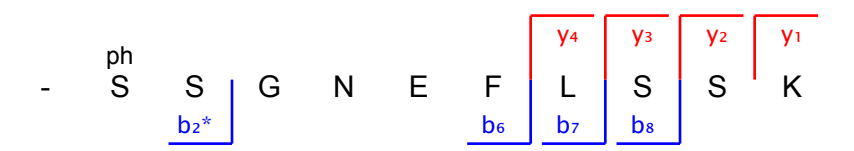
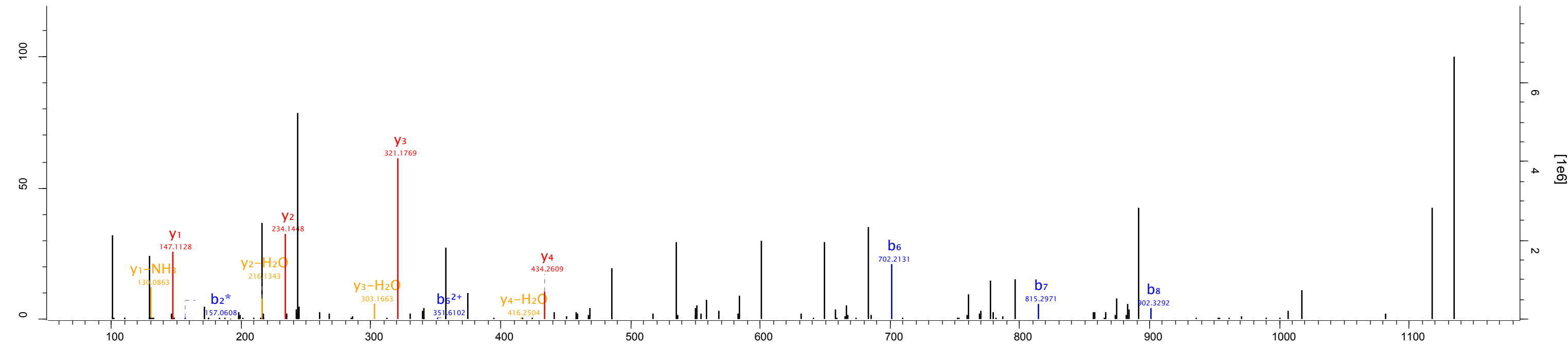


Raw file
20180707_MaS_A375SR_ML_proteome_2_19

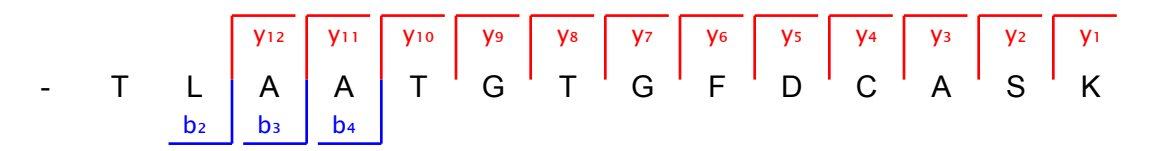
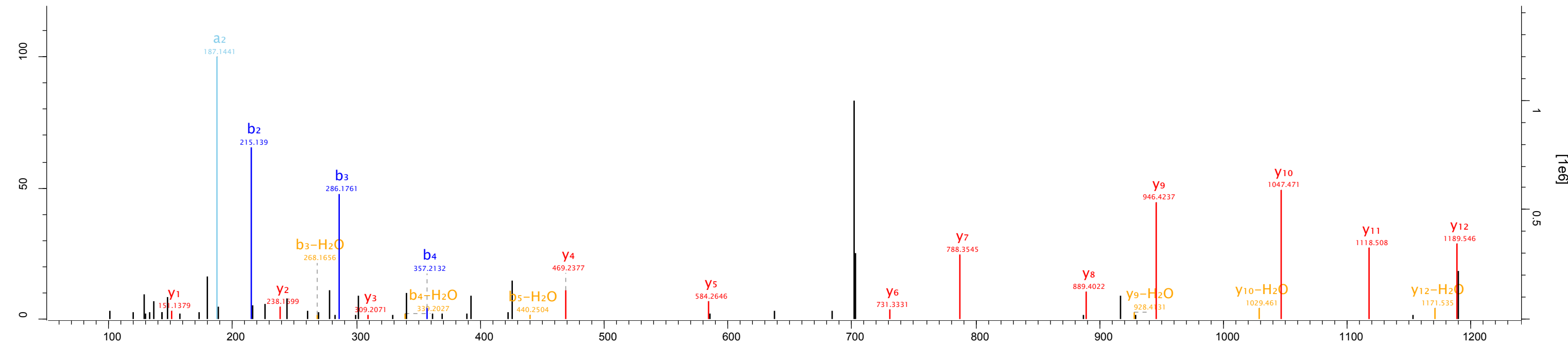
Scan 24656 Method FTMS; HCD Score 103.21 m/z 727.86 Gene names FBP1



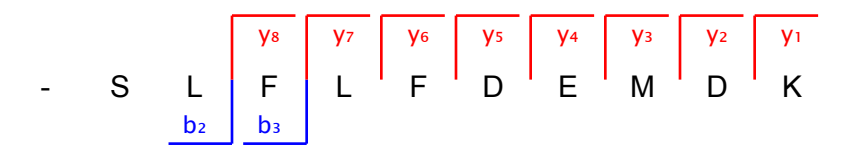
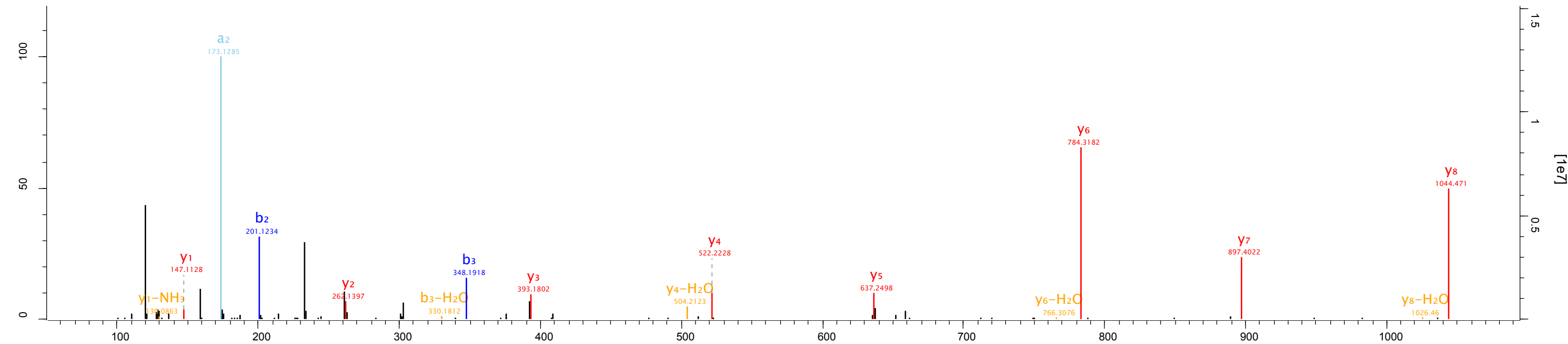
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 Scan 3436 Method FTMS; HCD Score 85.53 m/z 568.24 Gene names MAP3K19

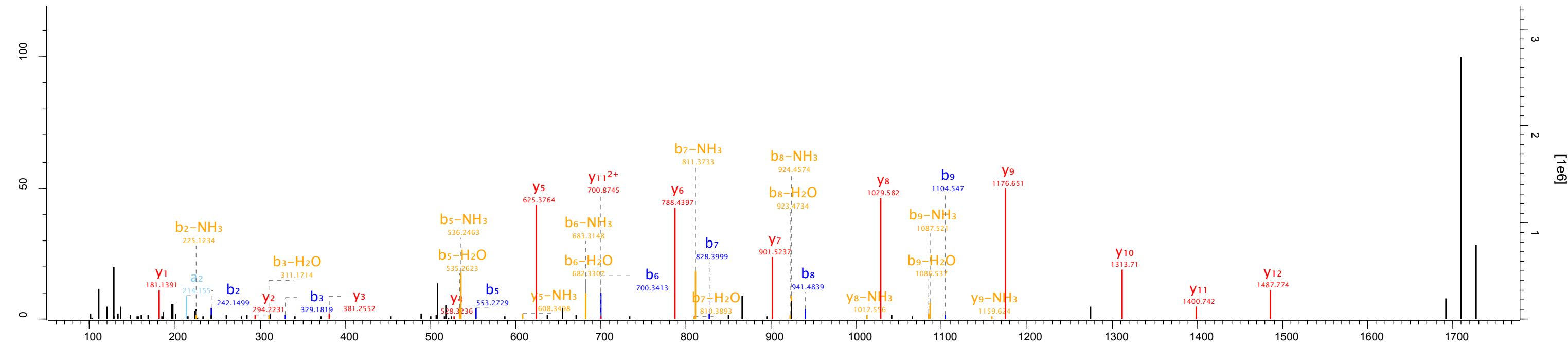


Raw file 20180707_MaS_A375SR_ML_proteome_2_22 Scan 12806 Method FTMS; HCD Score 71.98 m/z 702.84 Gene names ODC1



Raw file 20180707_MaS_A375SR_ML_proteome_2_23 Scan 29686 Method FTMS; HCD Score 81.02 m/z 622.8 Gene names TOR2A





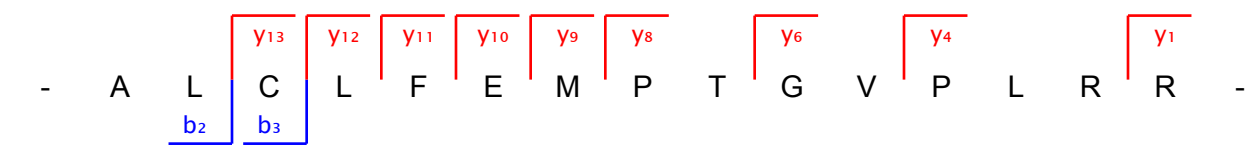
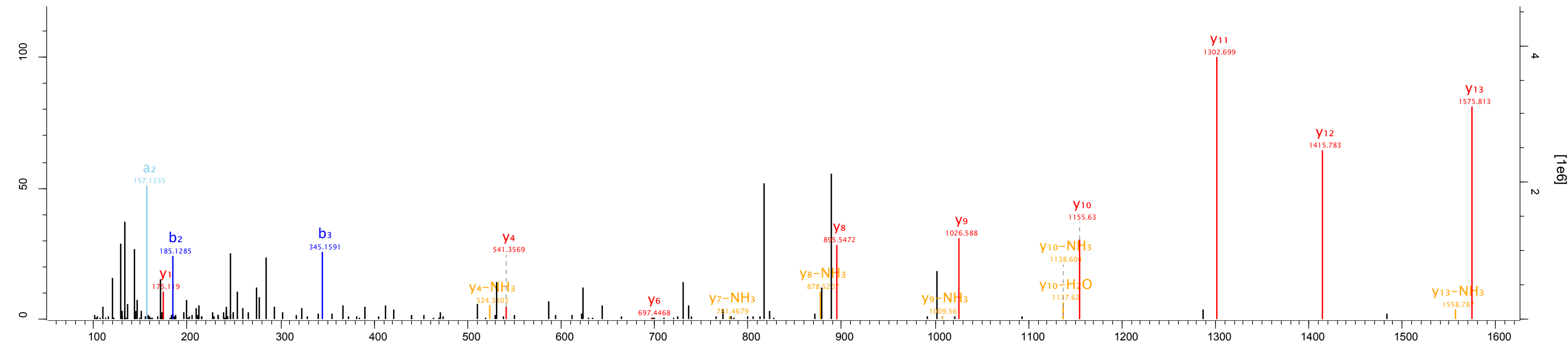
- Q L S S H F Q I Y P F S L R -

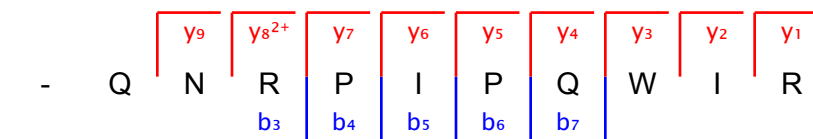
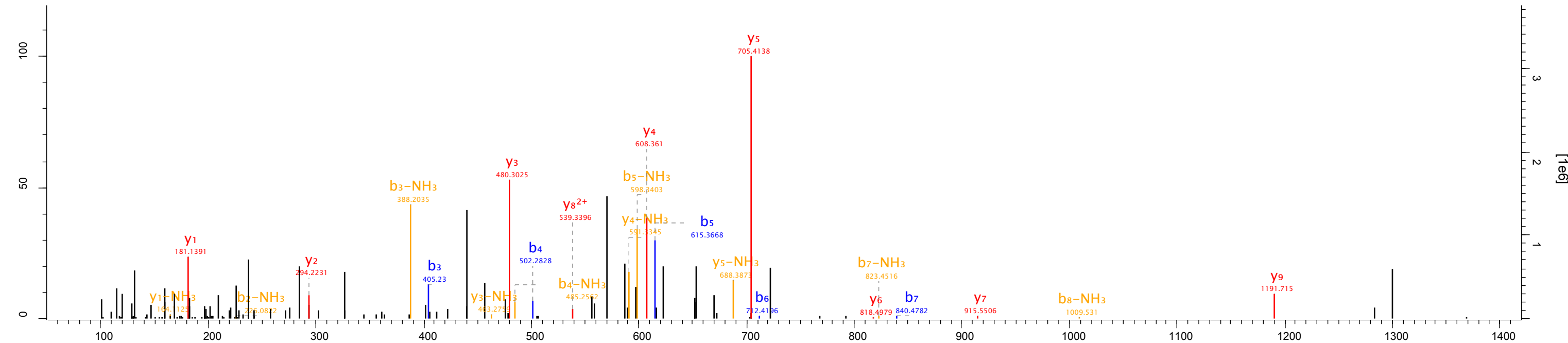
Fragmentation sites are indicated by boxes below the sequence:

- Red boxes: y12 (S), y11 (S), y10 (H), y9 (F), y8 (Q), y7 (I), y6 (Y), y5 (P), y4 (F), y3 (S), y2 (L), y1 (R)
- Blue boxes: b2 (L), b3 (S), b5 (H), b6 (F), b7 (Q), b8 (I), b9 (Y)

Raw file
20180707_MaS_A375SR_ML_proteome_2_25

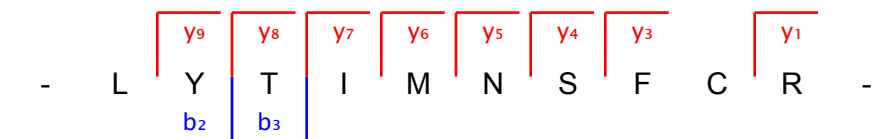
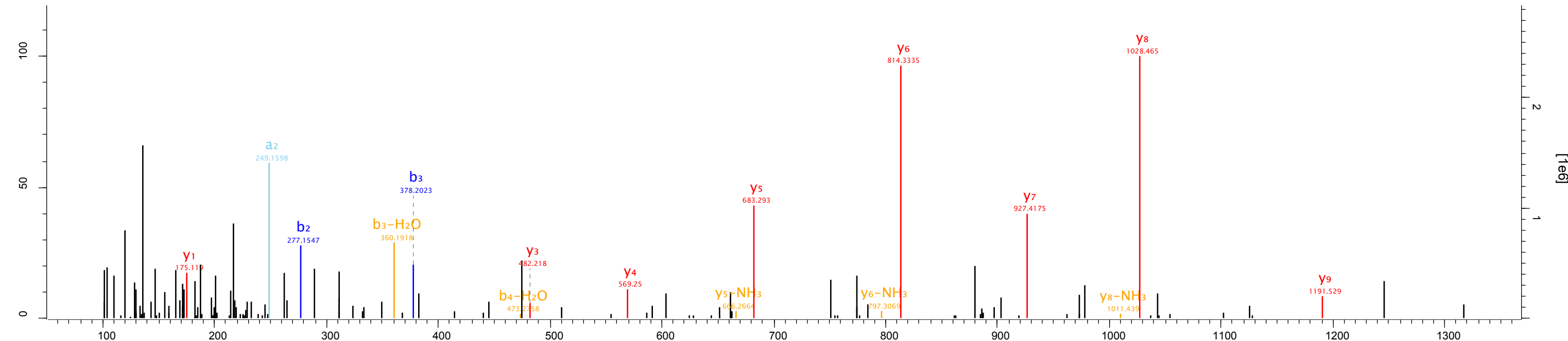
Scan 28346 Method FTMS; HCD Score 74.48 m/z 587.32 Gene names AOC1



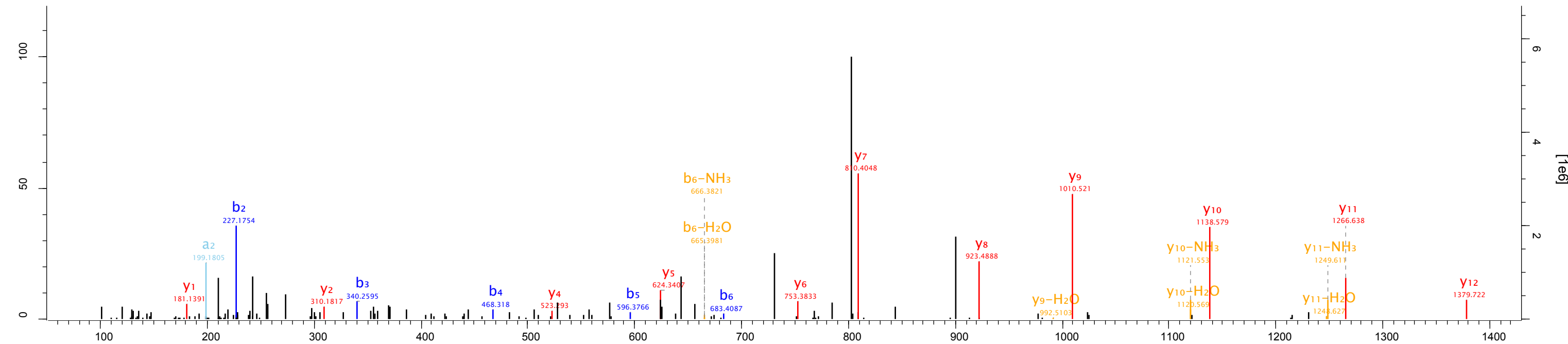


Raw file
20180707_MaS_A375SR_ML_proteome_2_27

Scan 24916 Method FTMS; HCD Score 63.62 m/z 652.81 Gene names CYTL1



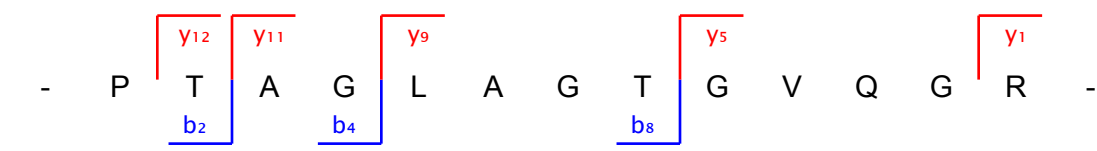
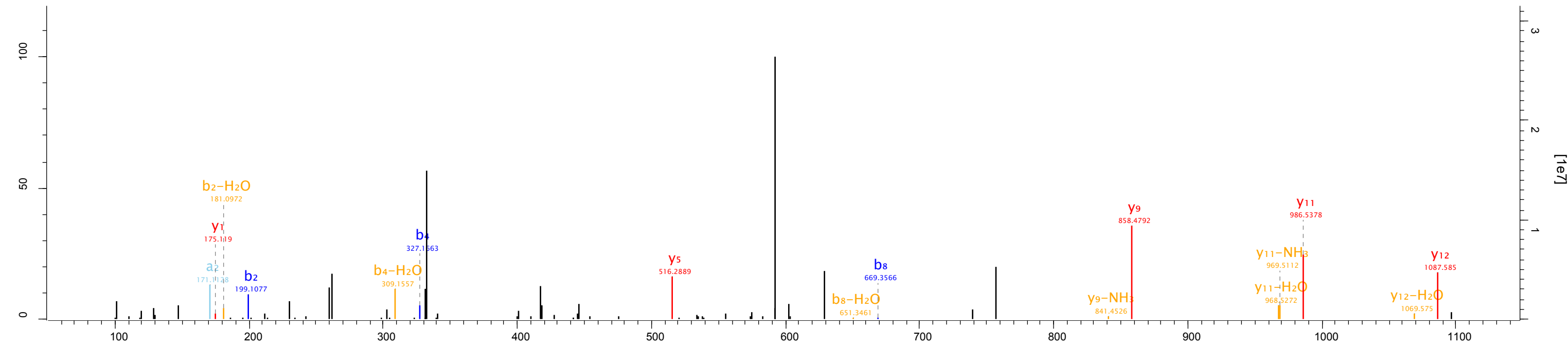
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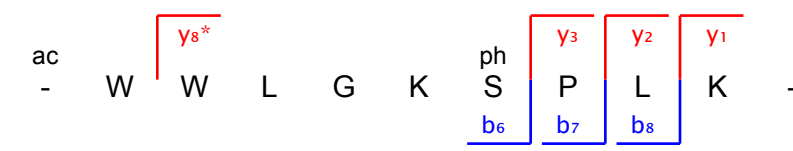
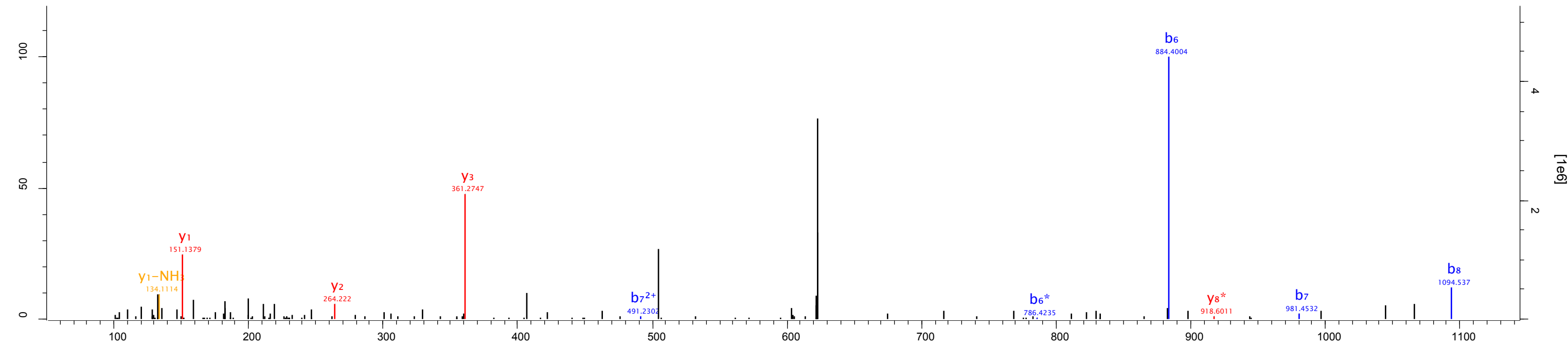
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b₂
b₃
b₄
b₅
b₆
y₁
y₂
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y₇
y₈
y₉
y₁₀
y₁₁
y₁₂

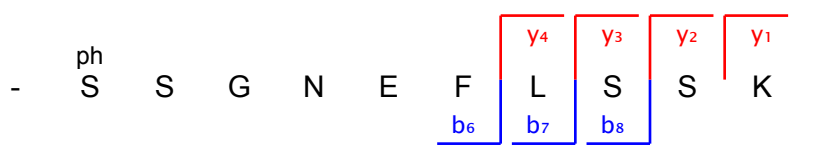
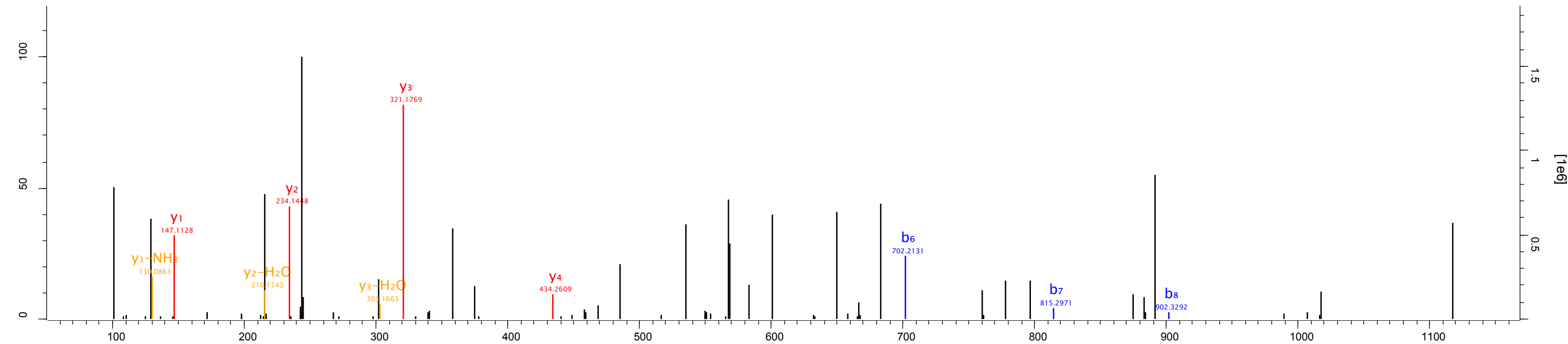
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 Scan 8146 Method FTMS; HCD Score 55.26 m/z 592.82

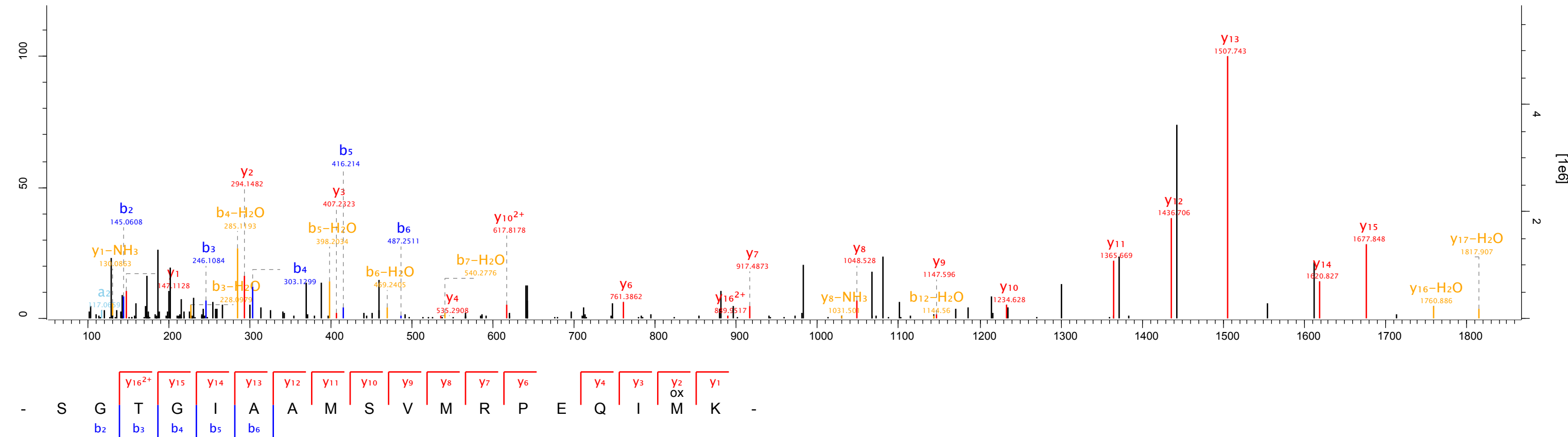


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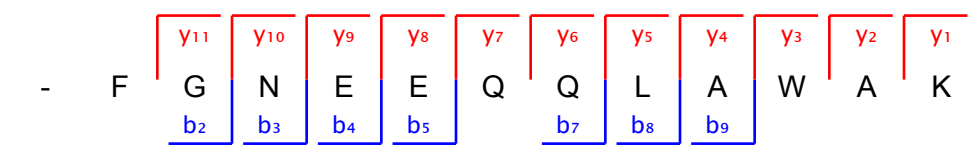
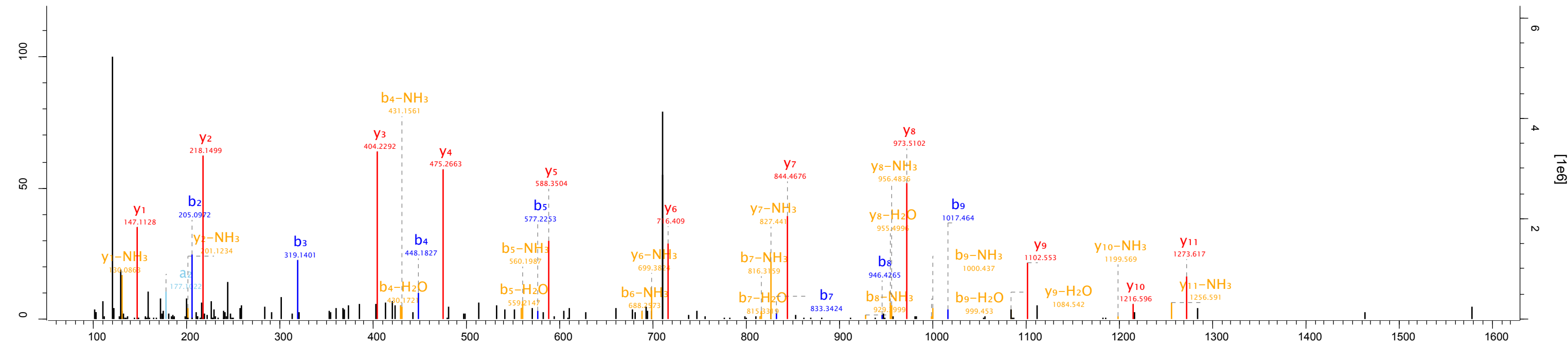
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 Scan 3496 Method FTMS; HCD Score 60.17 m/z 568.24 Gene names MAP3K19

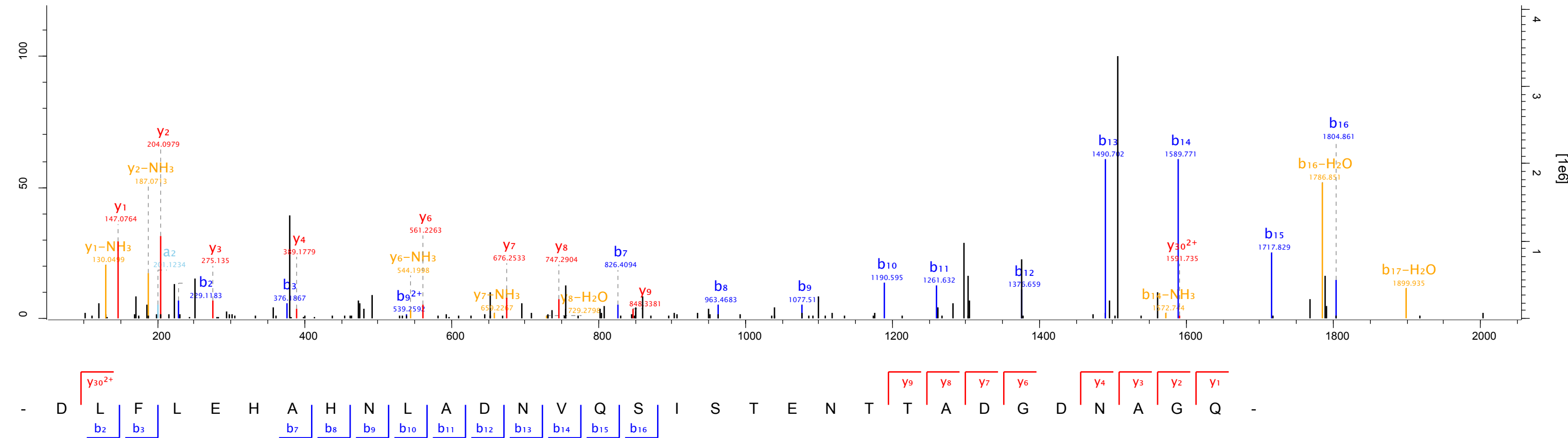




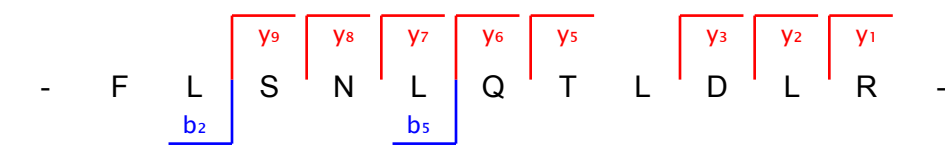
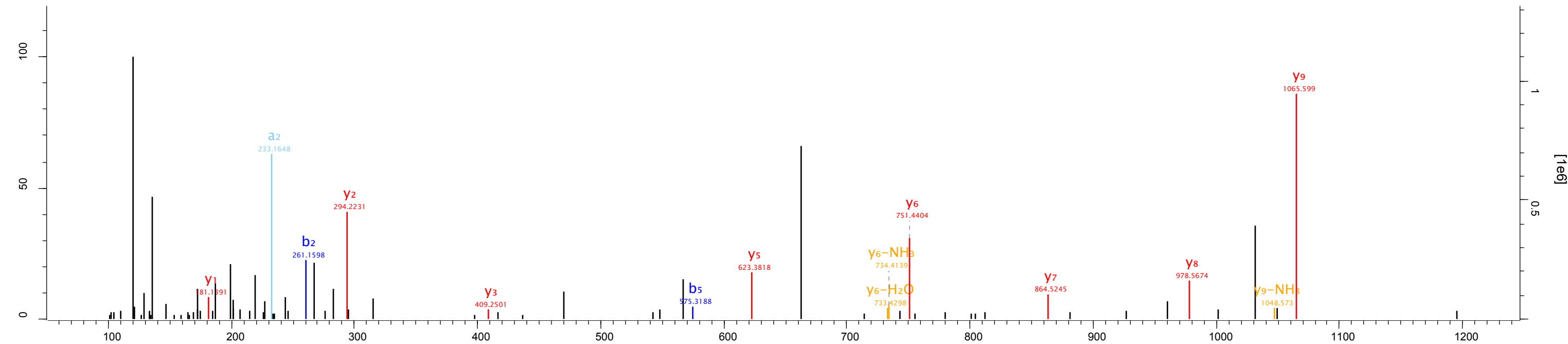
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20180707_MaS_A375SR_ML_proteome_22

Scan 17316 Method FTMS; HCD Score 216.53 m/z 710.85 Gene names SPATA22

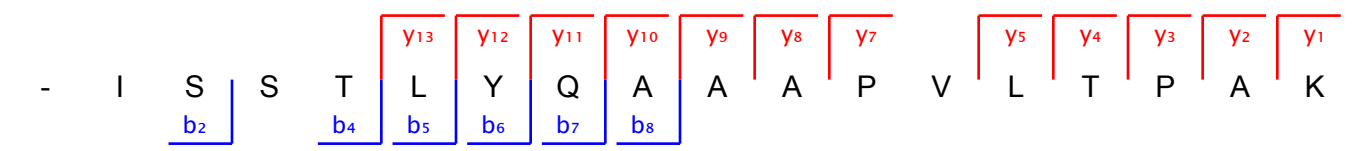
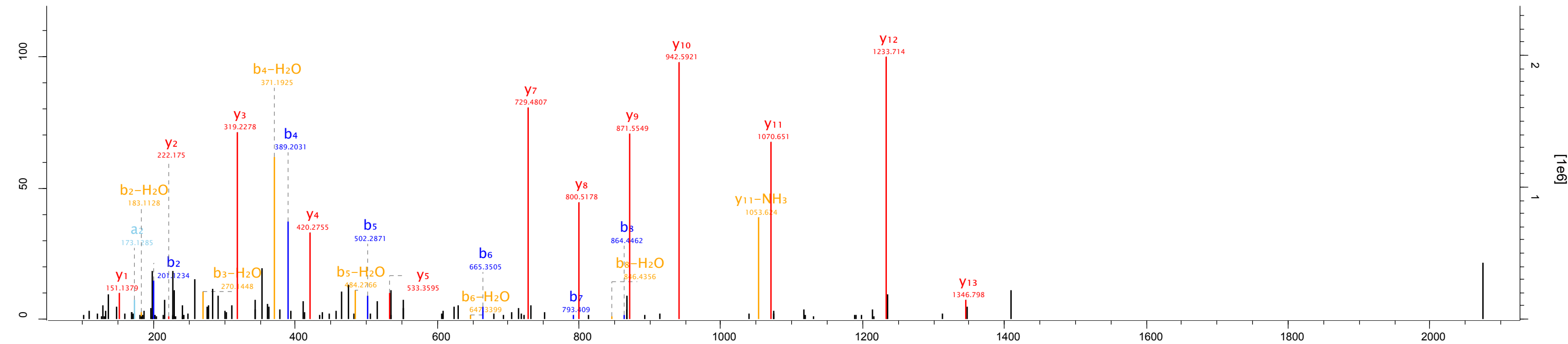




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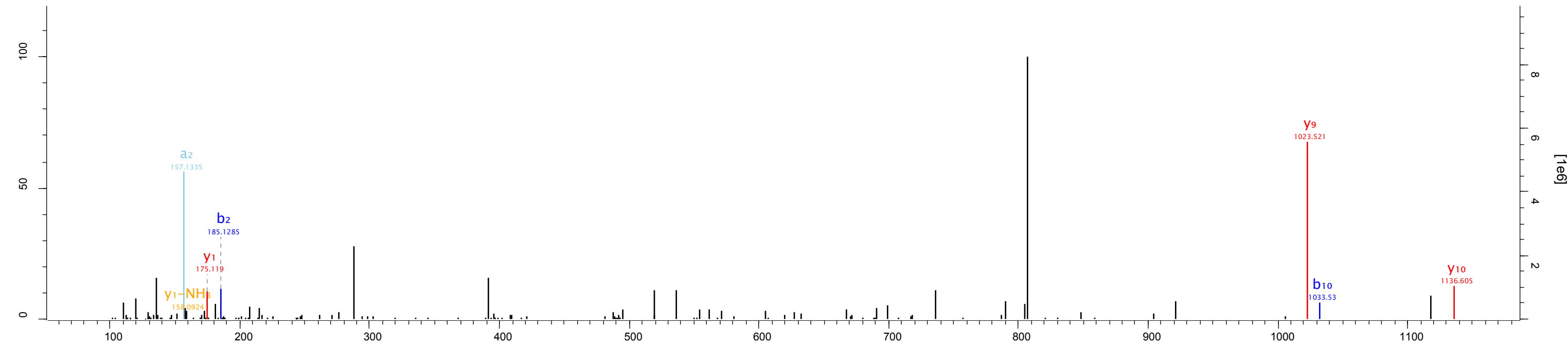


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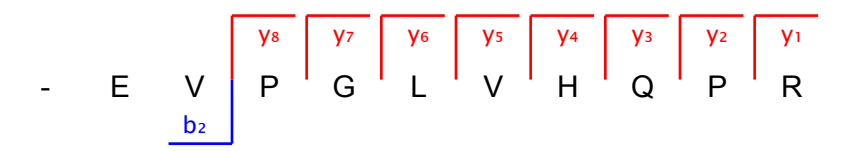
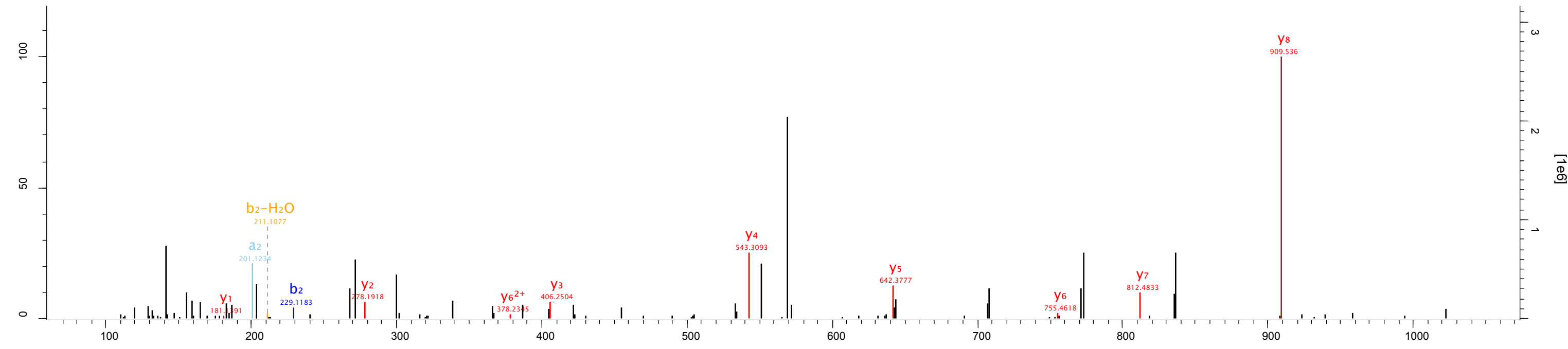


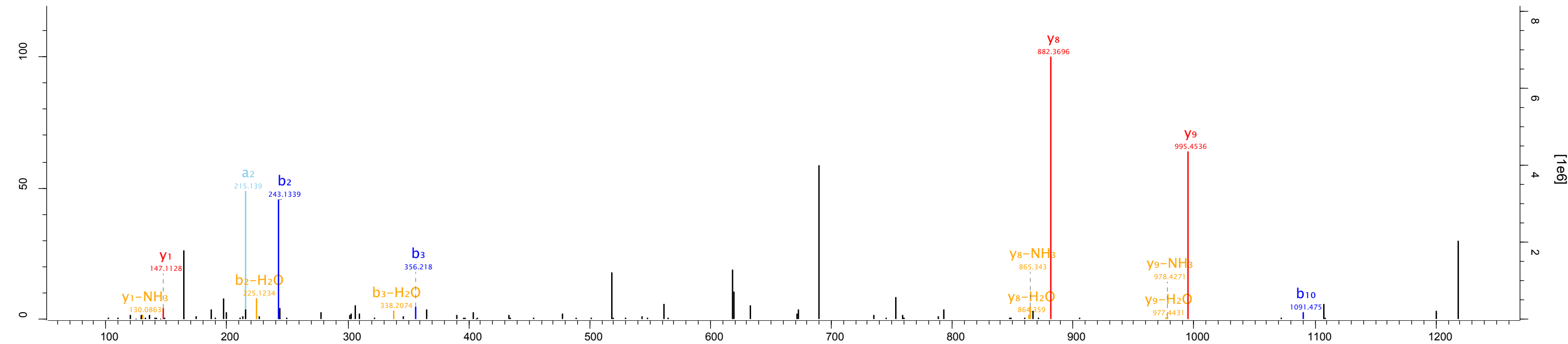
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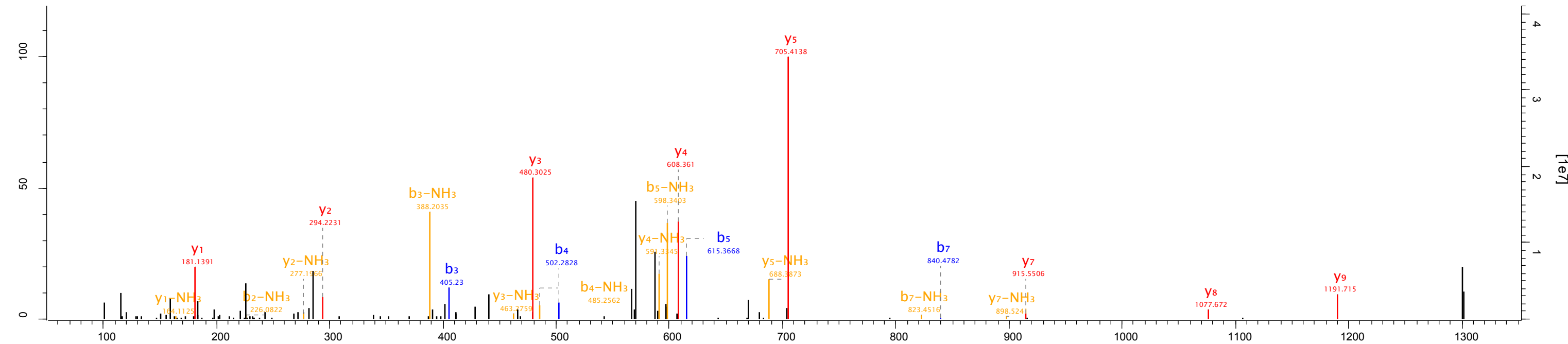
Scan 13666 Method FTMS; HCD Score 40.5 m/z 403.22



Raw file 20180707_MaS_A375SR_ML_proteome_24 Scan 9706 Method FTMS; HCD Score 37.7 m/z 569.33 Gene names C1orf21



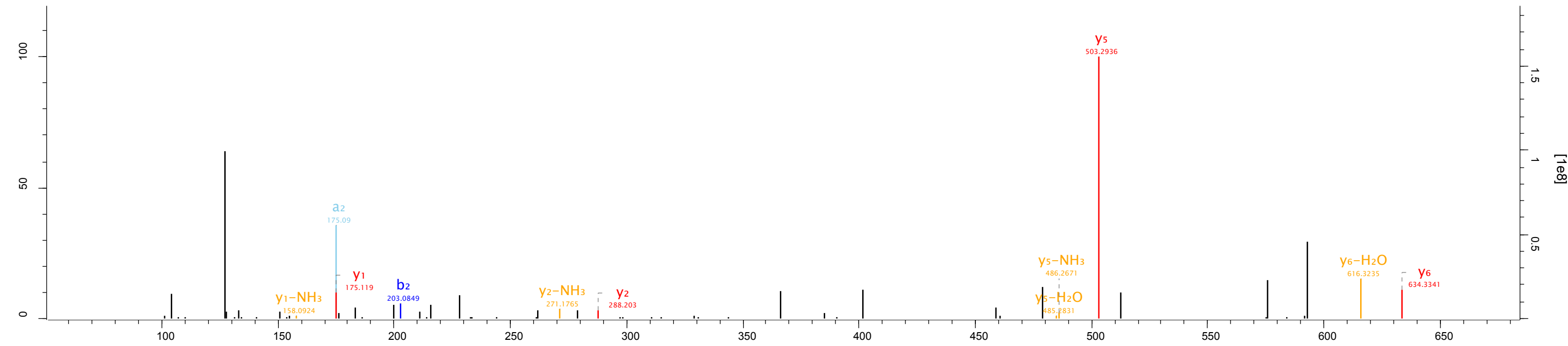




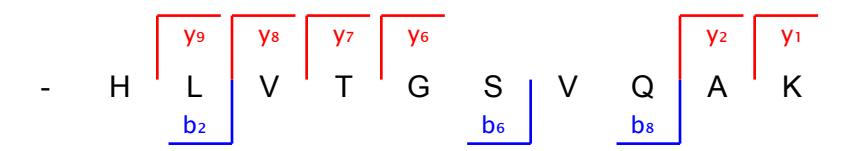
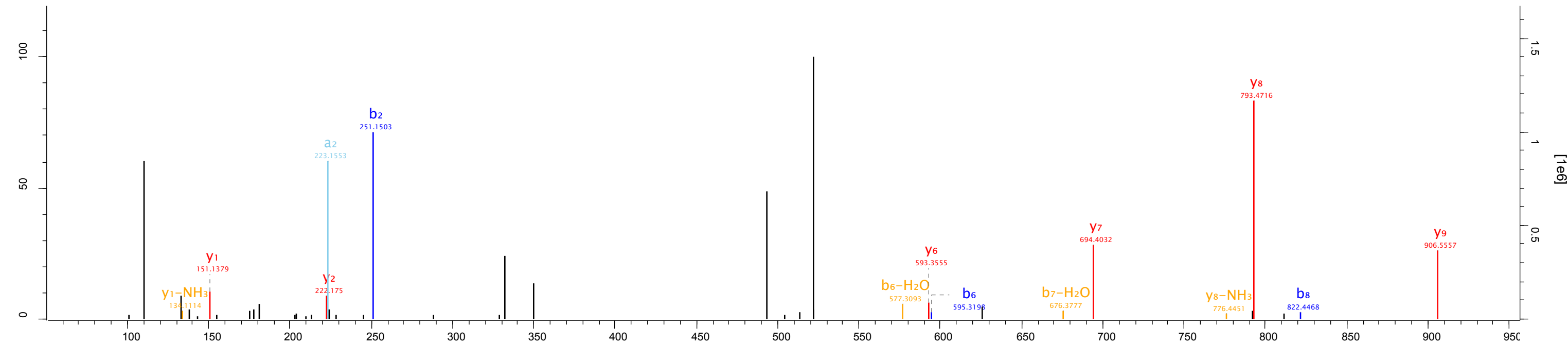
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 (Red boxes above: y9, y8, y7, y5, y4, y3, y2, y1)
 (Blue boxes below: b3, b4, b5, b7)

Raw file
20180707_MaS_A375SR_ML_proteome_27

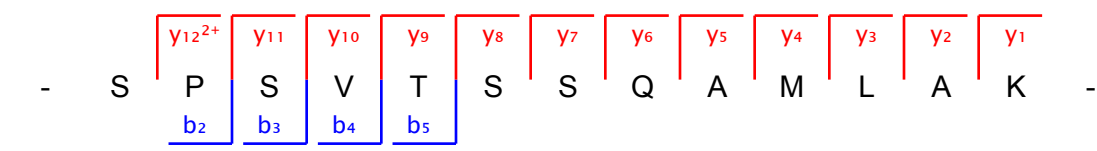
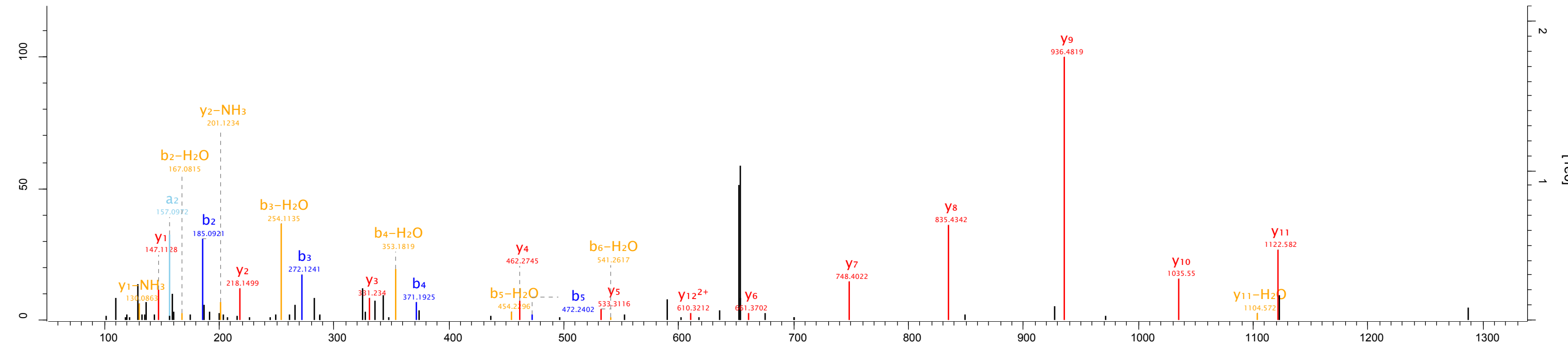
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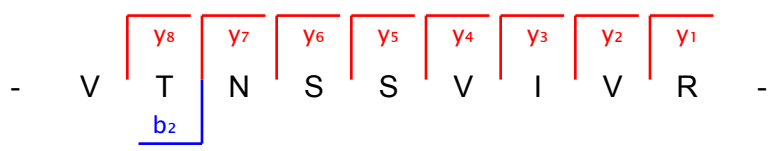
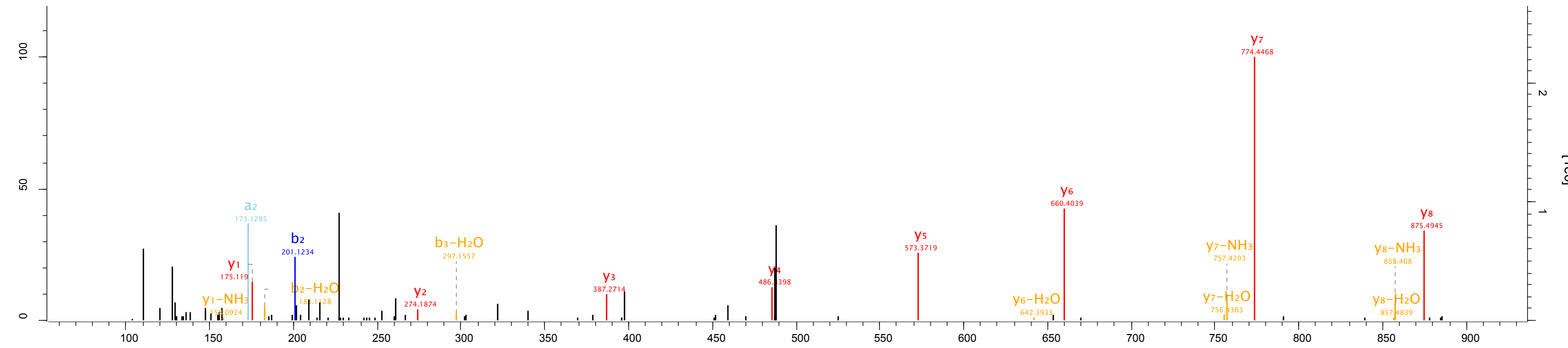
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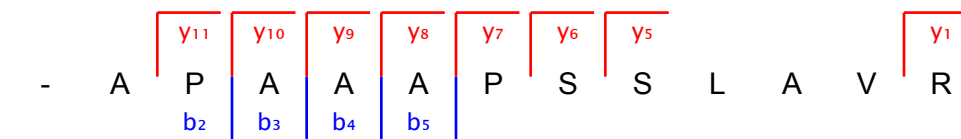
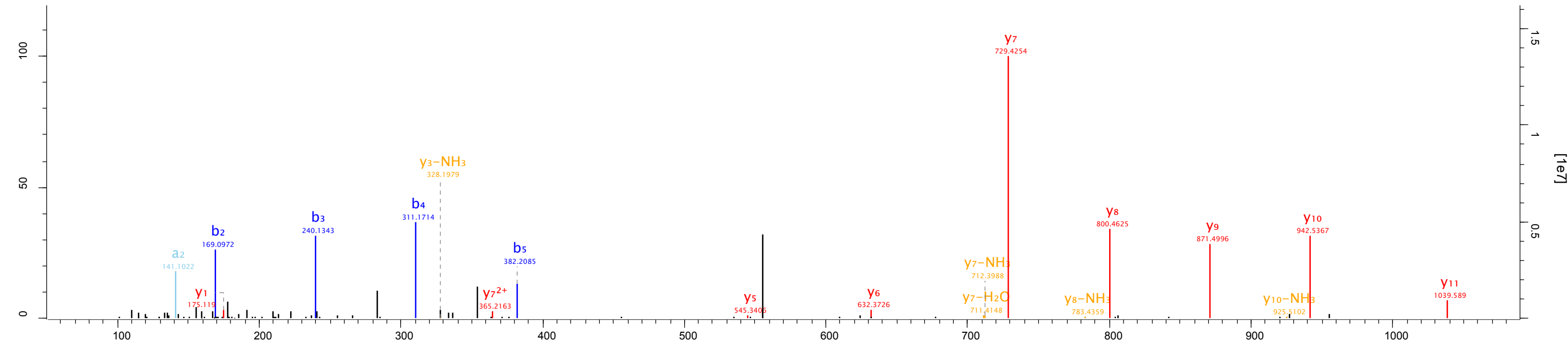
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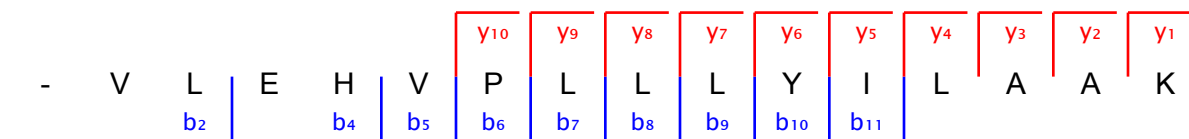
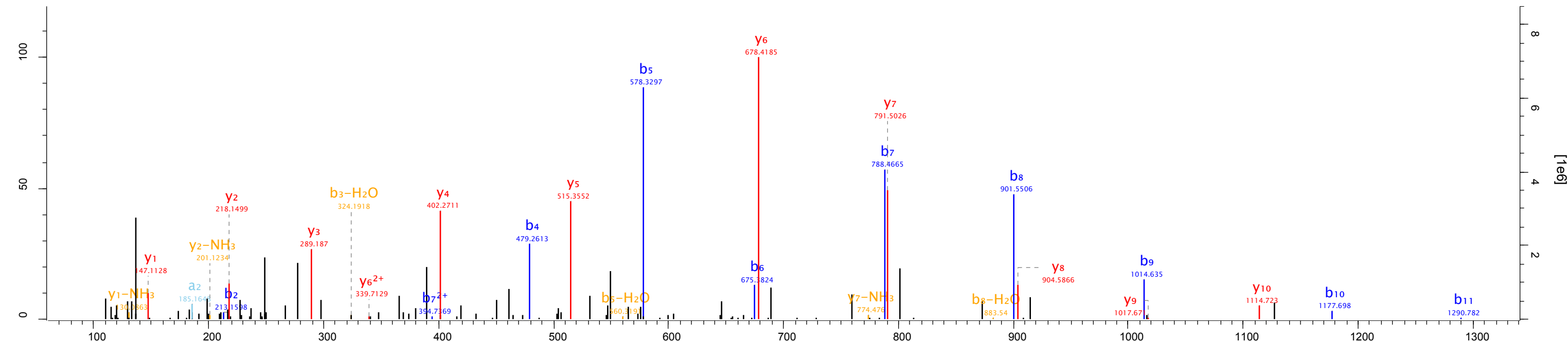


Raw file

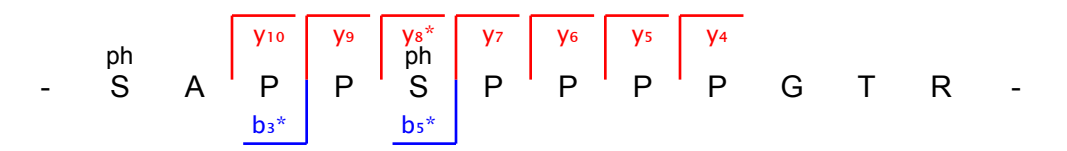
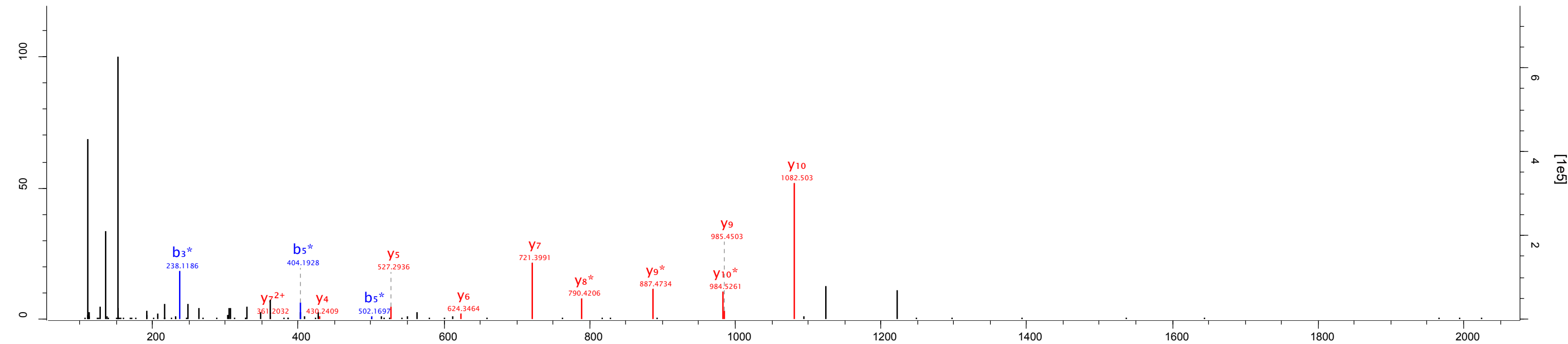
20180707_MaS_A375SR_ML_proteome_30

Scan	Method	Score	m/z
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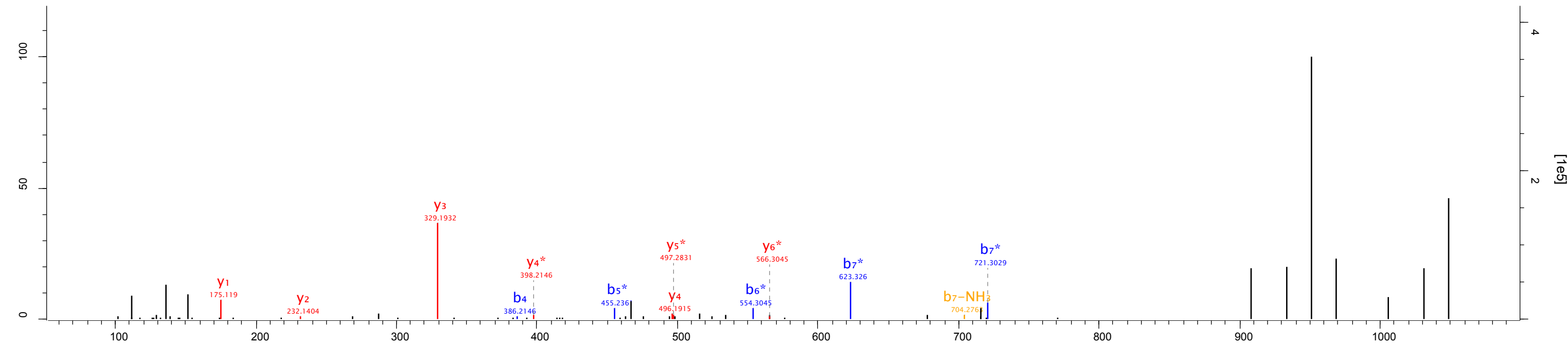




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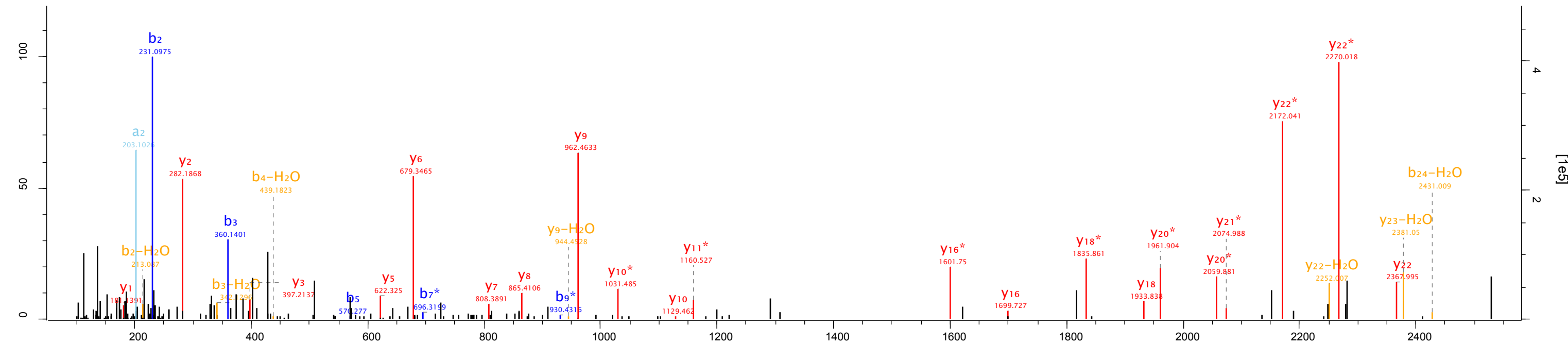
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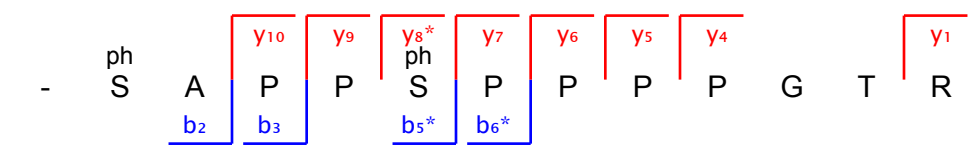
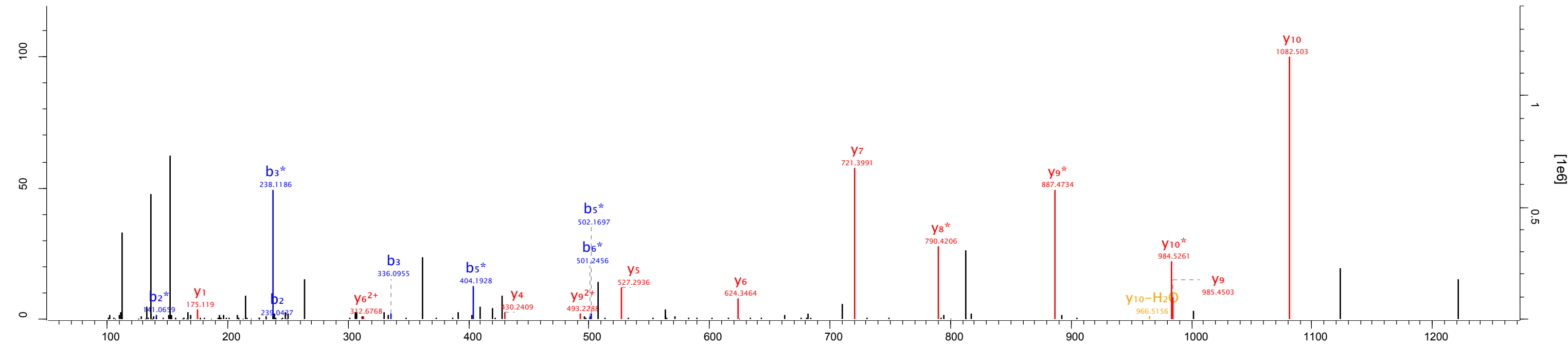
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ph
S y5*
V y4
ph
S y3
P y2
G y1
R -

b4 b5* b6* b7*

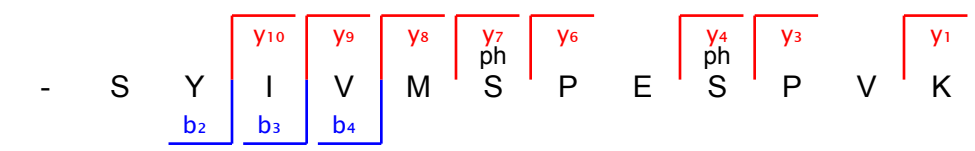
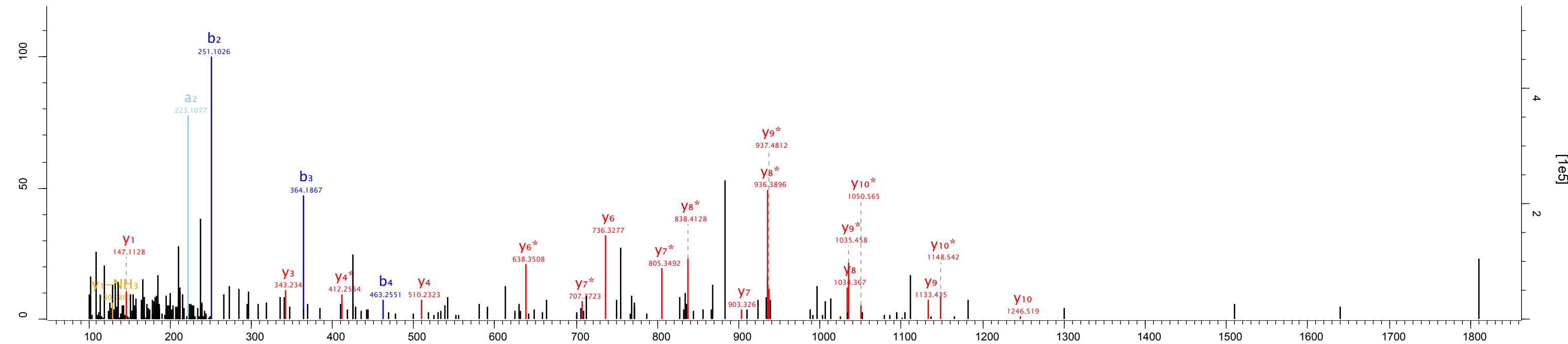
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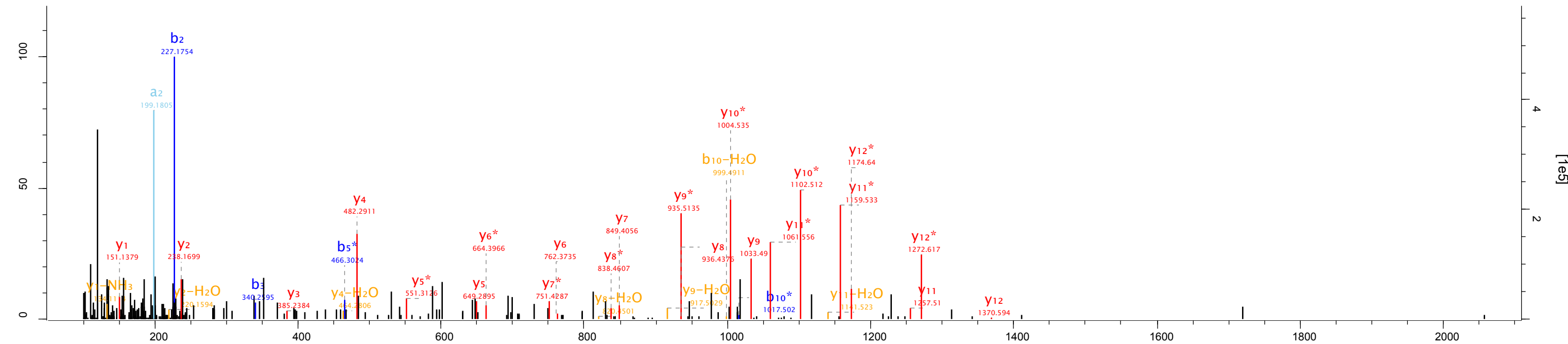
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Raw file 20150812_A375SR_Phospho_BR1_03 Scan 20047 Method FTMS; HCD Score 66.15 m/z 749.31 Gene names ZBTB44



Raw file 20150812_A375SR_Phospho_BR1_03 Scan 28507 Method FTMS; HCD Score 92.91 m/z 798.89 Gene names BCL11A



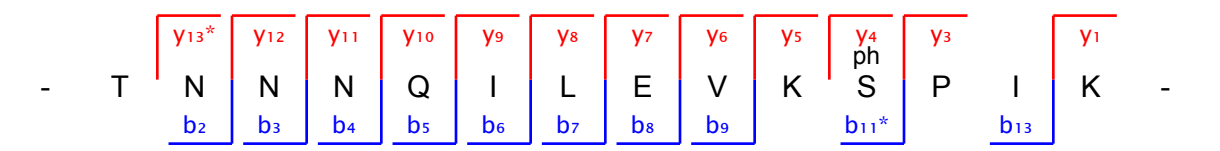
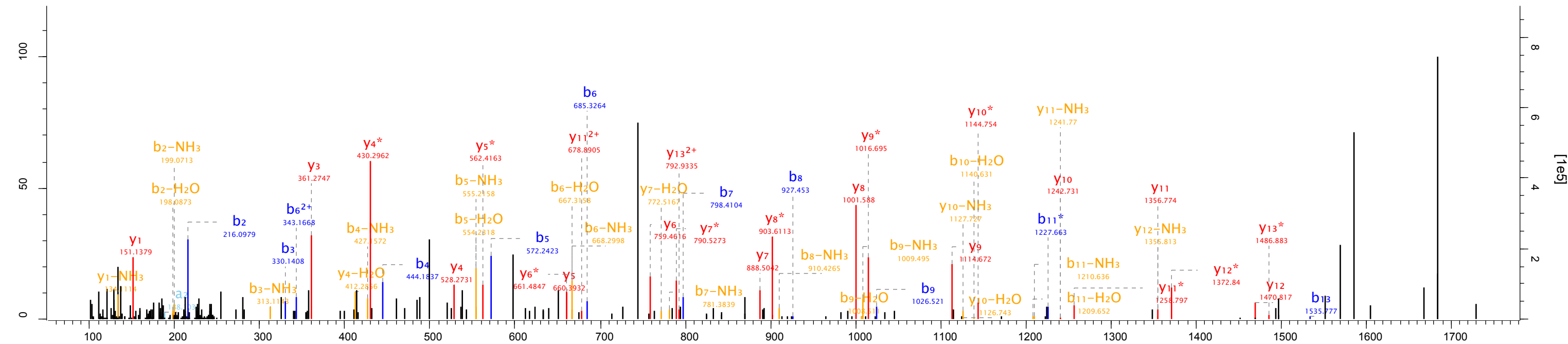
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Fragmentation mapping (b and y ions):

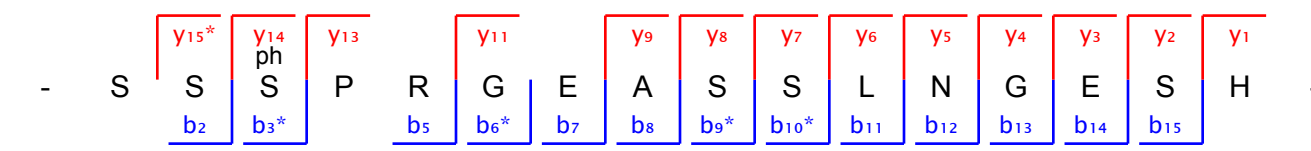
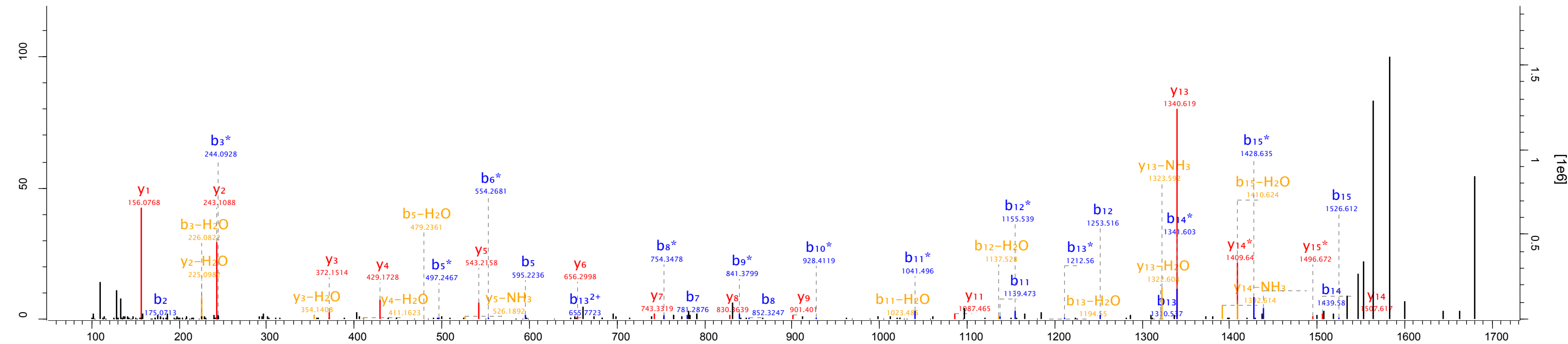
- b₂ (L)
- b₃ (L)
- b₅* (S)
- b₁₀* (S)
- y₁ (K)
- y₂ (S)
- y₃ (F)
- y₄ (P)
- y₅ (S)
- y₅ph (S)
- y₆ (L)
- y₇ (S)
- y₈ (S)
- y₉ (P)
- y₁₀* (S)
- y₁₁ (G)
- y₁₂ (L)

Raw file
20150812_A375SR_Phospho_BR1_06

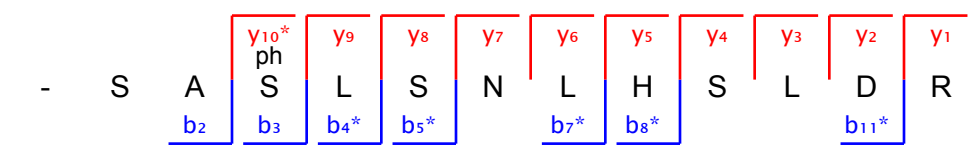
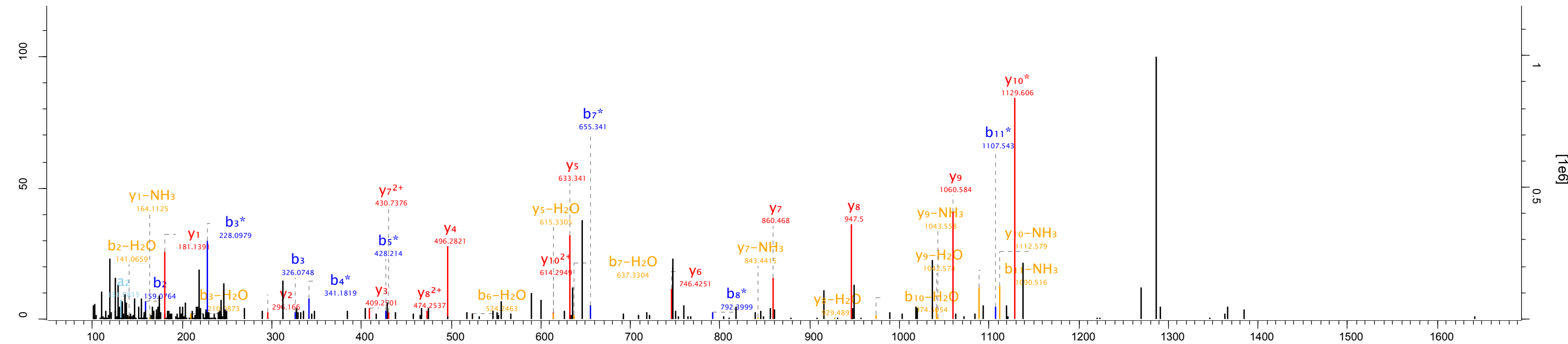
Scan 14007 Method FTMS; HCD Score 264.83 m/z 843.46 Gene names MLLT3



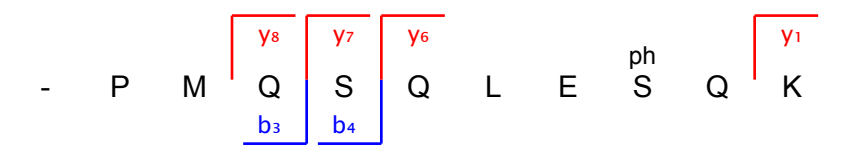
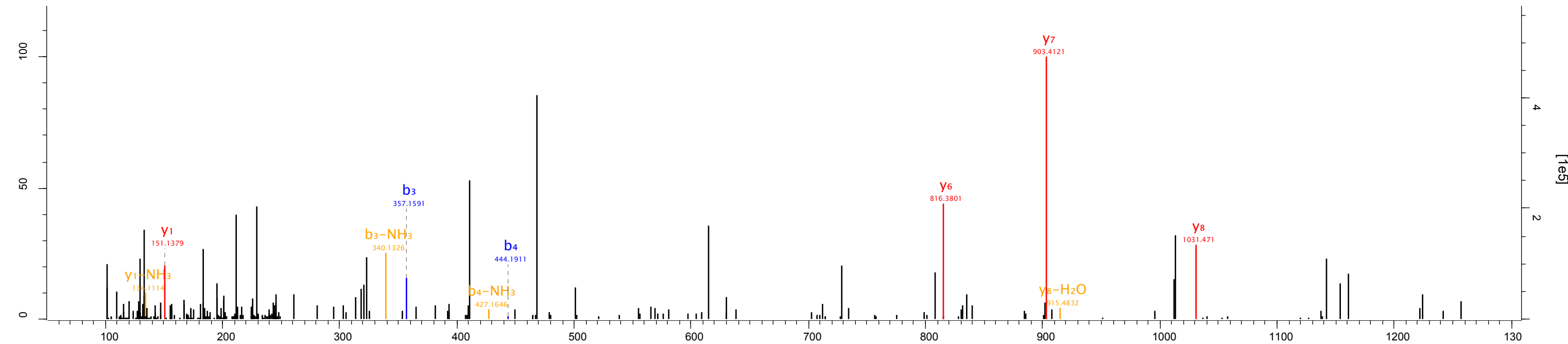
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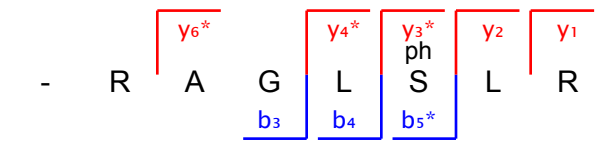
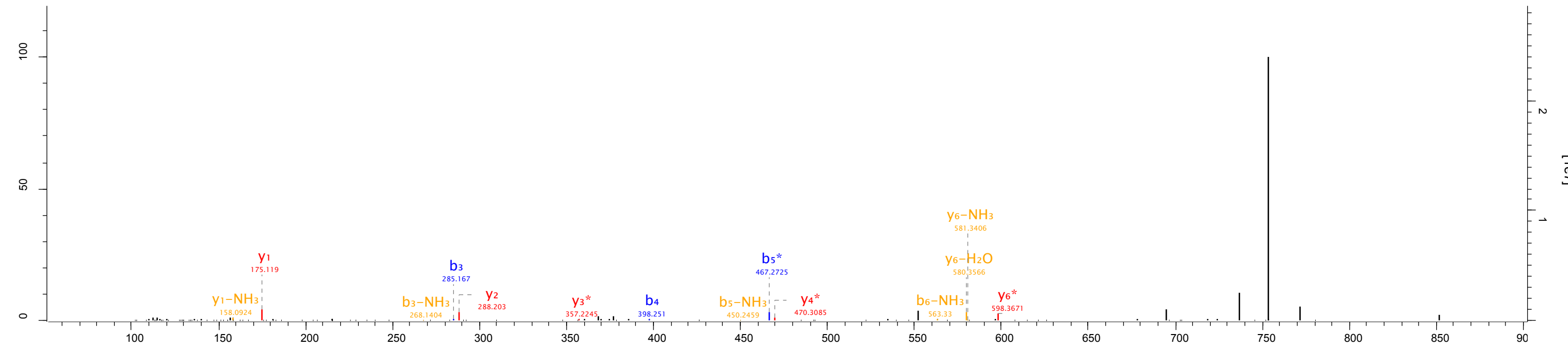
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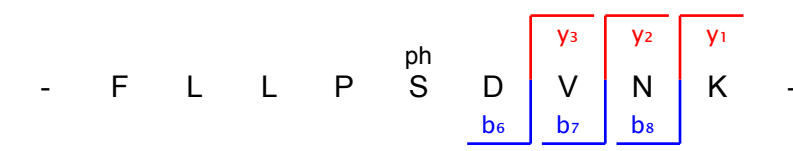
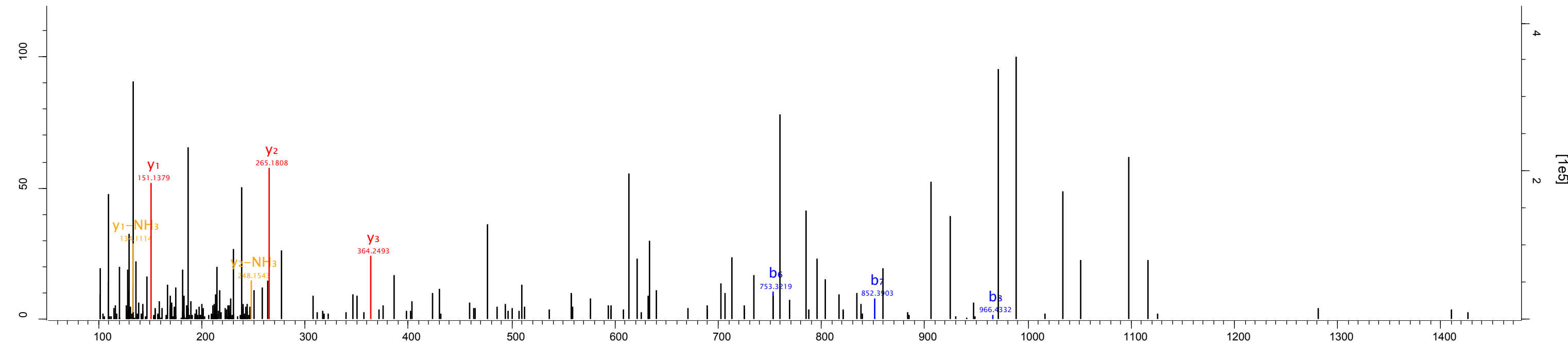
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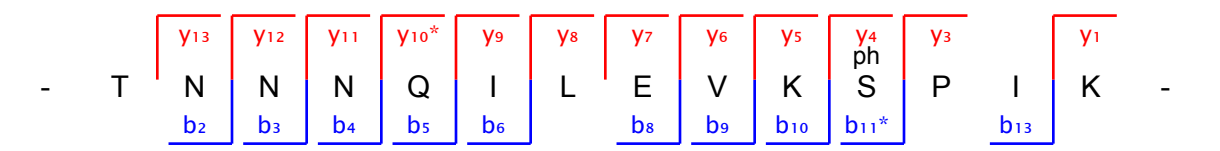
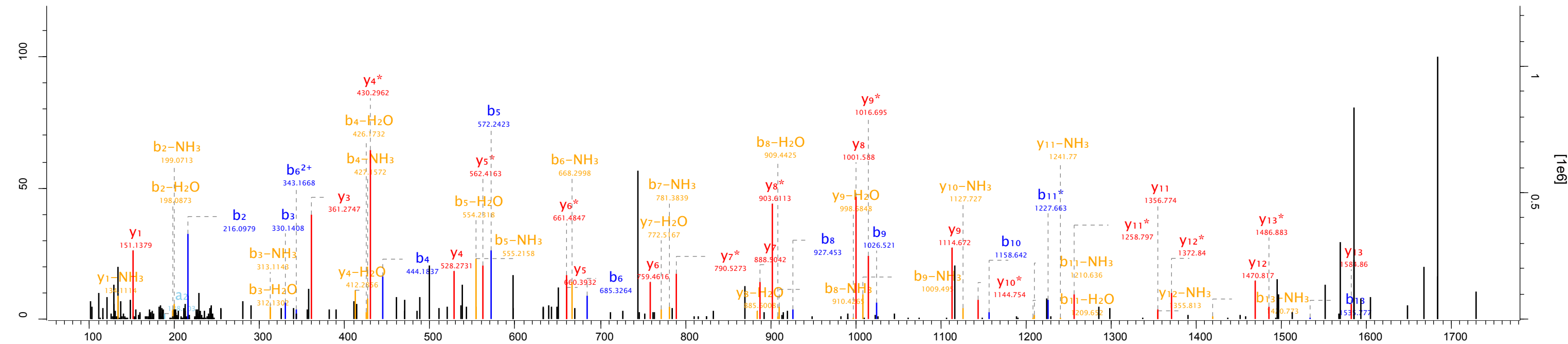
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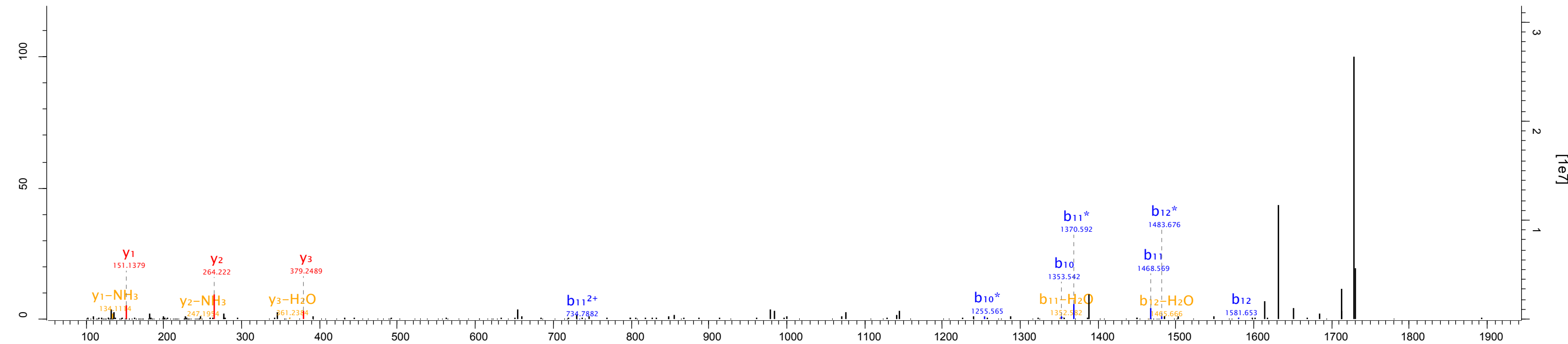
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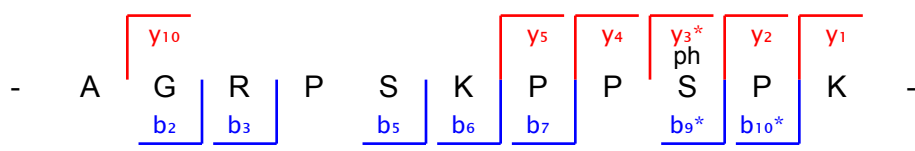
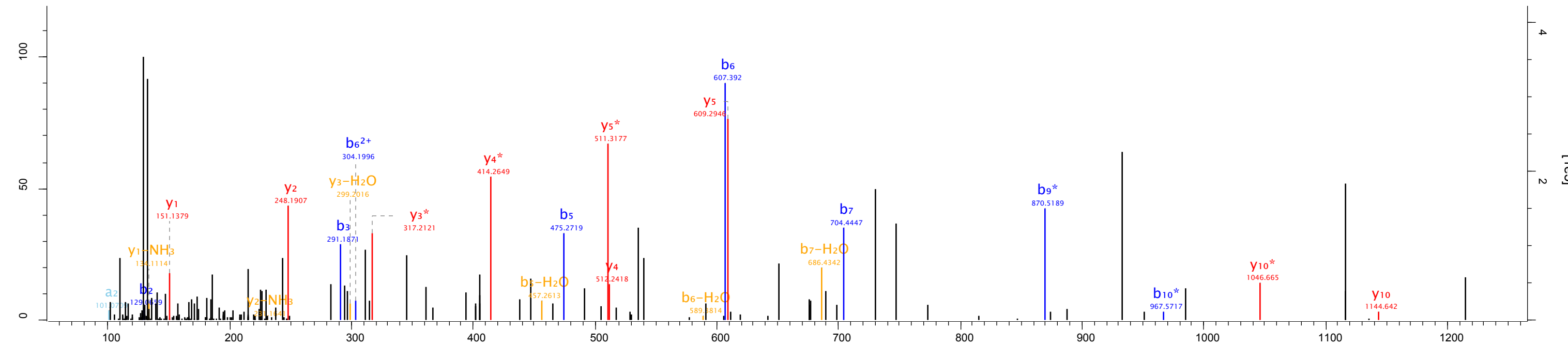
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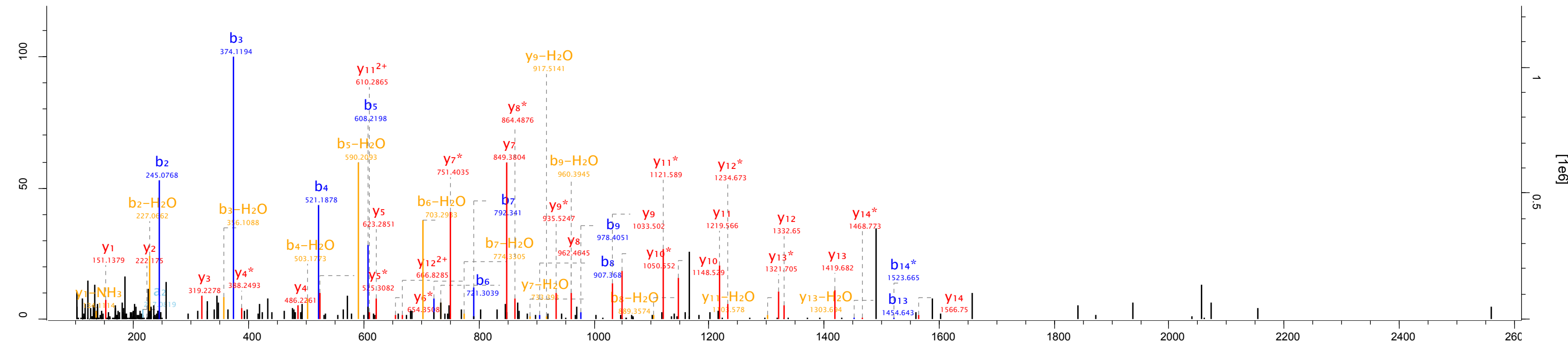
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 Scan: 2127 Method: FTMS; HCD Score: 72.9 m/z: 406.2 Gene names: TBC1D14



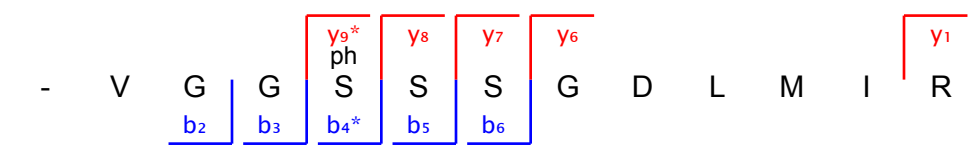
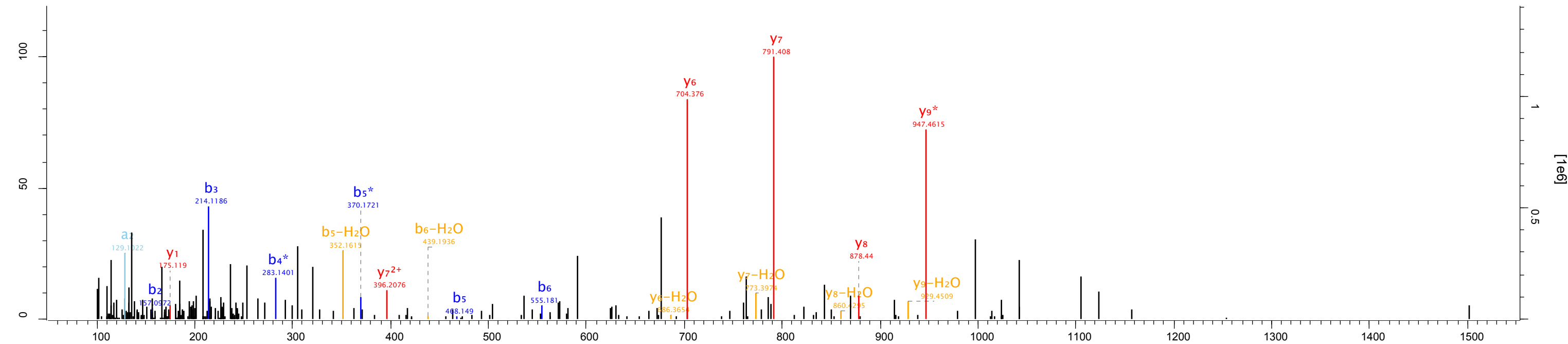
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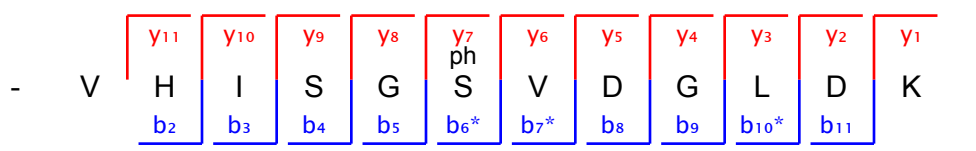
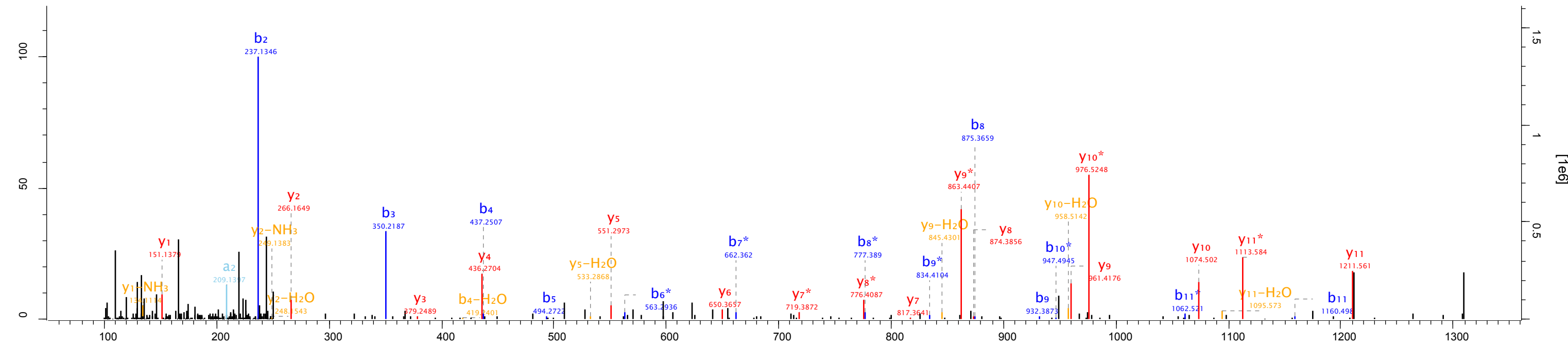
ac - S D E F S L A D A L P E H S P A K -

b₂
b₃
b₄
b₅
b₆
b₇
b₈
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b₁₃
b₁₄^{*}
y₁₄
y₁₃
y₁₂
y₁₁
y₁₀
y₉
y₈
y₇
y₆^{*}
y₅
y₄_{ph}
y₃
y₂
y₁

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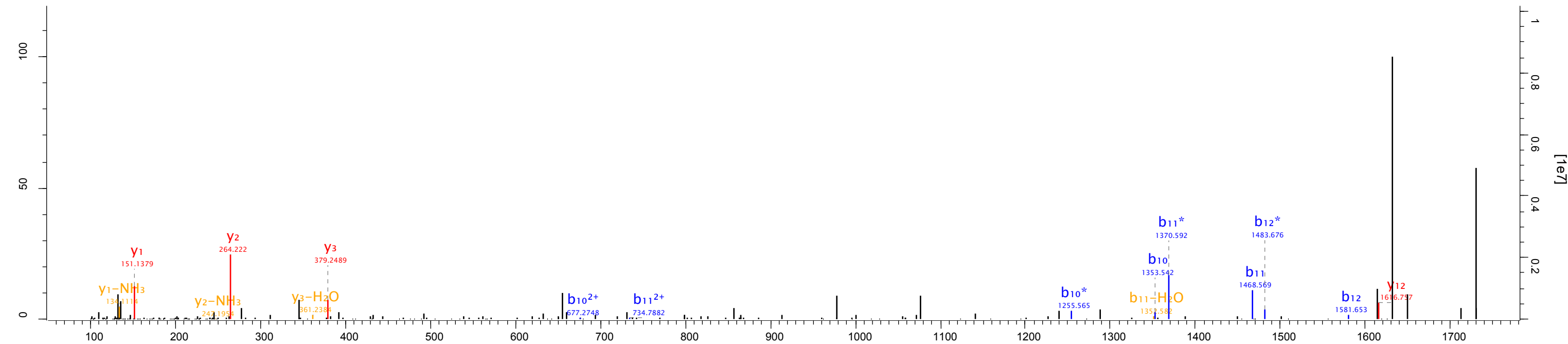


Raw file 20150812_A375SR_Phospho_BR1_09 Scan 11207 Method FTMS; HCD Score 114.28 m/z 655.82 Gene names PHACTR2



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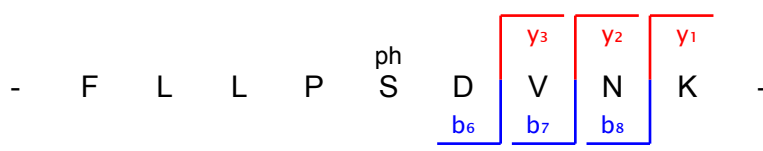
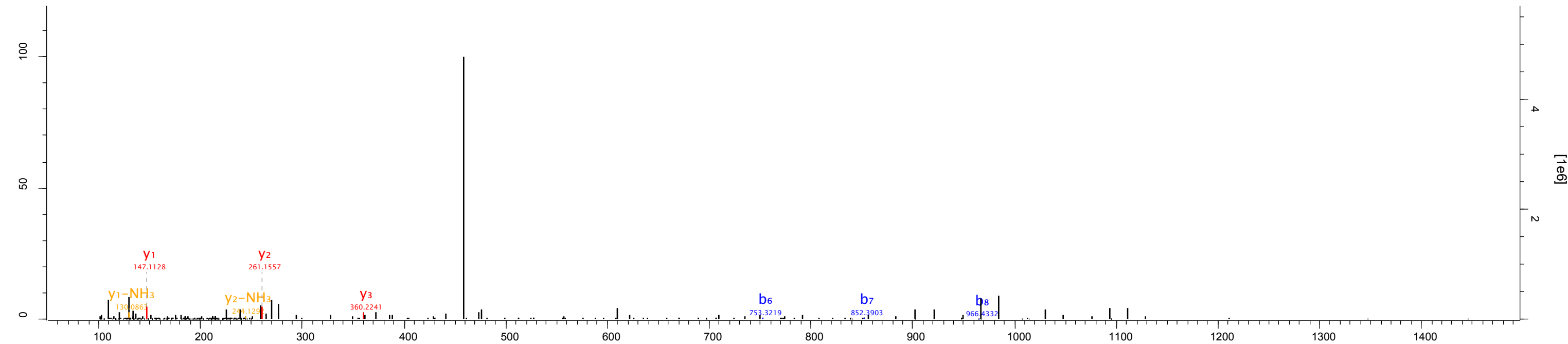
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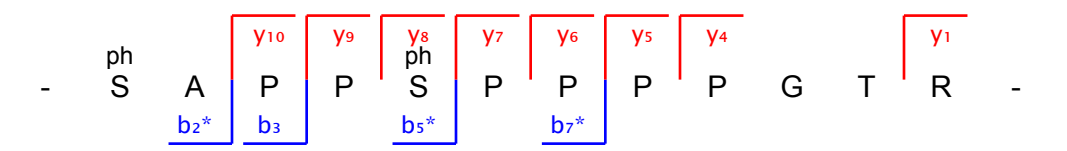
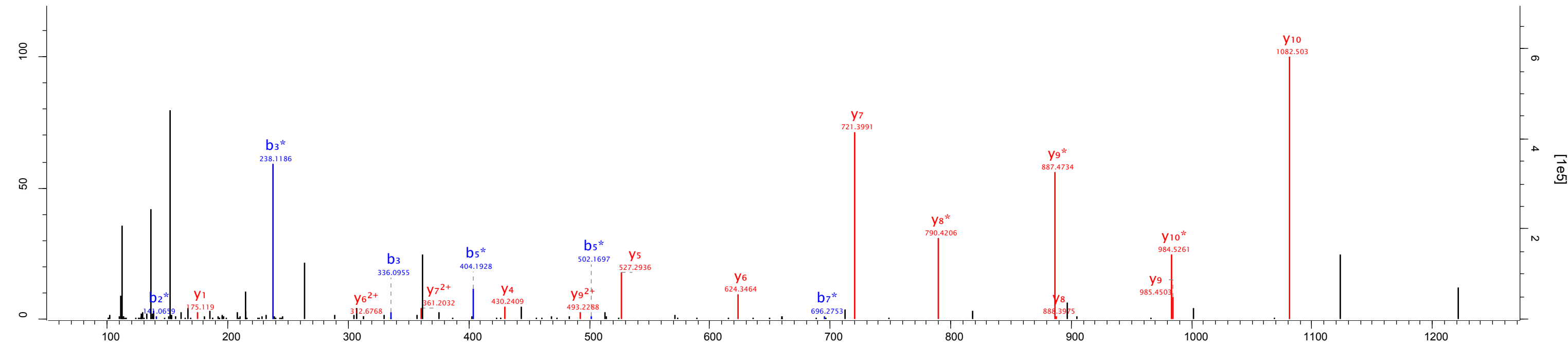
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y12
b10 y3 y2 y1
b11 b12

Raw file
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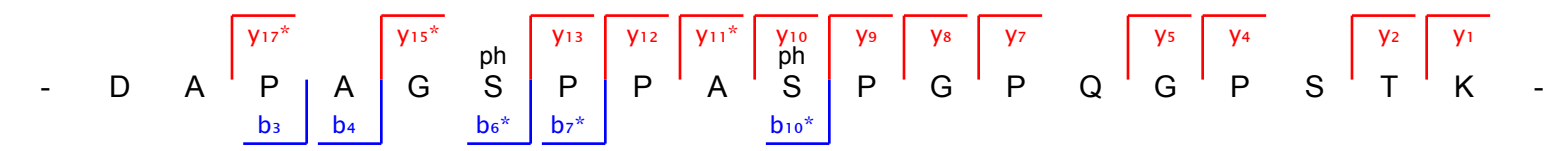
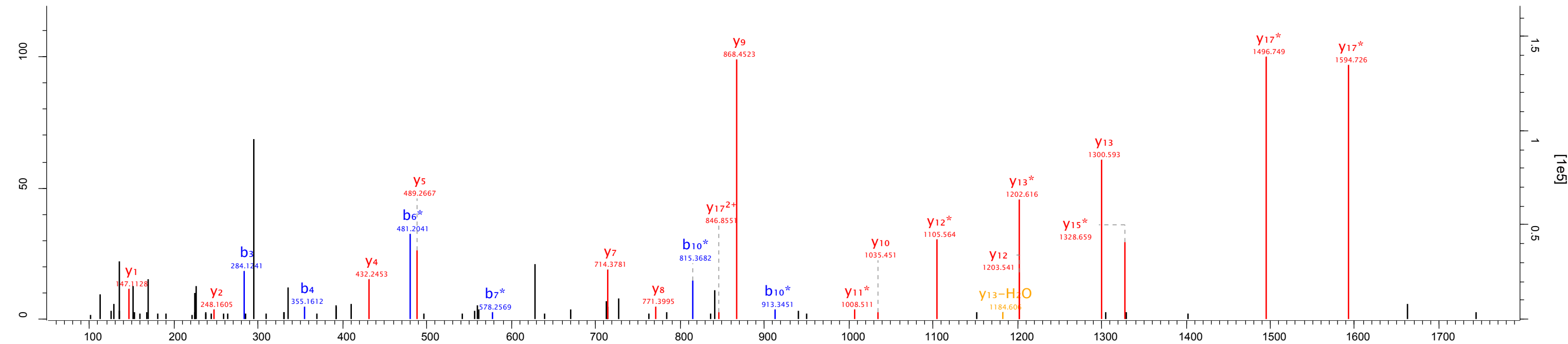
Scan 8727 Method FTMS; HCD Score 43.18 m/z 556.77



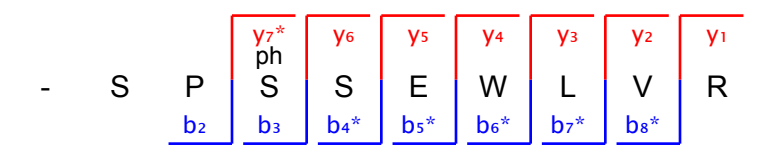
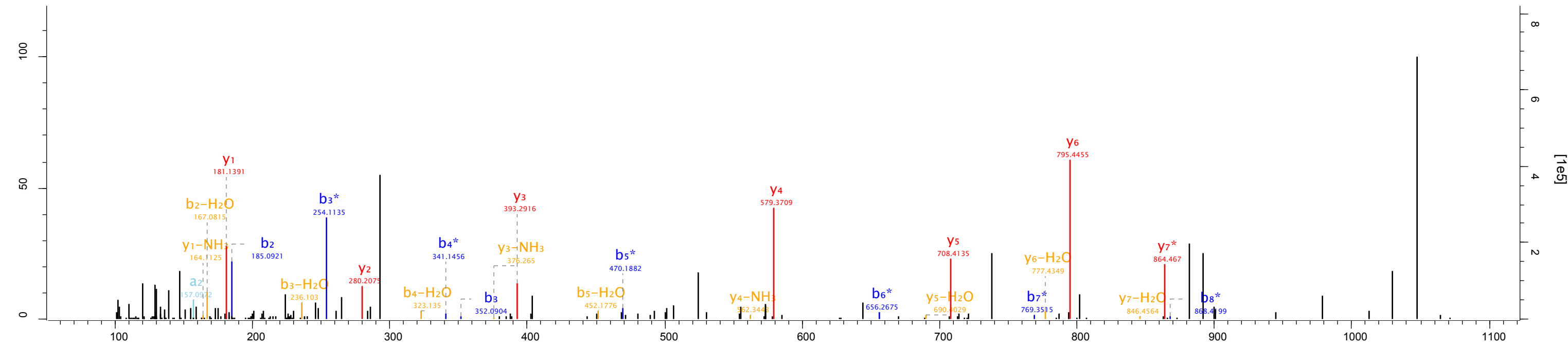
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 Scan: 6527 Method: FTMS; HCD Score: 49.04 m/z: 660.77 Gene names: GPSM3



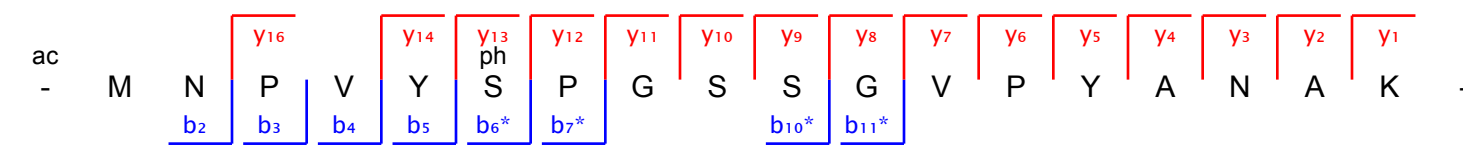
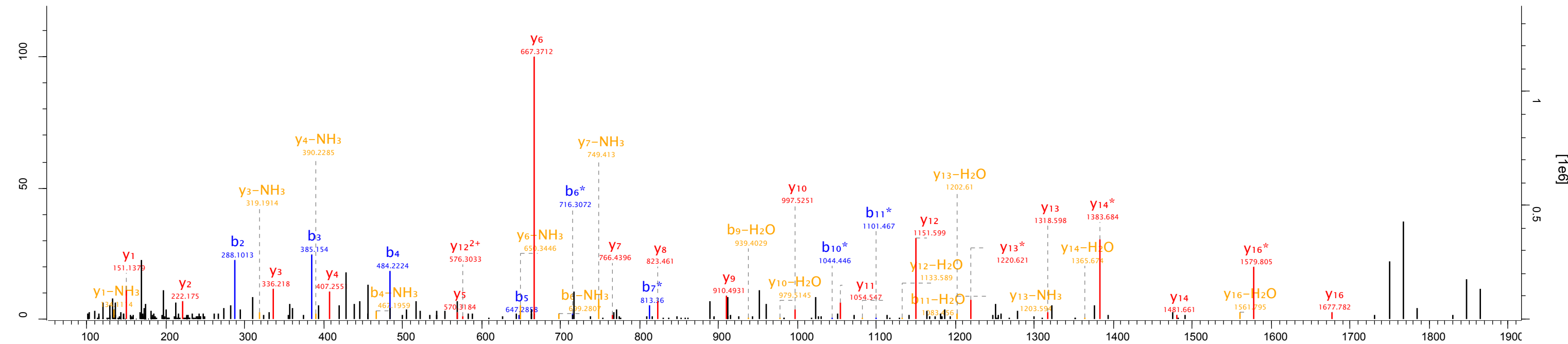
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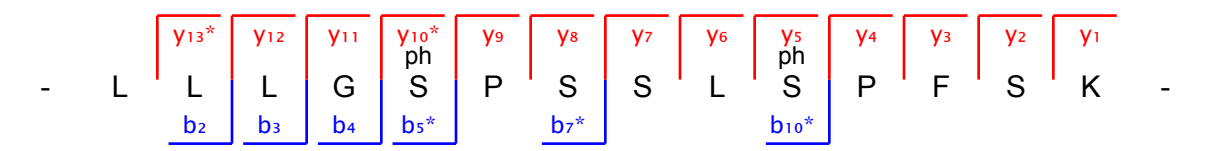
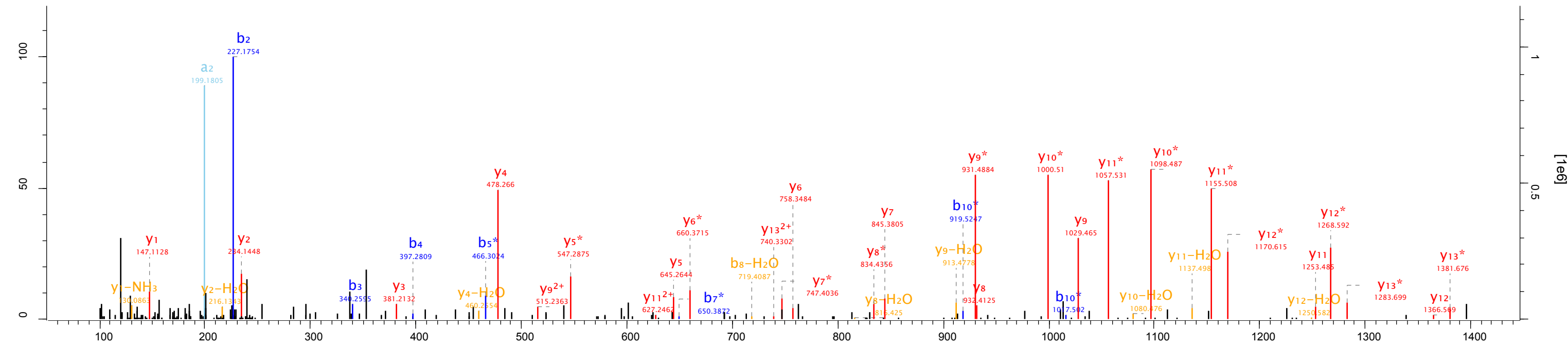
Raw file: 20150814_A375SR_Phospho_BR2_03
 Scan: 17257 Method: FTMS; HCD Score: 107.51 m/z: 573.77 Gene names: GPATCH2L



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 Scan: 20887 Method: FTMS; HCD Score: 108.5 m/z: 983.44 Gene names: FAM168B

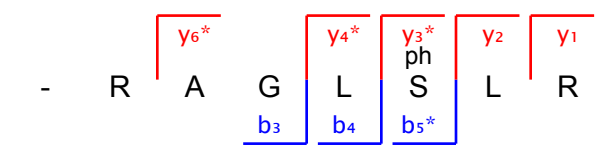
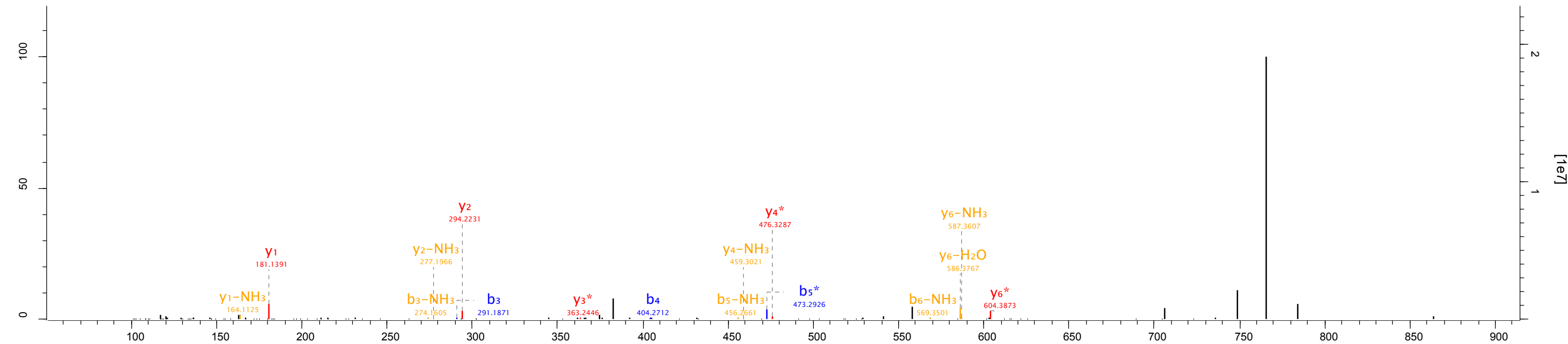


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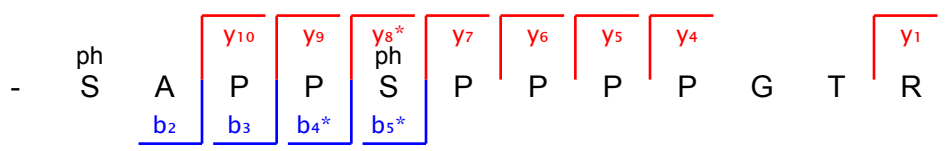
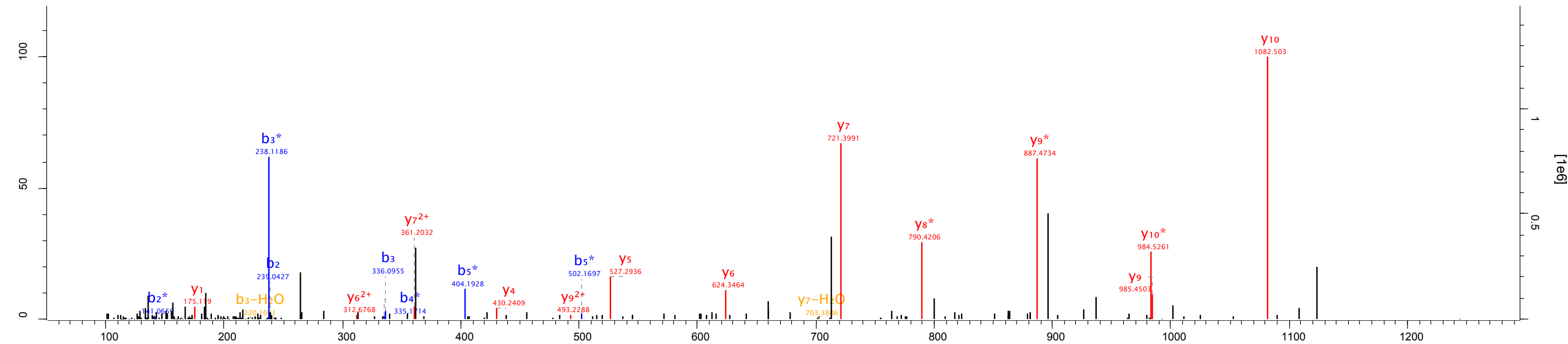


Raw file
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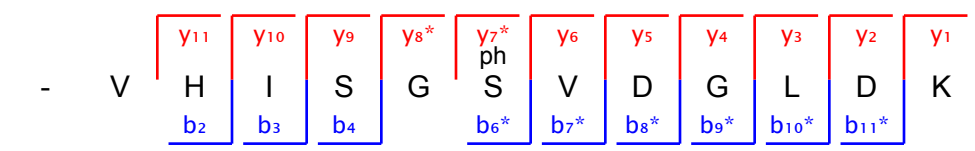
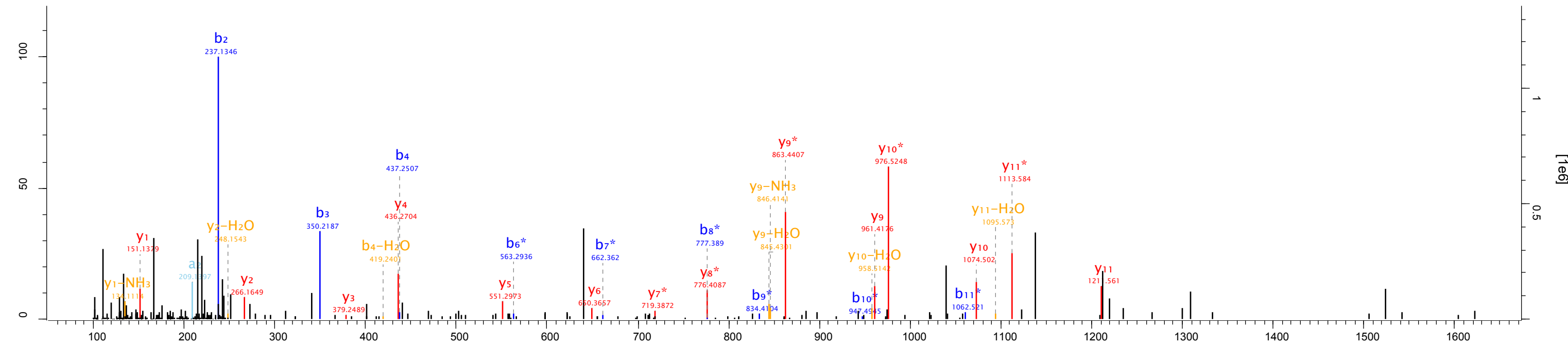
Scan	Method	Score	m/z
5707	FTMS; HCD	73.23	432.75



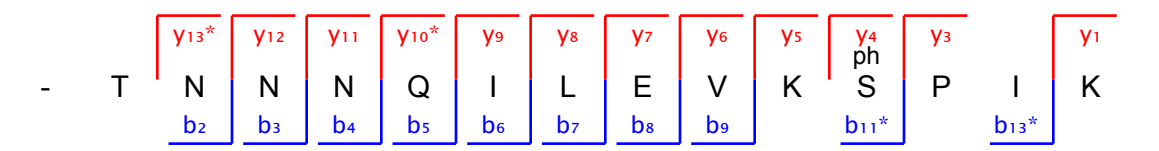
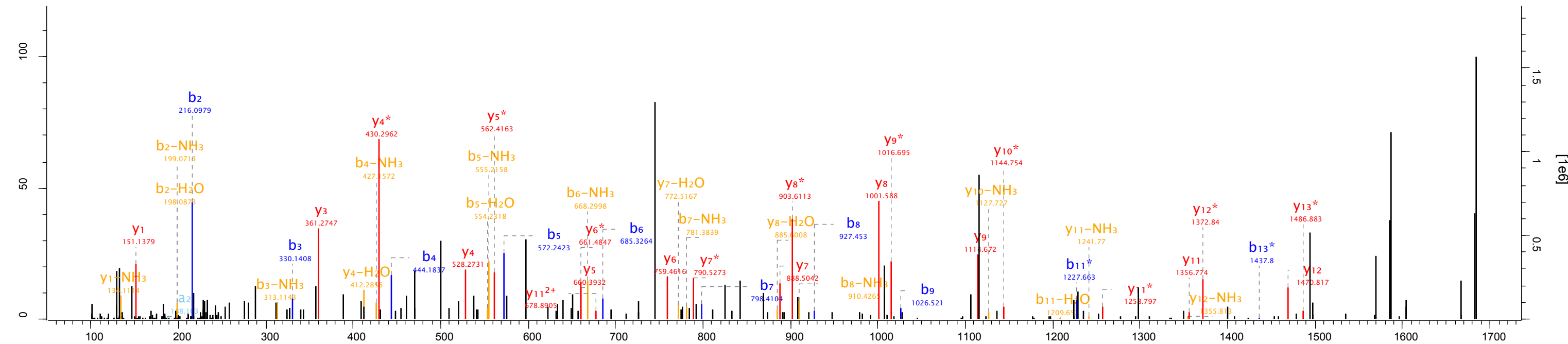
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 Scan 6007 Method FTMS; HCD Score 49.71 m/z 660.77 Gene names GPSM3



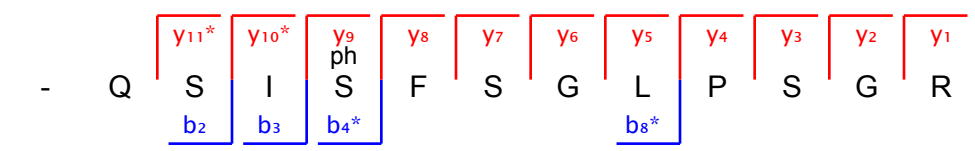
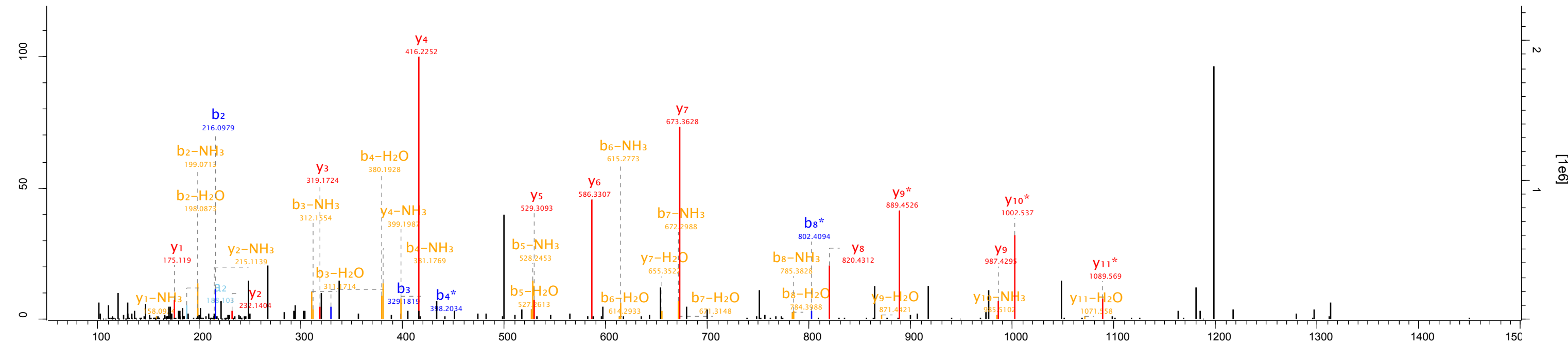
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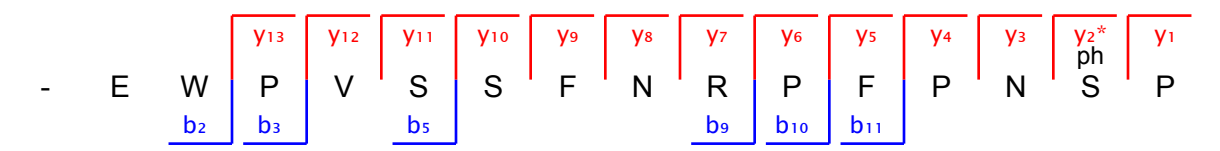
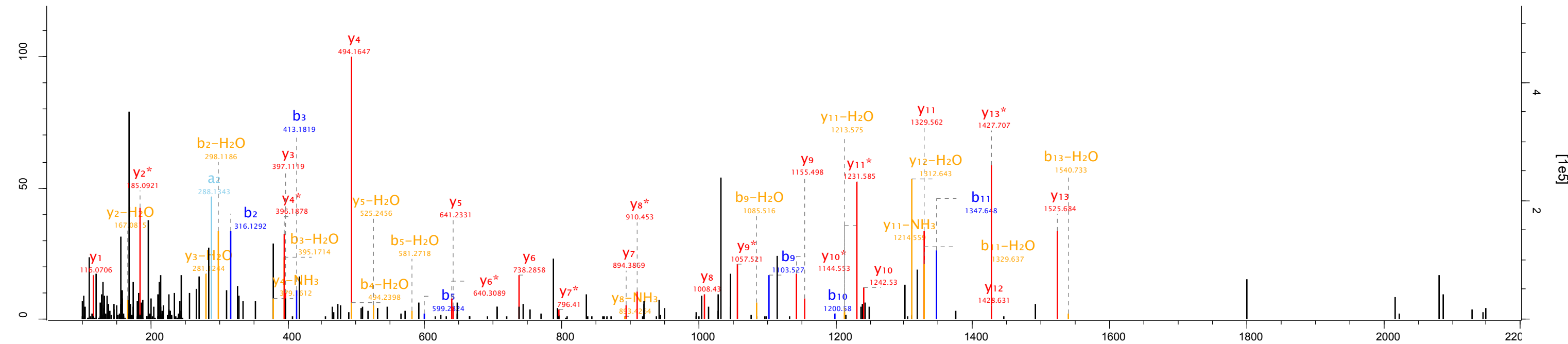
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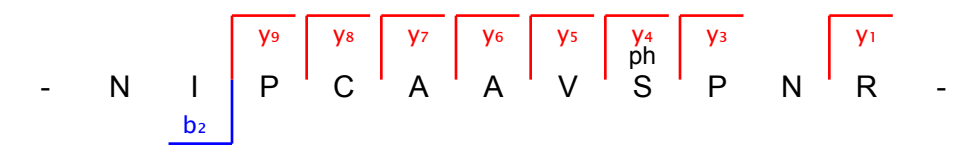
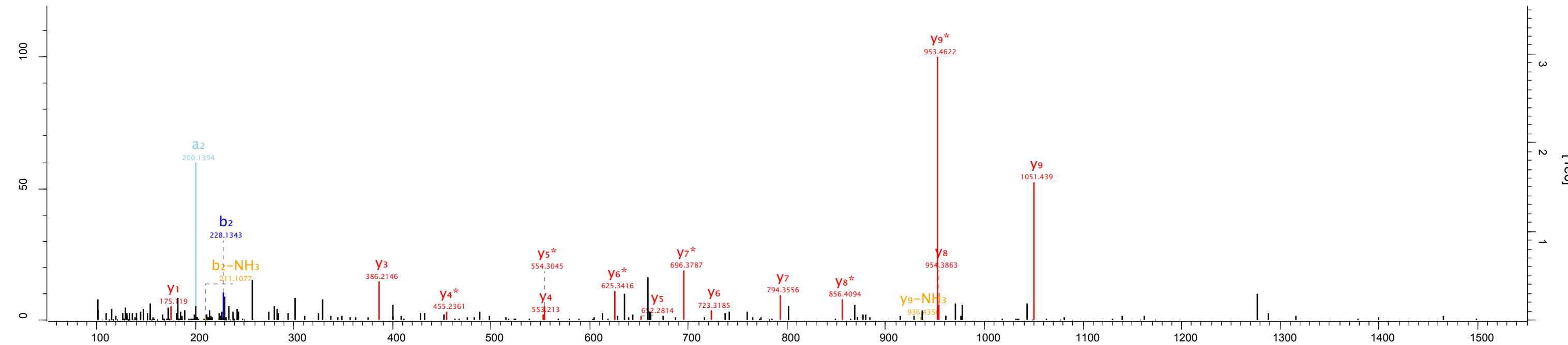
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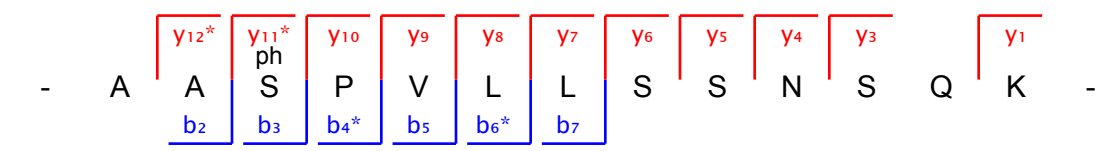
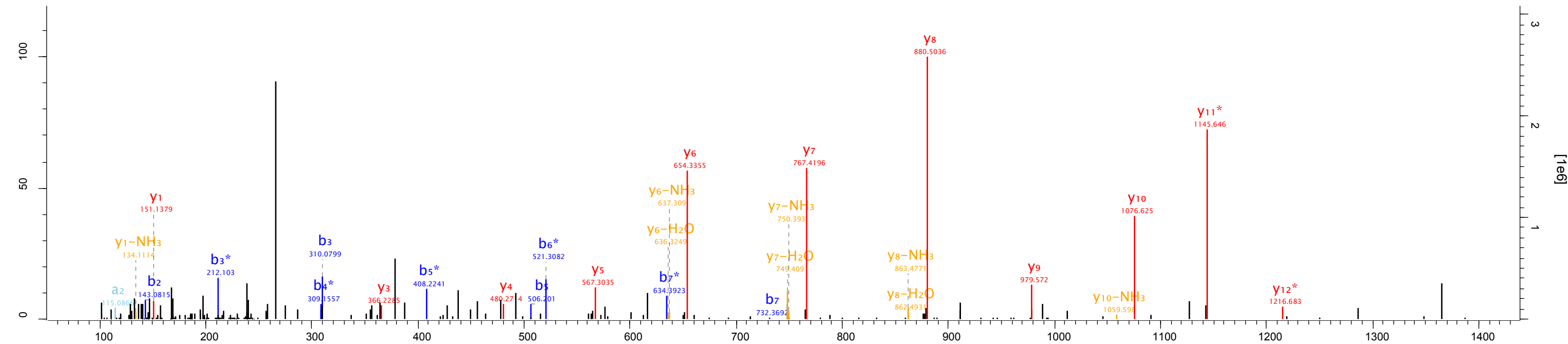
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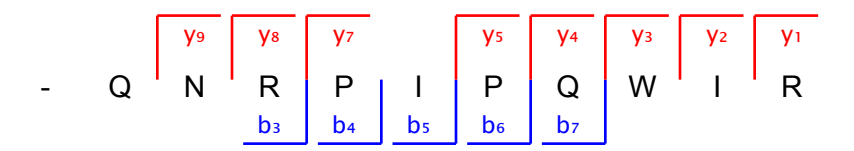
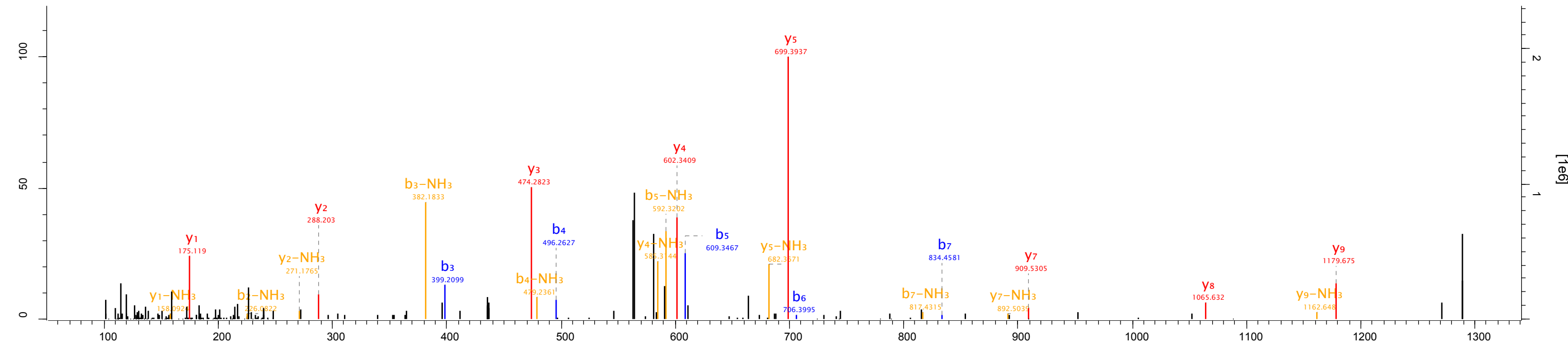
20150814_A375SR_Phospho_BR2_04 9187 FTMS; HCD 57.79 639.79 KLF10



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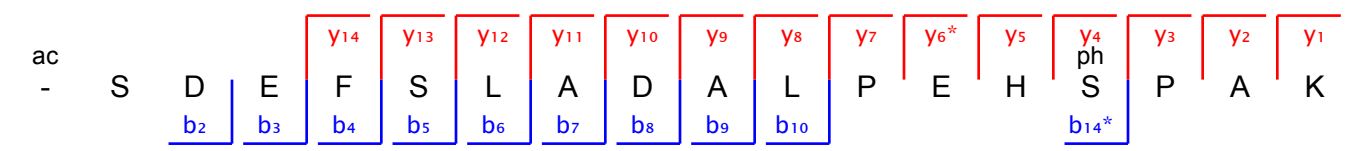
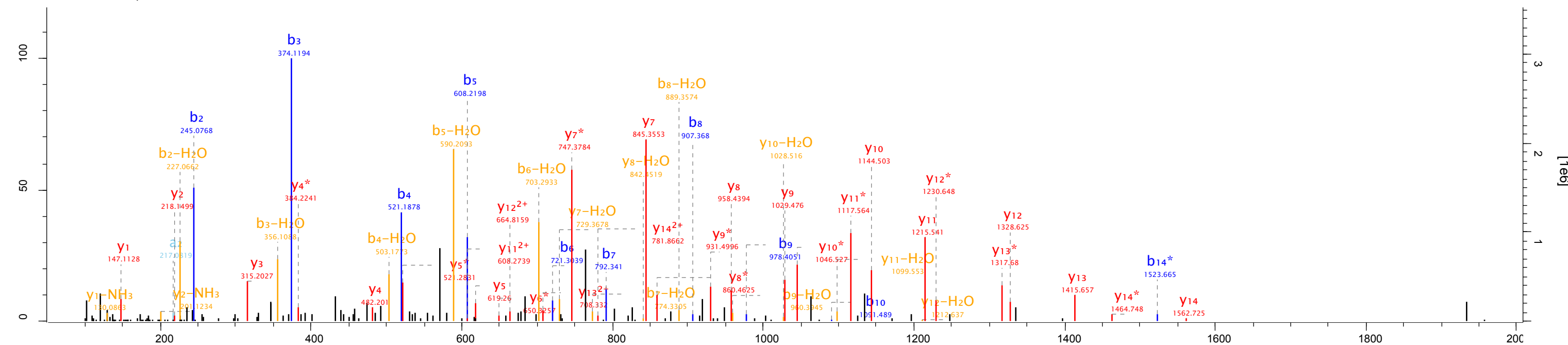


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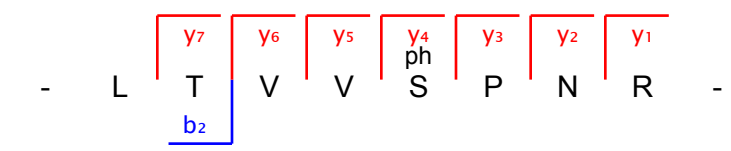
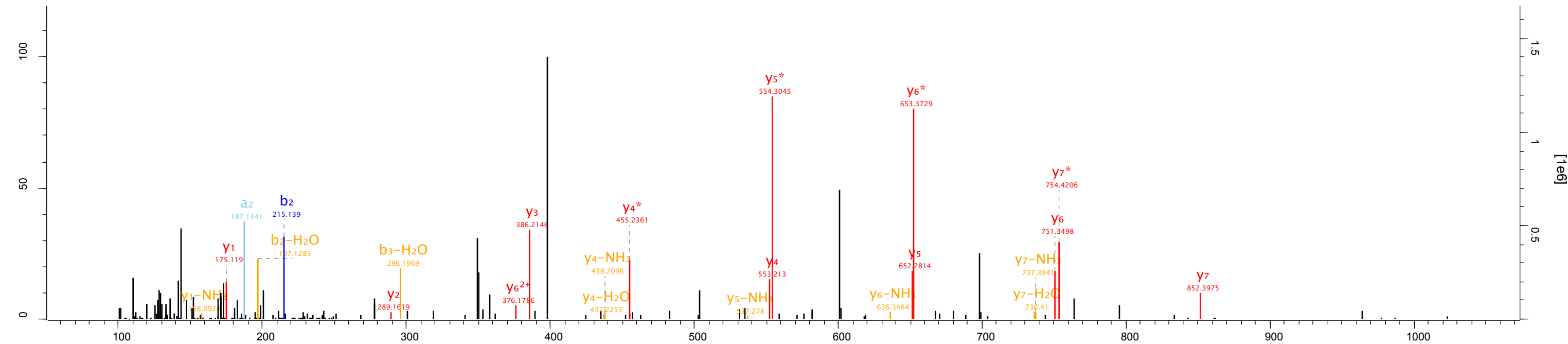


Raw file
20150814_A375SR_Phospho_BR2_05

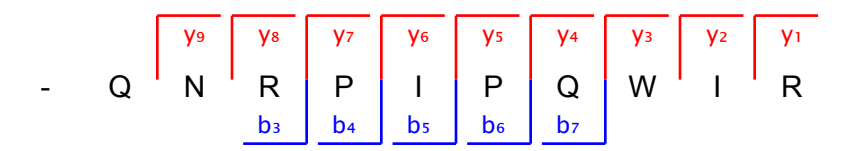
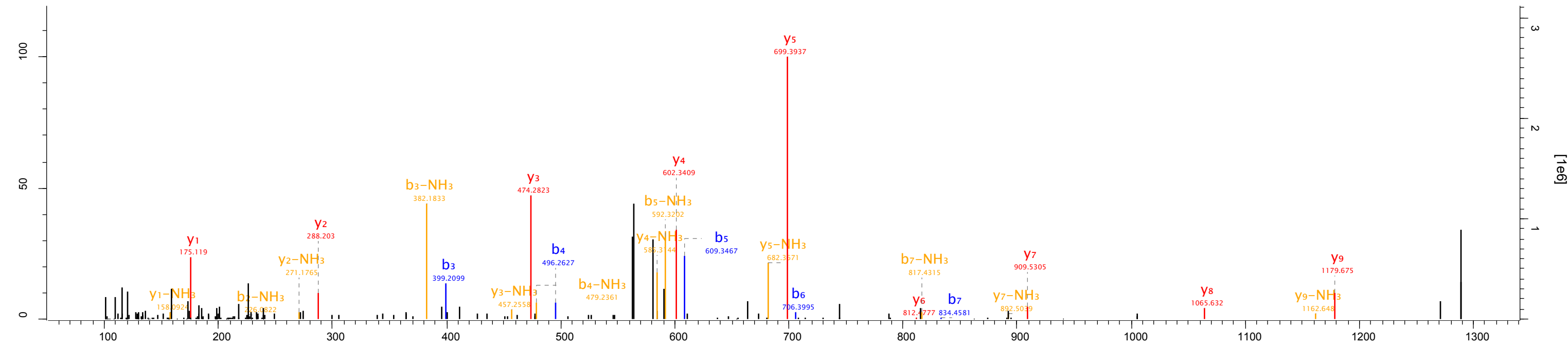
Scan 24027 Method FTMS; HCD Score 260.67 m/z 968.42 Gene names MAPK11P1L



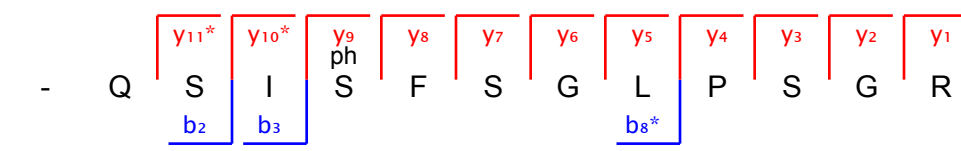
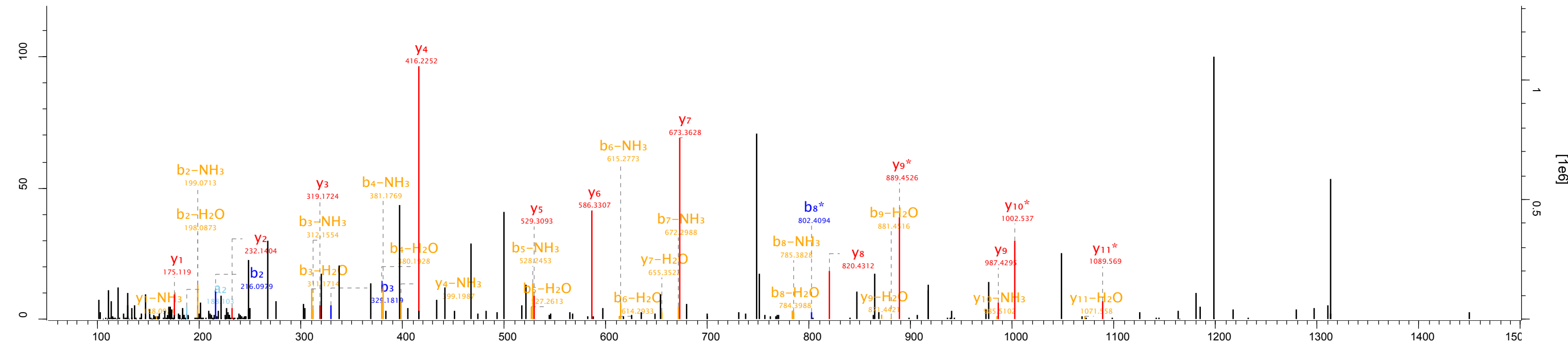
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 Scan: 8687 Method: FTMS; HCD Score: 103.31 m/z: 483.24 Gene names: C16orf72



Raw file: 20150814_A375SR_Phospho_BR2_06
 Scan: 14147
 Method: FTMS; HCD
 Score: 175.91
 m/z: 436.58
 Gene names: RPL39P5;RPL39

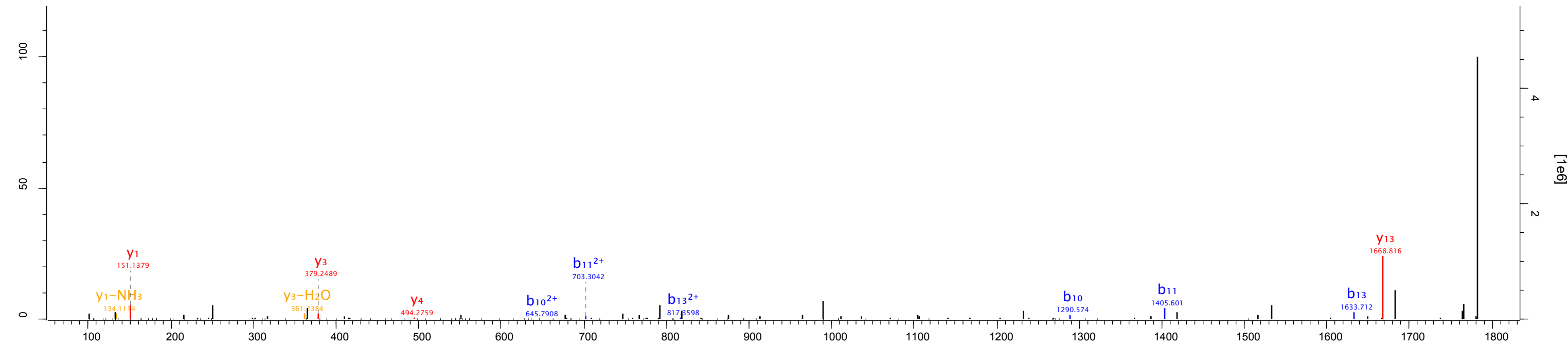


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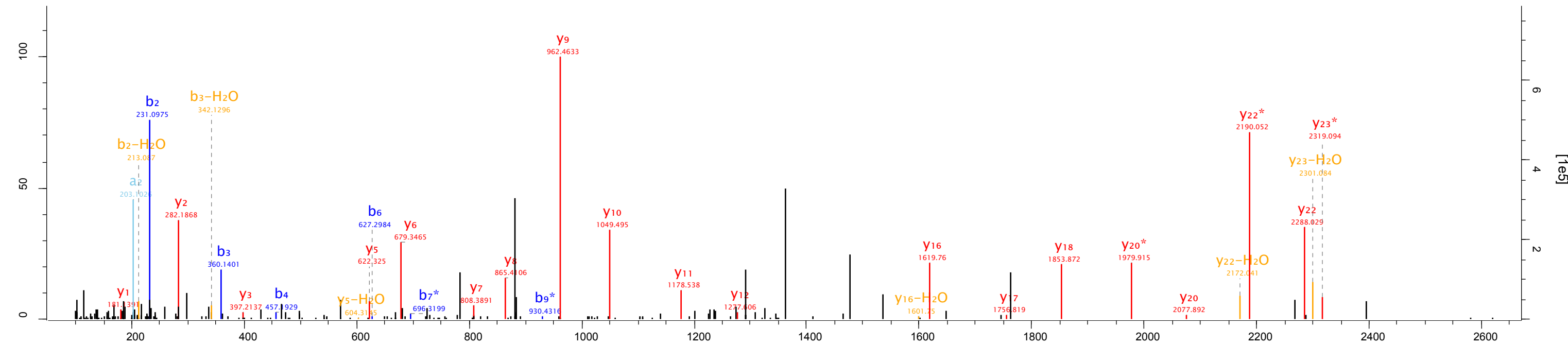


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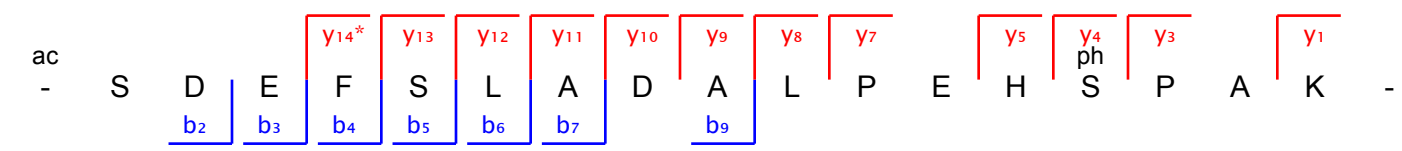
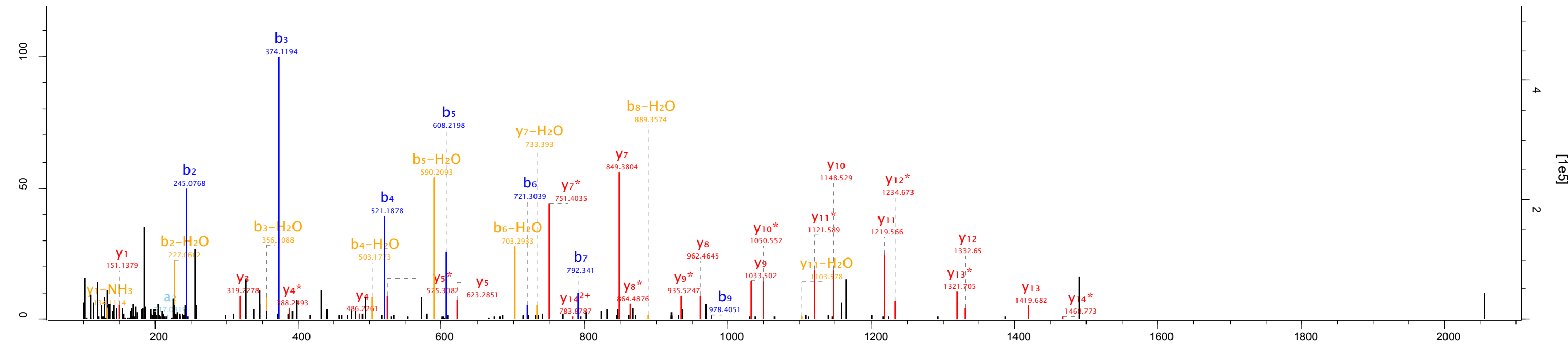
Scan 3387 Method FTMS; HCD Score 66.99 m/z 892.43



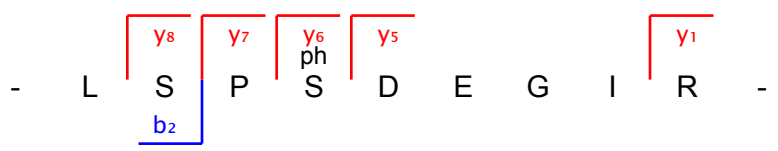
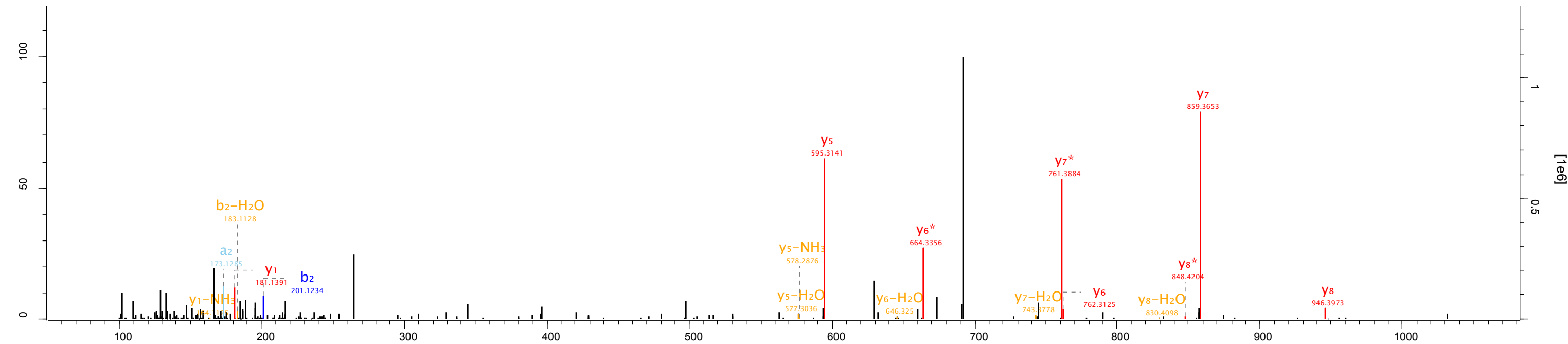
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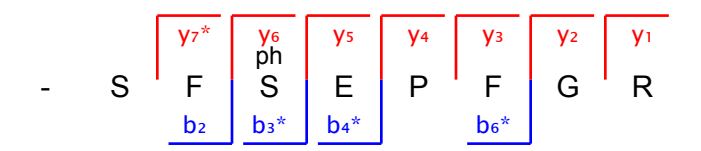
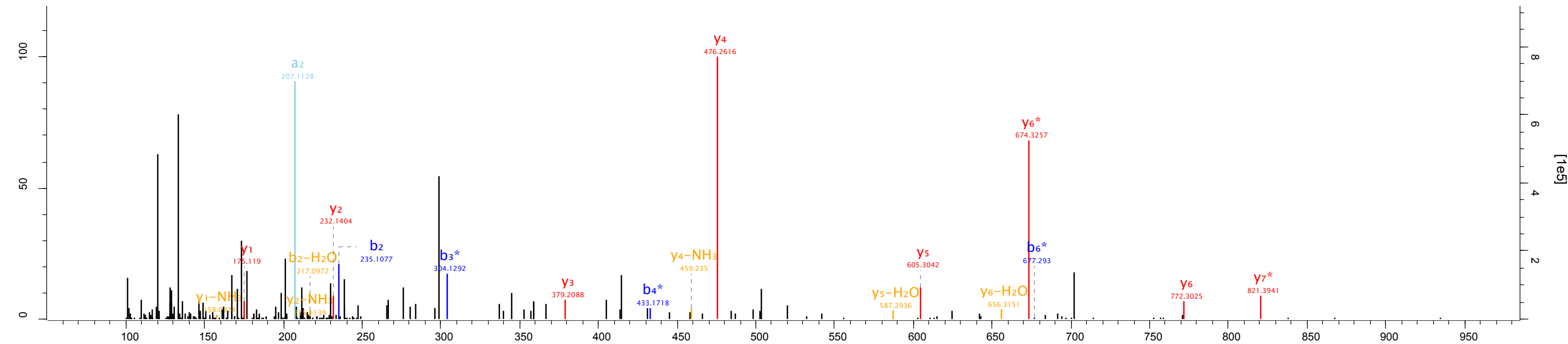
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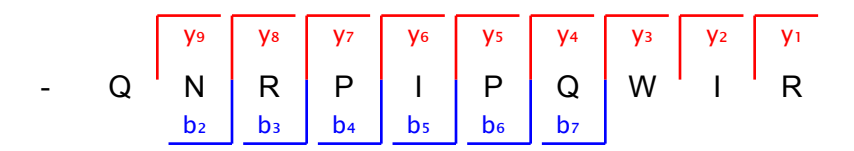
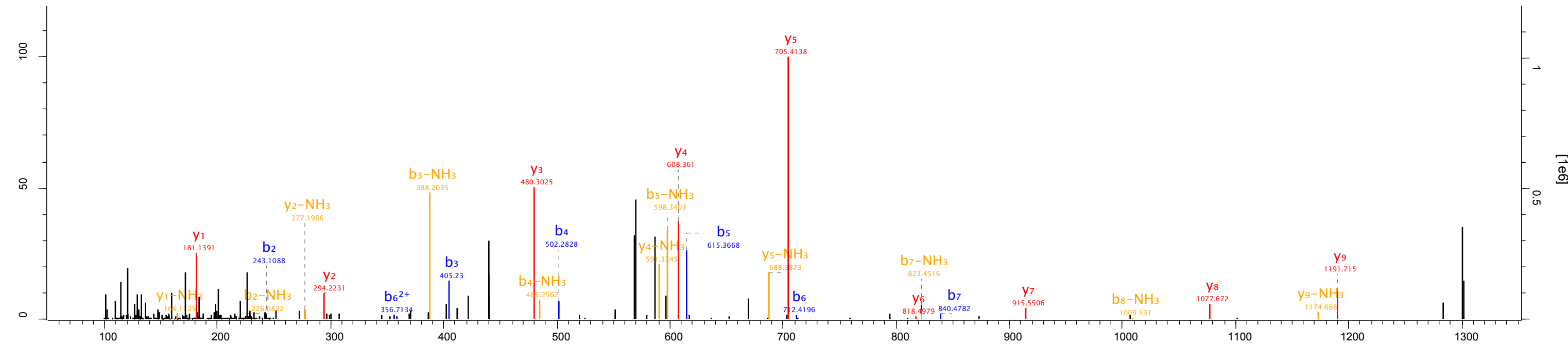
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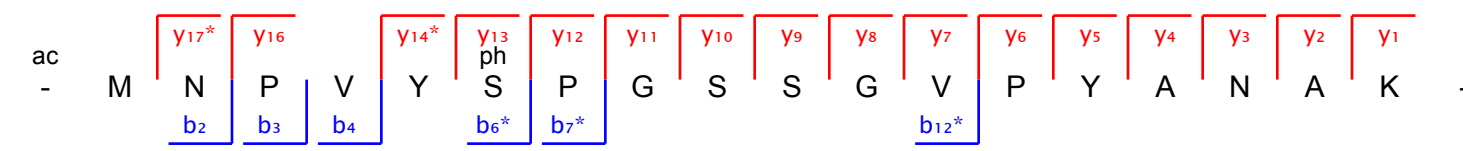
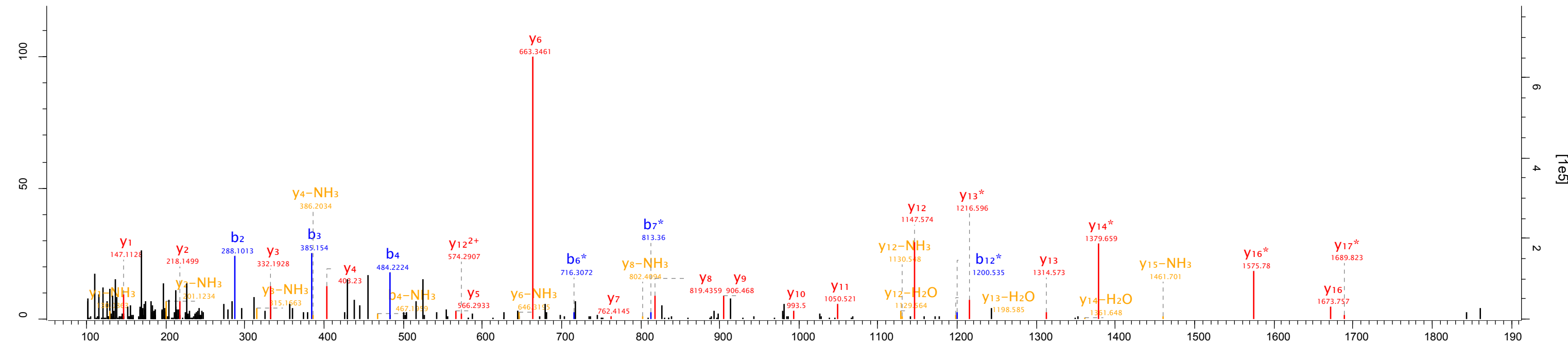
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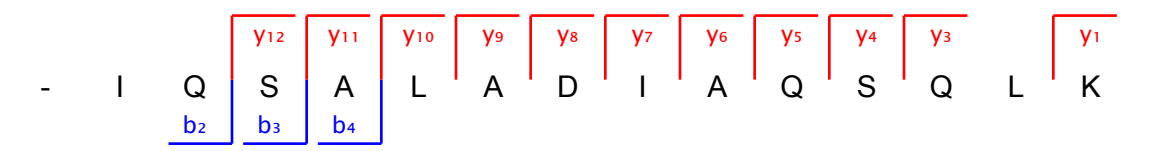
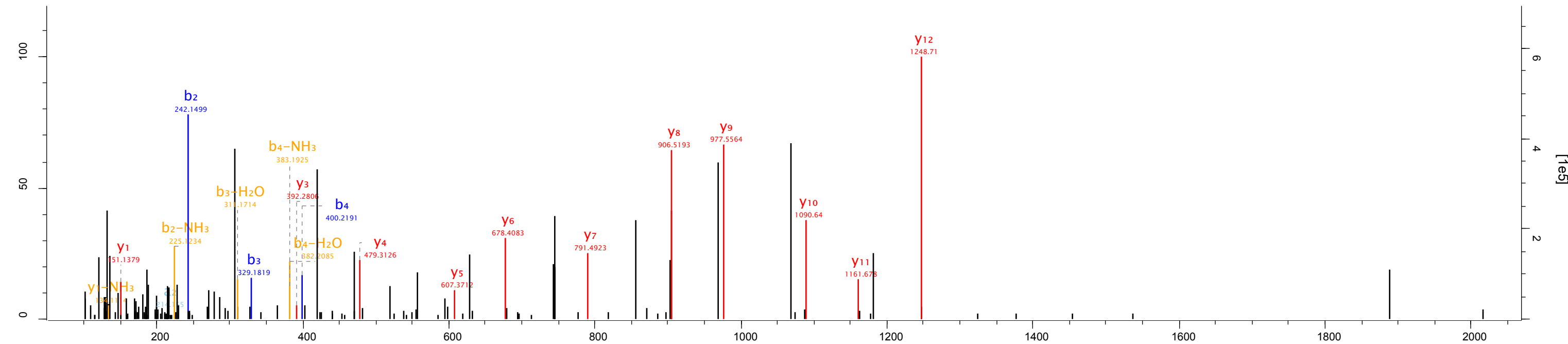
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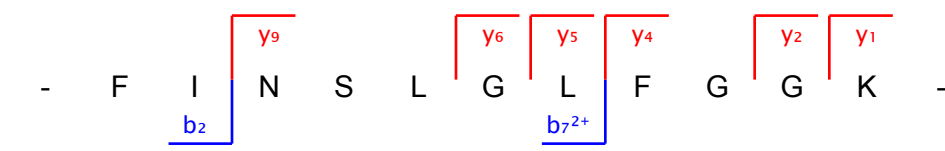
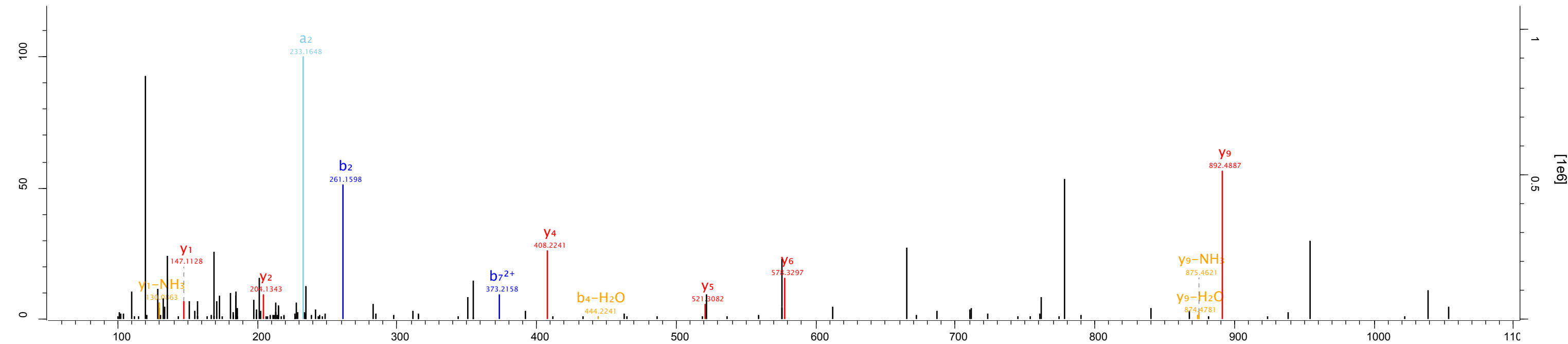
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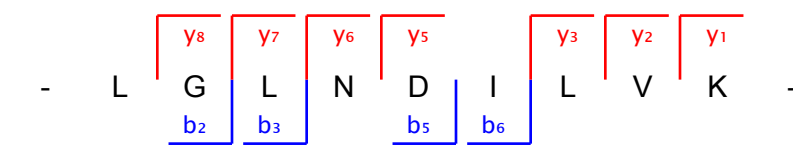
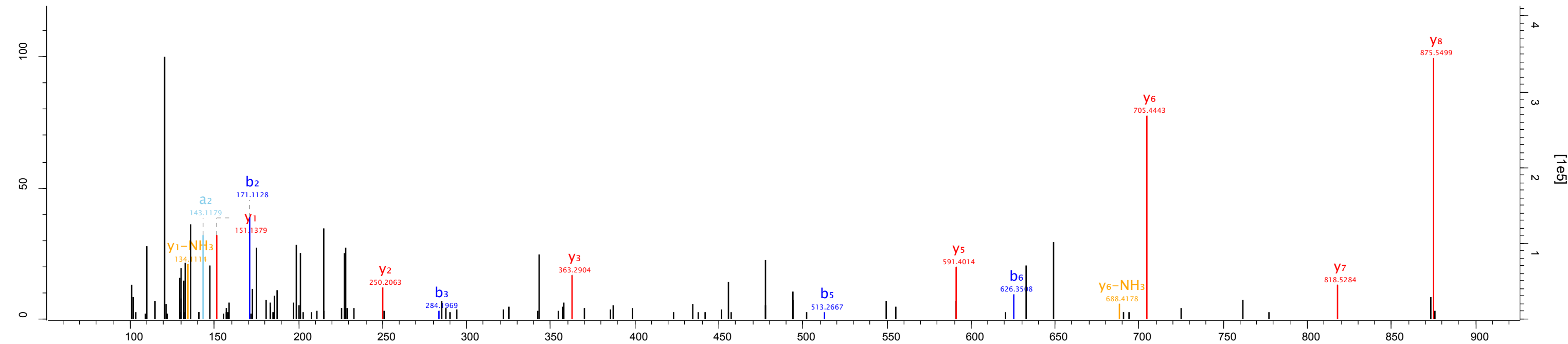
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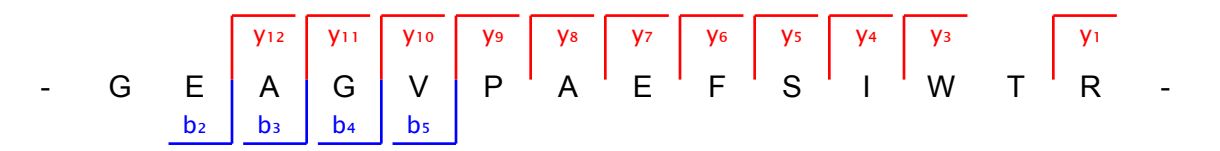
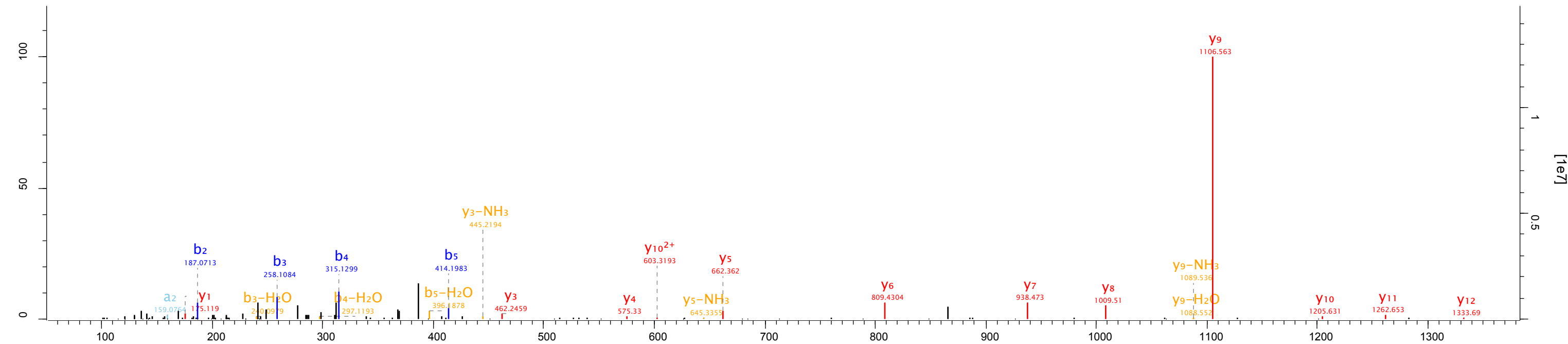
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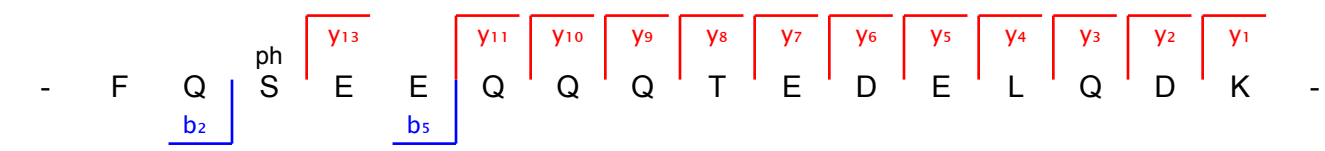
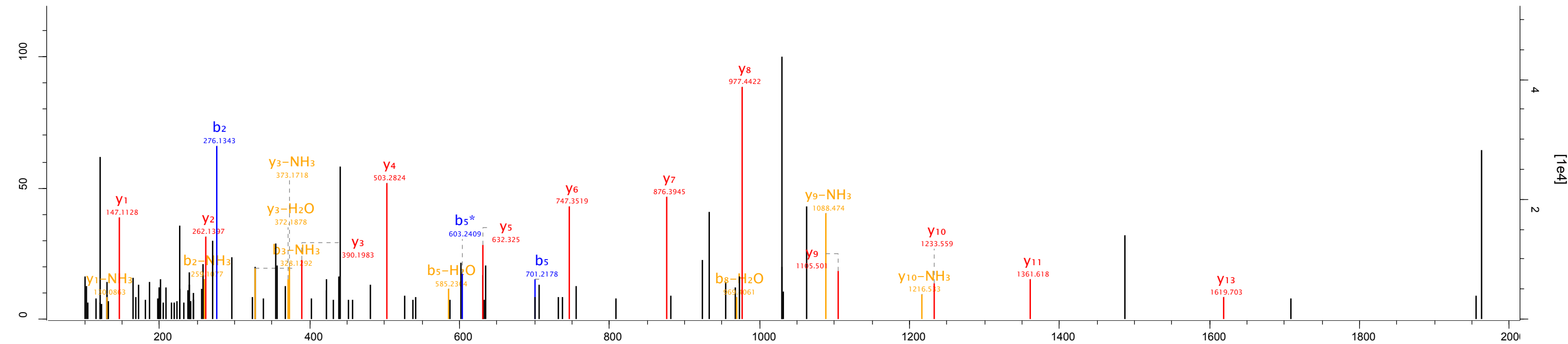
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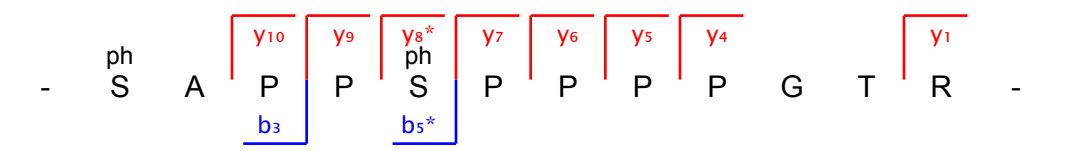
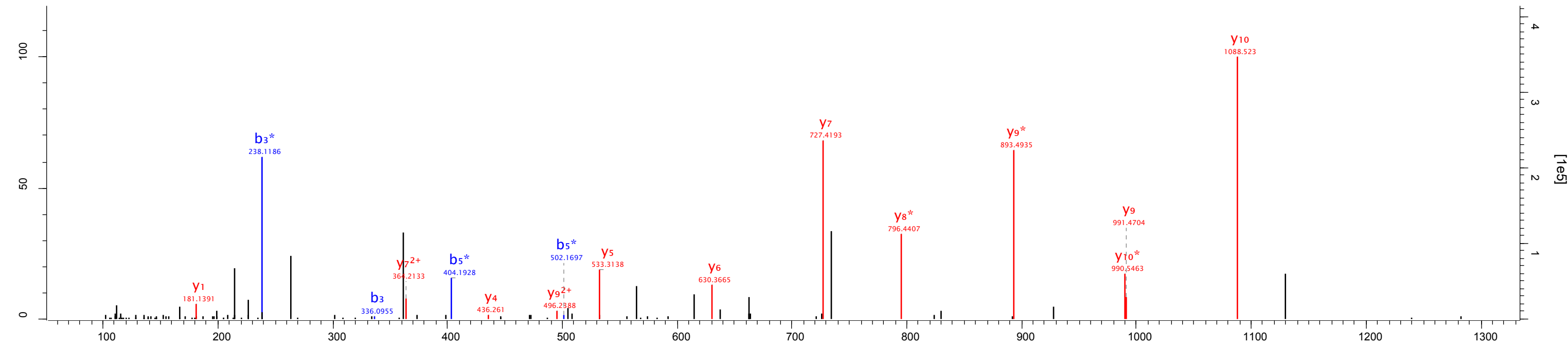
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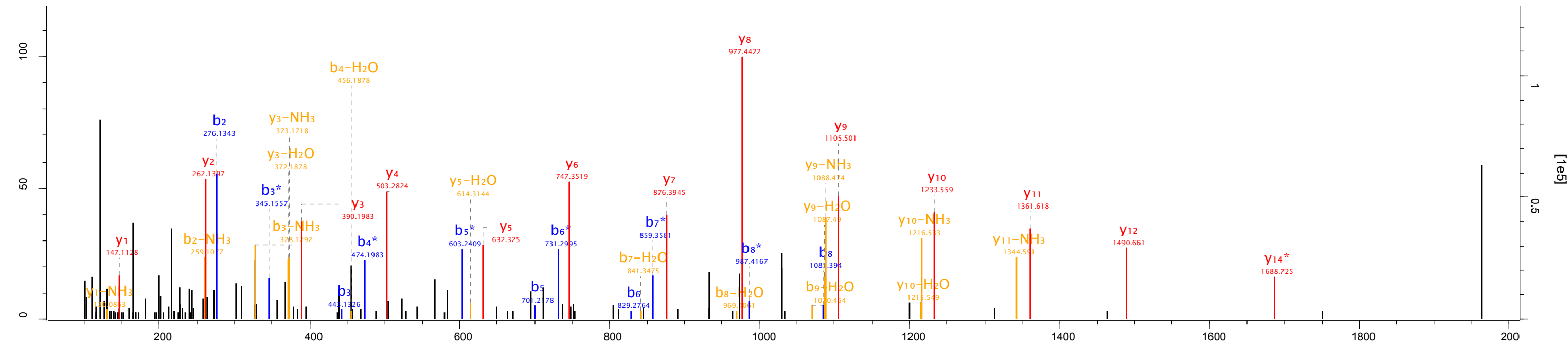
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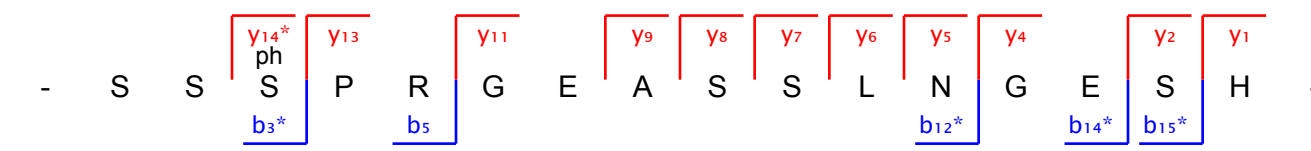
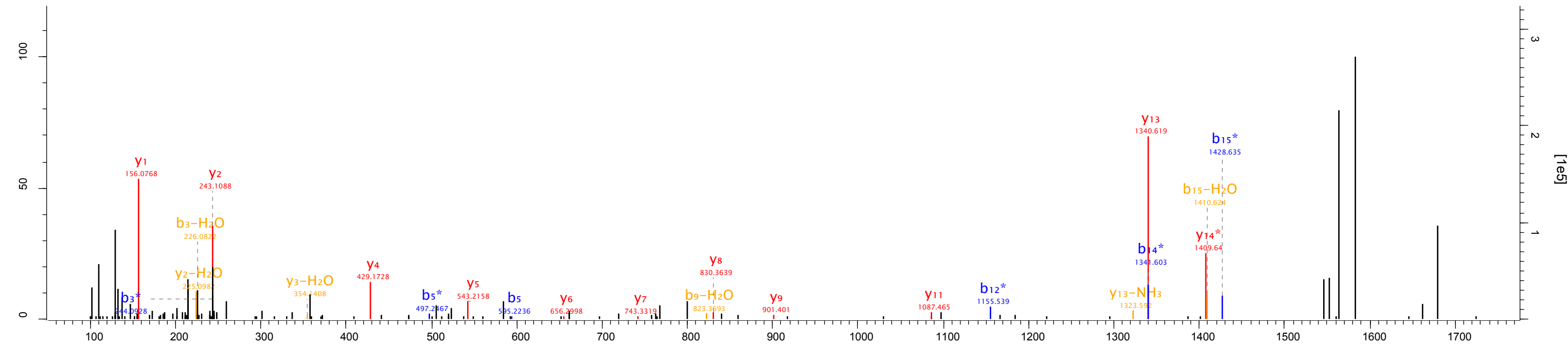
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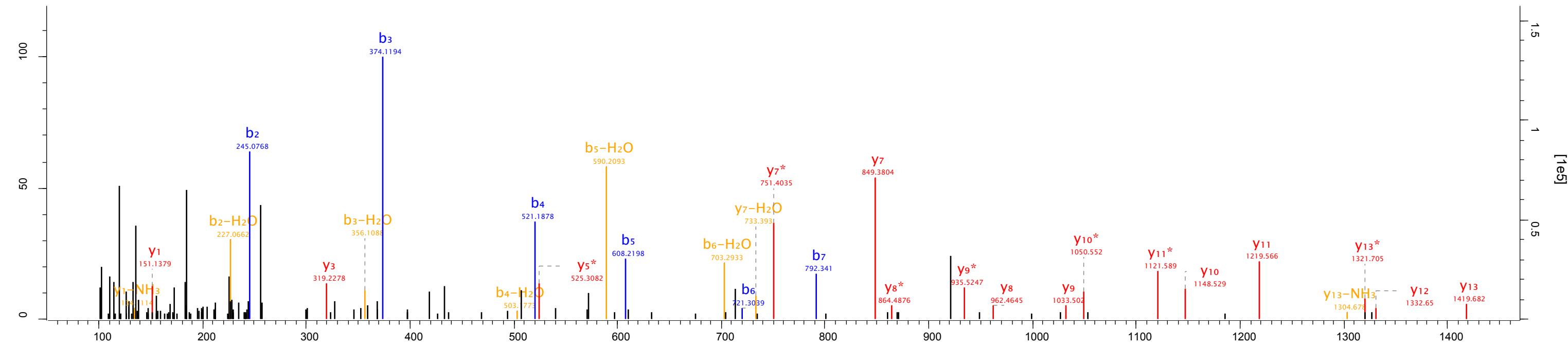
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b₂
b₃
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y₁₂
y₁₁
y₁₀
y₉
y₈
y₇
y₆
y₅
y₄
y₃
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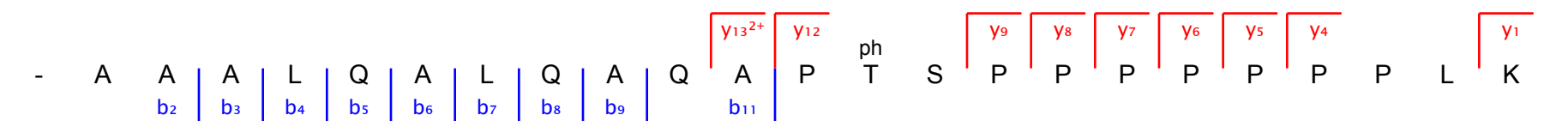
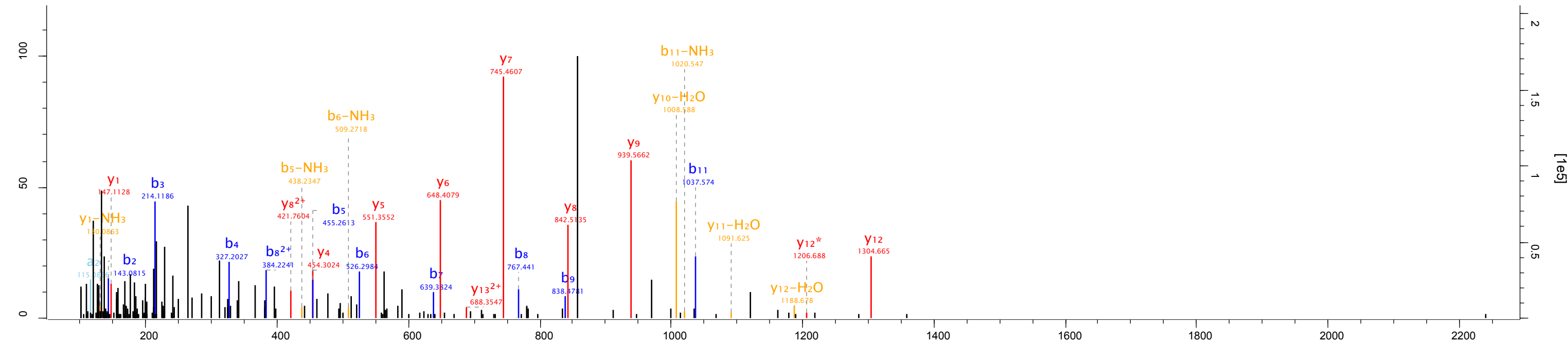
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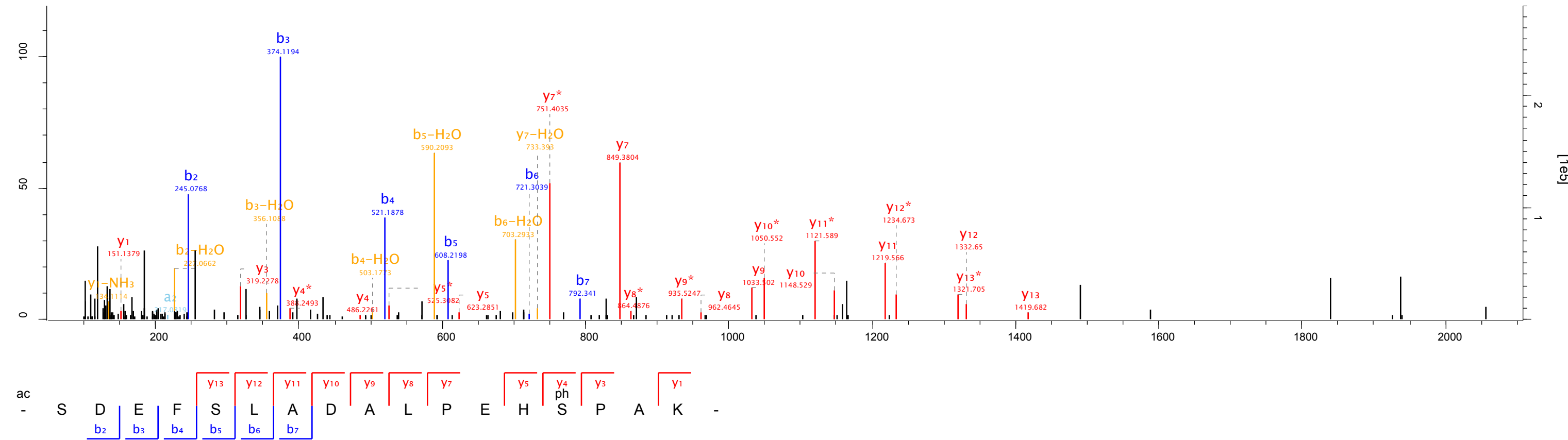
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Raw file
20150822_A375SR_Phospho_BR3_08

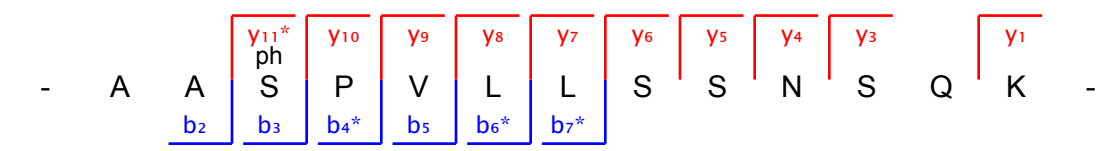
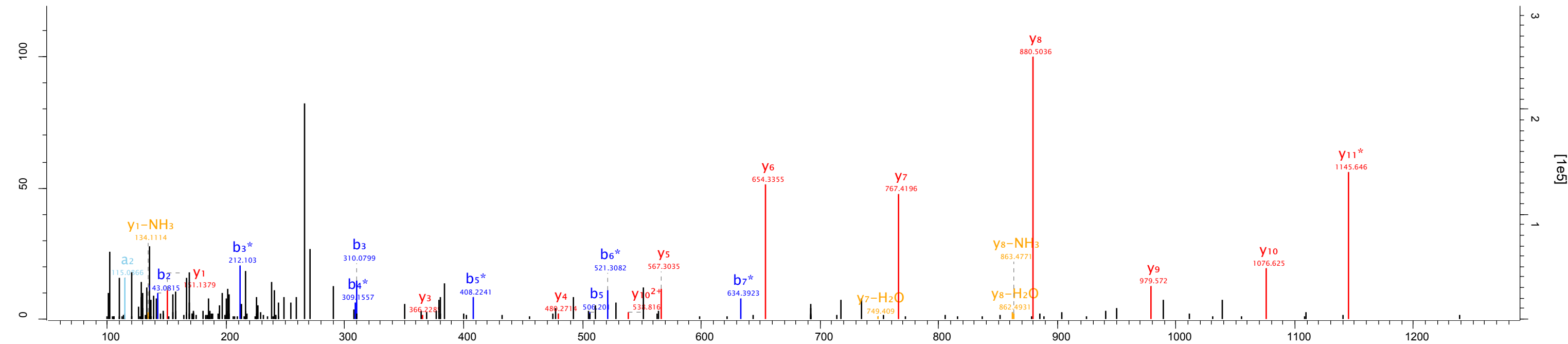
Scan 21597 Method FTMS; HCD Score 69.26 m/z 781.42 Gene names ZNF579



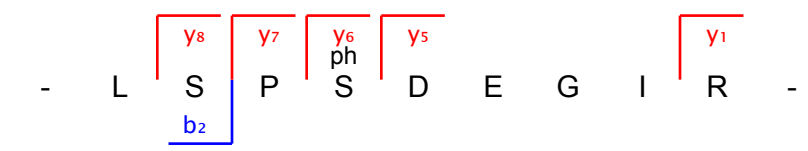
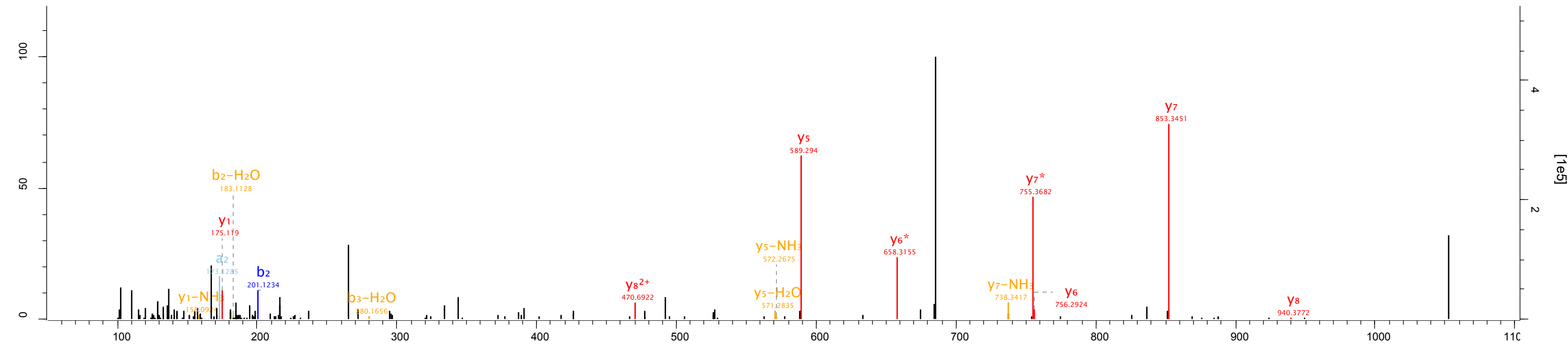
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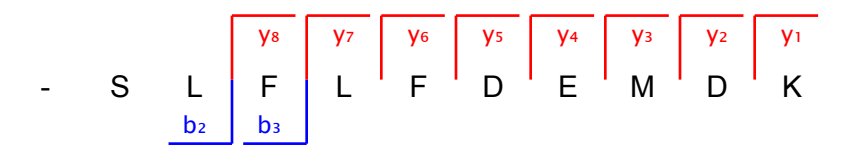
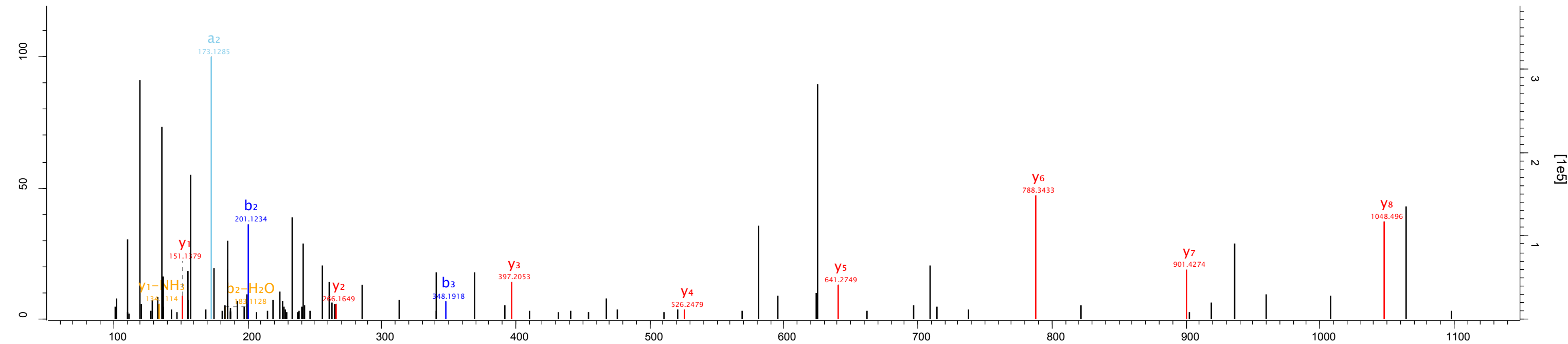
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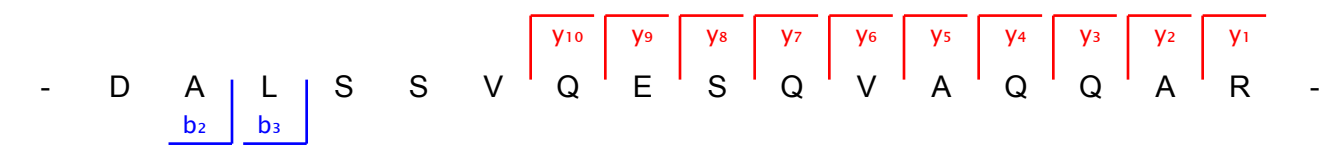
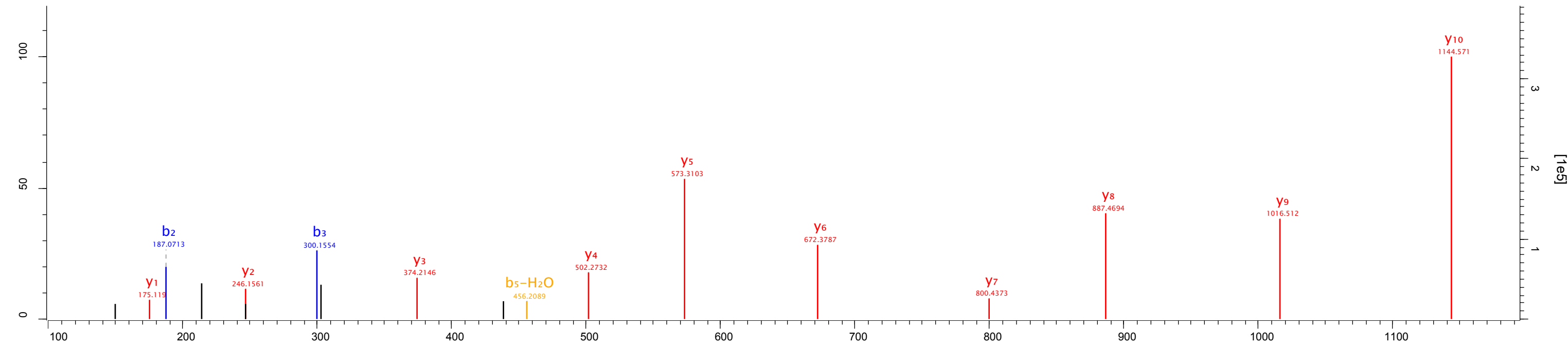


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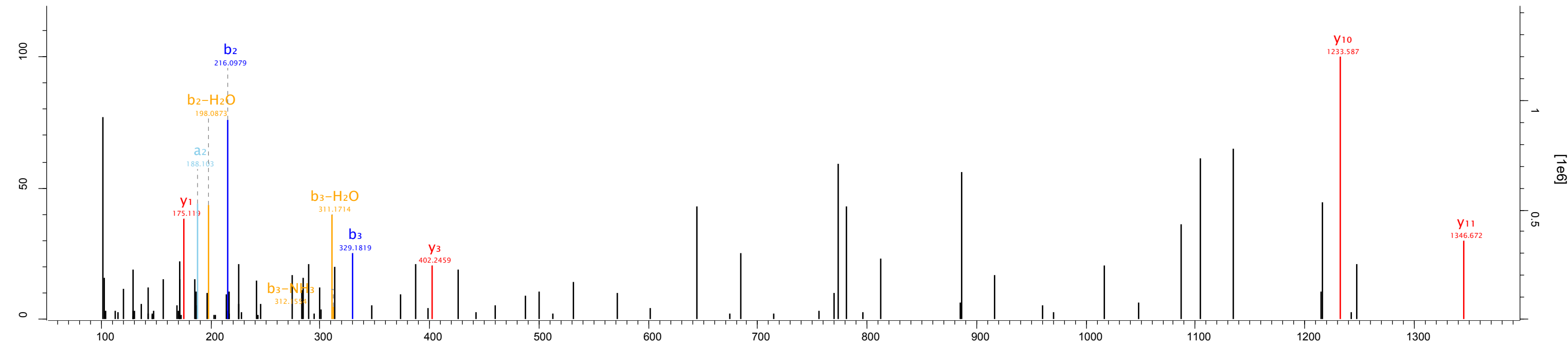


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20180707_MaS_A375SR_LM_proteome_01

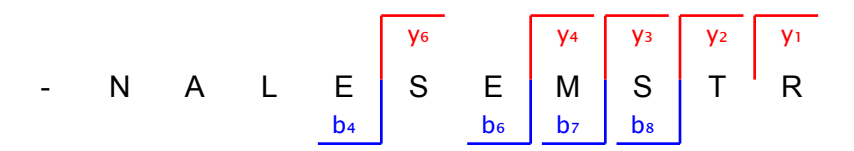
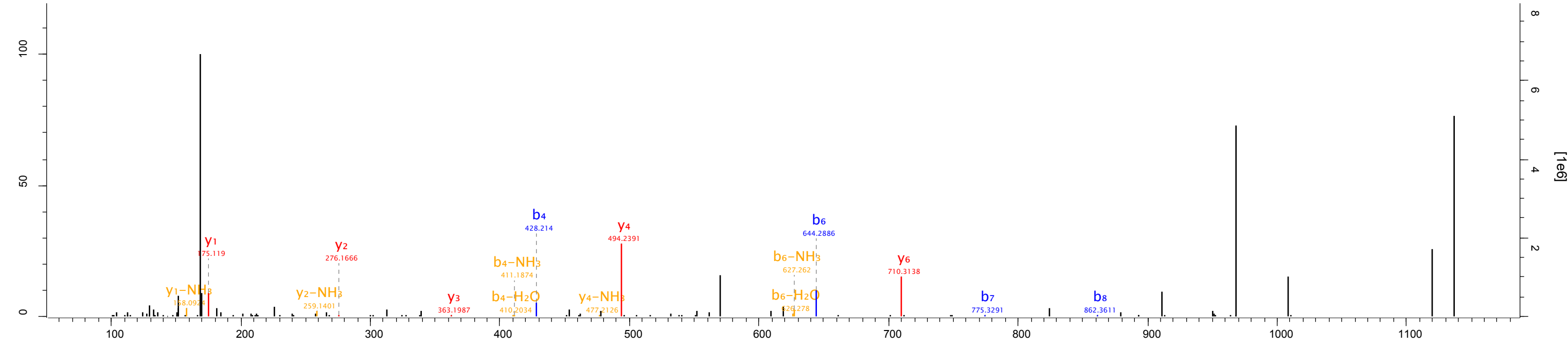
Scan 12837 Method FTMS; HCD Score 41.7 m/z 859.43 Gene names APOC3



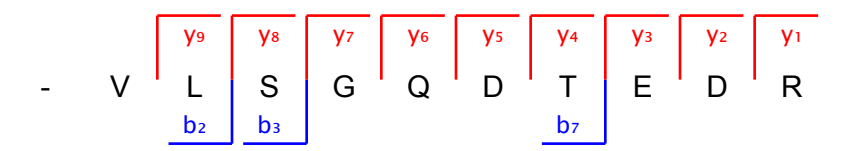
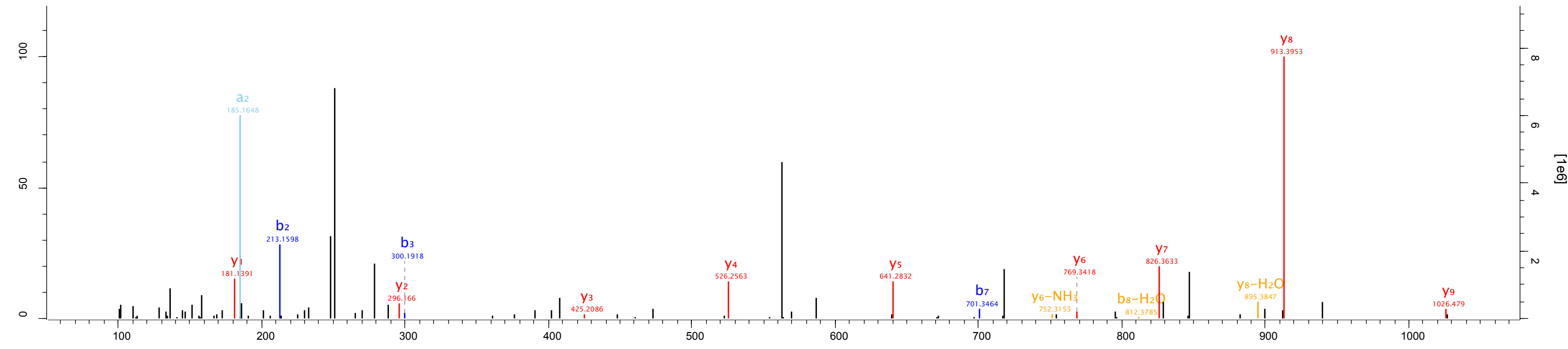
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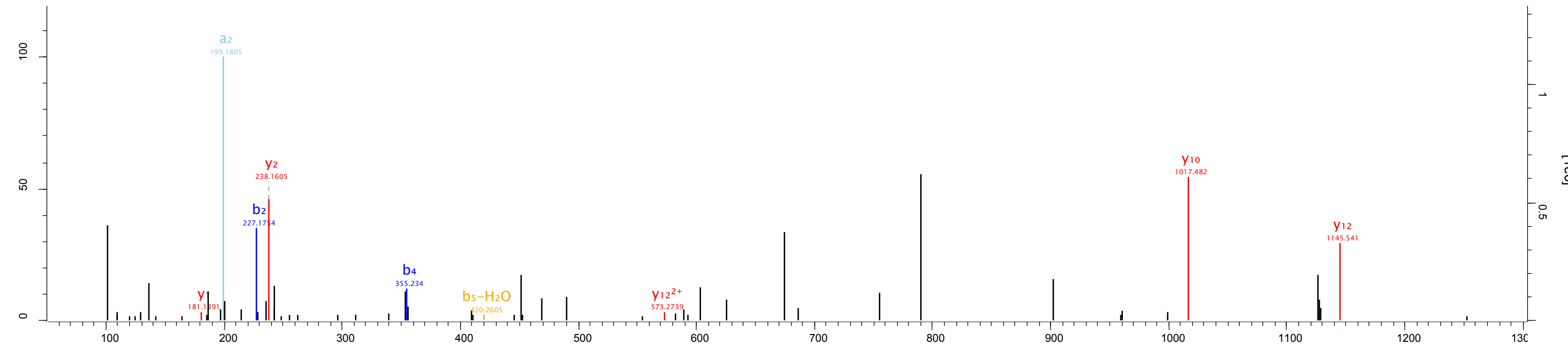
20180707_MaS_A375SR_LM_proteome_03 2917 FTMS; HCD 54.34 569.76 ZEB2



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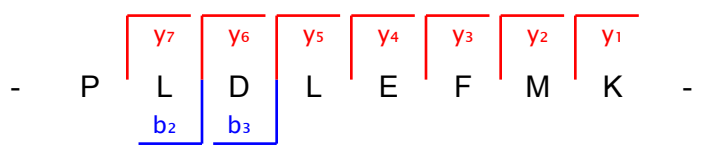
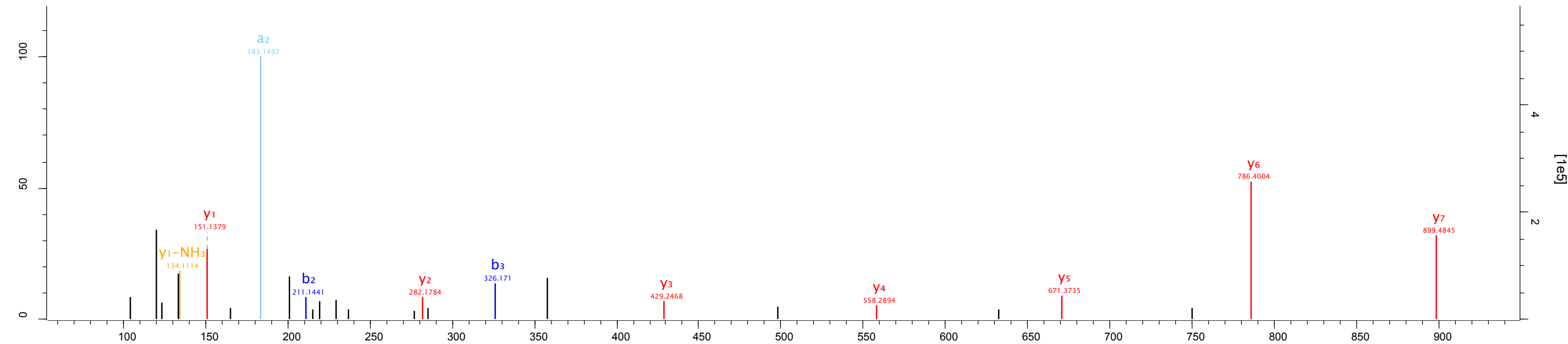


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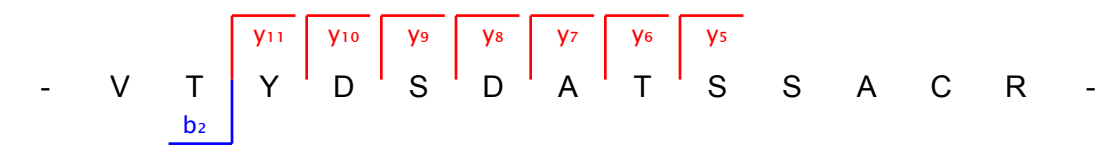
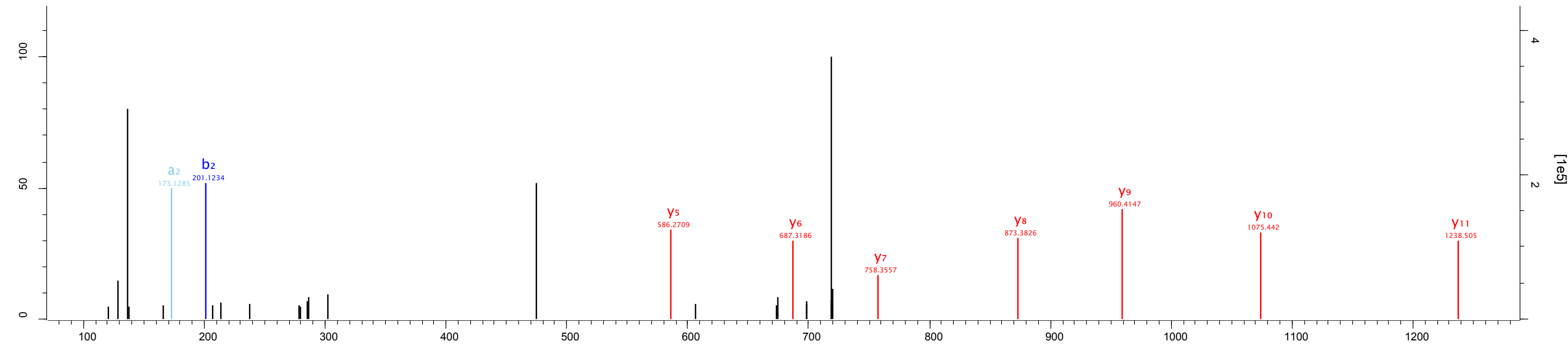
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Scan: 24727
Method: FTMS; HCD
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Gene names: SEPT3

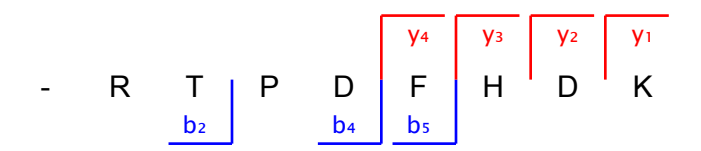
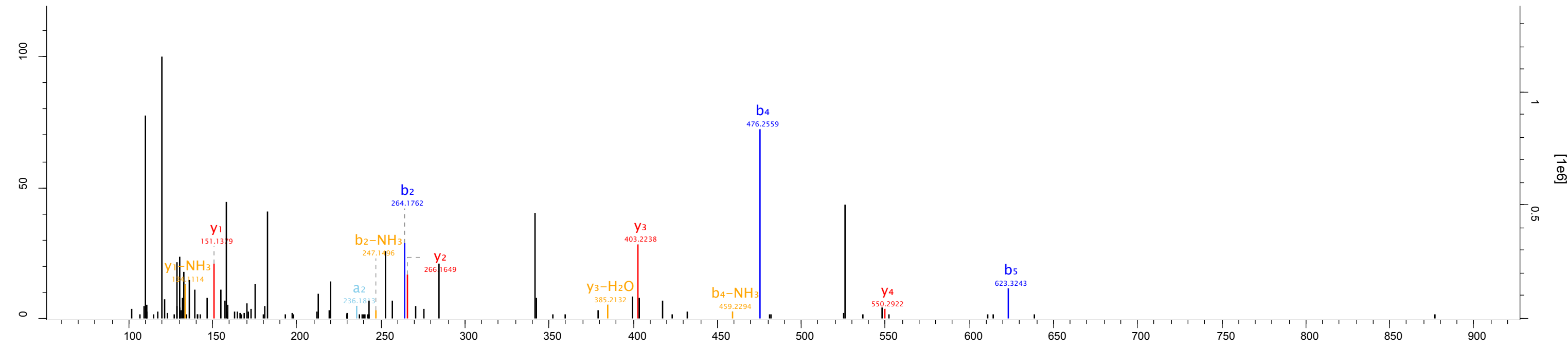


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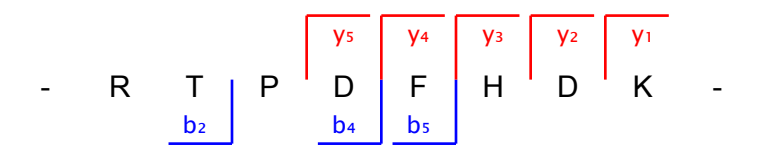
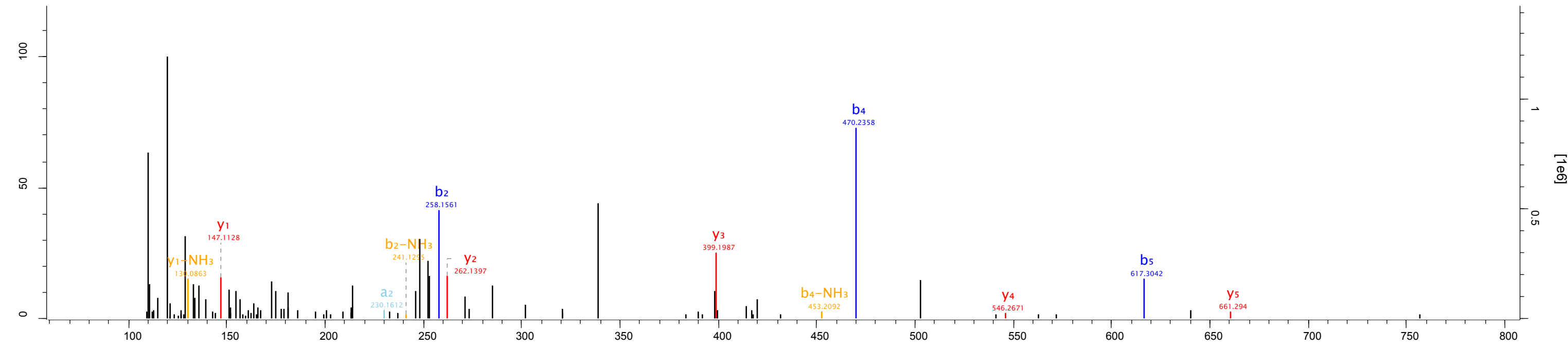
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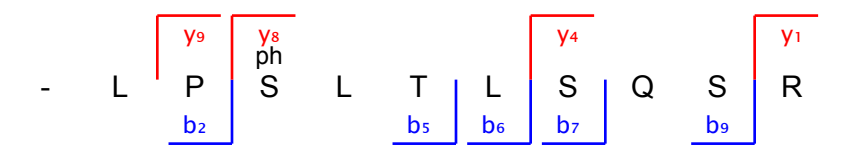
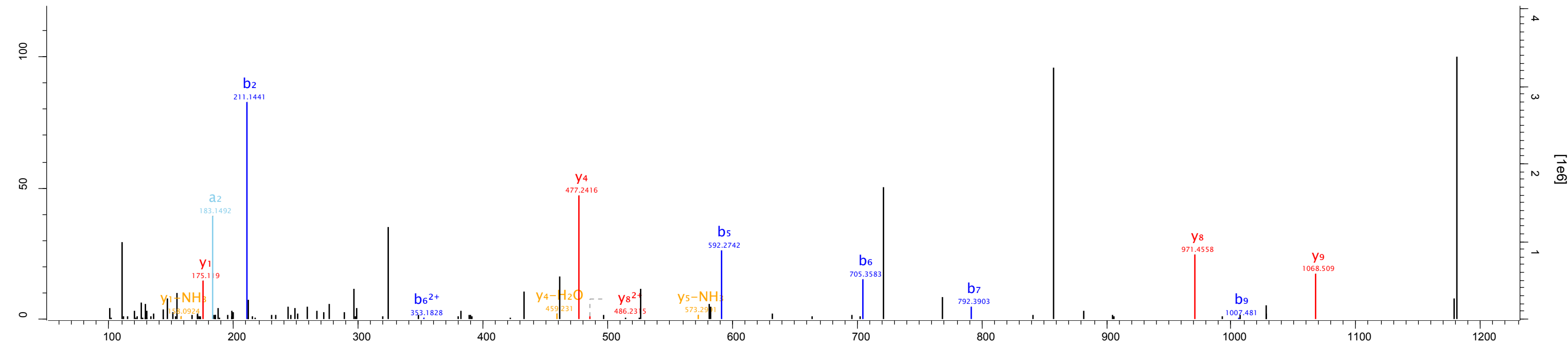
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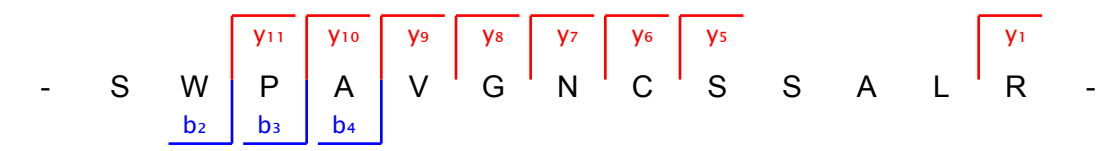
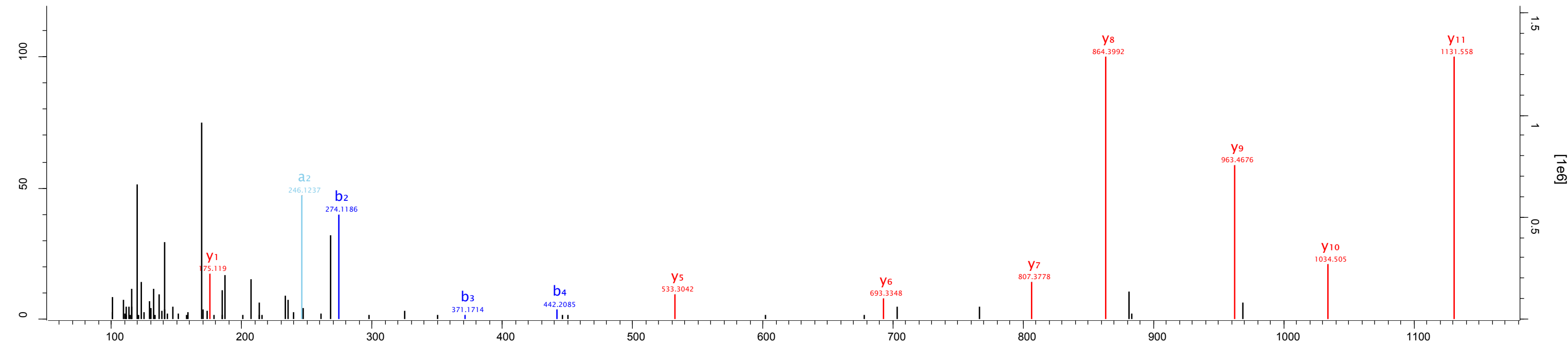
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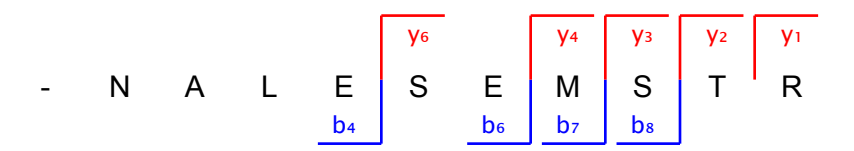
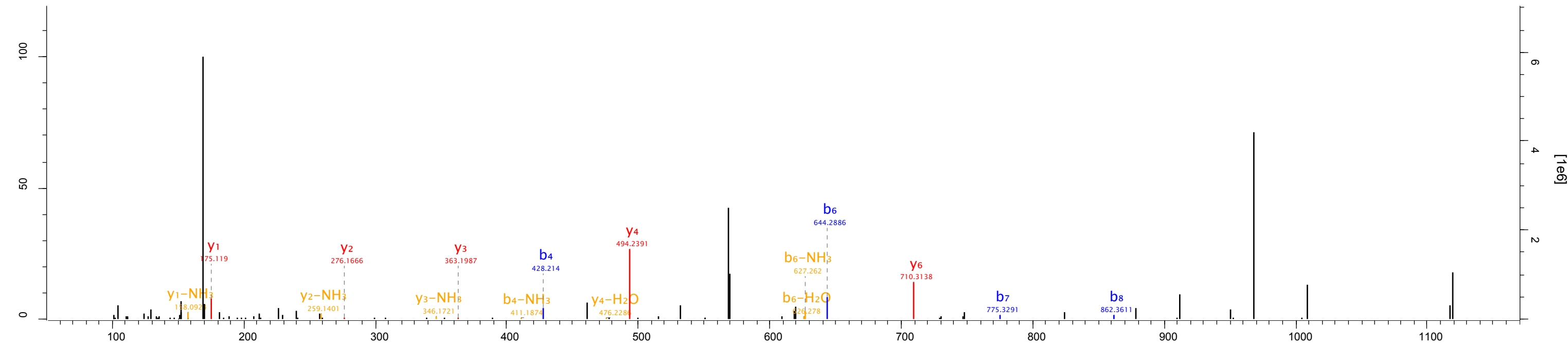
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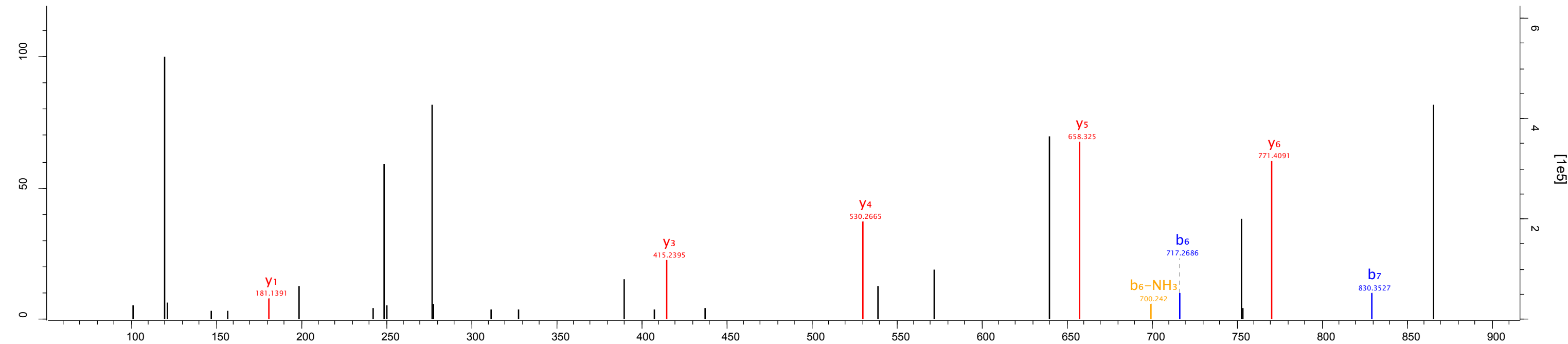


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Raw file
20180707_MaS_A375SR_LM_proteome_21

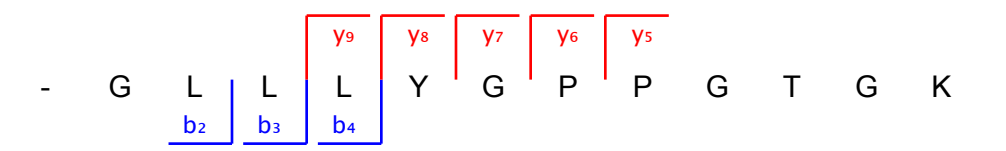
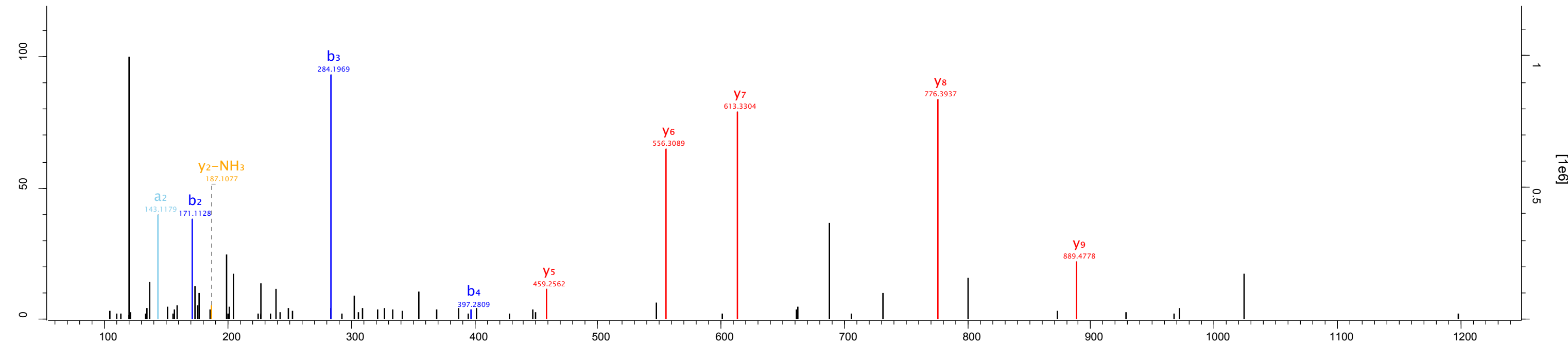
Scan Method Score m/z Gene names
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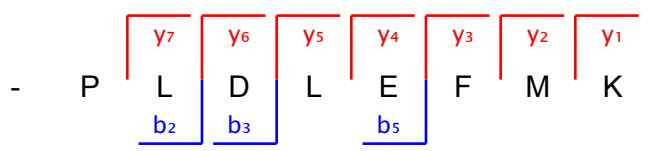
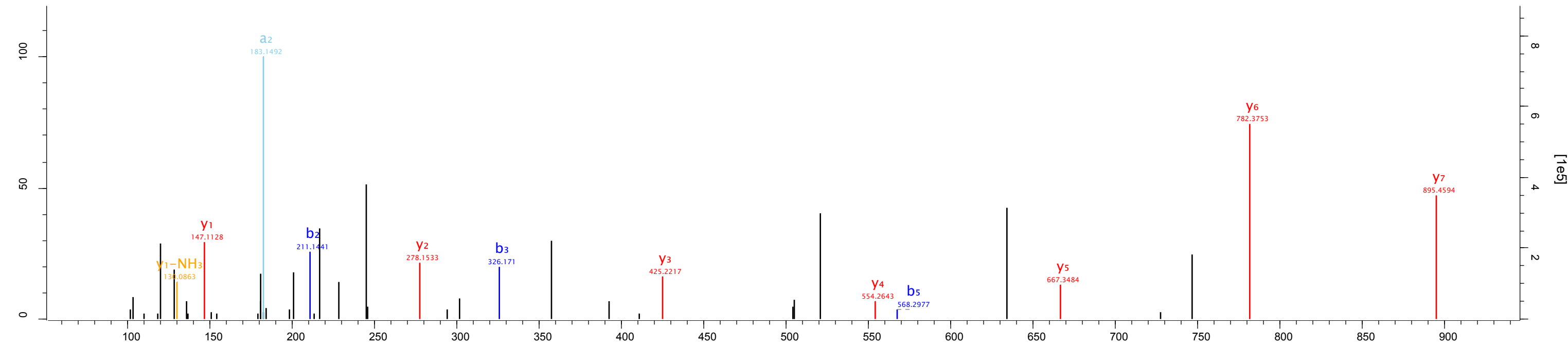
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Scan 21437 Method FTMS; HCD Score 35.52 m/z 586.84 Gene names KATNAL2



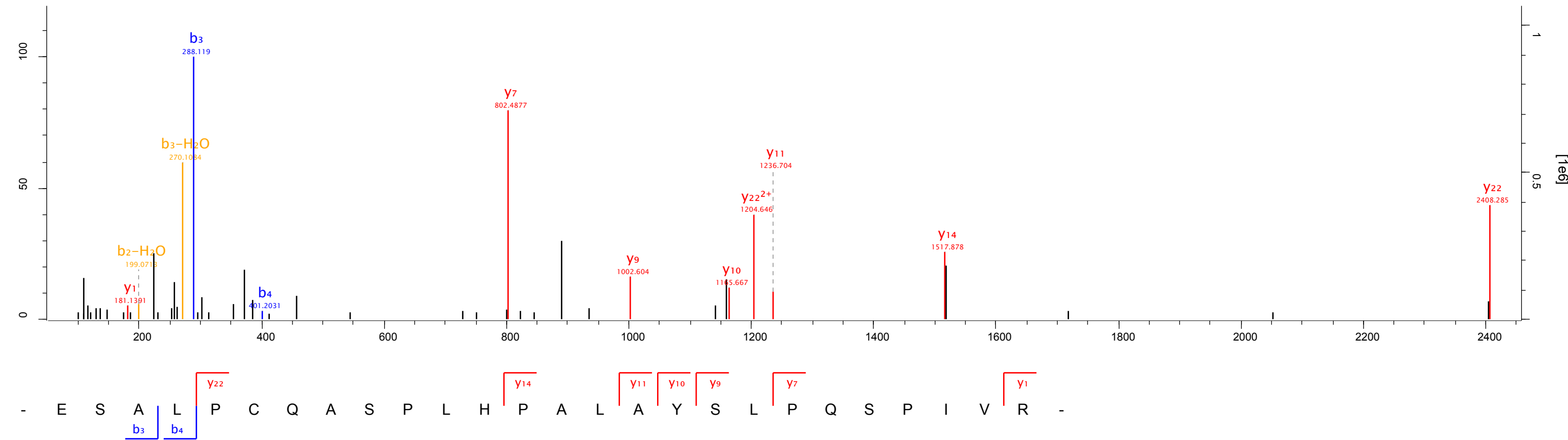
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Scan Method Score m/z Gene names
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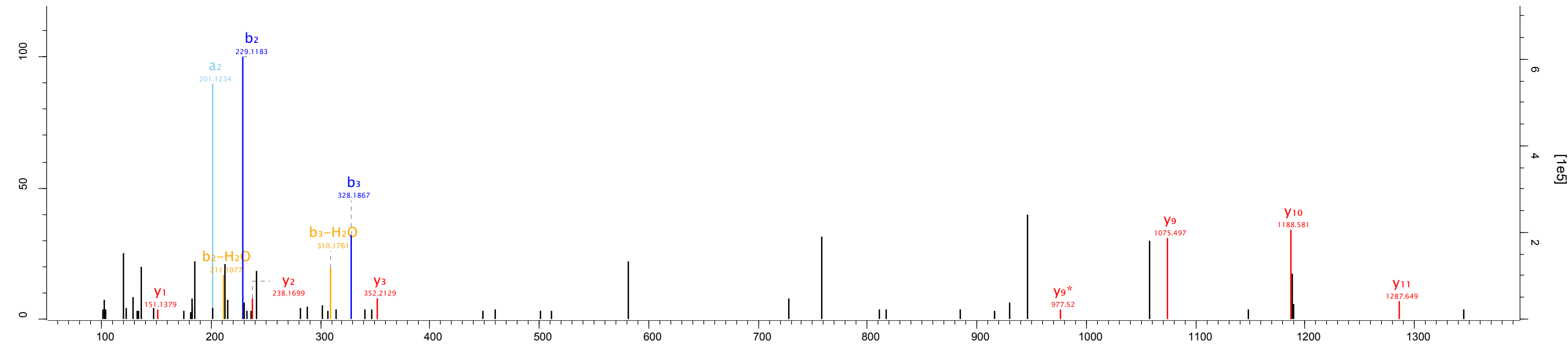


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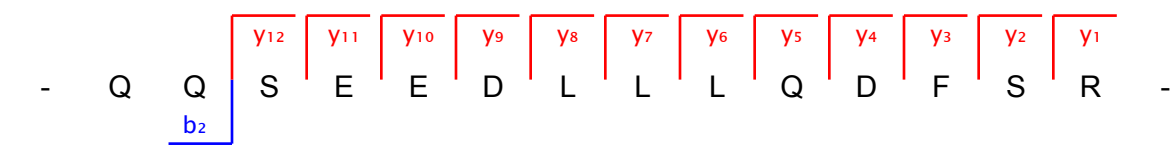
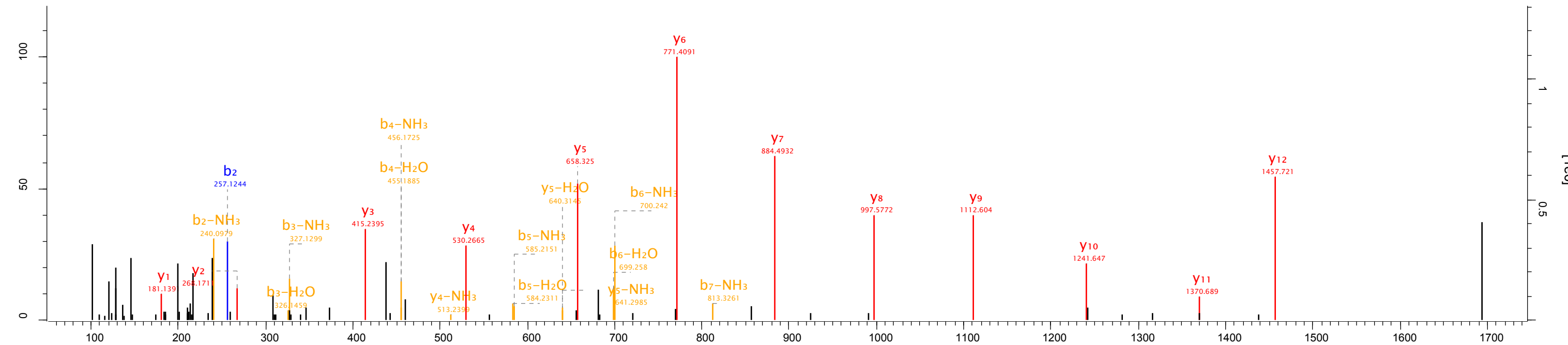
Scan Method Score m/z Gene names
26917 FTMS; HCD 17.93 936.83 C1orf85



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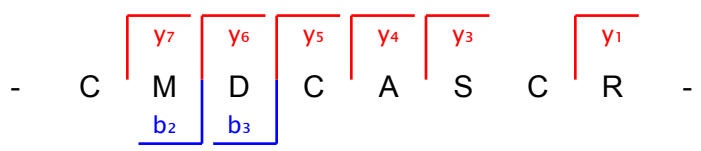
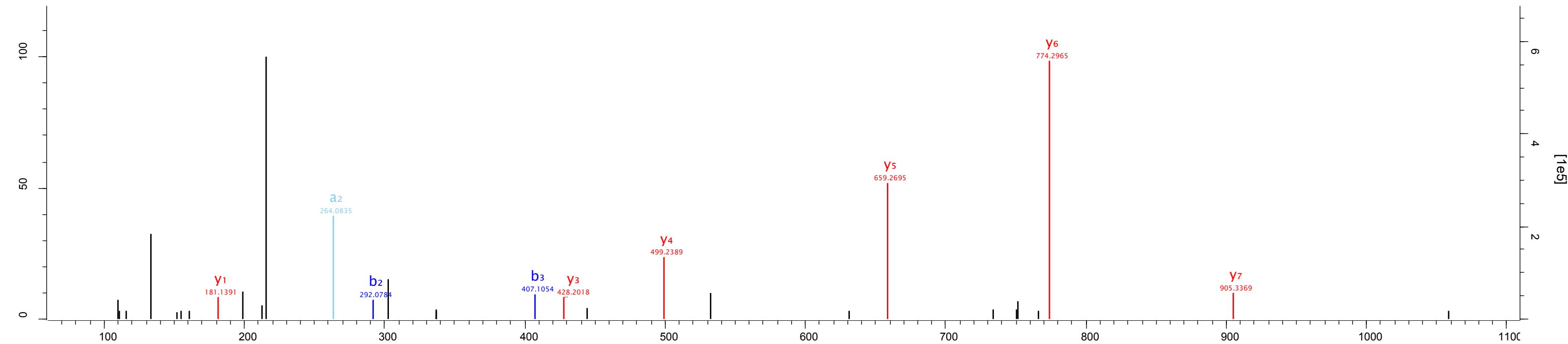


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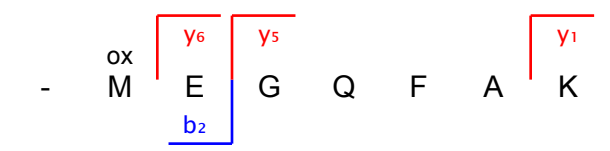
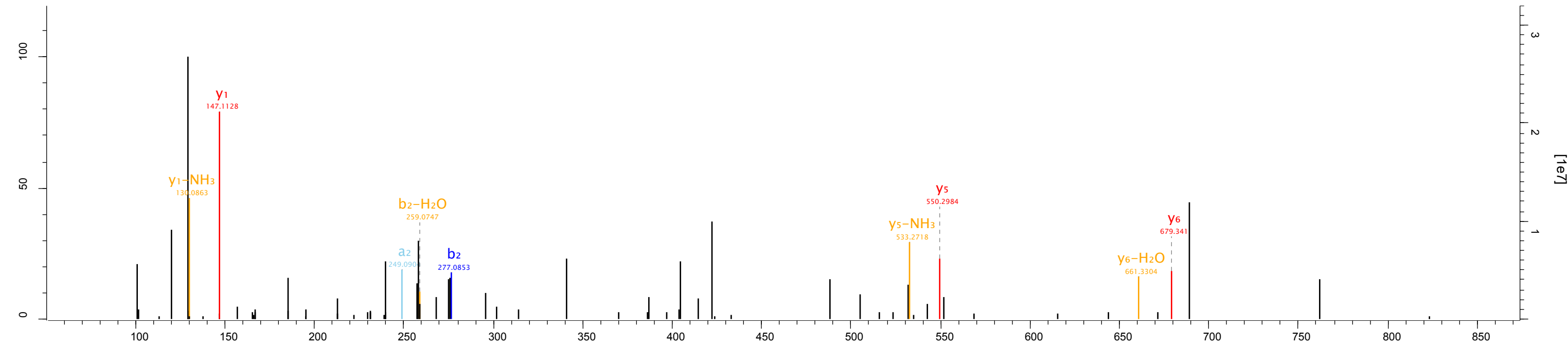
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Scan Method Score m/z Gene names
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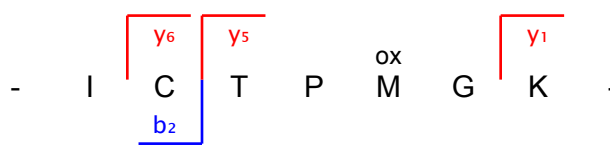
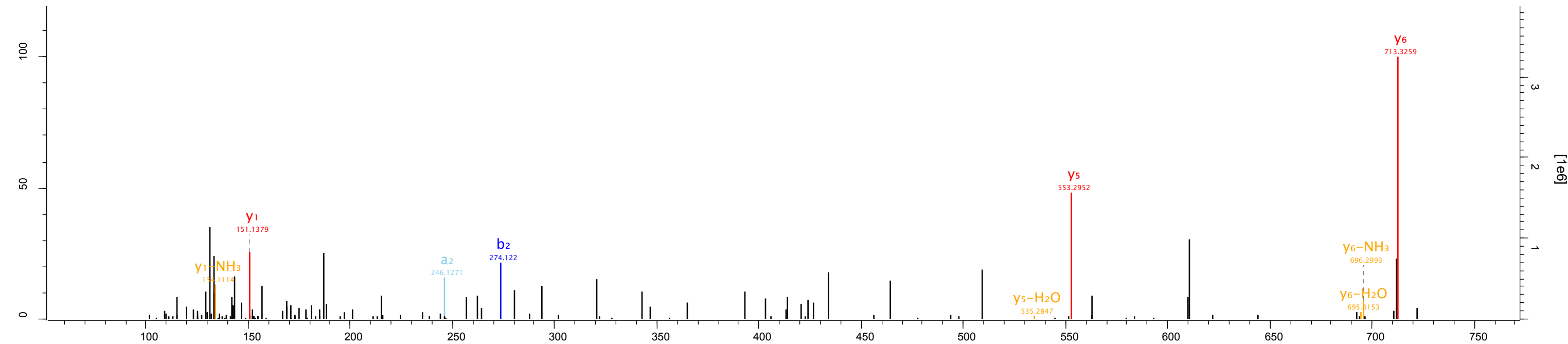


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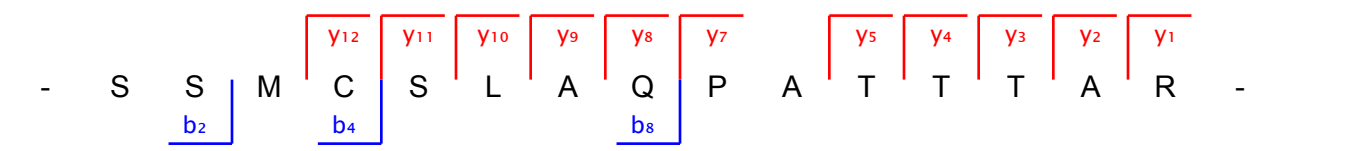
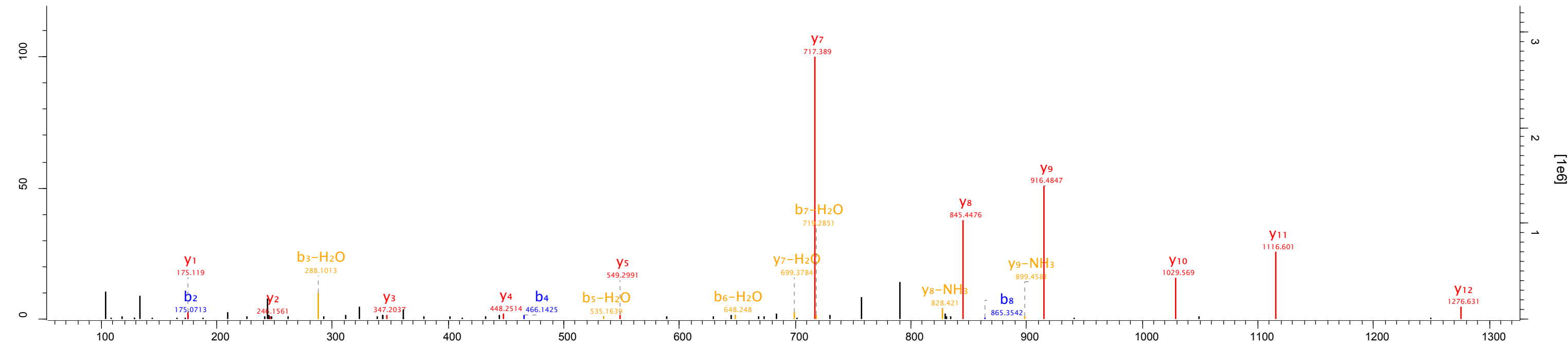
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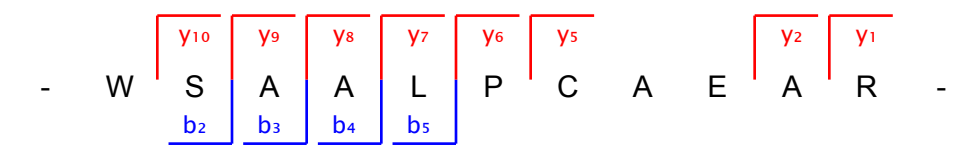
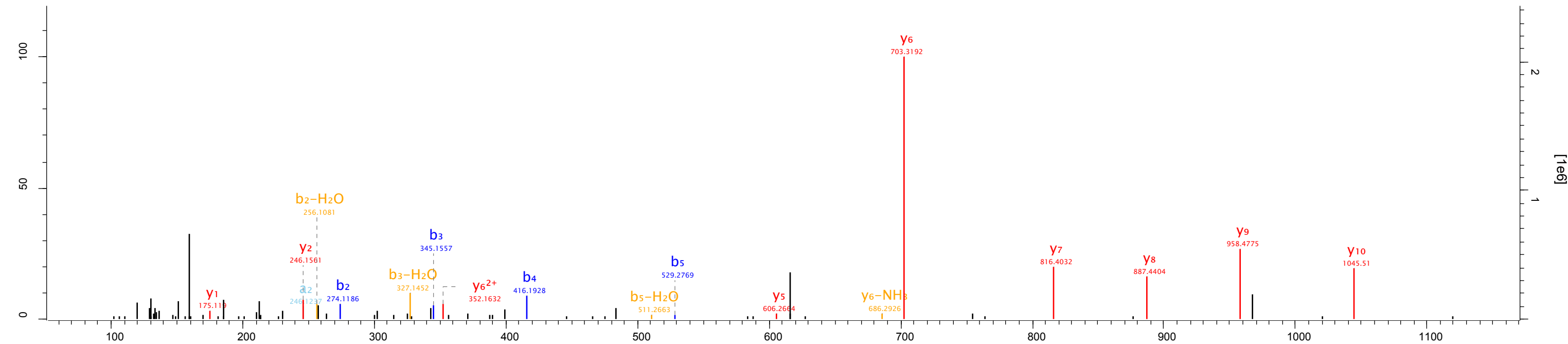
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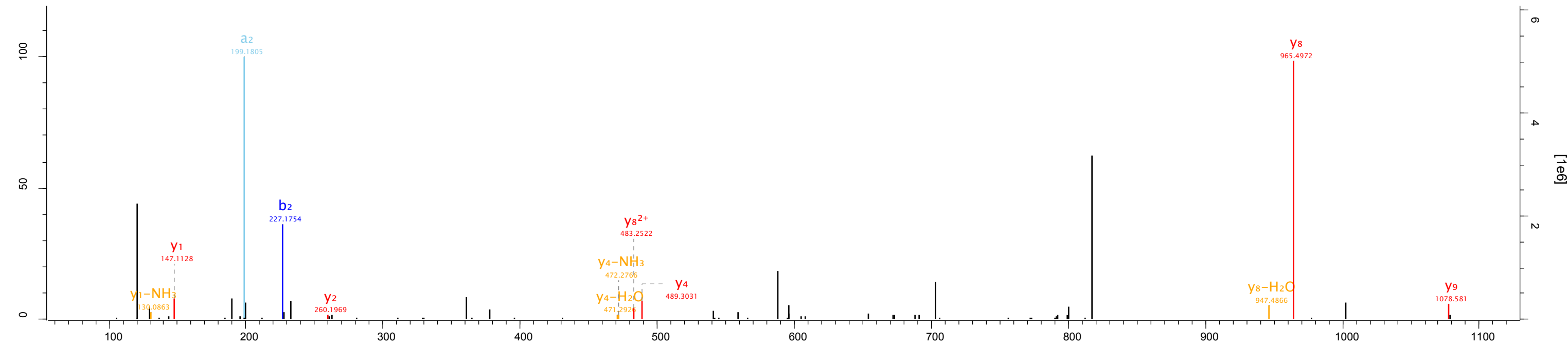


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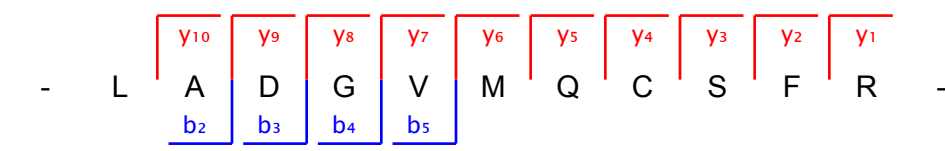
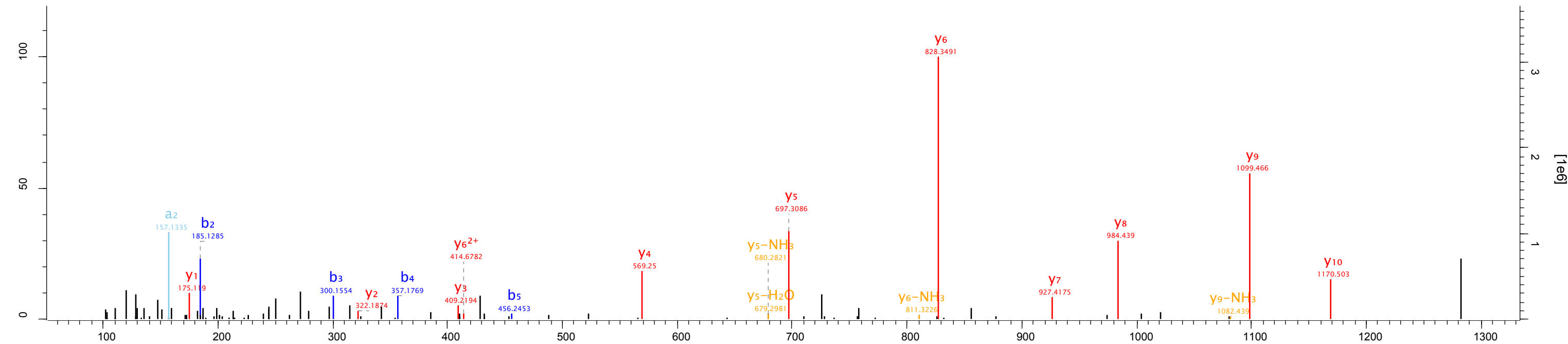


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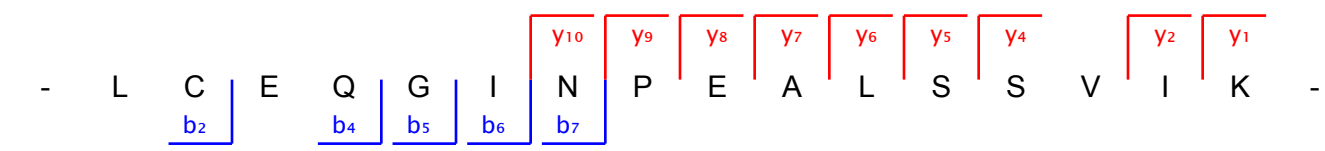
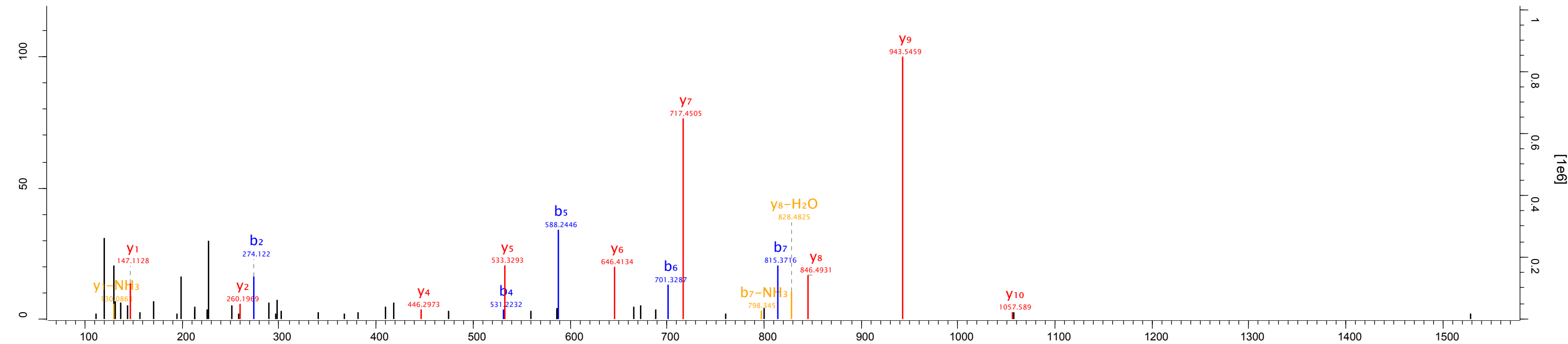


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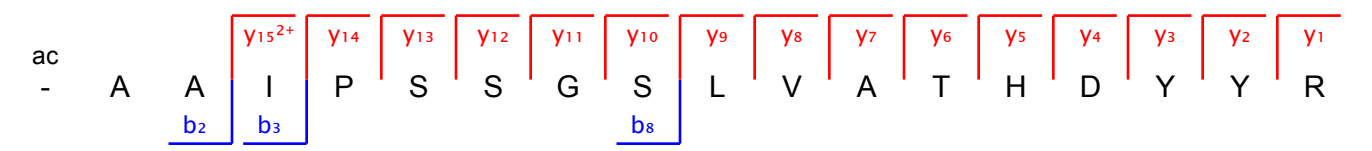
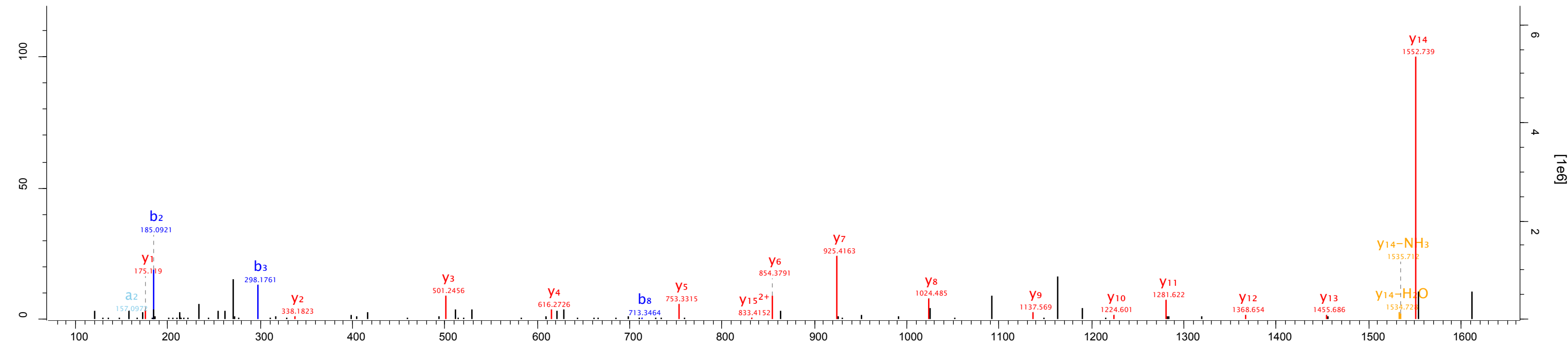
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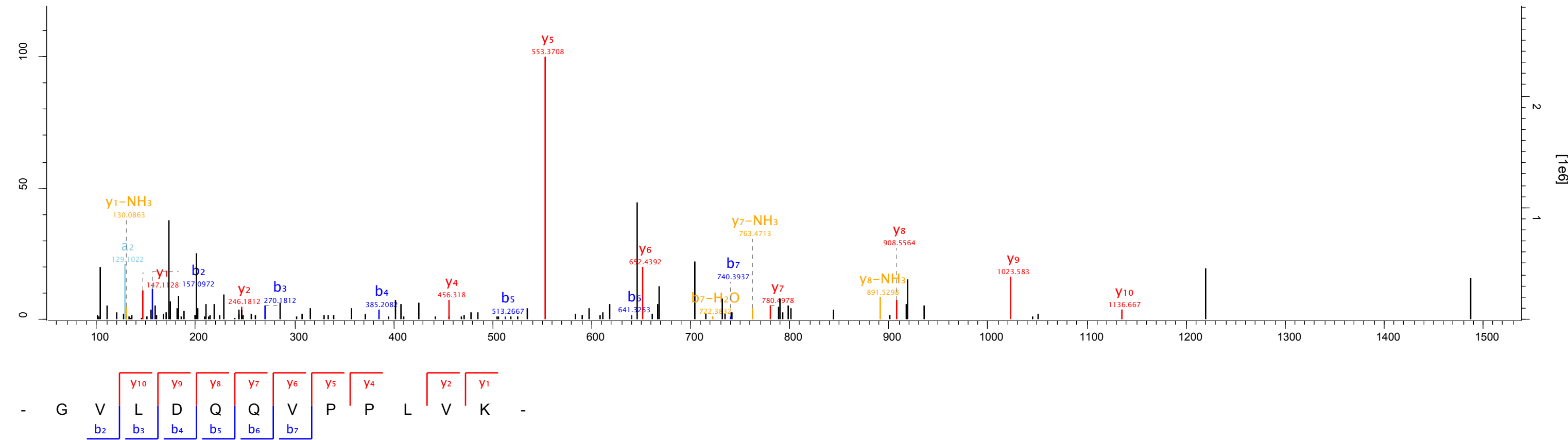
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m/z: 586.98
Gene names: MZT1



Raw file
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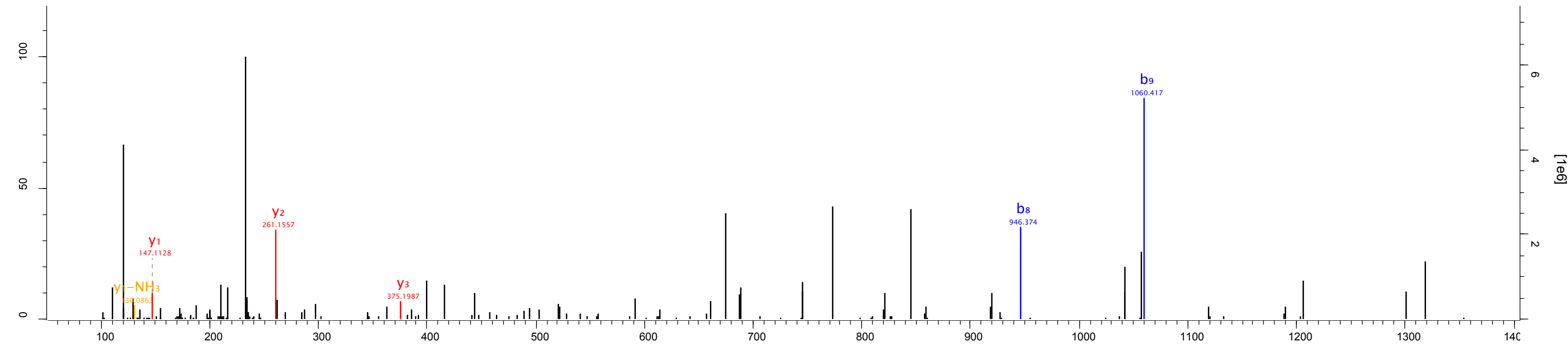
Scan 22797 Method FTMS; HCD Score 78.08 m/z 925.96 Gene names PDPDF





Raw file
20180707_MaS_A375SR_ML_proteome_06

Scan	Method	Score	m/z	Gene names
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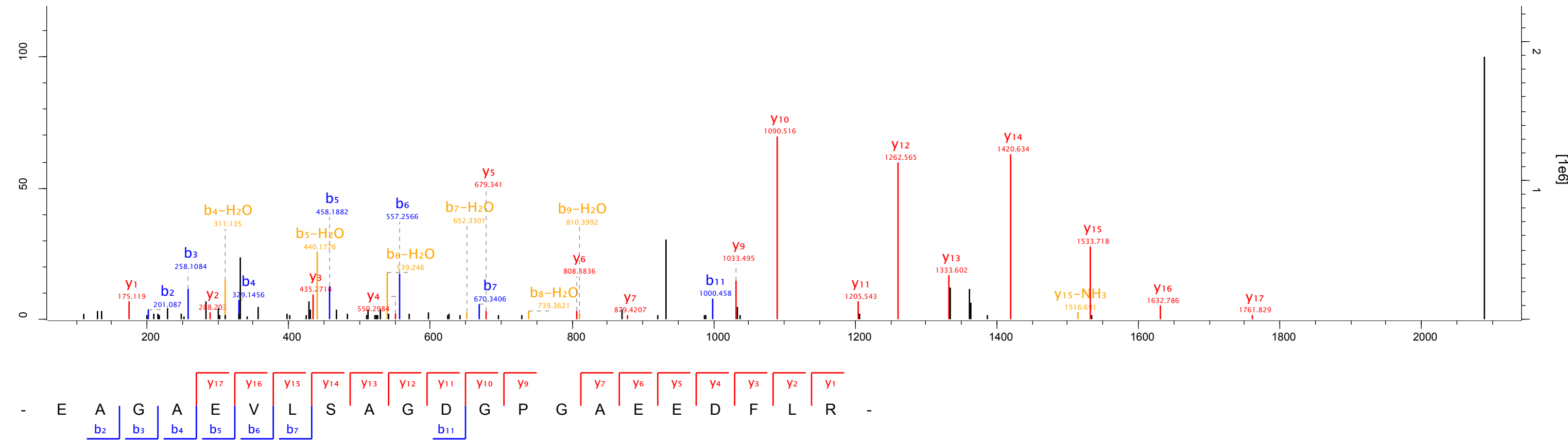


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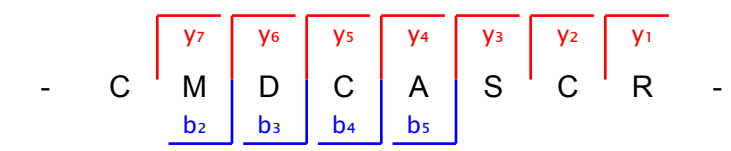
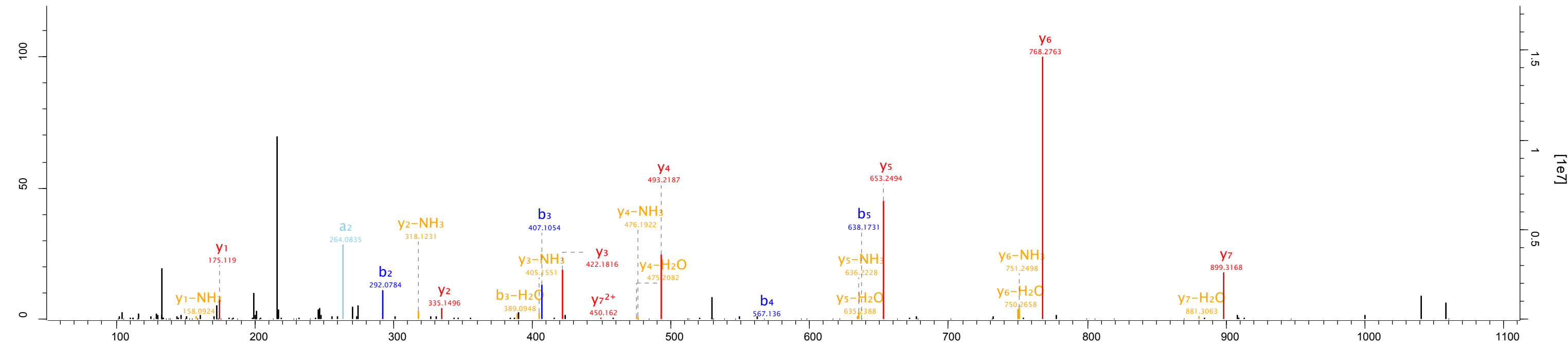
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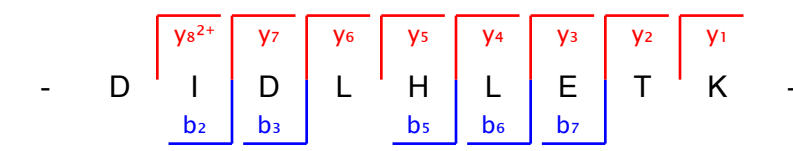
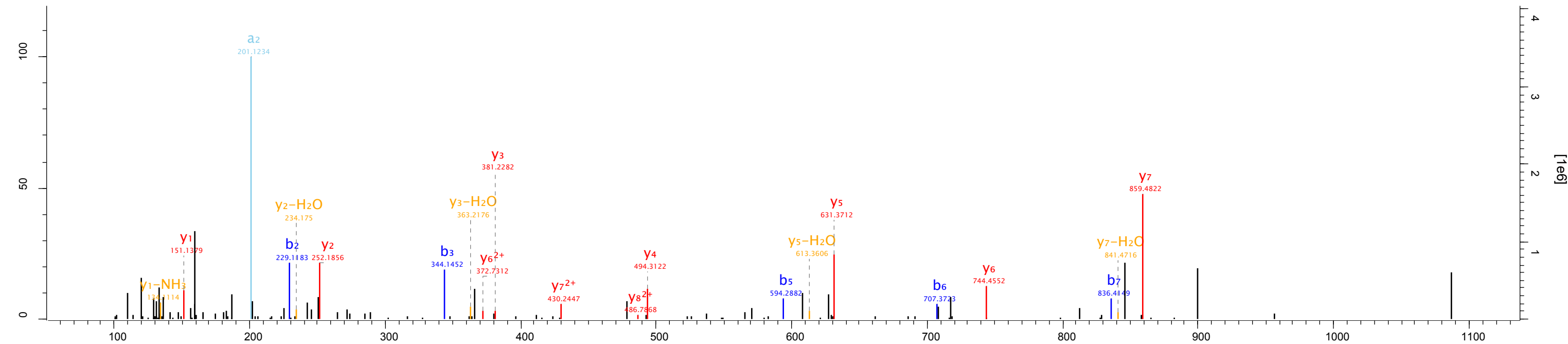


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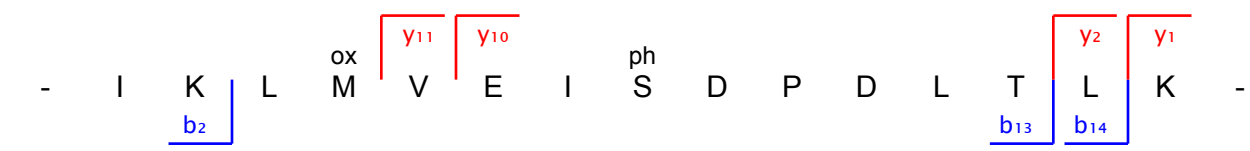
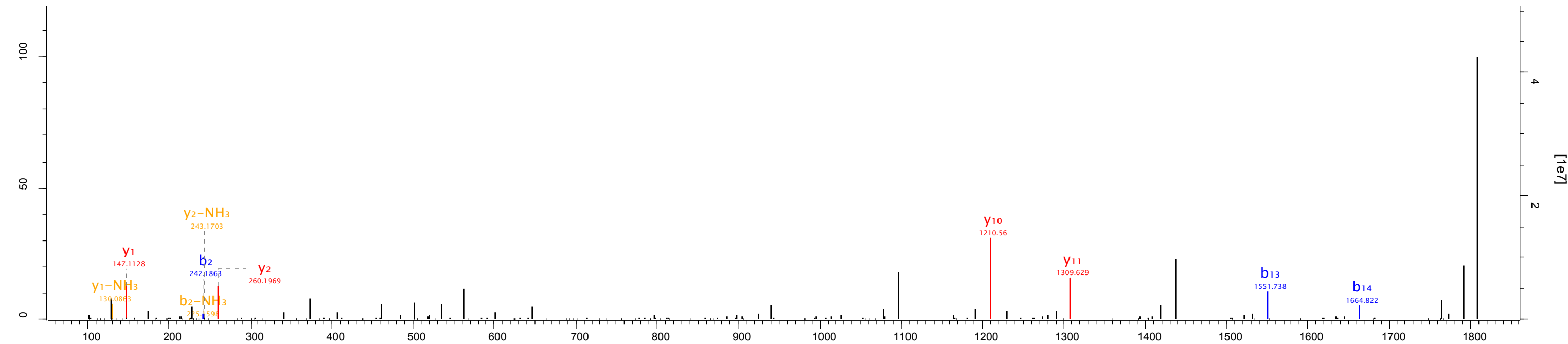
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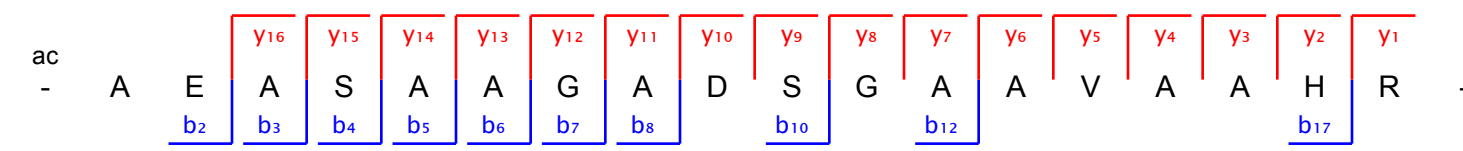
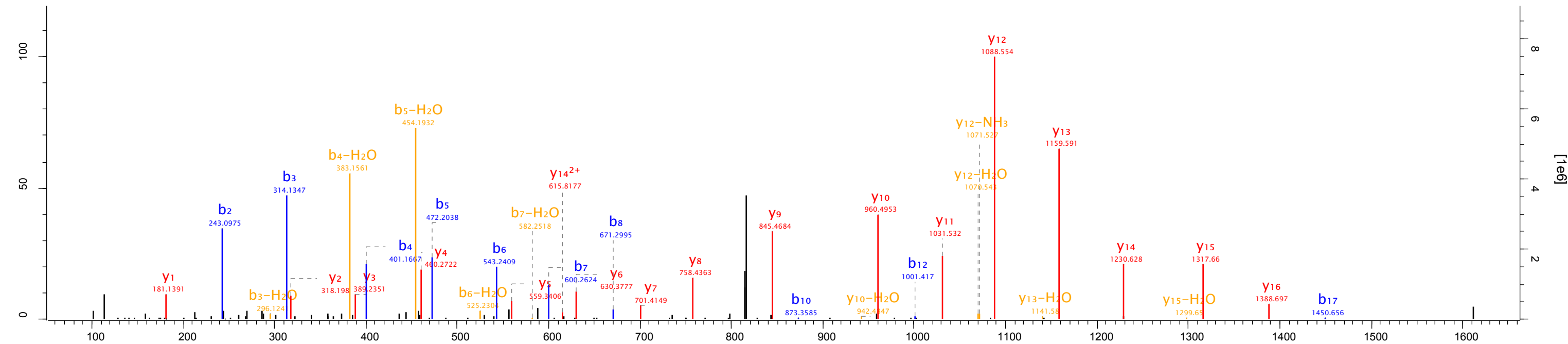
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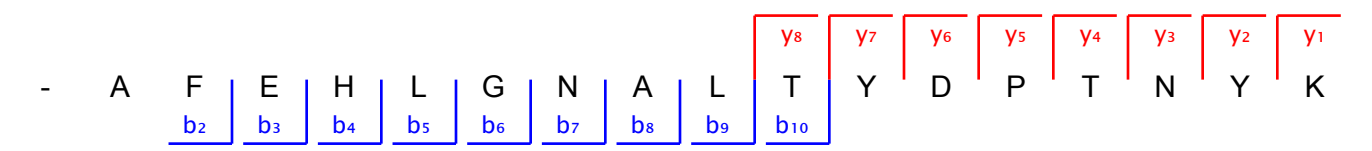
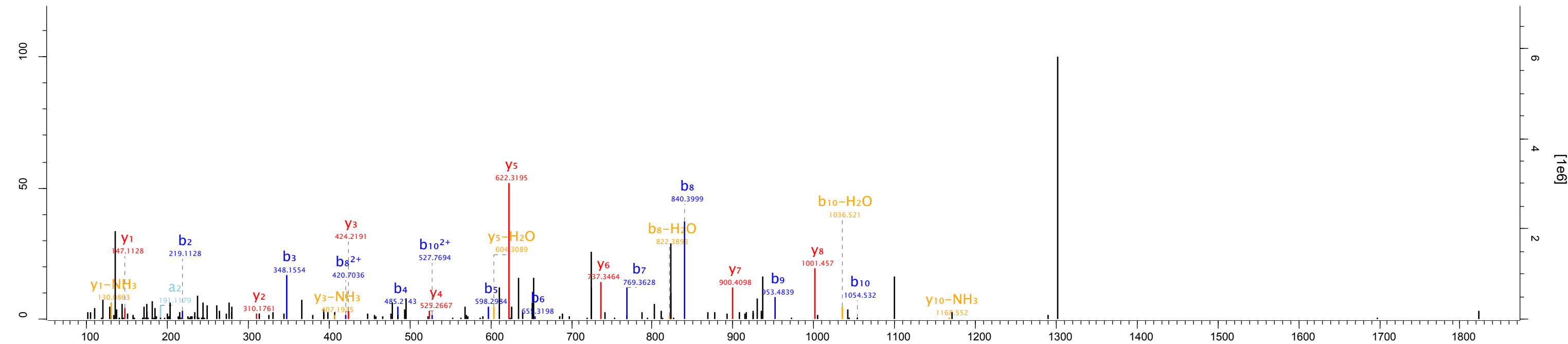


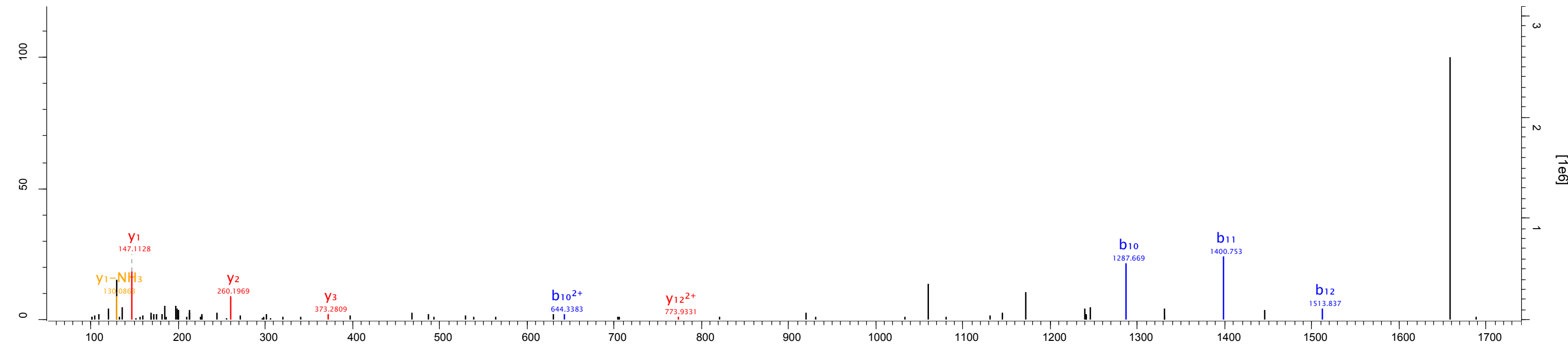
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Raw file
20180707_MaS_A375SR_ML_proteome_10

Scan Method Score m/z Gene names
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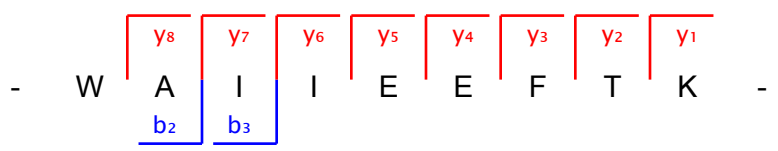
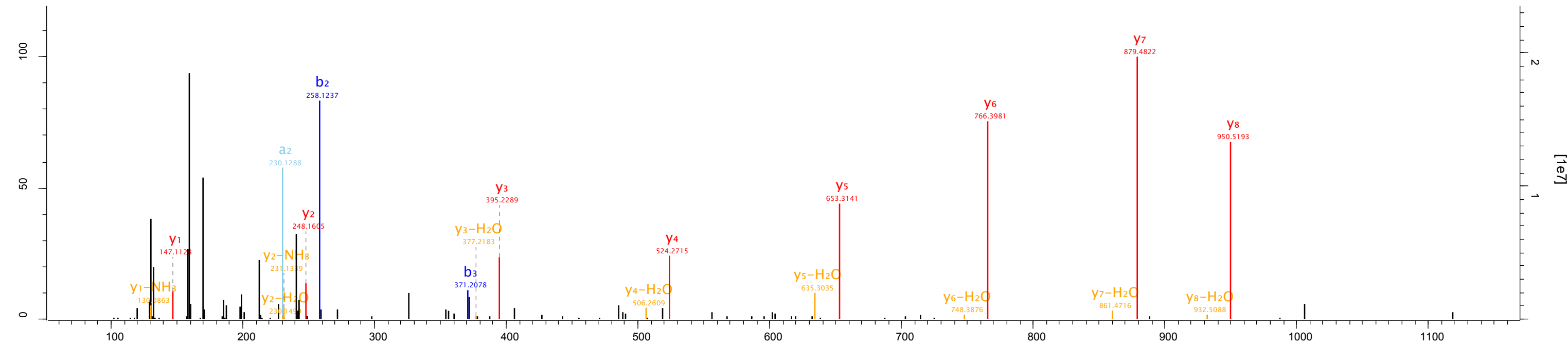
y_{12}^{2+}

b_{10} b_{11} b_{12} K -

y_3 y_2 y_1

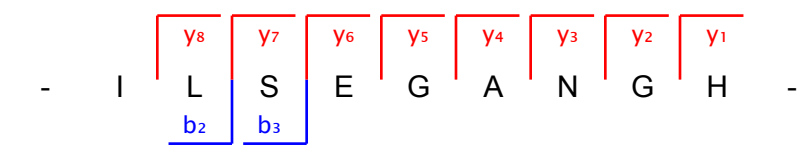
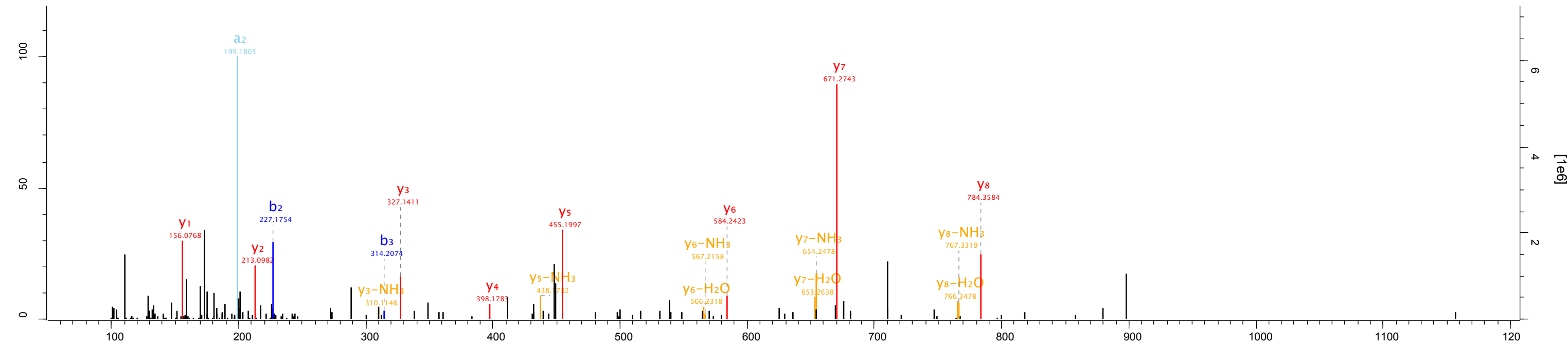
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Scan 28727 Method FTMS; HCD Score 113.62 m/z 568.8 Gene names MT-ND2

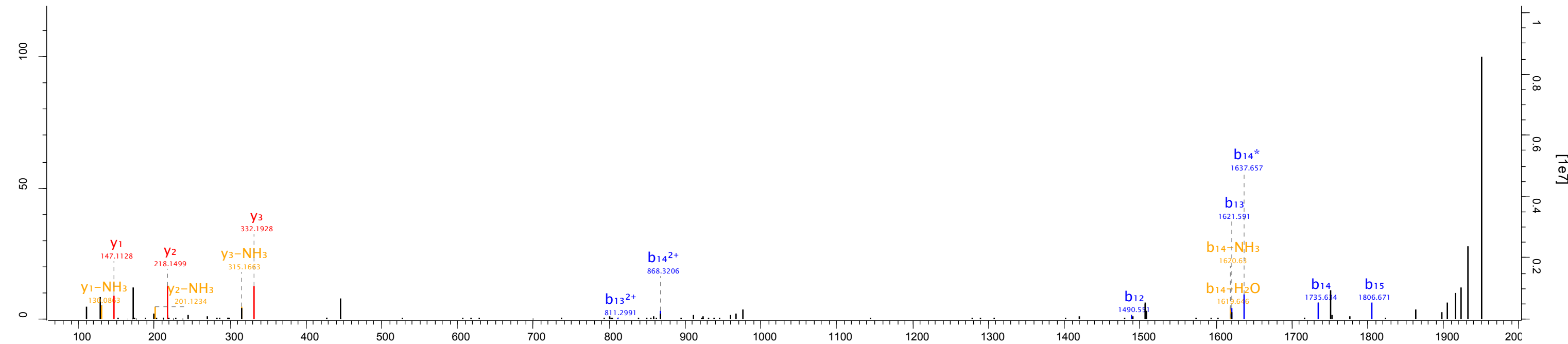


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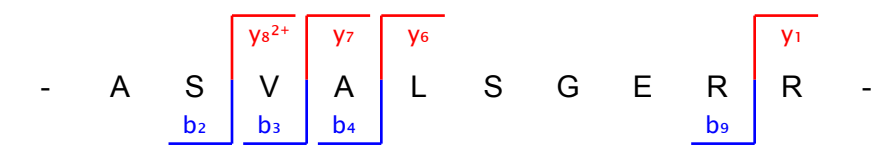
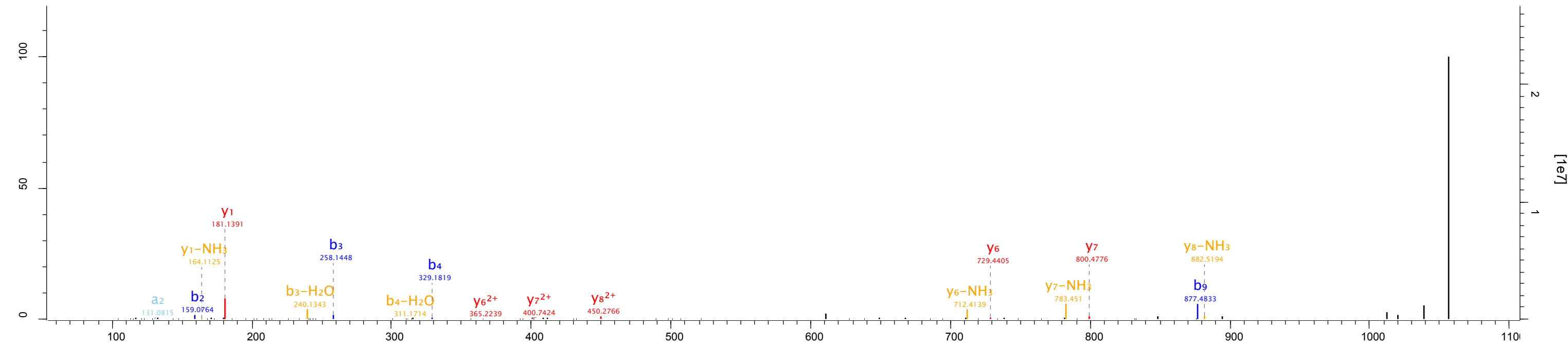
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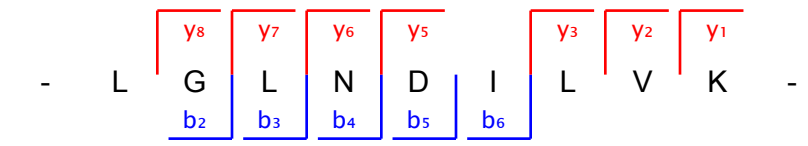
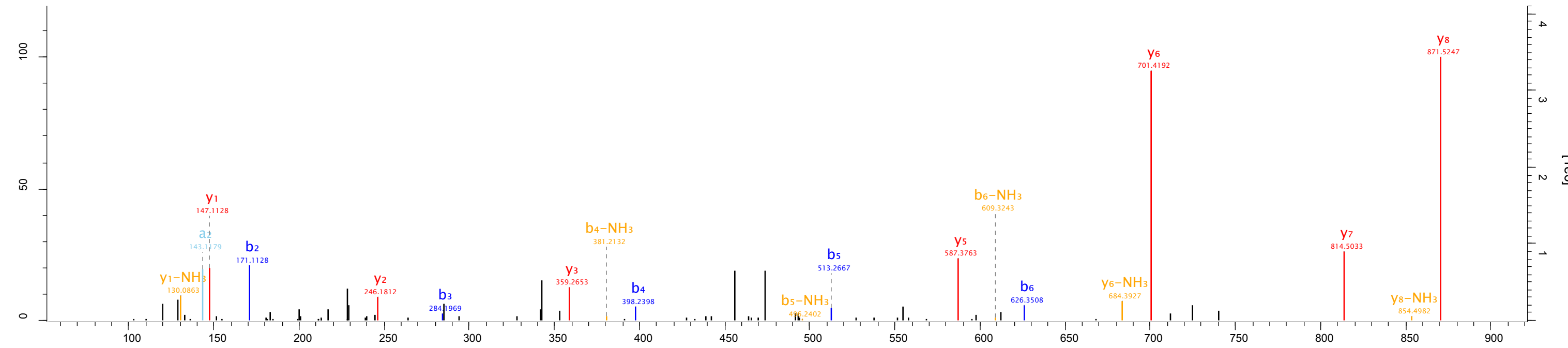
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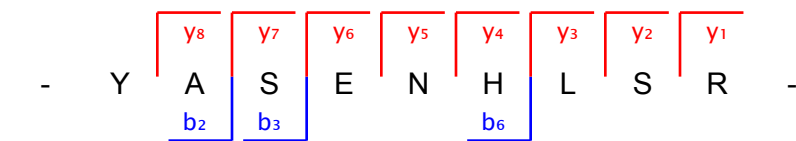
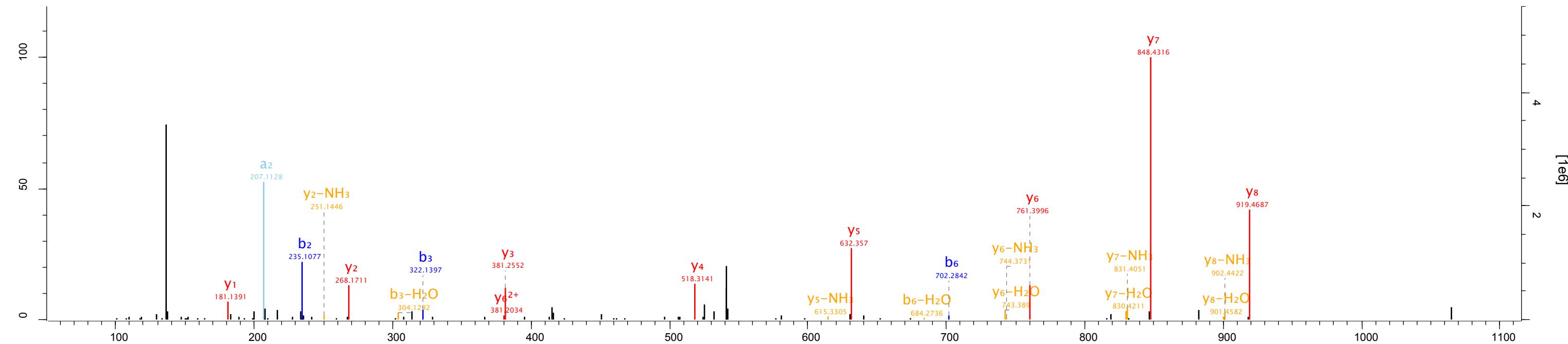


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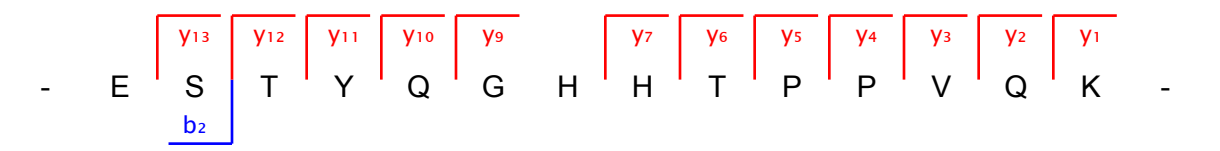
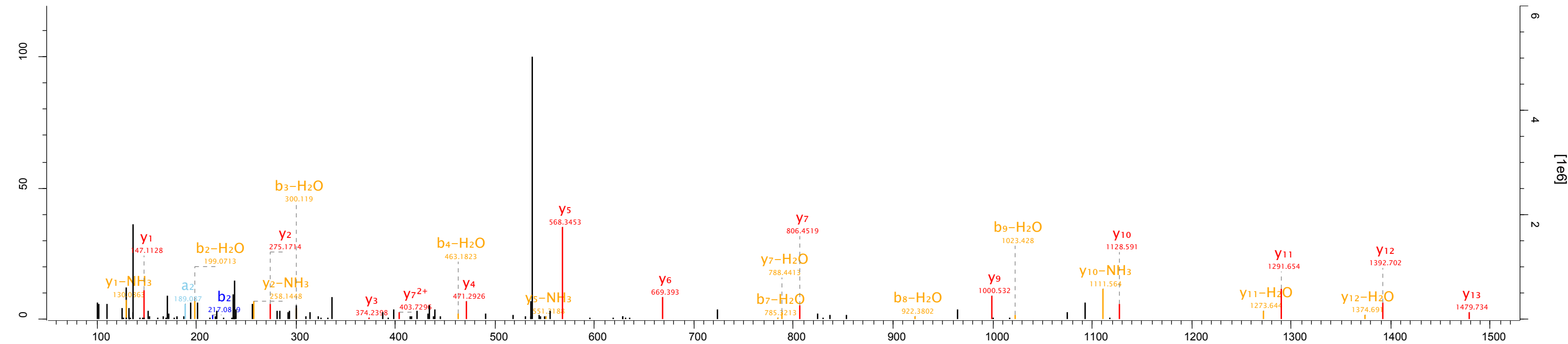


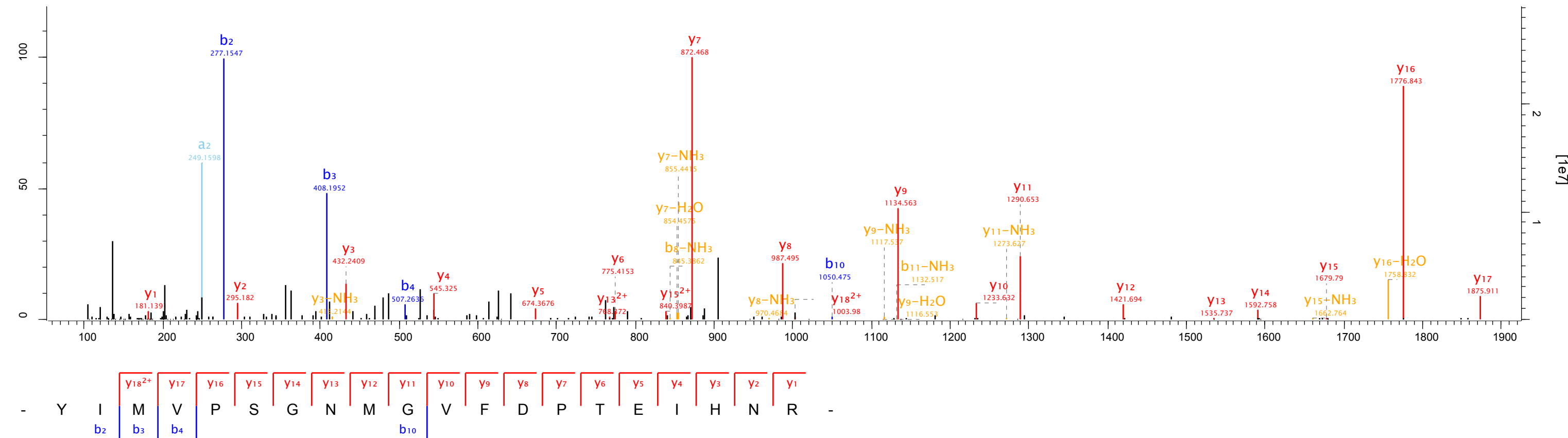
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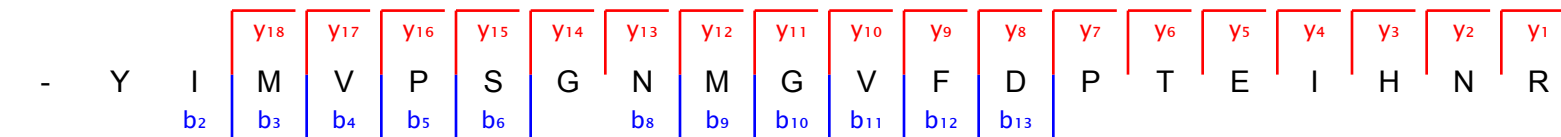
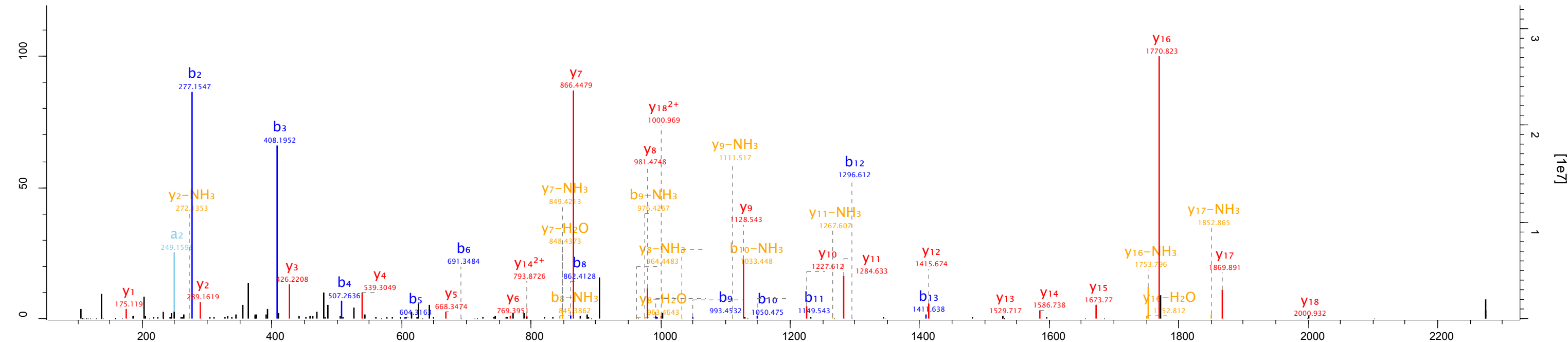
Scan Method Score m/z Gene names
3047 FTMS; HCD 148.94 541.77 TM4SF1



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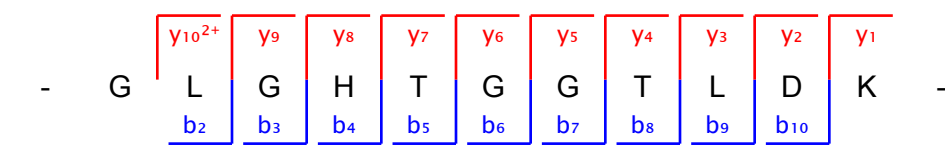
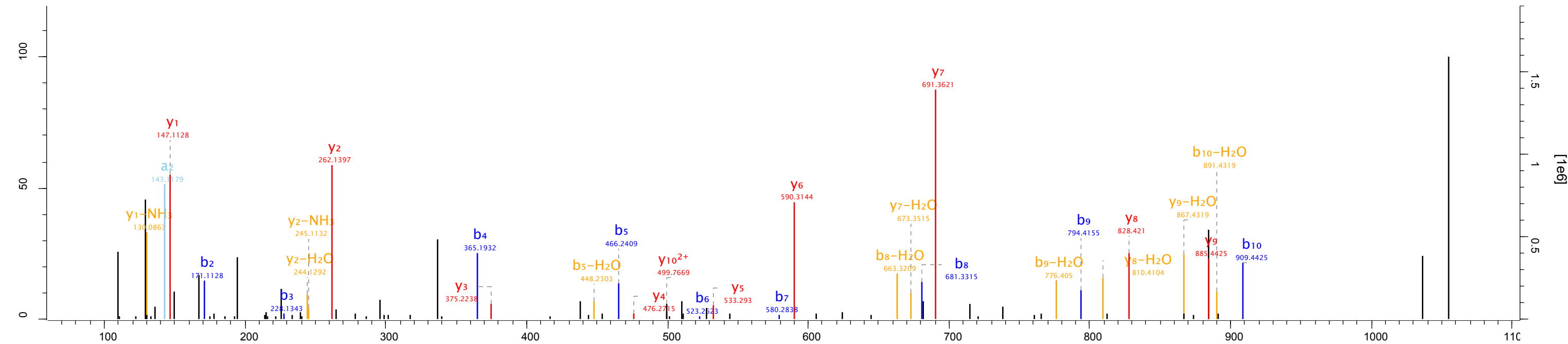




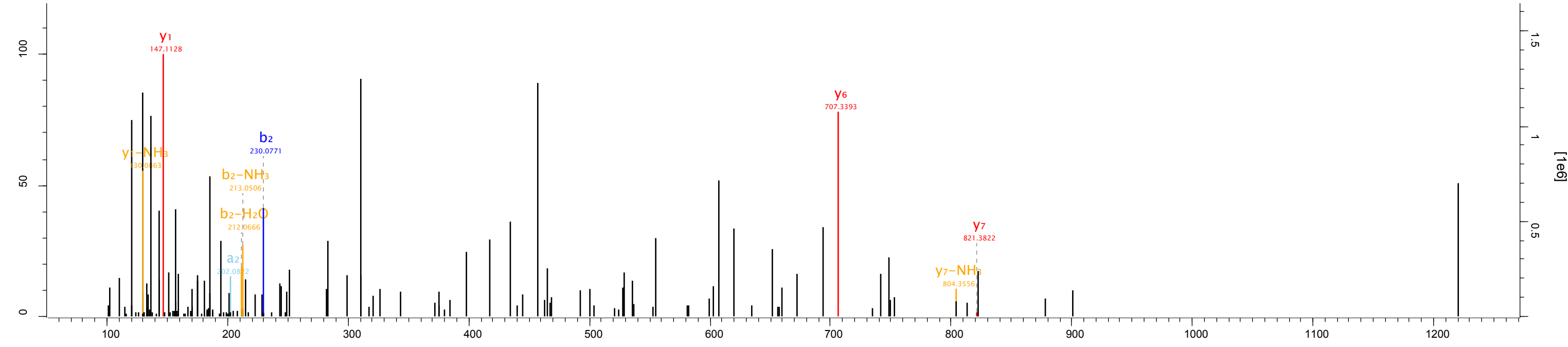


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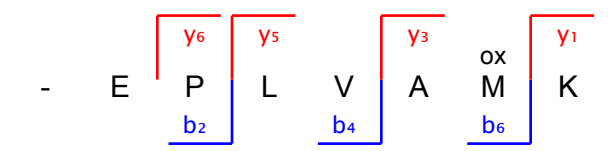
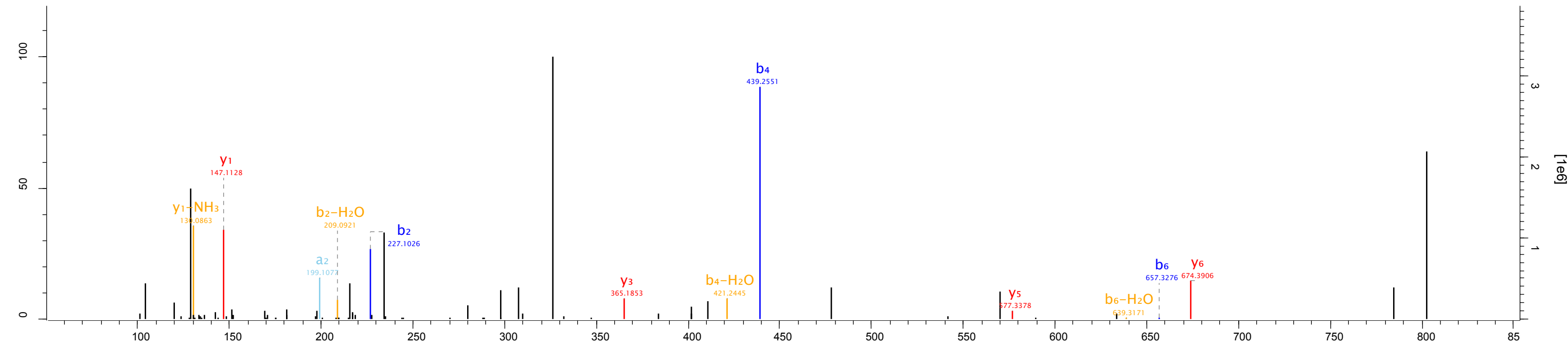
Scan 4397 Method FTMS; HCD Score 155.33 m/z 528.28 Gene names TYMP



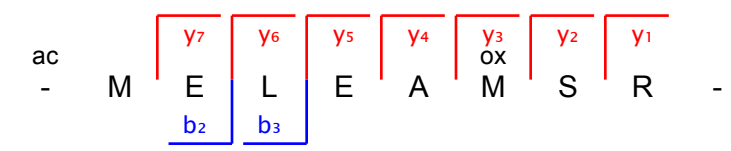
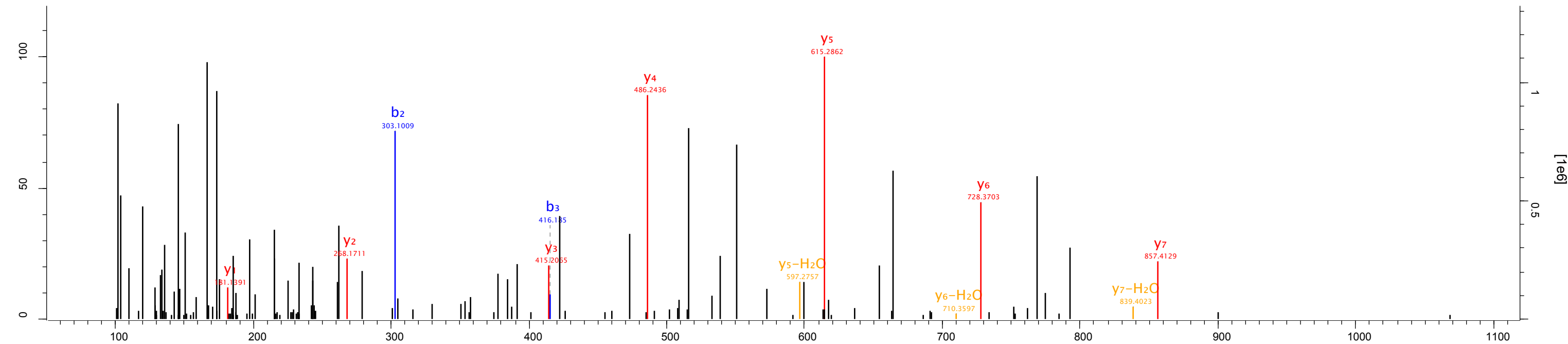
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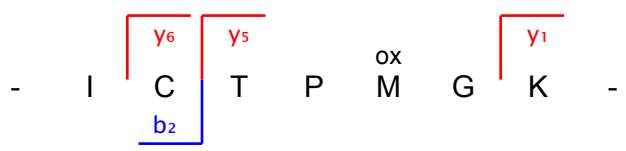
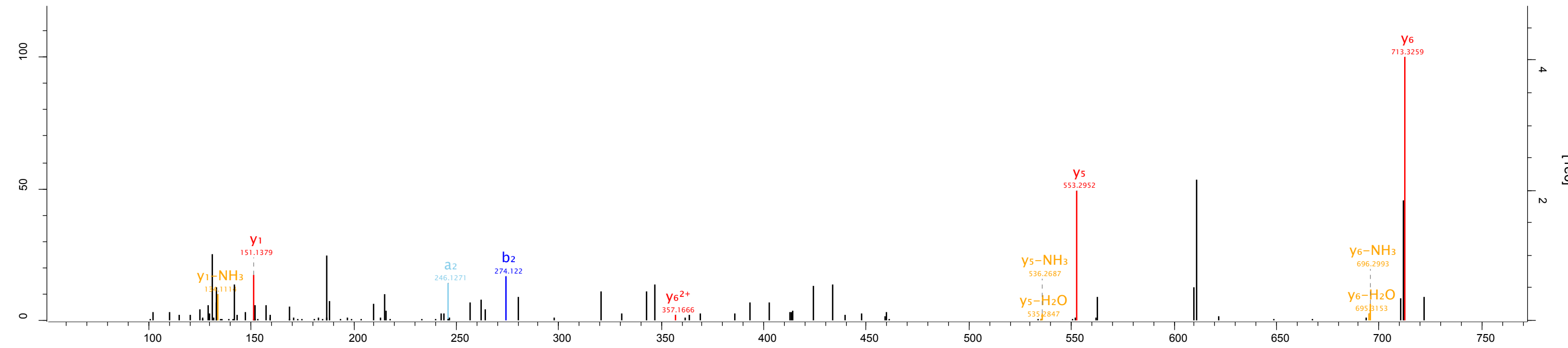
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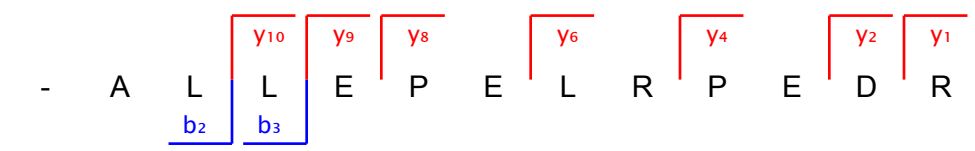
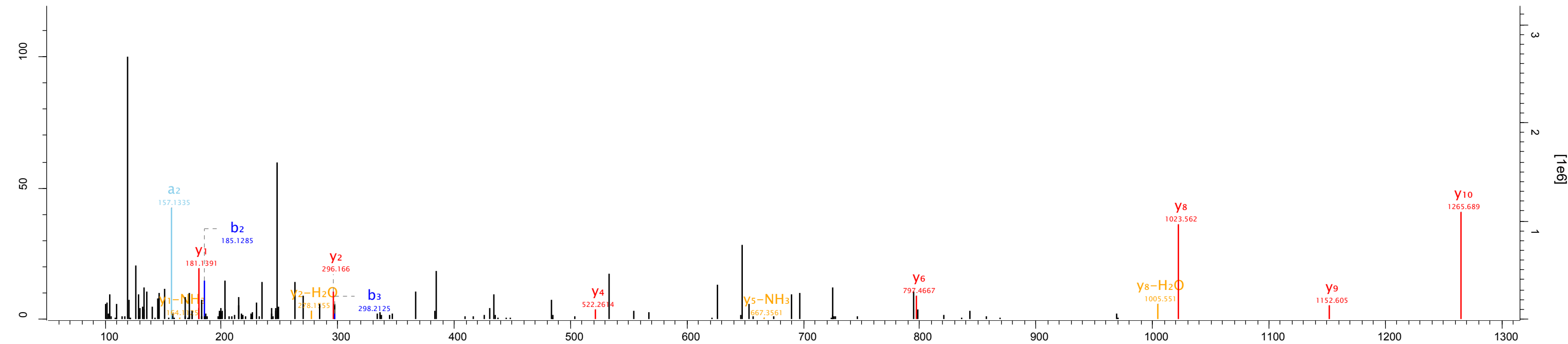
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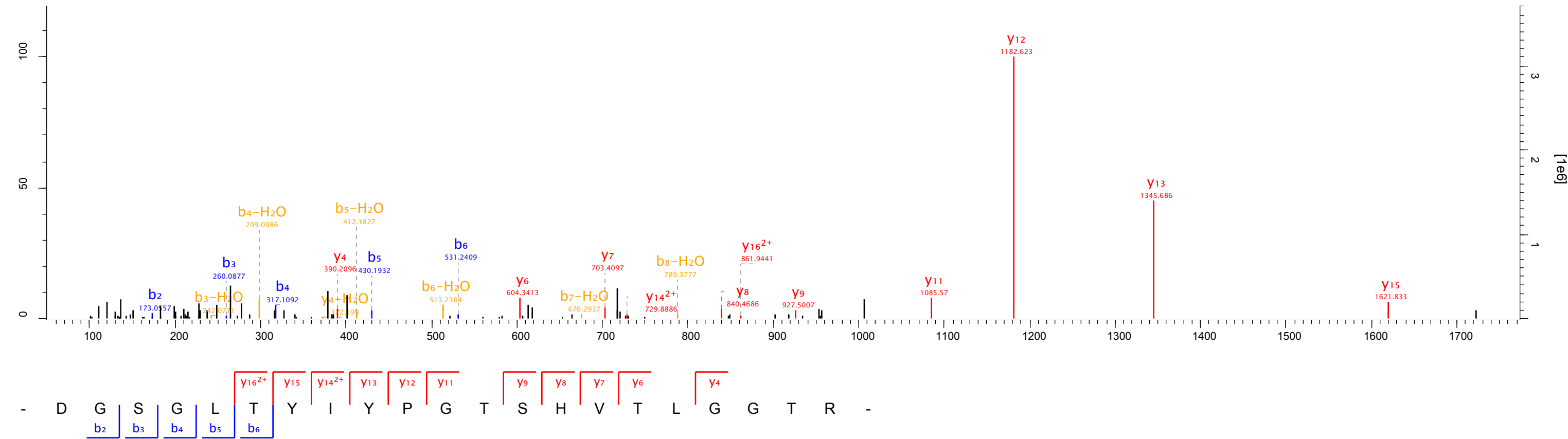
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 Scan: 16877 Method: FTMS; HCD Score: 40.38 m/z: 484.25 Gene names: ECE2

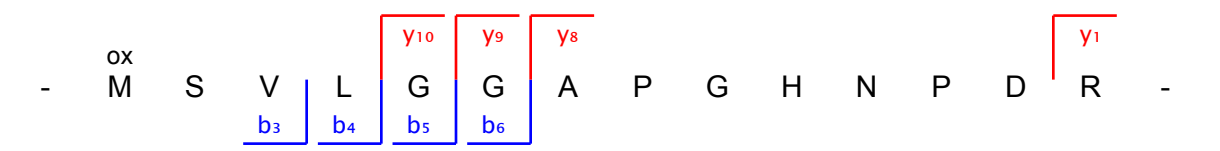
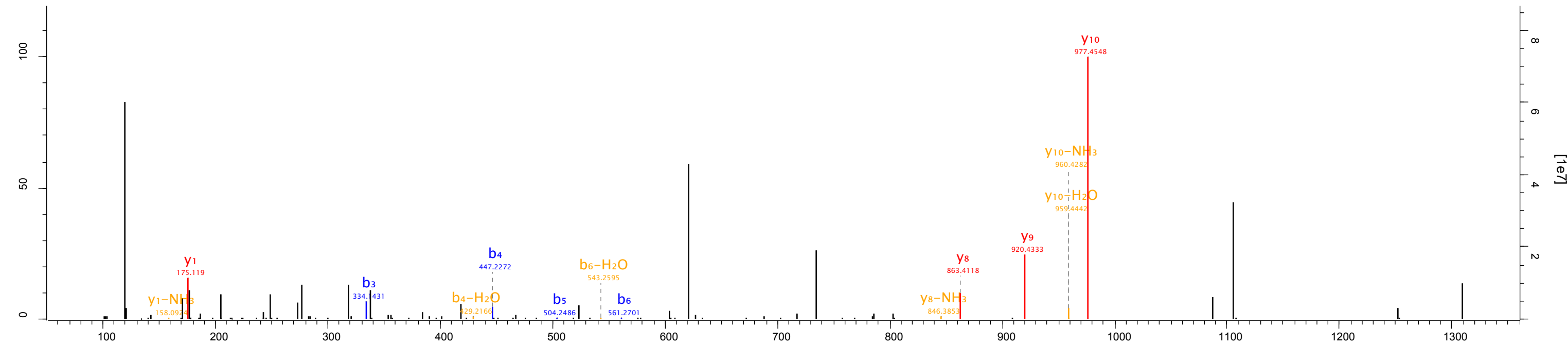


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 Scan: 22747 Method: FTMS; HCD Score: 46.95 m/z: 718.36 Gene names: DDO

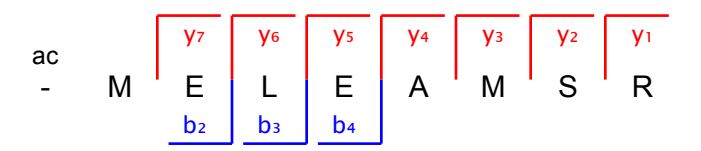
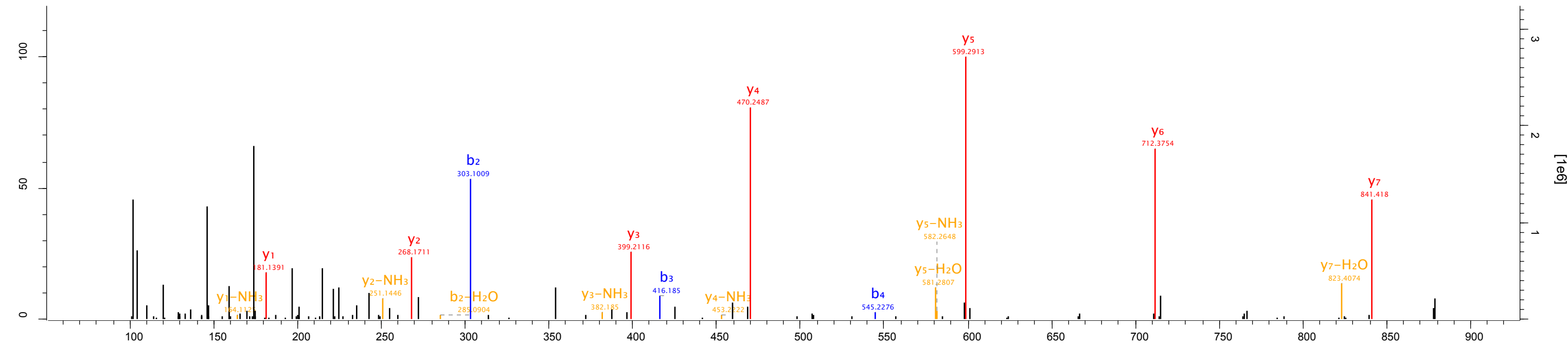


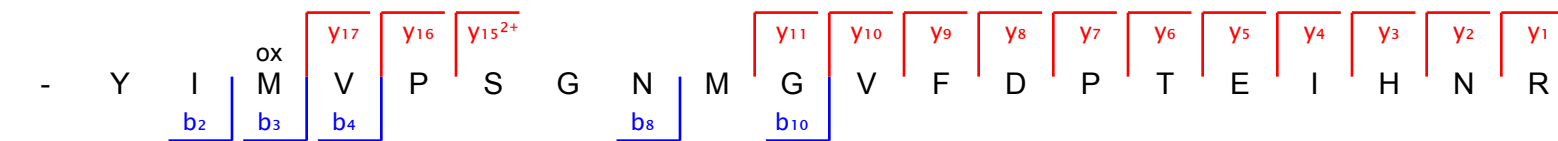
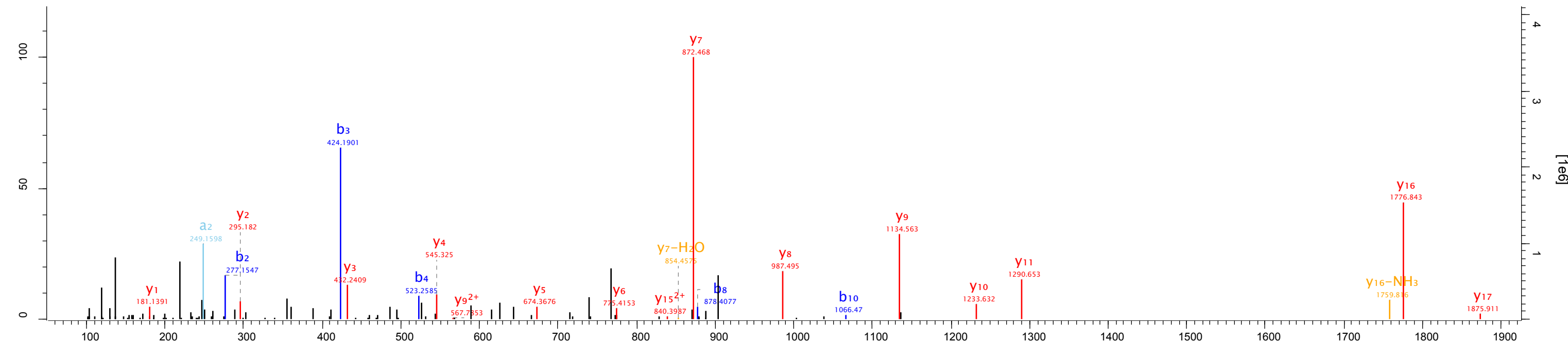
Raw file
20180707_MaS_A375SR_ML_proteome_15

Scan 23907 Method FTMS; HCD Score 43.76 m/z 712.34

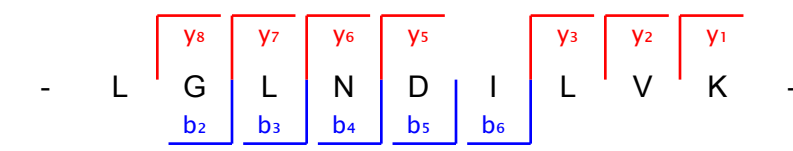
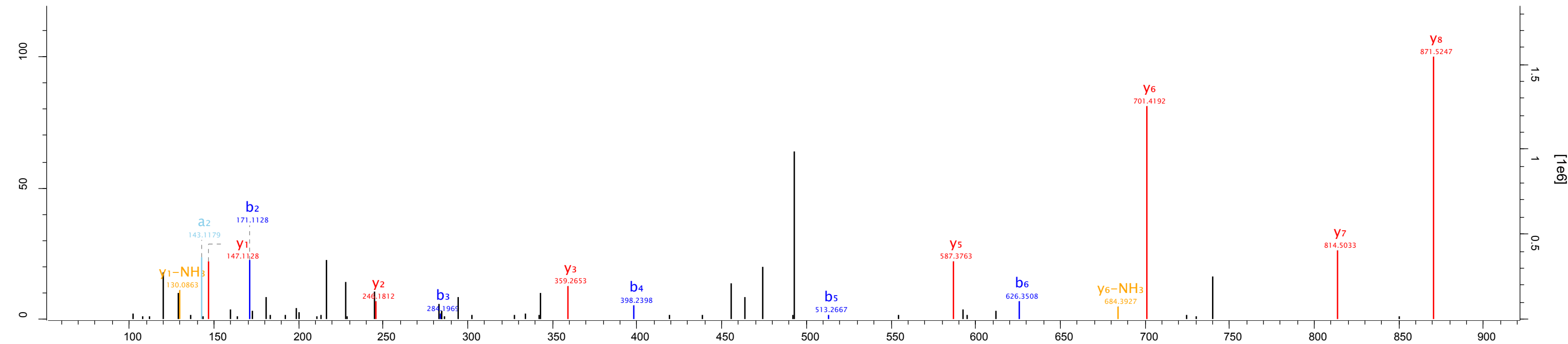


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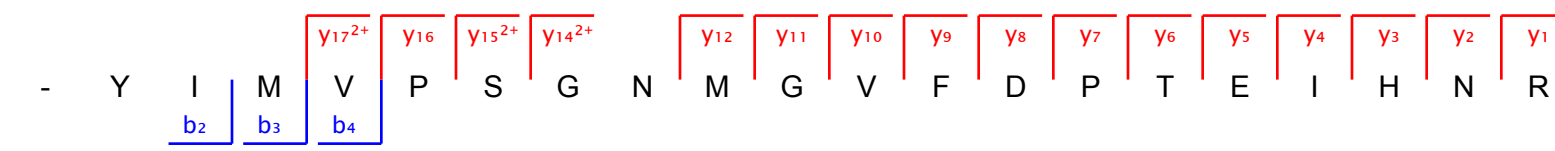
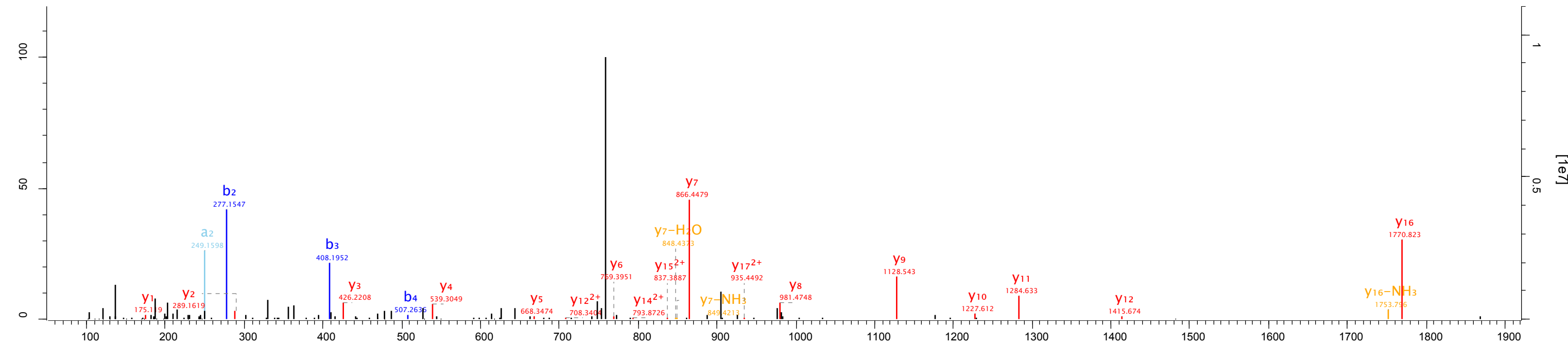


Raw file 20180707_MaS_A375SR_ML_proteome_15 Scan 26267 Method FTMS; HCD Score 77.19 m/z 492.81 Gene names STON2



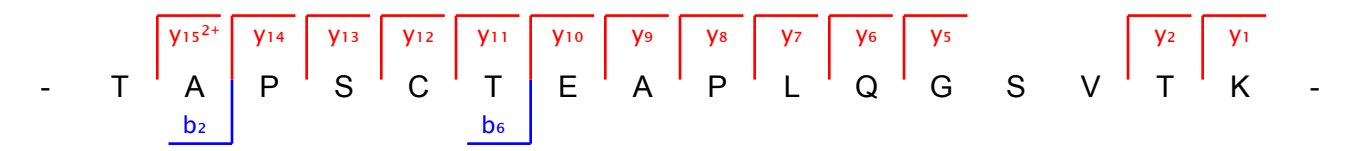
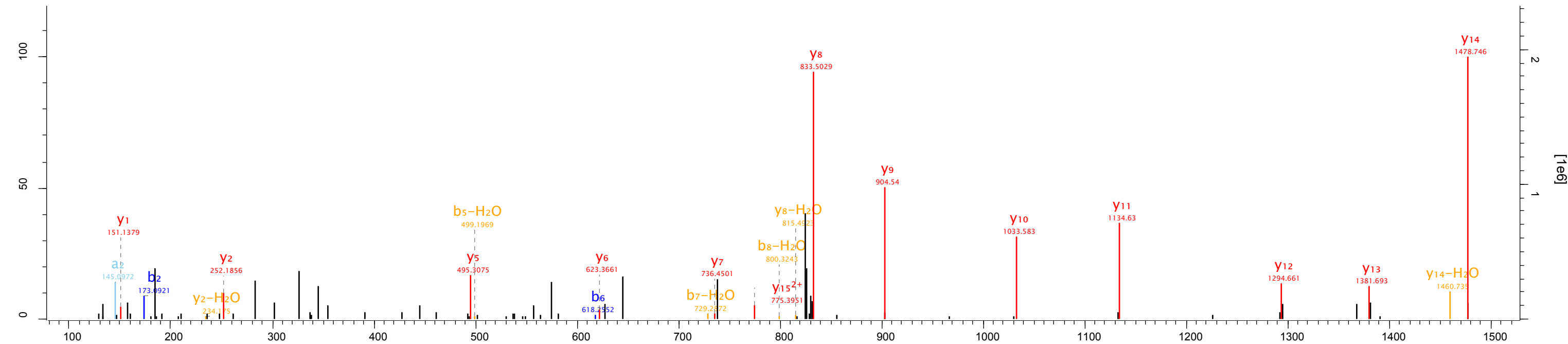
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20180707_MaS_A375SR_ML_proteome_15

Scan 27217 Method FTMS; HCD Score 62.23 m/z 759.7 Gene names CNIH4



Raw file
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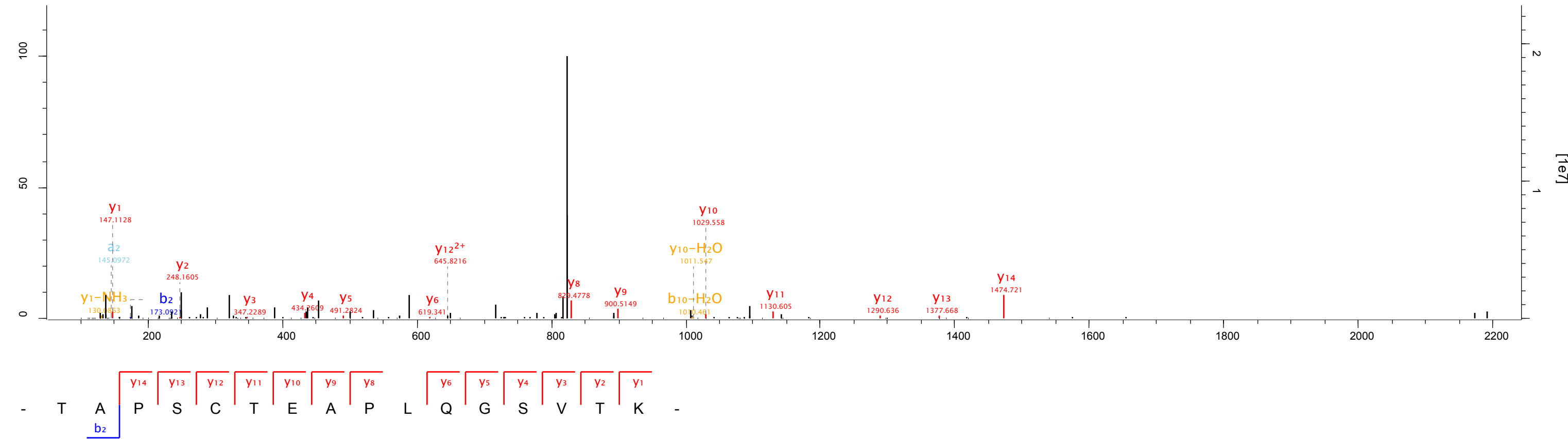
Scan 11387 Method FTMS; HCD Score 50.83 m/z 825.92 Gene names MKRN1



Raw file

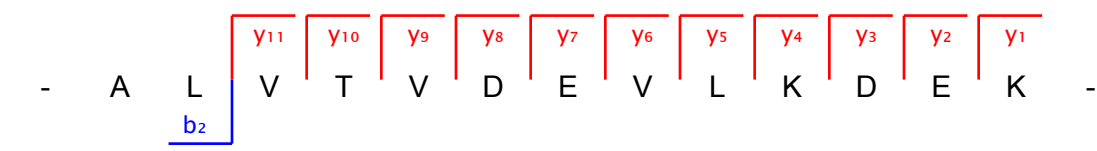
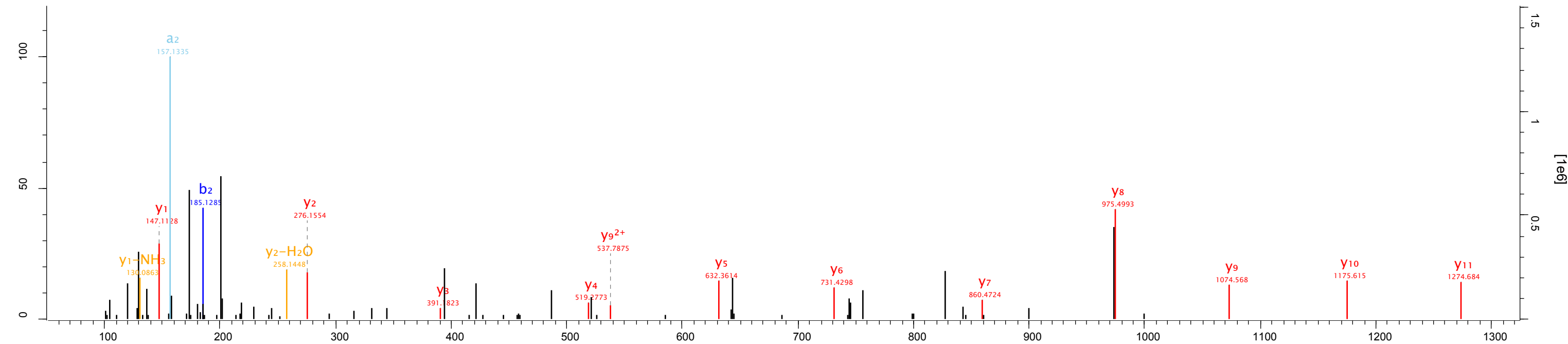
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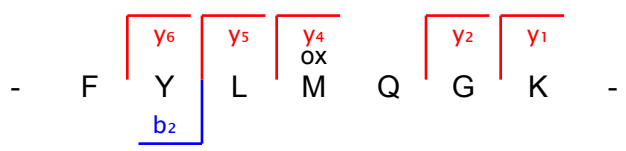
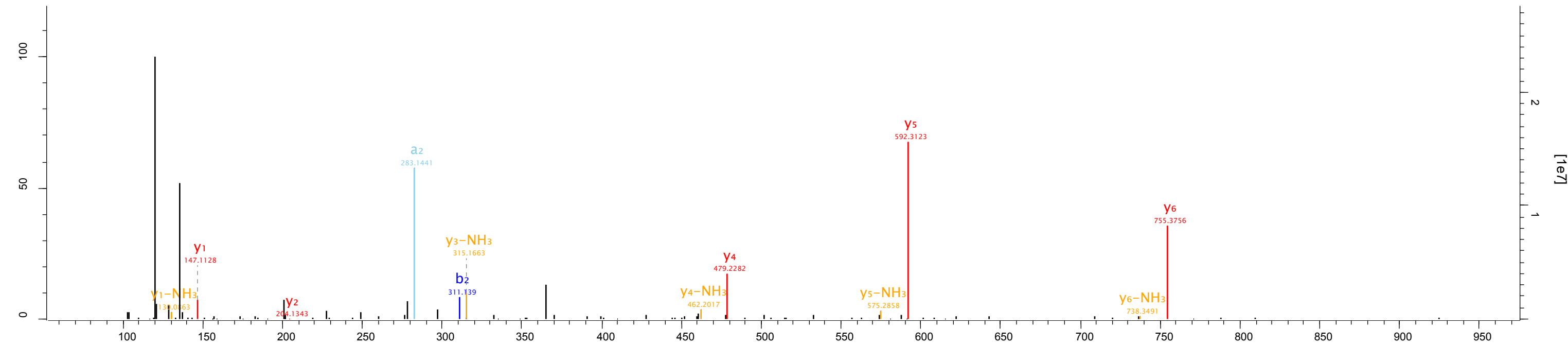
Scan	Method	Score	m/z	Gene names
11467	FTMS; HCD	29.76	823.91	MKRN1



Raw file
20180707_MaS_A375SR_ML_proteome_16

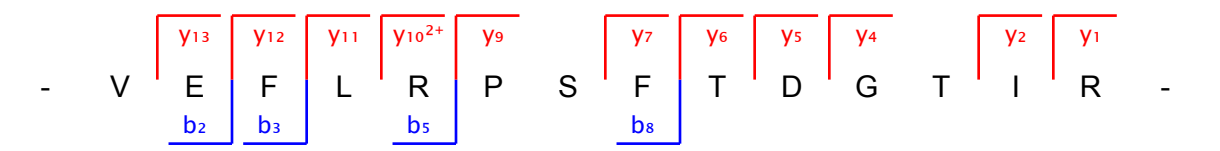
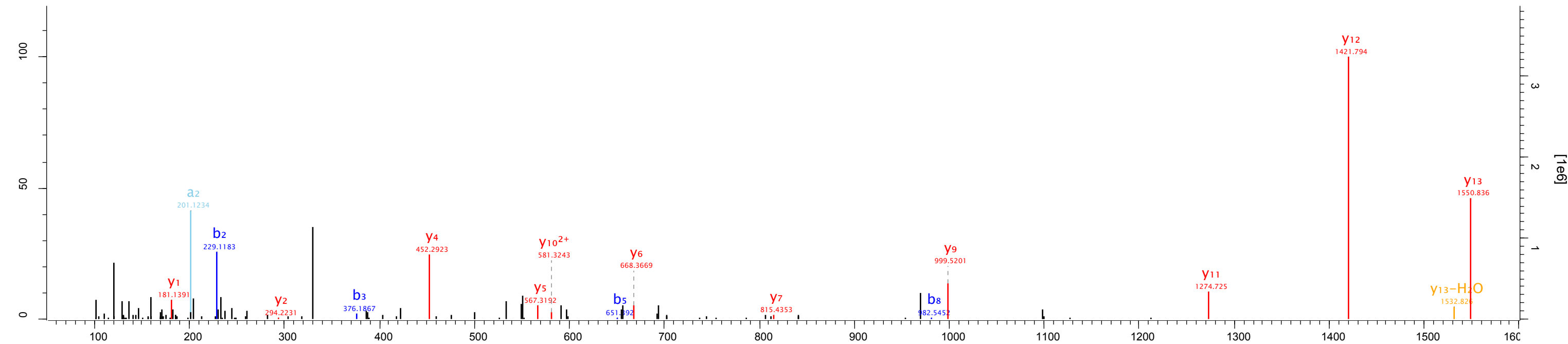
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Method: FTMS; HCD
Score: 71.88
m/z: 487.27
Gene names: WFIKKN2



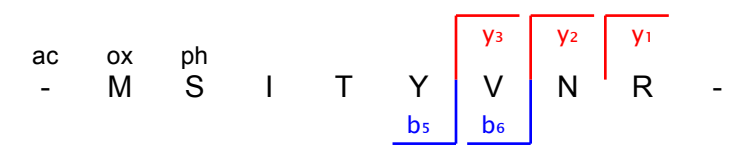
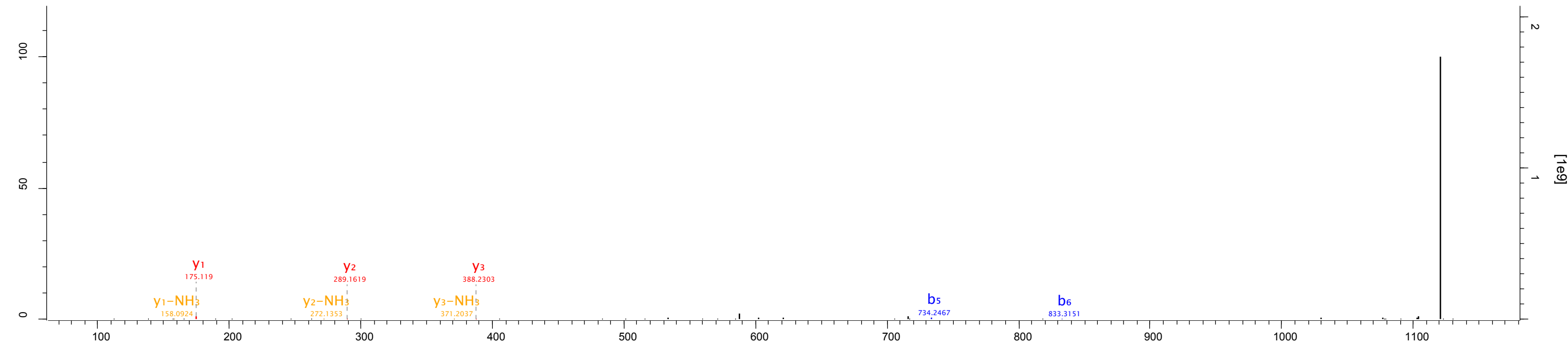


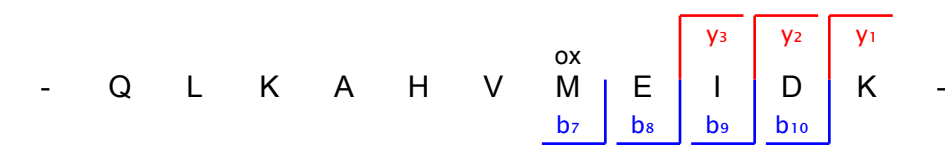
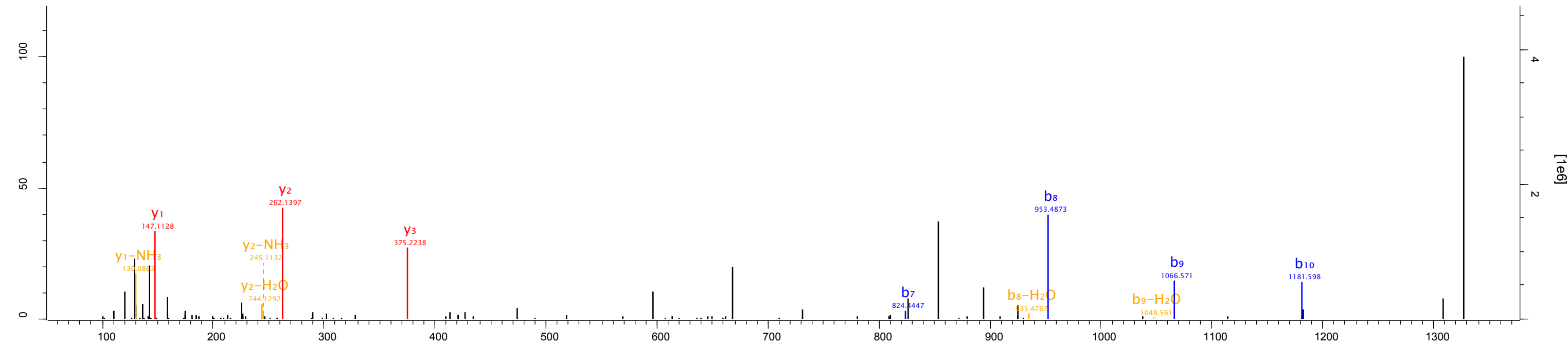
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20180707_MaS_A375SR_ML_proteome_18

Scan 23077 Method FTMS; HCD Score 53.98 m/z 550.64 Gene names PVRL1

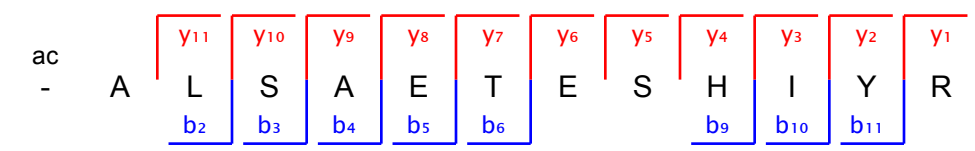
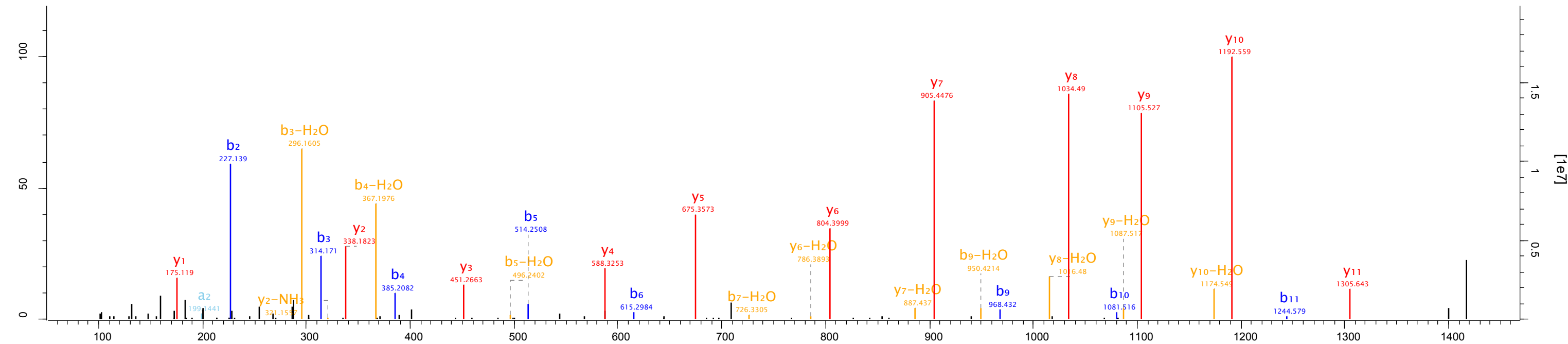


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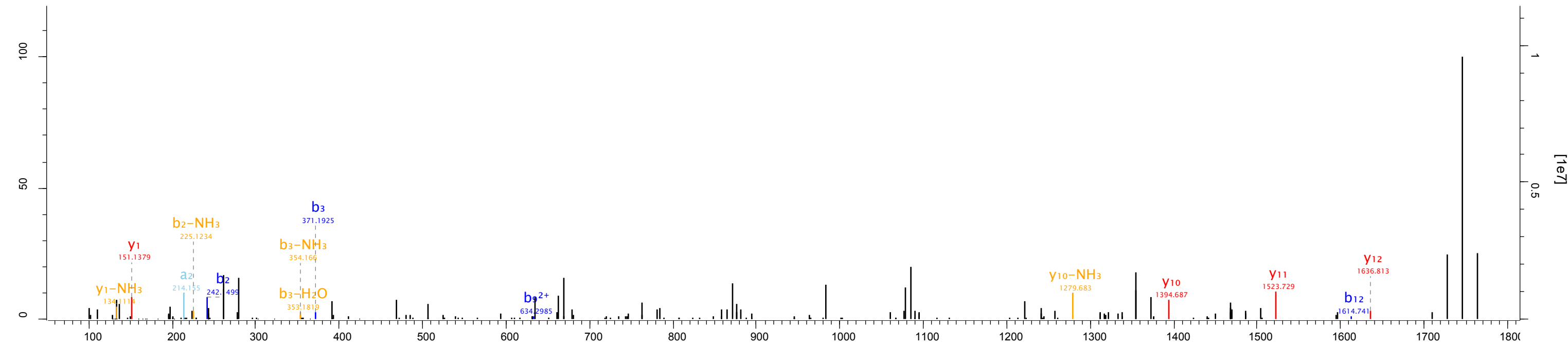


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 Scan: 16787 Method: FTMS; HCD Score: 216.06 m/z: 709.85 Gene names: CYB561D2

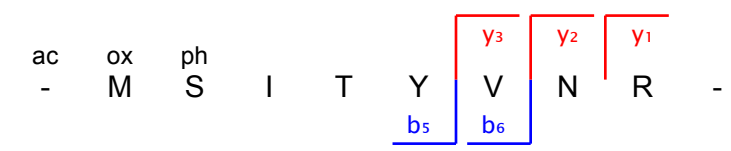
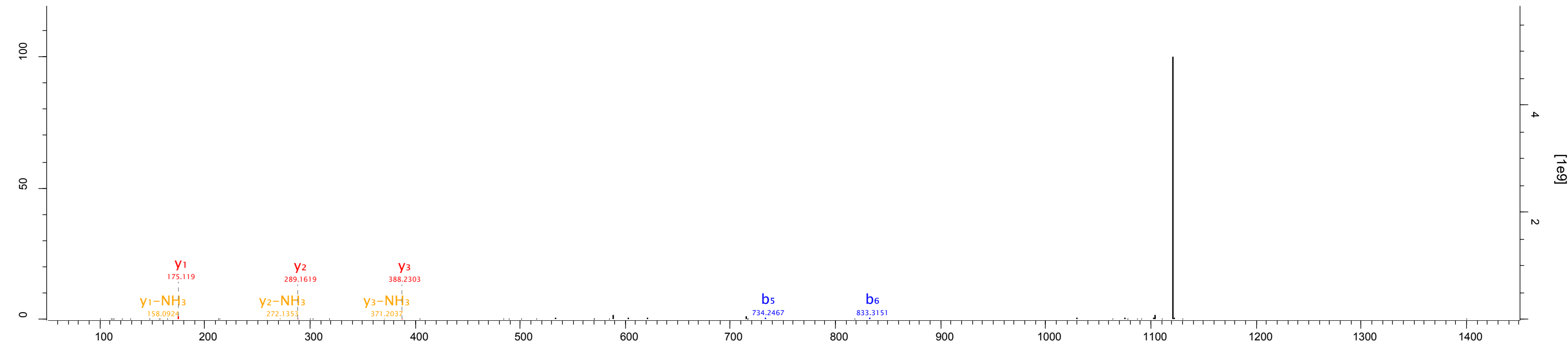


Raw file
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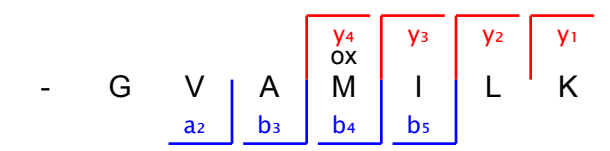
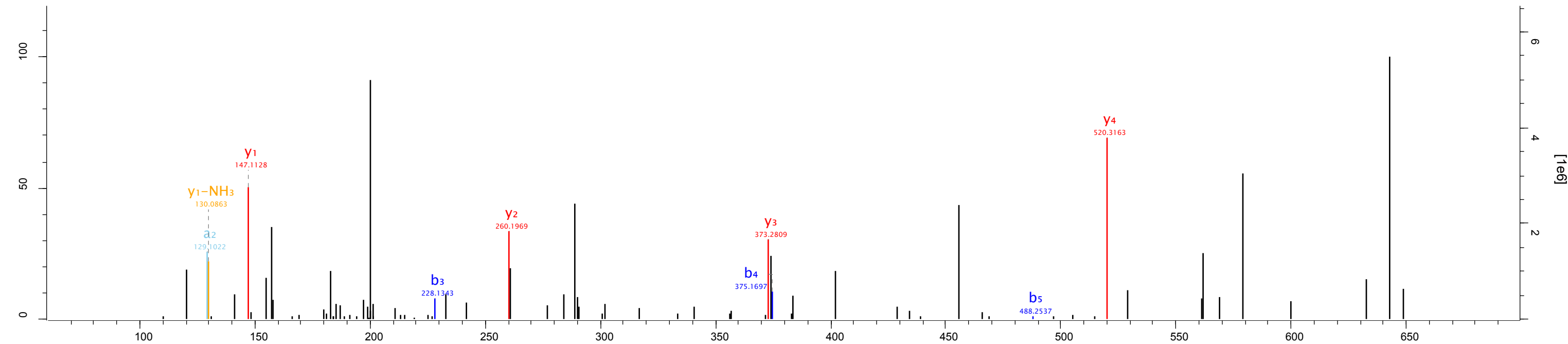
Scan 13607 Method FTMS; HCD Score 59.98 m/z 882.94 Gene names NLRP14

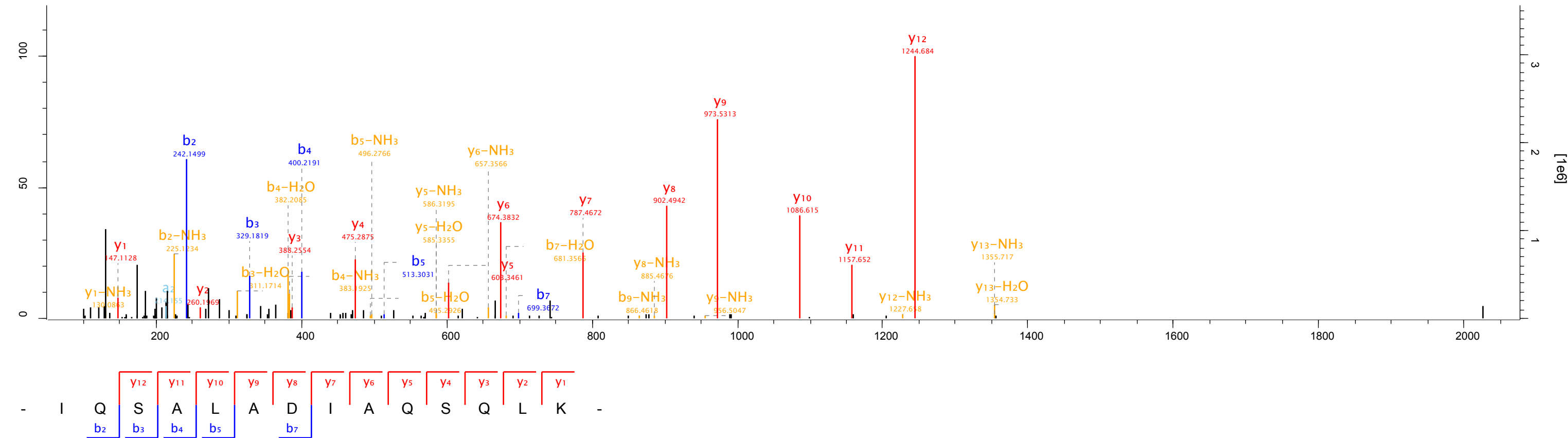


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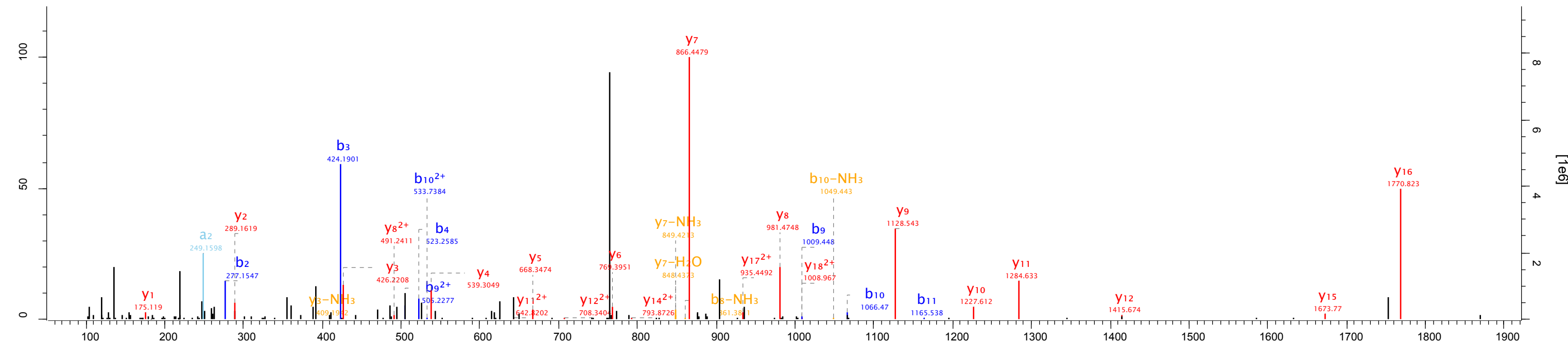
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 20180707_MaS_A375SR_ML_proteome_2_02
 Scan 15517 Method FTMS; HCD Score 59.61 m/z 374.22





Raw file
20180707_MaS_A375SR_ML_proteome_2_02

Scan 25137 Method FTMS; HCD Score 103.41 m/z 765.36 Gene names CNIH4



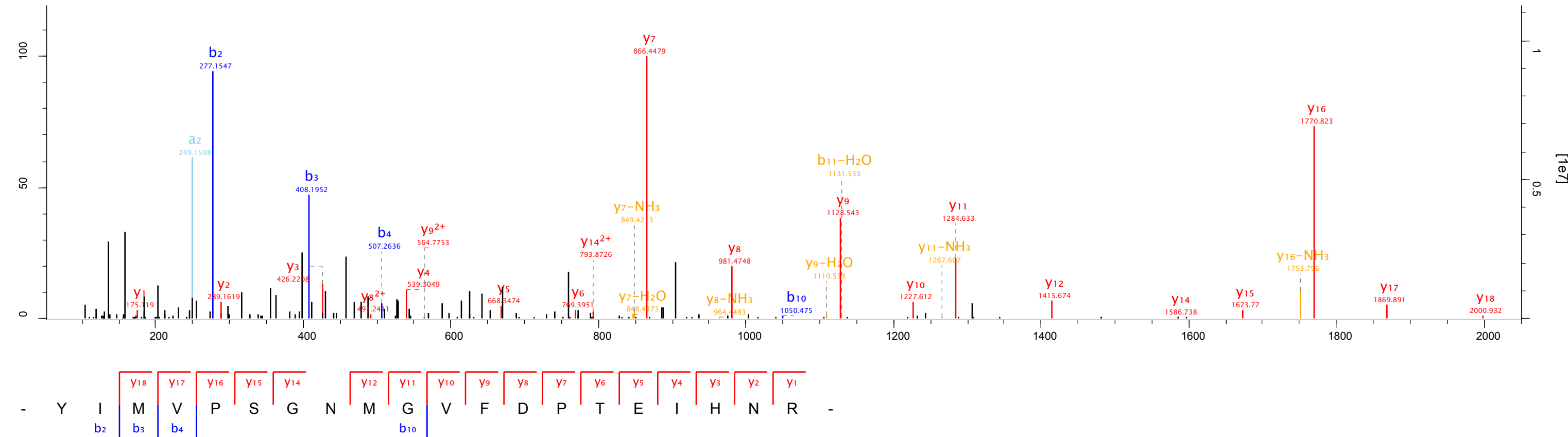
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Fragmentation mapping:

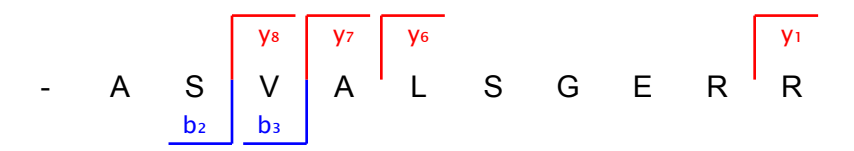
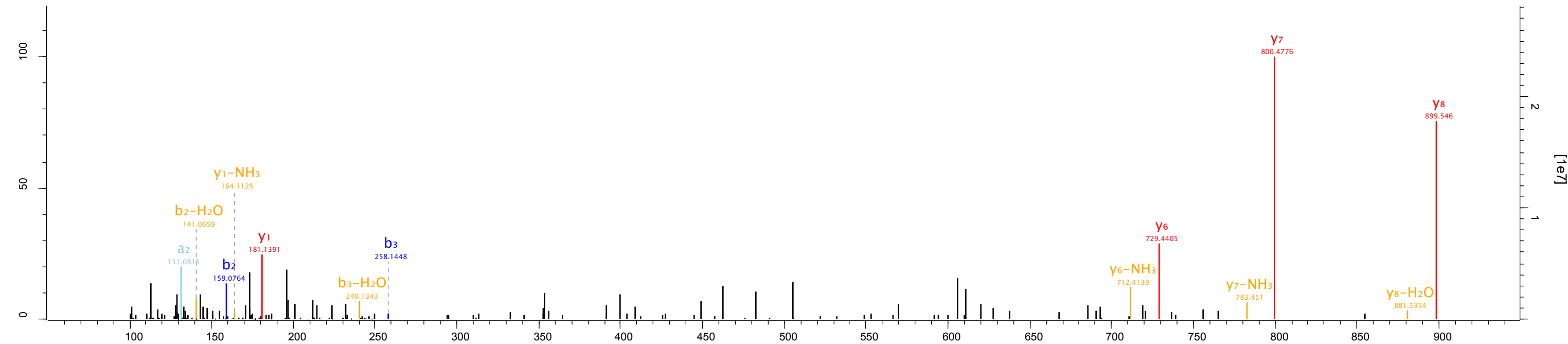
- Red boxes (y-ions): y18²⁺ (M), y17²⁺ (V), y16 (P), y15 (S), y14²⁺ (G), y12 (M), y11 (G), y10 (V), y9 (F), y8 (D), y7 (P), y6 (T), y5 (E), y4 (I), y3 (H), y2 (N), y1 (R)
- Blue boxes (b-ions): b2 (I), b3 (M), b4 (V), b9 (M), b10 (G), b11 (V)

Raw file
20180707_MaS_A375SR_ML_proteome_2_02

Scan 26997 Method FTMS; HCD Score 103.9 m/z 760.03 Gene names CNIH4

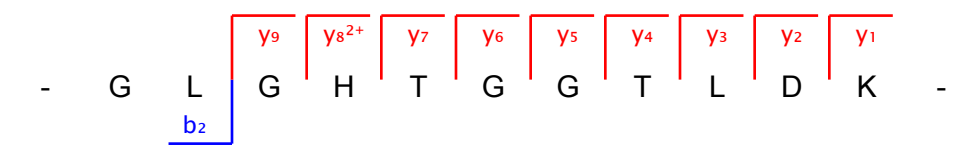
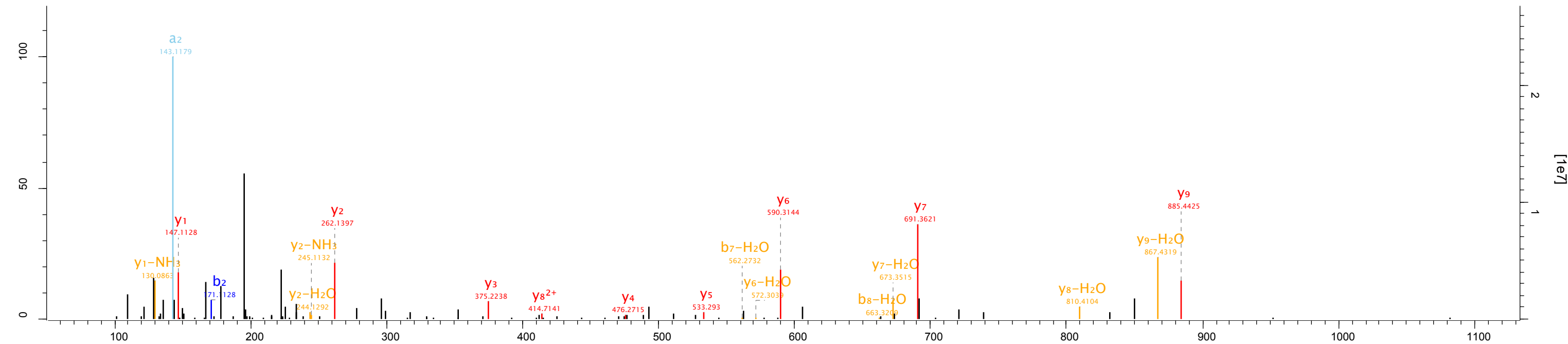


Raw file 20180707_MaS_A375SR_ML_proteome_2_02 Scan 2967 Method FTMS; HCD Score 52.49 m/z 353.21



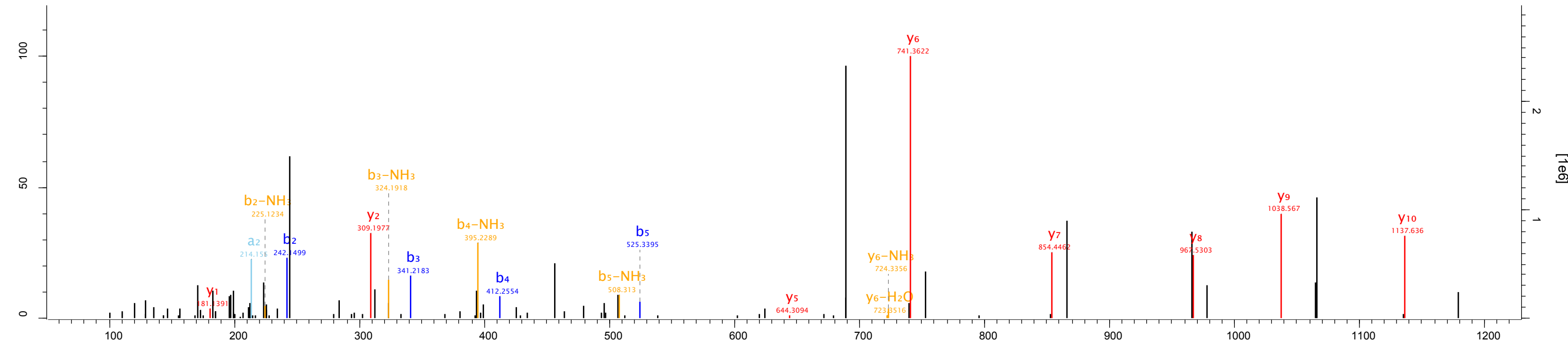
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20180707_MaS_A375SR_ML_proteome_2_02

Scan 4227 Method FTMS; HCD Score 67.08 m/z 352.52 Gene names TYMP



Raw file
20180707_MaS_A375SR_ML_proteome_2_03

Scan 25827 Method FTMS; HCD Score 79.49 m/z 689.89 Gene names TMEM106A

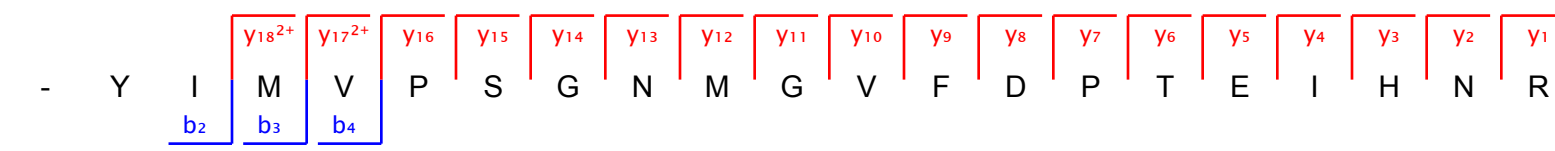
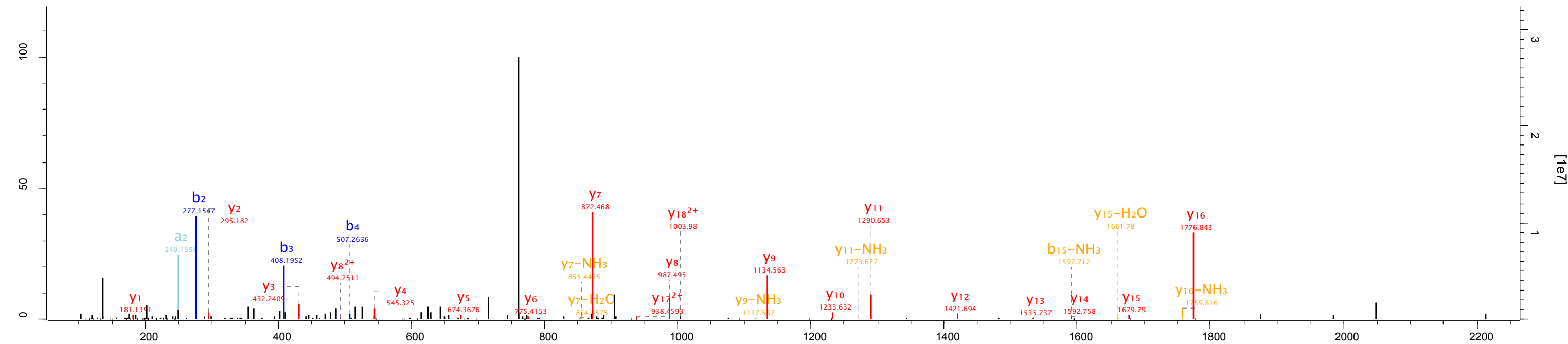


- Q L V A L I P Y G D Q R -

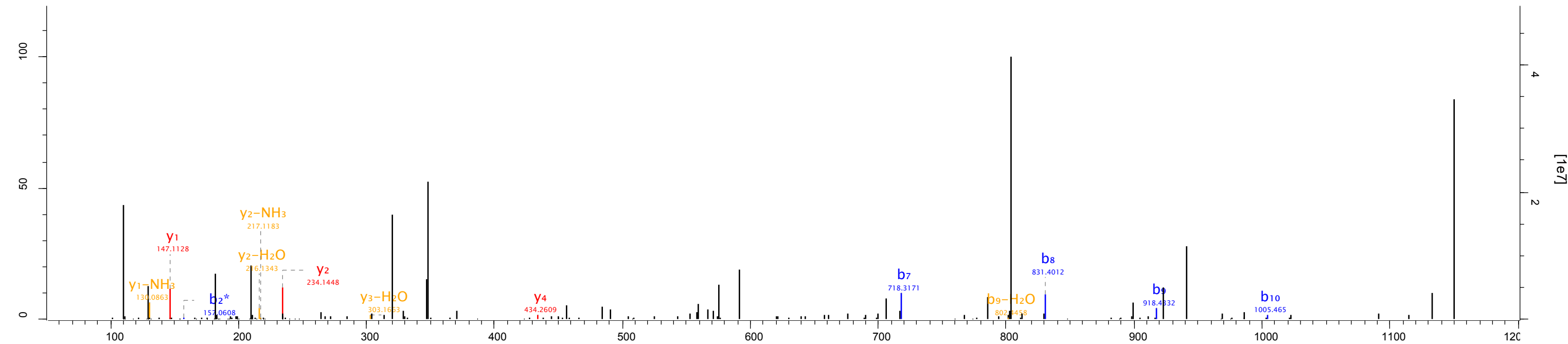
b₂ b₃ b₄ b₅ y₁₀ y₉ y₈ y₇ y₆ y₅ y₂ y₁

Raw file
20180707_MaS_A375SR_ML_proteome_2_03

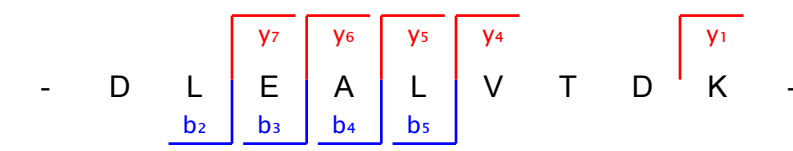
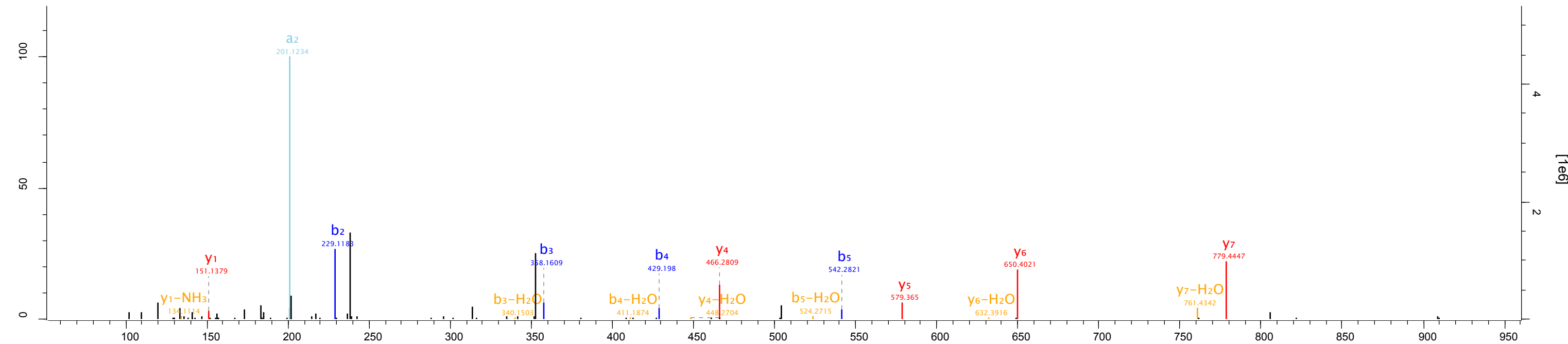
Scan 27527 Method FTMS; HCD Score 116.6 m/z 762.04 Gene names CNIH4



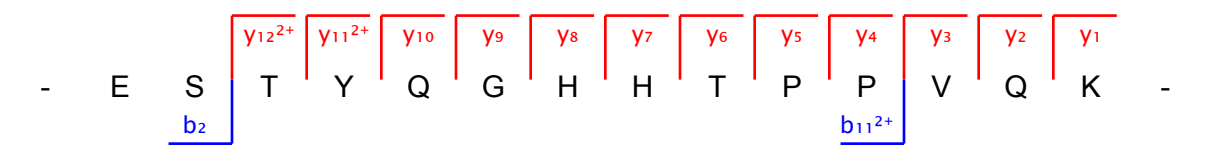
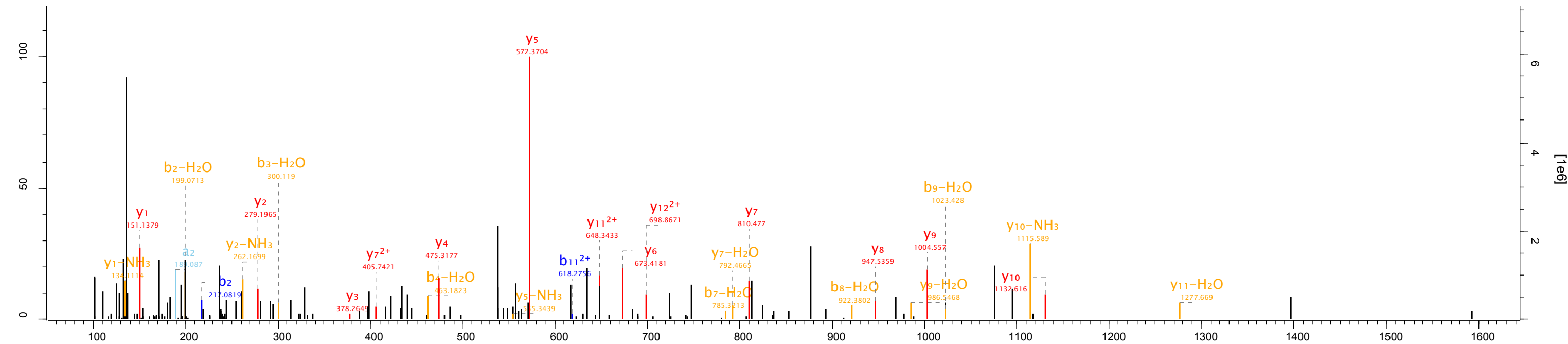
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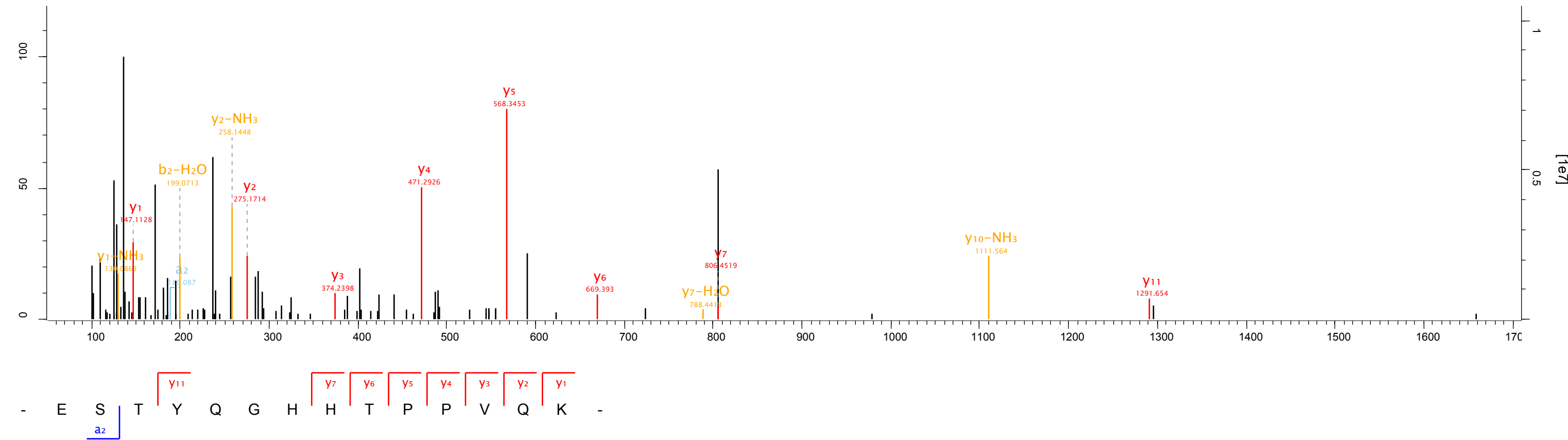


Raw file 20180707_MaS_A375SR_ML_proteome_2_04 Scan 23507 Method FTMS; HCD Score 72.61 m/z 504.28 Gene names PGM5

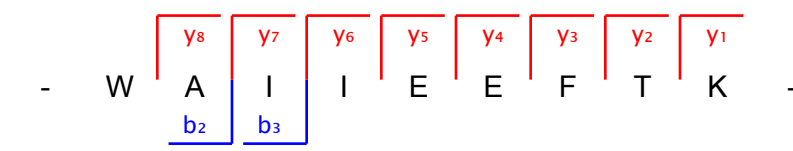
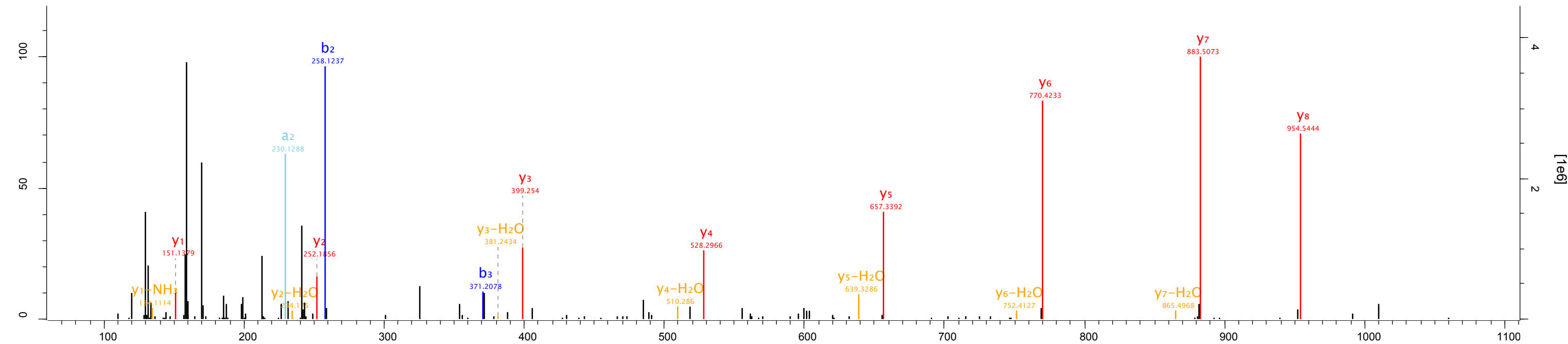


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 Scan: 3007 Method: FTMS; HCD Score: 83.53 m/z: 538.61 Gene names: MT-CO3

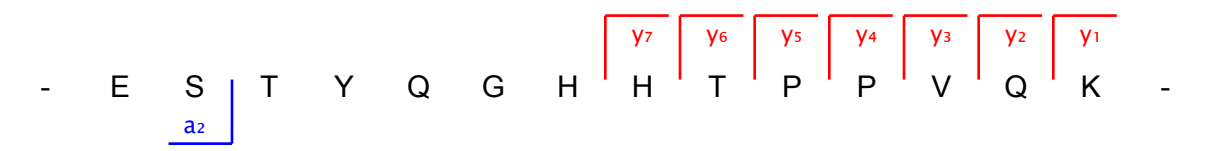
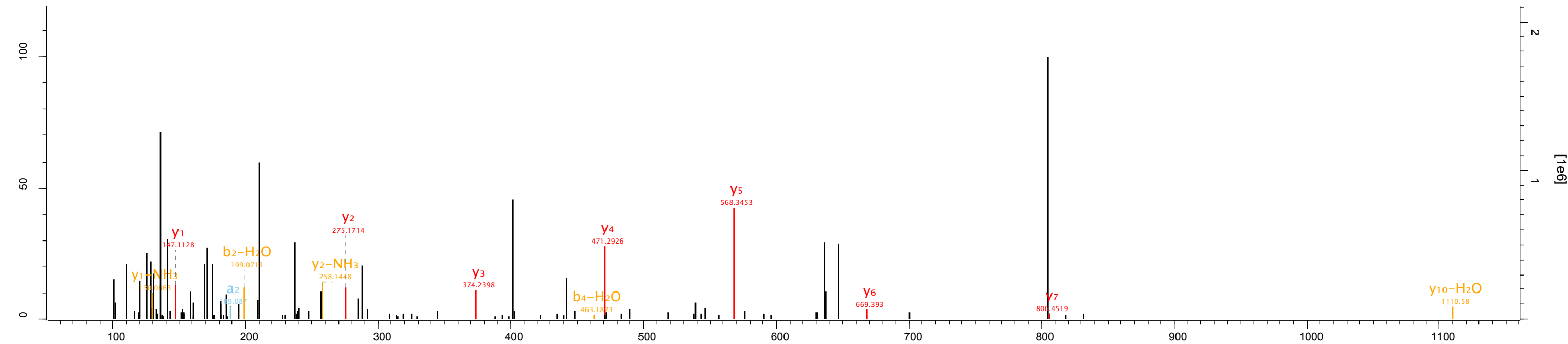




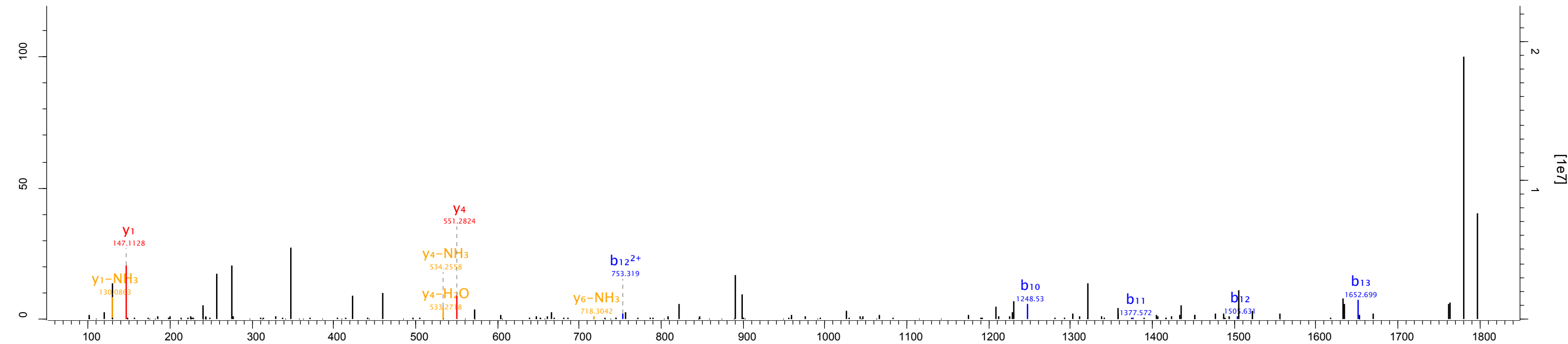
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Raw file 20180707_MaS_A375SR_ML_proteome_2_05 Scan 3507 Method FTMS; HCD Score 18.83 m/z 402.95 Gene names MT-CO3



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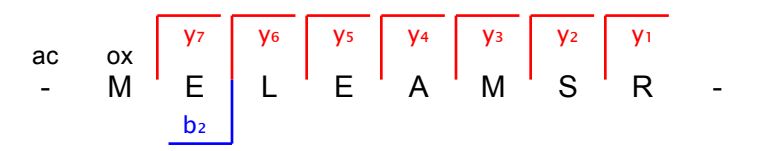
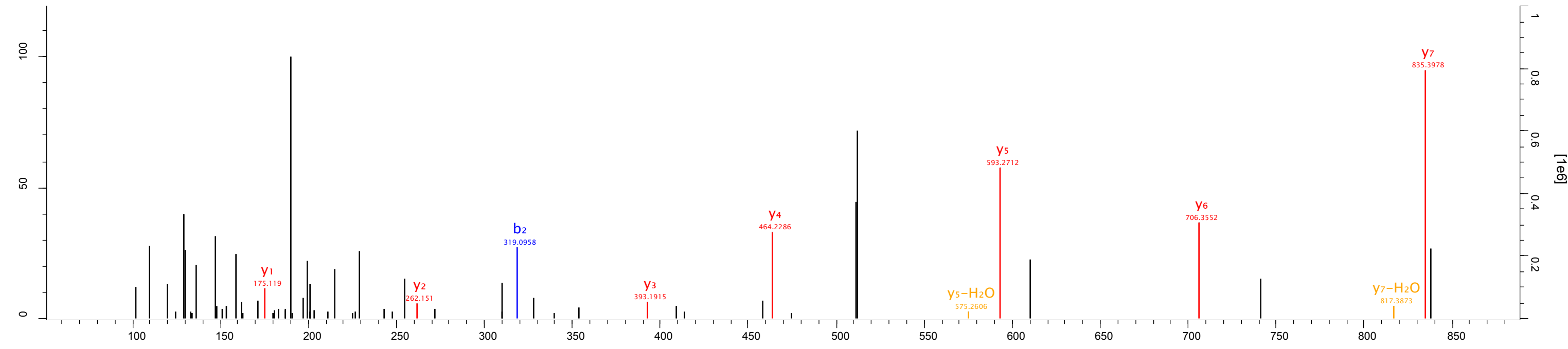


- R L I G Y S E F D S E Q F K -

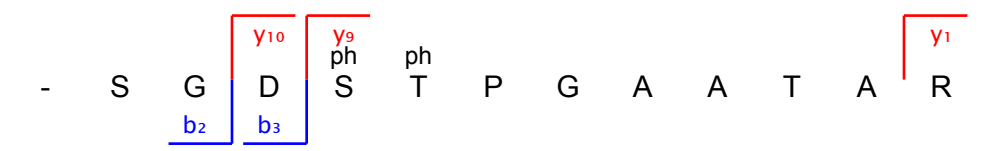
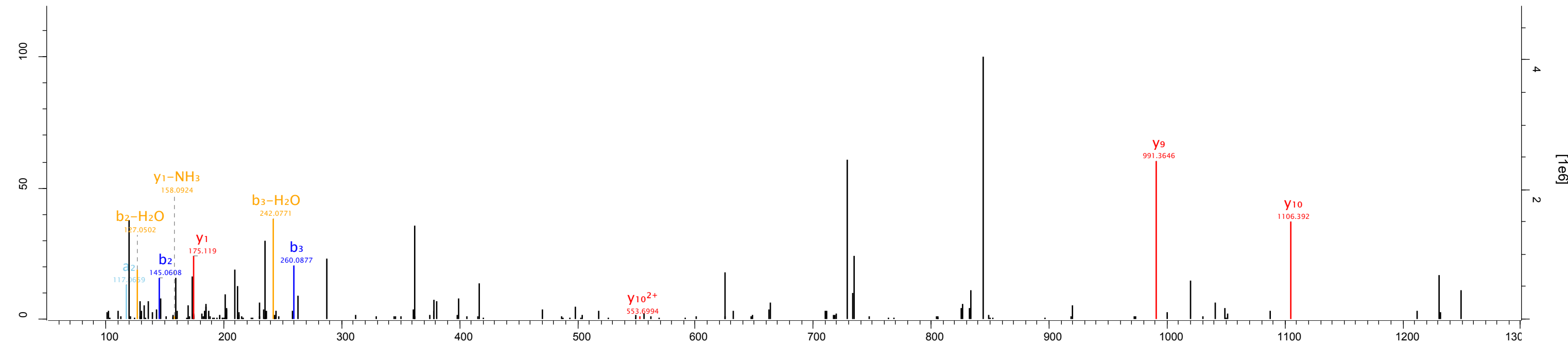
ph

b₁₀ b₁₁ b₁₂ b₁₃ y₄ y₁

Raw file: 20180707_MaS_A375SR_ML_proteome_2_07
 Scan: 18097 Method: FTMS; HCD Score: 45.37 m/z: 512.73 Gene names: TMEM258

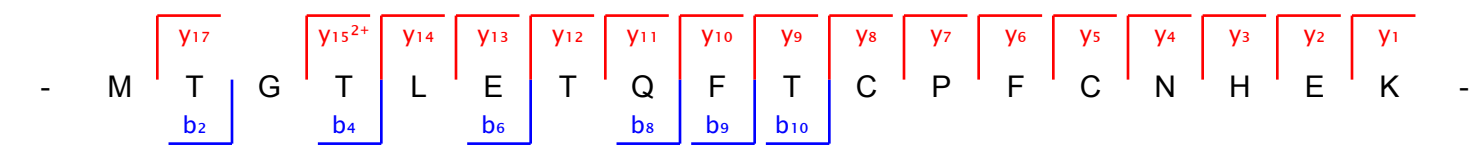
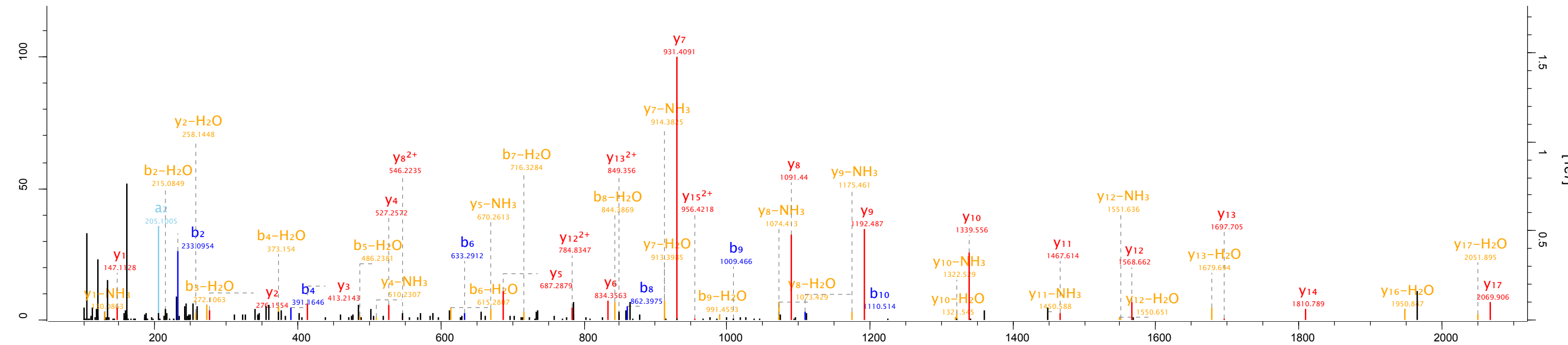


Raw file 20180707_MaS_A375SR_ML_proteome_2_10 Scan 15887 Method FTMS; HCD Score 42.24 m/z 625.73



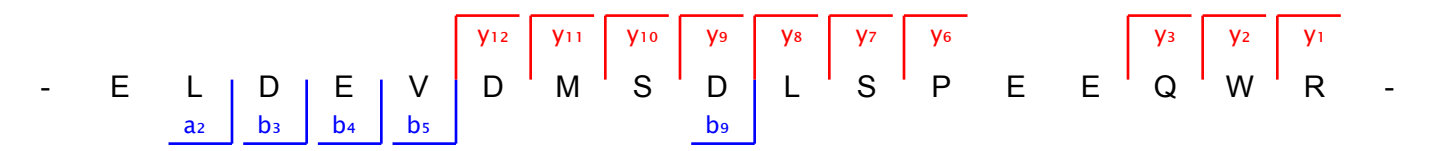
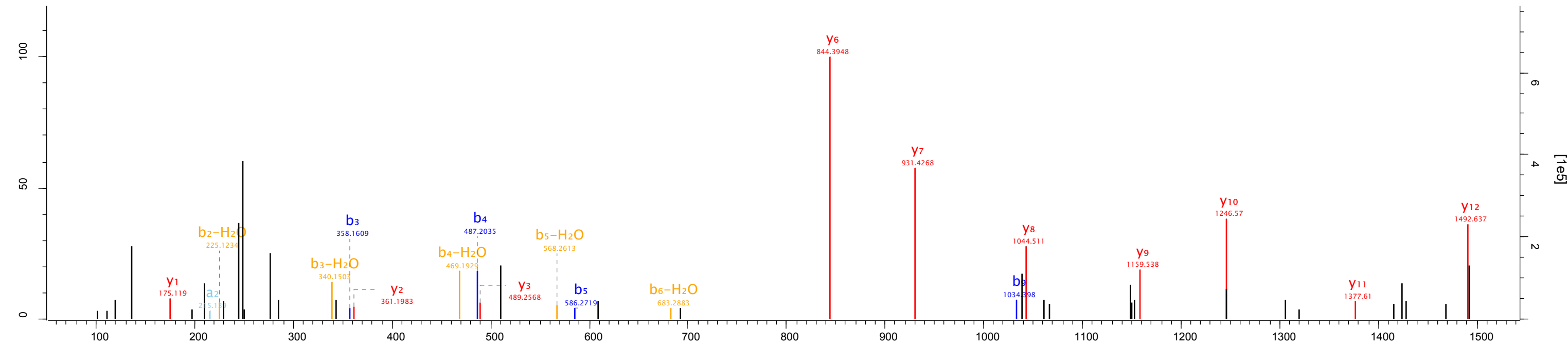
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20180707_MaS_A375SR_ML_proteome_2_10

Scan 21677 Method FTMS; HCD Score 214.54 m/z 734.66 Gene names ELOF1

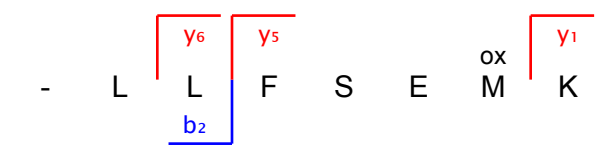
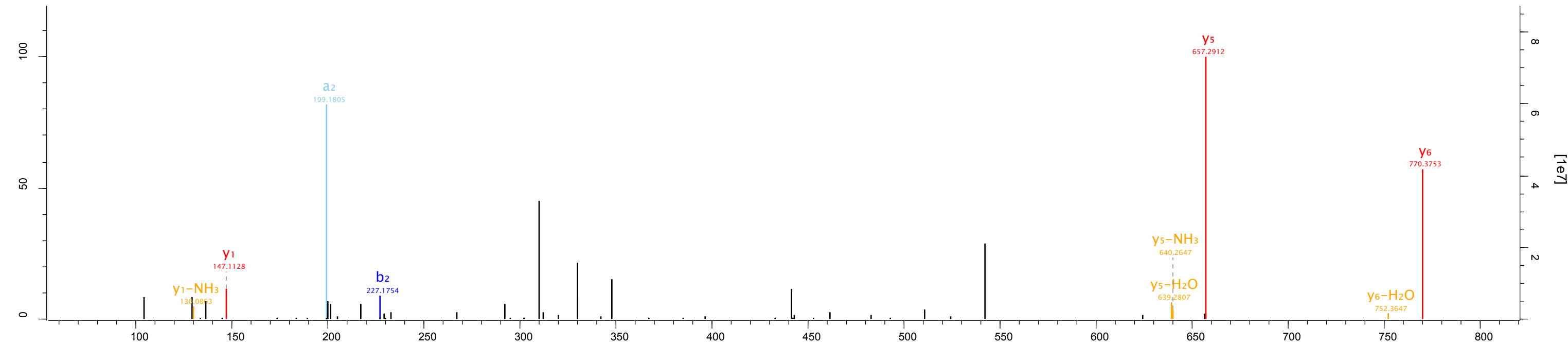


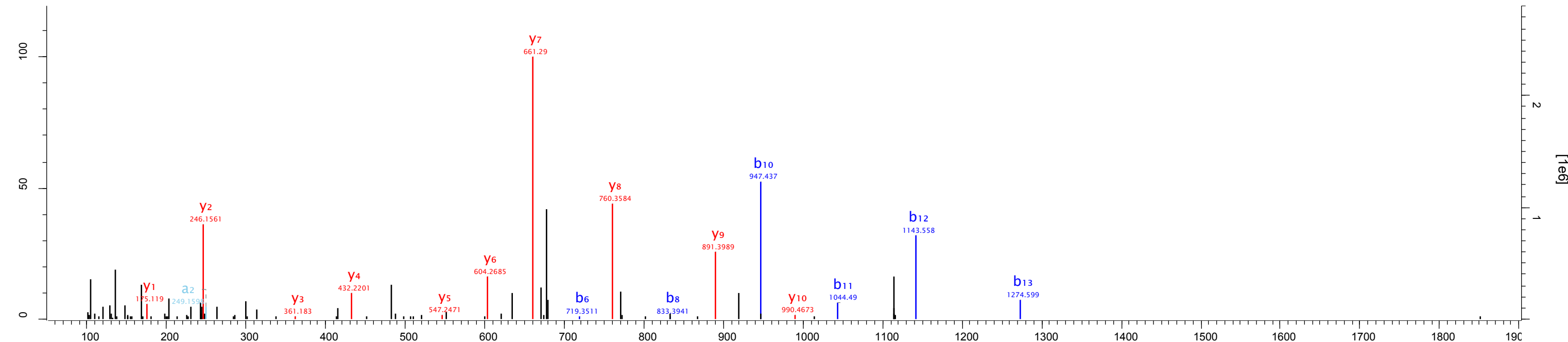
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20180707_MaS_A375SR_ML_proteome_2_10

Scan 26967 Method FTMS; HCD Score 66.02 m/z 1039.46 Gene names RNF121



Raw file: 20180707_MaS_A375SR_ML_proteome_2_11
 Scan: 12407 Method: FTMS; HCD Score: 64.78 m/z: 442.23 Gene names: C1orf234

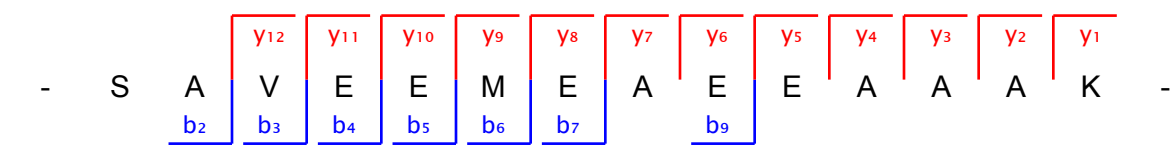
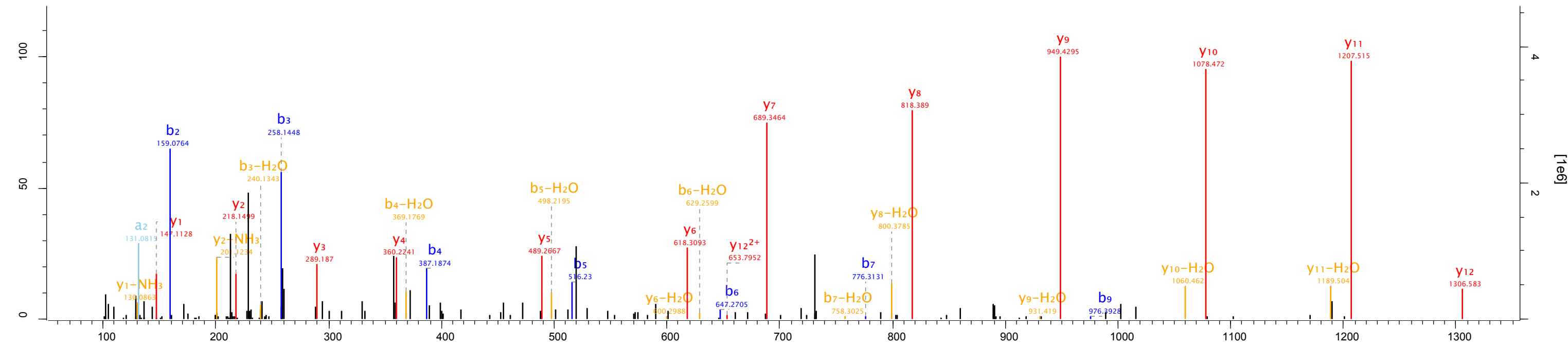


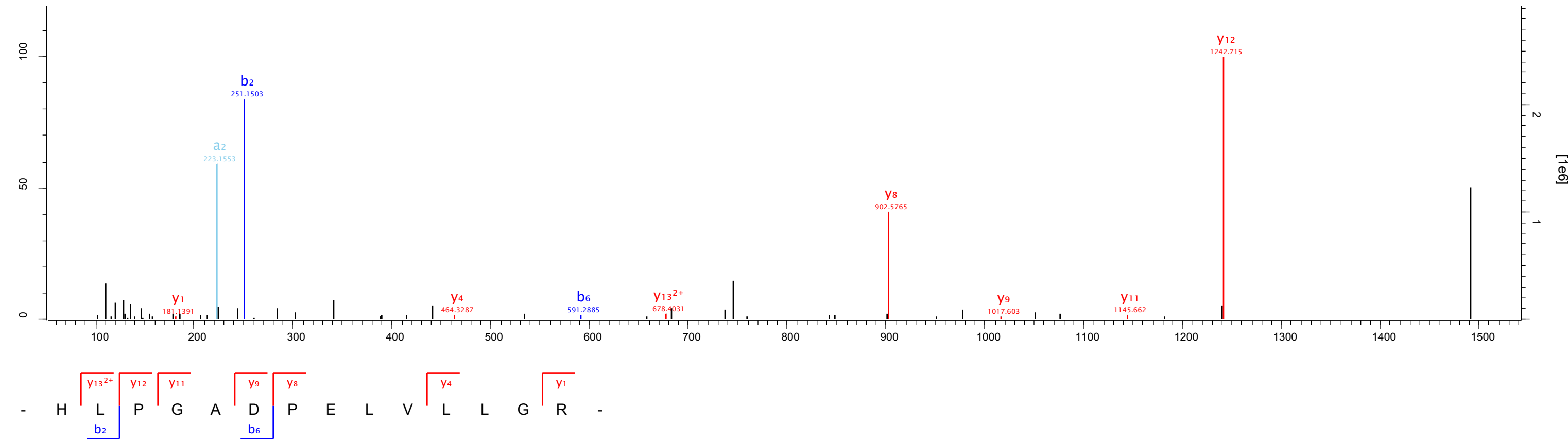


- L Y S H F A G G G P V M V G G D A D A R -

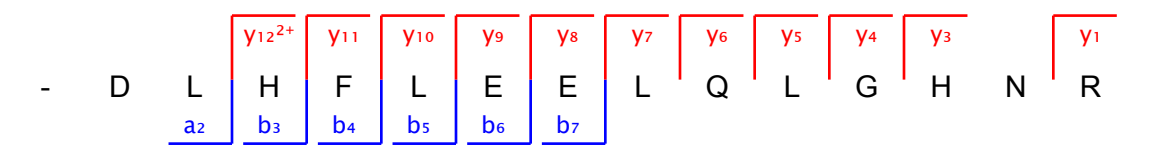
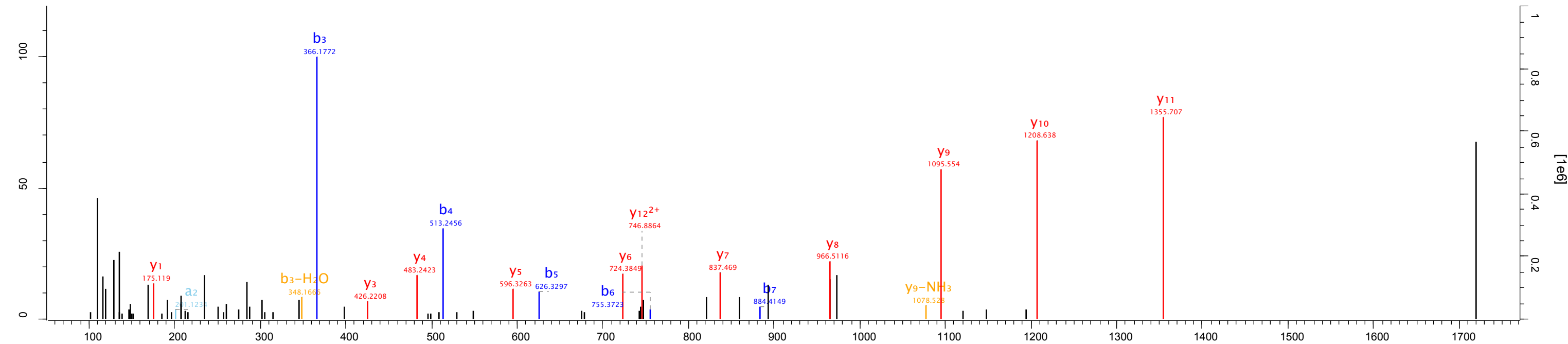
Fragmentation sites are indicated by brackets below the sequence:

- Blue brackets (b ions): a2 (Y-S), b6 (A-G), b8 (G-G), b10 (G-P), b11 (P-V), b12 (V-M), b13 (M-V)
- Red brackets (y ions): y10 (V-M), y9 (M-V), y8 (V-G), y7 (G-G), y6 (G-D), y5 (D-A), y4 (A-D), y3 (D-A), y2 (A-R), y1 (R)



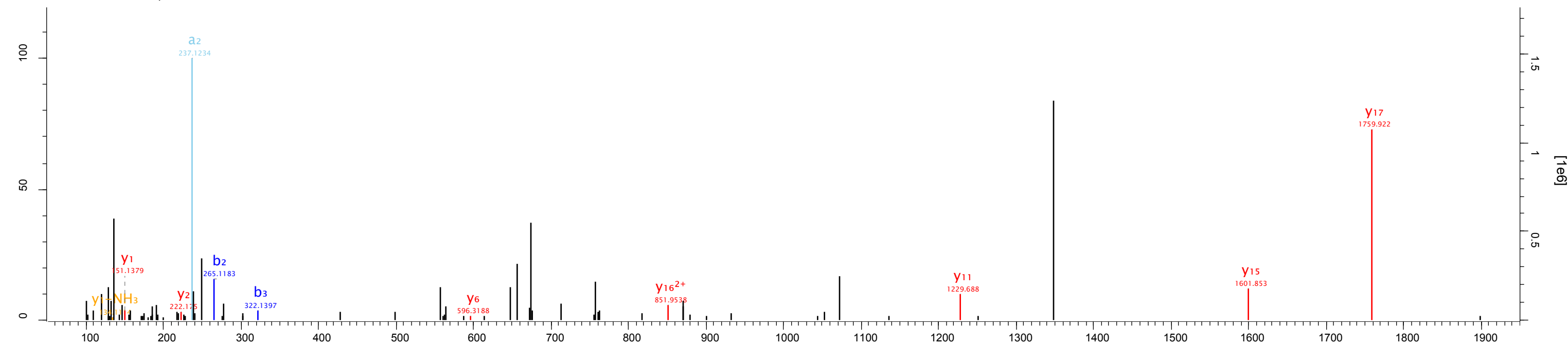


Raw file 20180707_MaS_A375SR_ML_proteome_2_14
 Scan 25857 Method FTMS; HCD Score 83.09 m/z 860.95 Gene names IGFALS



Raw file
20180707_MaS_A375SR_ML_proteome_2_15

Scan 18277 Method FTMS; HCD Score 11.36 m/z 675.35 Gene names TMEM243



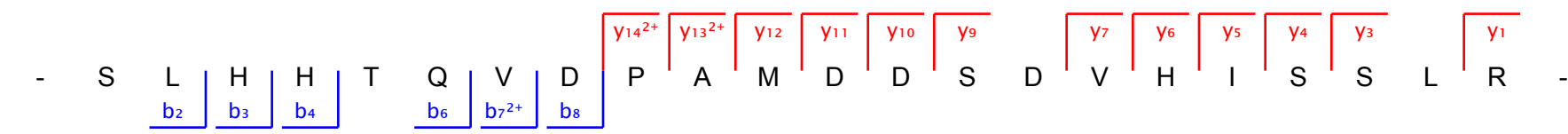
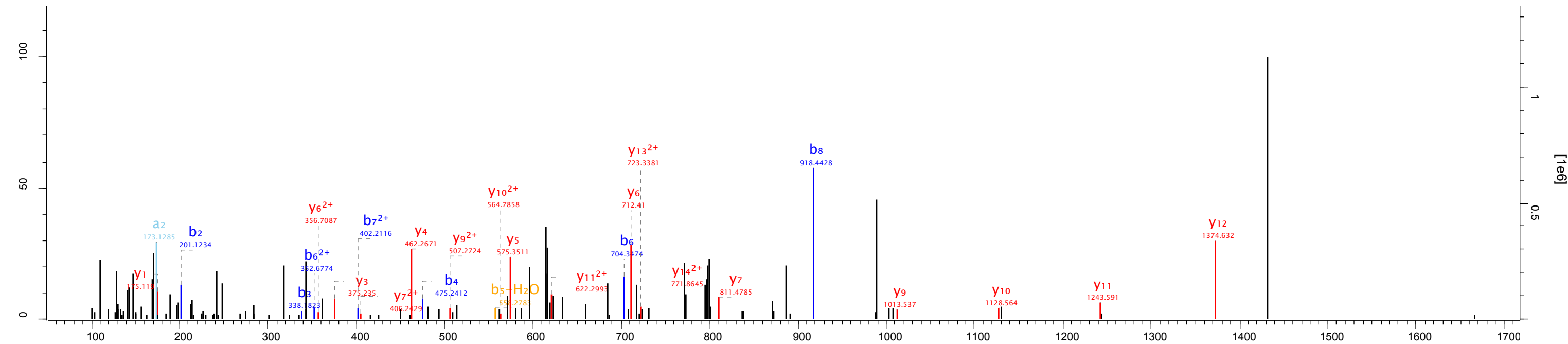
- T Y G T S G L D N R P L F G E T S A K -

Fragmentation mapping (b and y ions) is shown below the sequence:

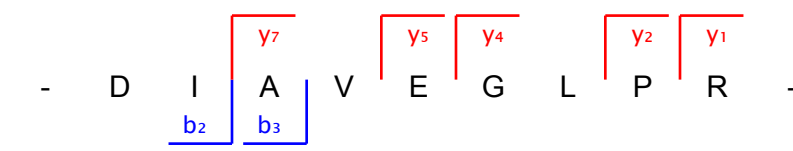
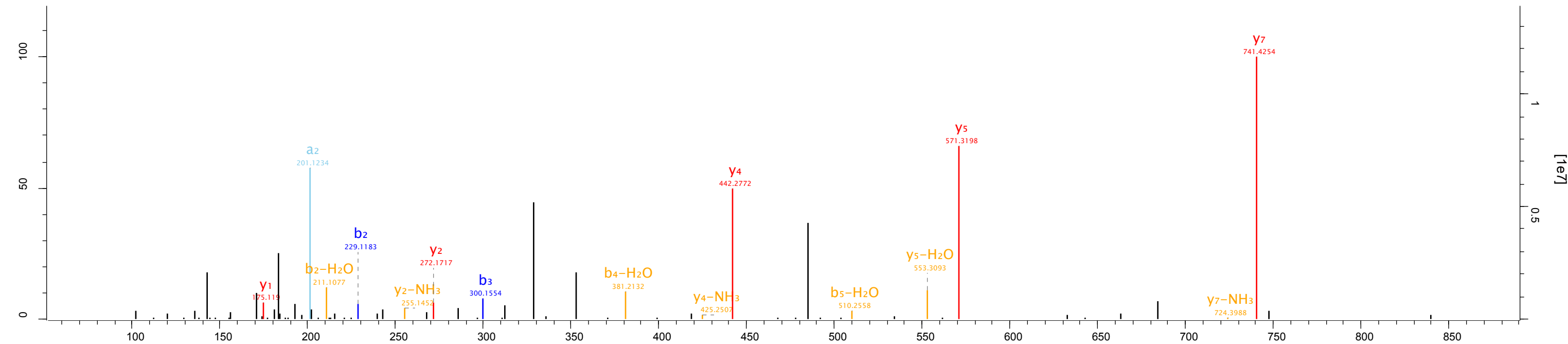
- b₂ (blue) is associated with Y.
- b₃ (blue) is associated with G.
- y₁₇ (red) is associated with G.
- y₁₆²⁺ (red) is associated with T.
- y₁₅ (red) is associated with S.
- y₁₁ (red) is associated with N.
- y₆ (red) is associated with G.
- y₂ (red) is associated with A.
- y₁ (red) is associated with K.

Raw file
20180707_MaS_A375SR_ML_proteome_2_17

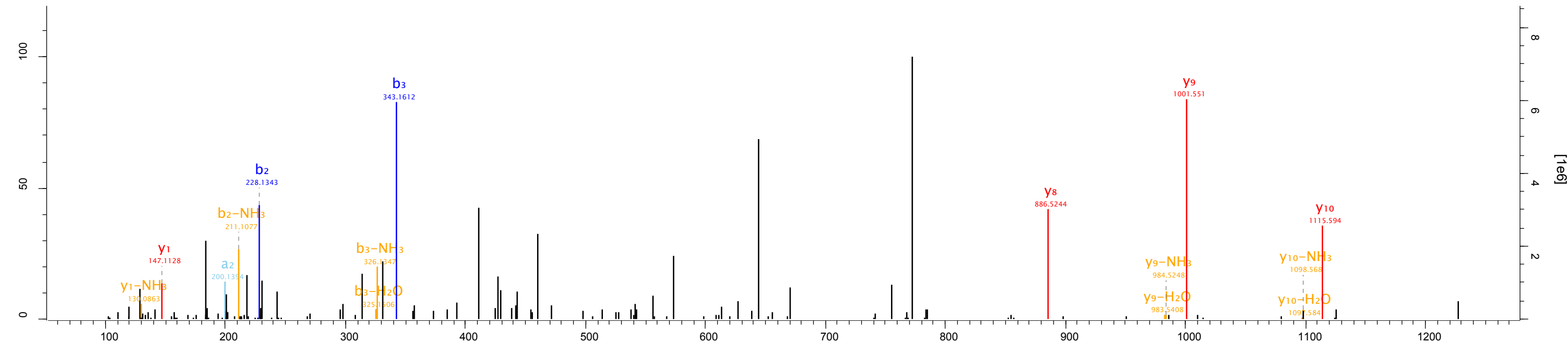
Scan 14677 Method FTMS; HCD Score 47.47 m/z 615.8 Gene names WSB2



Raw file 20180707_MaS_A375SR_ML_proteome_2_17 Scan 17587 Method FTMS; HCD Score 89.7 m/z 485.27

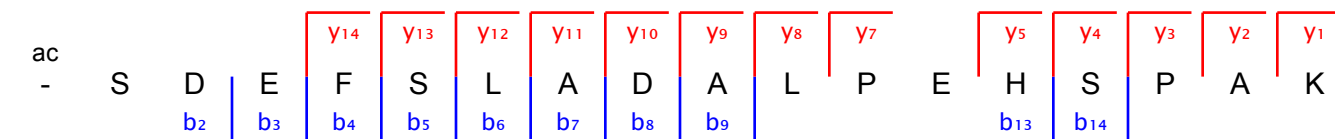
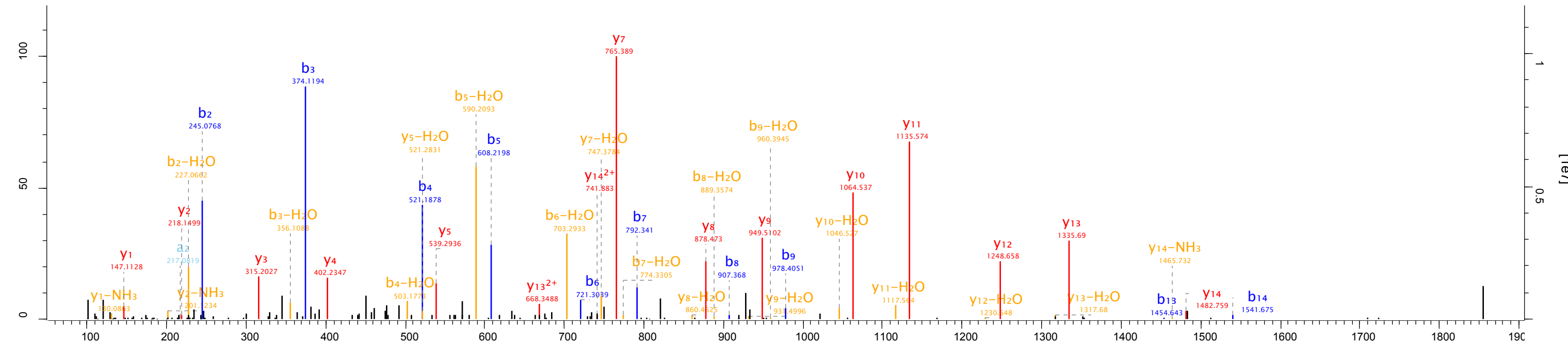


Raw file
 20180707_MaS_A375SR_ML_proteome_2_17
 Scan 23897 Method FTMS; HCD Score 74.84 m/z 614.84

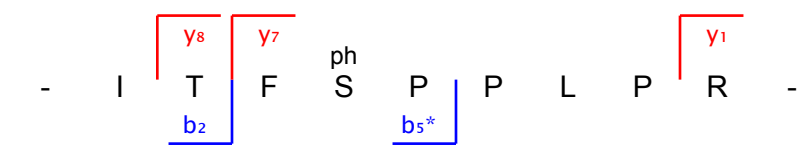
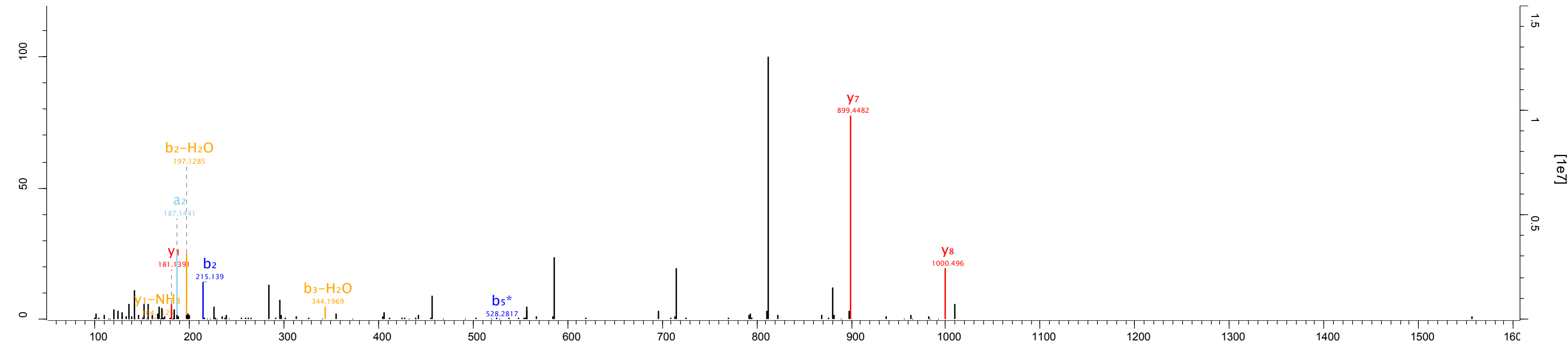


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20180707_MaS_A375SR_ML_proteome_2_17

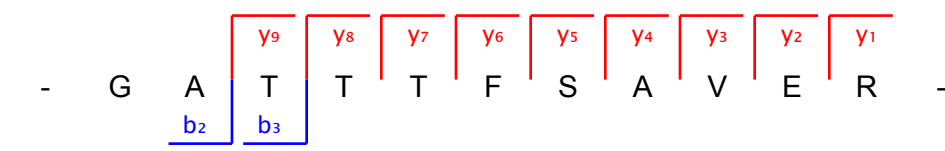
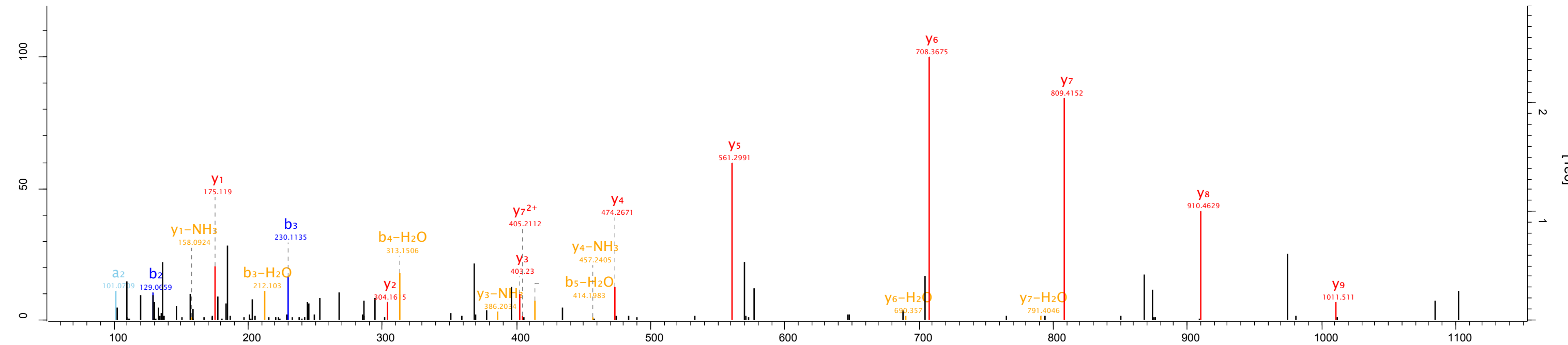
Scan 27207 Method FTMS; HCD Score 224.55 m/z 928.94 Gene names MAPK1IP1L



Raw file 20180707_MaS_A375SR_ML_proteome_2_18 Scan 15977 Method FTMS; HCD Score 52.48 m/z 557.3 Gene names IL4I1

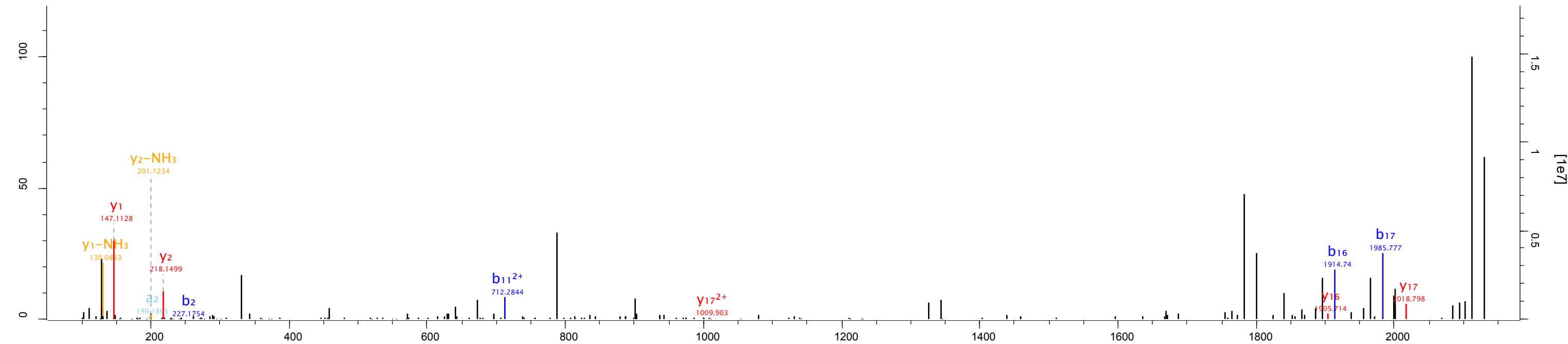


Raw file: 20180707_MaS_A375SR_ML_proteome_2_19
 Scan: 12257 Method: FTMS; HCD Score: 79.23 m/z: 570.29 Gene names: DPT



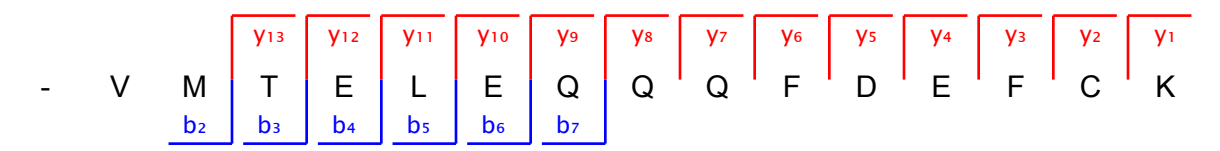
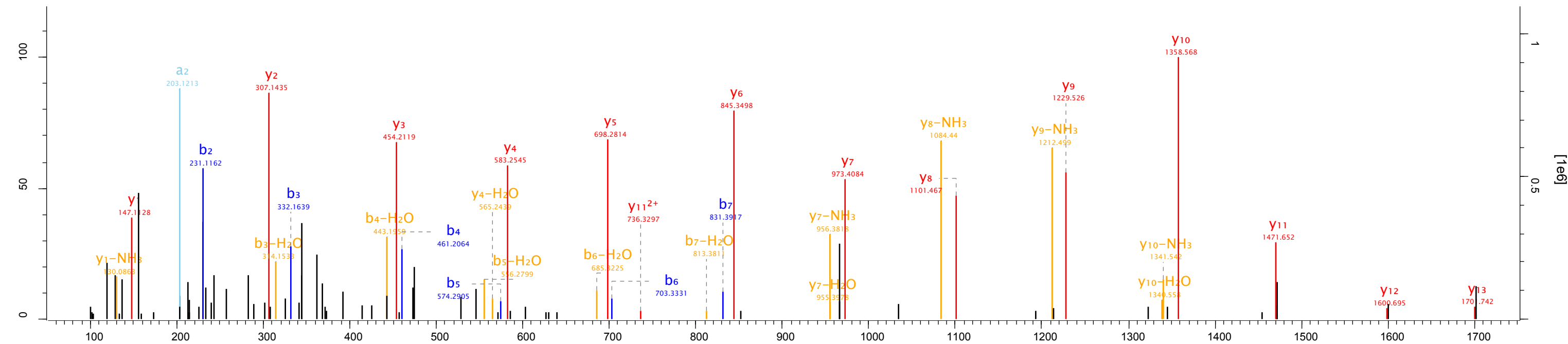
Raw file
20180707_MaS_A375SR_ML_proteome_2_19

Scan	Method	Score	m/z	Gene names
18537	FTMS; HCD	41.7	711.64	LINC00614



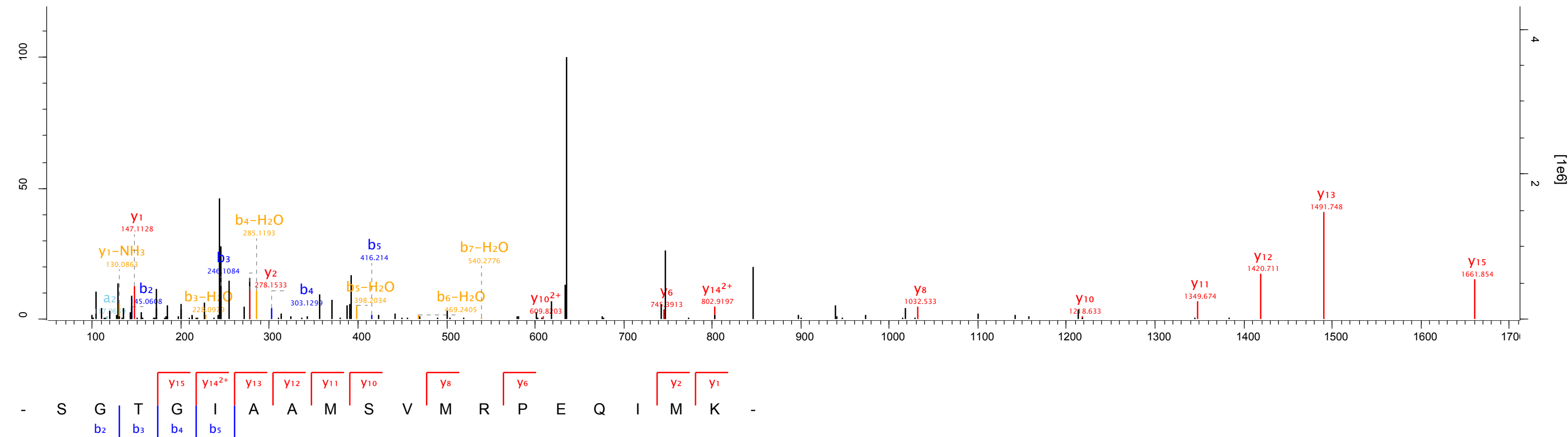
Raw file
20180707_MaS_A375SR_ML_proteome_2_19

Scan 23227 Method FTMS; HCD Score 230.36 m/z 966.93 Gene names CCDC23

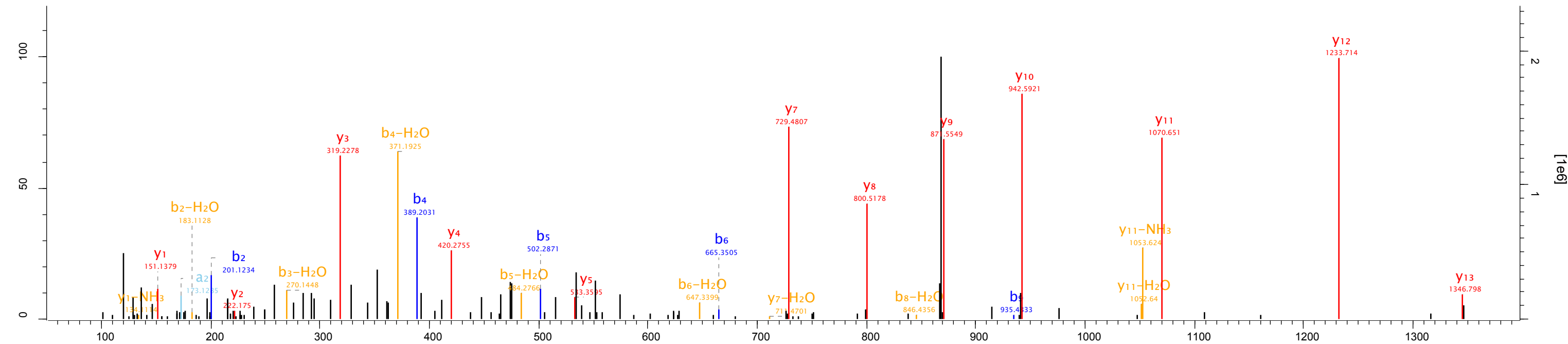


Raw file
20180707_MaS_A375SR_ML_proteome_2_19

Scan 23587 Method FTMS; HCD Score 31.4 m/z 636.32 Gene names ATP6V0C



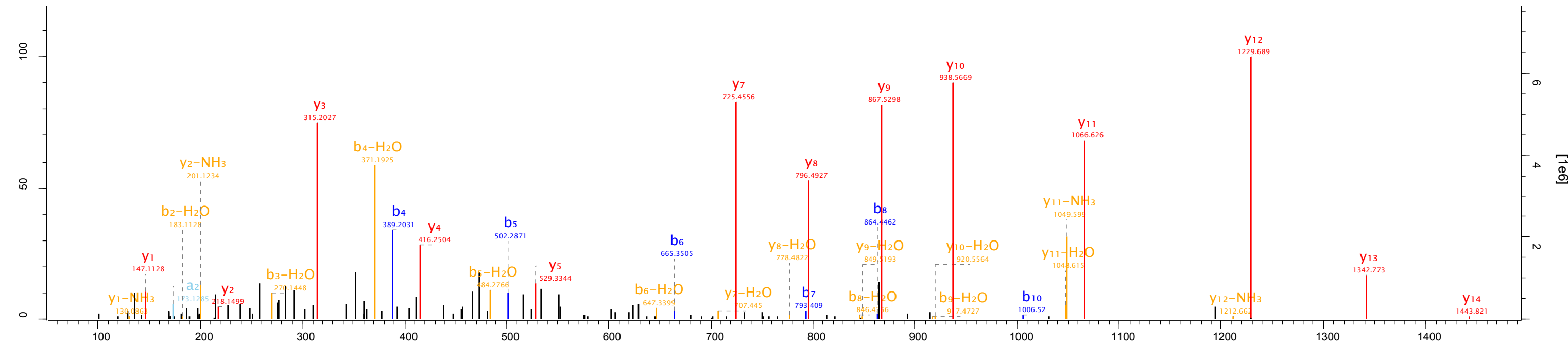
Raw file 20180707_MaS_A375SR_ML_proteome_2_20 Scan 22727 Method FTMS; HCD Score 103.13 m/z 868 Gene names KRTCAP2



- I S S T L Y Q A A A P V L T P A K -

Fragmentation sites are indicated by brackets below the sequence:

- b₂ (under S)
- b₄ (under T)
- b₅ (under L)
- b₆ (under Y)
- b₉ (under A)
- y₁ (under K)
- y₂ (under A)
- y₃ (under P)
- y₄ (under A)
- y₅ (under L)
- y₇ (under P)
- y₈ (under A)
- y₉ (under A)
- y₁₀ (under A)
- y₁₁ (under Q)
- y₁₂ (under Y)
- y₁₃ (under L)



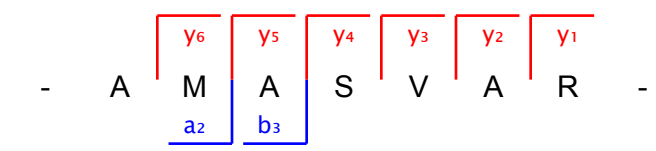
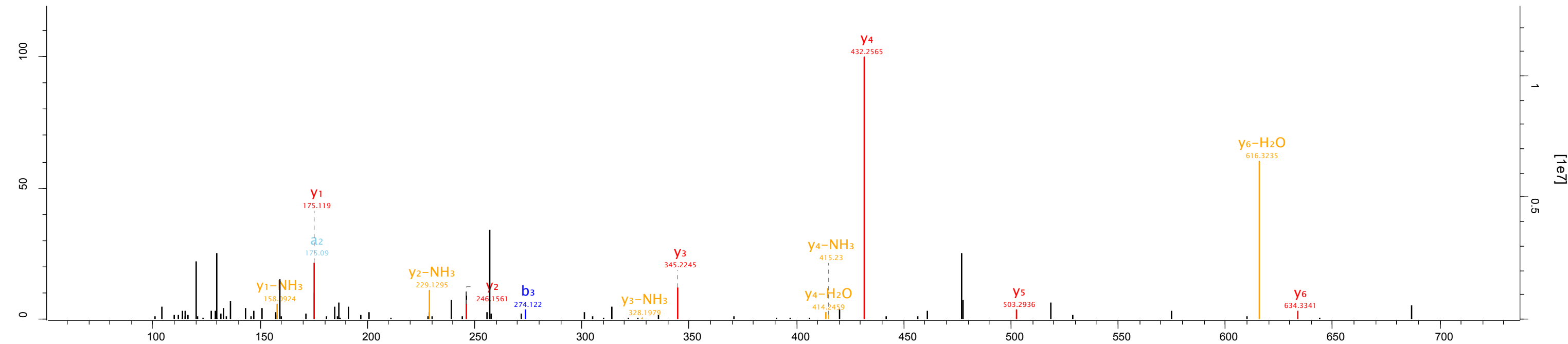
- I S S T L Y Q A A P V L T P A K -

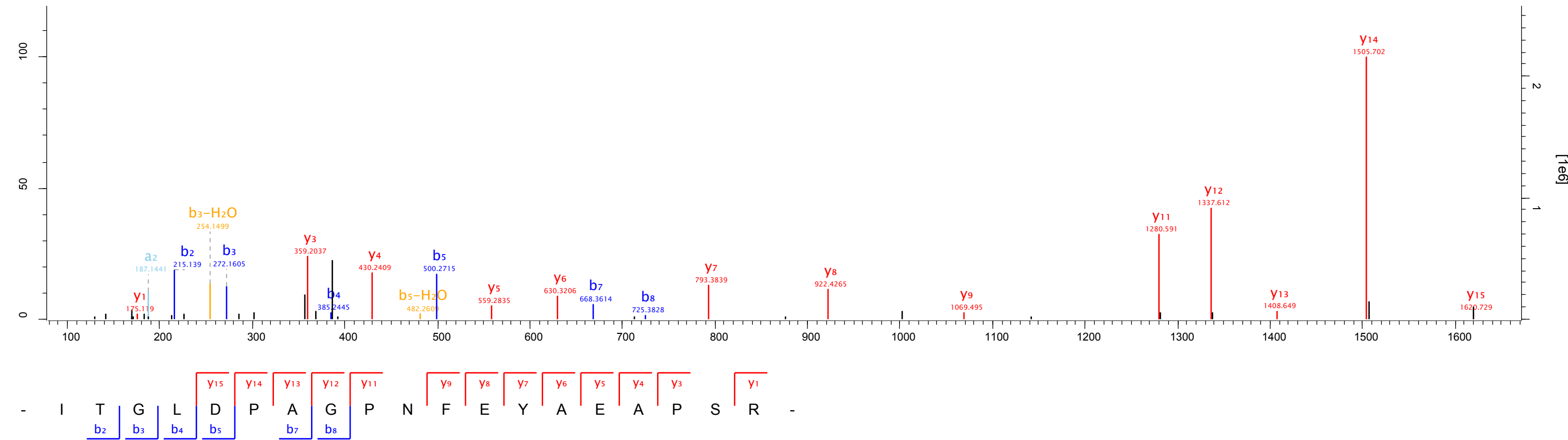
Fragmentation sites are indicated by brackets below the sequence:

- Fragmentation sites for y ions (red brackets): y14, y13, y12, y11, y10, y9, y8, y7, y5, y4, y3, y2, y1.
- Fragmentation sites for b ions (blue brackets): b4, b5, b6, b7, b8, b10.

Raw file
20180707_MaS_A375SR_ML_proteome_2_20

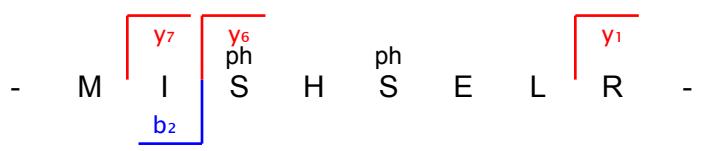
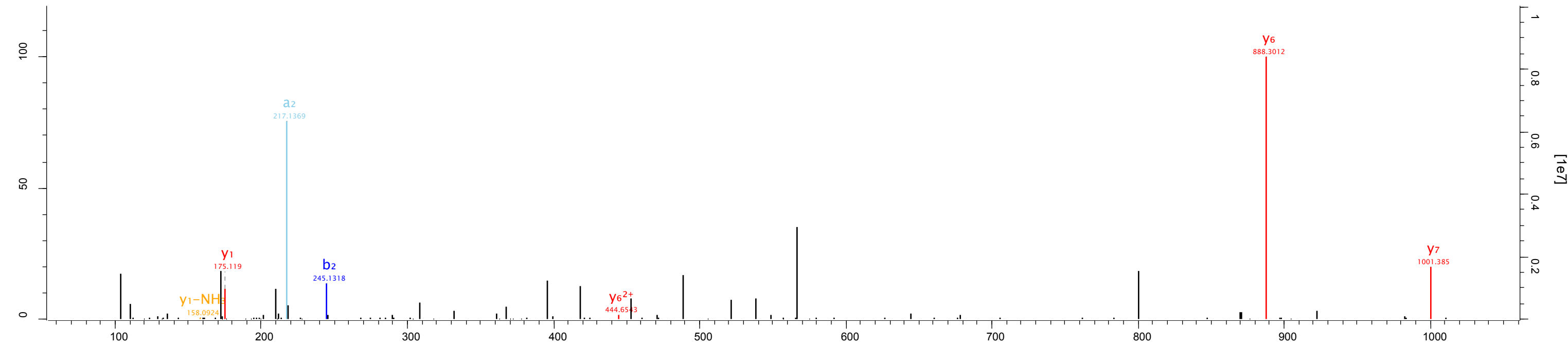
Scan 6197 Method FTMS; HCD Score 85.36 m/z 353.19 Gene names ART4





Raw file
20180707_MaS_A375SR_ML_proteome_2_22

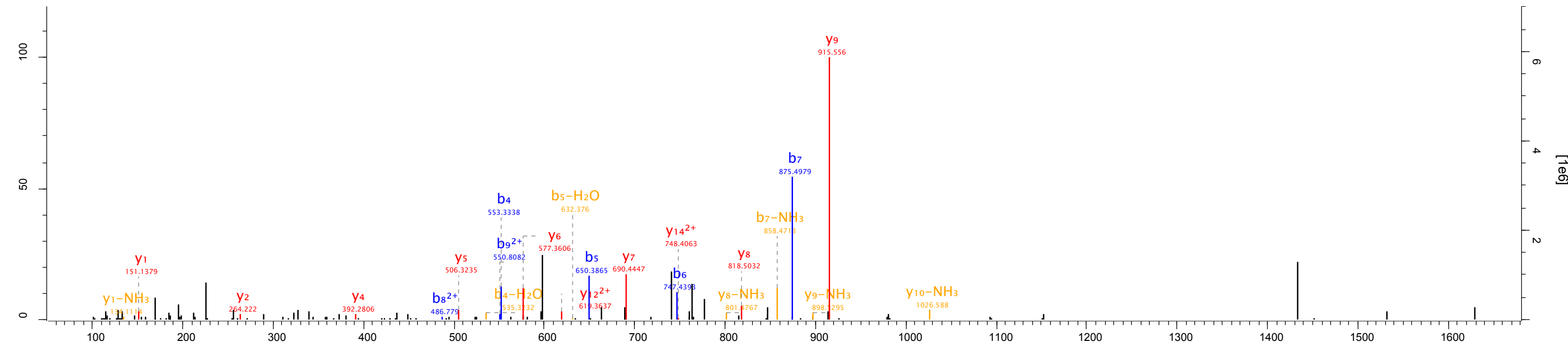
Scan 9187 Method FTMS; HCD Score 68.91 m/z 566.72 Gene names PSPHP1



Raw file

20180707_MaS_A375SR_ML_proteome_2_22

Scan	Method	Score	m/z	Gene names
9757	FTMS; HCD	69.26	597.69	C20orf24

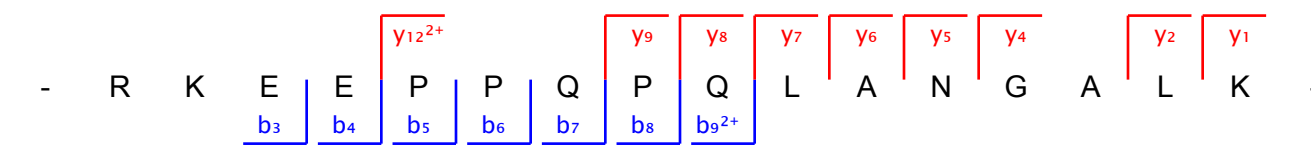
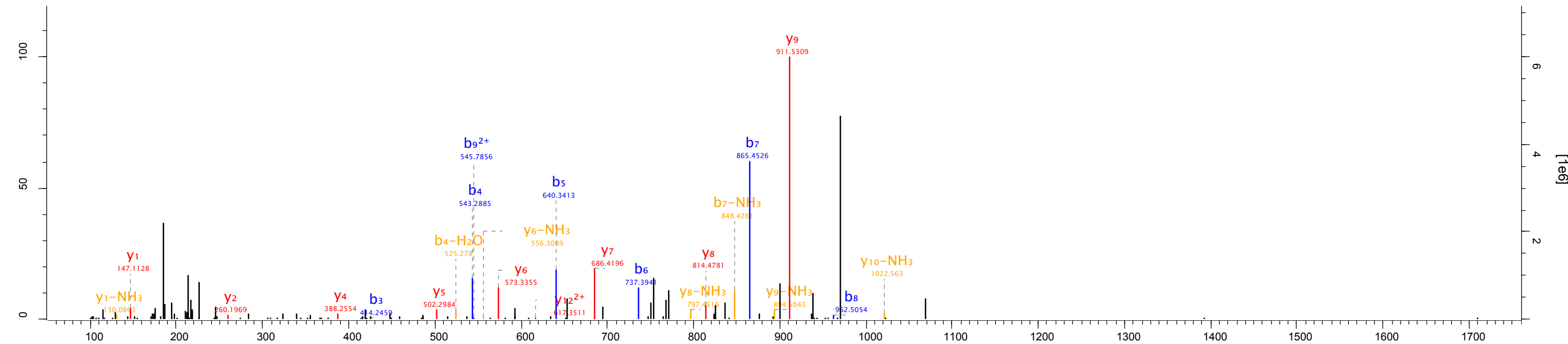


- R K E E P P Q P Q L A N G A L K -

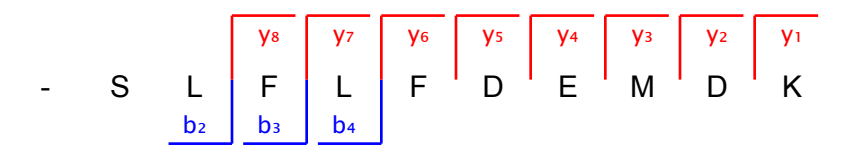
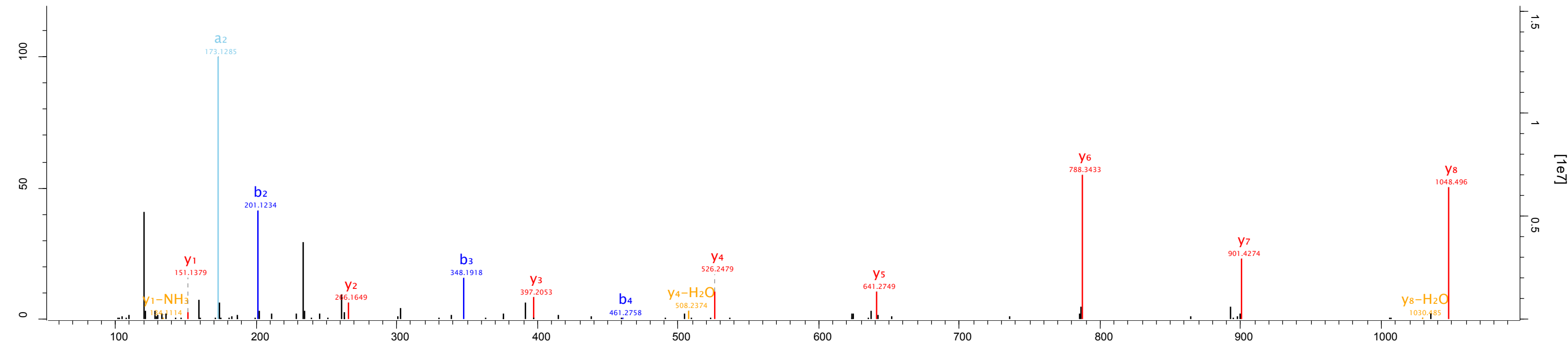
y₁₄²⁺
y₁₂²⁺
y₉
y₈
y₇
y₆
y₅
y₄
y₂
y₁

b₄
b₅
b₆
b₇
b₈²⁺
b₉²⁺

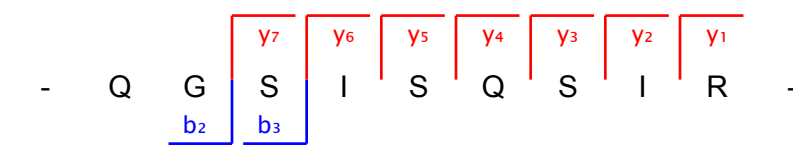
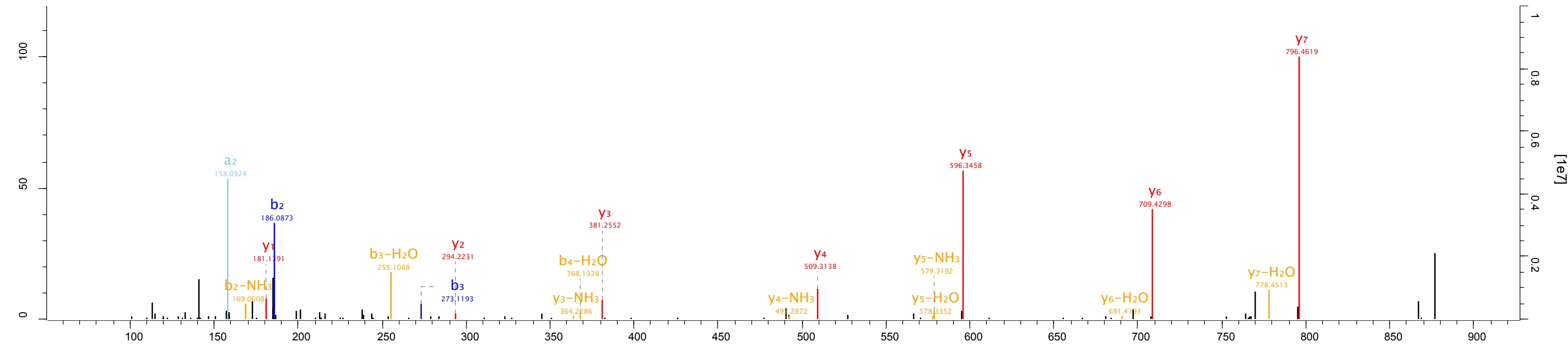
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 Scan 9887 Method FTMS; HCD Score 48.88 m/z 593 Gene names C20orf24

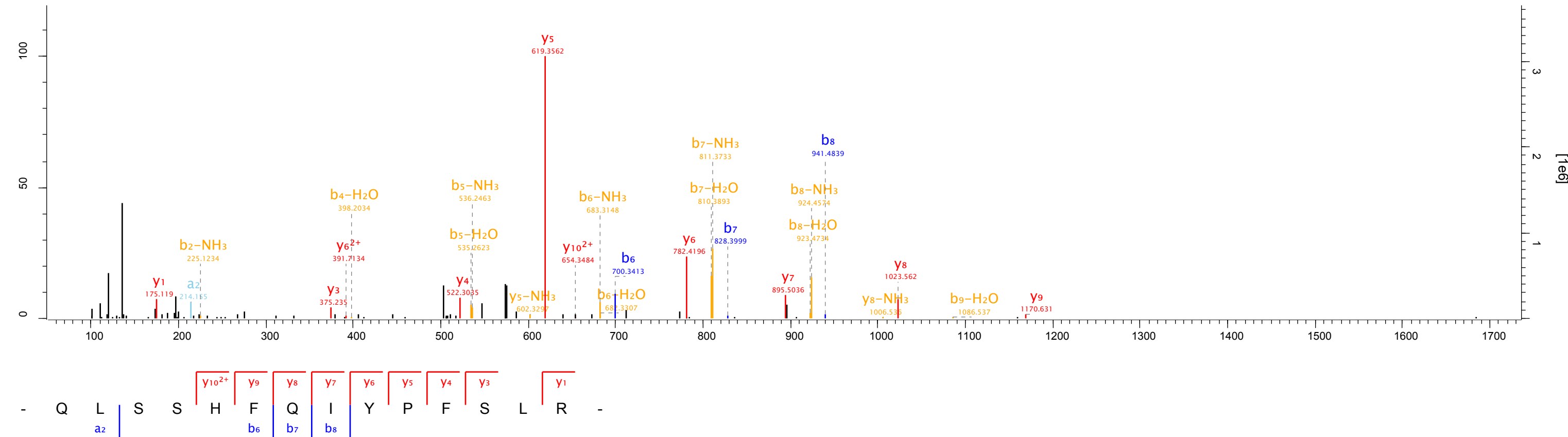


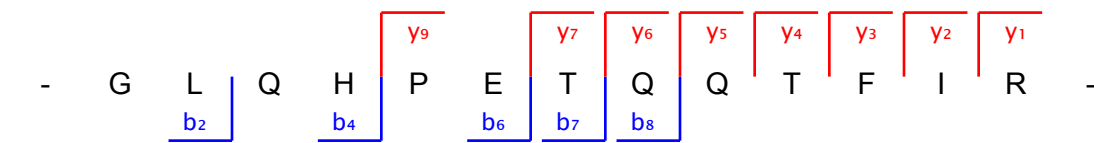
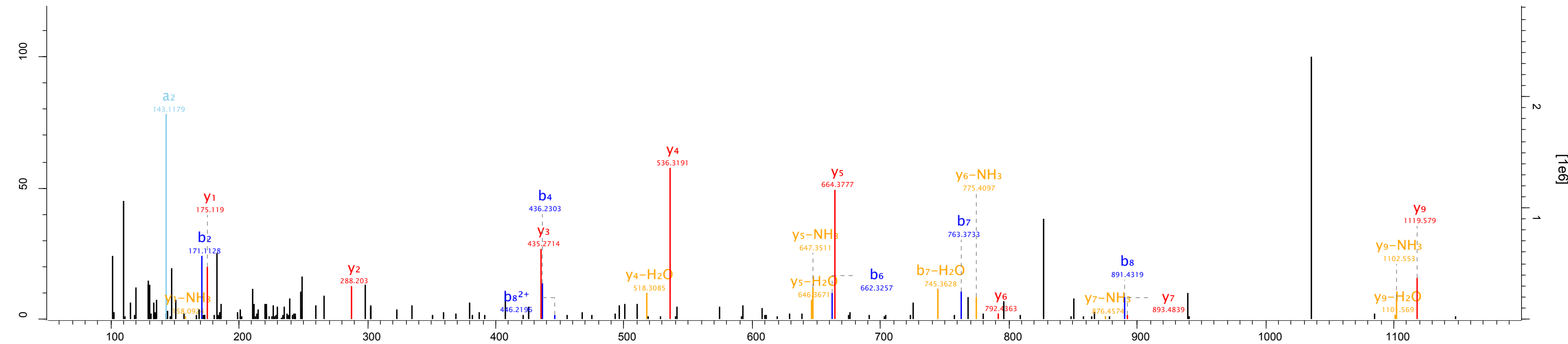
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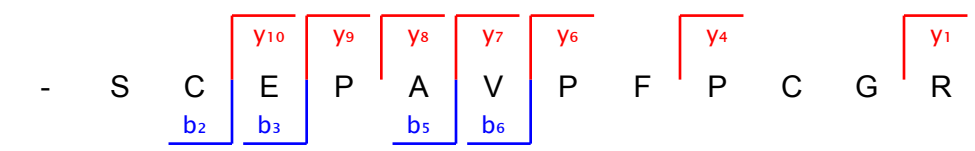
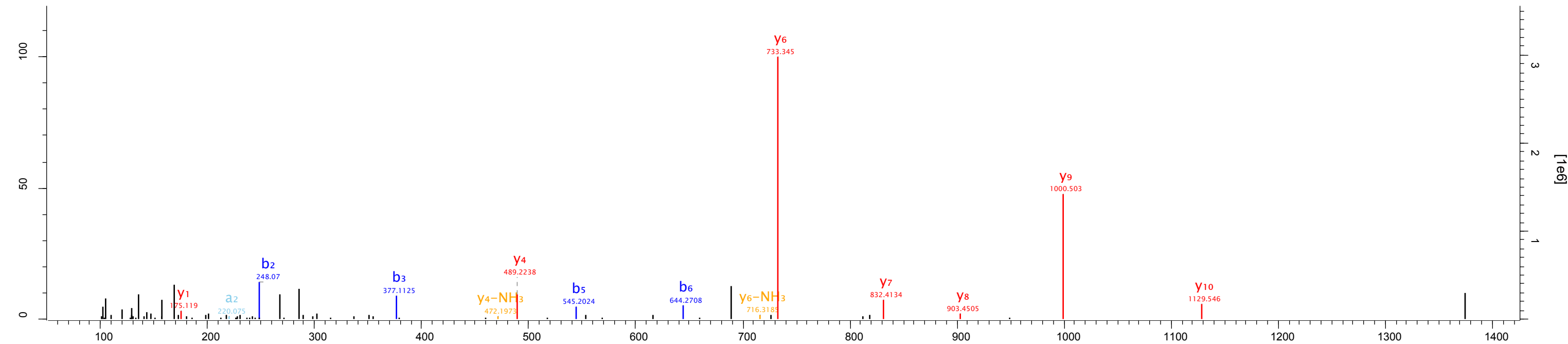
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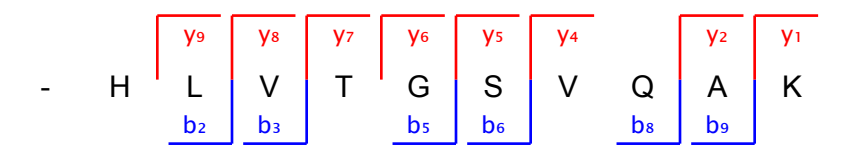
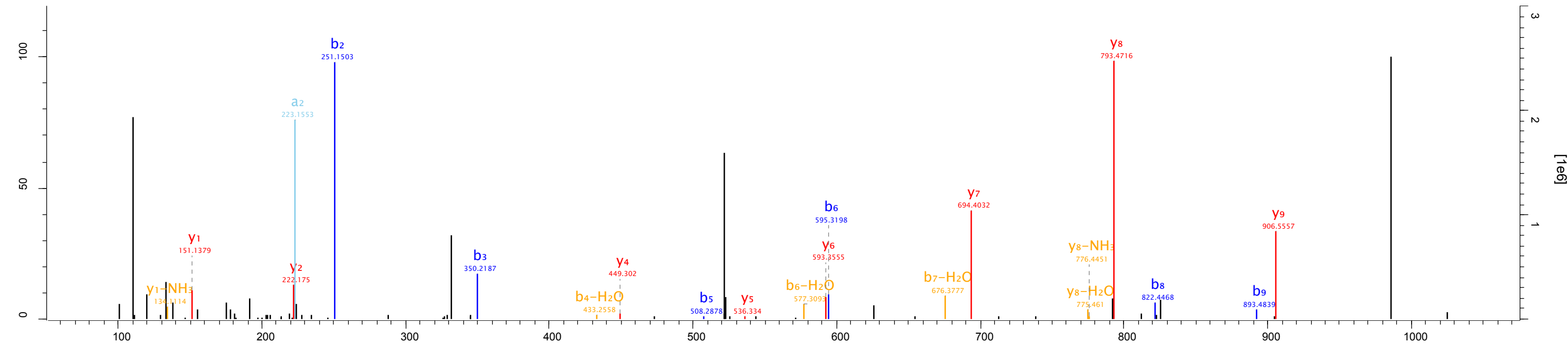




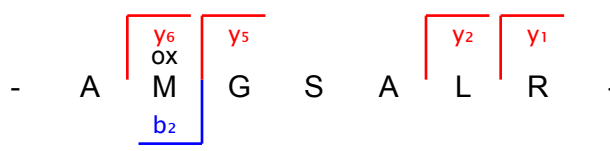
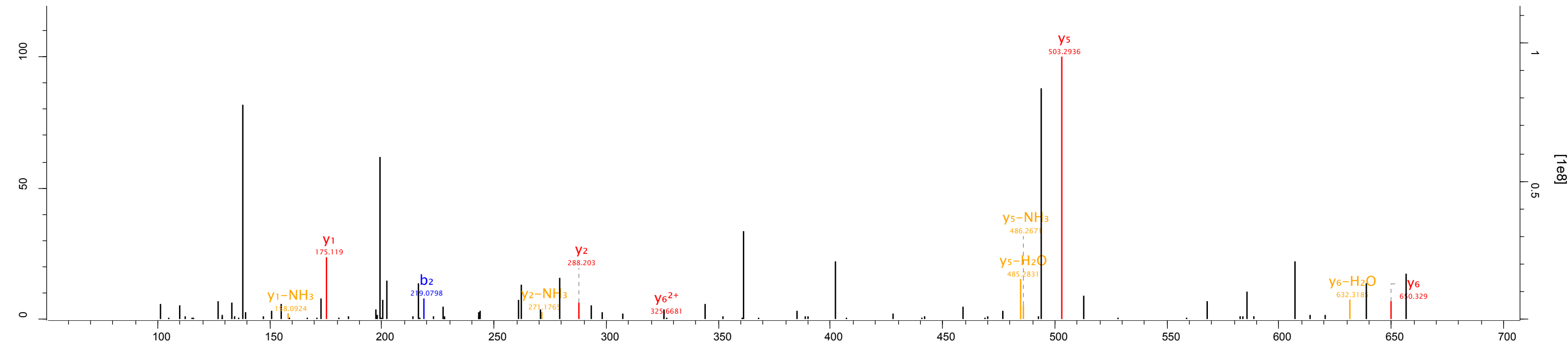
Raw file 20180707_MaS_A375SR_ML_proteome_2_26 Scan 17007 Method FTMS; HCD Score 57.16 m/z 688.81 Gene names F9

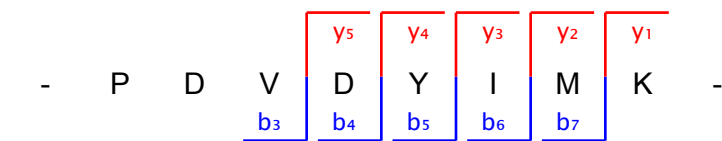
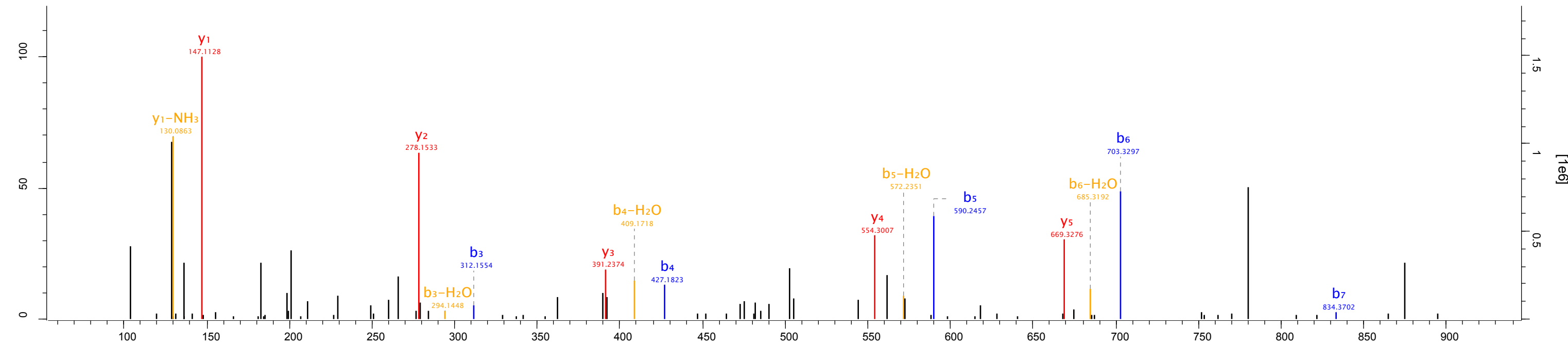


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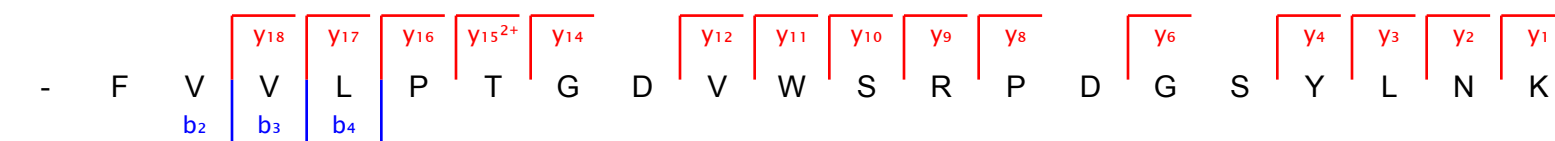
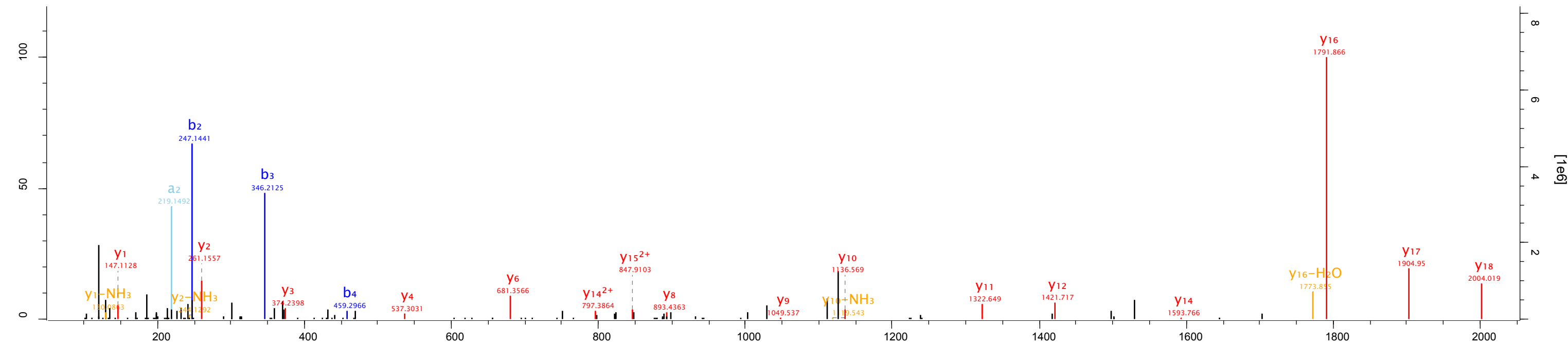
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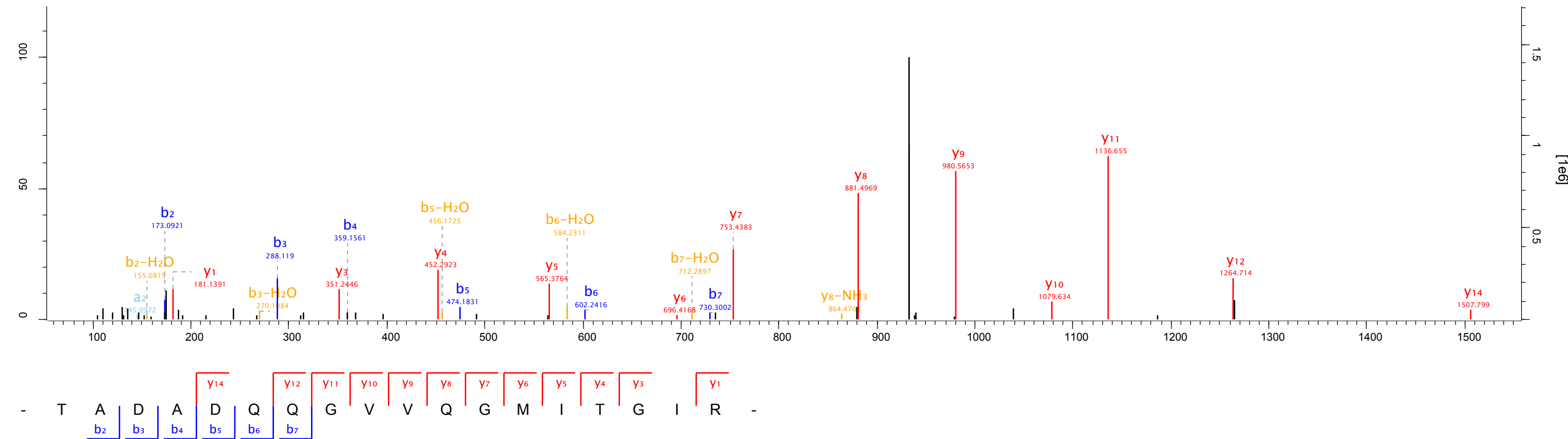




Raw file
20180707_MaS_A375SR_ML_proteome_2_28

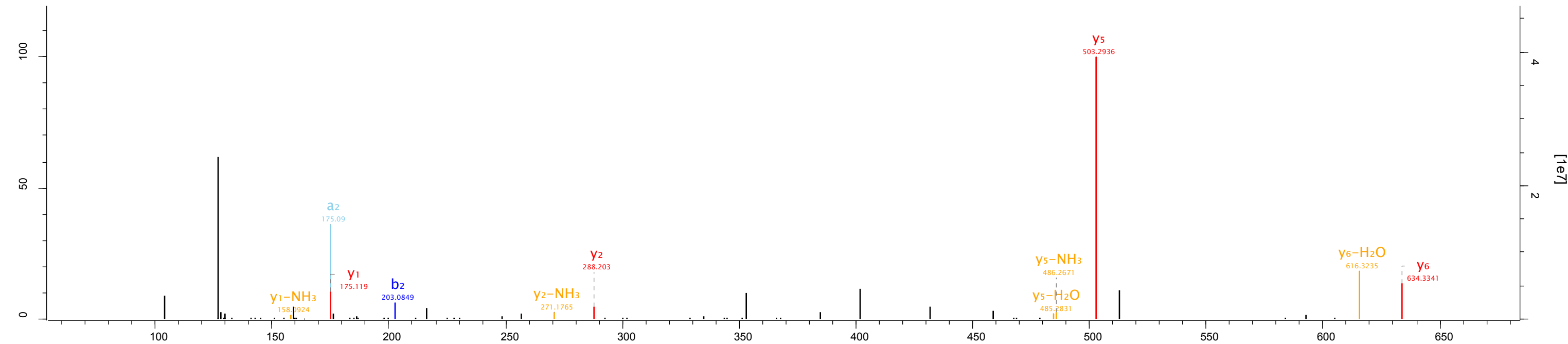
Scan 26627 Method FTMS; HCD Score 111.77 m/z 750.72 Gene names FGFR1





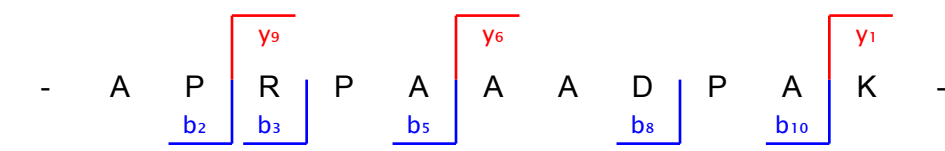
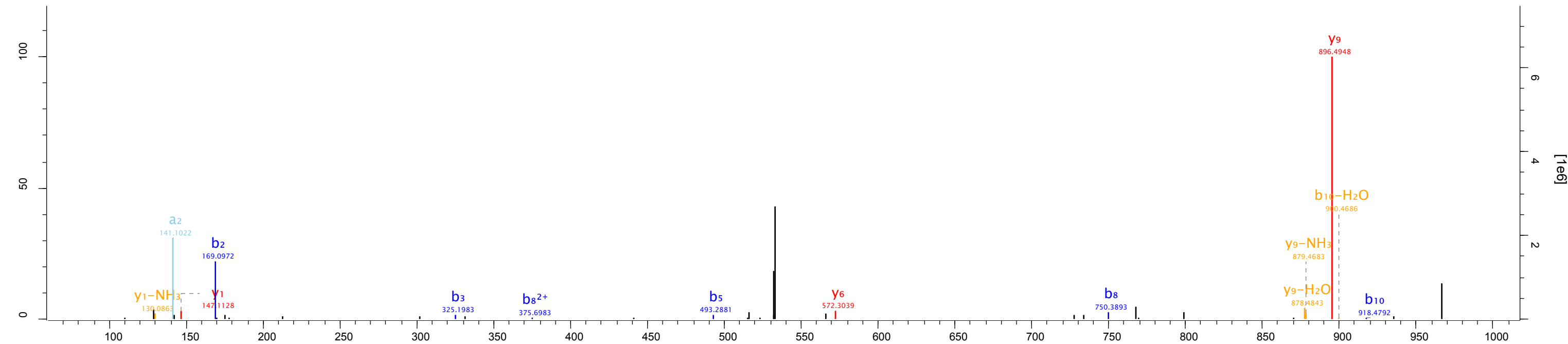
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20180707_MaS_A375SR_ML_proteome_2_29

Scan 6457 Method FTMS; HCD Score 79.45 m/z 353.19

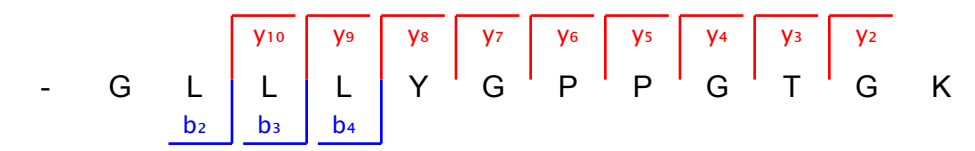
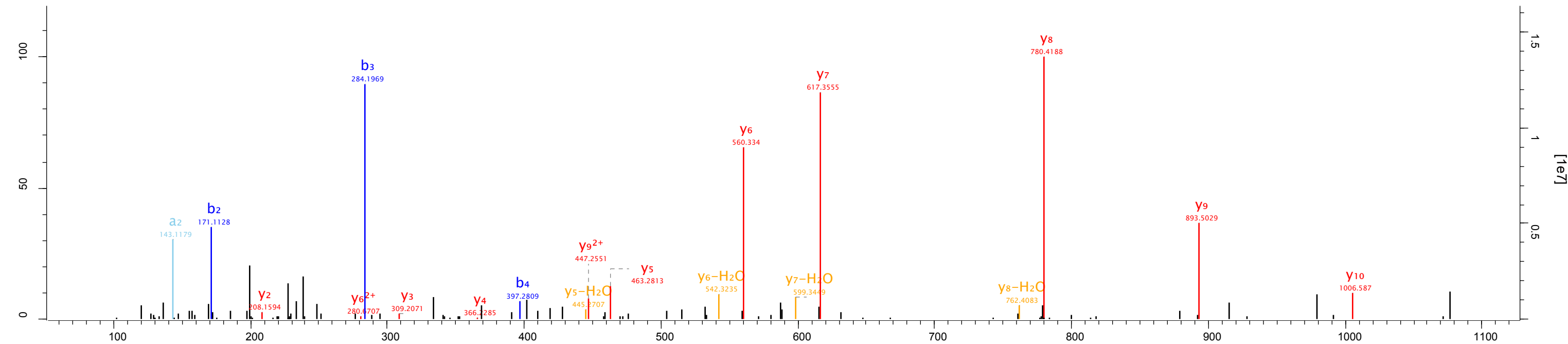


Raw file
20180707_MaS_A375SR_ML_proteome_2_30

Scan 4057 Method FTMS; HCD Score 57.15 m/z 532.8

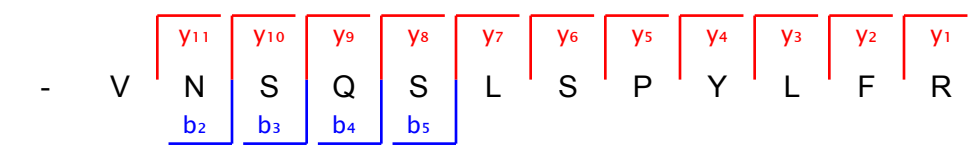
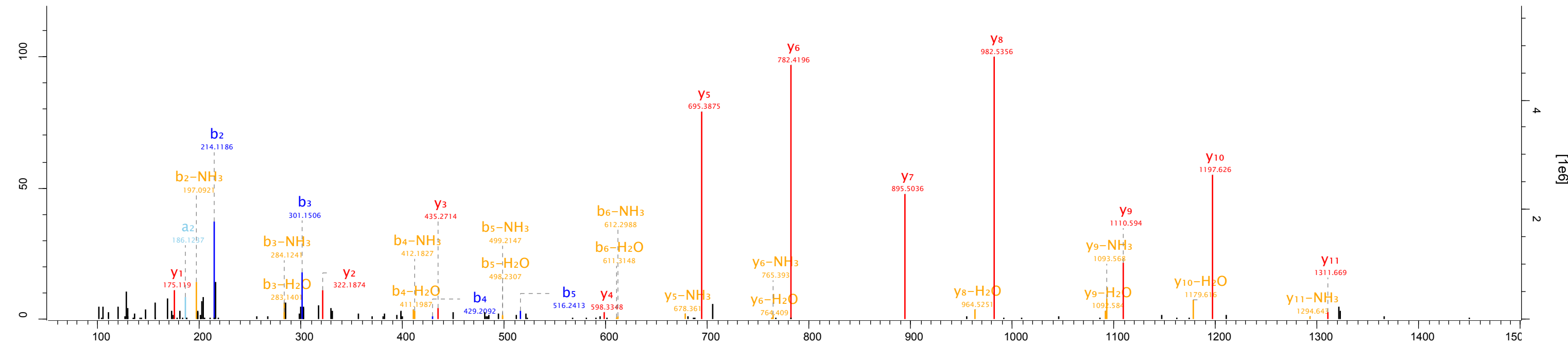


Raw file 20180707_MaS_A375SR_ML_proteome_20 Scan 22137 Method FTMS; HCD Score 80.69 m/z 588.85 Gene names KATNAL2



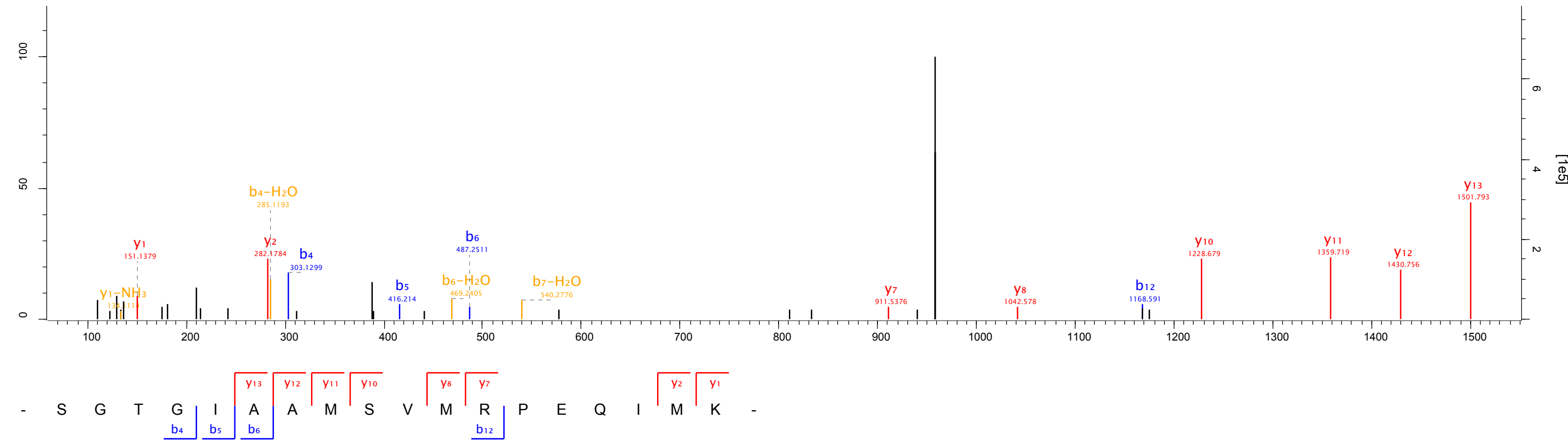
Raw file
20180707_MaS_A375SR_ML_proteome_21

Scan 25447 Method FTMS; HCD Score 169.89 m/z 705.87 Gene names SPP2

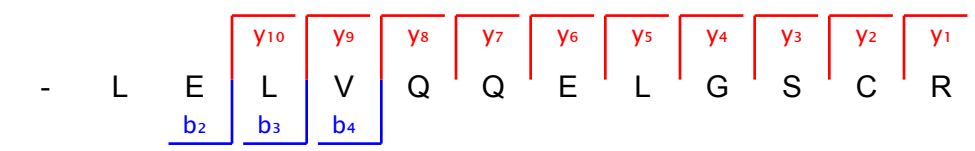
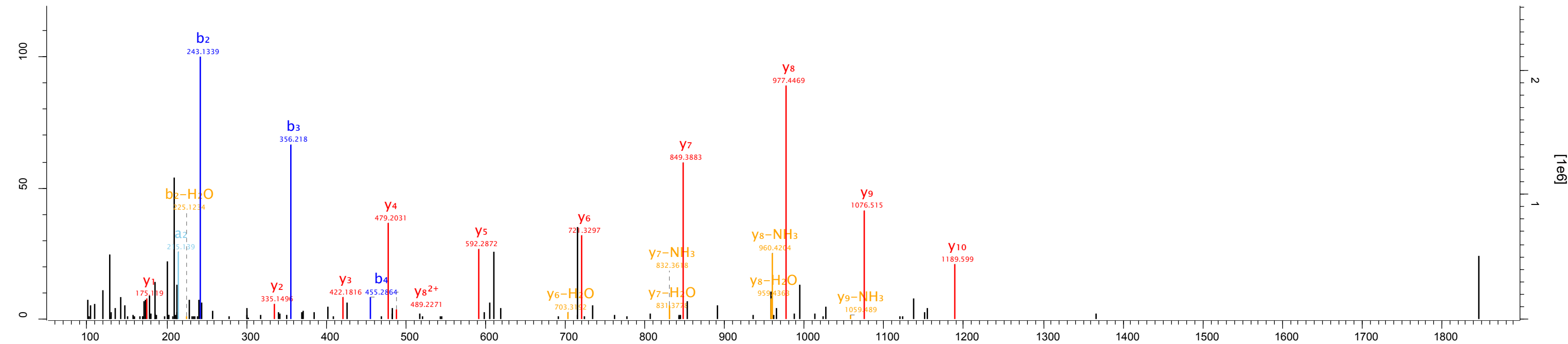


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20180707_MaS_A375SR_ML_proteome_22

Scan 21557 Method FTMS; HCD Score 49.54 m/z 959 Gene names ATP6V0C

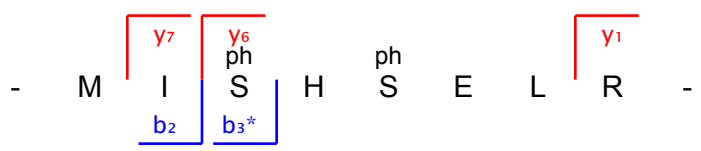
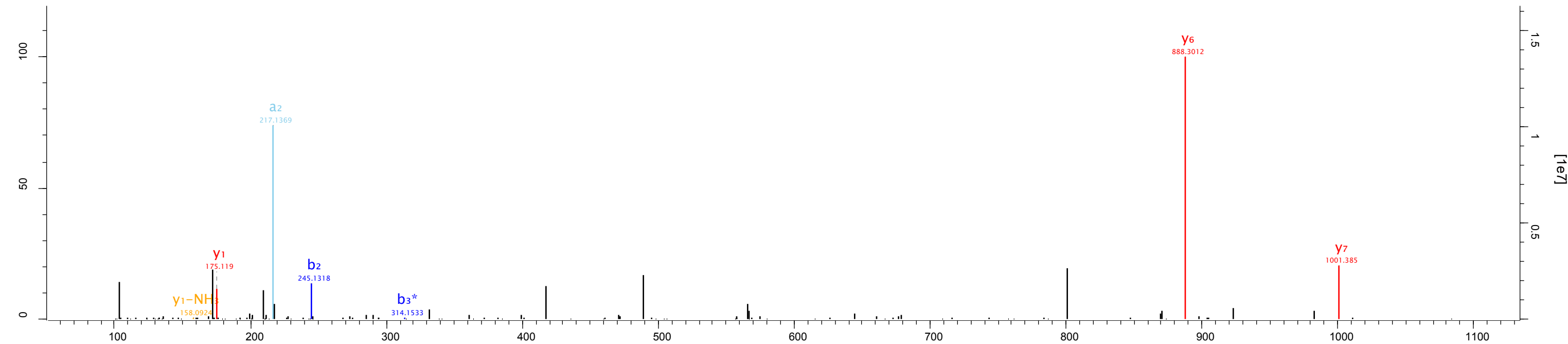


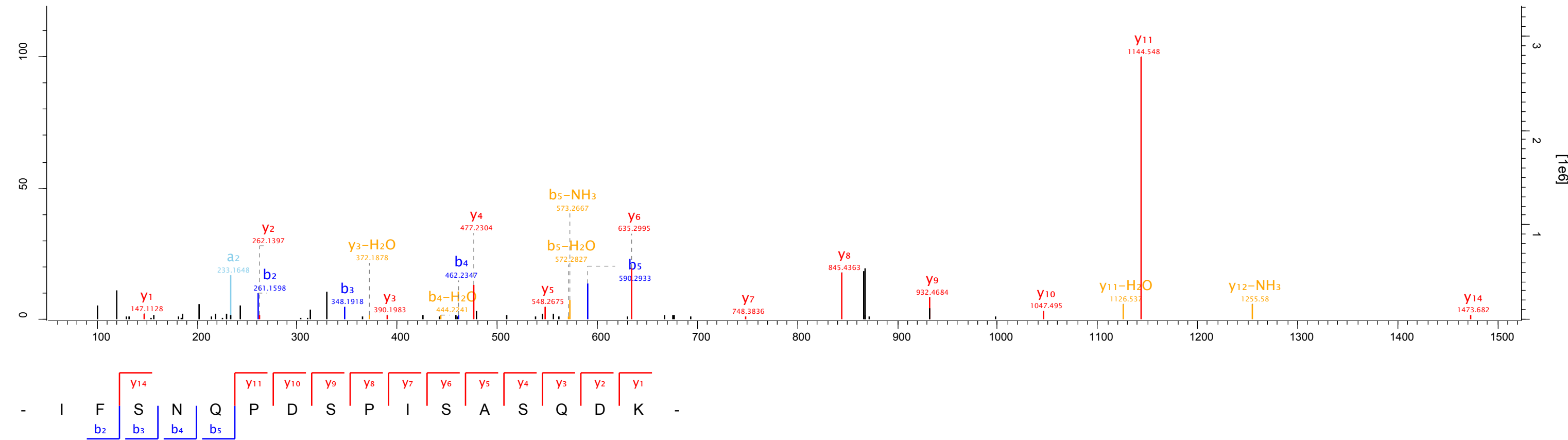
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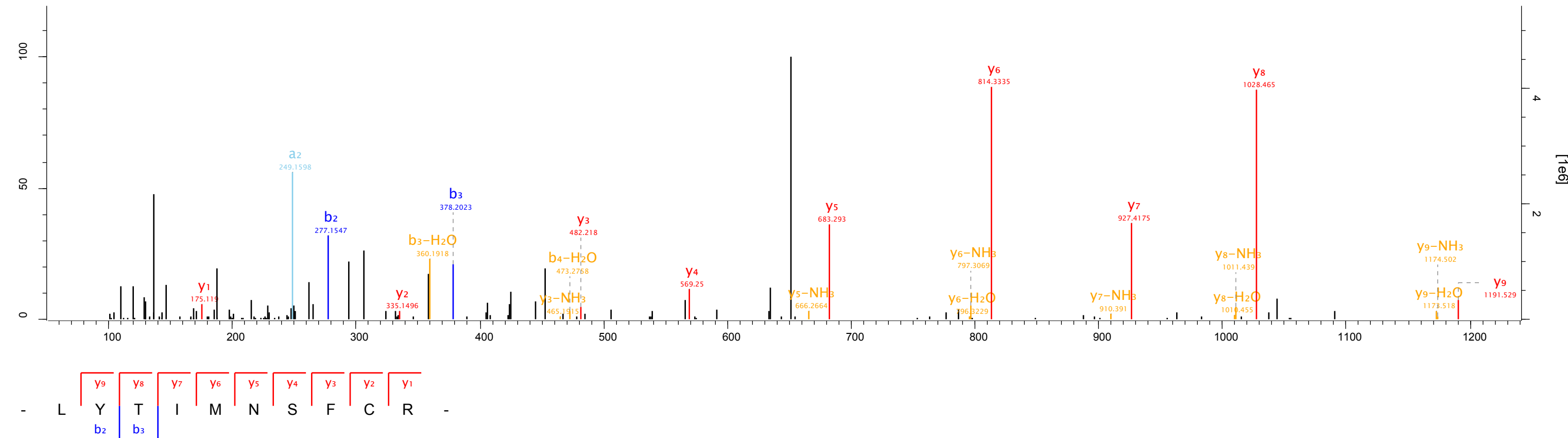


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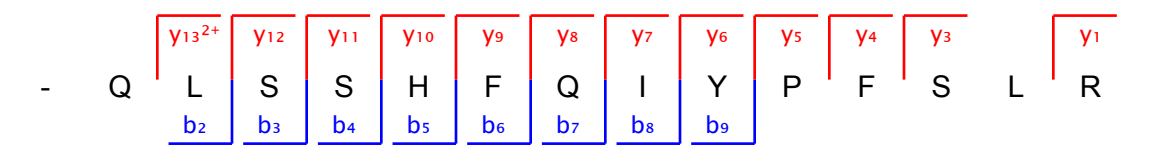
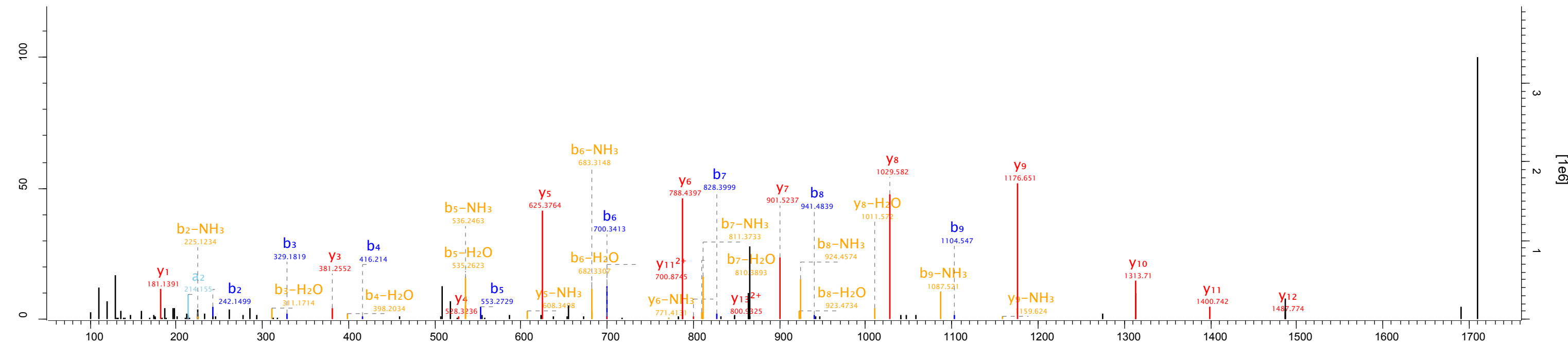




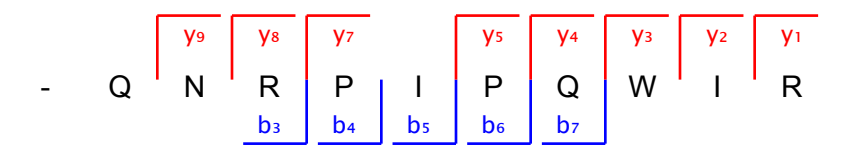
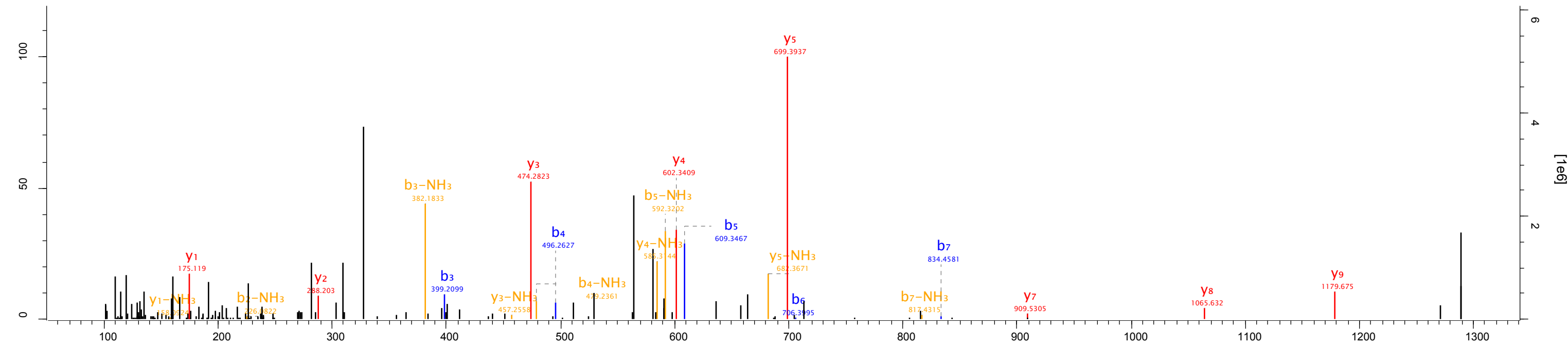


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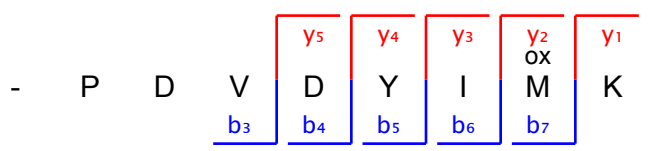
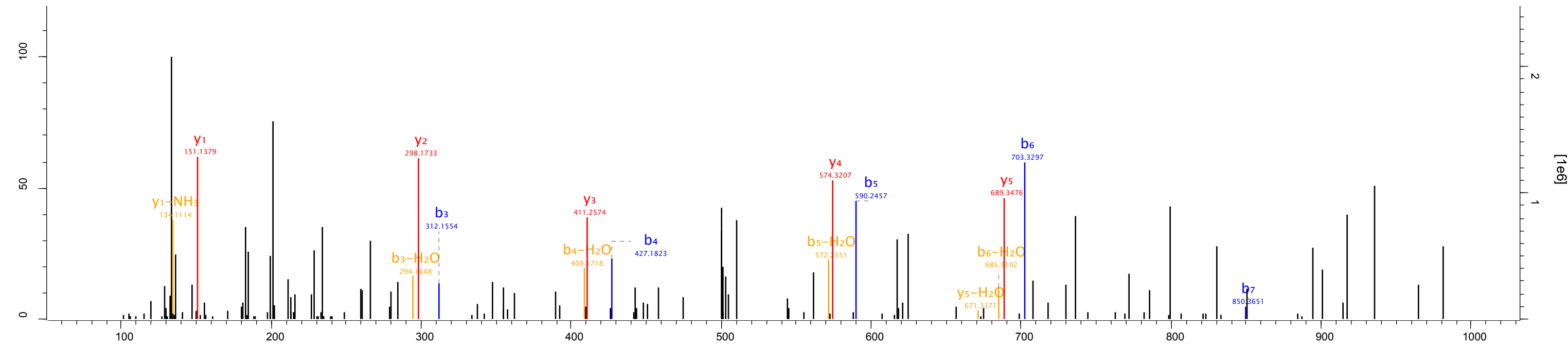
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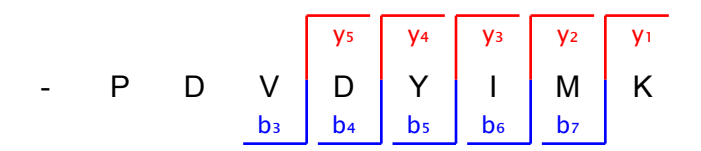
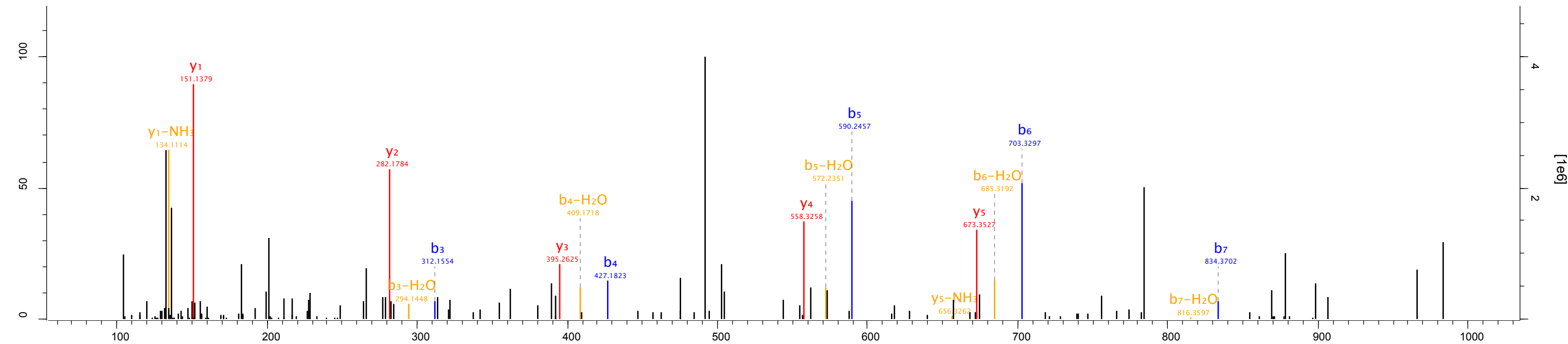
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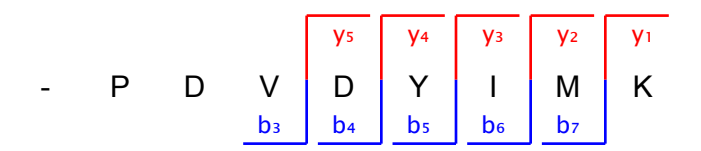
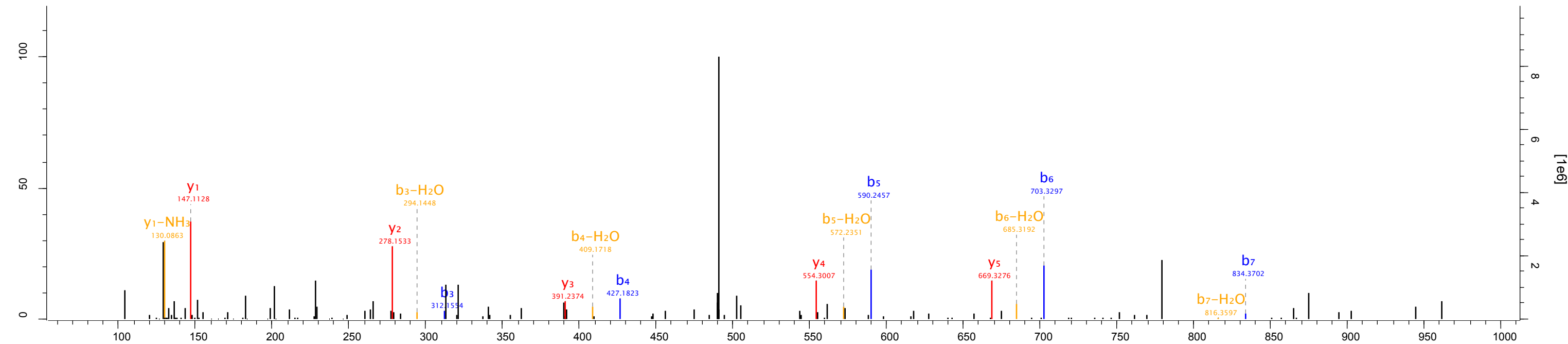
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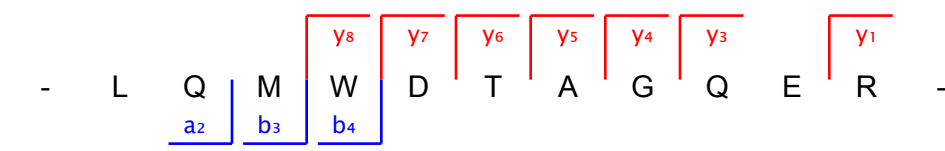
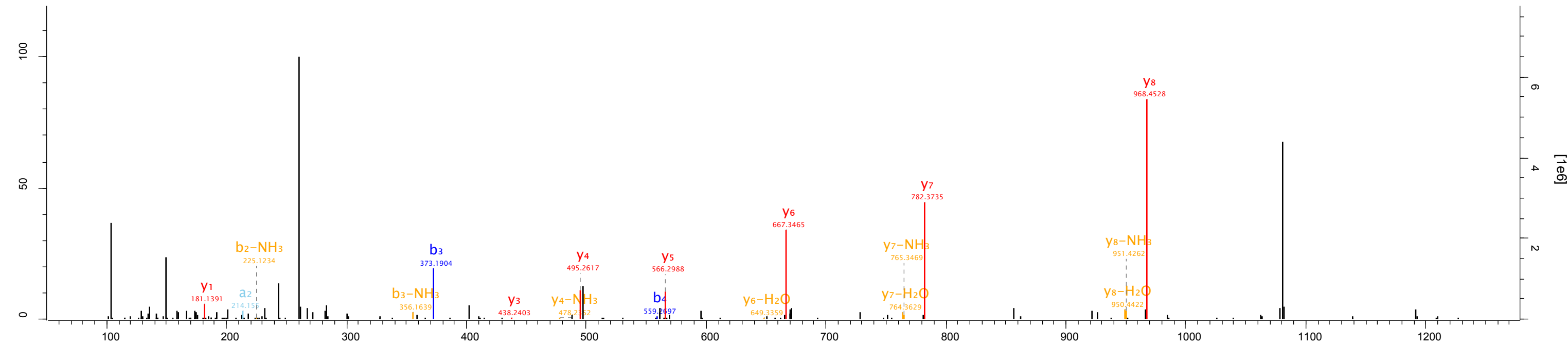


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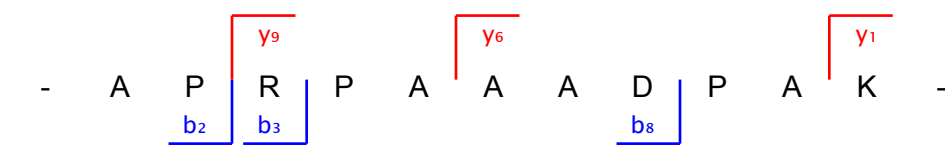
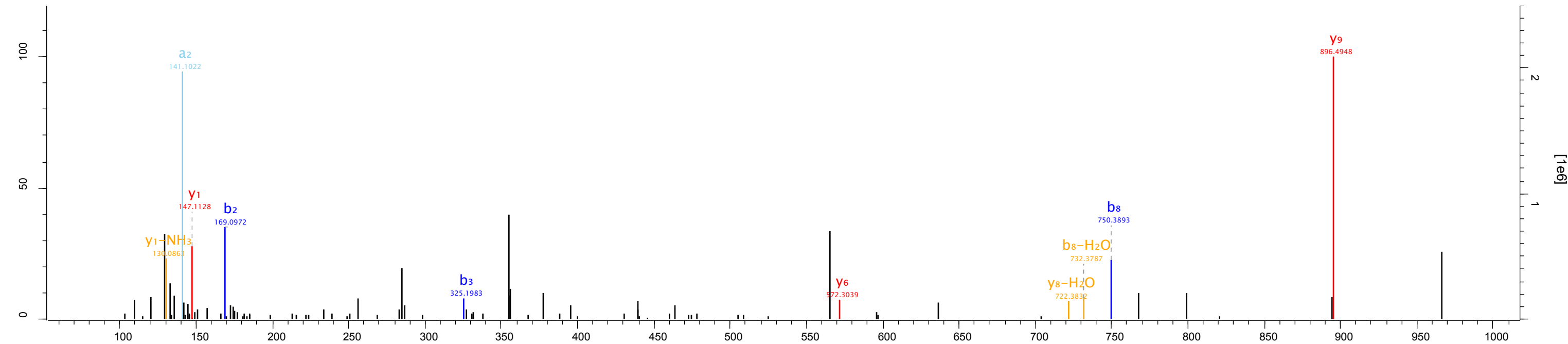
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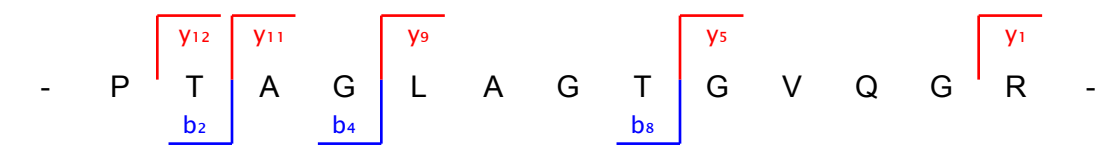
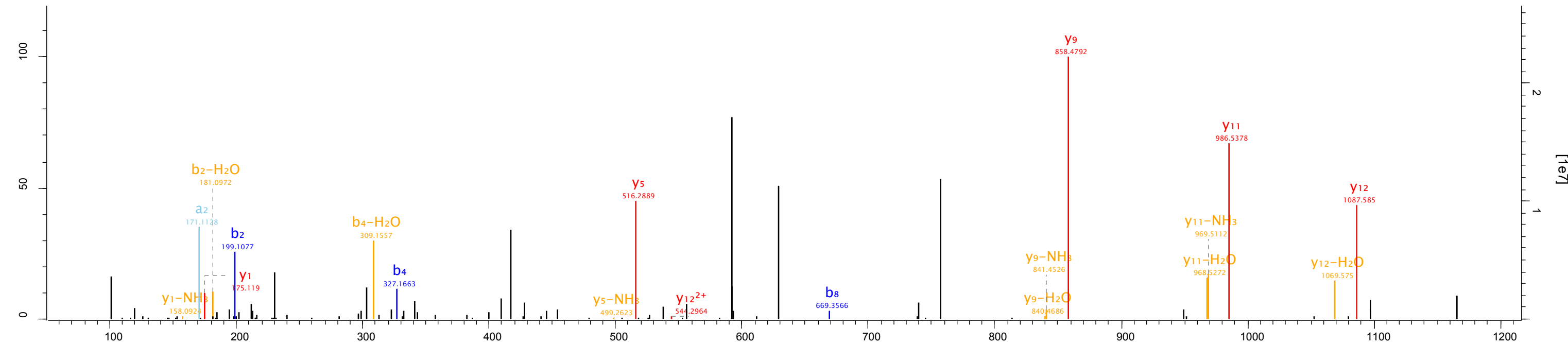


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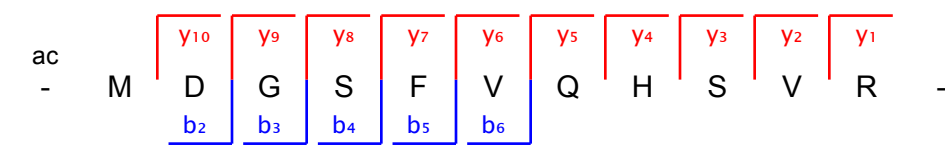
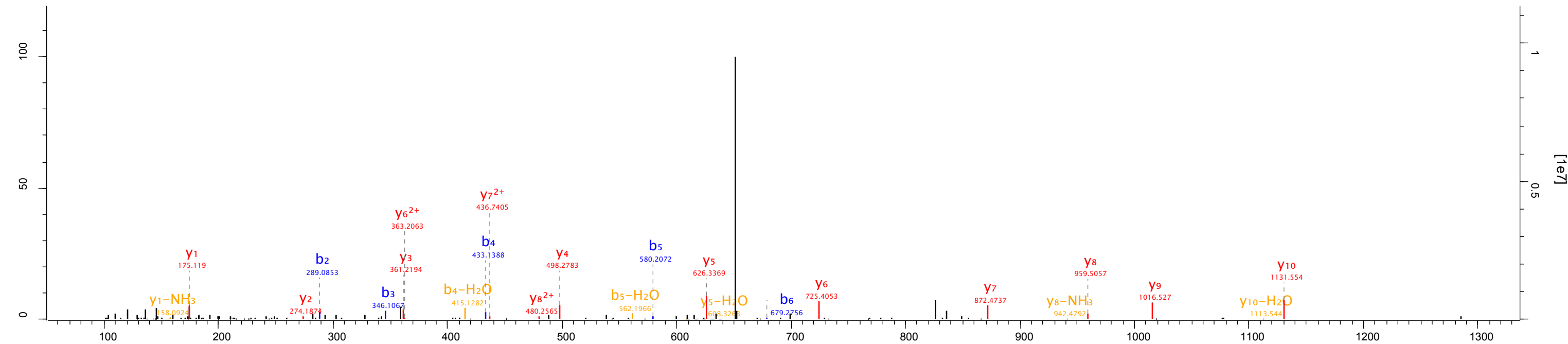
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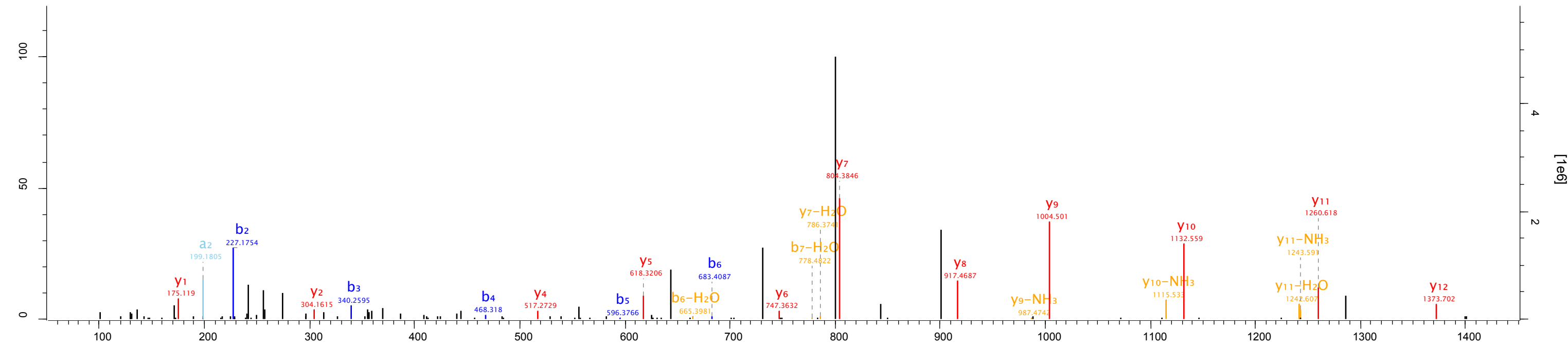
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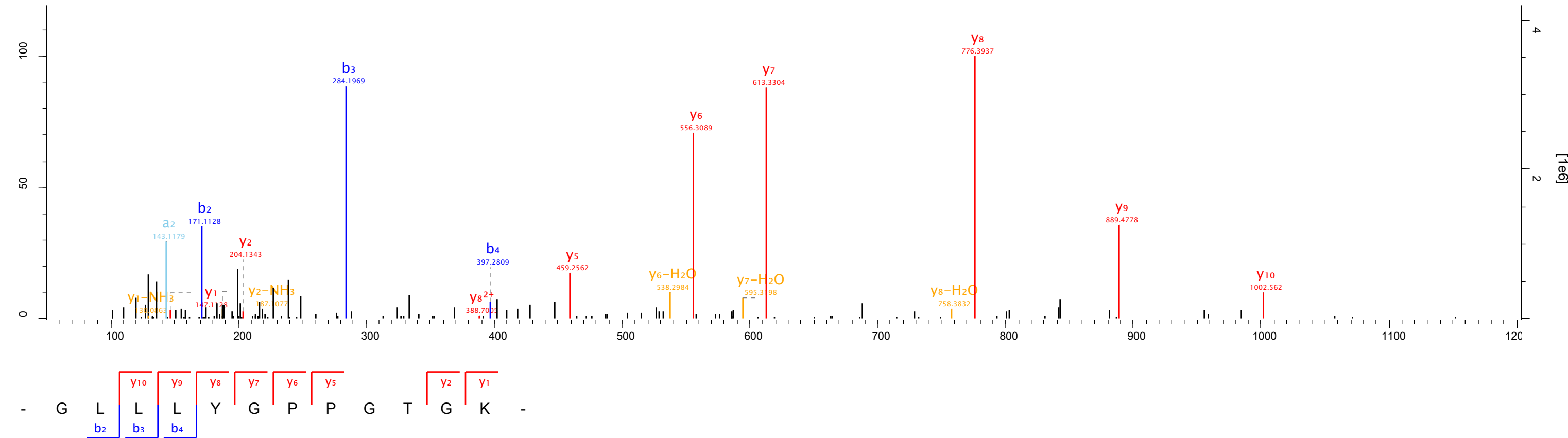


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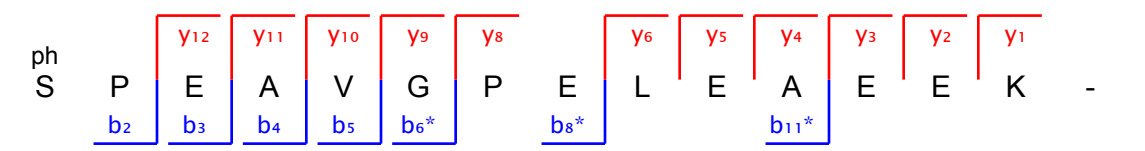
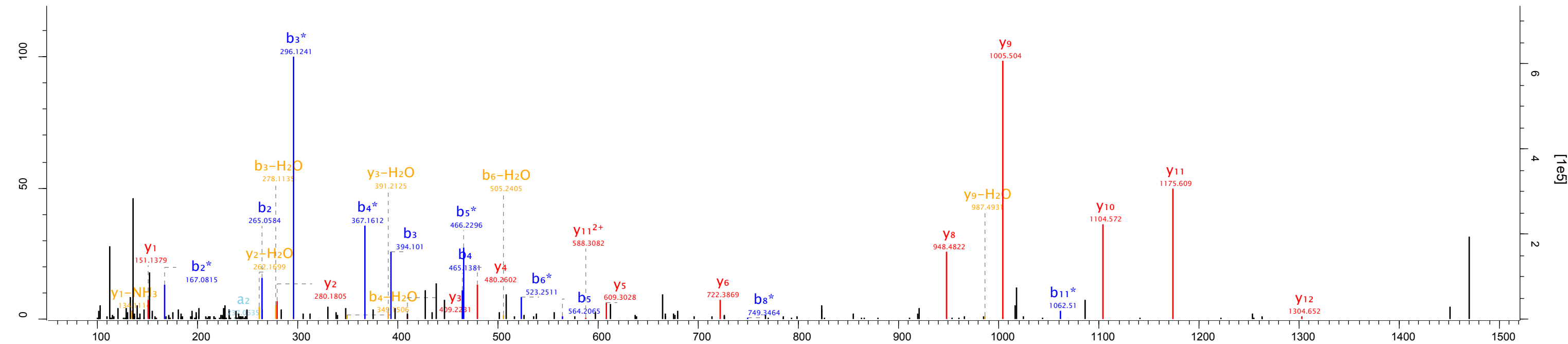


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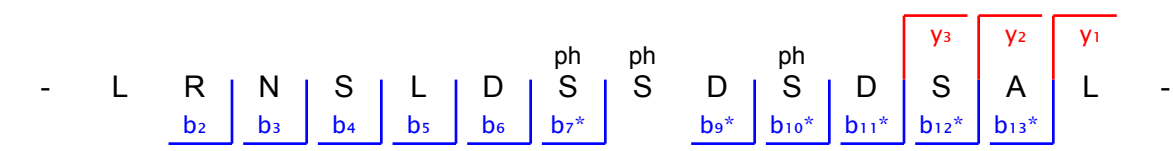
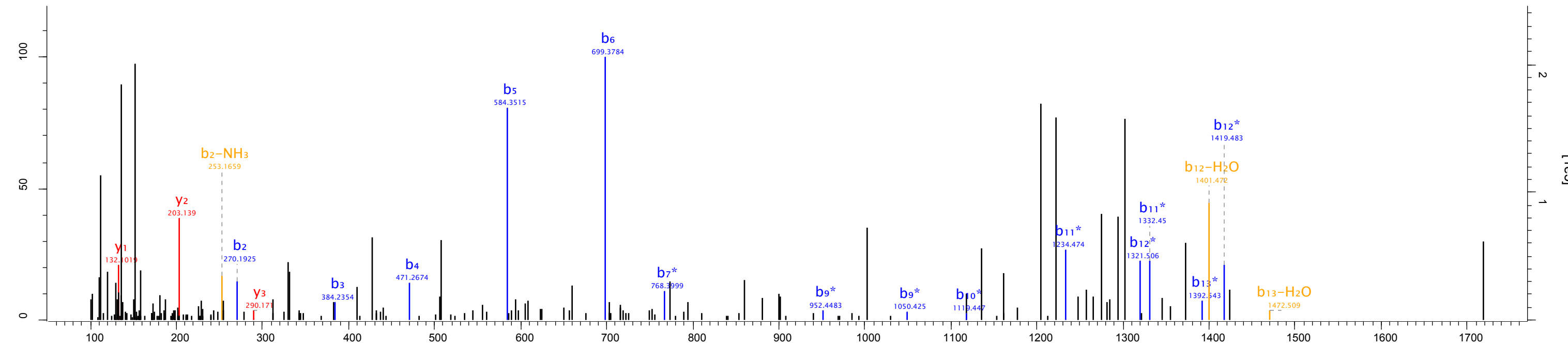
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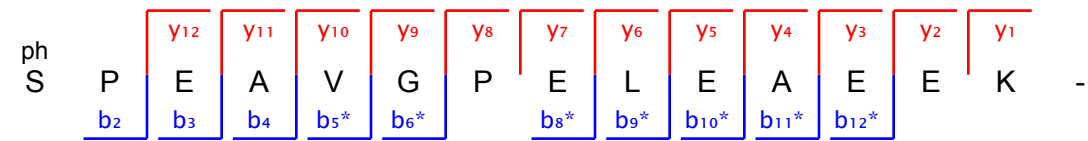
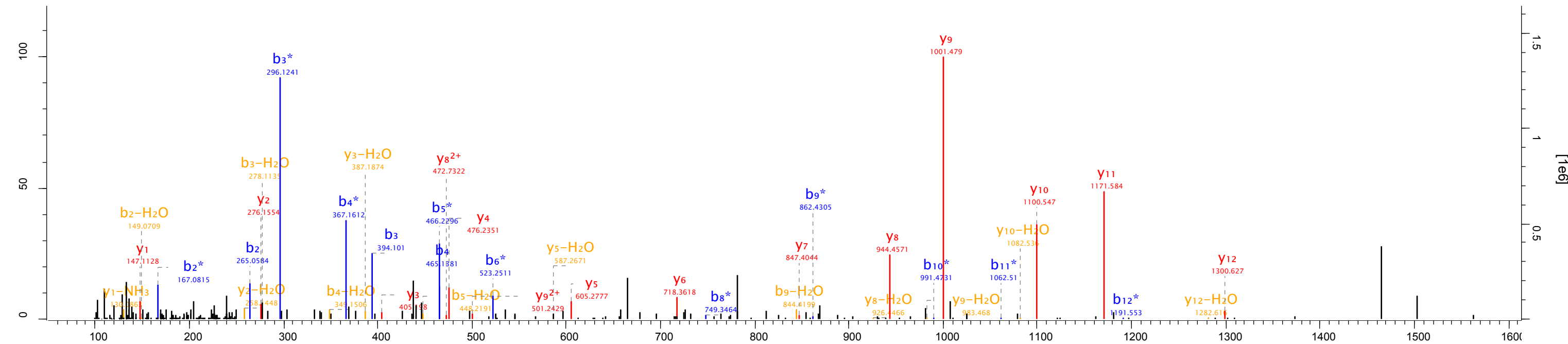
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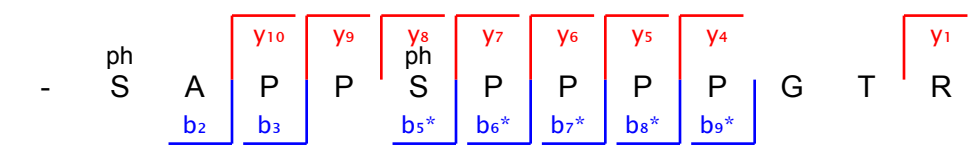
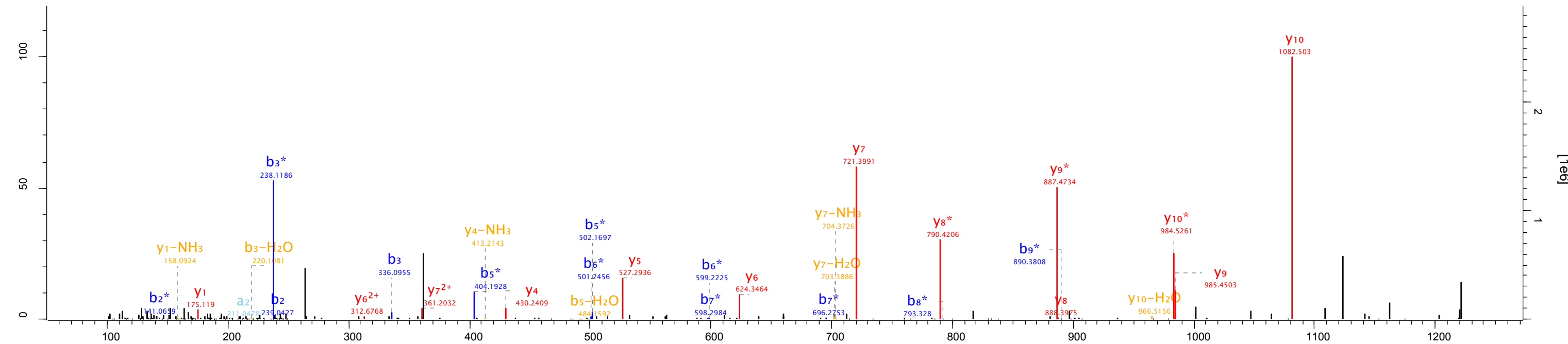
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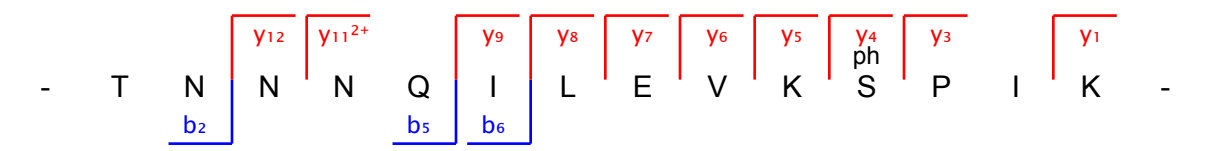
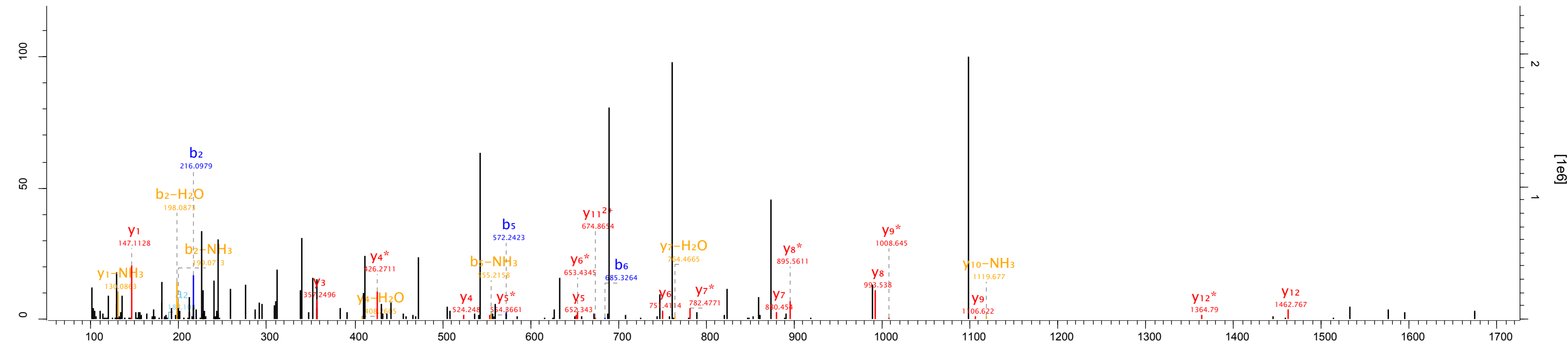
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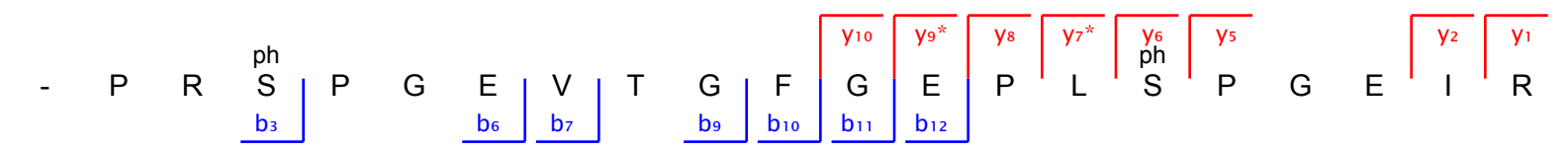
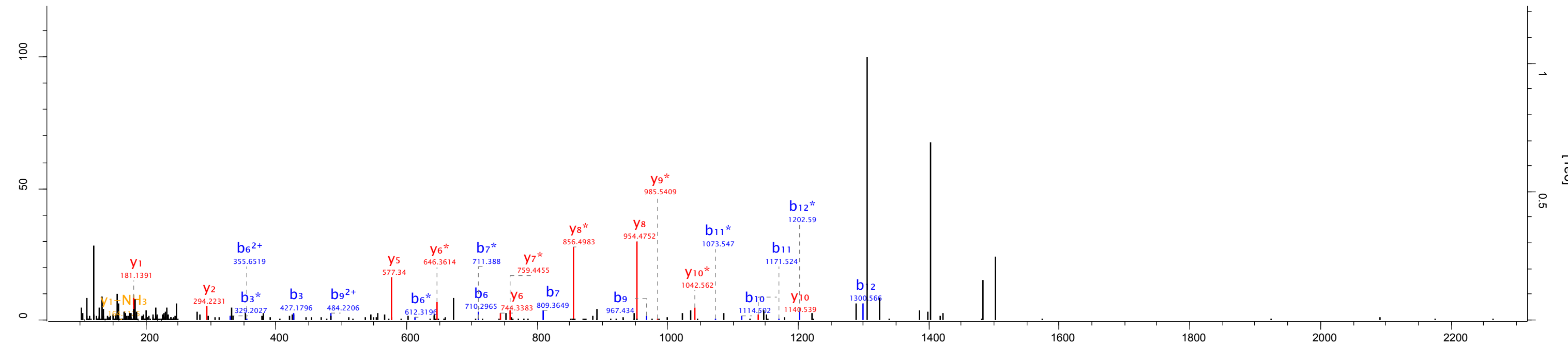
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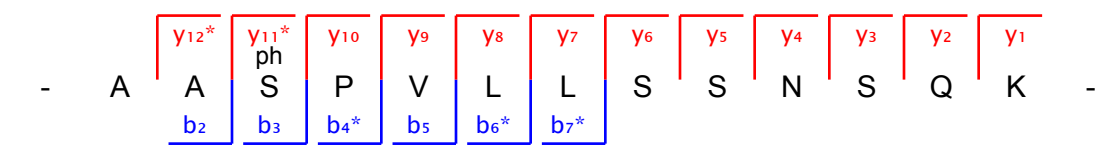
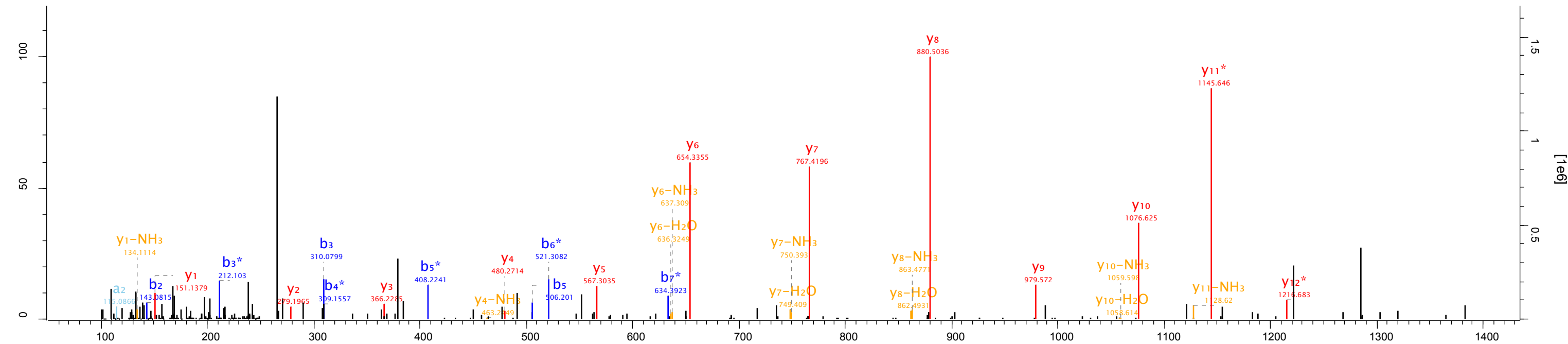
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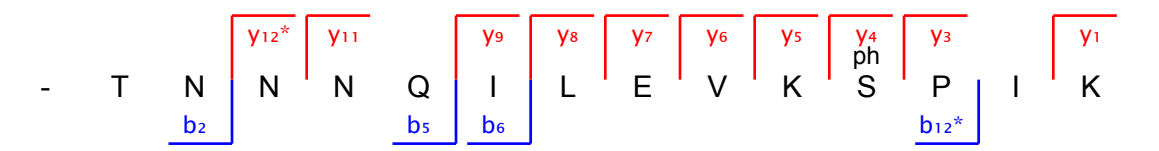
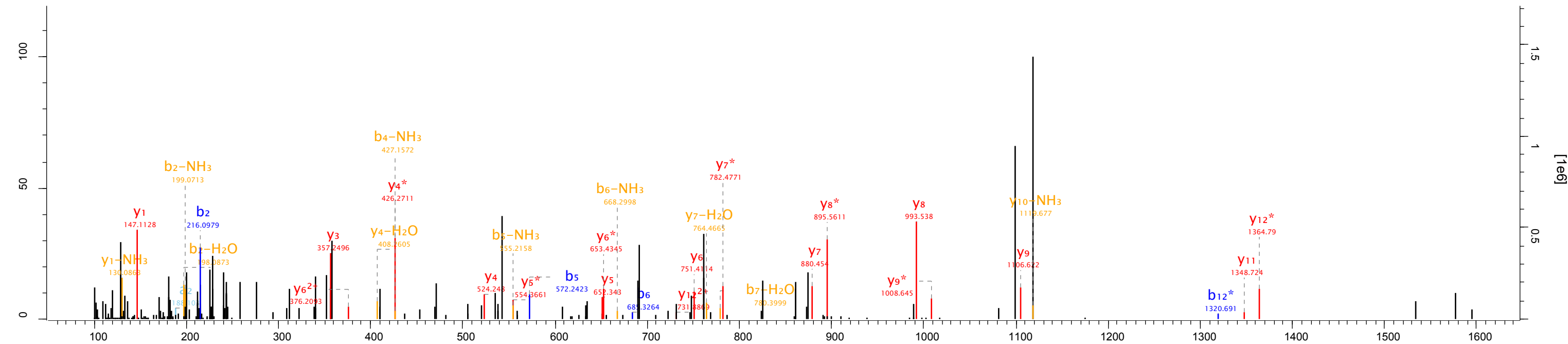
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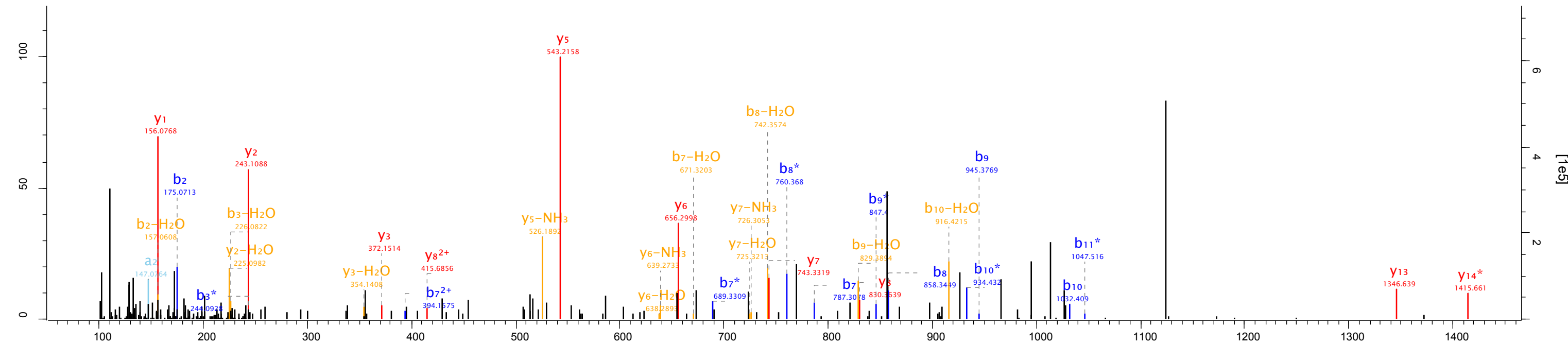


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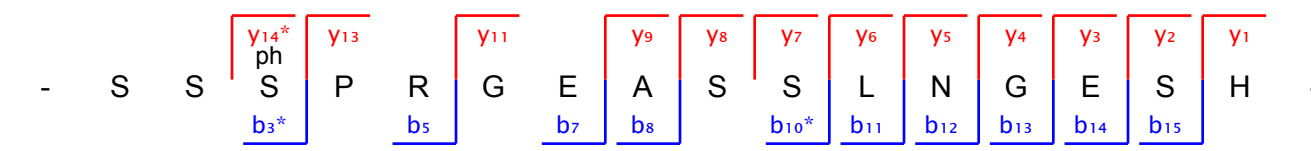
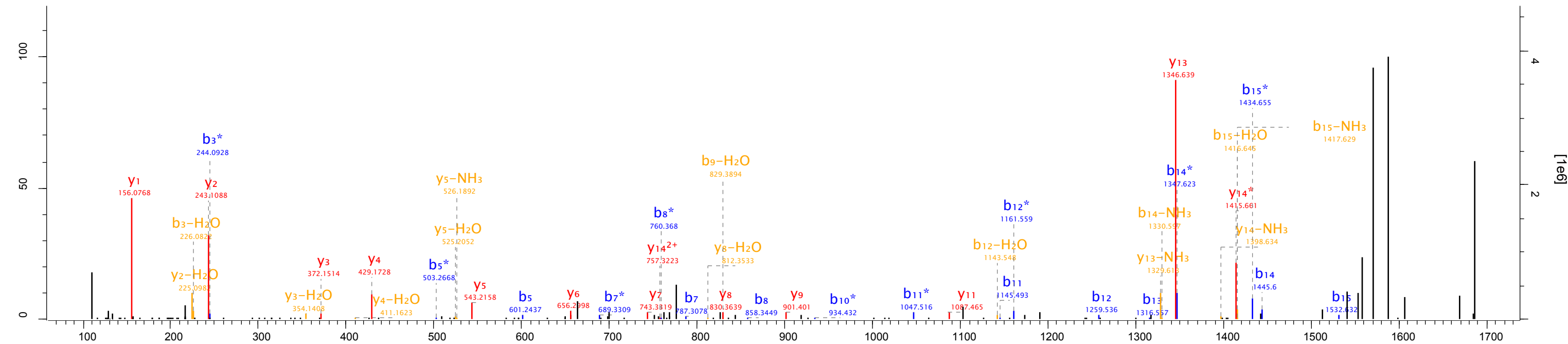




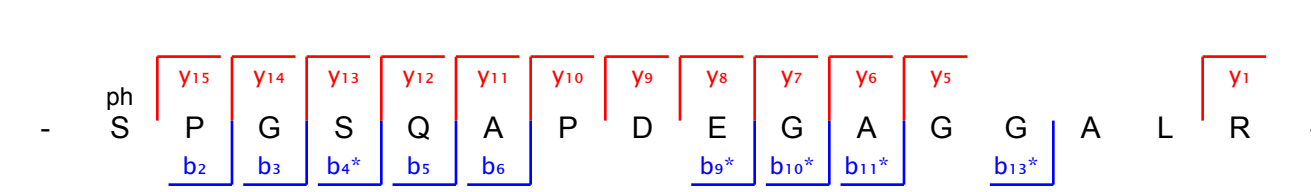
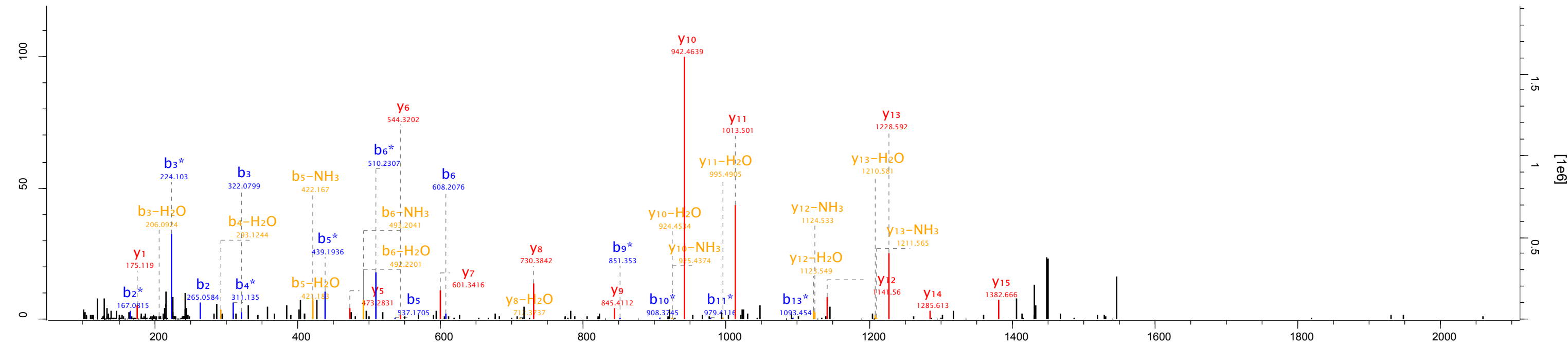
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b₂ b₃^{*} b₇ b₈ b₉ b₁₀ b₁₁^{*}

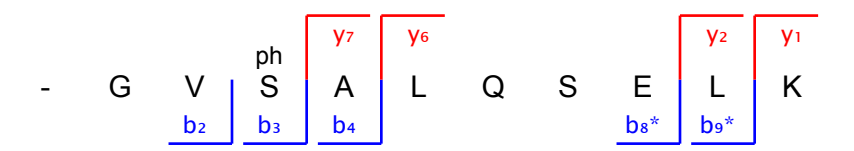
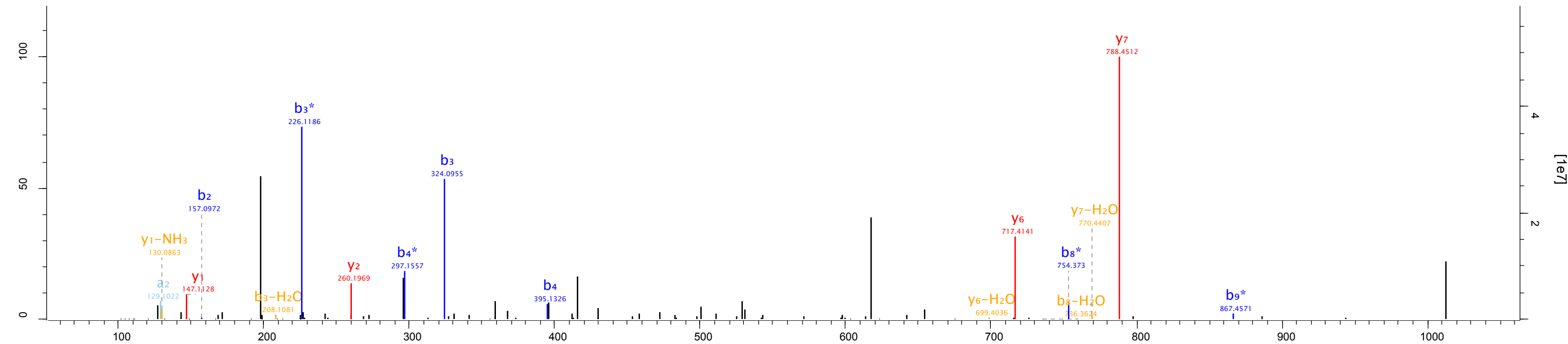
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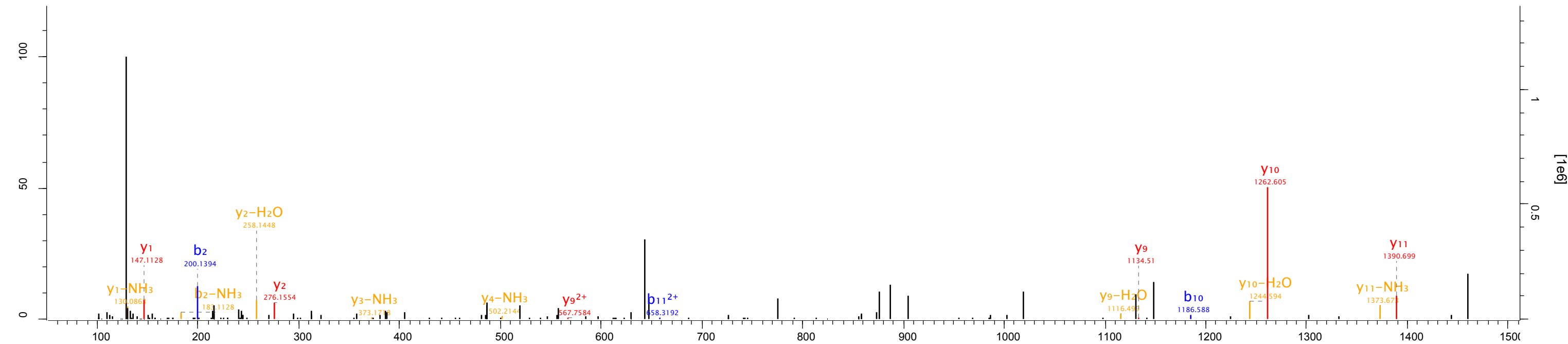


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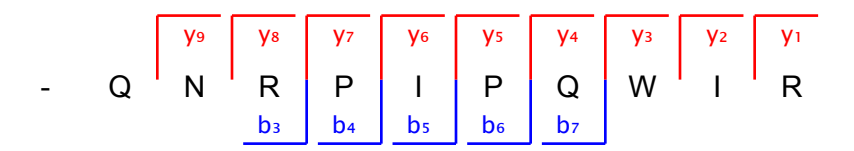
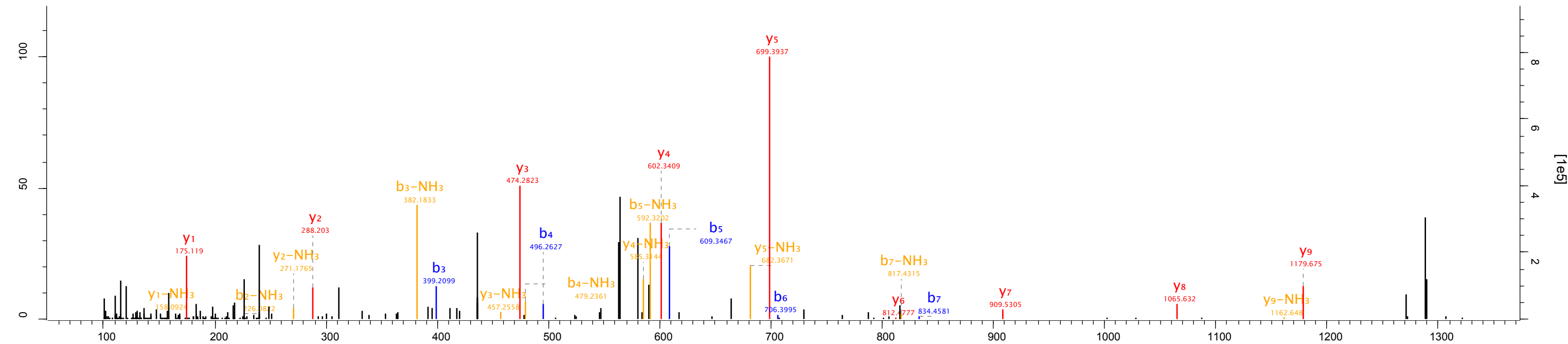


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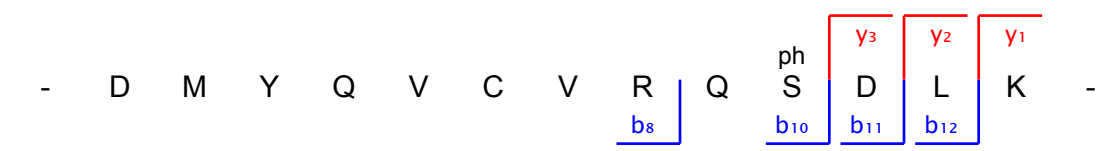
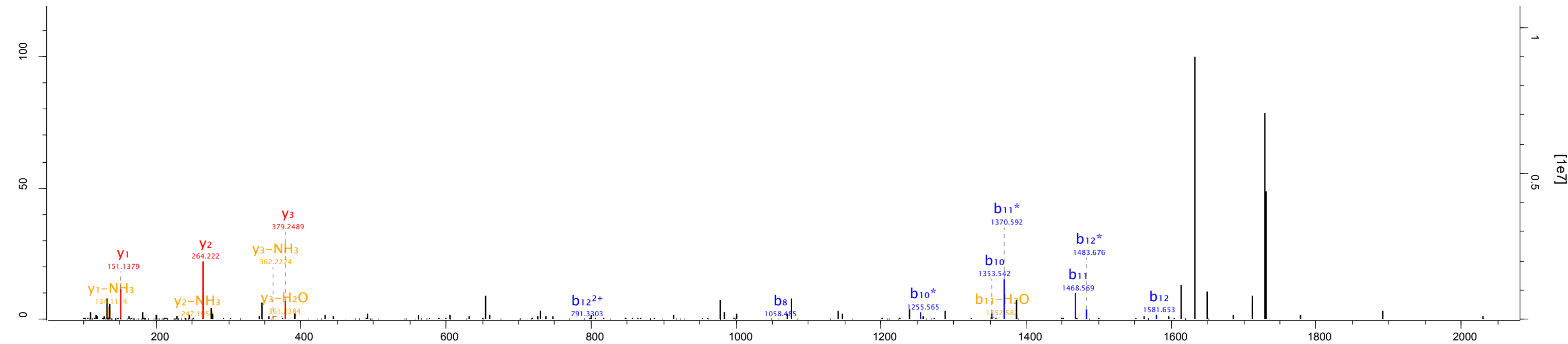
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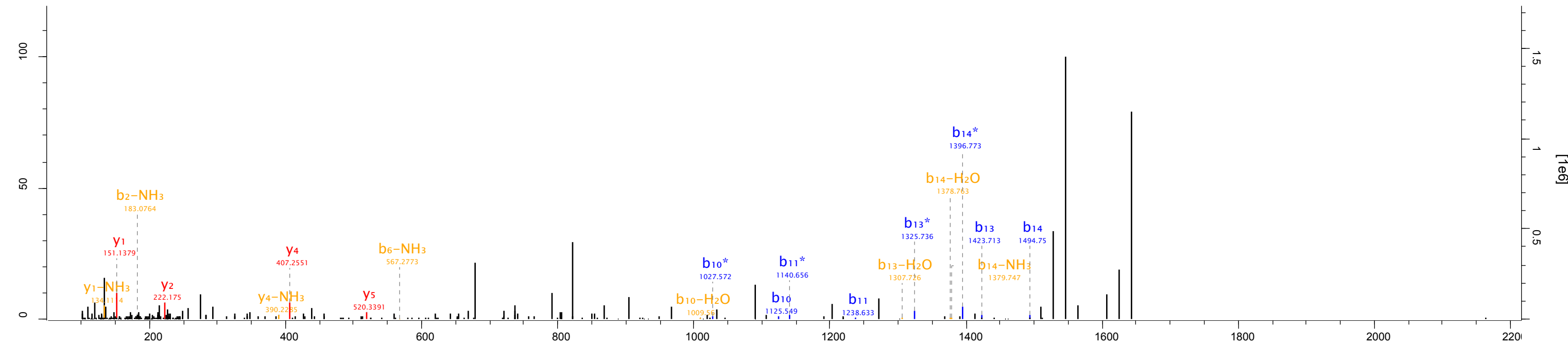
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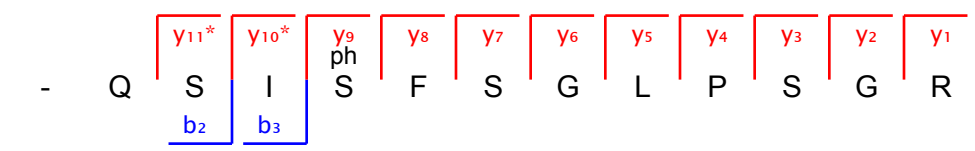
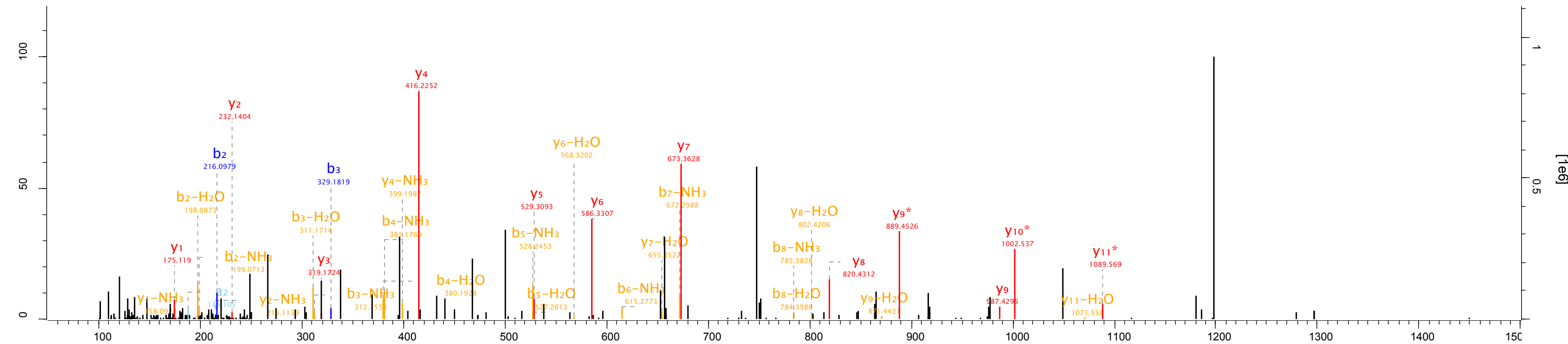
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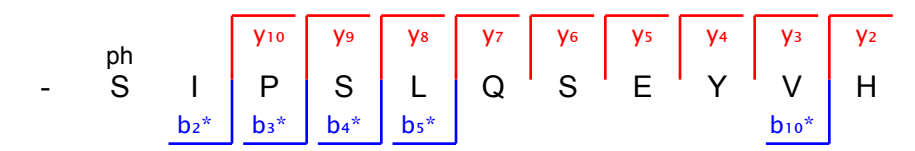
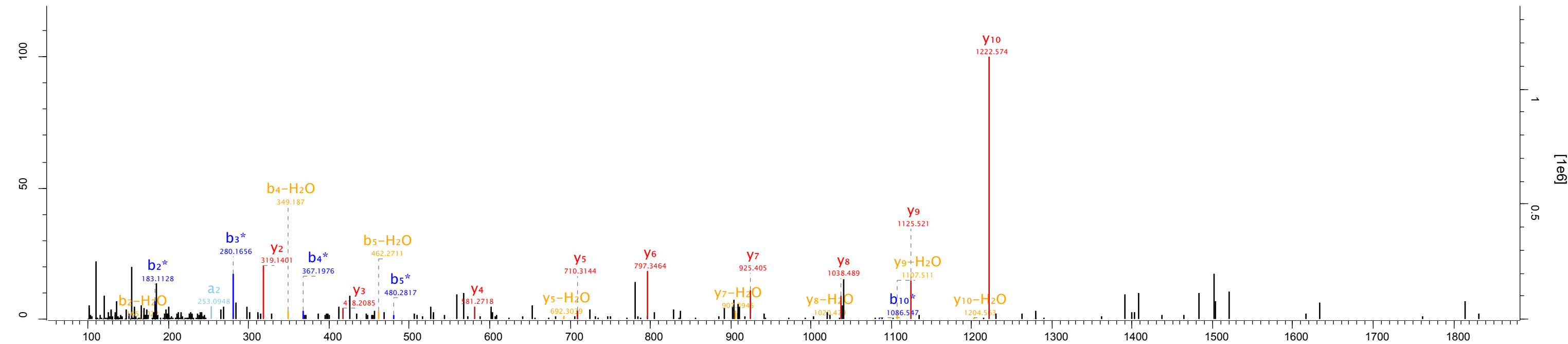
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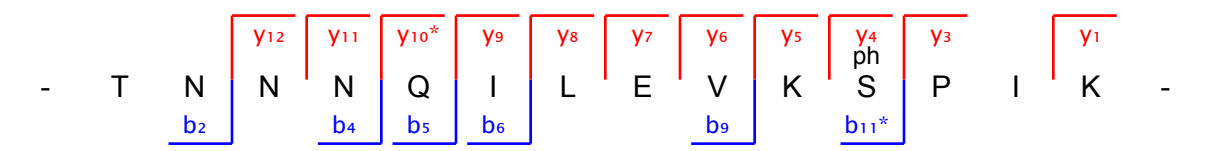
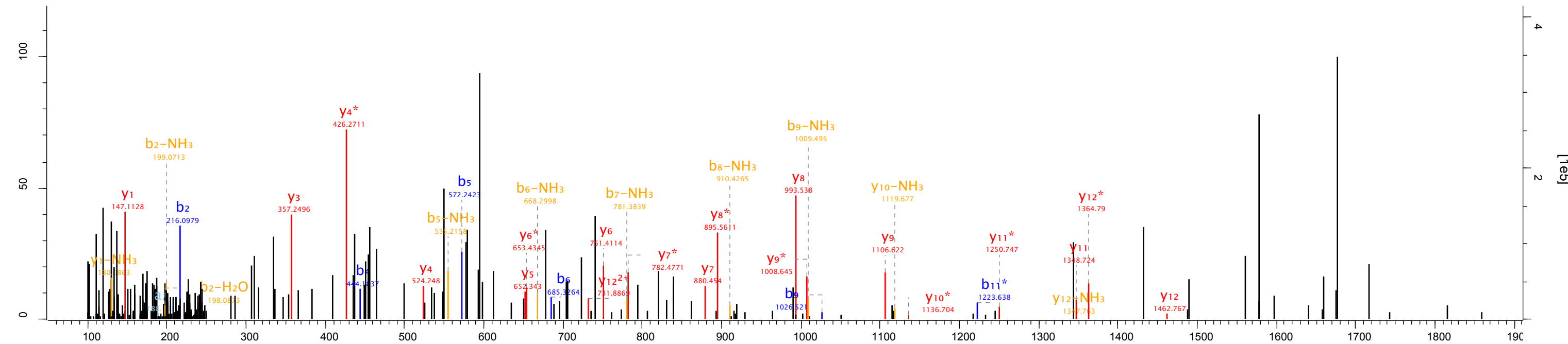
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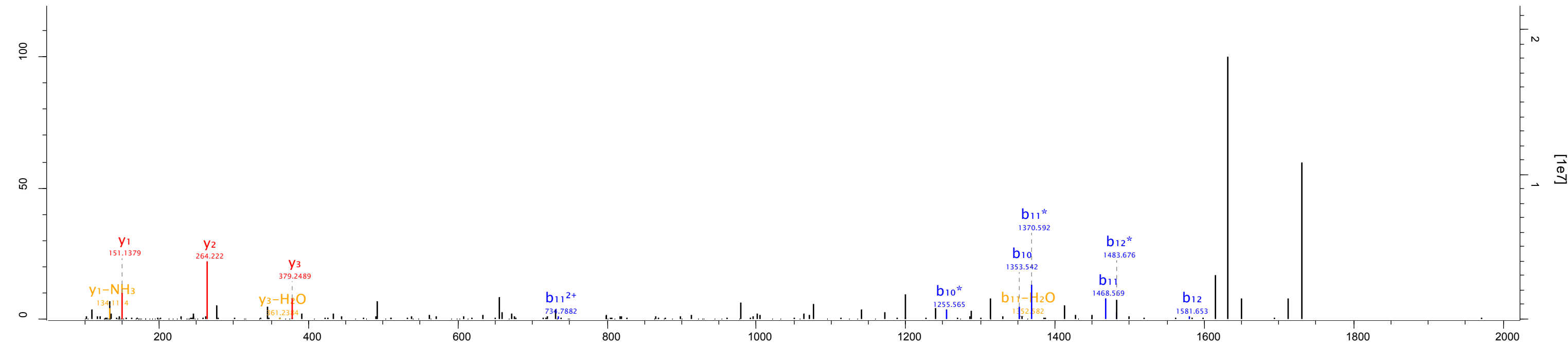
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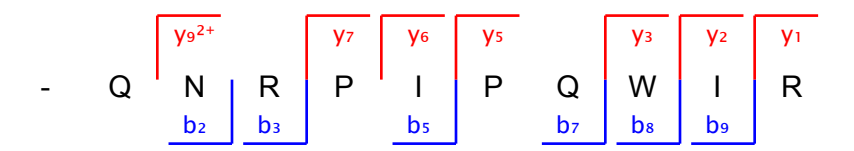
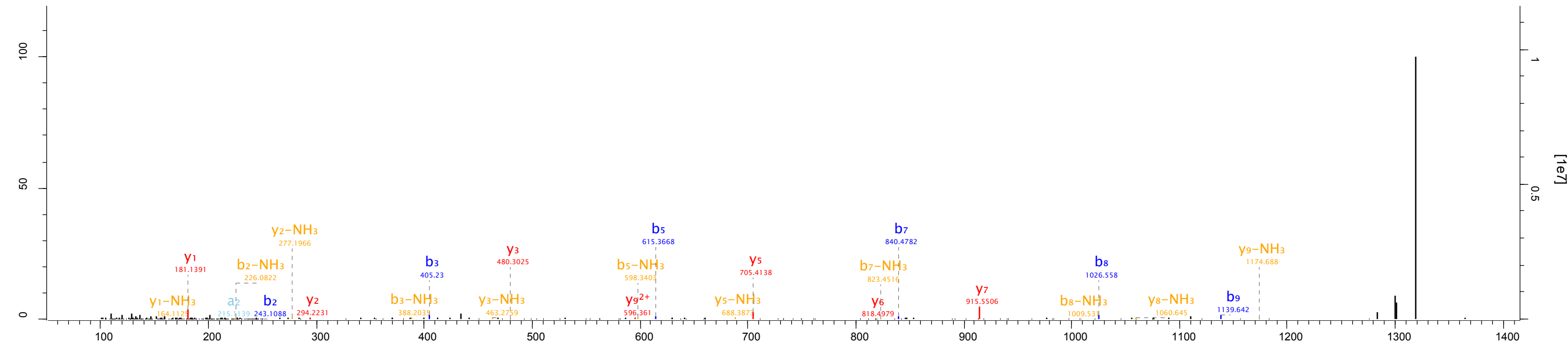
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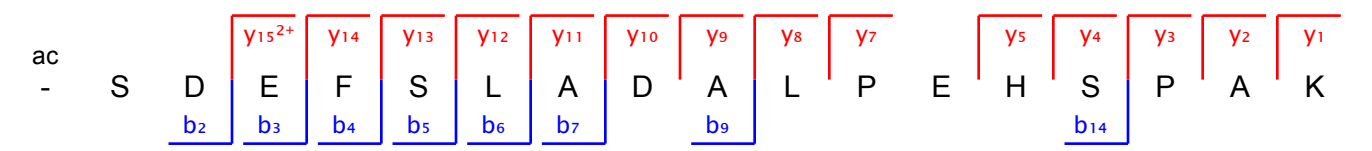
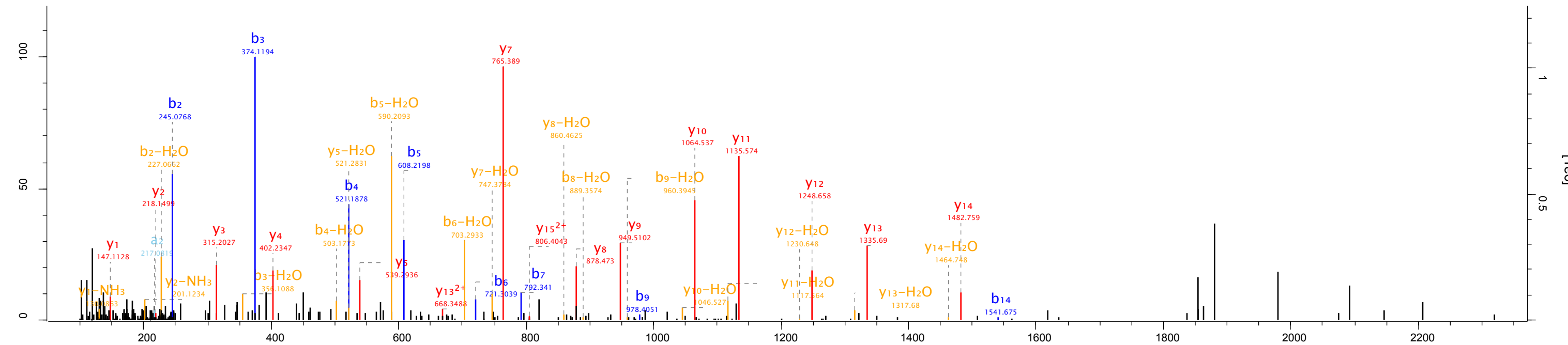
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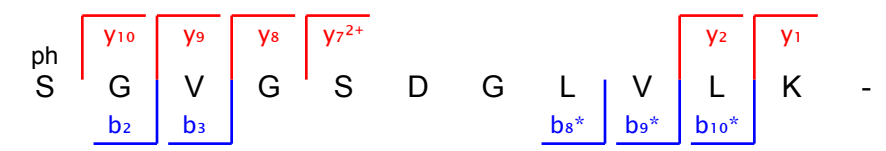
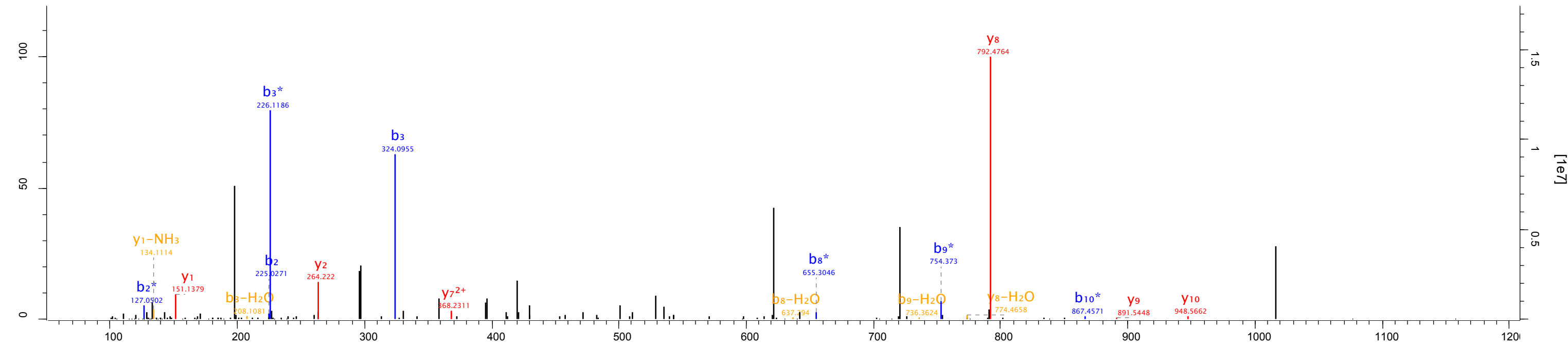
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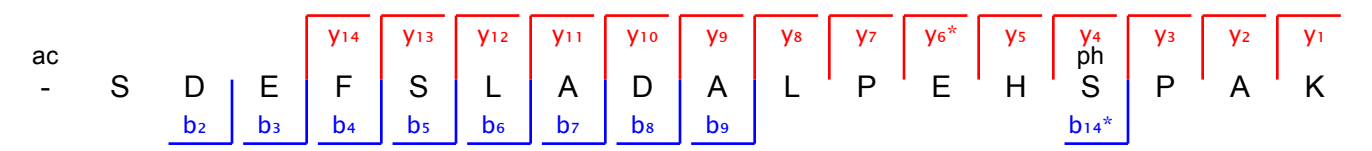
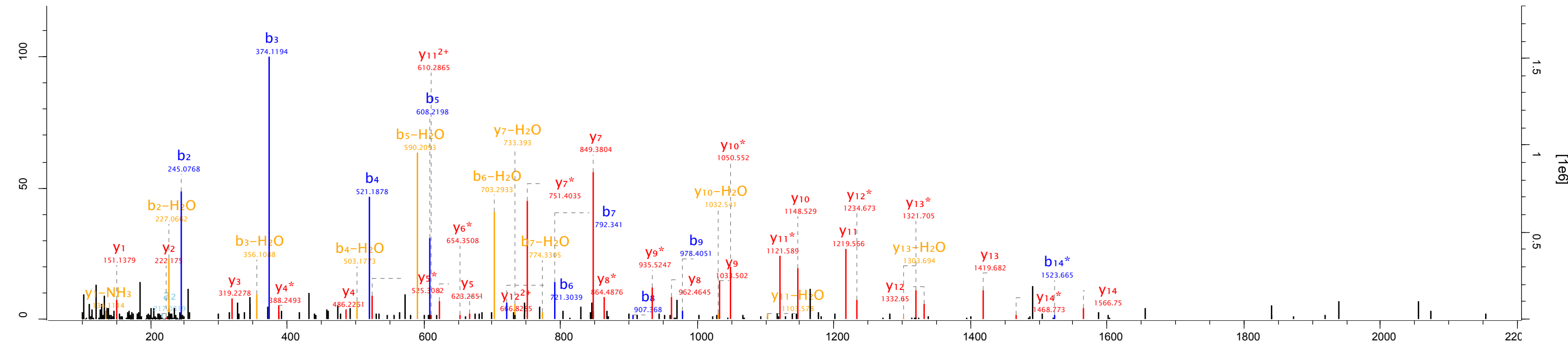
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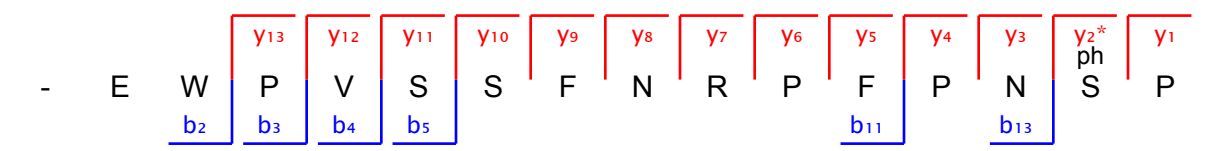
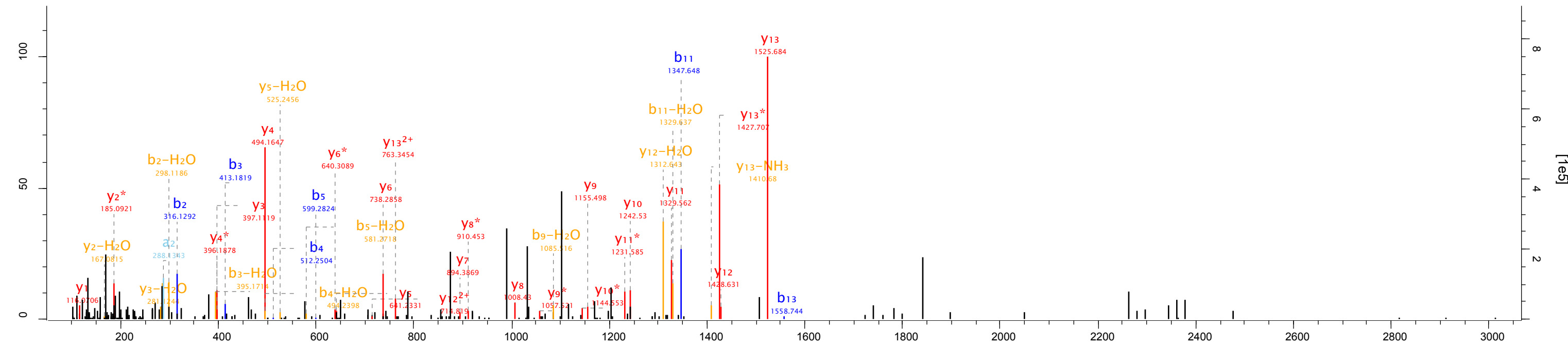
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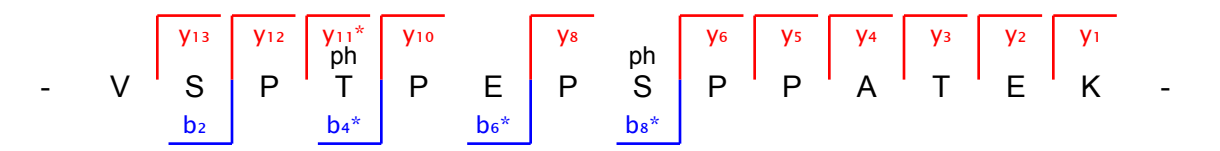
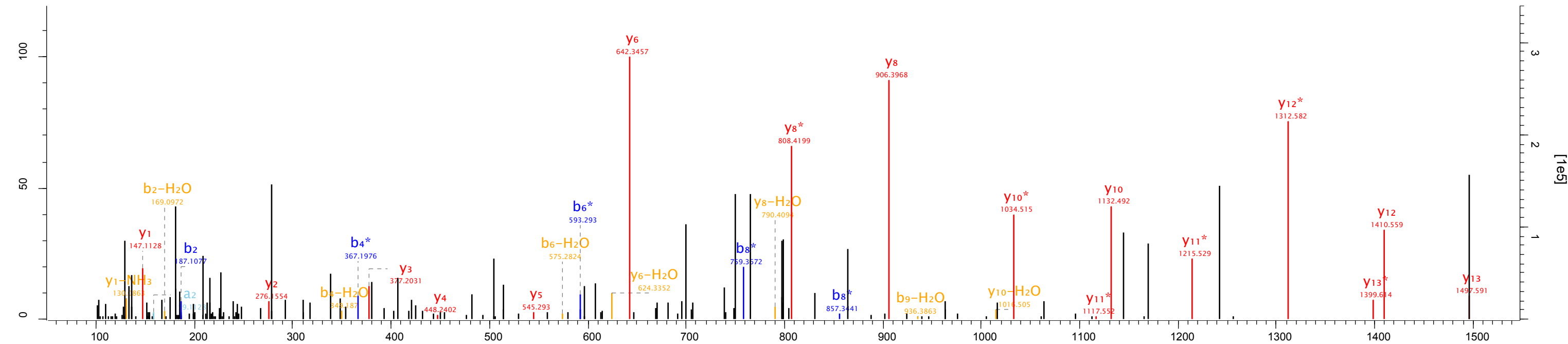
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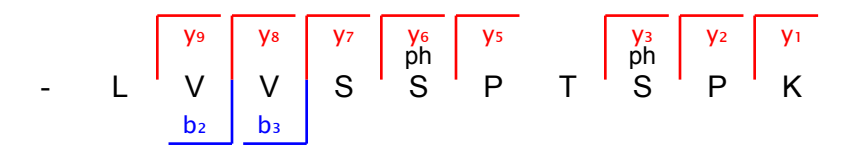
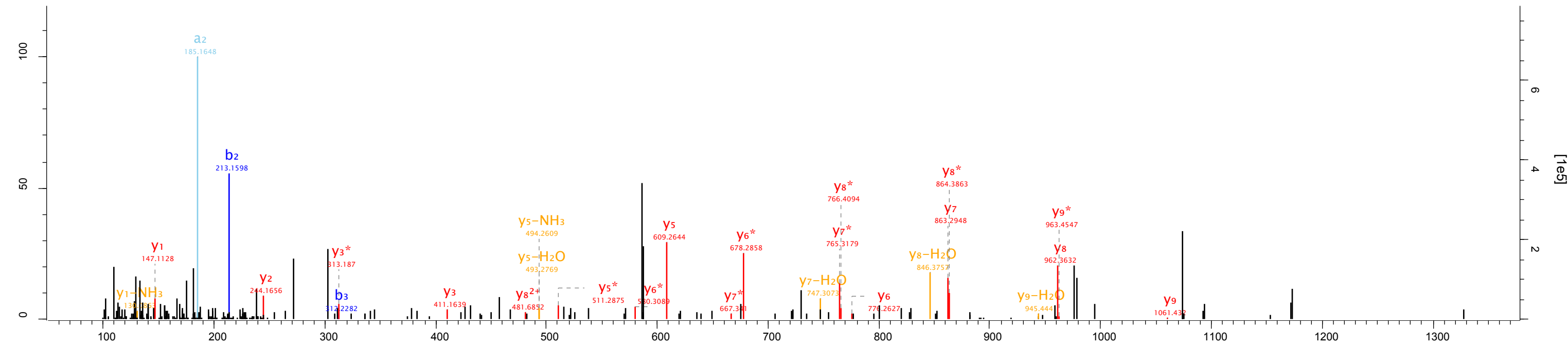
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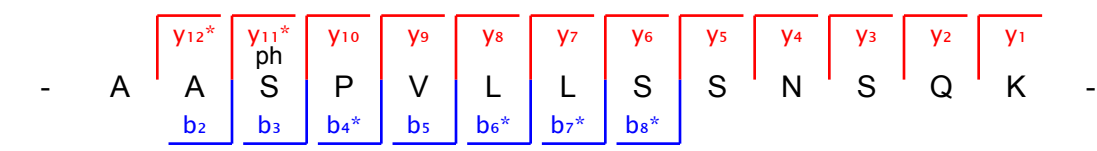
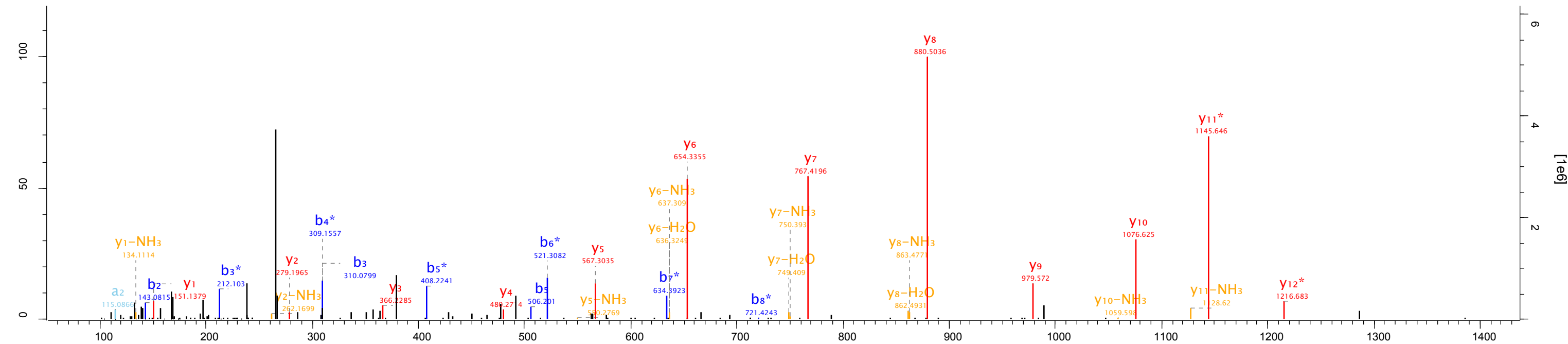
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 Scan: 7498 Method: FTMS; HCD Score: 49.66 m/z: 798.83 Gene names: AMER1



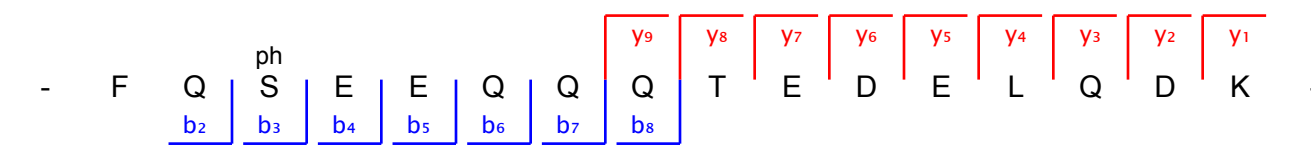
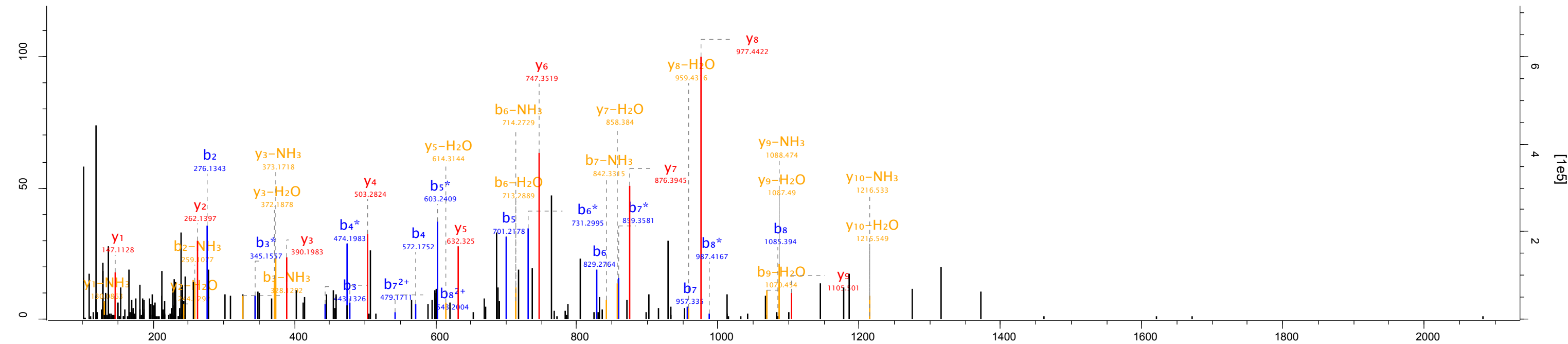
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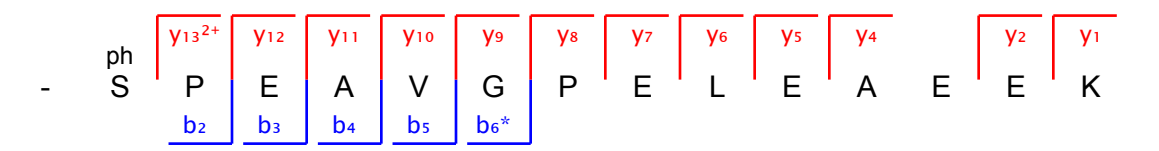
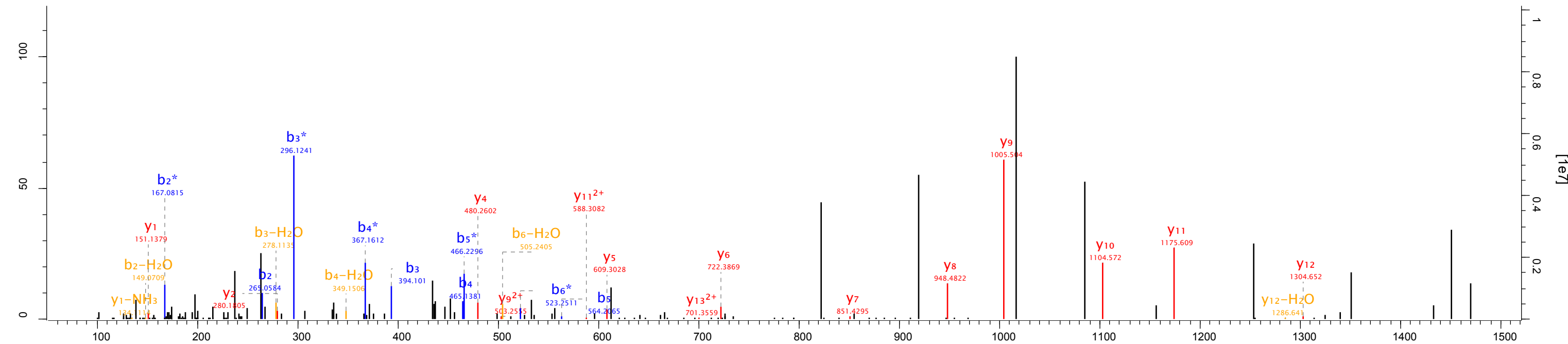
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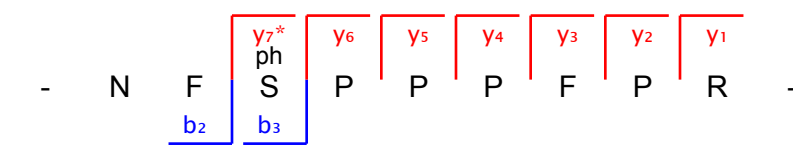
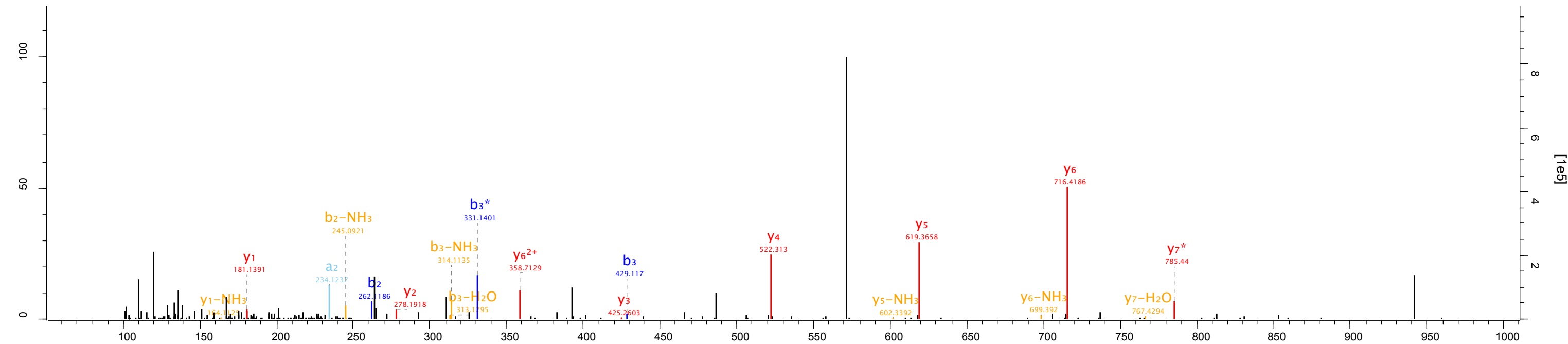
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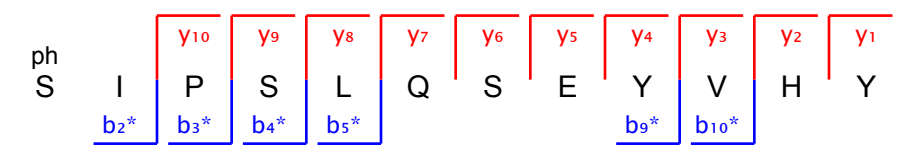
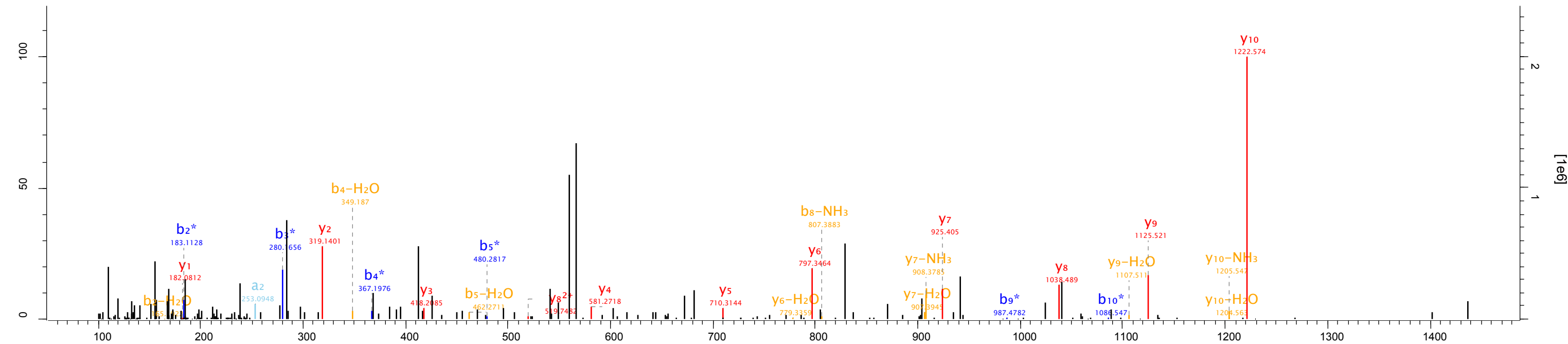
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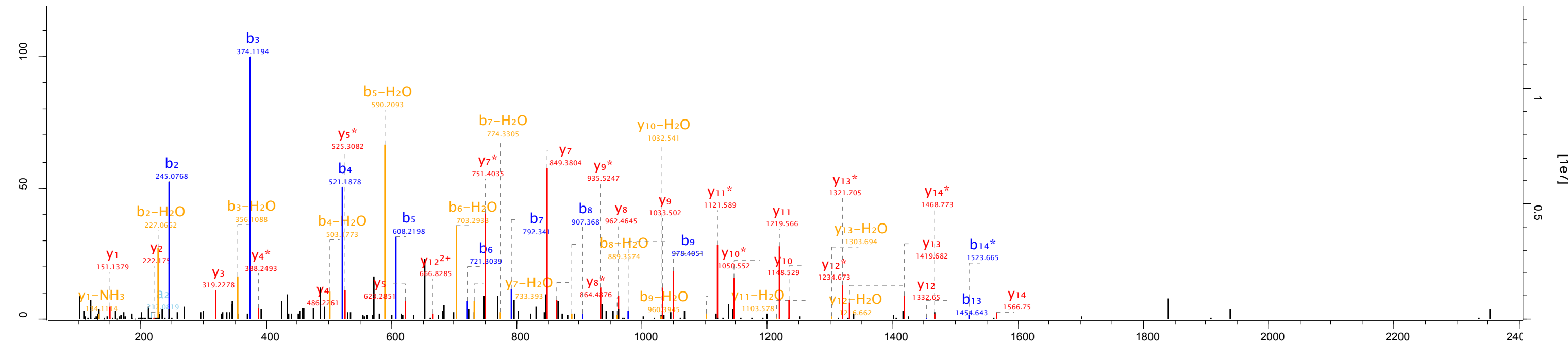


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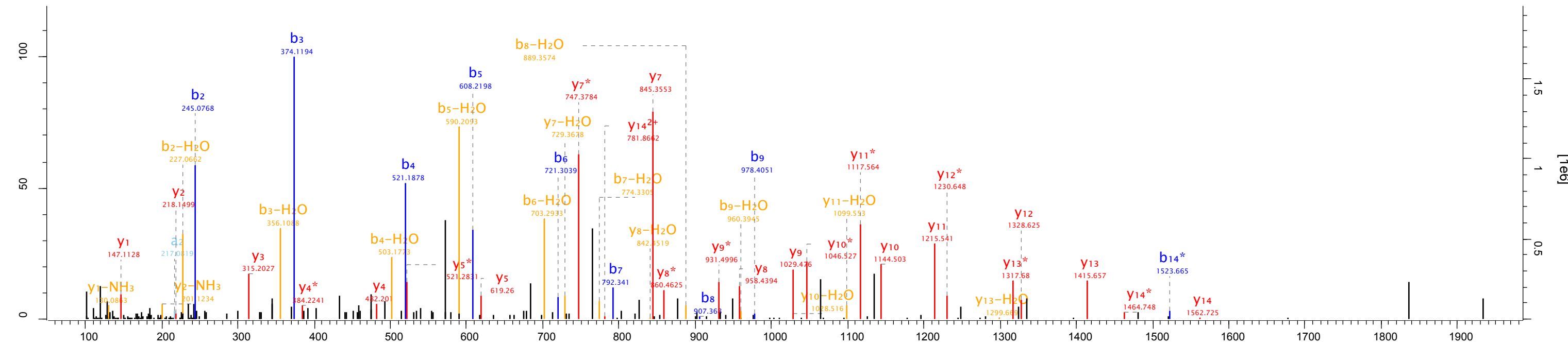
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Scan 23798 Method FTMS; HCD Score 194.24 m/z 970.43 Gene names MAPK11P1L



ac
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b2 b3 b4 b5 b6 b7 b8 b9 b13 b14*

Raw file 20150814_A375SR_Phospho_BR2_04 Scan 23838 Method FTMS; HCD Score 242.22 m/z 968.92 Gene names MAPK11P1L

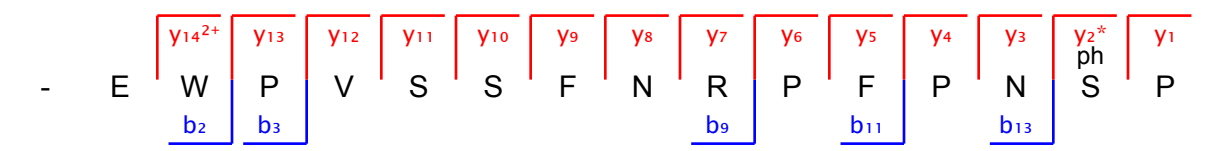
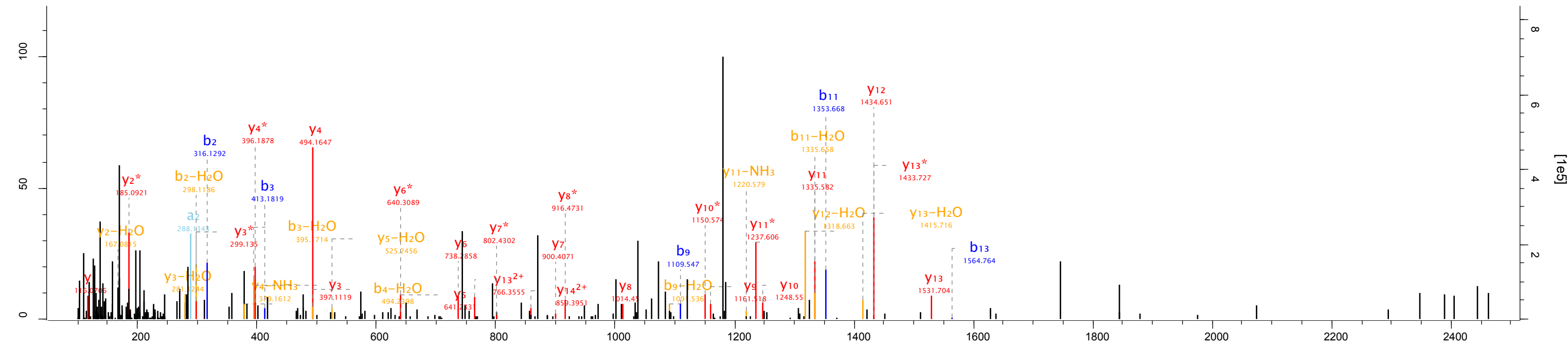


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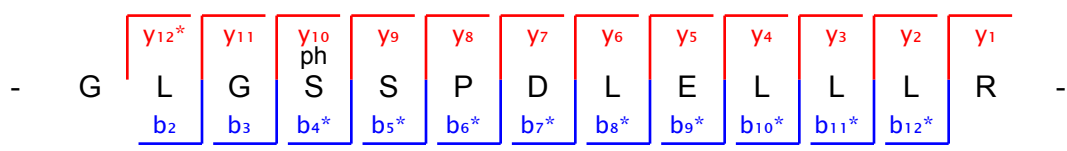
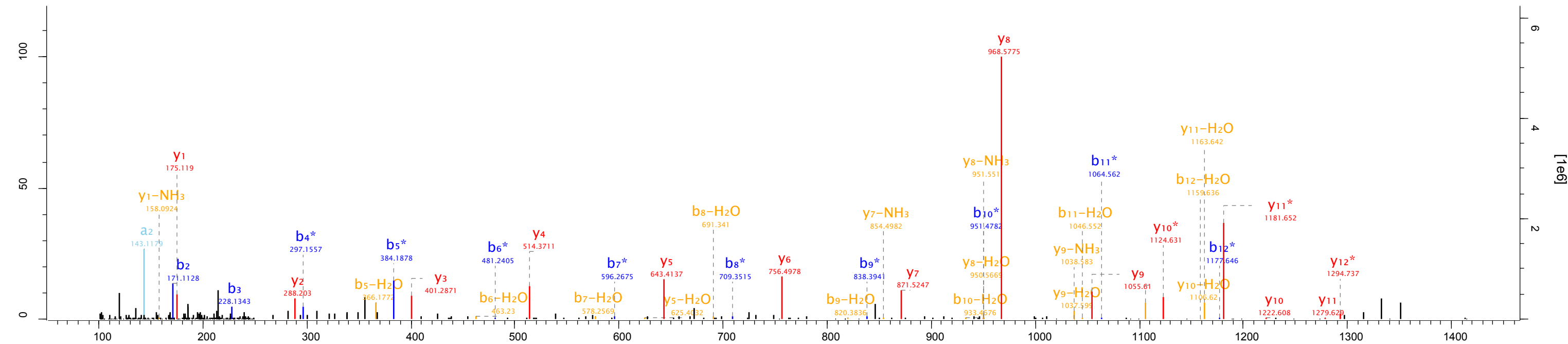
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y14 y13 y12 y11 y10 y9 y8 y7 y5 y4 ph y3 y2 y1

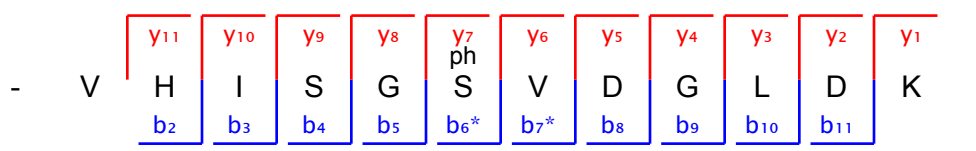
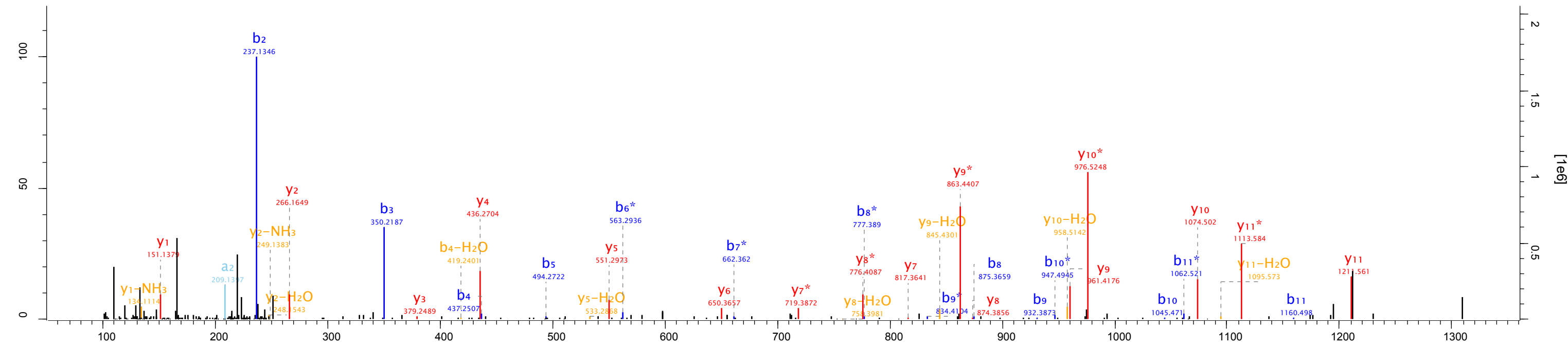
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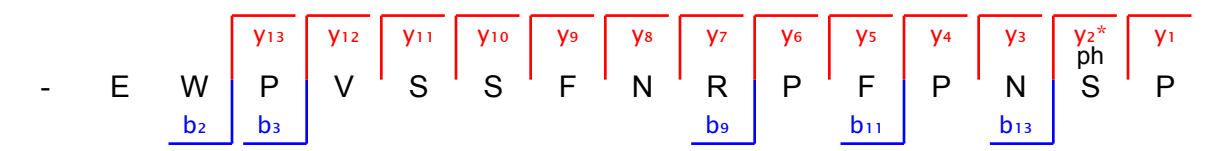
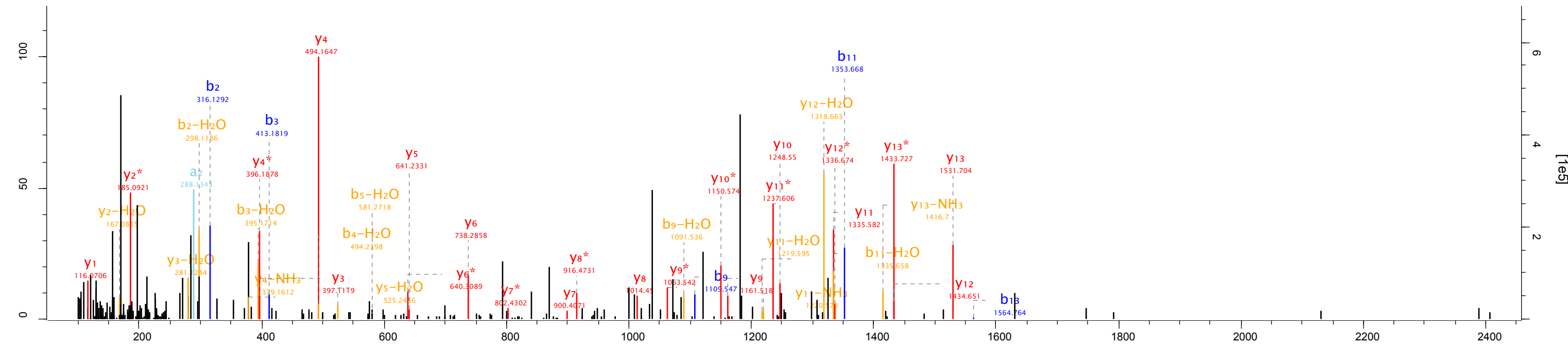
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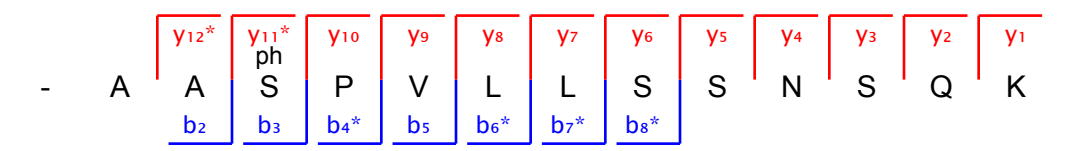
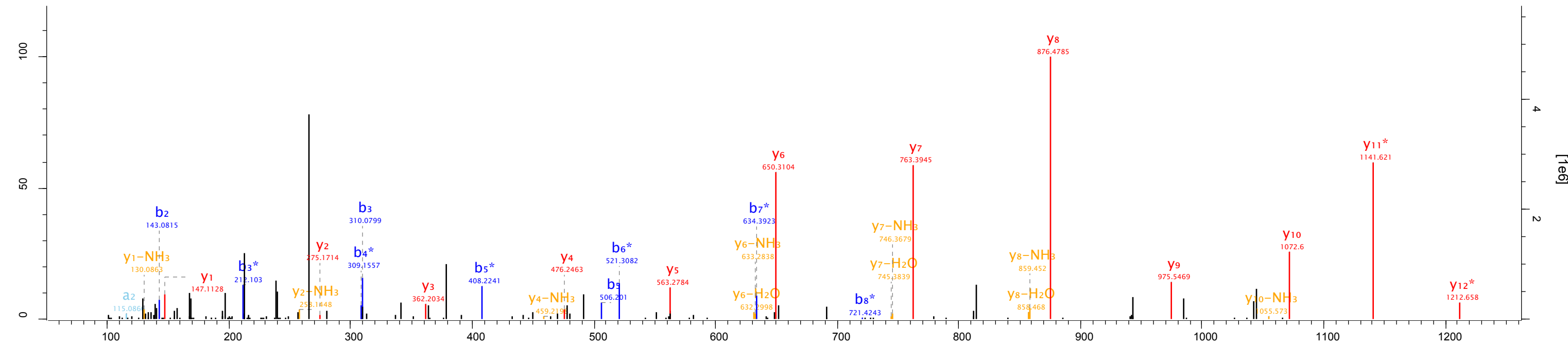
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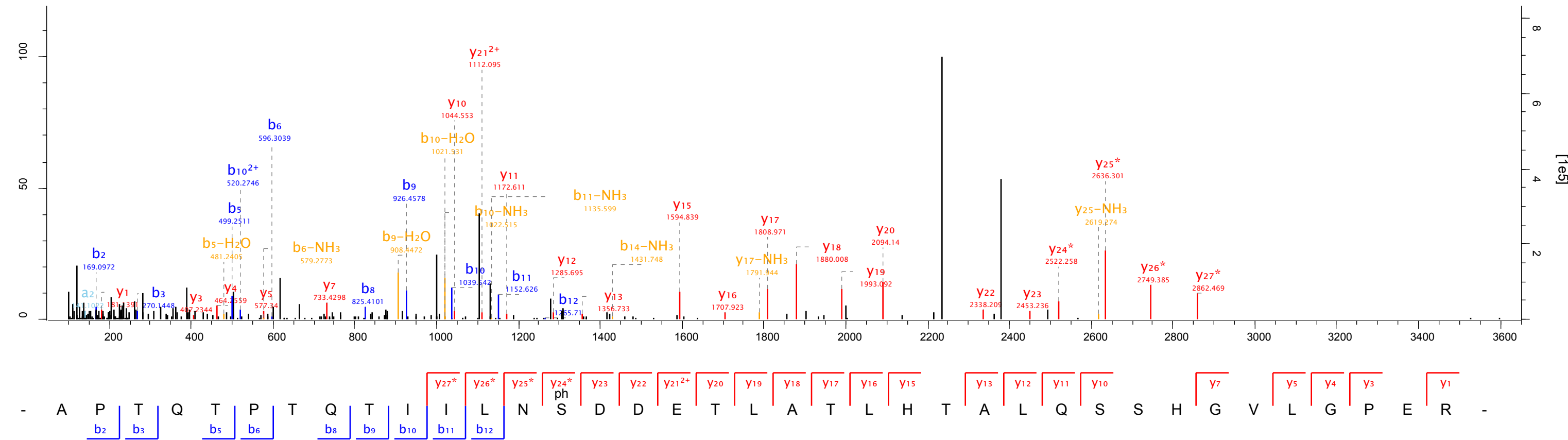
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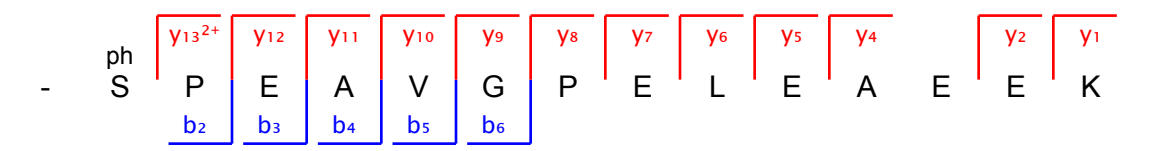
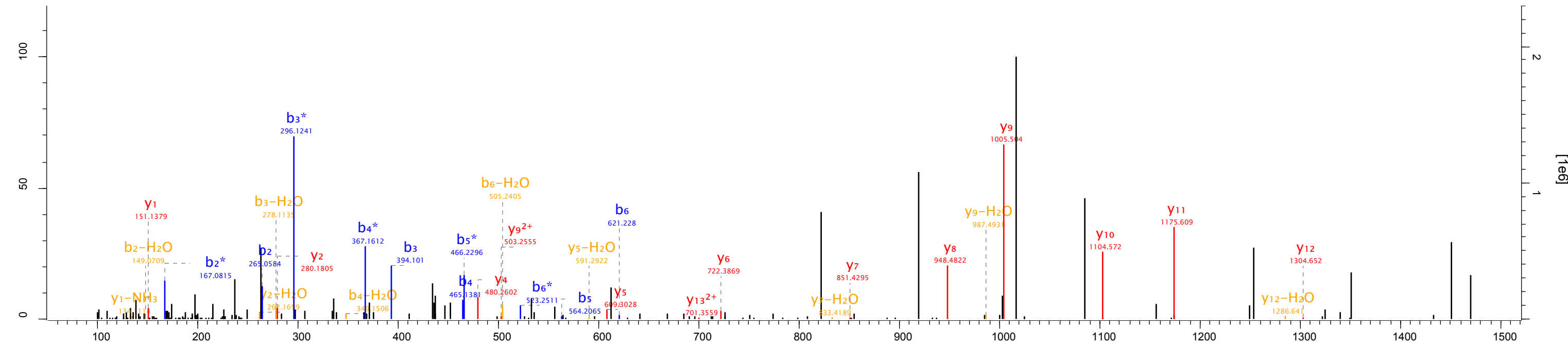
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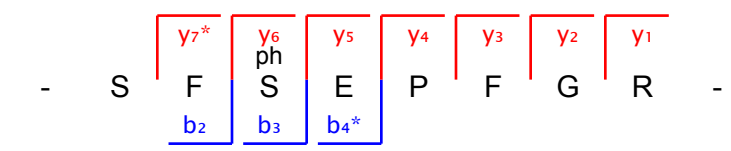
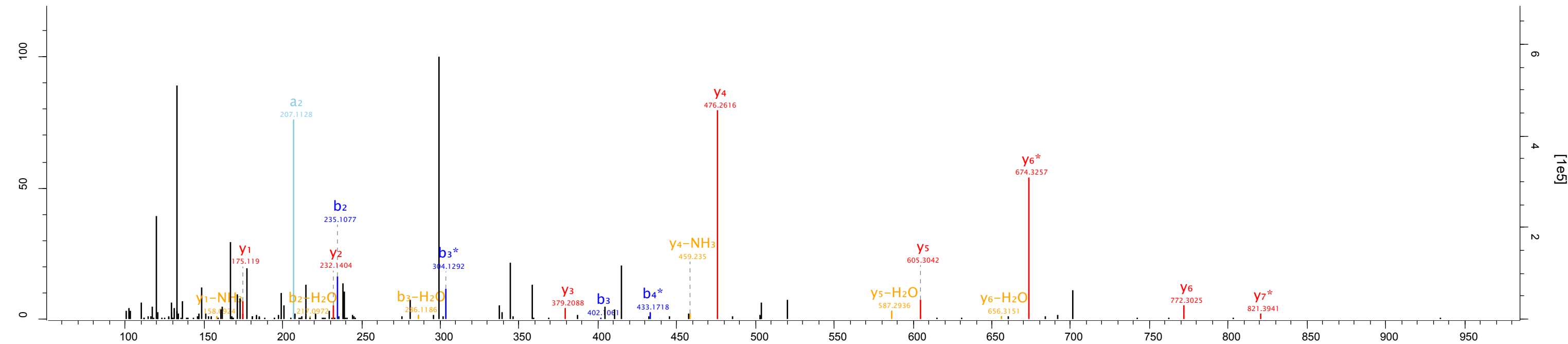
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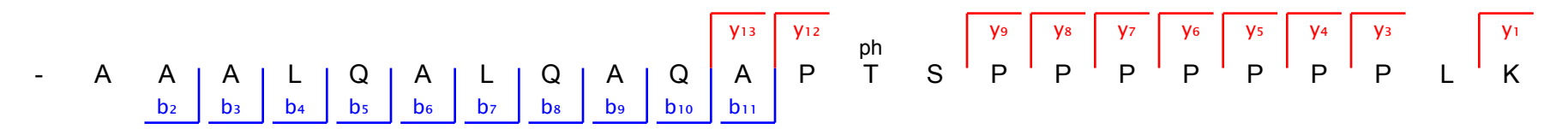
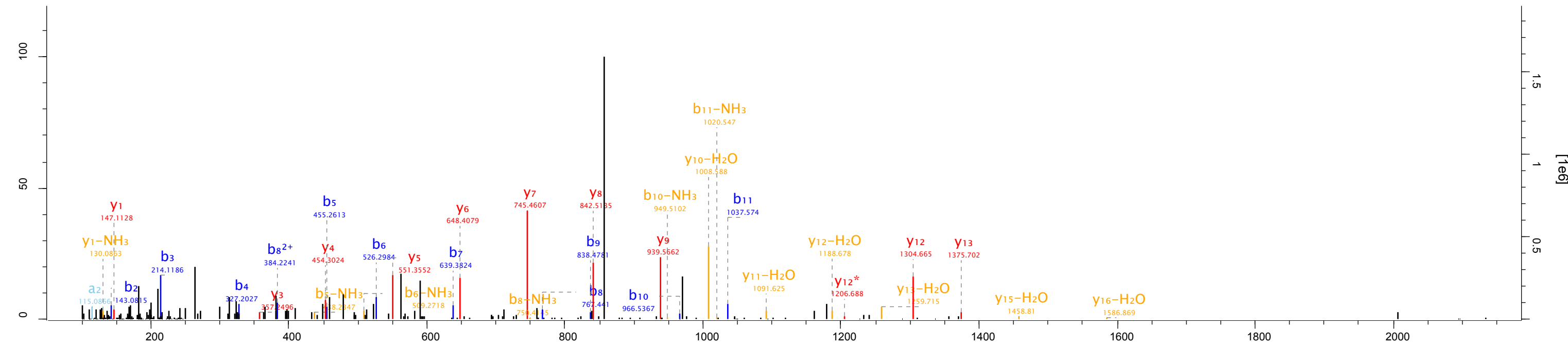
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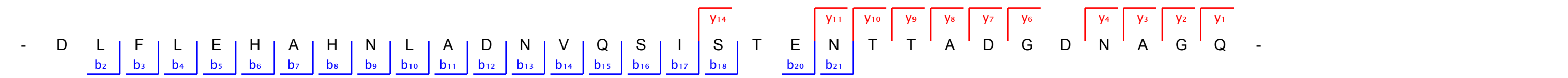
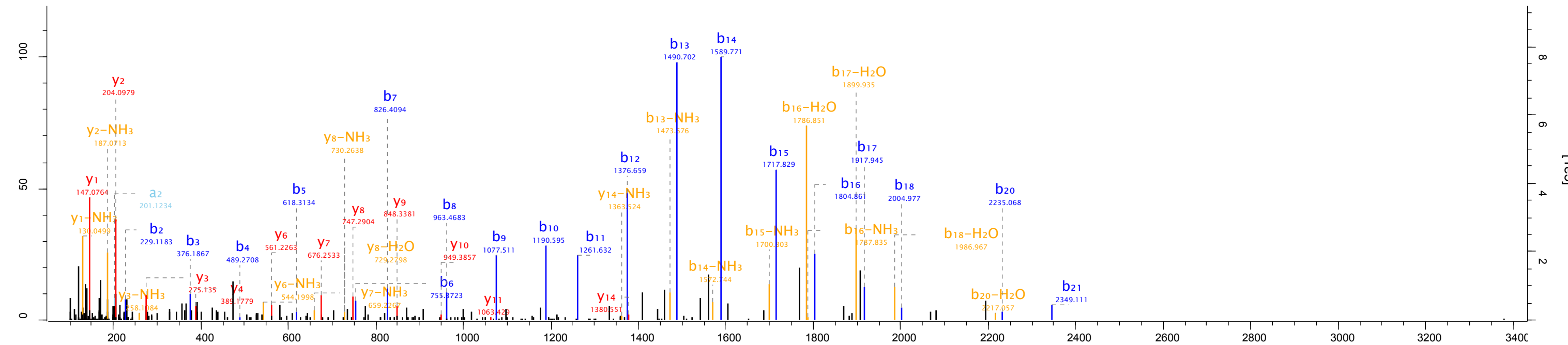
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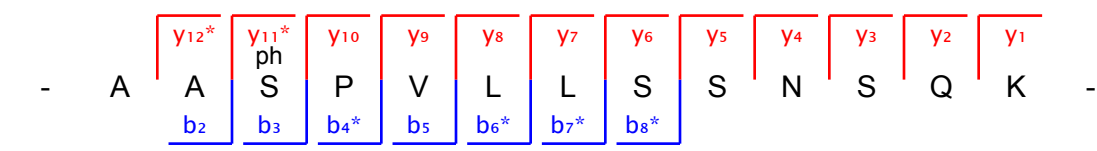
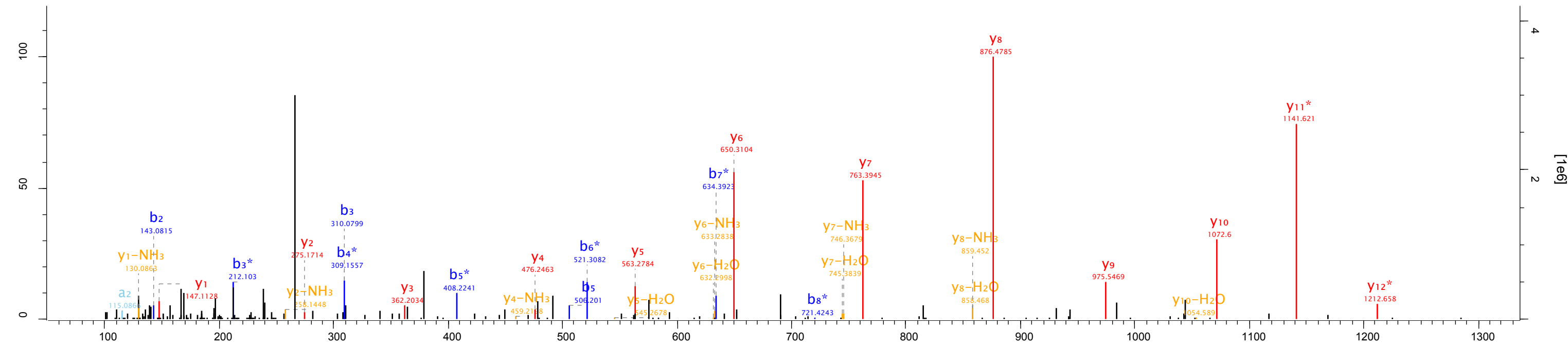
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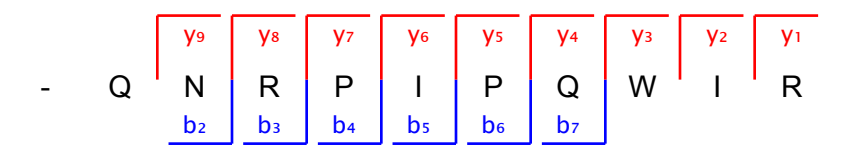
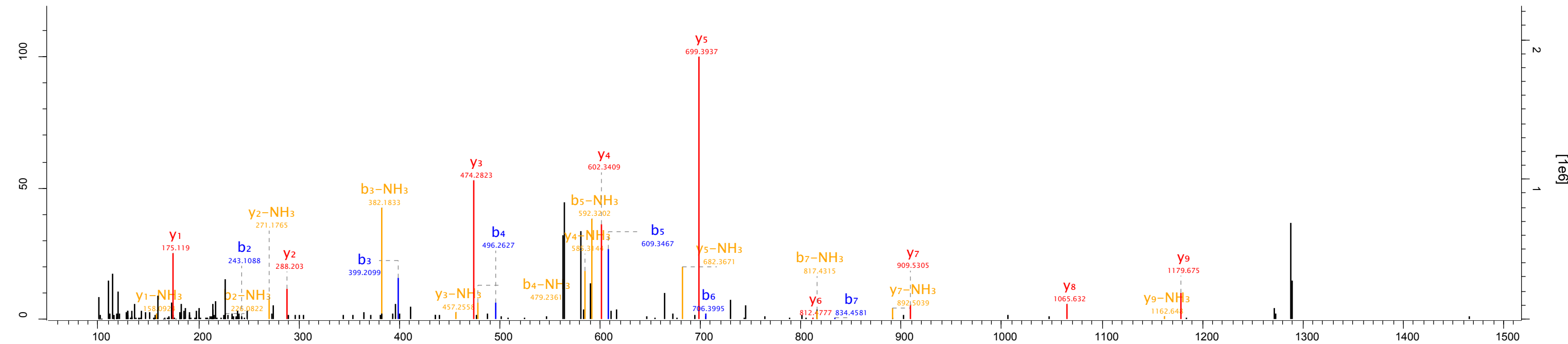
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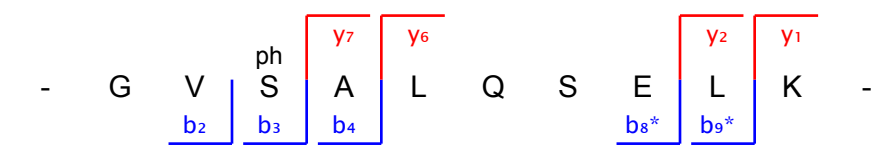
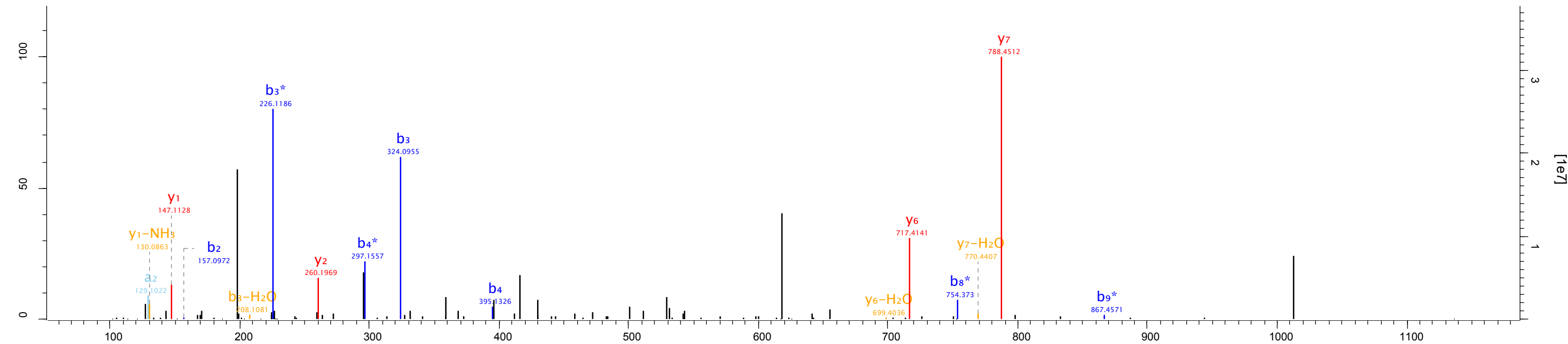
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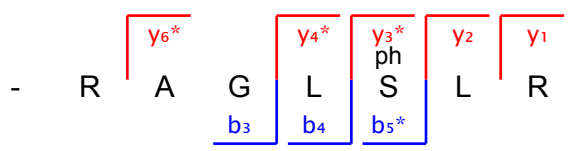
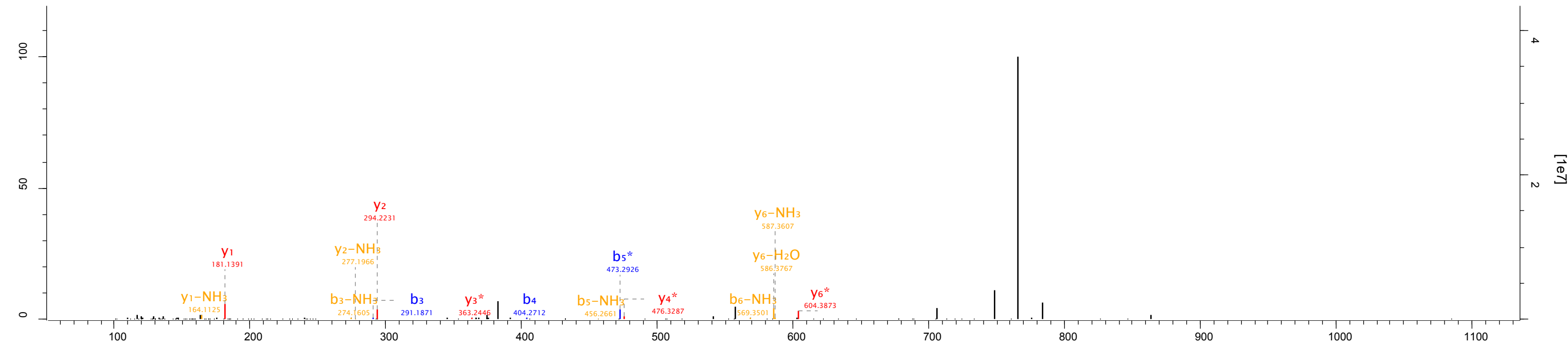
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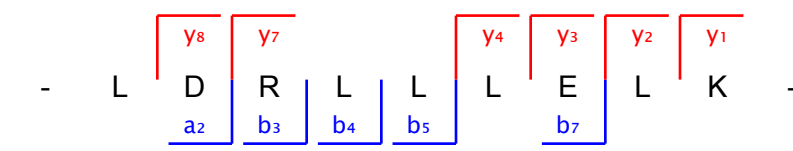
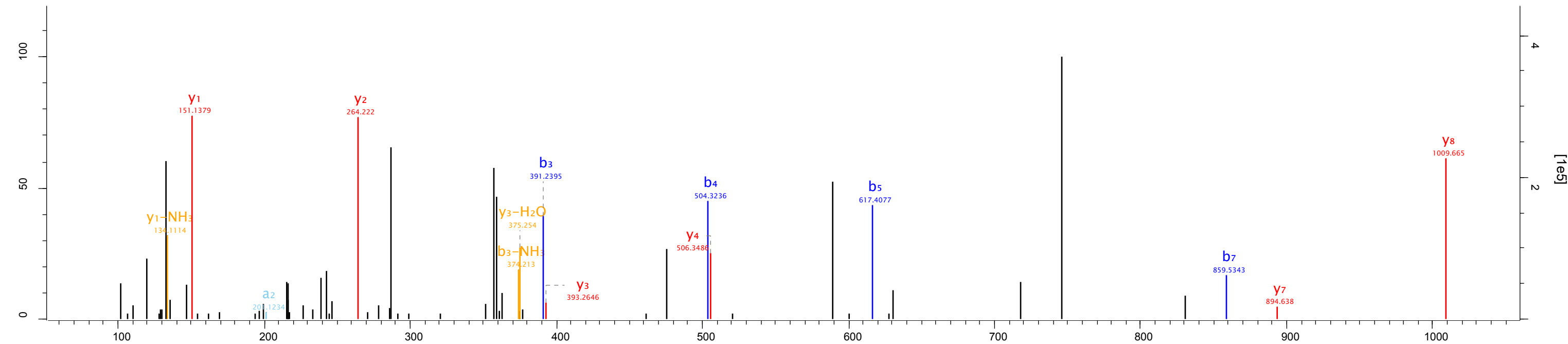
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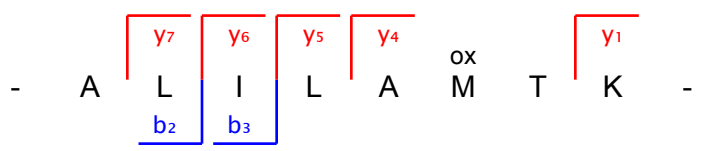
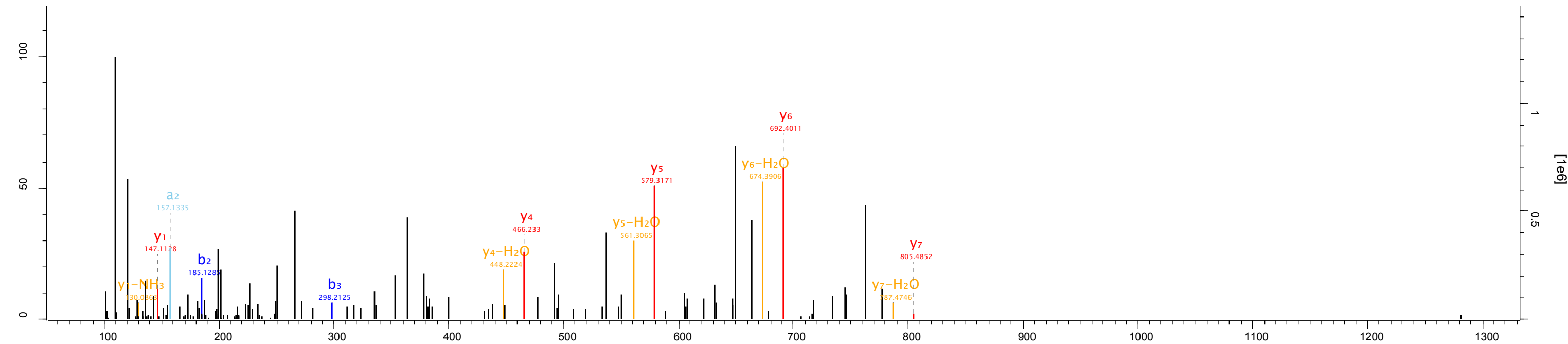
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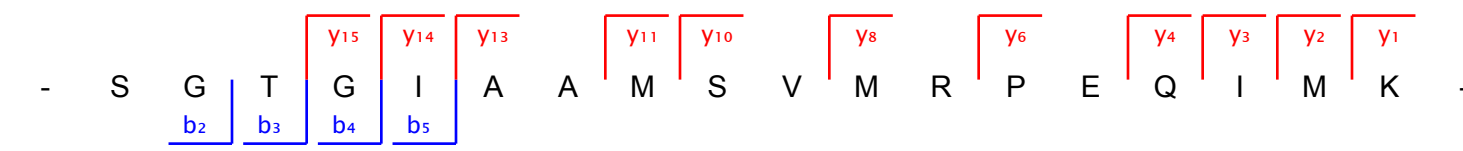
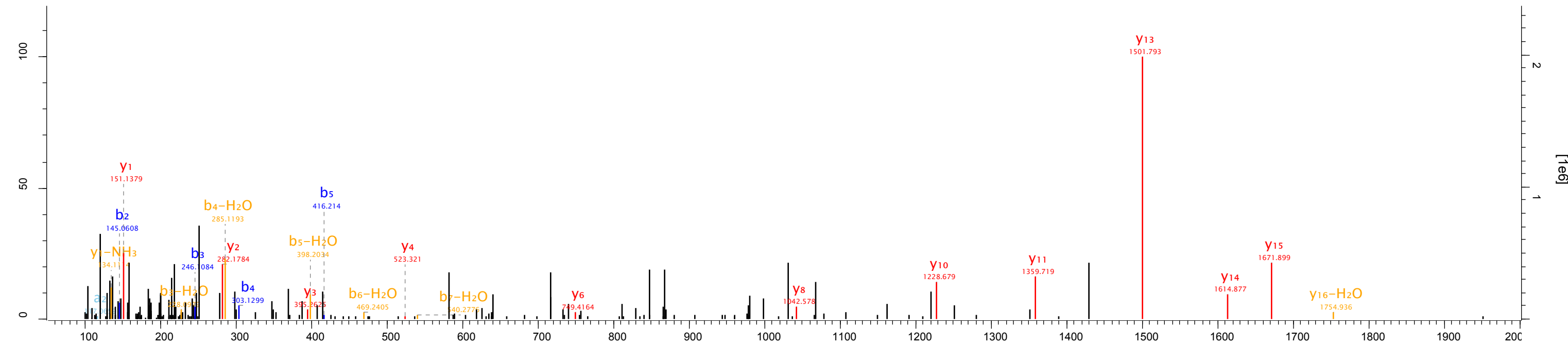
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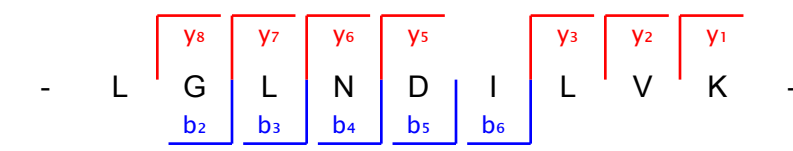
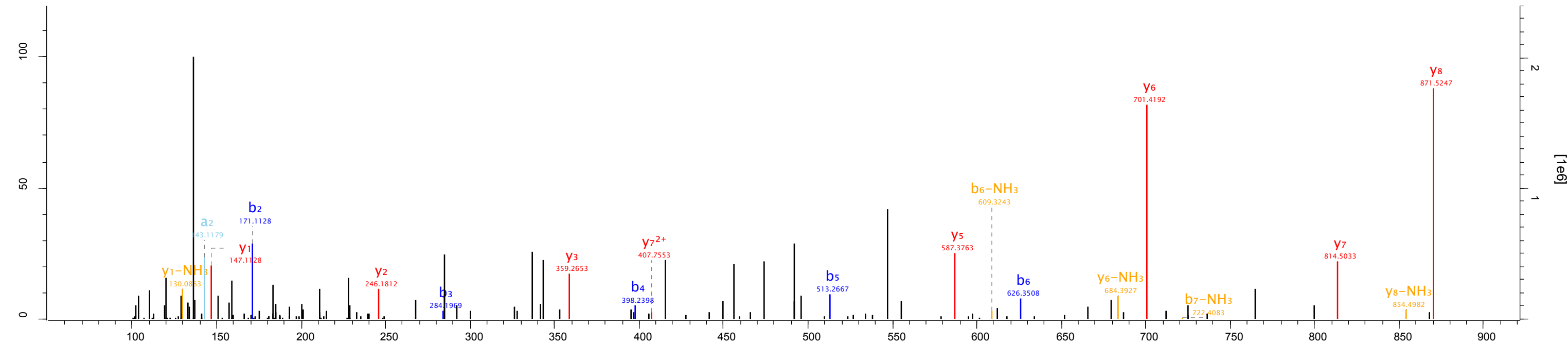
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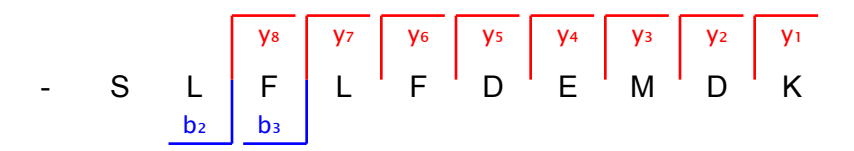
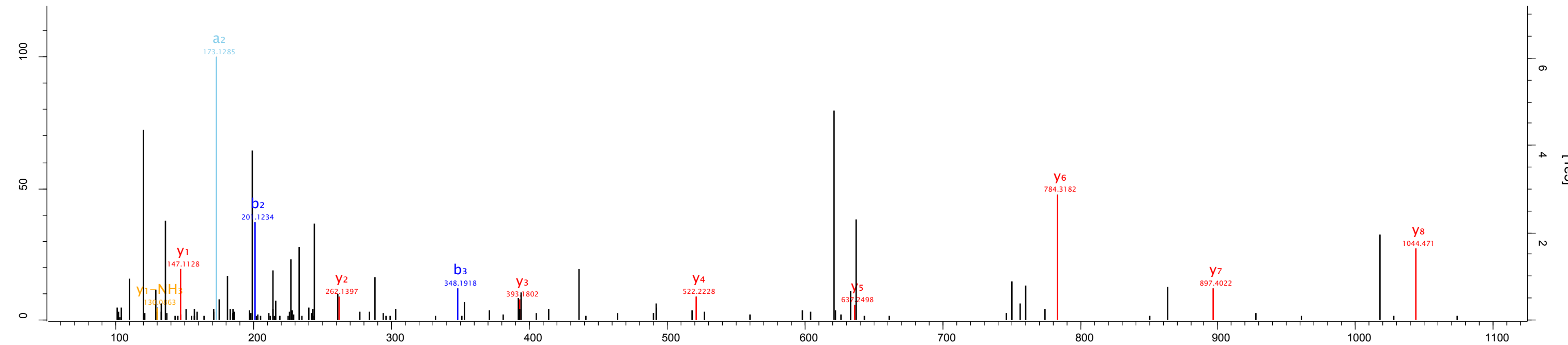
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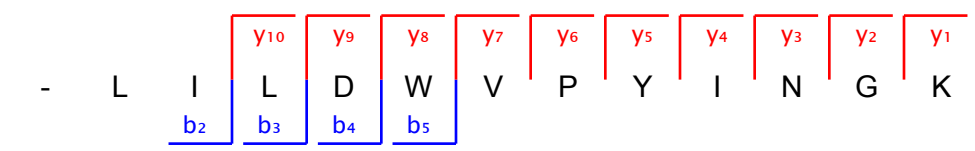
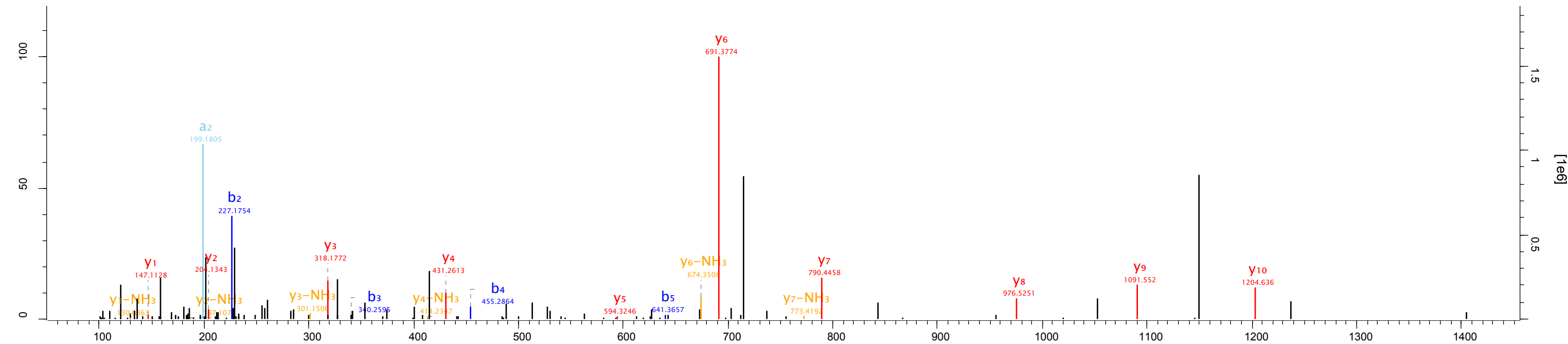
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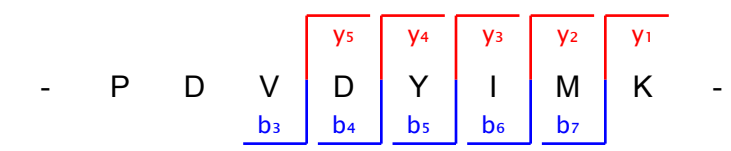
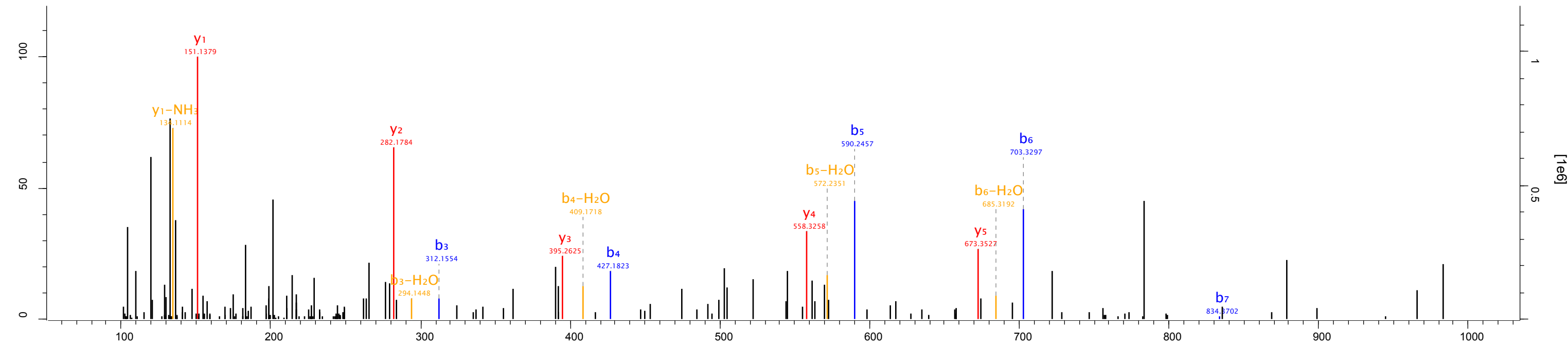
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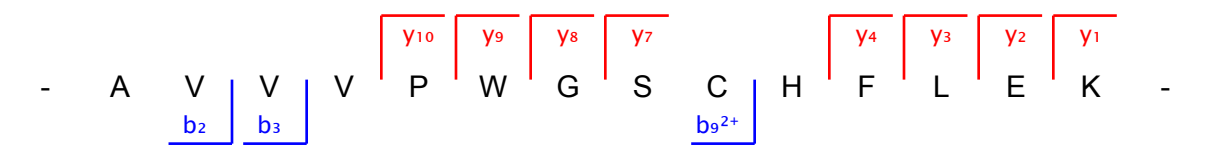
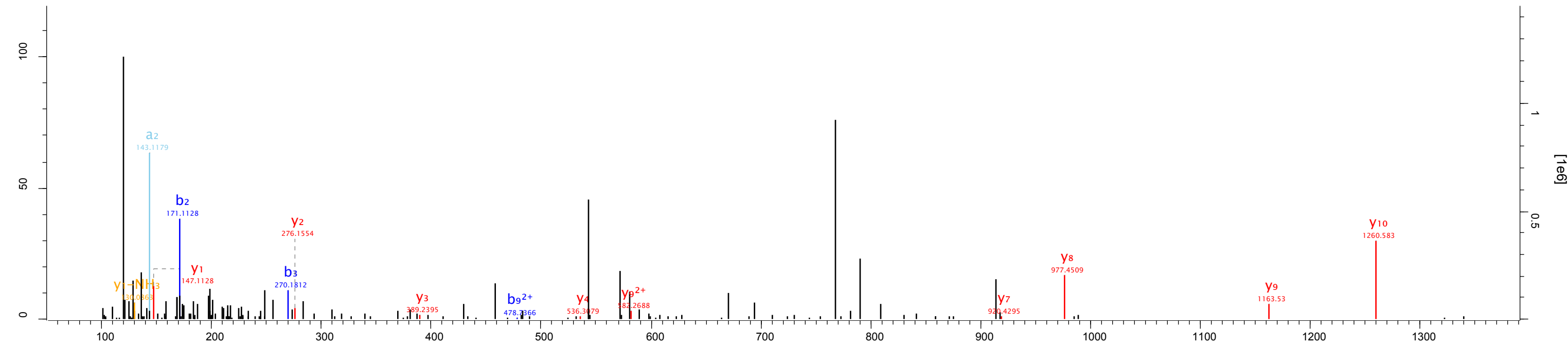
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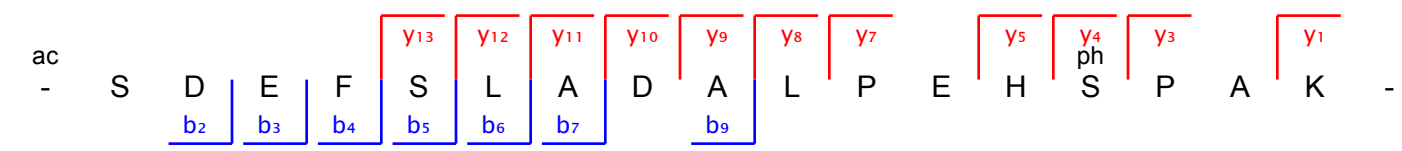
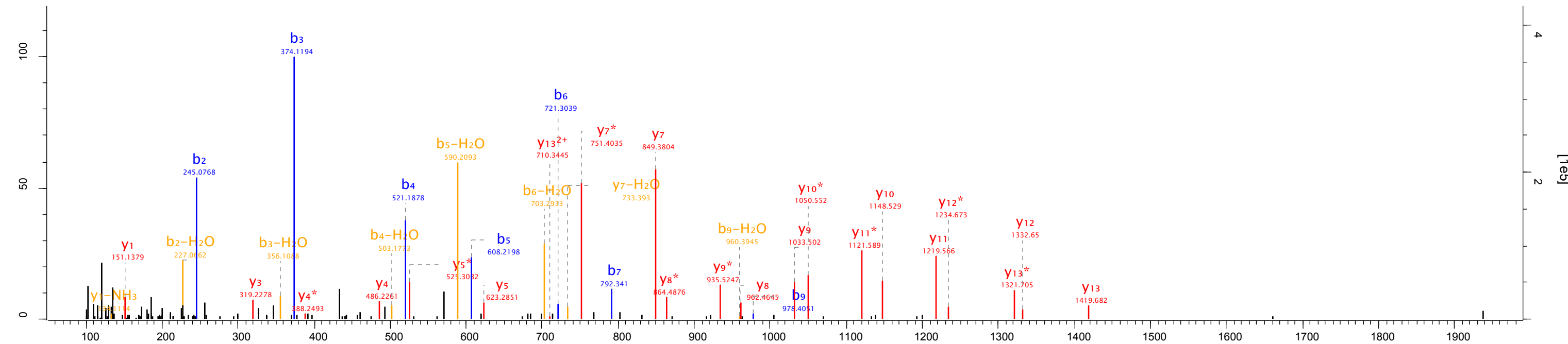
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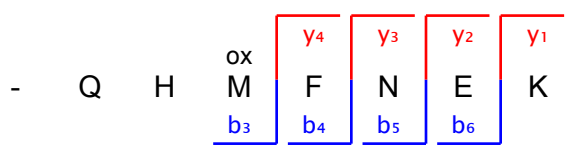
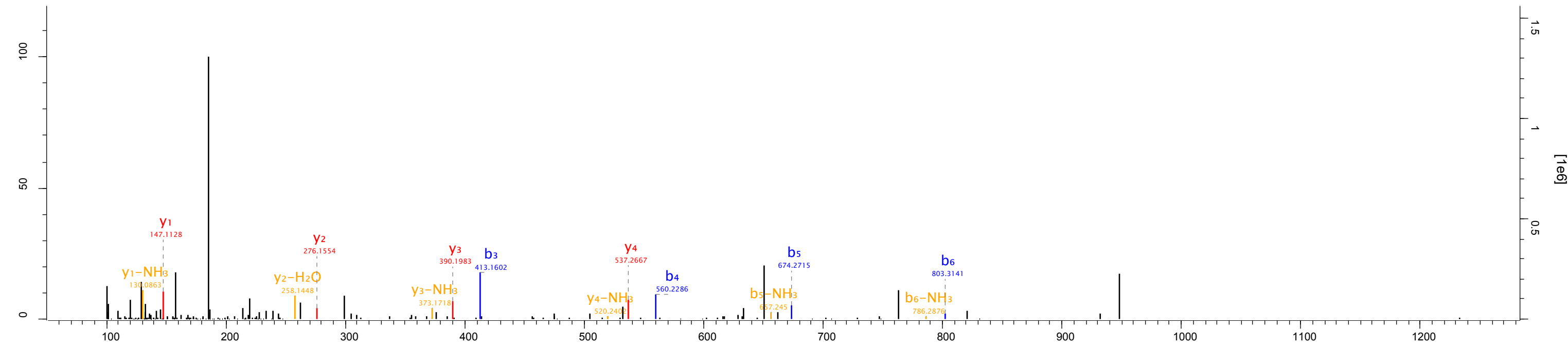
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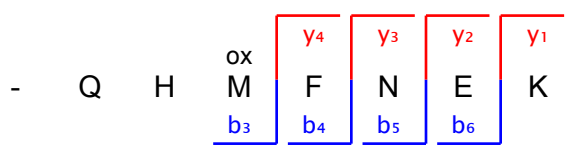
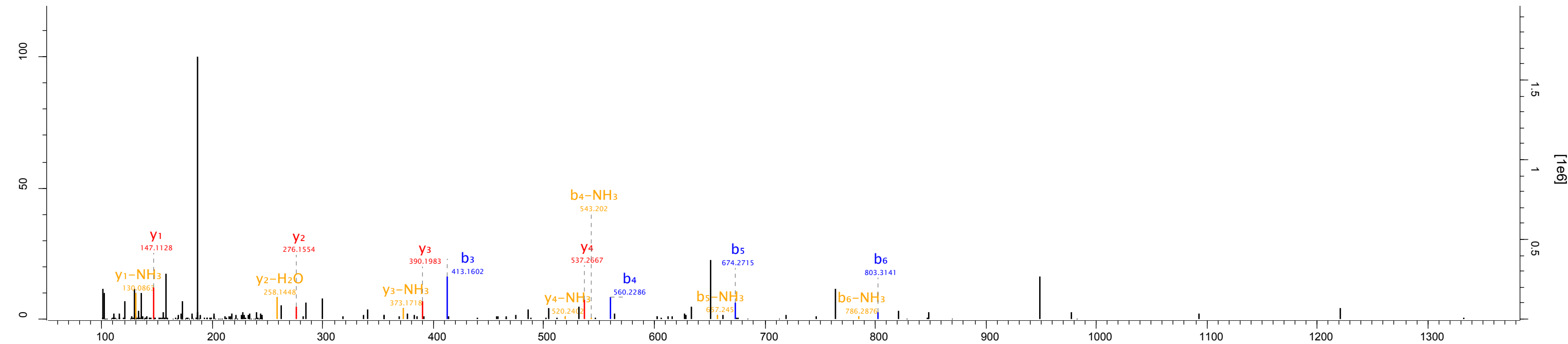
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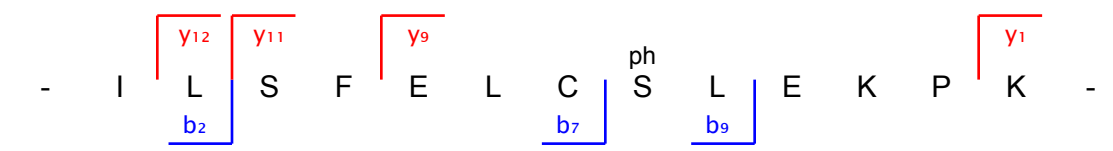
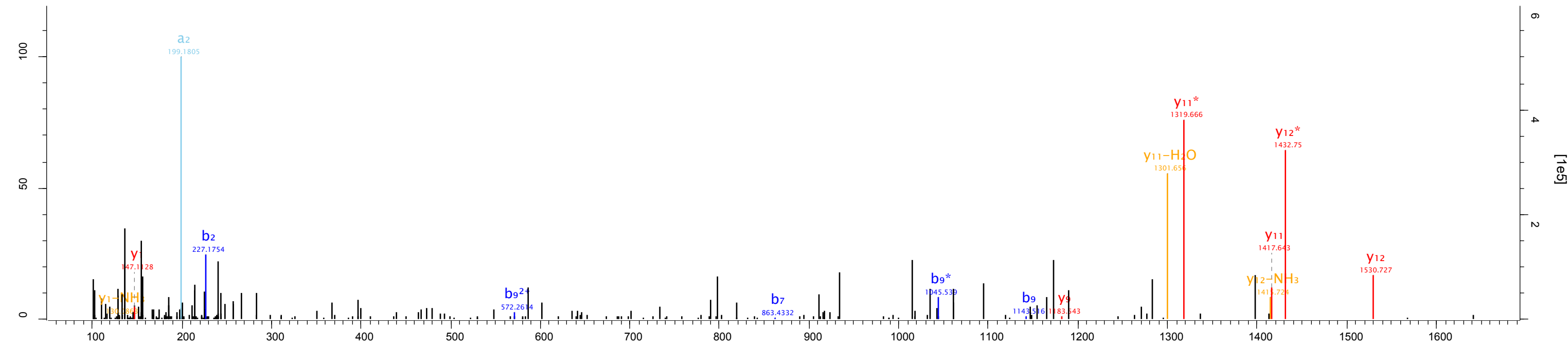
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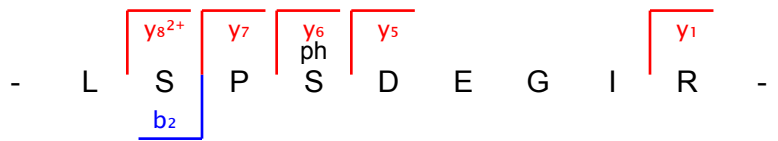
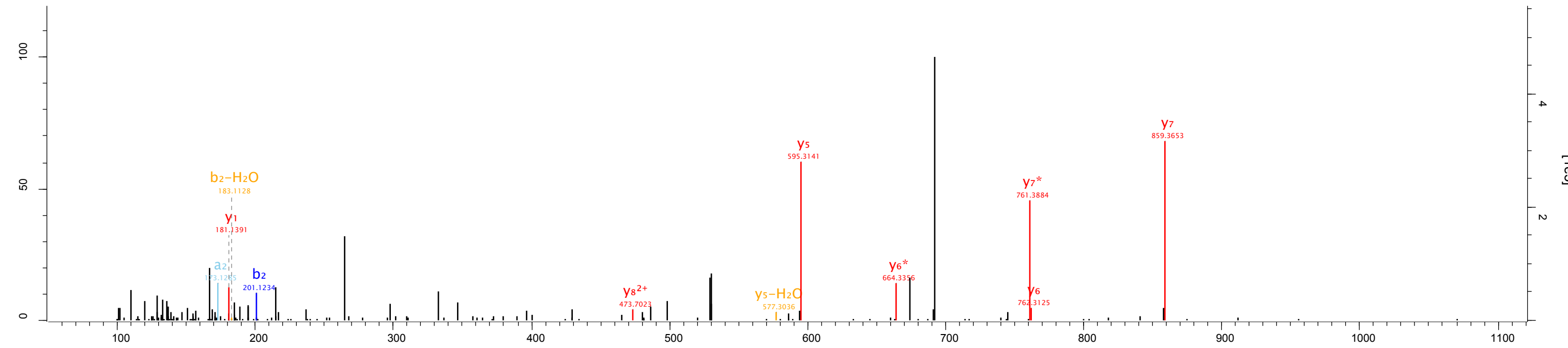
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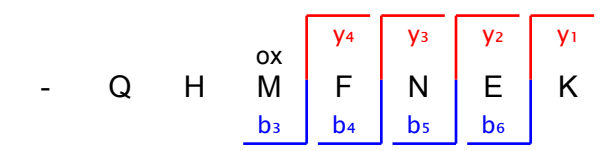
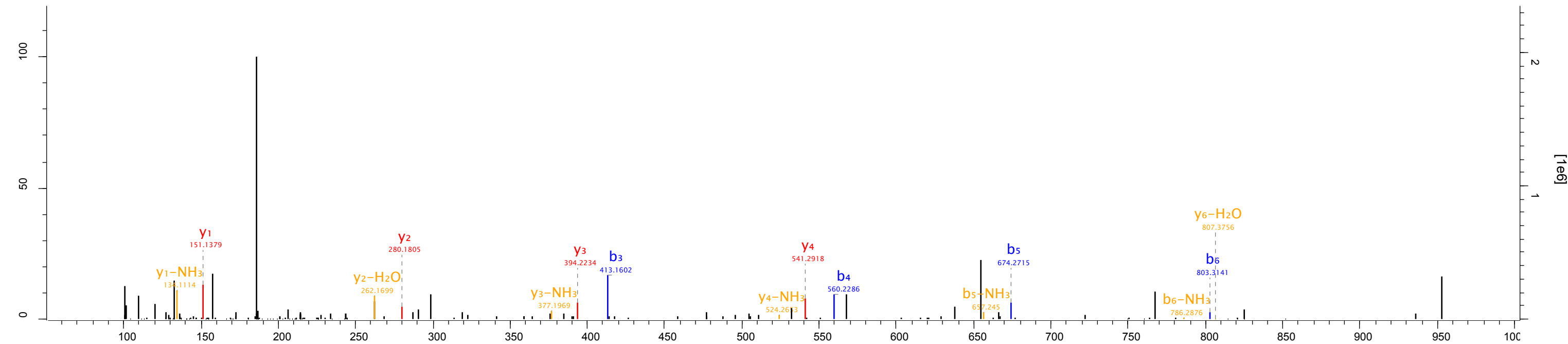
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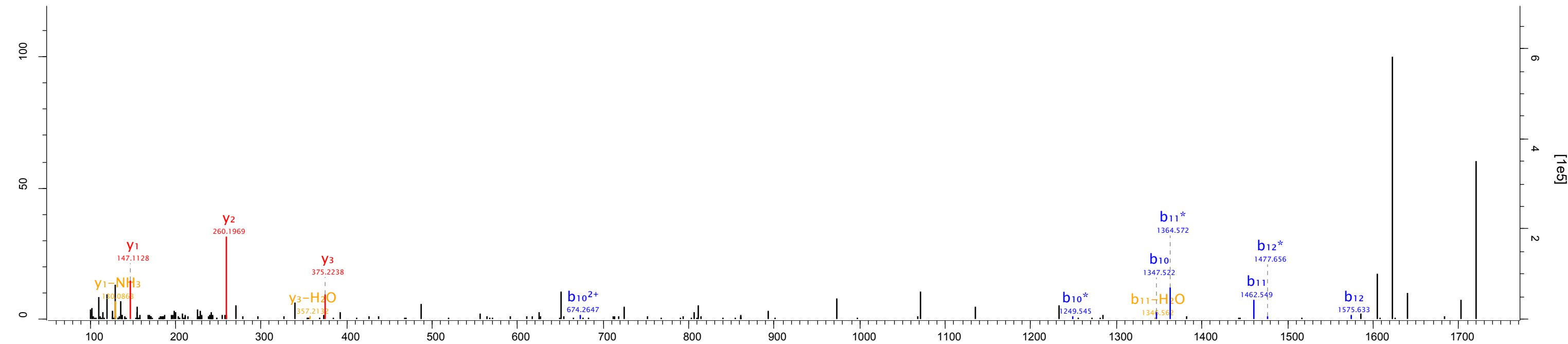
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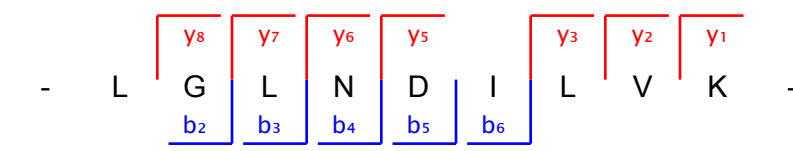
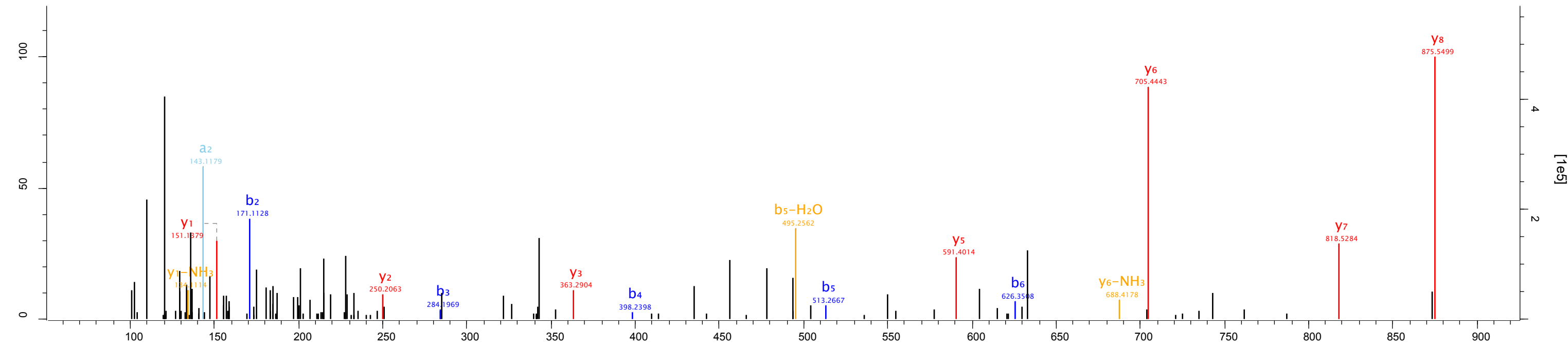
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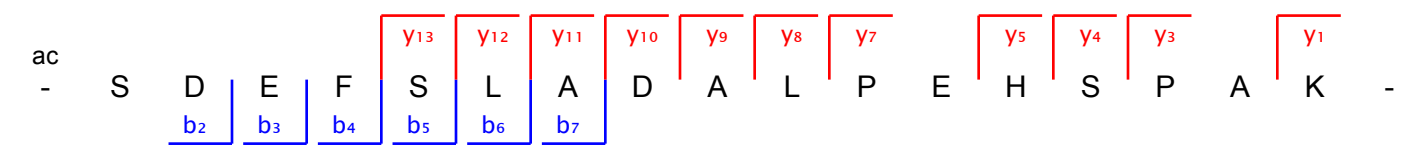
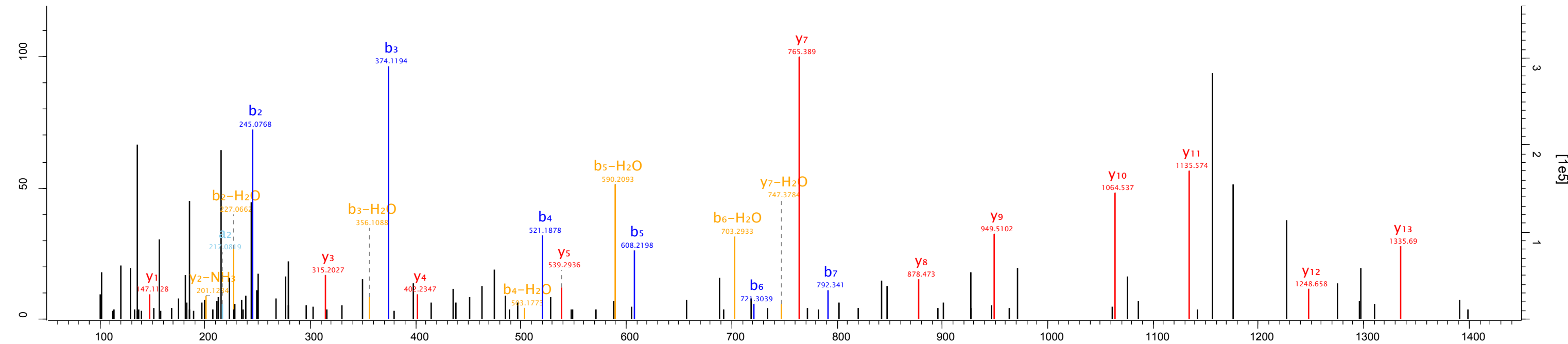
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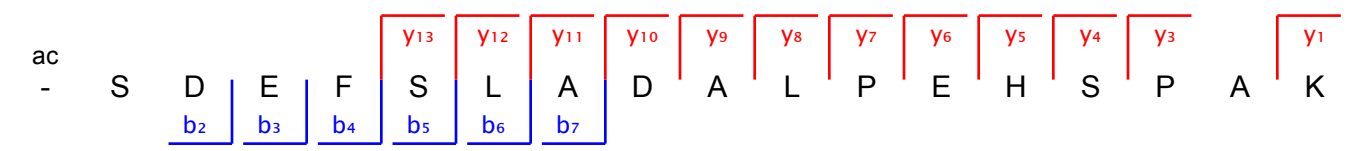
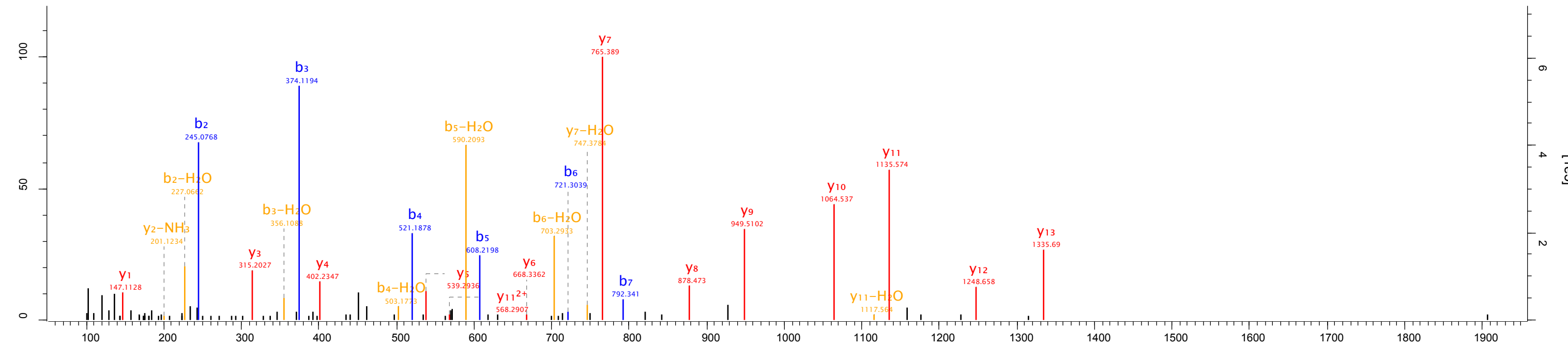
Raw file: 20150822_A375SR-Proteome_BR3
 Scan: 75288 Method: FTMS; HCD Score: 68.85 m/z: 494.82 Gene names: STON2



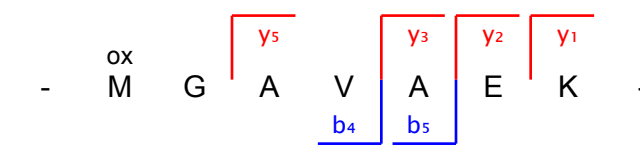
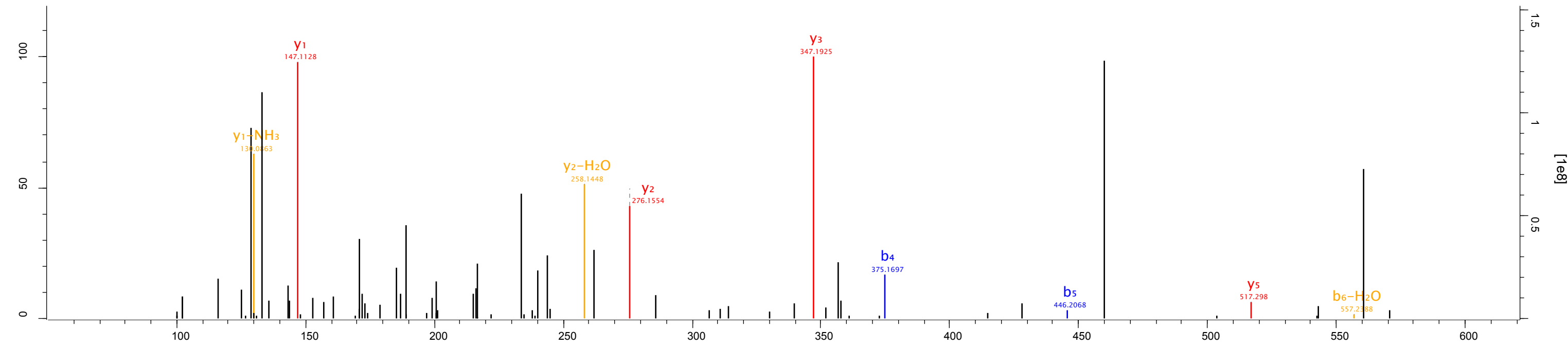
Raw file: 20150822_A375SR-Proteome_BR3
 Scan: 83118 Method: FTMS; HCD Score: 70.12 m/z: 928.44 Gene names: MAPK1IP1L

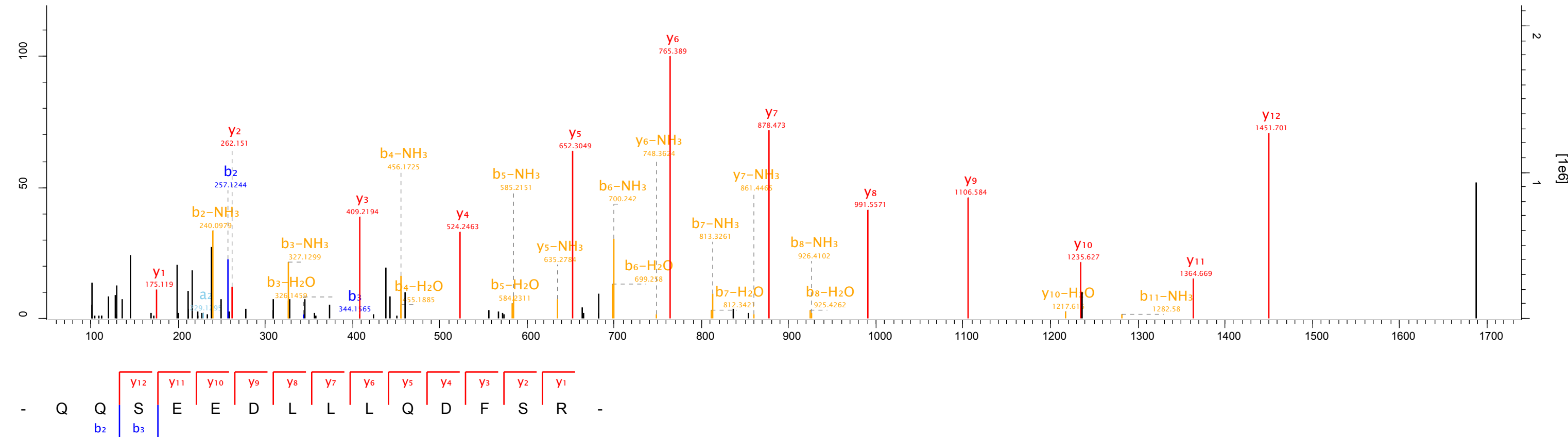


Raw file: 20150822_A375SR-Proteome_BR3
 Scan: 83428 Method: FTMS; HCD Score: 130.29 m/z: 928.44 Gene names: MAPK11P1L



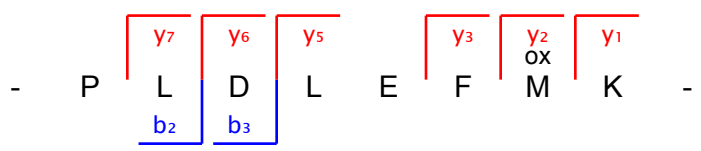
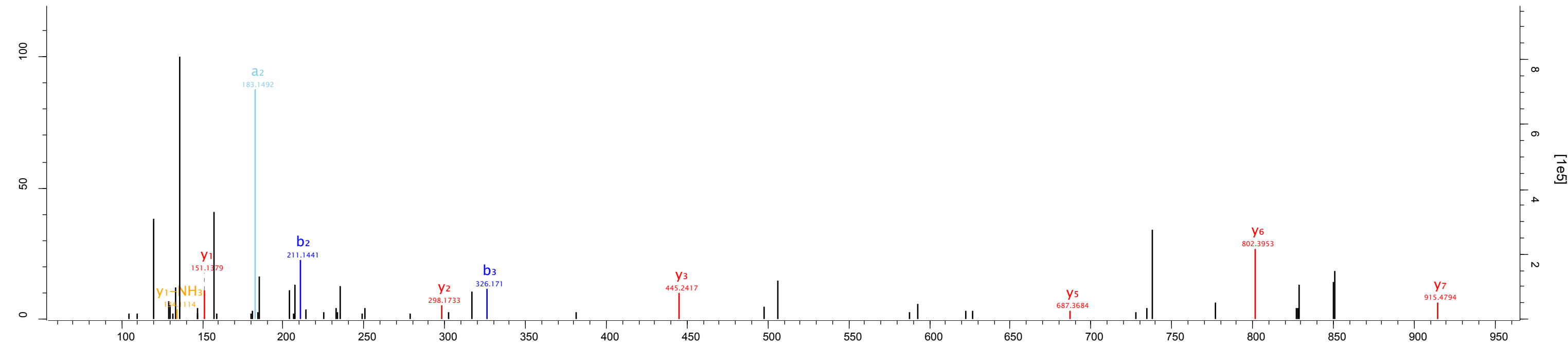
Raw file 20180707_MaS_A375SR_LM_proteome_03 Scan 3308 Method FTMS; HCD Score 60.79 m/z 361.18





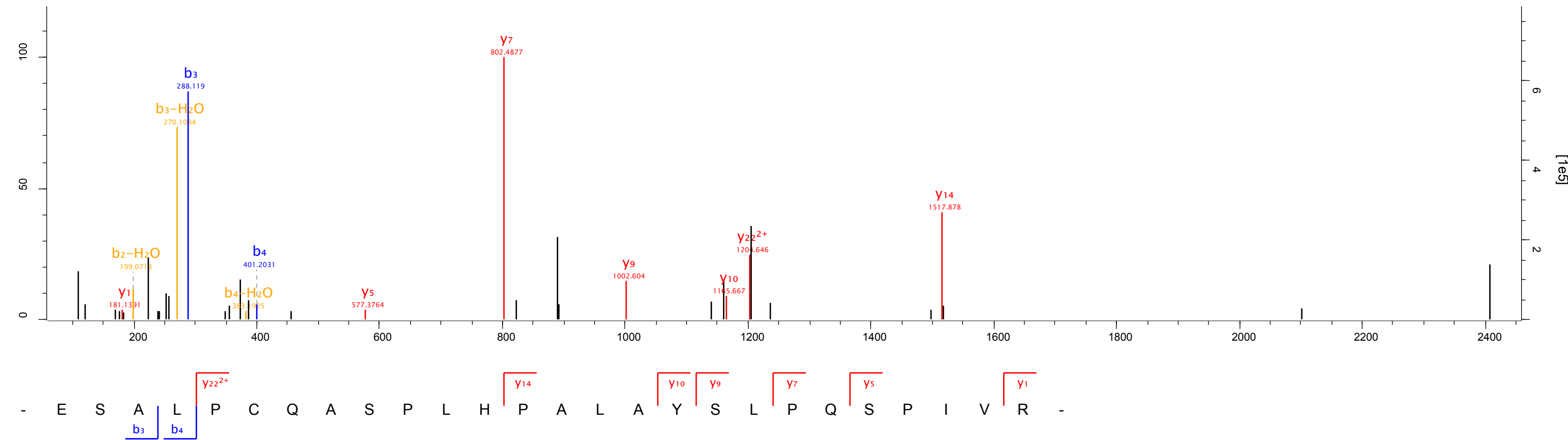
Raw file
20180707_MaS_A375SR_LM_proteome_07

Scan: 19688
Method: FTMS; HCD
Score: 43.08
m/z: 506.77
Gene names: SEPT3



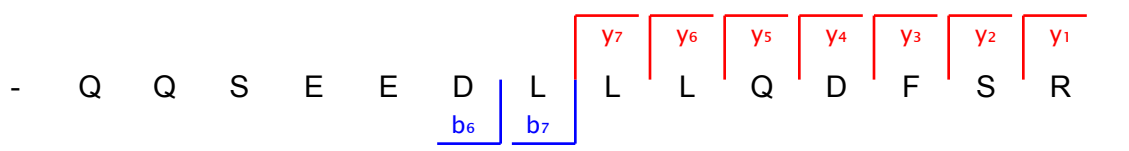
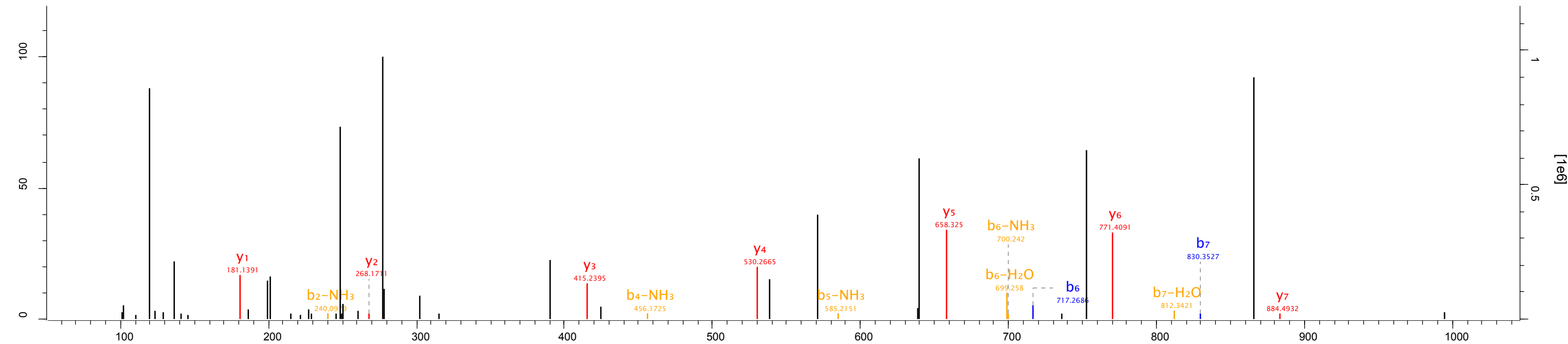
Raw file
20180707_MaS_A375SR_LM_proteome_07

Scan Method Score m/z Gene names
26358 FTMS; HCD 16.47 937.17 C1orf85

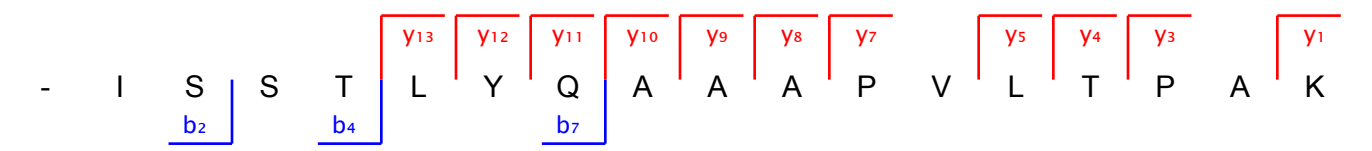
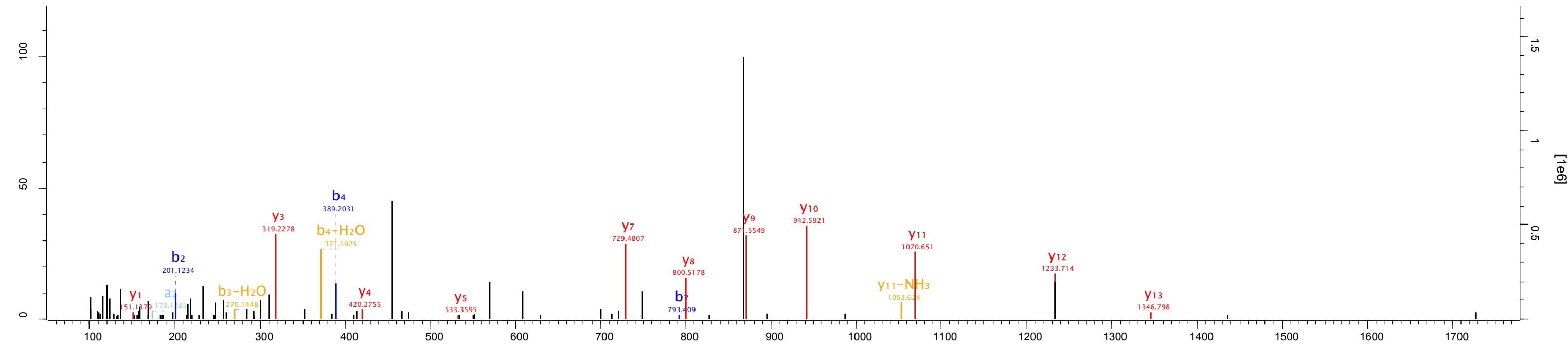


Raw file
20180707_MaS_A375SR_LM_proteome_07

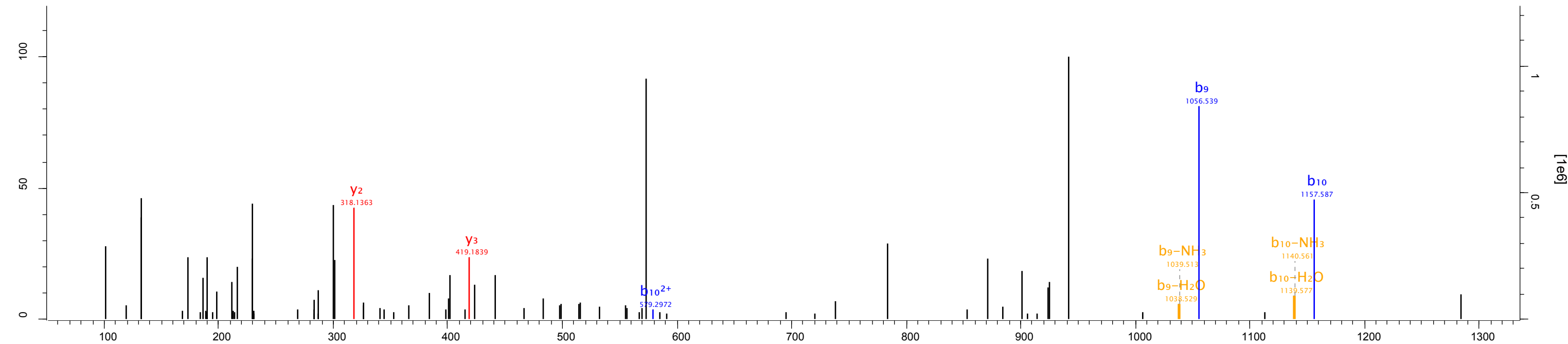
Scan Method Score m/z Gene names
26998 FTMS; HCD 31.91 571.95 SSR3



Raw file 20180707_MaS_A375SR_LM_proteome_09 Scan 23038 Method FTMS; HCD Score 48.91 m/z 868.5 Gene names KRTCAP2



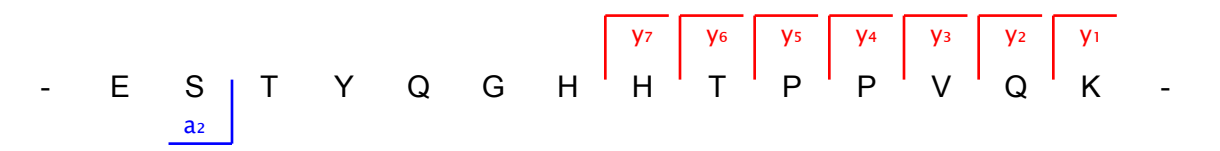
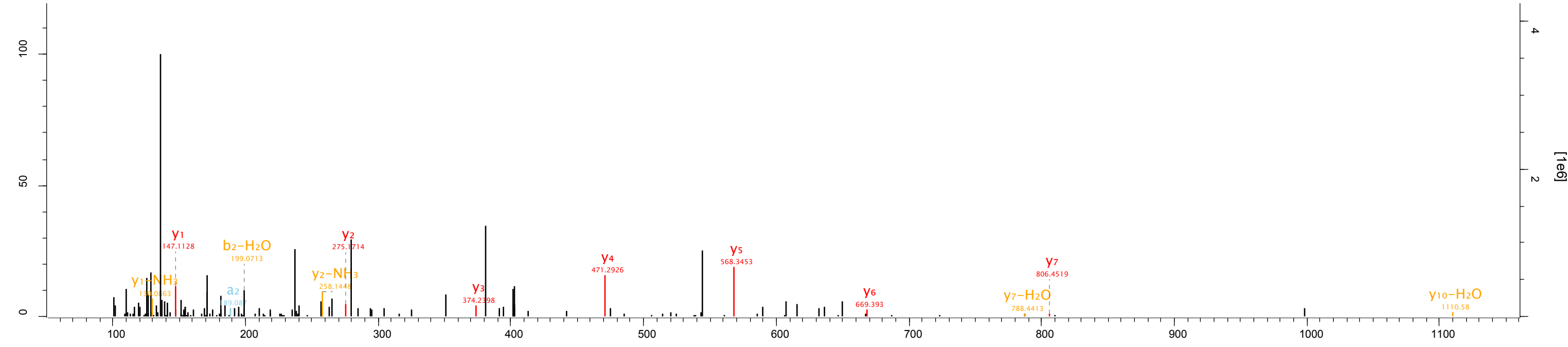
Raw file 20180707_MaS_A375SR_LM_proteome_09 Scan 2478 Method FTMS; HCD Score 62.47 m/z 738.36



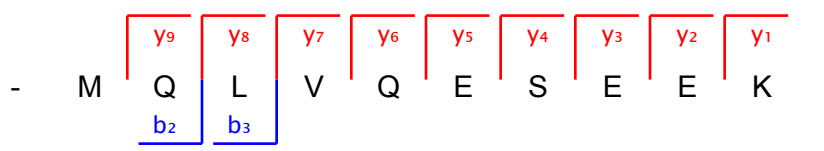
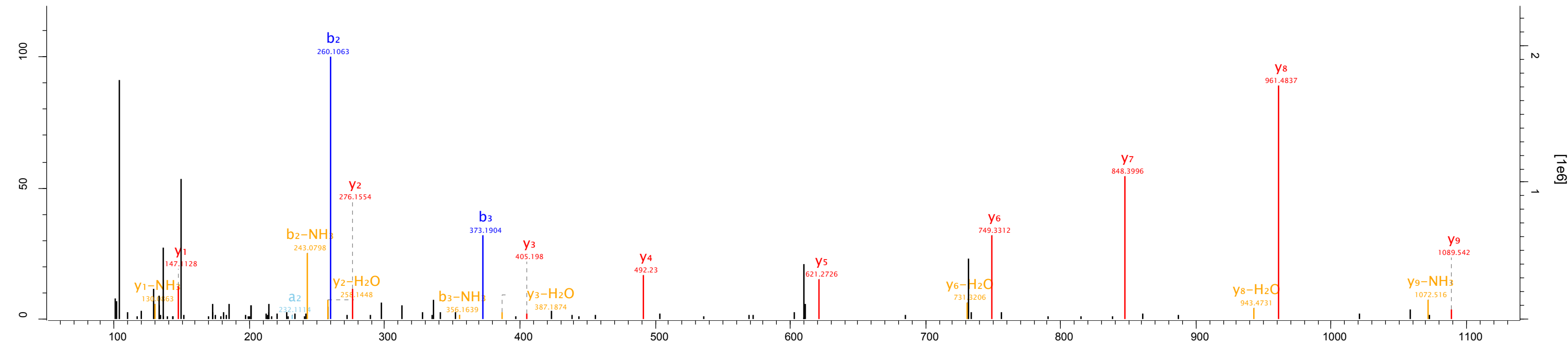
- M E L L Q I A Q E T S K -

Fragmentation mapping:

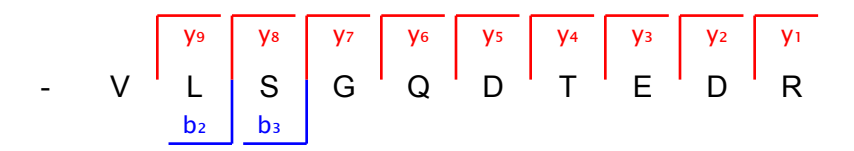
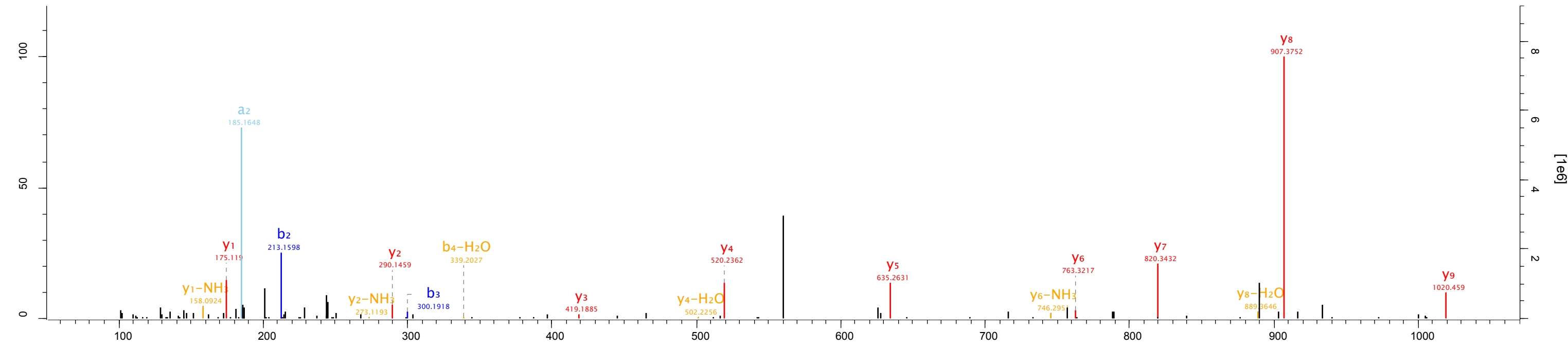
- b_9 (blue box) covers E and T.
- b_{10} (blue box) covers T and S.
- y_3 (red box) covers T.
- y_2 (red box) covers S.



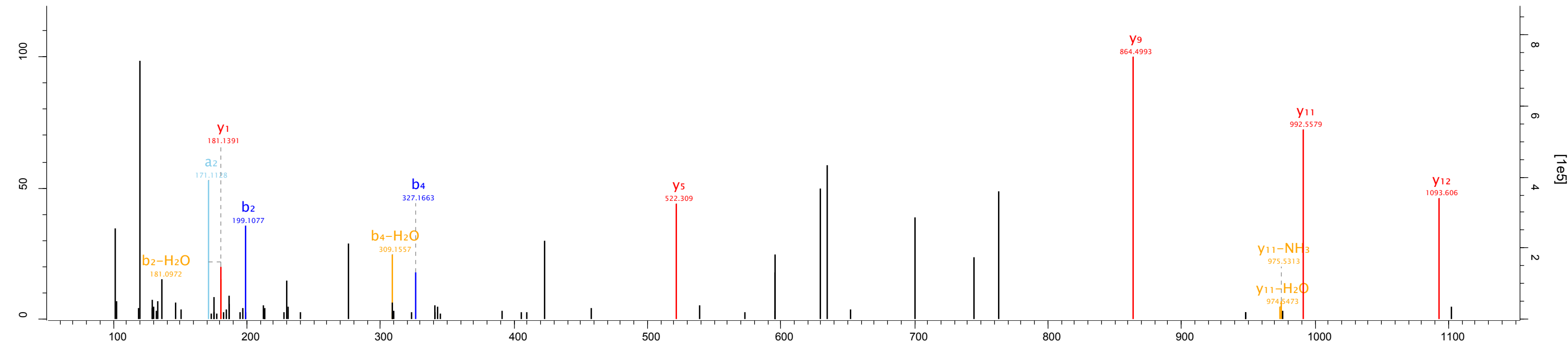
Raw file: 20180707_MaS_A375SR_LM_proteome_18
 Scan: 11598 Method: FTMS; HCD Score: 99.28 m/z: 610.8



Raw file: 20180707_MaS_A375SR_LM_proteome_18
 Scan: 4728 Method: FTMS; HCD Score: 76.93 m/z: 560.27 Gene names: SFT2D2

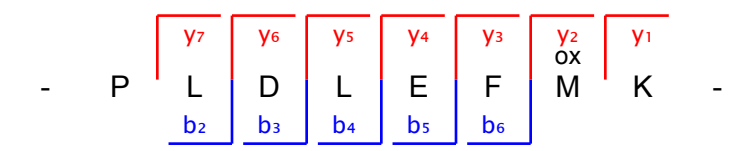
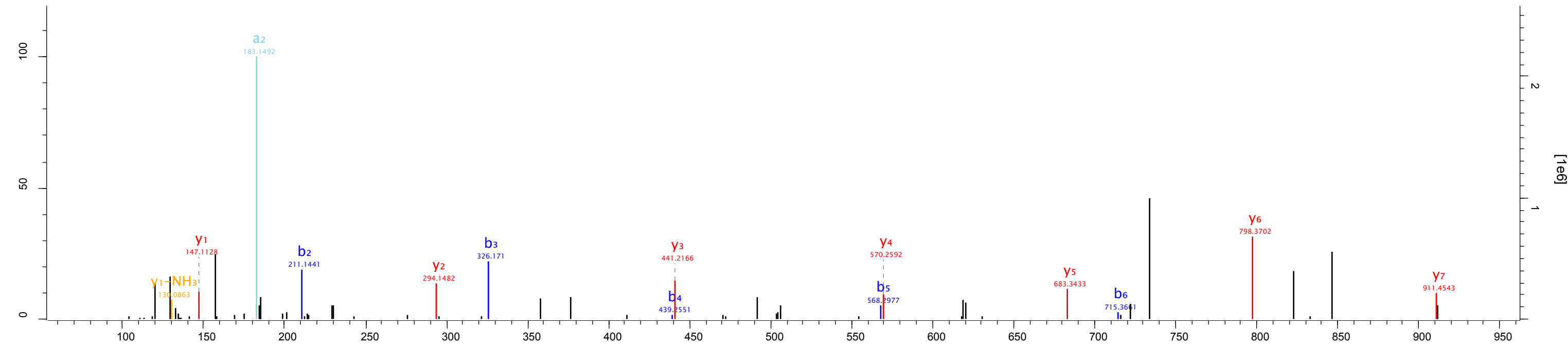


Raw file 20180707_MaS_A375SR_LM_proteome_18 Scan 8658 Method FTMS; HCD Score 47.71 m/z 596.33

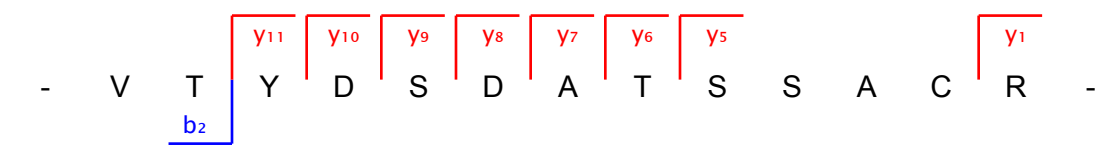
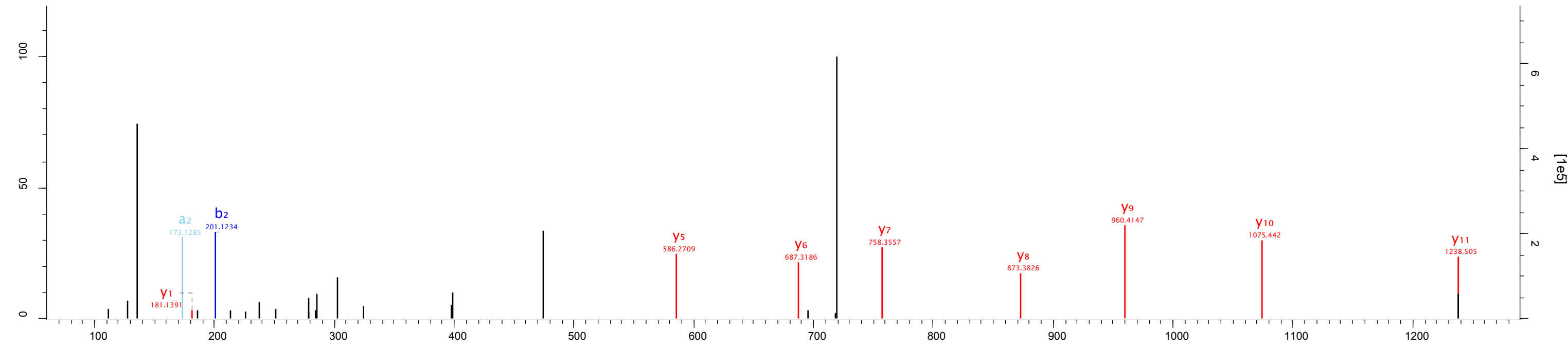


Raw file
20180707_MaS_A375SR_LM_proteome_21

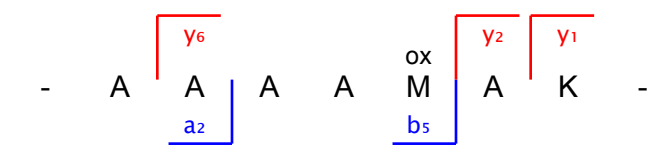
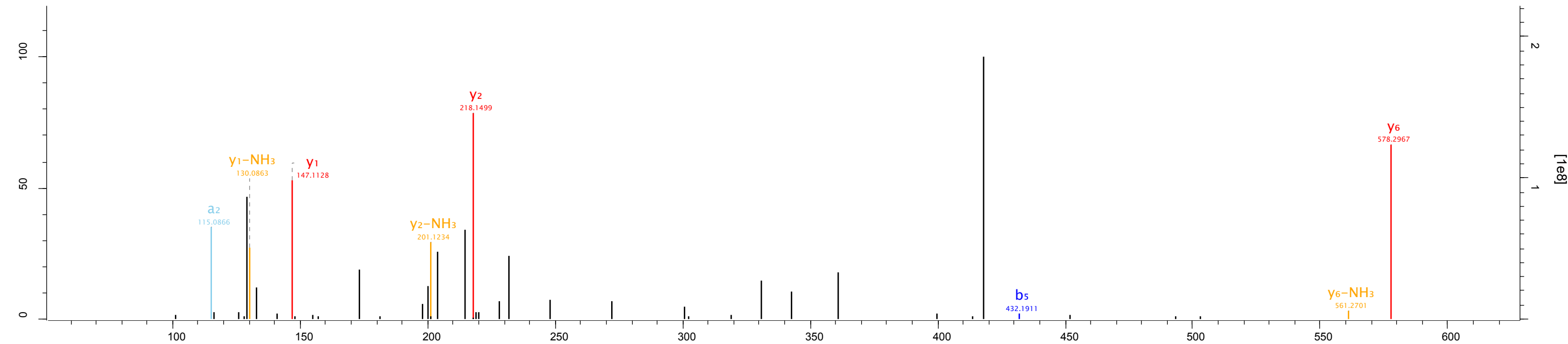
Scan: 20158
Method: FTMS; HCD
Score: 76.22
m/z: 504.76
Gene names: SEPT3



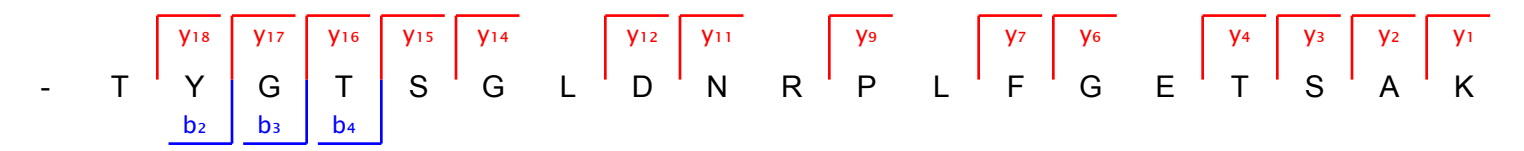
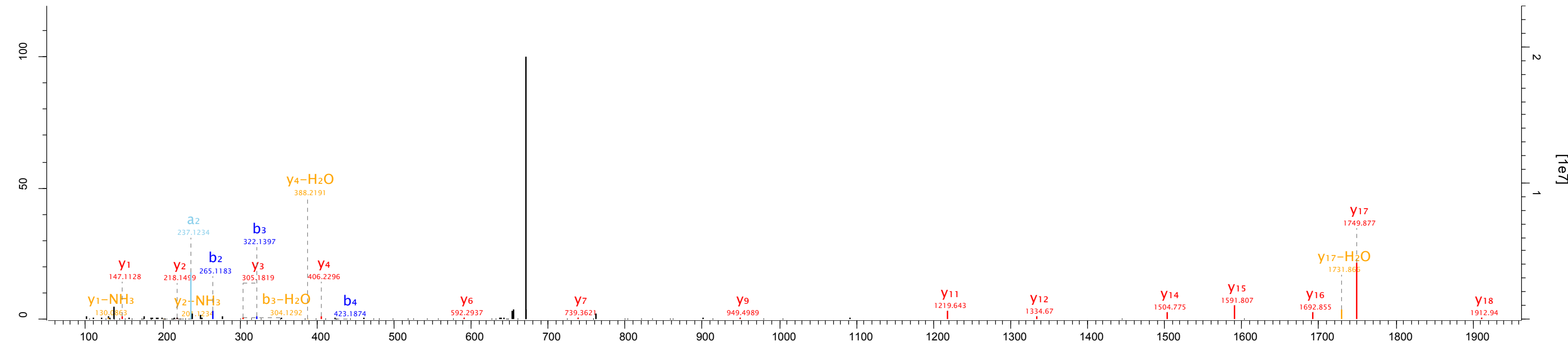
Raw file 20180707_MaS_A375SR_LM_proteome_22 Scan 6848 Method FTMS; HCD Score 35.66 m/z 719.82 Gene names LEPROT



Raw file 20180707_MaS_A375SR_LM_proteome_27 Scan 2908 Method FTMS; HCD Score 62 m/z 325.17

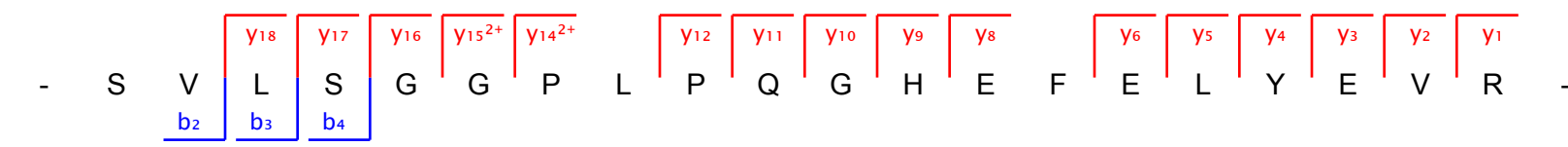
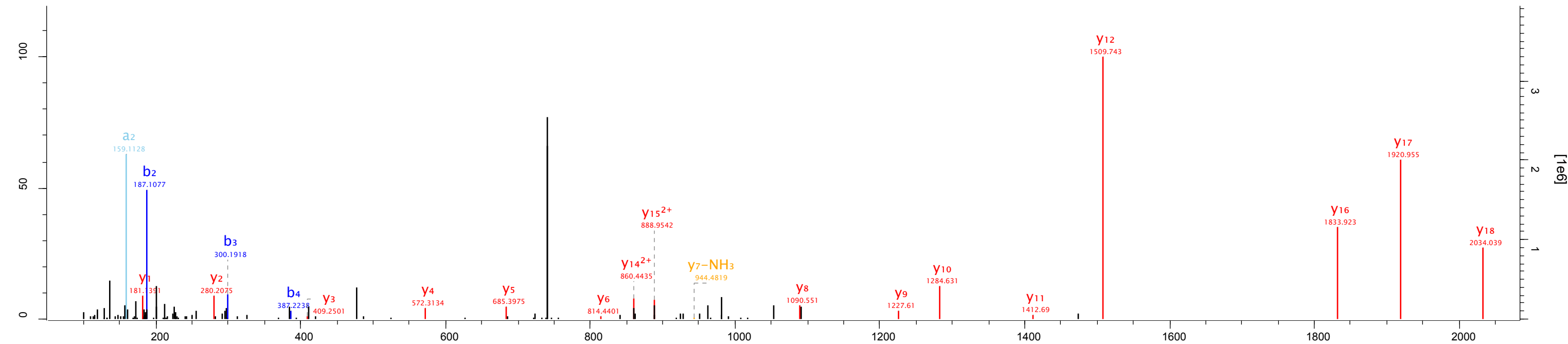


Raw file: 20180707_MaS_A375SR_ML_proteome_01
 Scan: 16538 Method: FTMS; HCD Score: 61.94 m/z: 672 Gene names: TMEM243



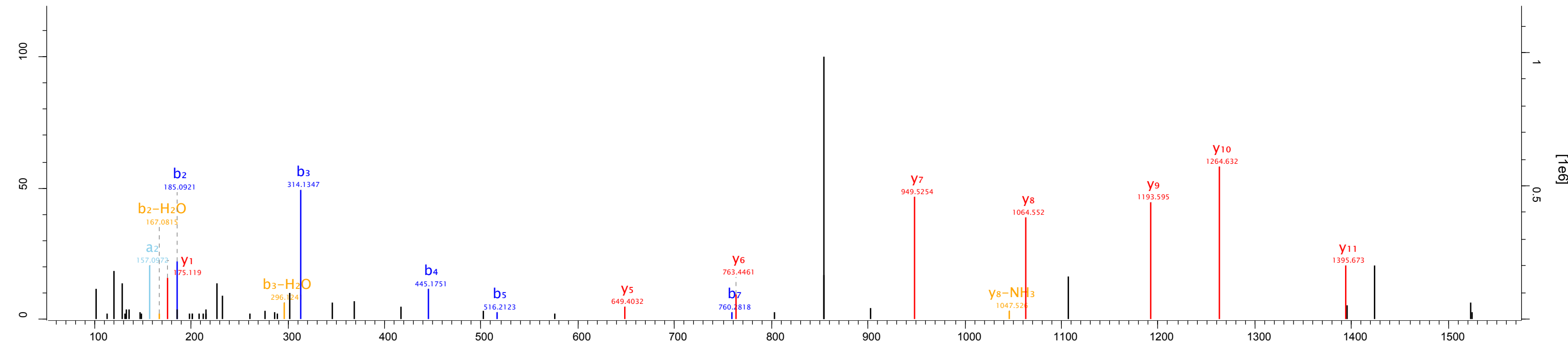
Raw file
20180707_MaS_A375SR_ML_proteome_01

Scan 24618 Method FTMS; HCD Score 66.64 m/z 741.05 Gene names CA8



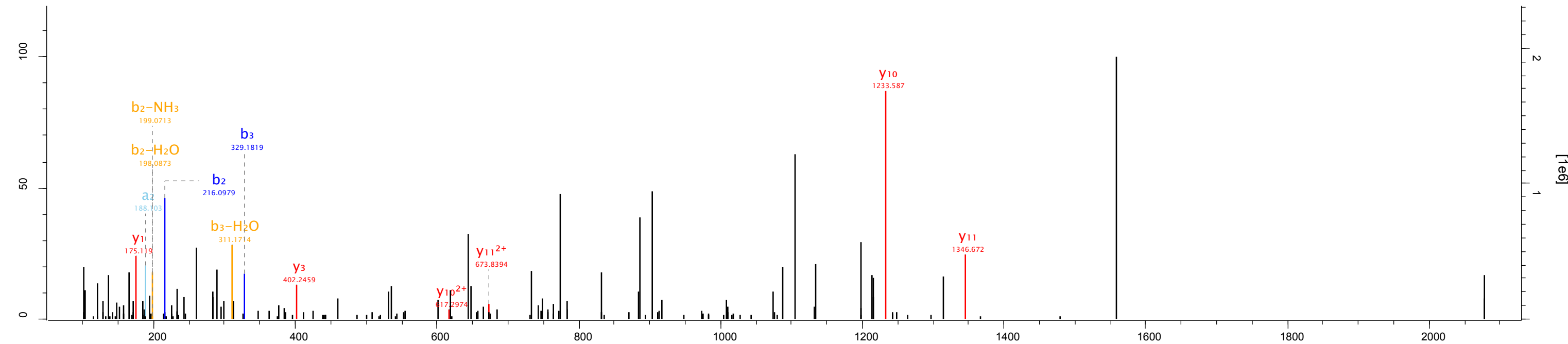
Raw file
20180707_MaS_A375SR_ML_proteome_01

Scan 27408 Method FTMS; HCD Score 68.97 m/z 854.9 Gene names TMEM248



- S P E M A E D W N T F L L R -

Fragmentation mapping:
- b2 (P) - b3 (E) - b4 (M) - b5 (A) - b7 (D) - y11 (M) - y10 (A) - y9 (E) - y8 (D) - y7 (W) - y6 (N) - y5 (T) - y1 (R)



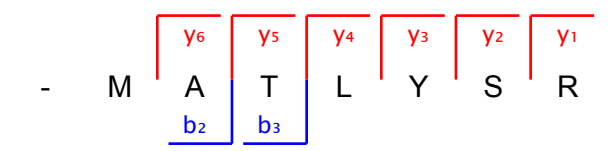
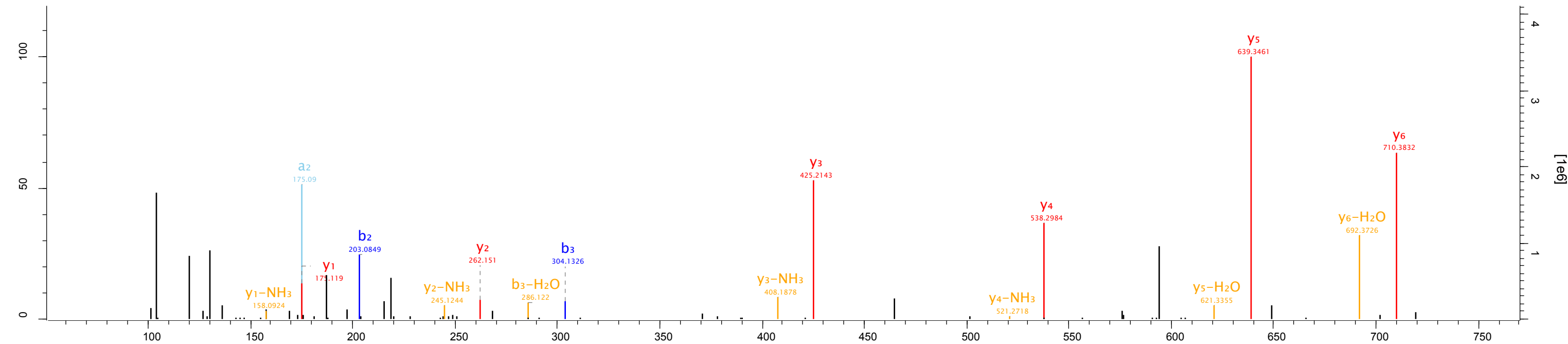
- S Q L D ph T L P P E V N L R -

Fragmentation sites are indicated by brackets below the sequence:

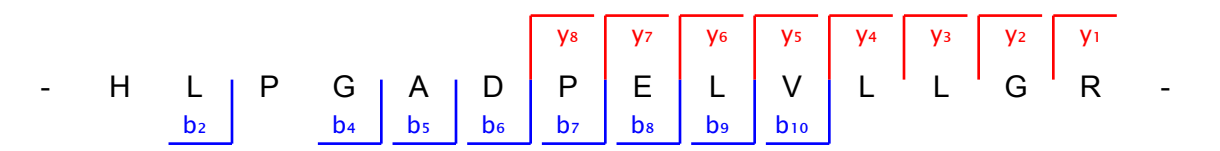
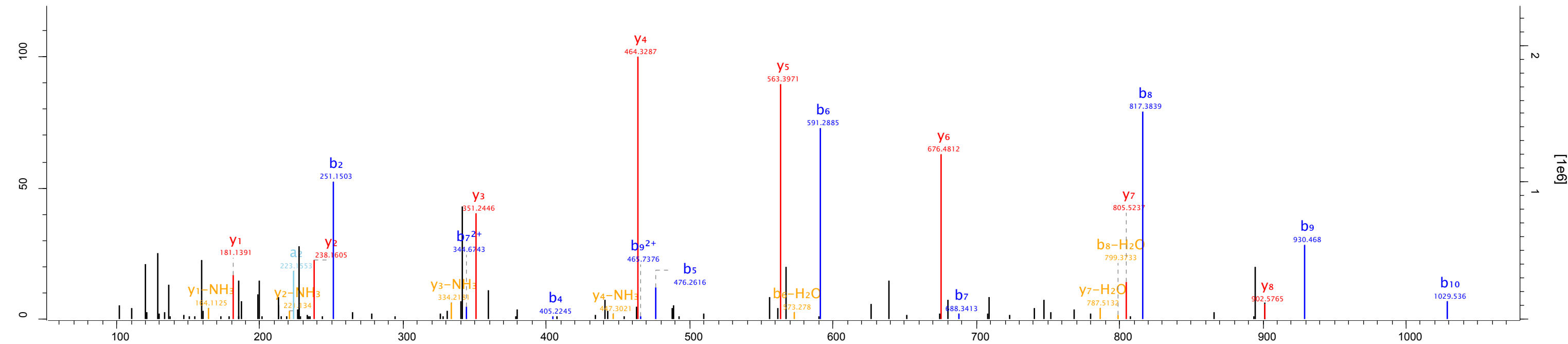
- Blue brackets: b₂ (under Q), b₃ (under L)
- Red brackets: y₁₁ (over L), y₁₀ (over D), y₃ (over N), y₁ (over R)

Raw file
20180707_MaS_A375SR_ML_proteome_02

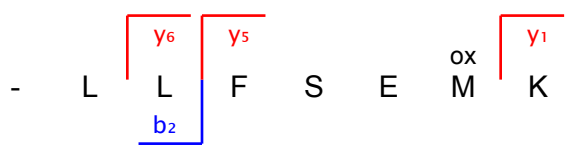
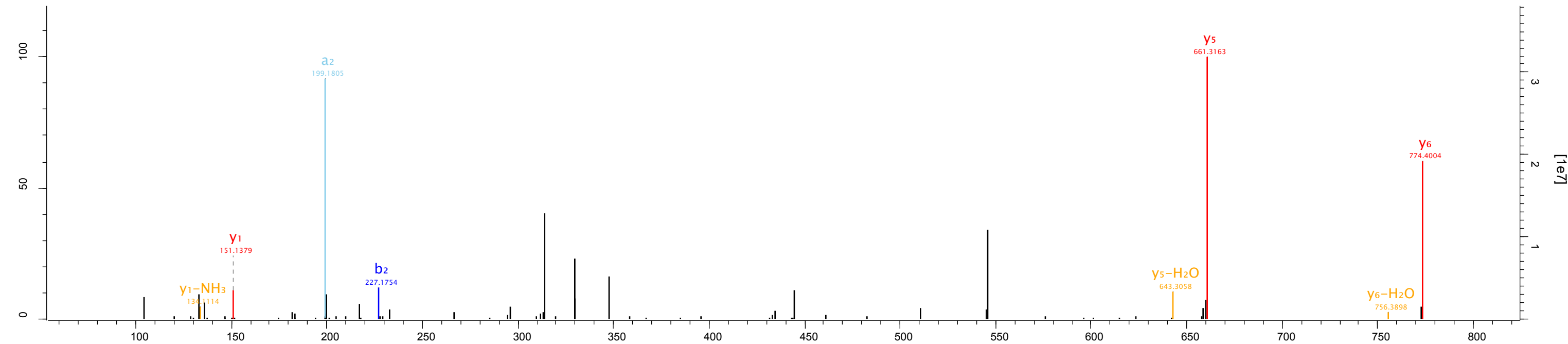
Scan Method Score m/z Gene names
9058 FTMS; HCD 107.59 421.21 PTGDS



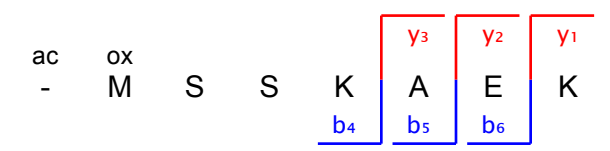
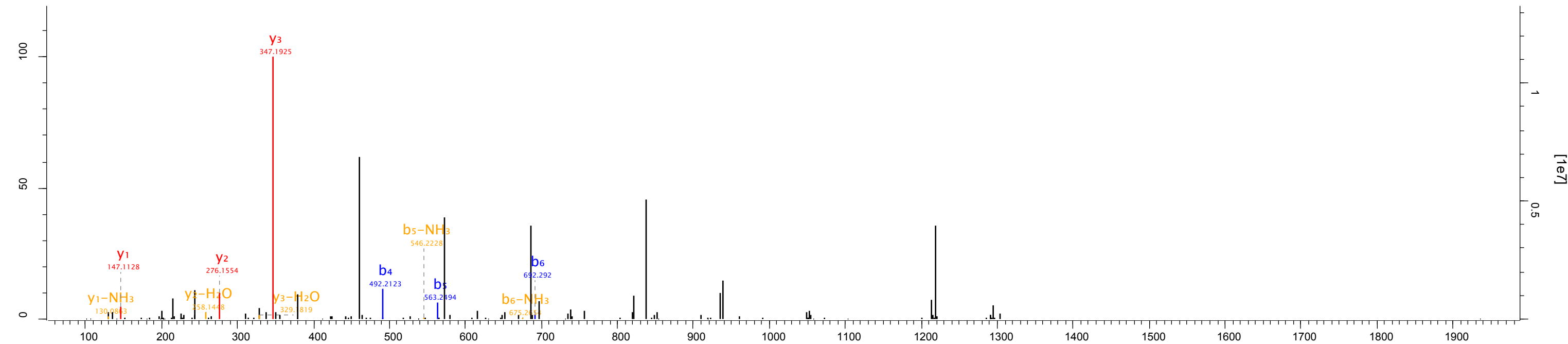
Raw file: 20180707_MaS_A375SR_ML_proteome_03
 Scan: 21198 Method: FTMS; HCD Score: 97.96 m/z: 498.29 Gene names: SELM



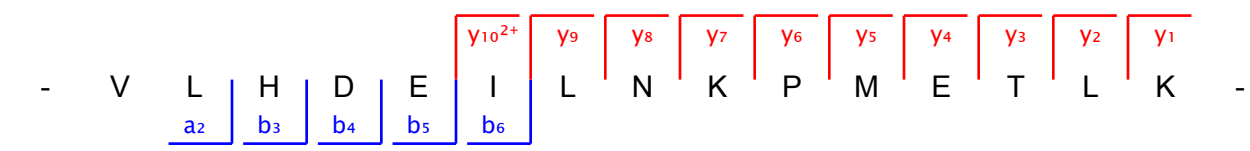
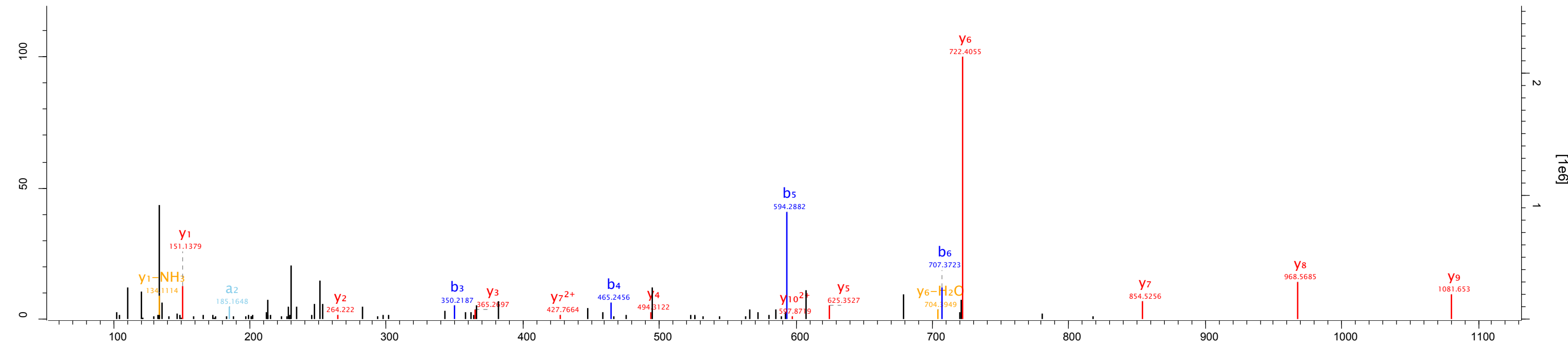
Raw file 20180707_MaS_A375SR_ML_proteome_06 Scan 12378 Method FTMS; HCD Score 46.66 m/z 444.25 Gene names C1orf234



Raw file: 20180707_MaS_A375SR_ML_proteome_06
 Scan: 13128 Method: FTMS; HCD Score: 54.2 m/z: 838.4 Gene names: DNAH2

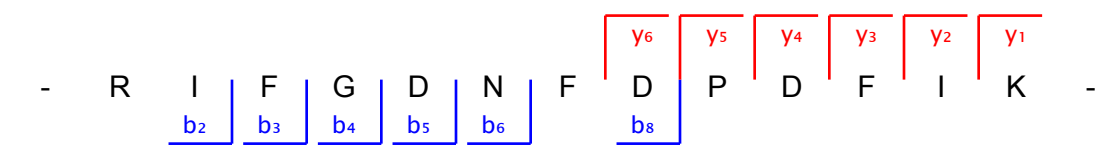
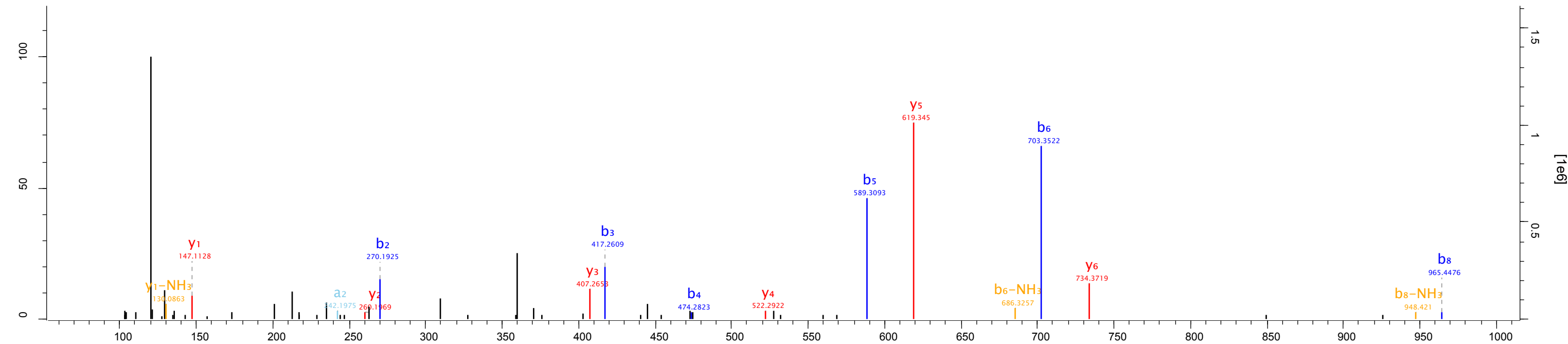


Raw file 20180707_MaS_A375SR_ML_proteome_06 Scan 17308 Method FTMS; HCD Score 54.81 m/z 448.01 Gene names SLC35A3

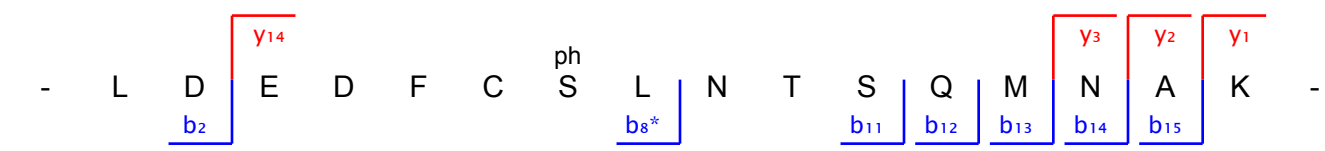
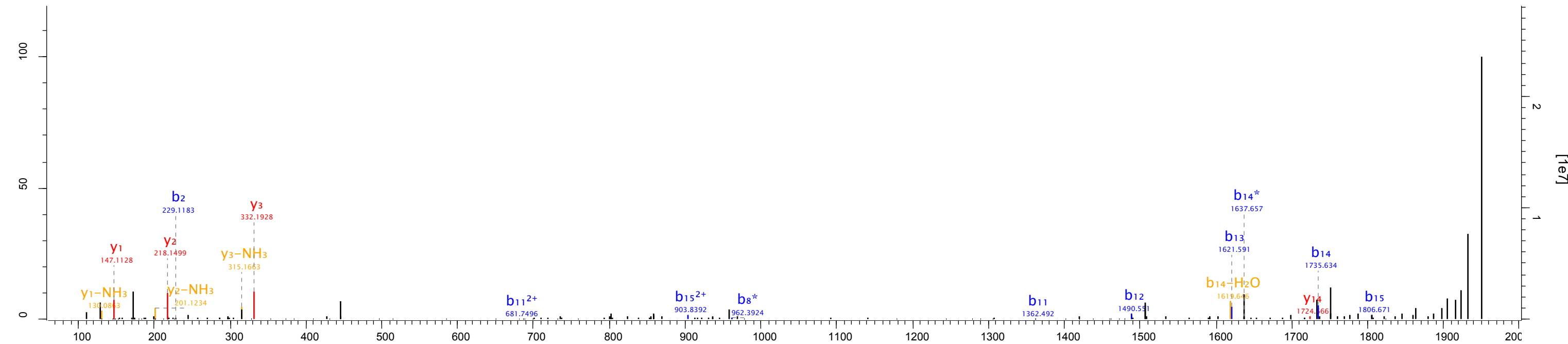


Raw file
20180707_MaS_A375SR_ML_proteome_06

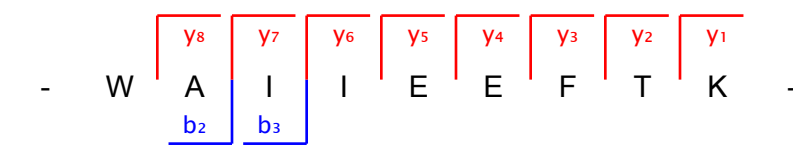
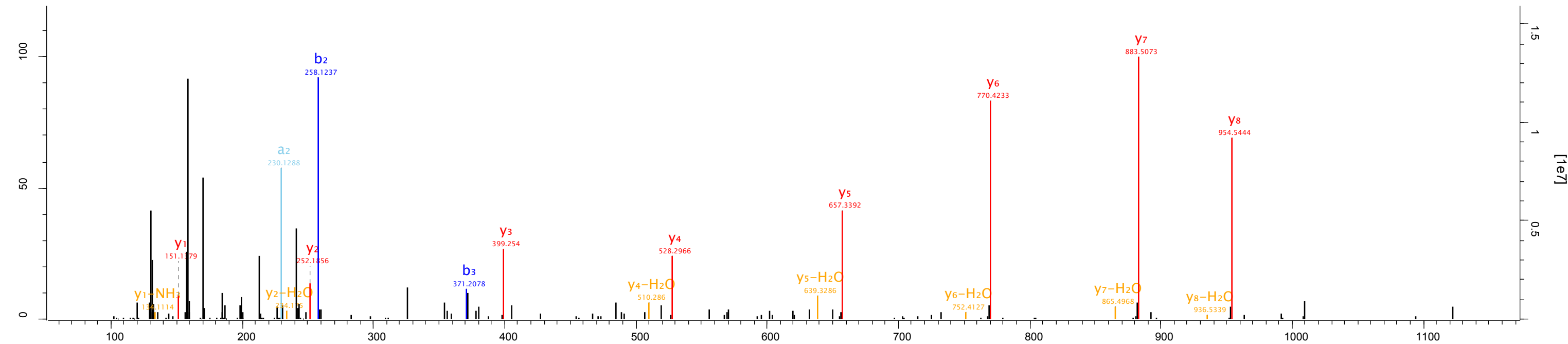
Scan 25838 Method FTMS; HCD Score 71.56 m/z 528.6 Gene names SGK3



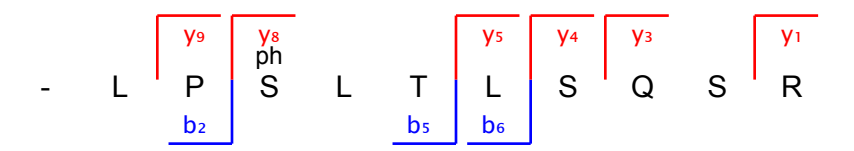
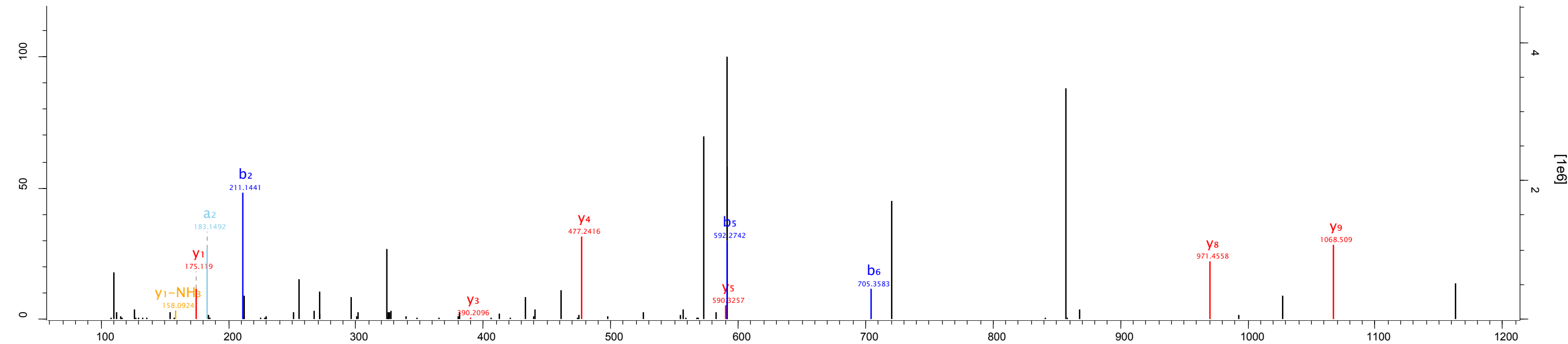
Raw file 20180707_MaS_A375SR_ML_proteome_09 Scan 9288 Method FTMS; HCD Score 46.89 m/z 977.39



Raw file: 20180707_MaS_A375SR_ML_proteome_10
 Scan: 28708 Method: FTMS; HCD Score: 101.65 m/z: 570.82 Gene names: MT-ND2

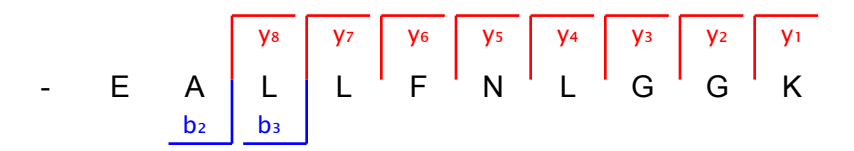
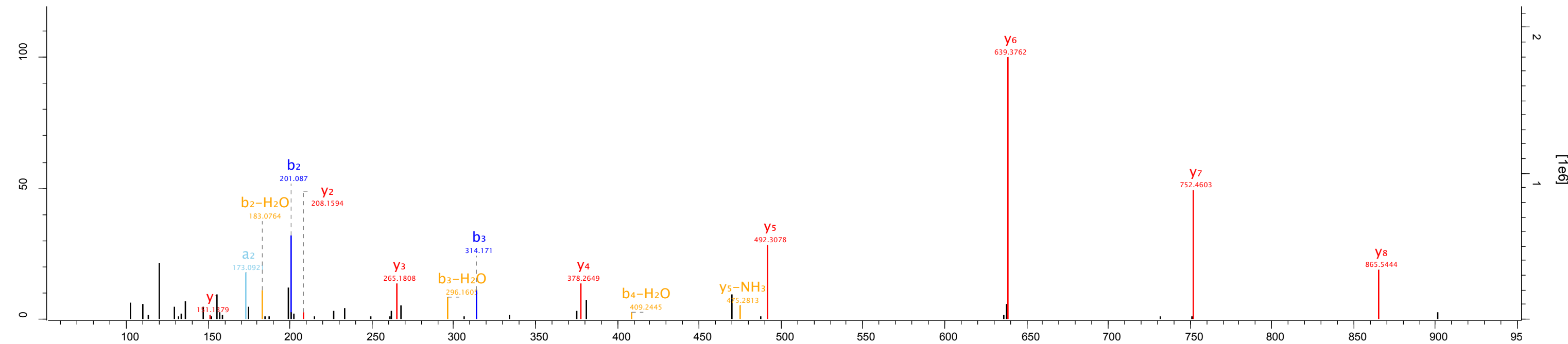


Raw file 20180707_MaS_A375SR_ML_proteome_10 Scan 7588 Method FTMS; HCD Score 41.16 m/z 591.8



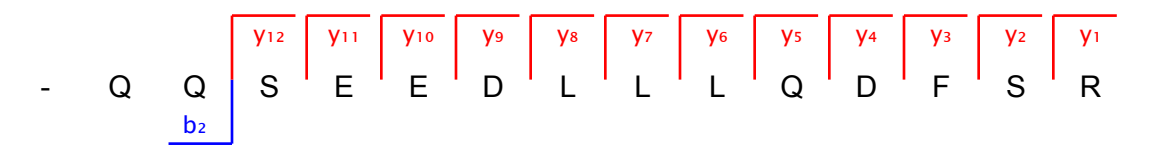
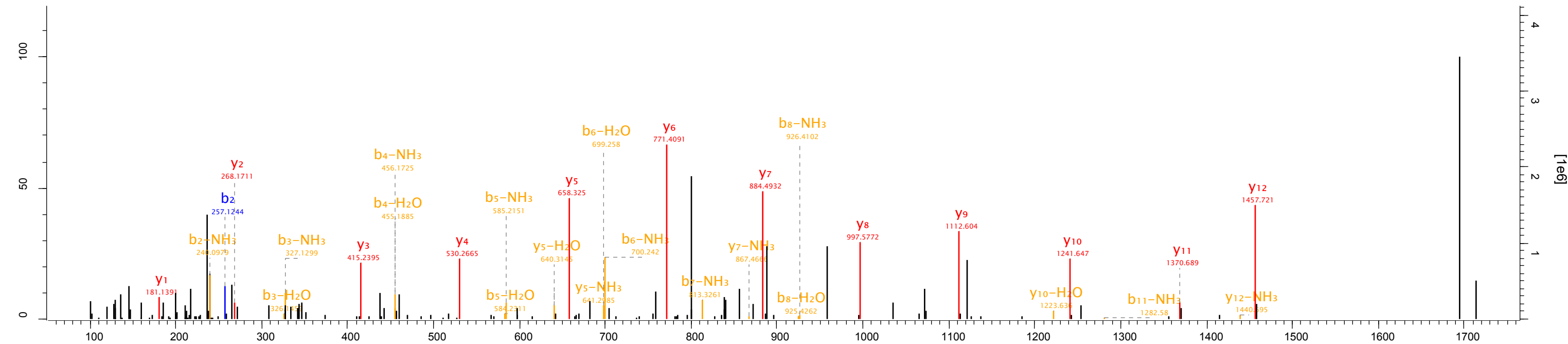
Raw file
20180707_MaS_A375SR_ML_proteome_11

Scan 27988 Method FTMS; HCD Score 70.06 m/z 533.32 Gene names CYB561

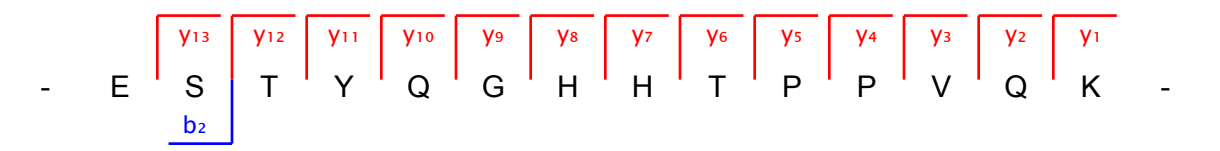
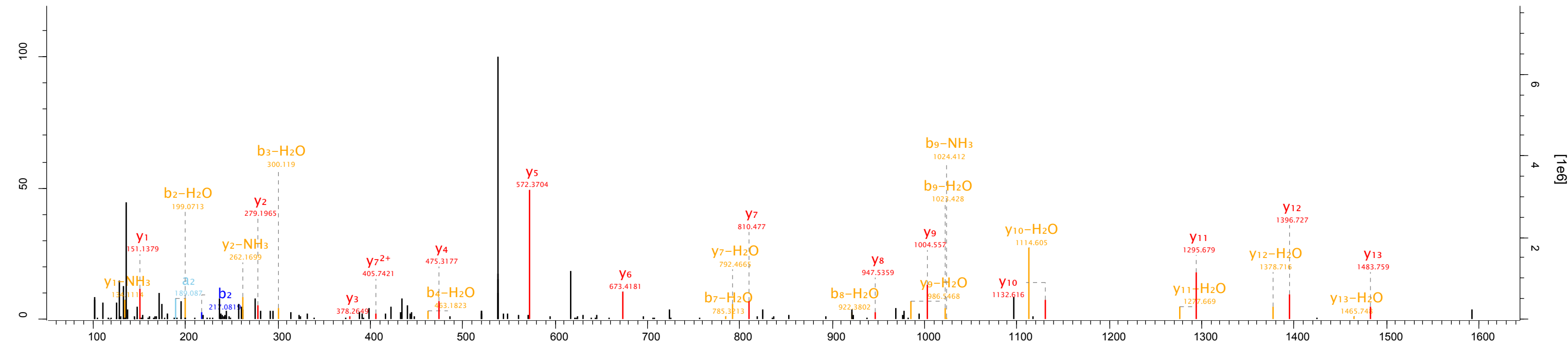


Raw file
20180707_MaS_A375SR_ML_proteome_11

Scan 28698 Method FTMS; HCD Score 65.37 m/z 857.92 Gene names SSR3



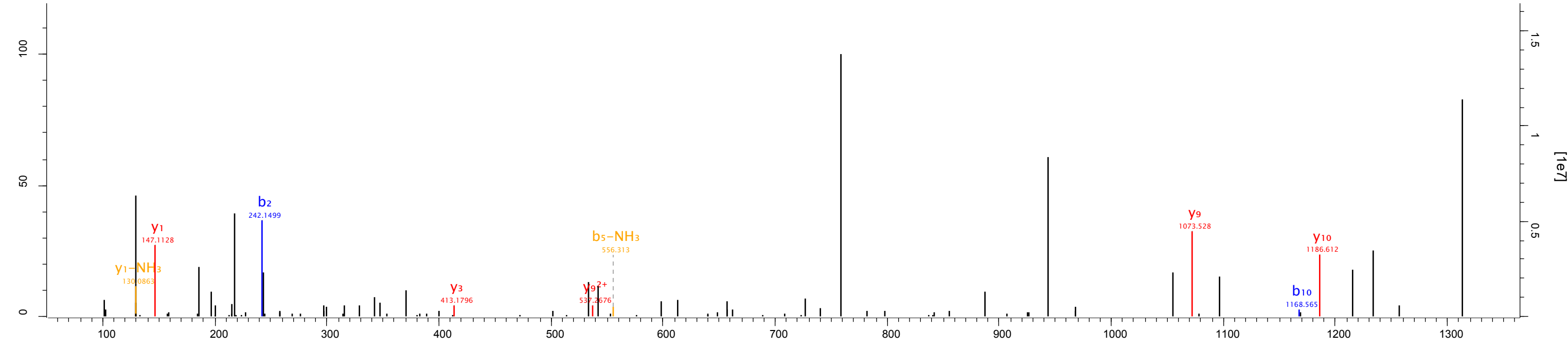
Raw file: 20180707_MaS_A375SR_ML_proteome_11
 Scan: 3308 Method: FTMS; HCD Score: 94.09 m/z: 538.61 Gene names: MT-CO3



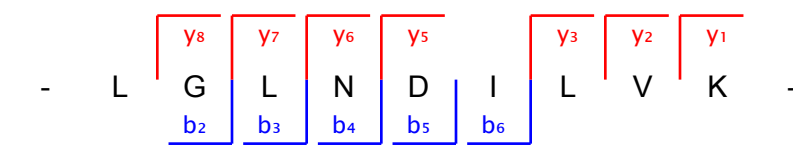
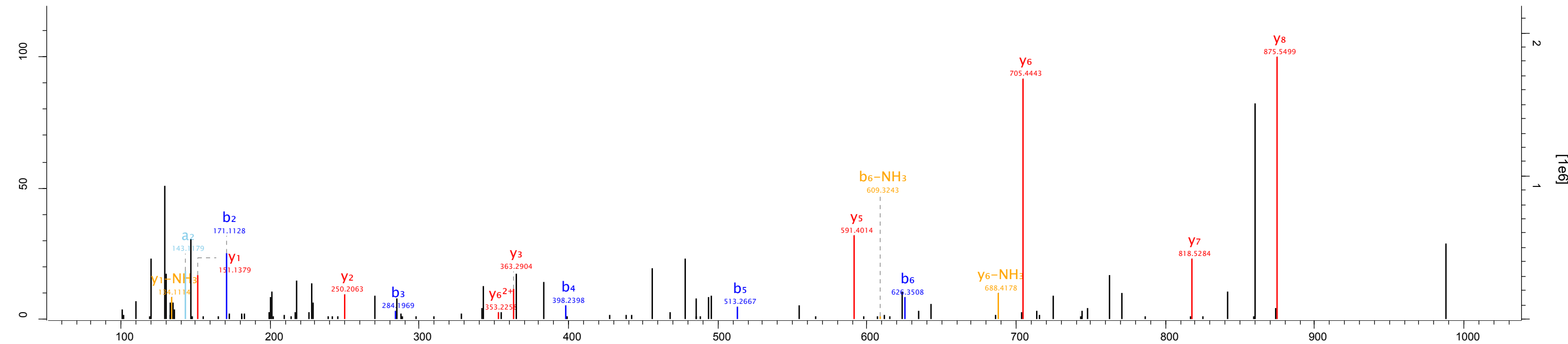
Raw file

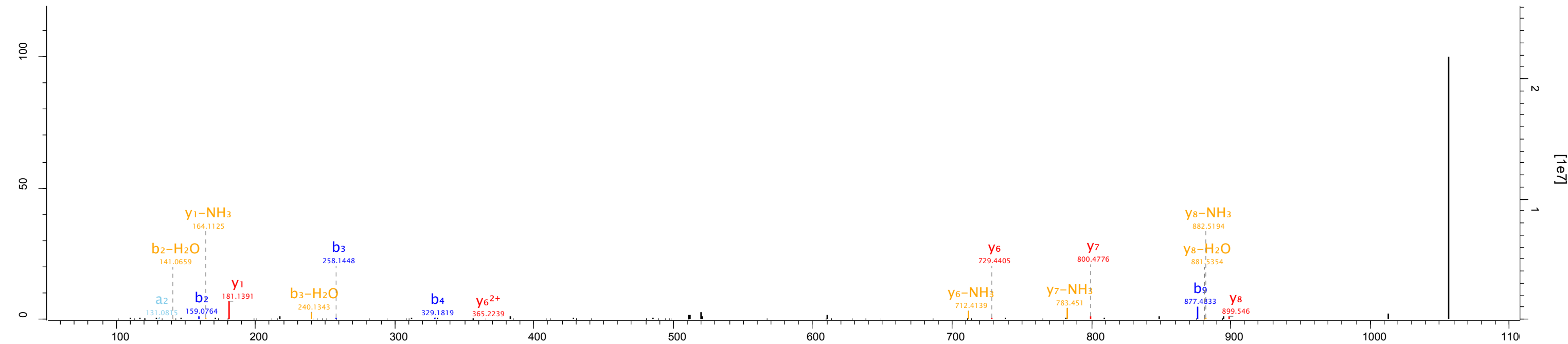
20180707_MaS_A375SR_ML_proteome_12

Scan	Method	Score	m/z
11058	FTMS; HCD	46.84	657.84



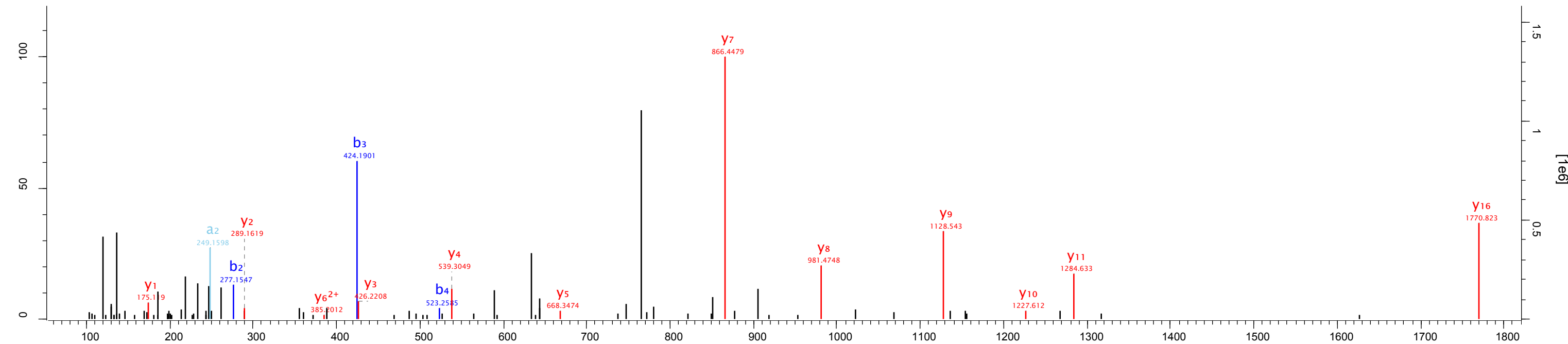
Raw file 20180707_MaS_A375SR_ML_proteome_12 Scan 26468 Method FTMS; HCD Score 70.4 m/z 494.82 Gene names STON2





- A S V A L S G E R R -

Fragmentation mapping:
- b2 (S) b3 (V) b4 (A) b9 (R)
- y8 (V) y7 (A) y6 (L) y1 (R)

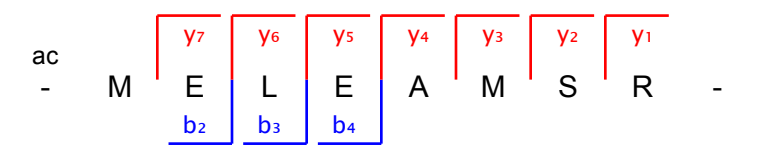
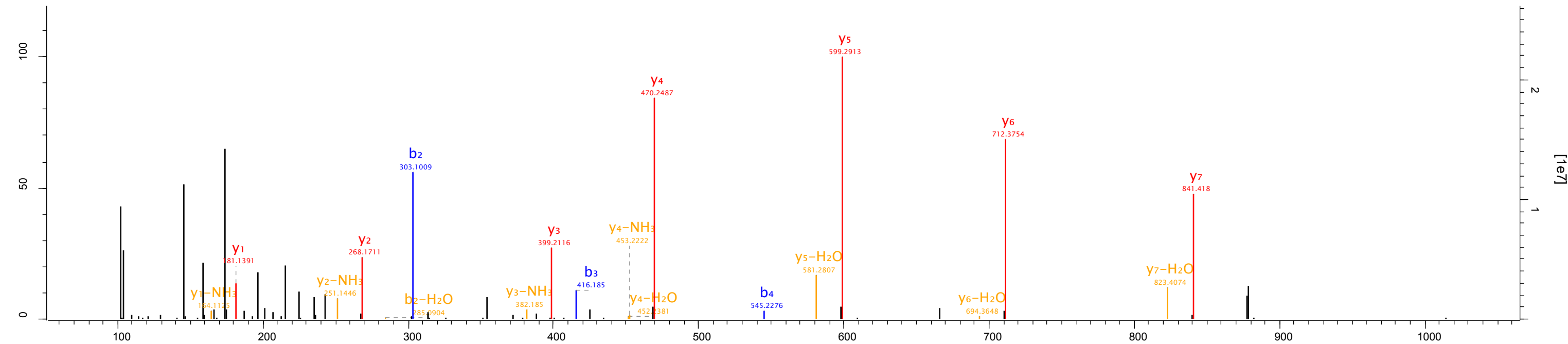


- Y I M^{ox} V P S G N M G V F D P T E I H N R -

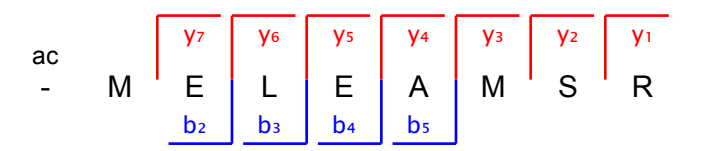
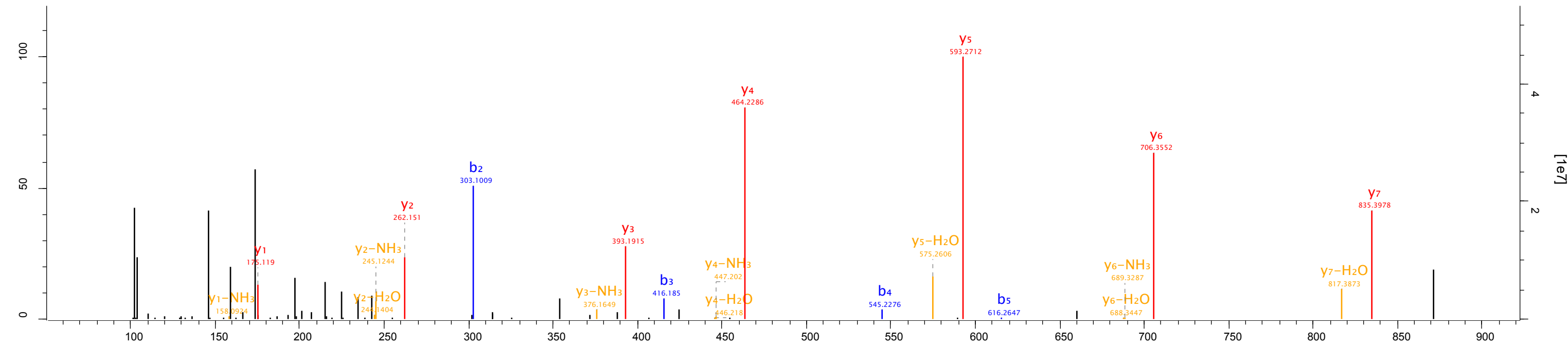
Fragmentation mapping (b and y ions) is shown below the sequence:

- b₂ (I-M)
- b₃ (M-oxM)
- b₄ (M-V)
- y₁₆ (V-P)
- y₁₁ (M-G)
- y₁₀ (G-V)
- y₉ (V-F)
- y₈ (F-D)
- y₇ (D-P)
- y_{6²⁺} (P-T)
- y₅ (T-E)
- y₄ (E-I)
- y₃ (I-H)
- y₂ (H-N)
- y₁ (N-R)

Raw file: 20180707_MaS_A375SR_ML_proteome_14
 Scan: 24738 Method: FTMS; HCD Score: 107.69 m/z: 507.74 Gene names: TMEM258

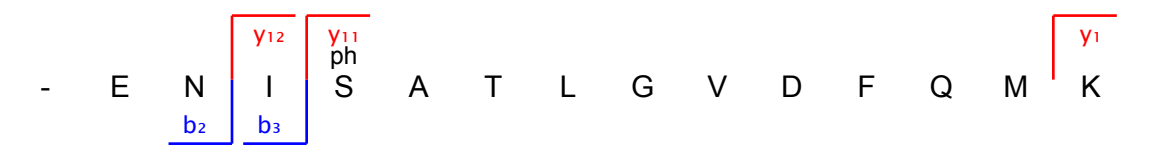
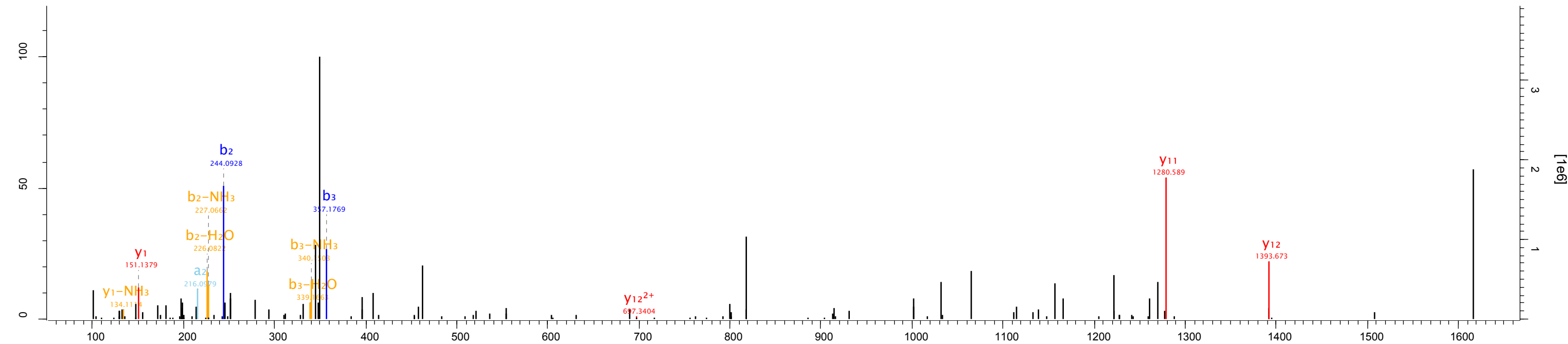


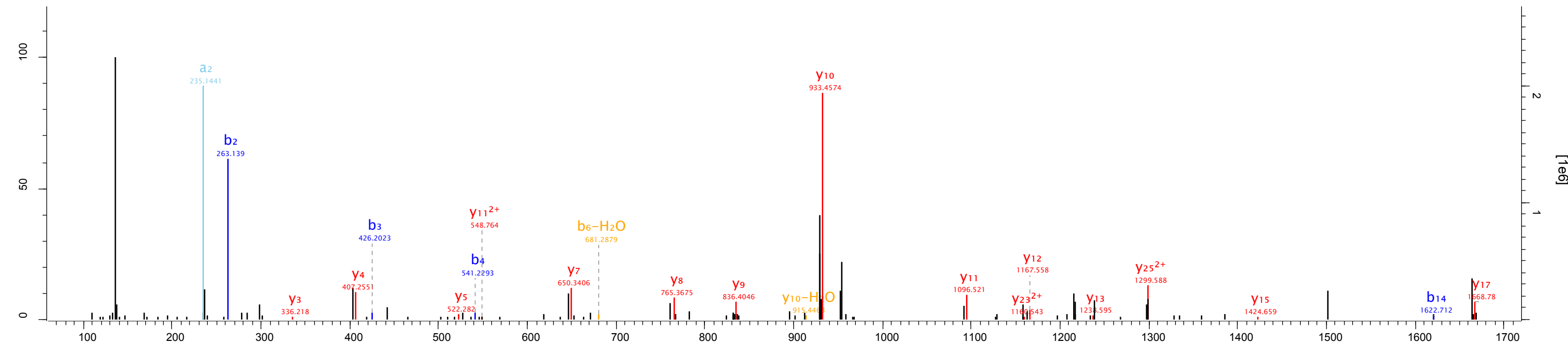
Raw file: 20180707_MaS_A375SR_ML_proteome_14
 Scan: 24758 Method: FTMS; HCD Score: 128.38 m/z: 504.73 Gene names: TMEM258



Raw file
20180707_MaS_A375SR_ML_proteome_16

Scan 16038 Method FTMS; HCD Score 53.45 m/z 818.88 Gene names RASEF





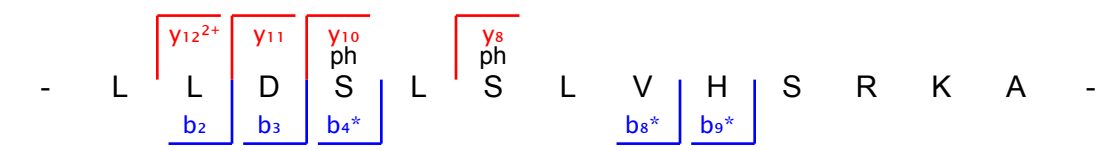
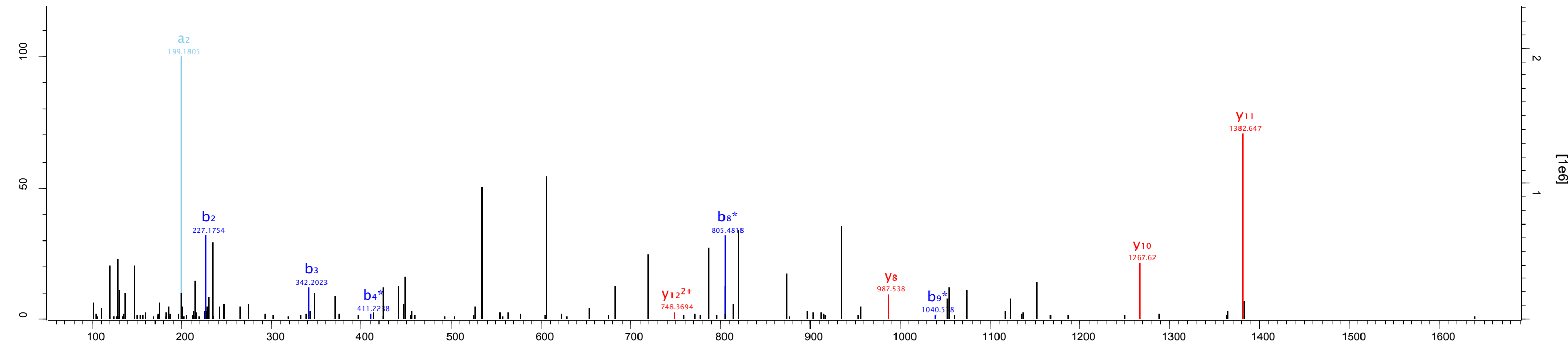
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Fragmentation labels (b and y ions) are shown below the sequence:

- b₂ (under Y)
- b₃ (under Y)
- b₄ (under D)
- b₁₄ (under E)
- y₃ (under G)
- y₄ (under D)
- y₅ (under A)
- y₇ (under G)
- y₈ (under A)
- y₉ (under Y)
- y₁₀ (under P)
- y₁₁ (under A)
- y₁₂ (under A)
- y₁₃ (under A)
- y₁₅ (under G)
- y₁₇ (under F)
- y_{23²⁺} (under Y)
- y_{25²⁺} (under Y)

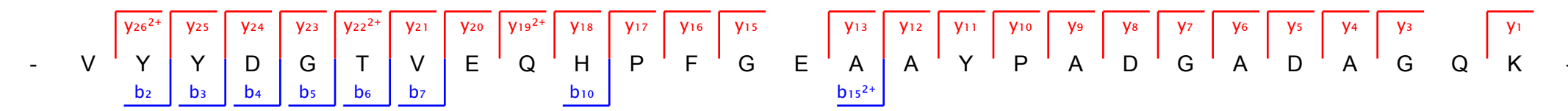
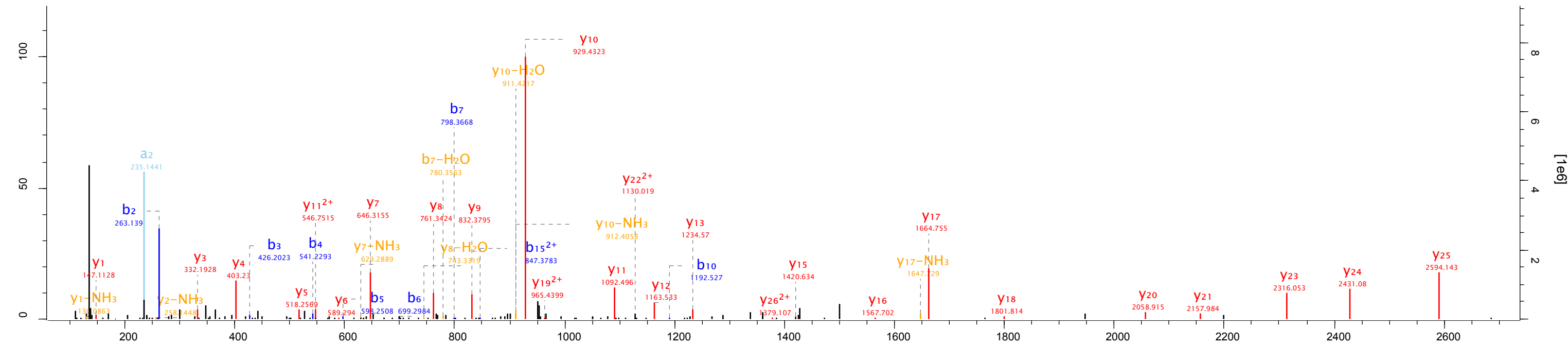
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20180707_MaS_A375SR_ML_proteome_17

Scan: 28018
Method: FTMS; HCD
Score: 50.35
m/z: 805.41
Gene names: IQCK

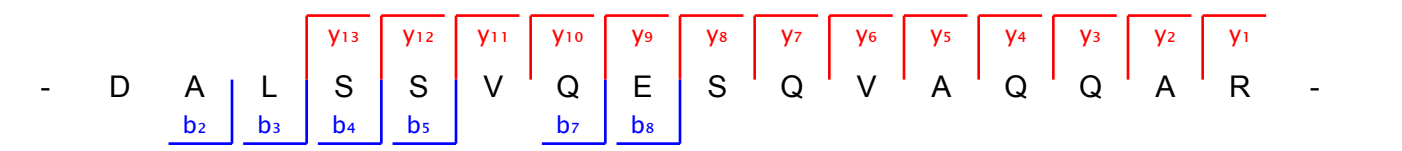
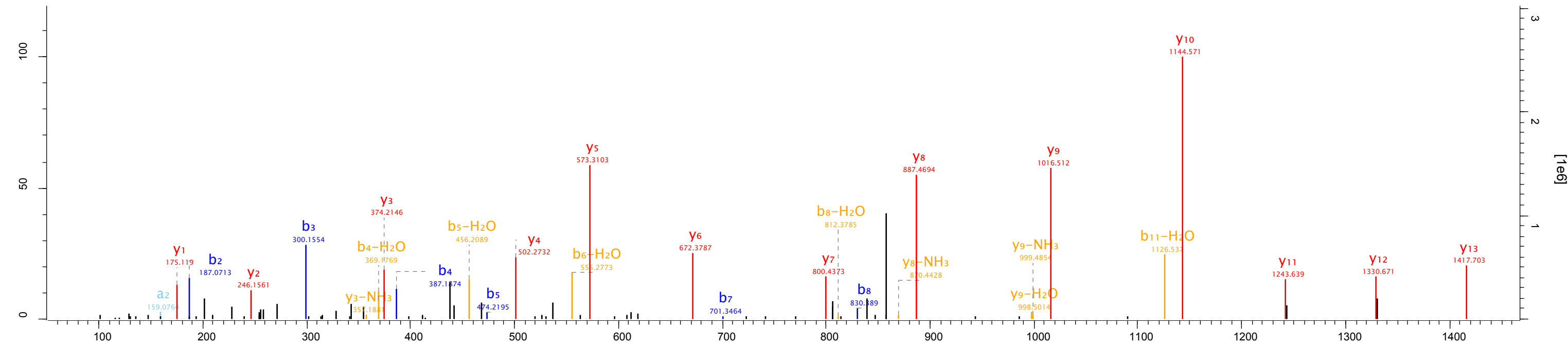


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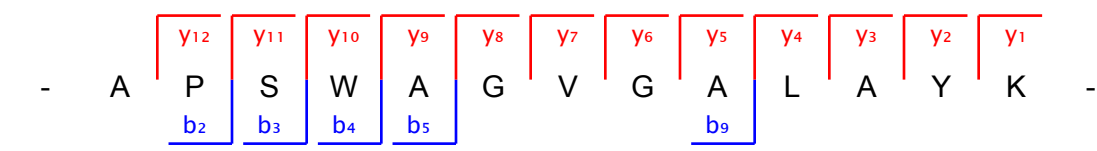
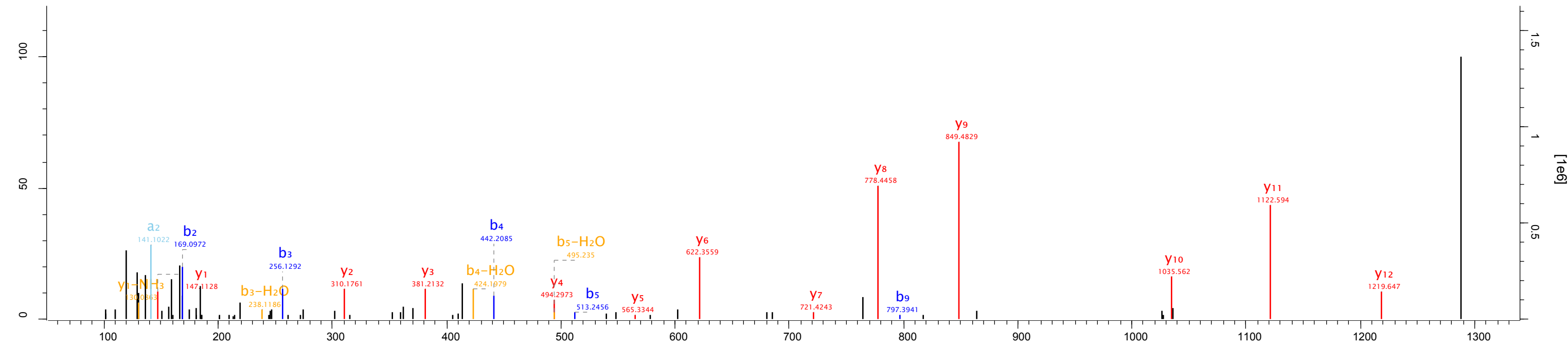
Scan 18448 Method FTMS; HCD Score 110.89 m/z 953.1 Gene names C6orf120



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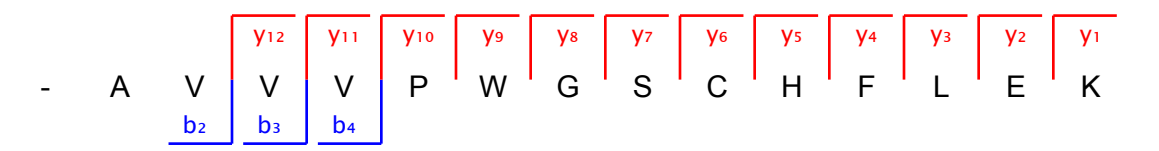
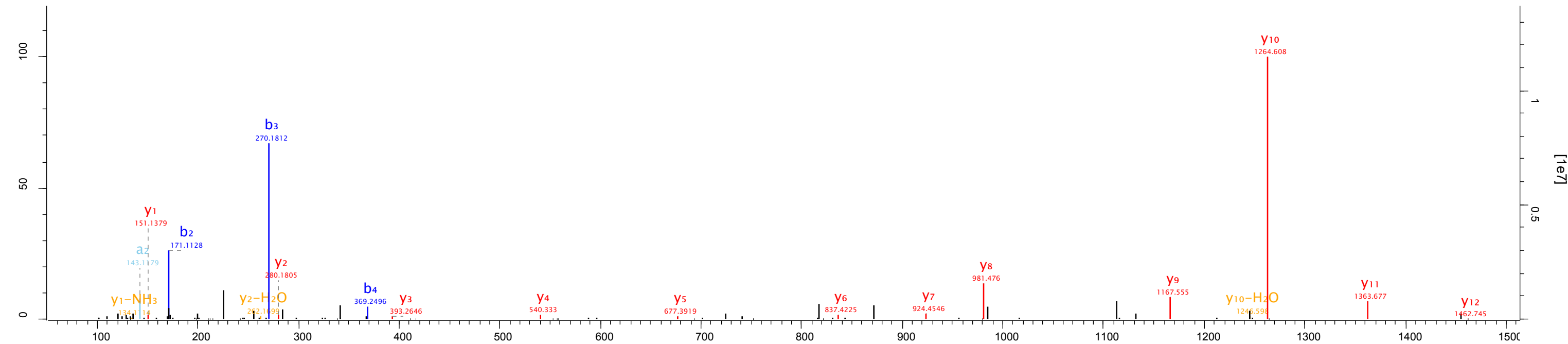


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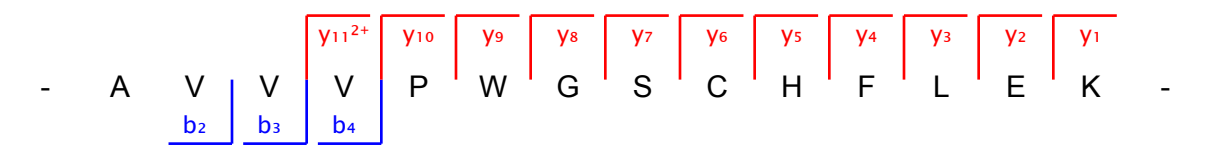
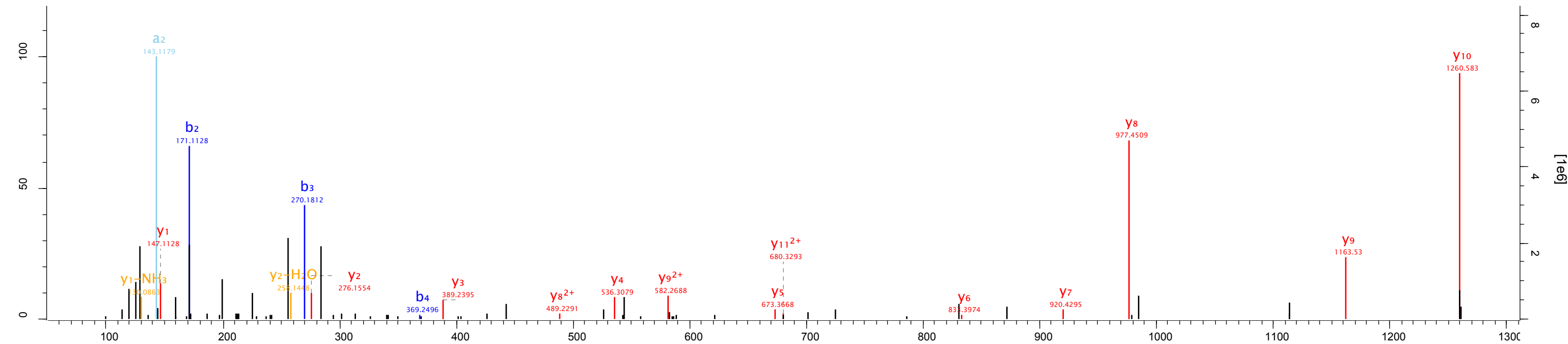


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Scan 24758 Method FTMS; HCD Score 74.79 m/z 817.43 Gene names SPPL2A

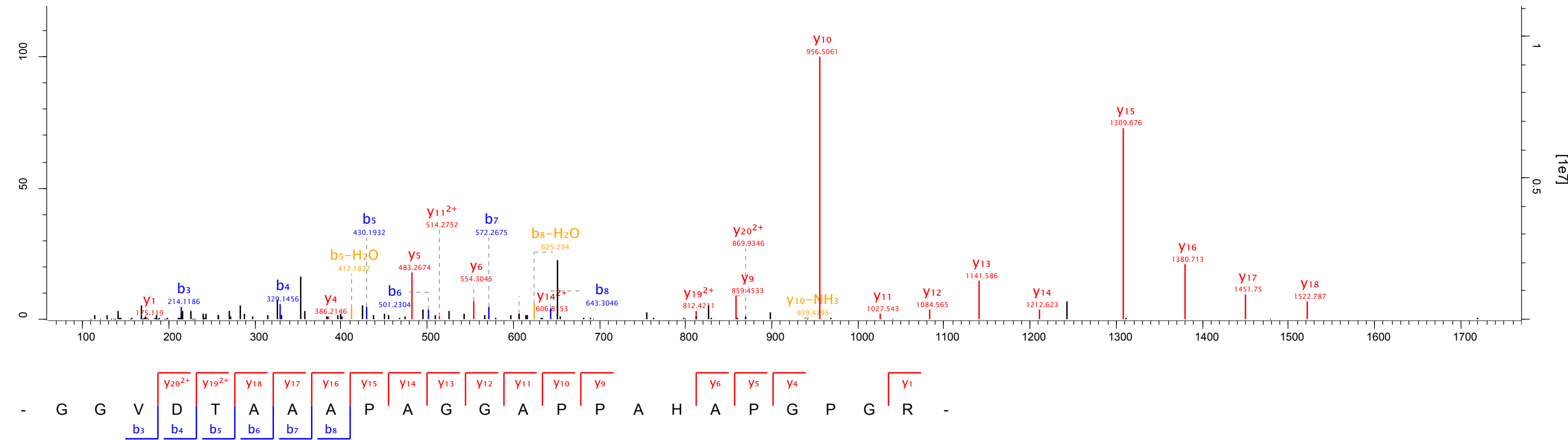


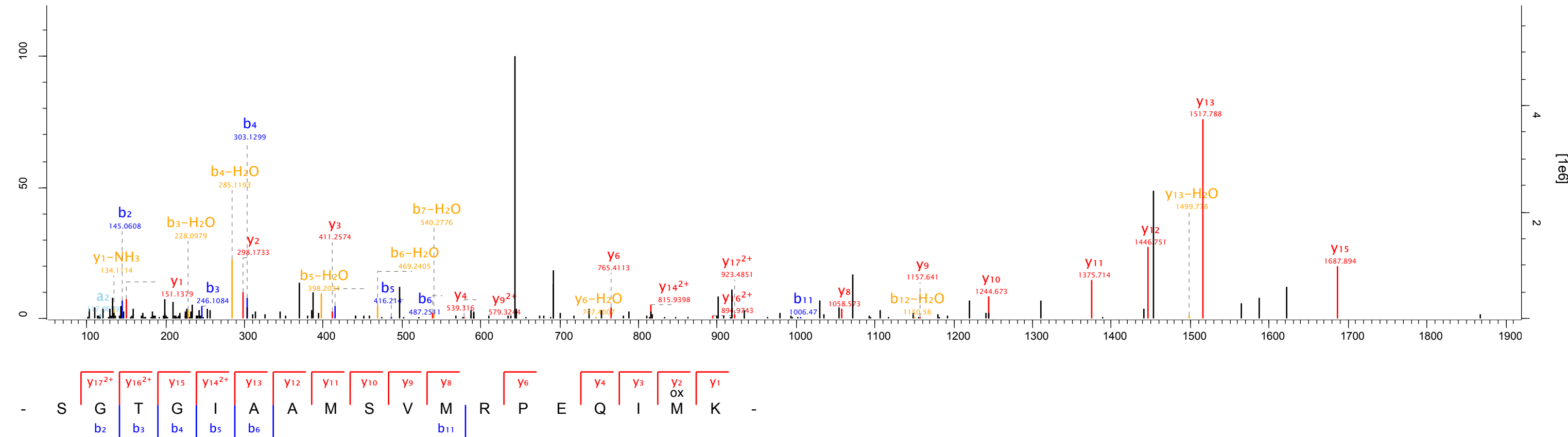
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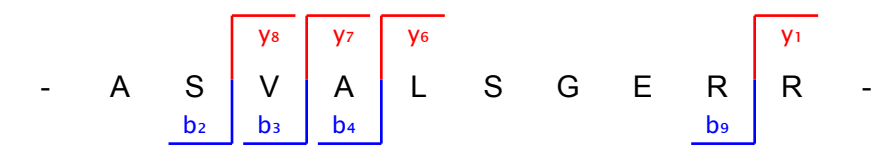
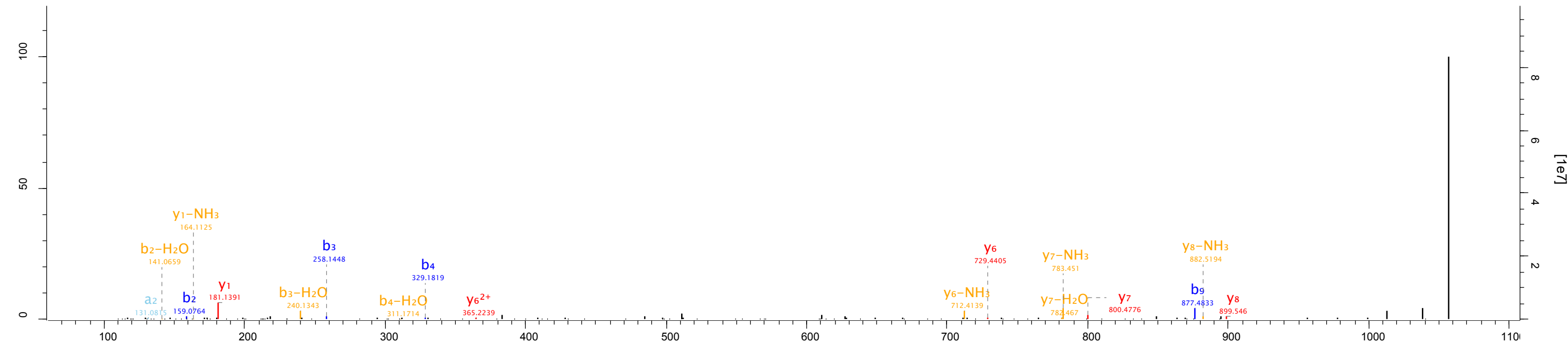
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Scan Method Score m/z Gene names
8188 FTMS; HCD 72.59 651.66 LAGE3

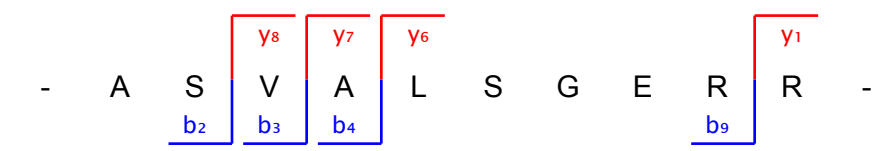
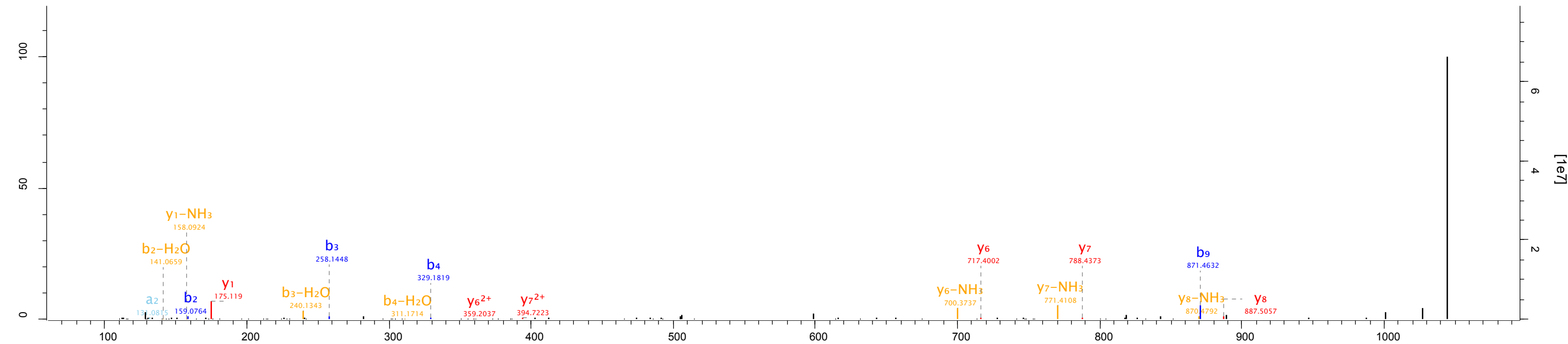




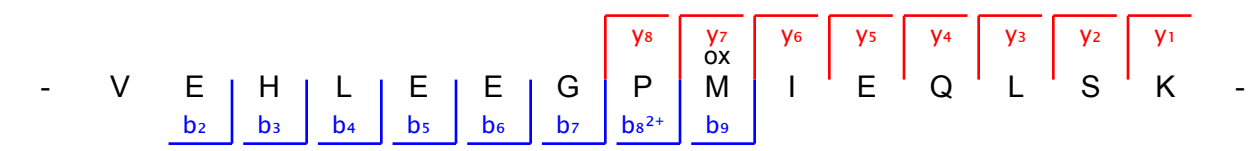
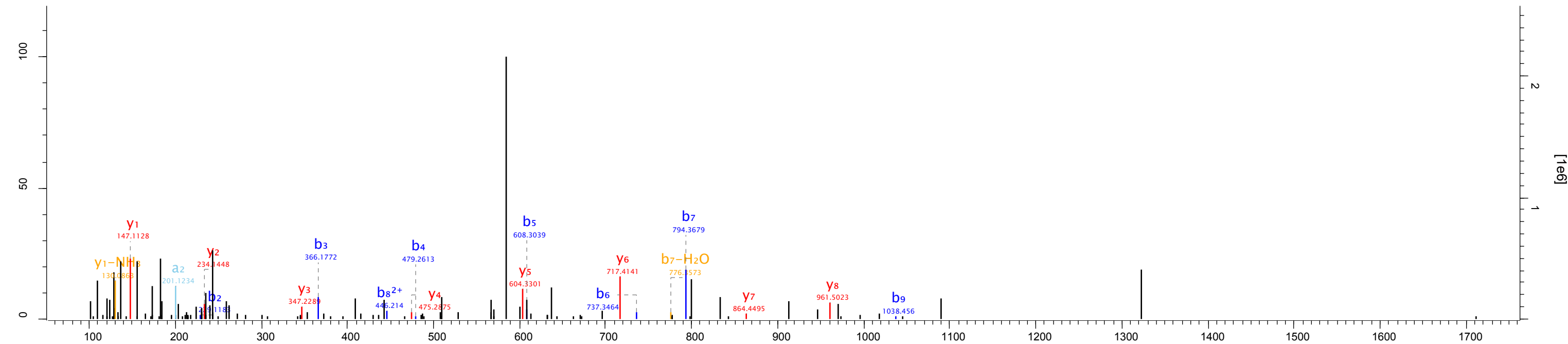
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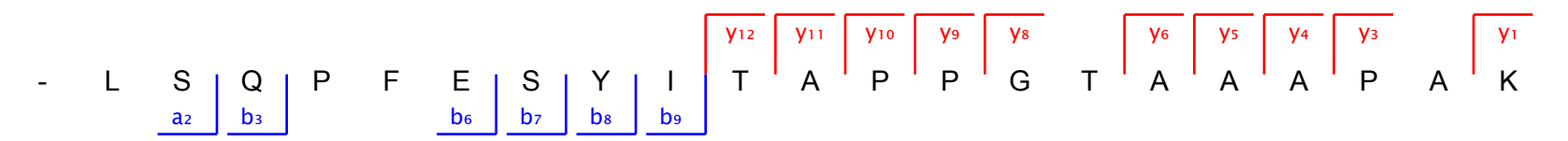
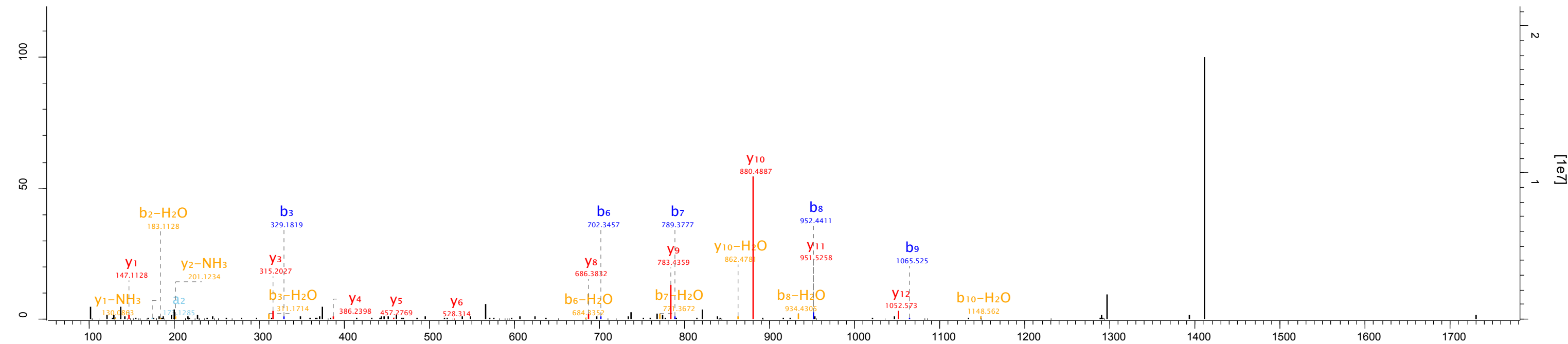


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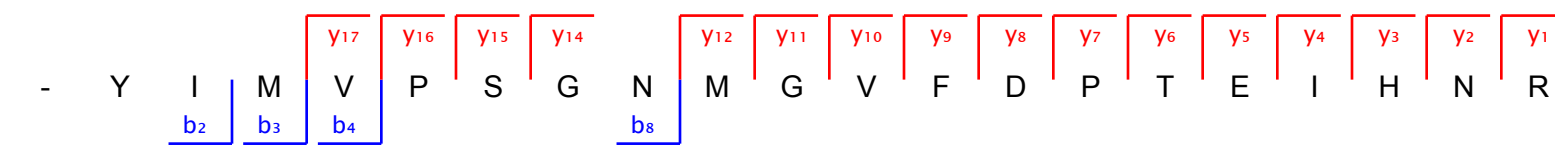
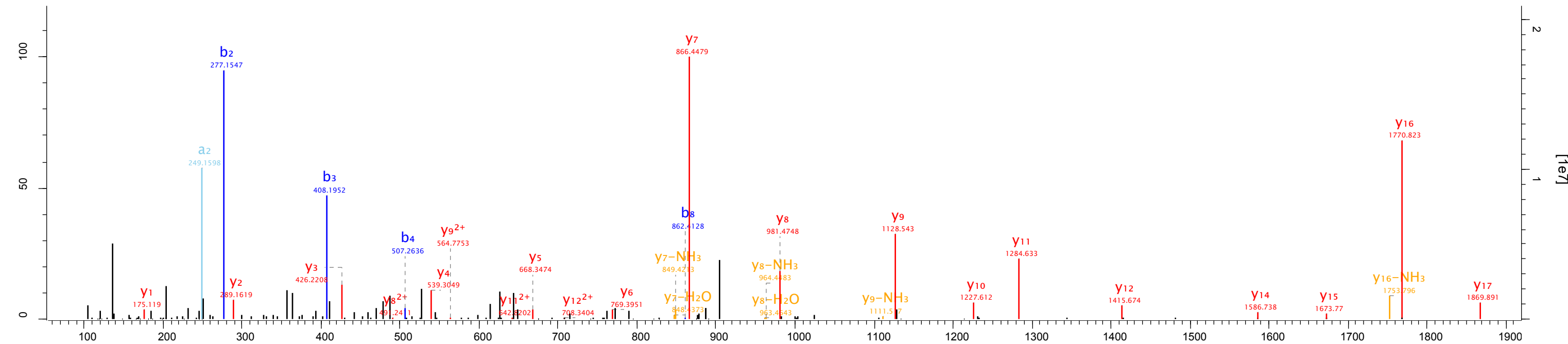
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Scan 25308 Method FTMS; HCD Score 32.24 m/z 706.7 Gene names TMEM261



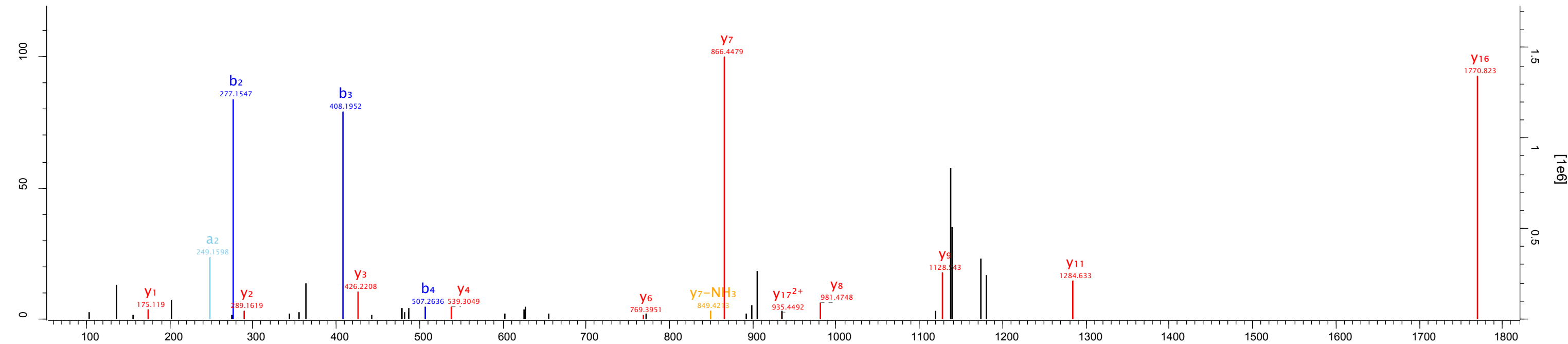
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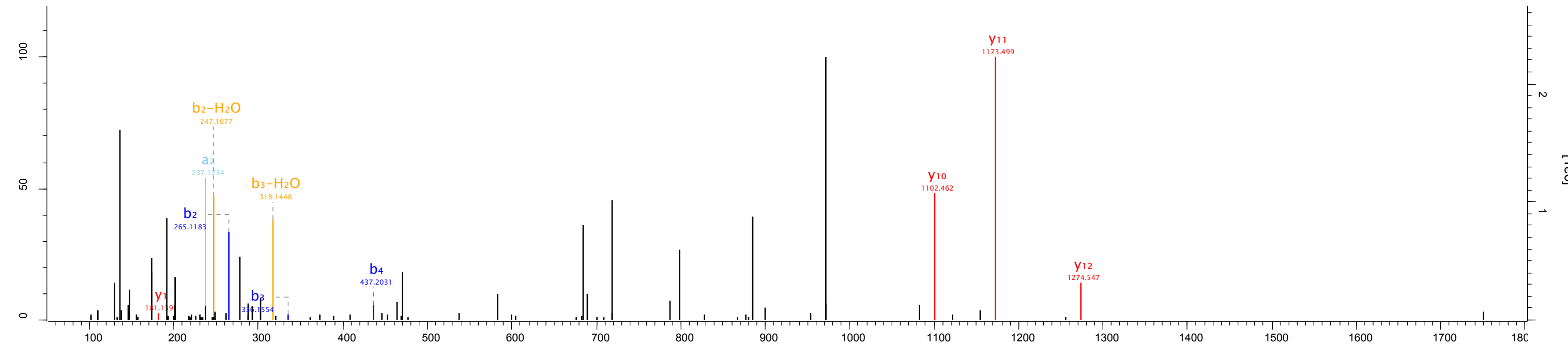


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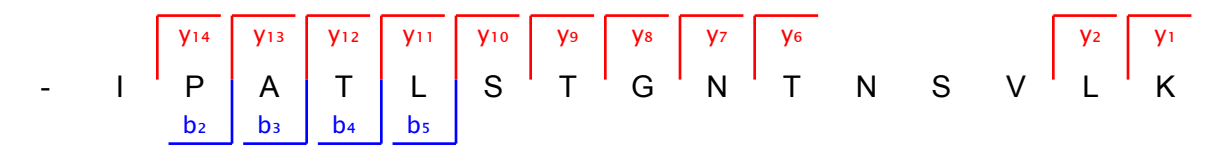
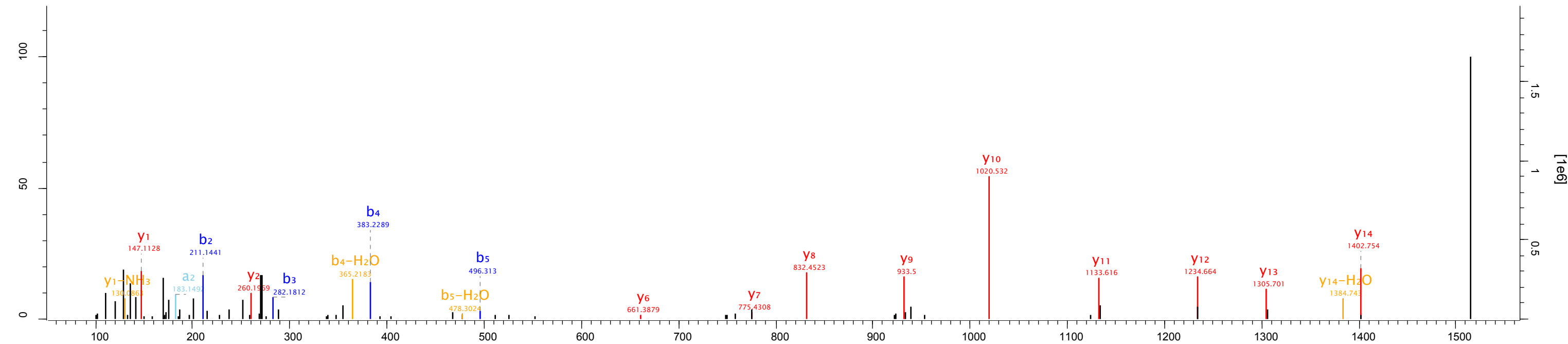
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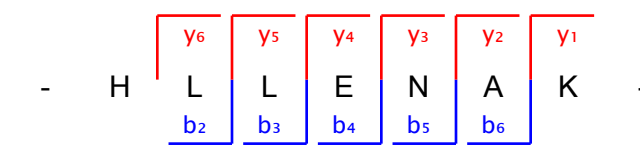
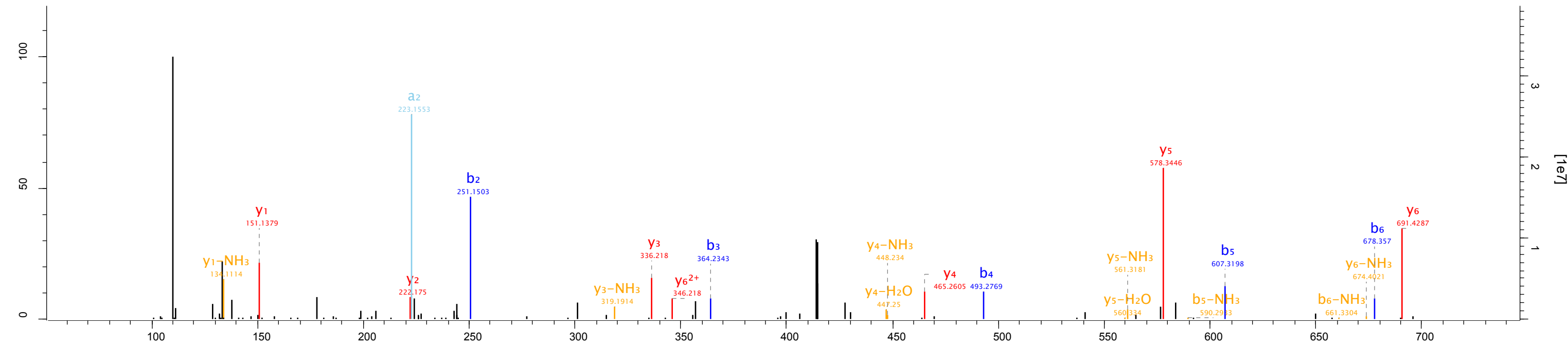
b₂
b₃
b₄

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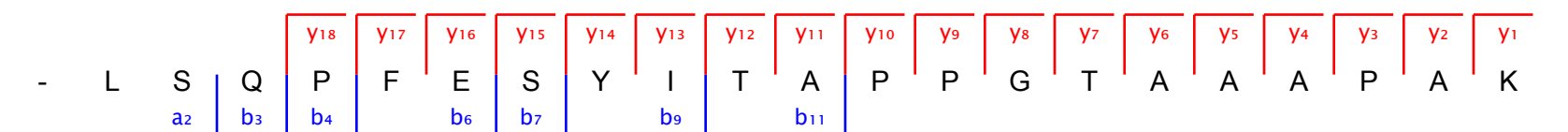
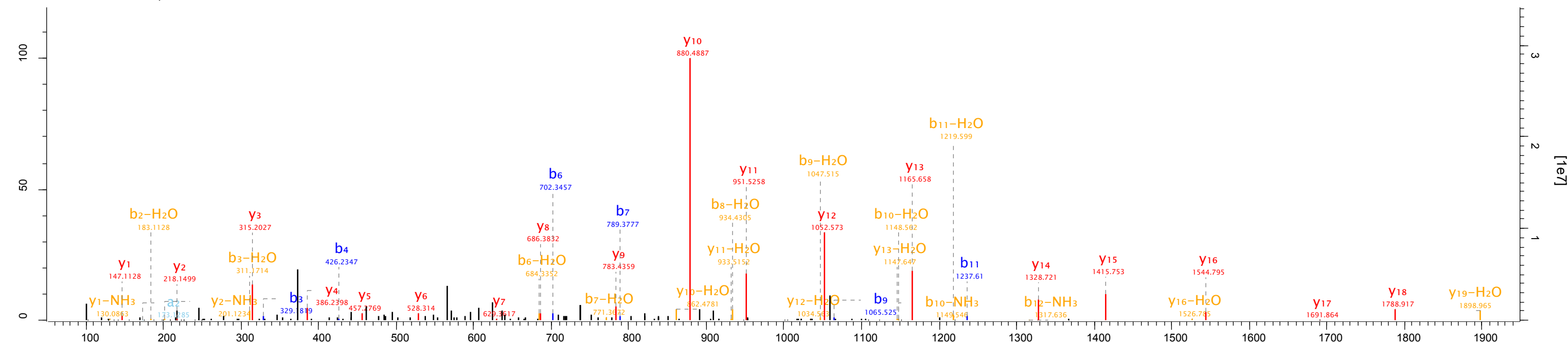
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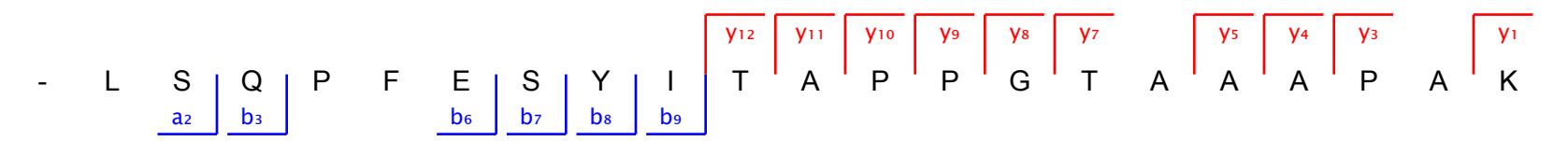
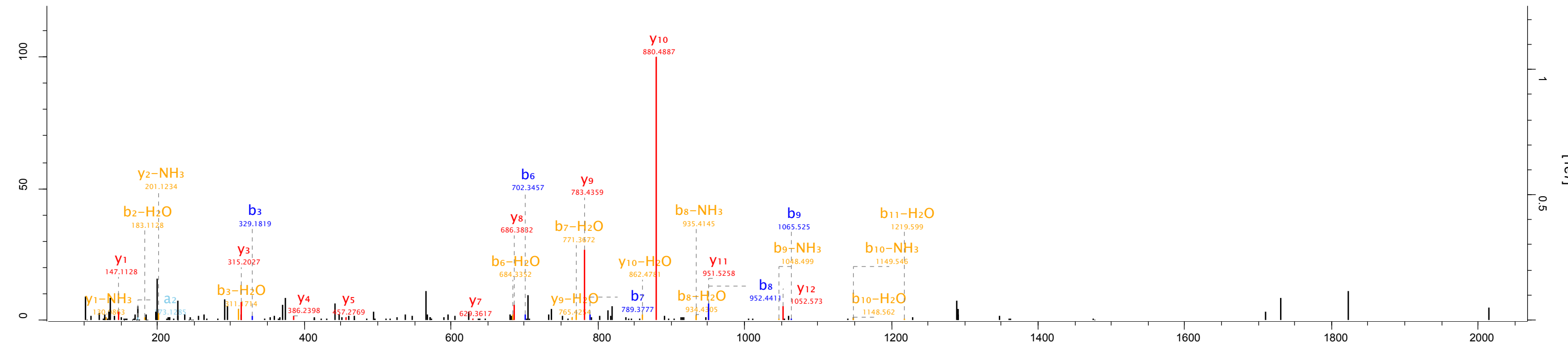


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Scan 24918 Method FTMS; HCD Score 118.36 m/z 1059.55 Gene names TMEM261

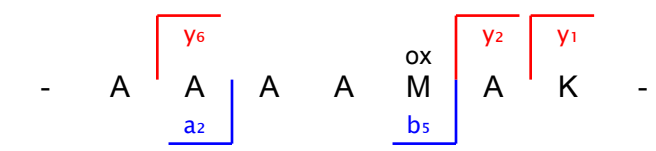
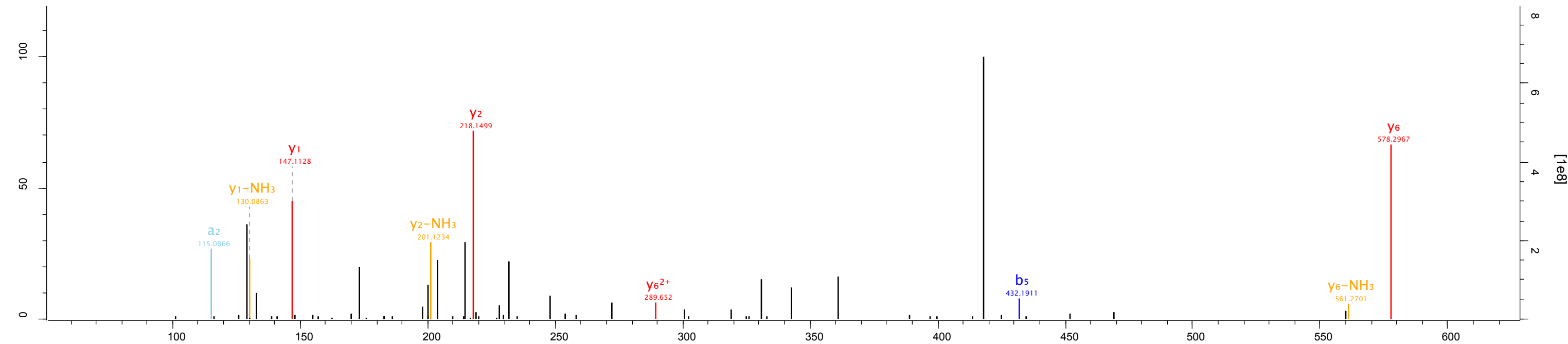


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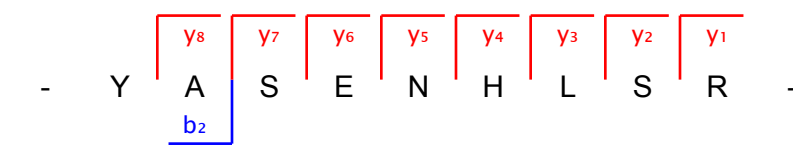
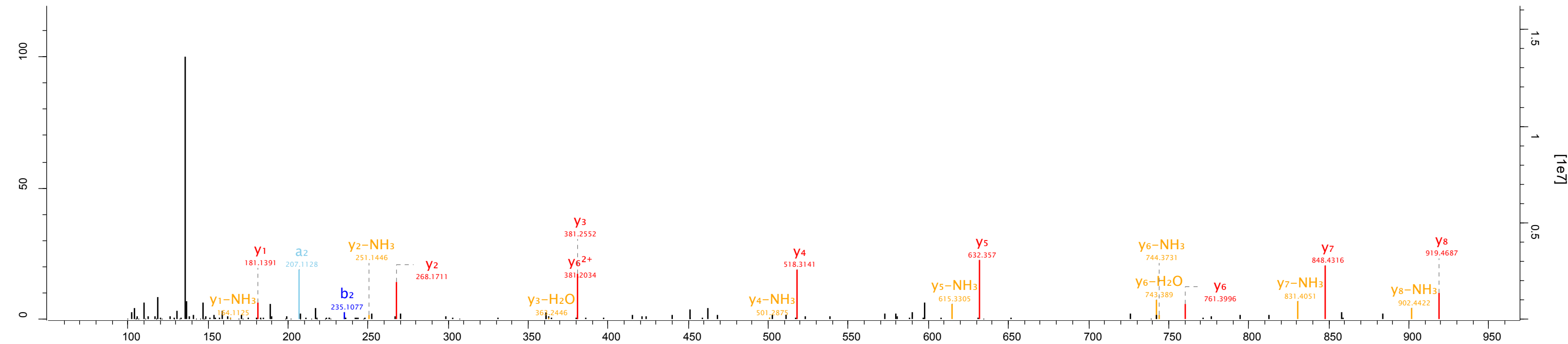


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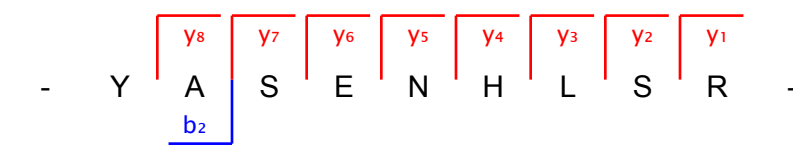
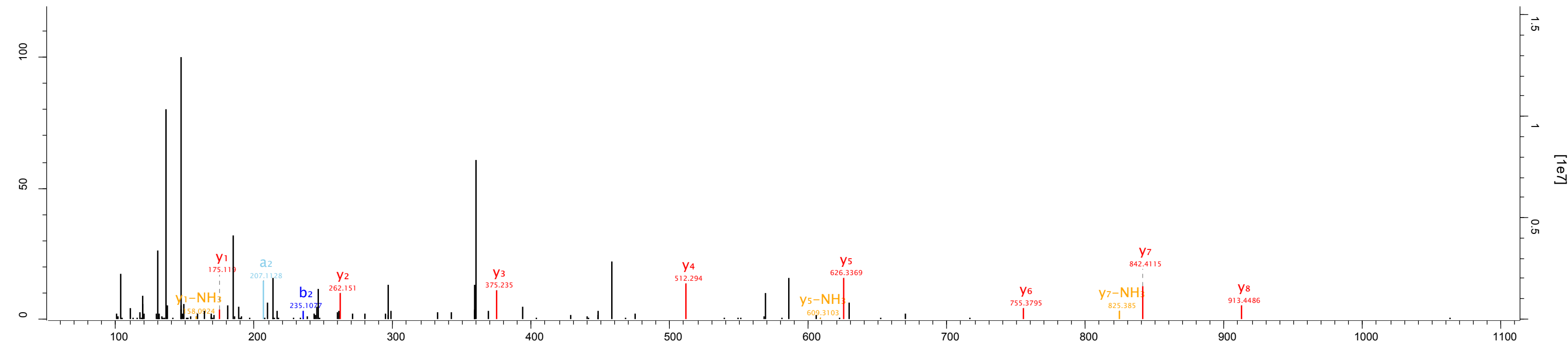


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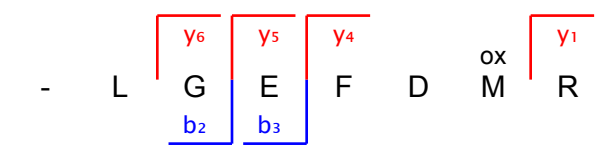
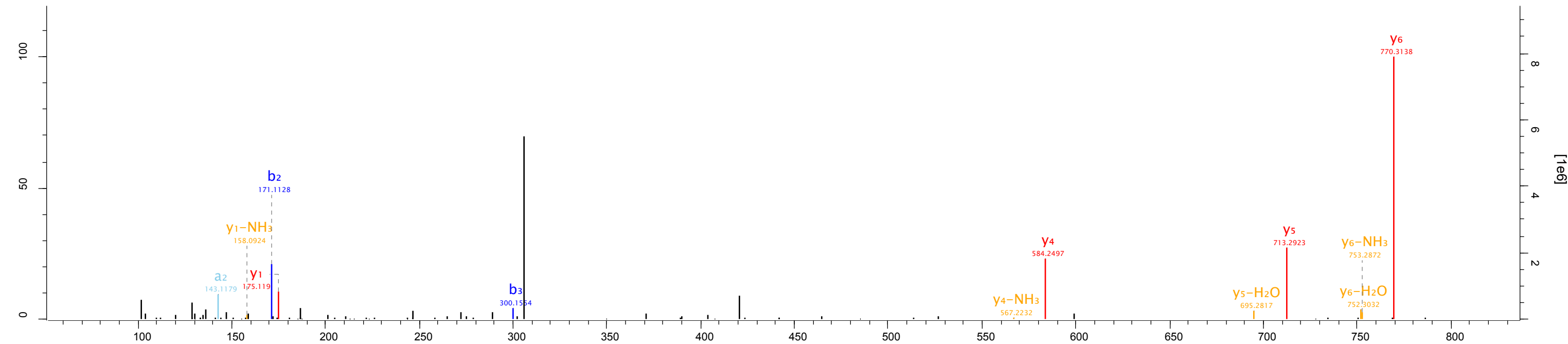


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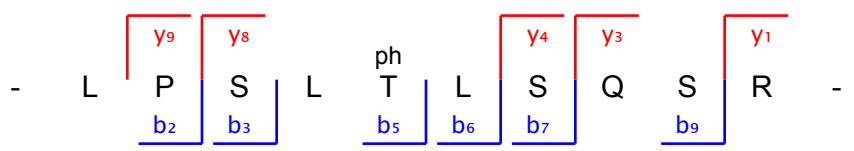
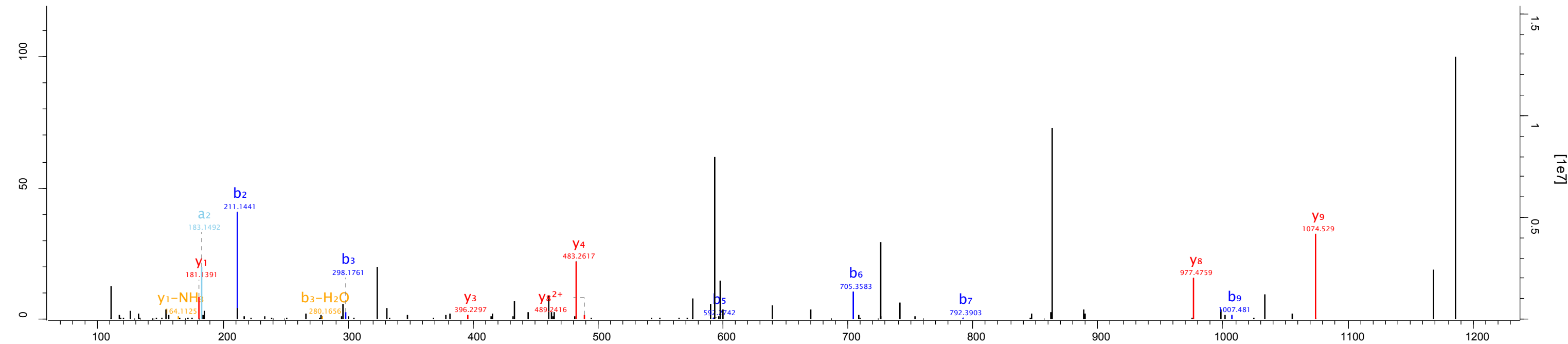
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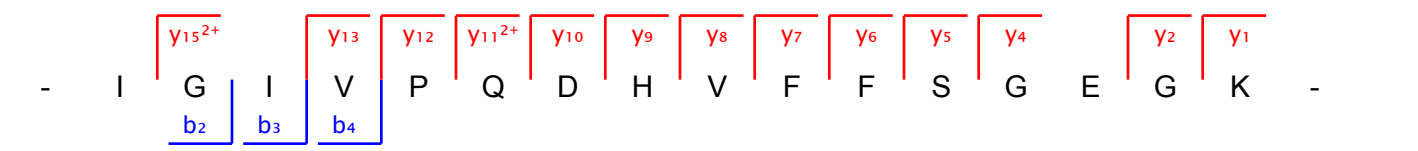
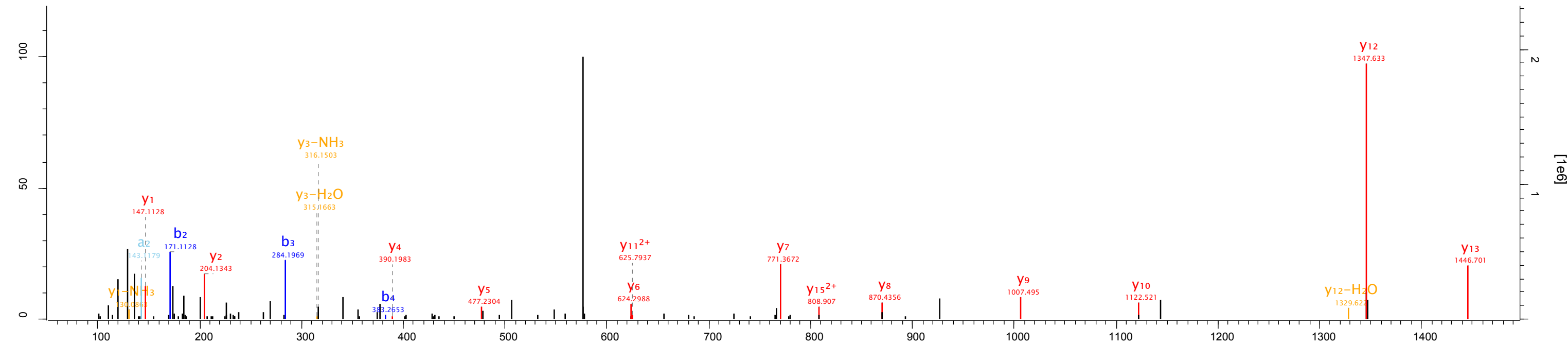
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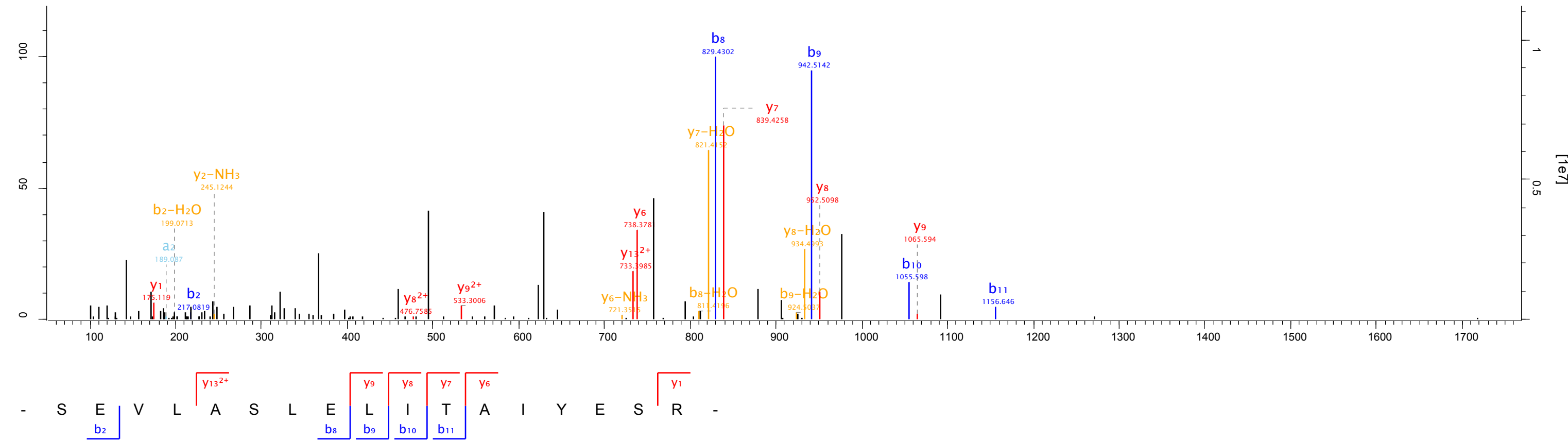


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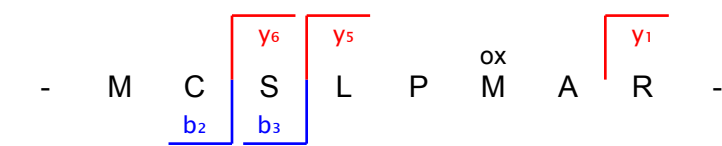
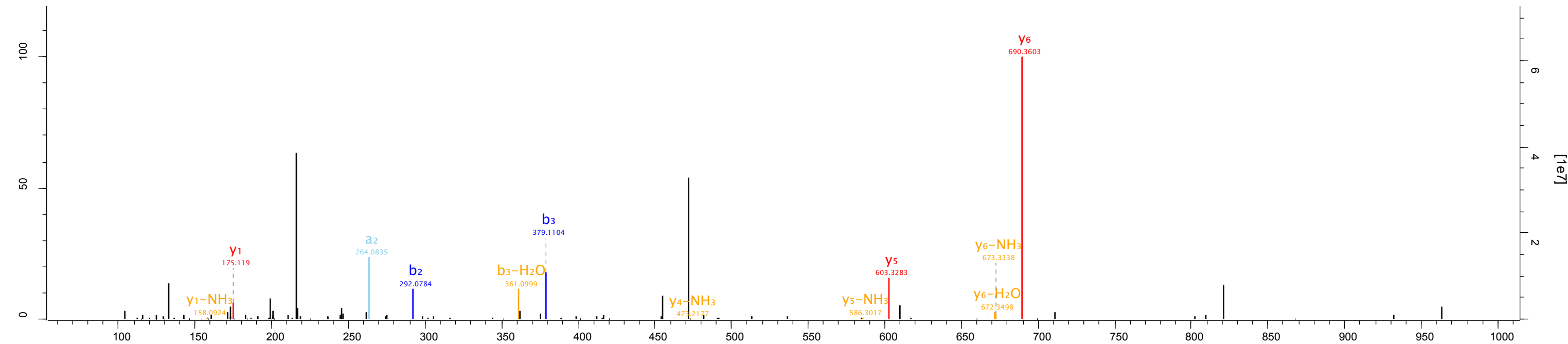




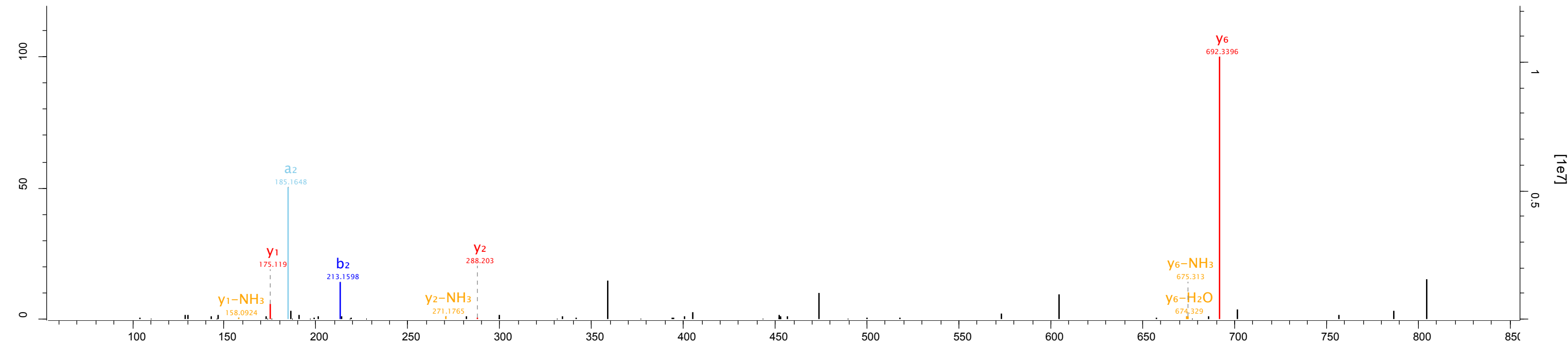
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20180707_MaS_A375SR_ML_proteome_2_09

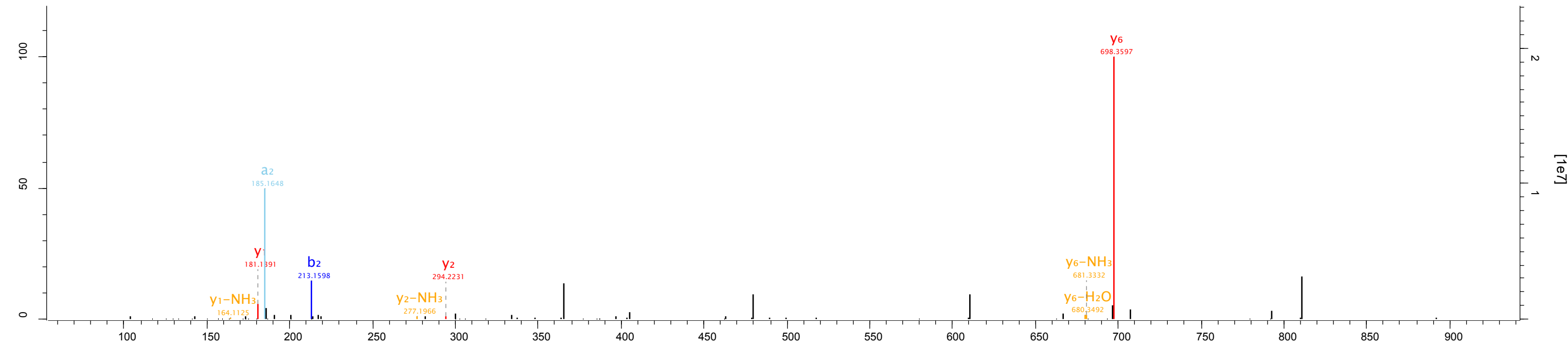
Scan	Method	Score	m/z	Gene names
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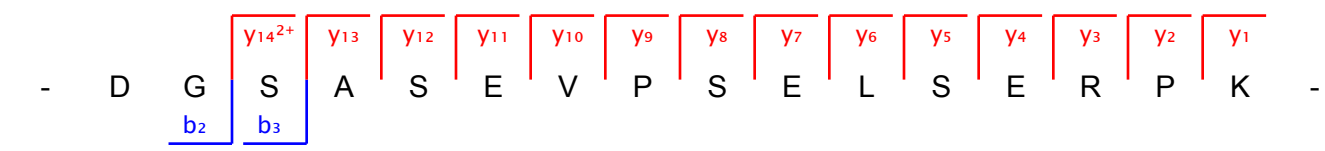
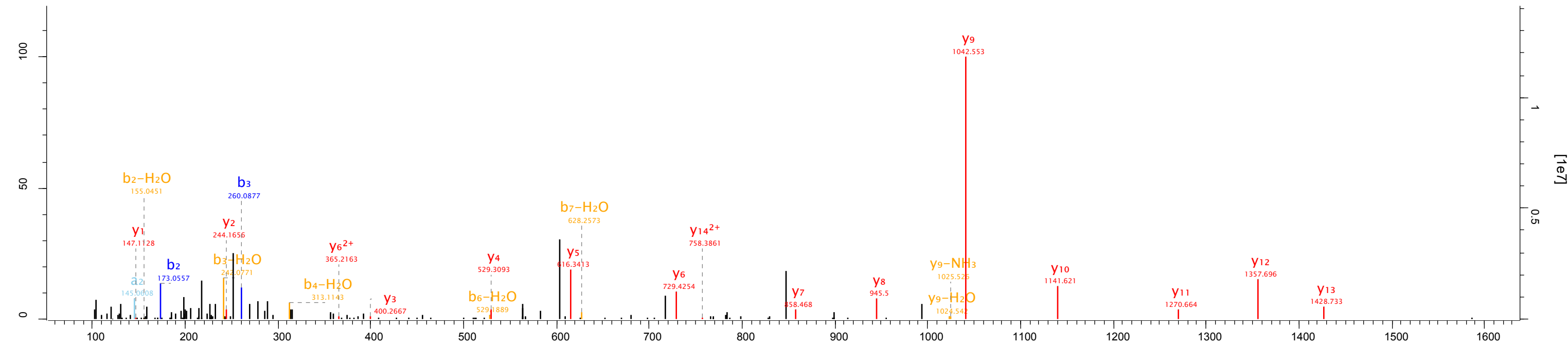
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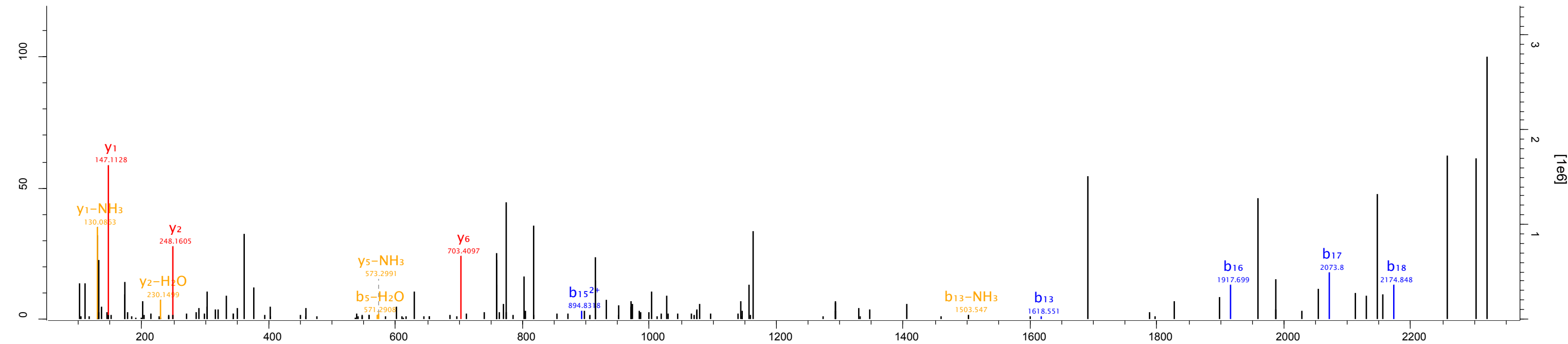
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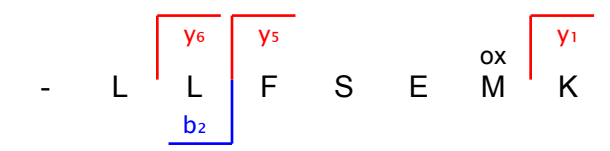
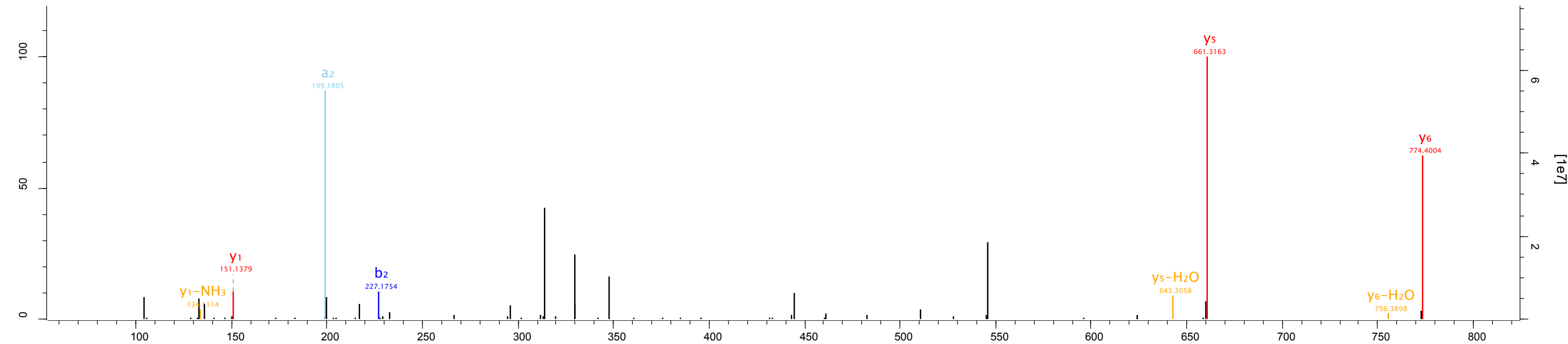


ac - ox M S A L K Q S T S E A S V L G E R T K -

Fragmentation mapping: b13 (V), b15 2+ (L), b16 (G), b17 (E), b18 (R), y6 (L), y2 (T), y1 (K)

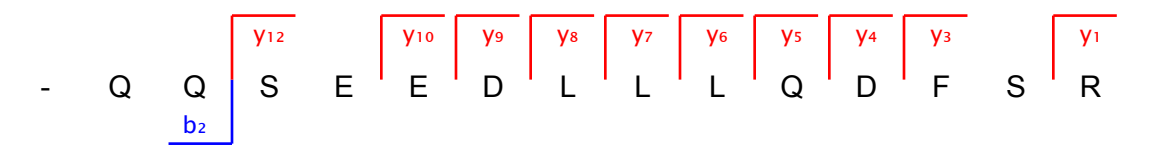
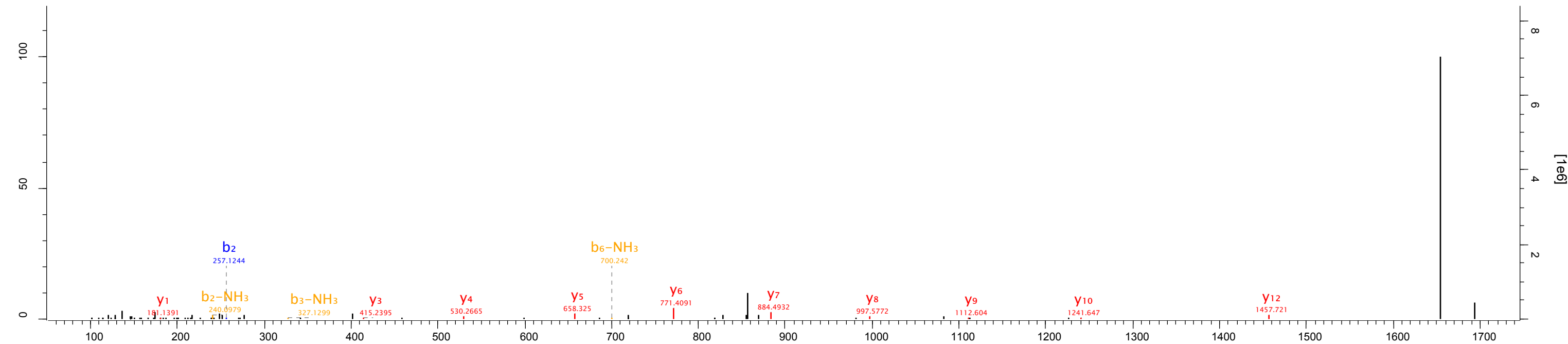
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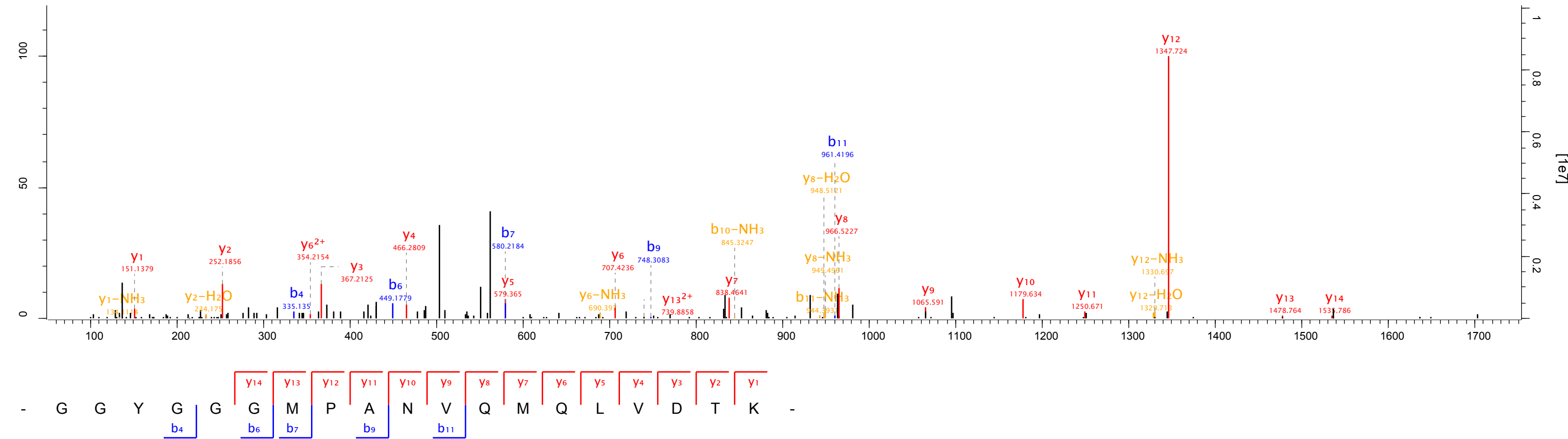
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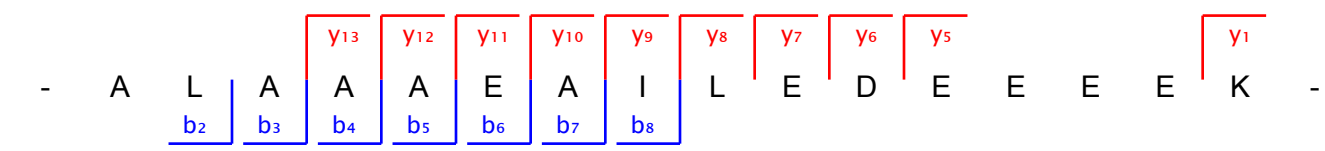
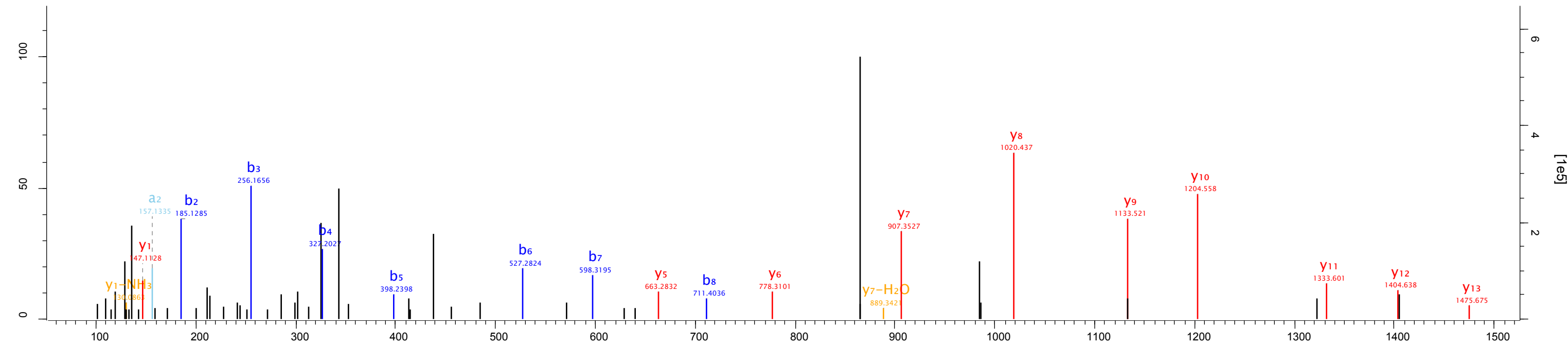
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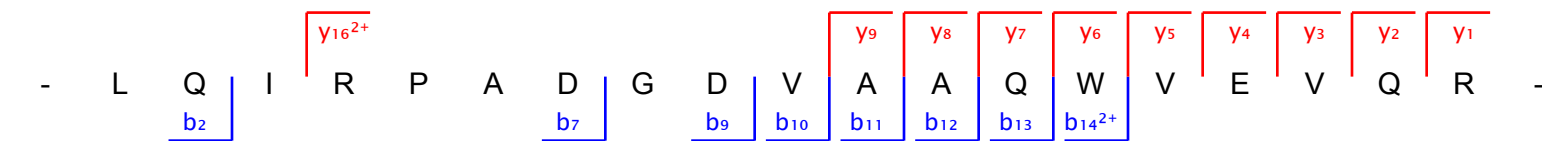
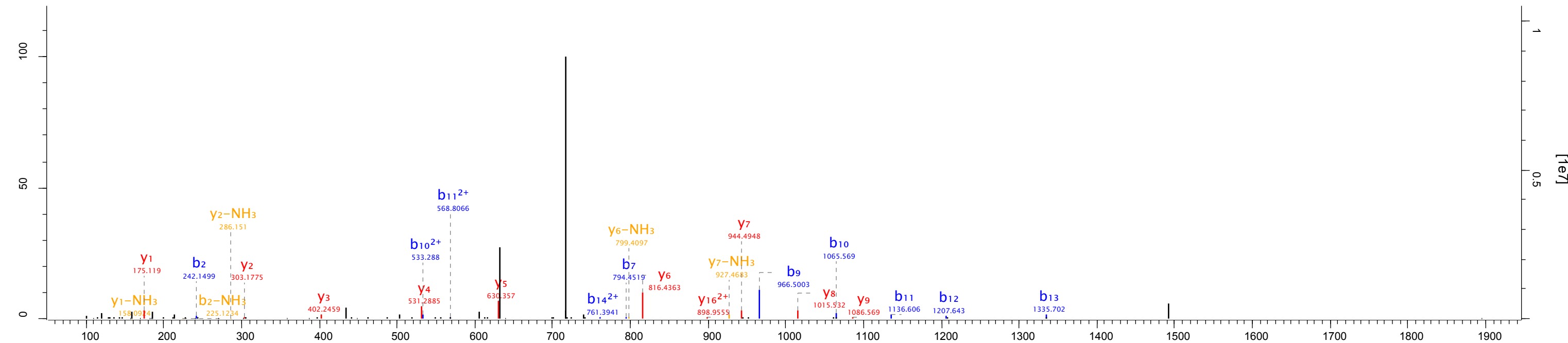
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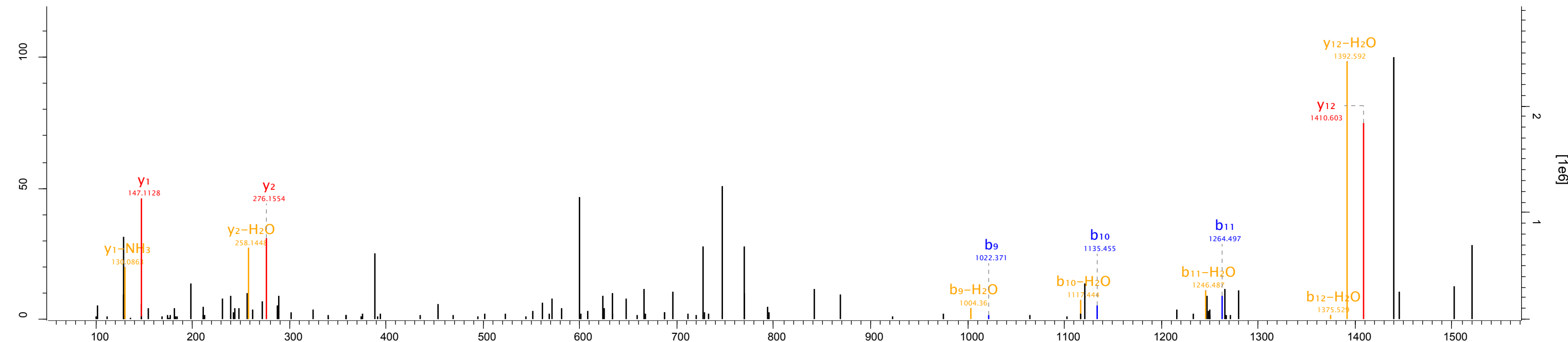
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Raw file
20180707_MaS_A375SR_ML_proteome_2_13

Scan 8128 Method FTMS; HCD Score 58.17 m/z 770.33 Gene names GOLGA8F;GOLGA8DP



- E A M S G F M D H L E E K -

ox

y12

y2

y1

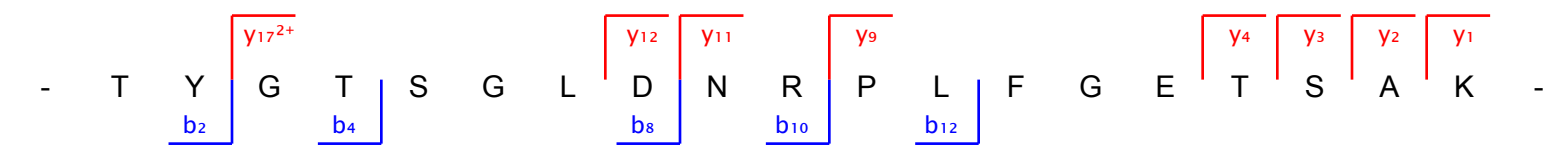
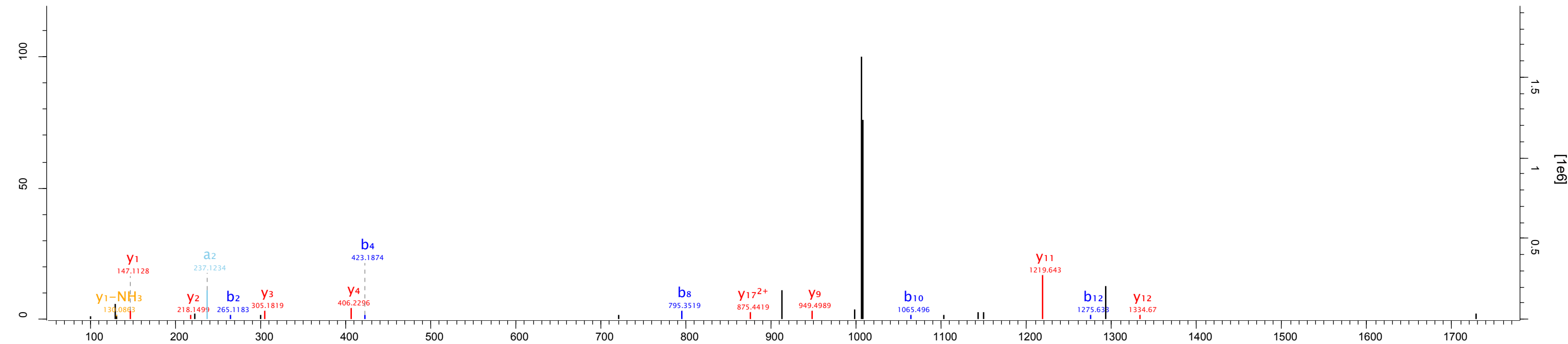
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b10

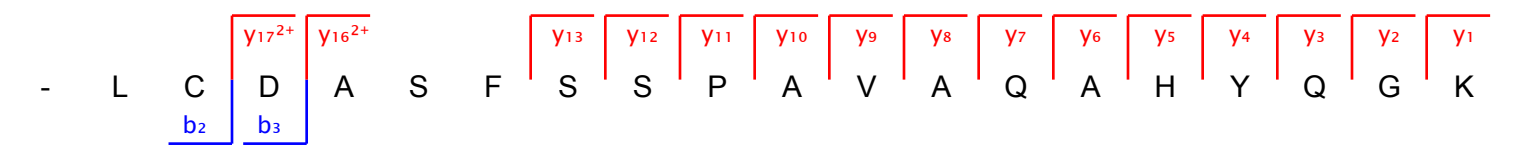
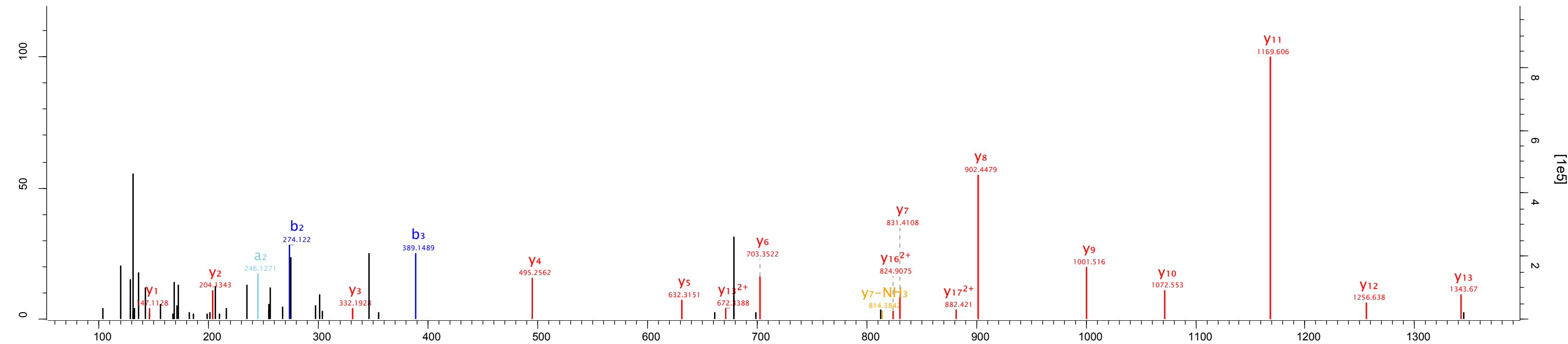
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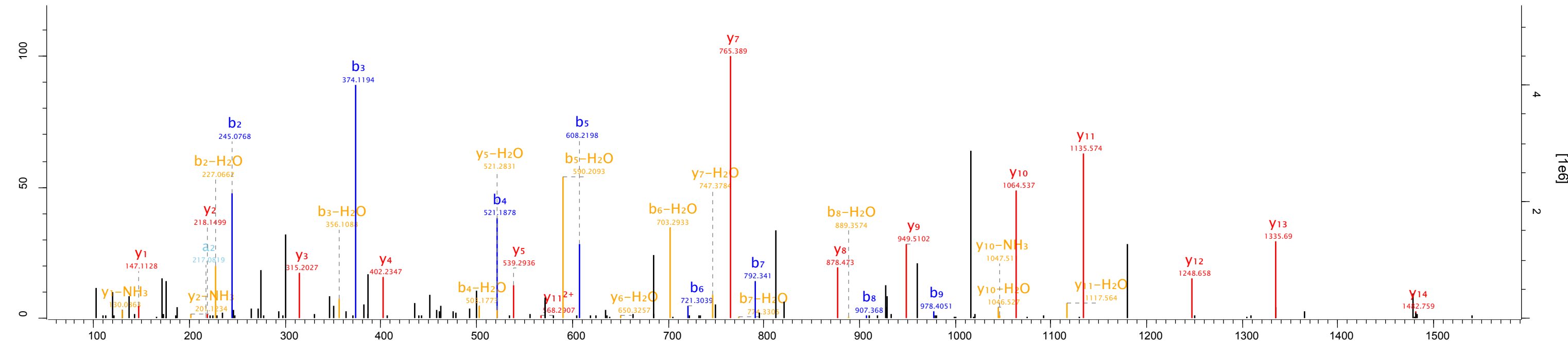


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20180707_MaS_A375SR_ML_proteome_2_16

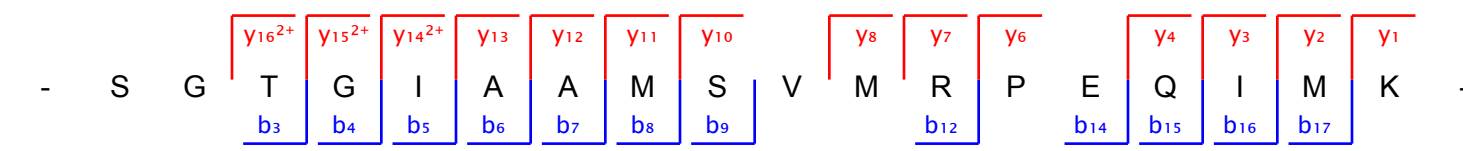
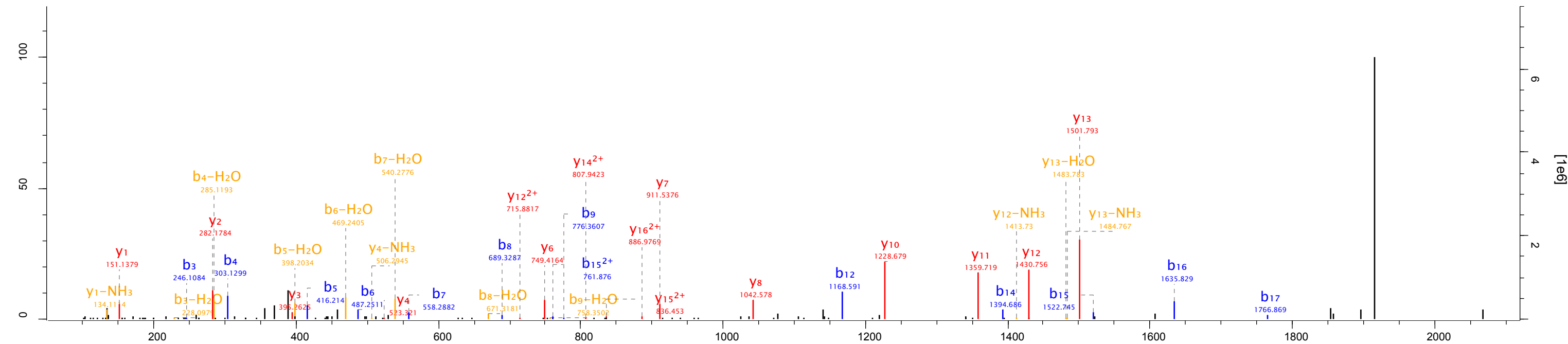
Scan 26448 Method FTMS; HCD Score 142.74 m/z 928.94 Gene names MAPK1IP1L



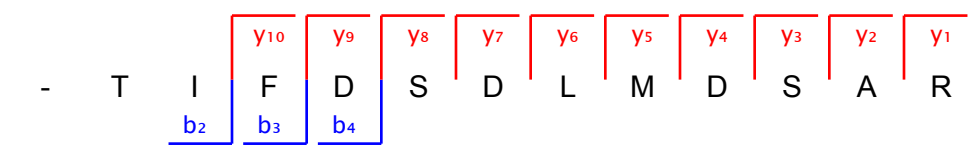
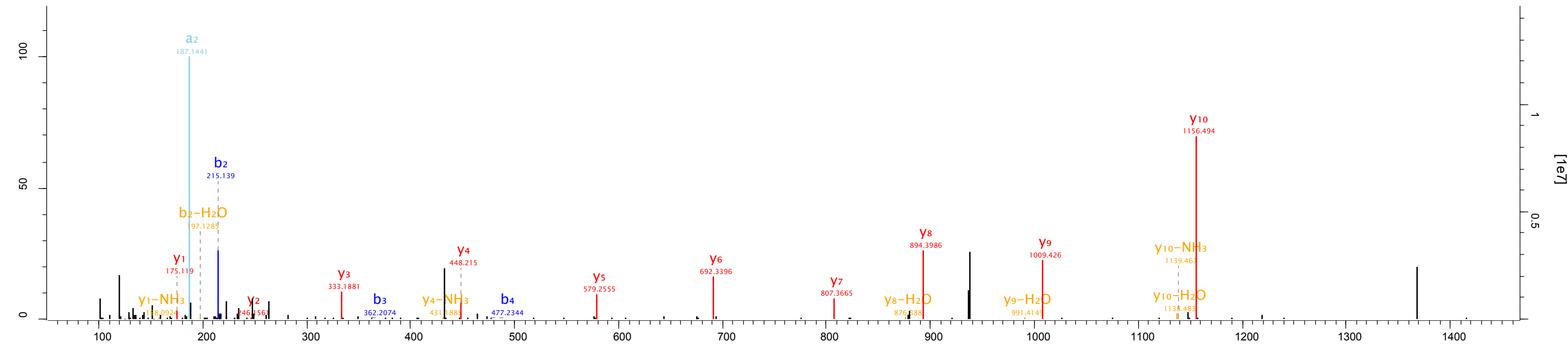
ac
- S D E F S L A D A L P E H S P A K -
b₂ b₃ b₄ b₅ b₆ b₇ b₈ b₉ y₁₄ y₁₃ y₁₂ y₁₁ y₁₀ y₉ y₈ y₇ y₅ y₄ y₃ y₂ y₁

Raw file
20180707_MaS_A375SR_ML_proteome_2_18

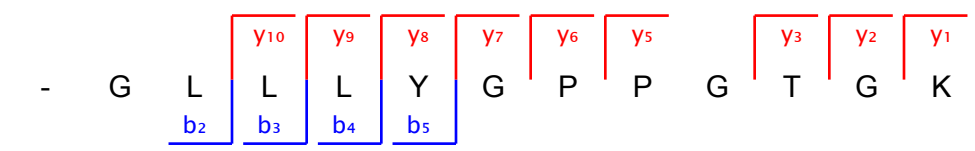
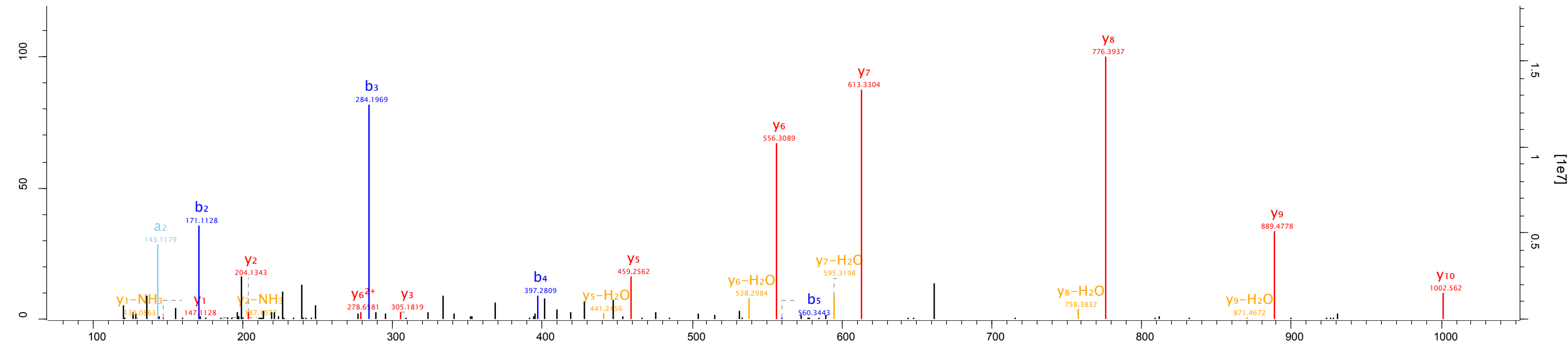
Scan 23578 Method FTMS; HCD Score 155.79 m/z 959.01 Gene names ATP6V0C



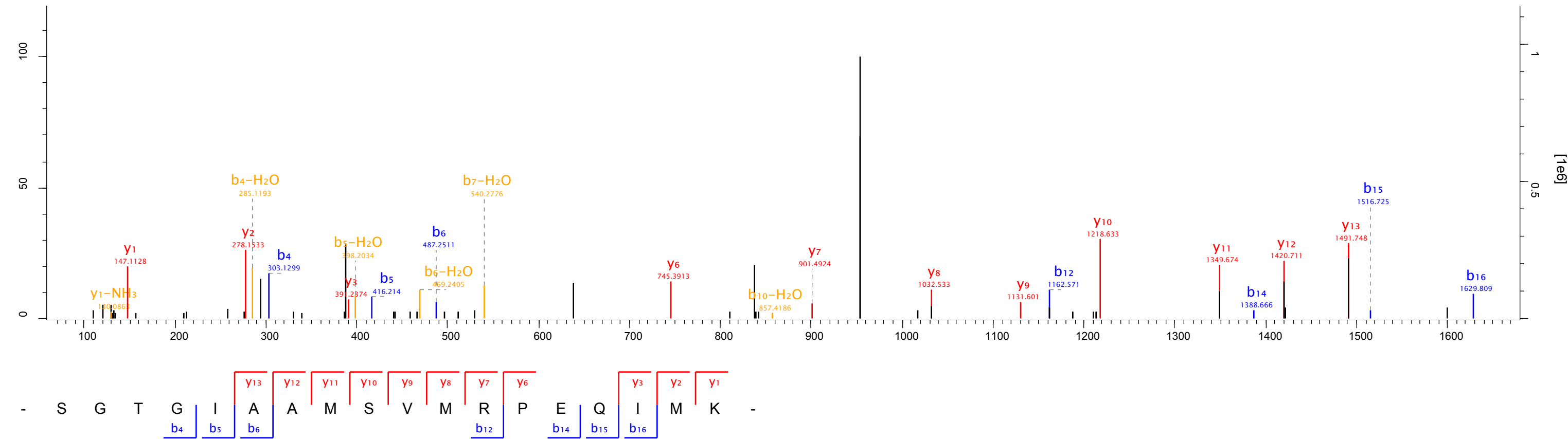
Raw file 20180707_MaS_A375SR_ML_proteome_2_18 Scan 25278 Method FTMS; HCD Score 81.57 m/z 685.82 Gene names PMEPA1



Raw file 20180707_MaS_A375SR_ML_proteome_2_19 Scan 22038 Method FTMS; HCD Score 72.29 m/z 586.84 Gene names KATNAL2

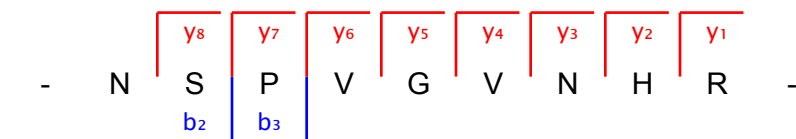
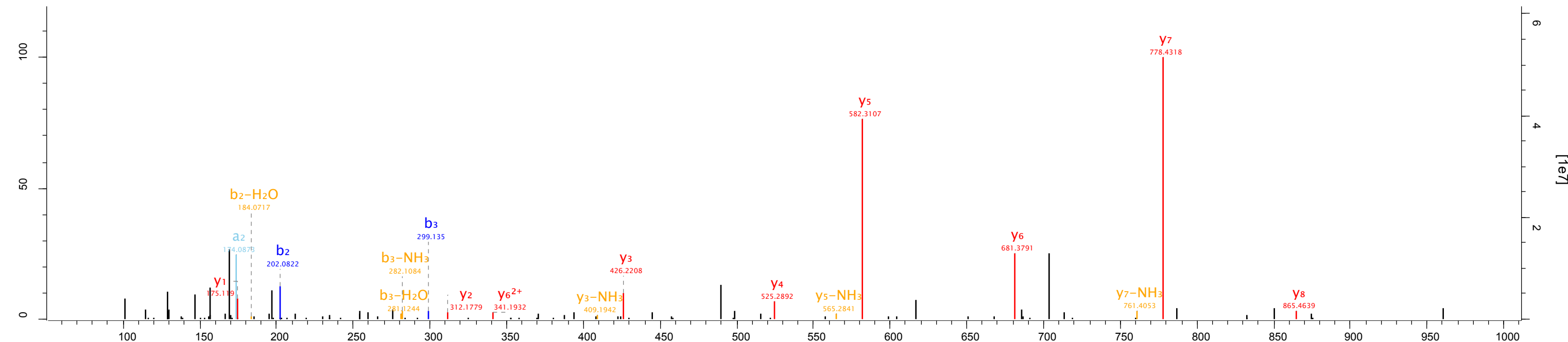


Raw file: 20180707_MaS_A375SR_ML_proteome_2_19
 Scan: 23638 Method: FTMS; HCD Score: 79.49 m/z: 954.48 Gene names: ATP6V0C

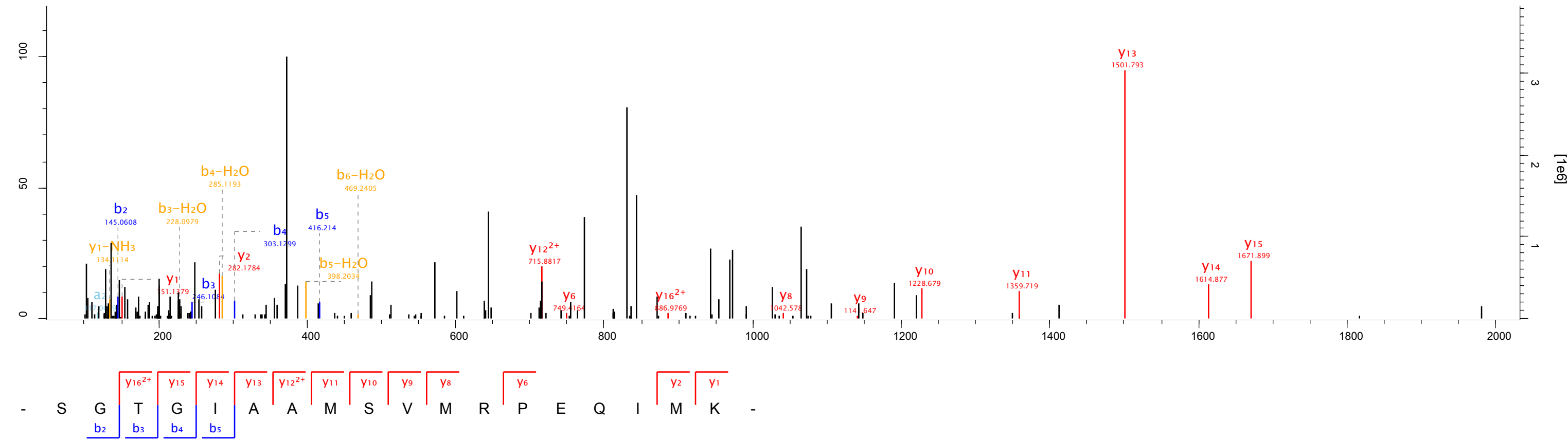


Raw file
20180707_MaS_A375SR_ML_proteome_2_19

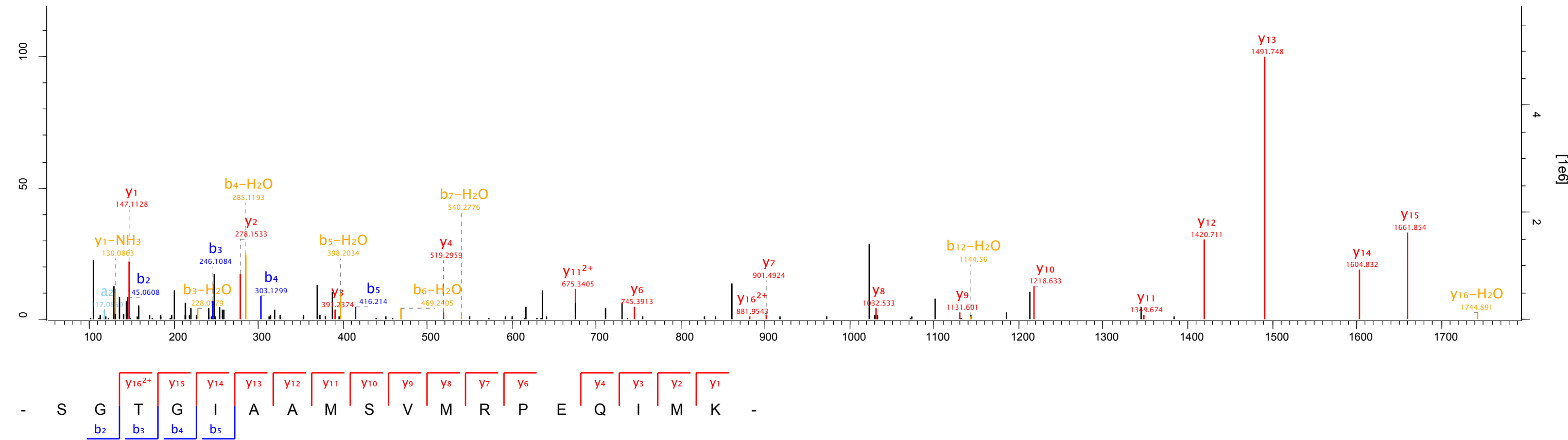
Scan 2548 Method FTMS; HCD Score 96.03 m/z 490.26 Gene names TIMM17A



Raw file 20180707_MaS_A375SR_ML_proteome_2_20 Scan 21818 Method FTMS; HCD Score 28.75 m/z 639.67 Gene names ATP6V0C

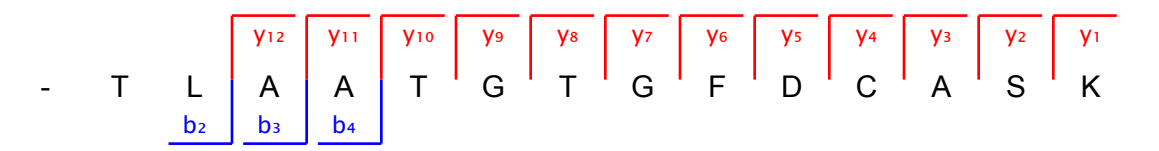
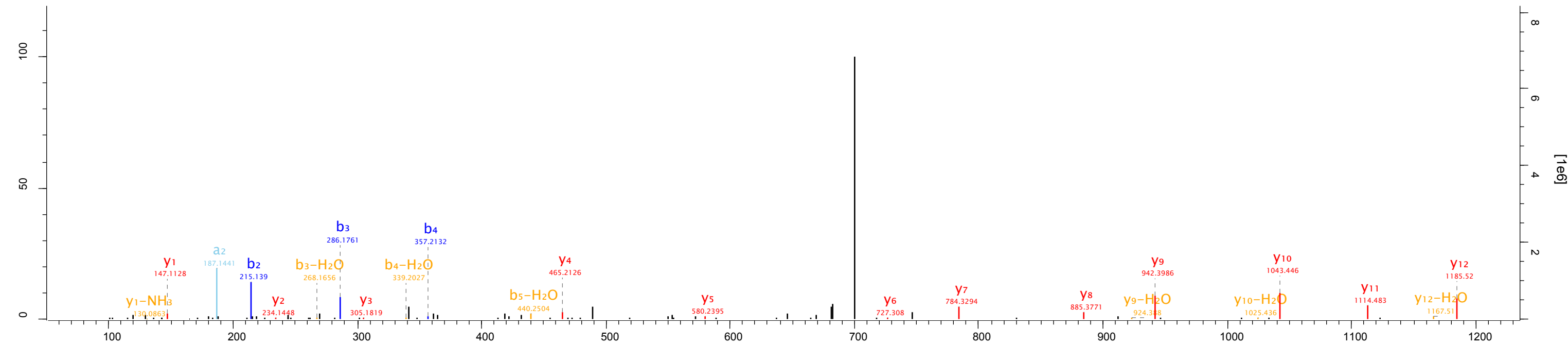


Raw file 20180707_MaS_A375SR_ML_proteome_2_21 Scan 24048 Method FTMS; HCD Score 89.37 m/z 636.32 Gene names ATP6V0C

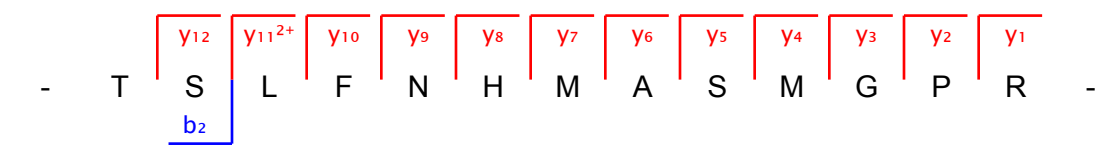
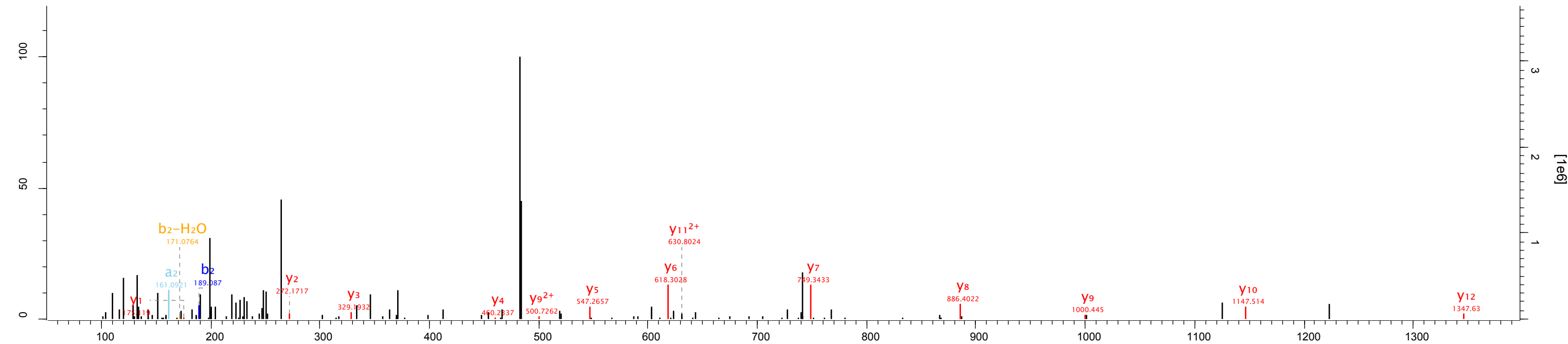


Raw file
20180707_MaS_A375SR_ML_proteome_2_22

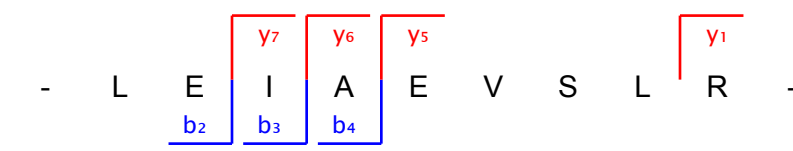
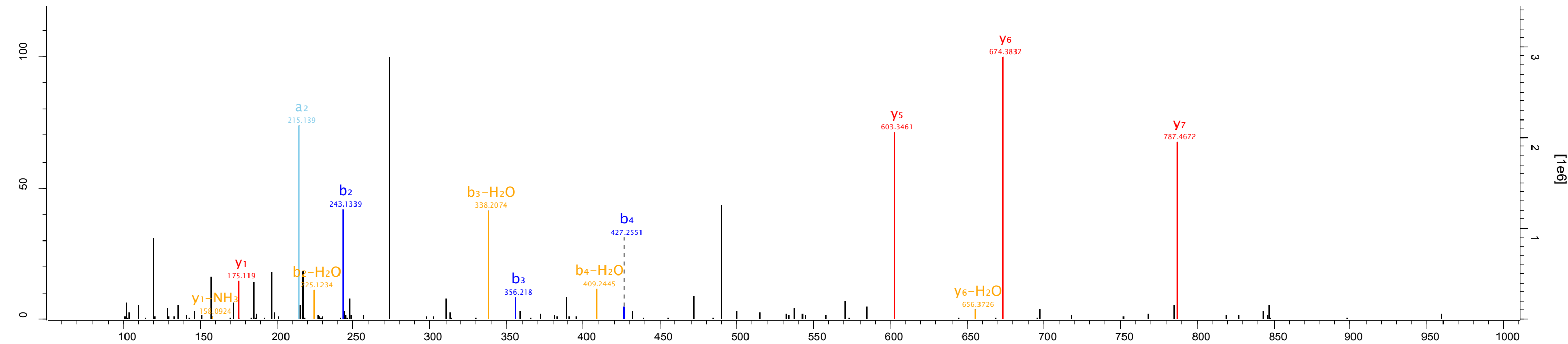
Scan 12788 Method FTMS; HCD Score 63.68 m/z 700.83 Gene names ODC1



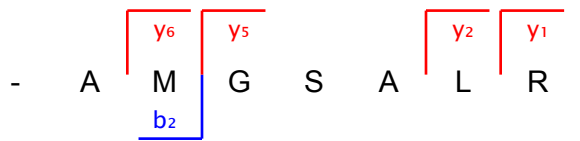
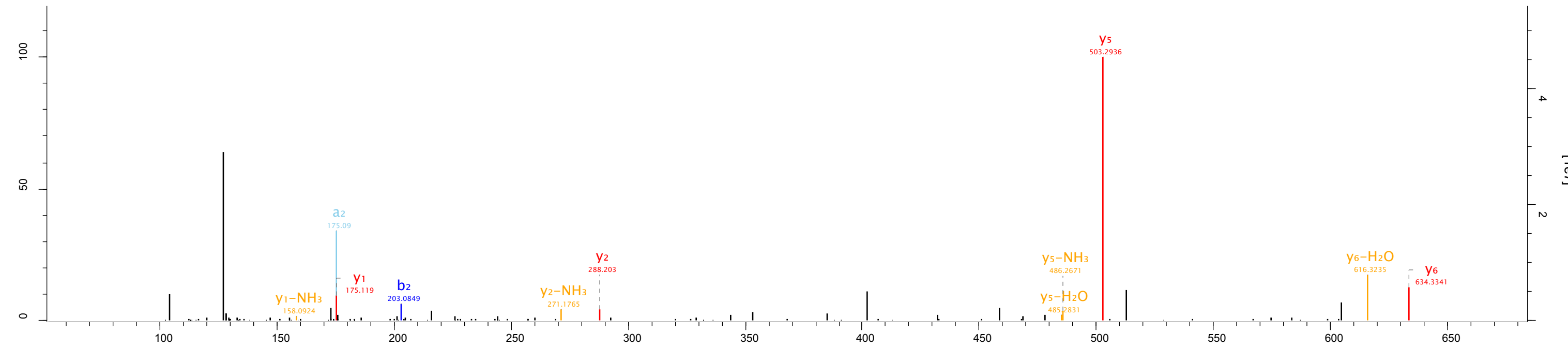
Raw file 20180707_MaS_A375SR_ML_proteome_2_22 Scan 18828 Method FTMS; HCD Score 27.26 m/z 483.97 Gene names TMEM39B



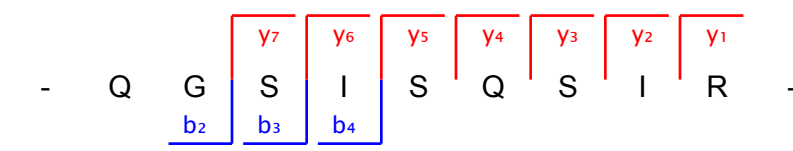
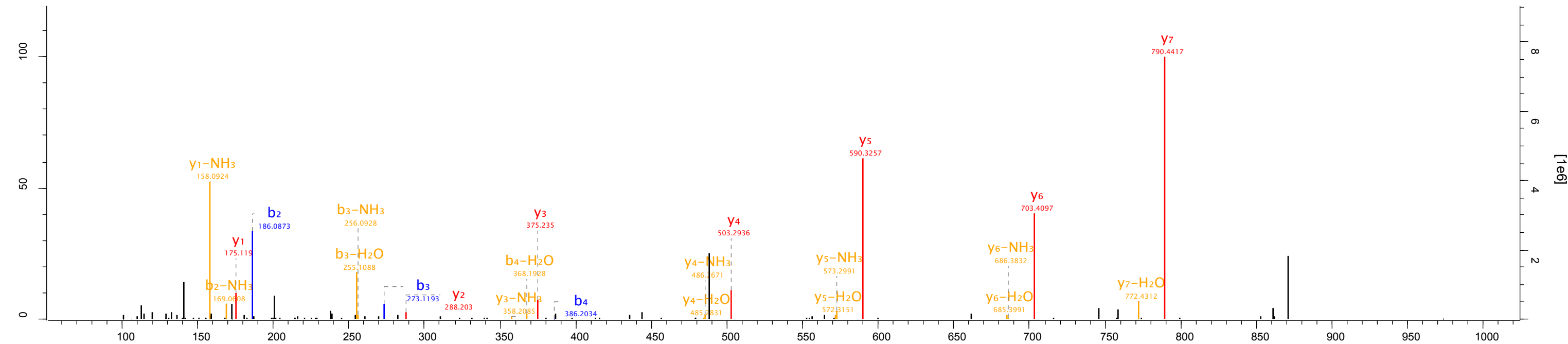
Raw file 20180707_MaS_A375SR_ML_proteome_2_22 Scan 23658 Method FTMS; HCD Score 76.68 m/z 515.3



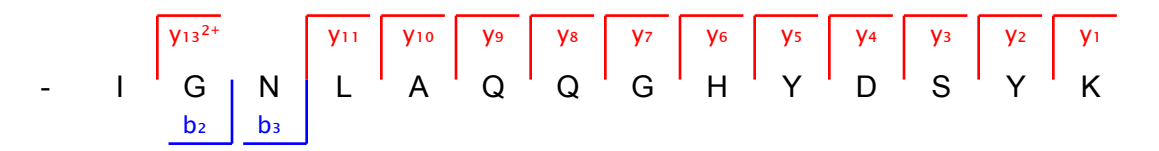
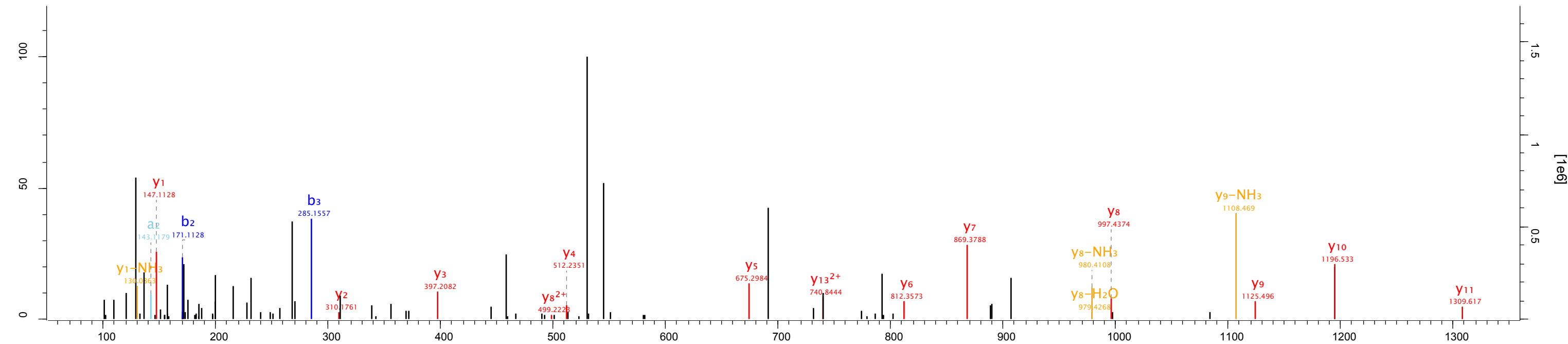
Raw file 20180707_MaS_A375SR_ML_proteome_2_22 Scan 6008 Method FTMS; HCD Score 79.45 m/z 353.19



Raw file 20180707_MaS_A375SR_ML_proteome_2_23 Scan 9818 Method FTMS; HCD Score 128.86 m/z 488.26

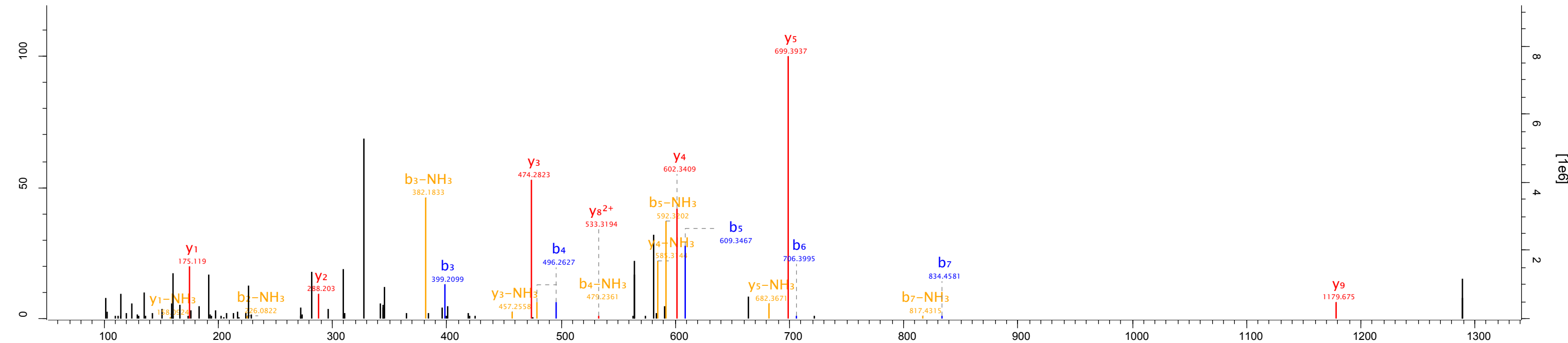


Raw file: 20180707_MaS_A375SR_ML_proteome_2_25
 Scan: 10078 Method: FTMS; HCD Score: 68.04 m/z: 531.93 Gene names: PAX9



Raw file

20180707_MaS_A375SR_ML_proteome_2_25

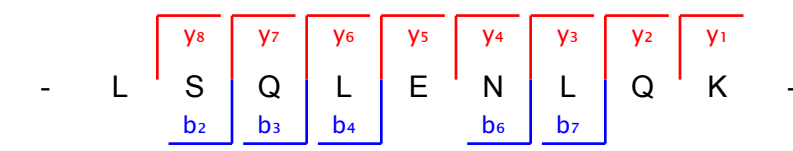
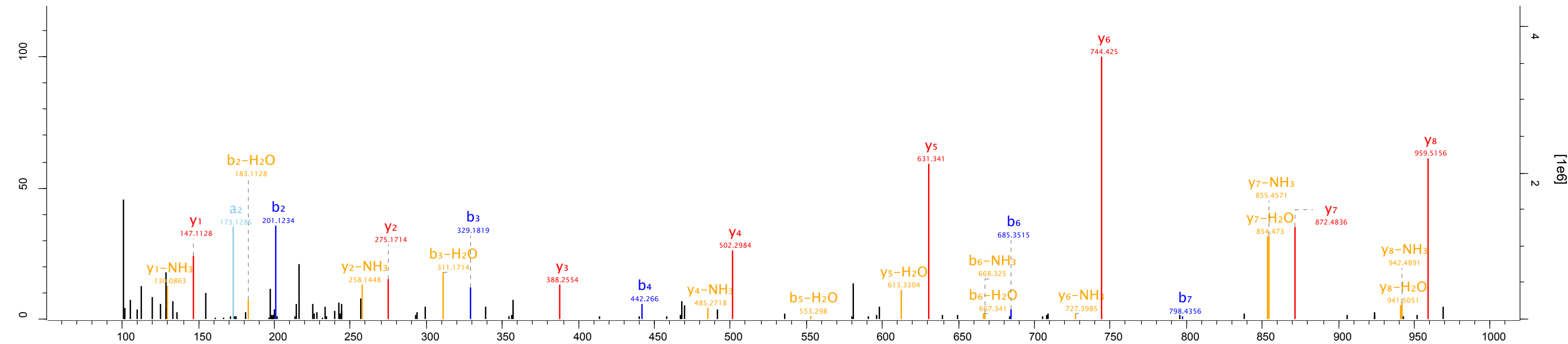
Scan
16208Method
FTMS; HCDScore
138.98m/z
436.58Gene names
RPL39P5;RPL39

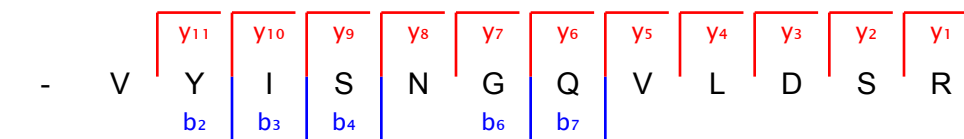
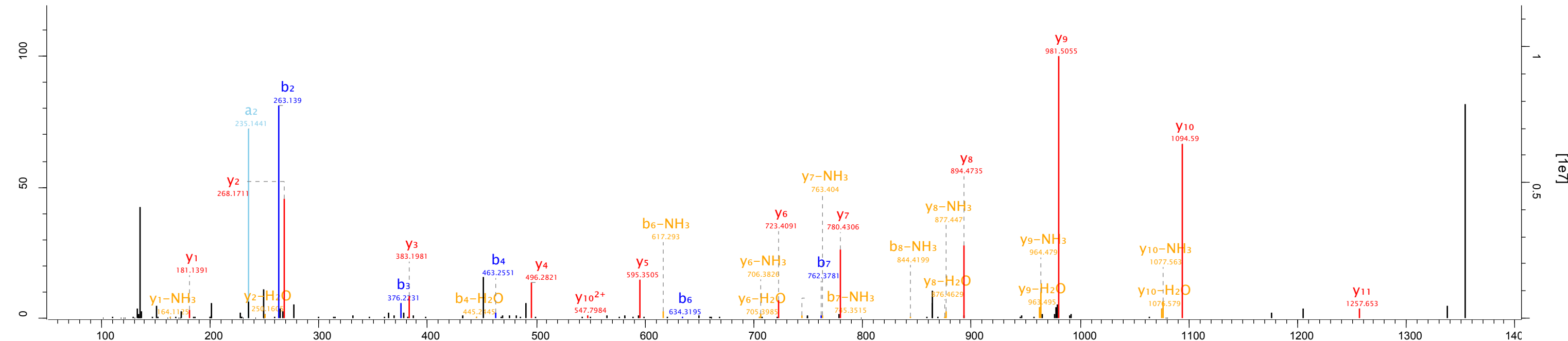
- Q N R P I P Q W I R -

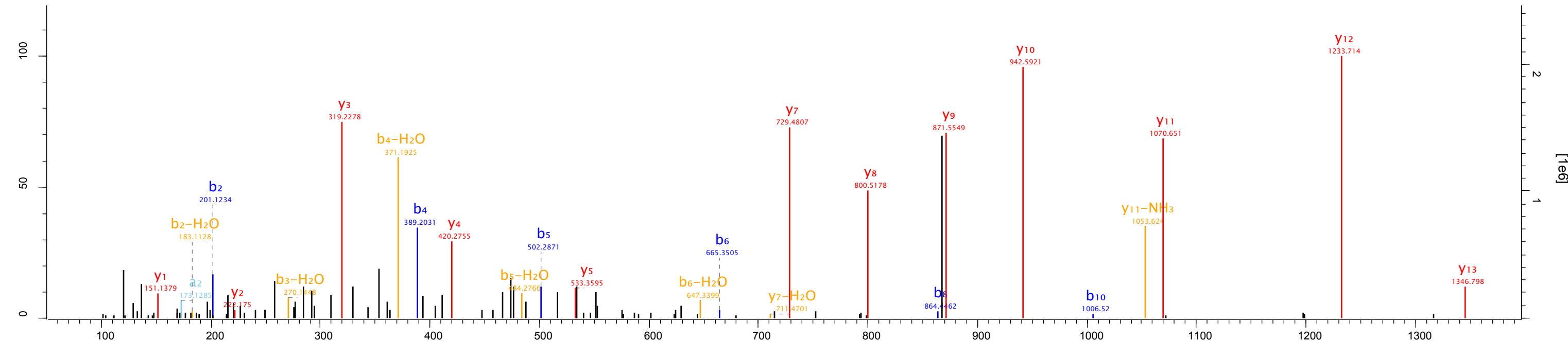
b₃ b₄ b₅ b₆ b₇

y₉ y₈²⁺ y₅ y₄ y₃ y₂ y₁

Raw file 20180707_MaS_A375SR_ML_proteome_2_27
 Scan 11958 Method FTMS; HCD Score 205.83 m/z 536.8 Gene names ATP5S





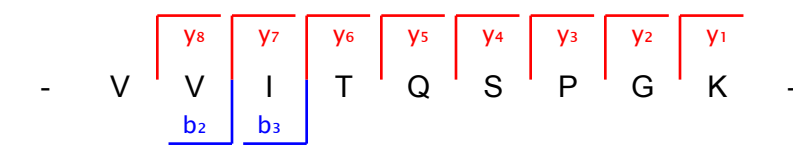
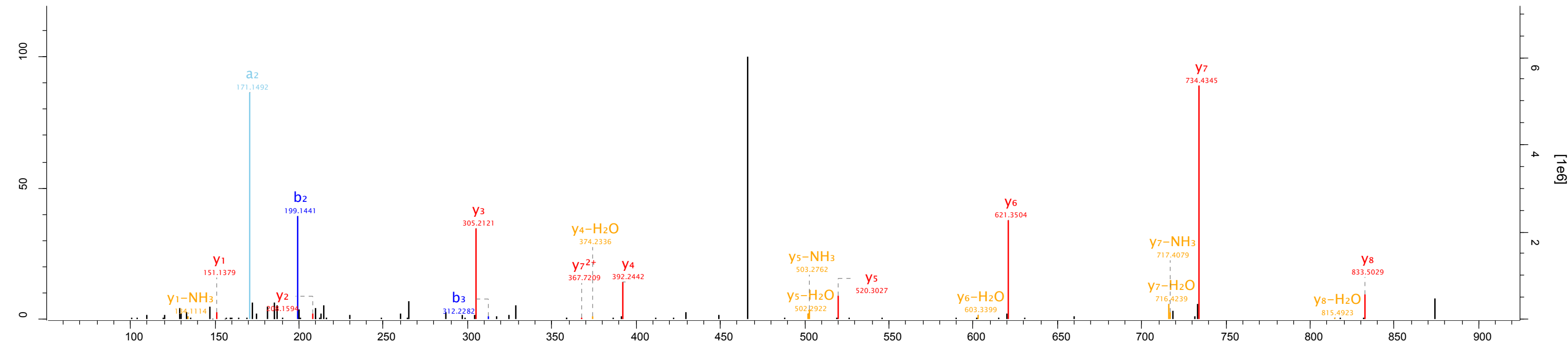


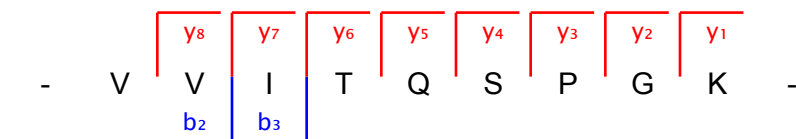
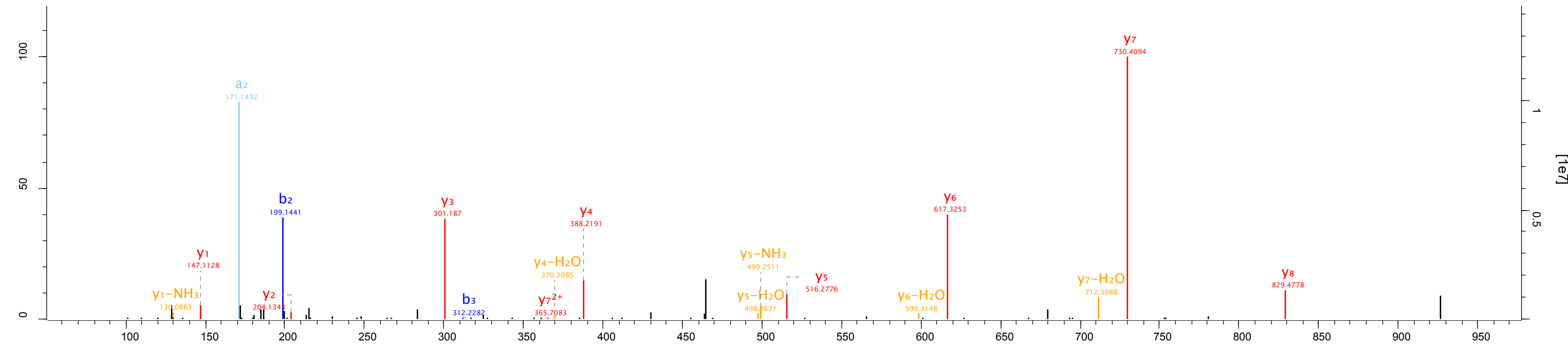
- I S S T L Y Q A A P V L T P A K -

Fragmentation scheme (b and y ions) shown below the sequence:

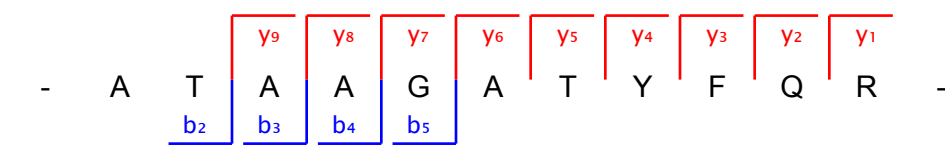
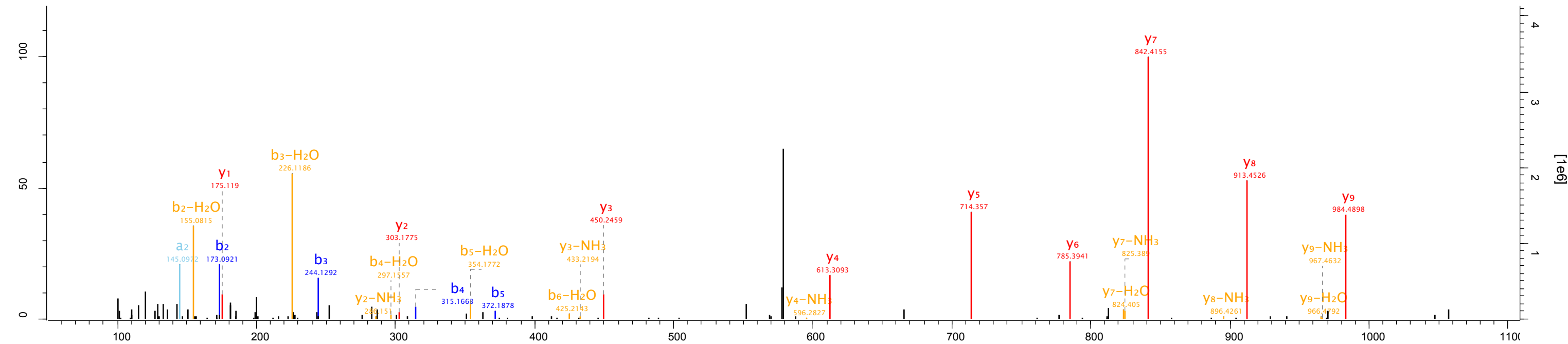
- b2: S
- b4: ST
- b5: STL
- b6: STLY
- b8: STLYQA
- b10: STLYQAAP
- y1: AK
- y2: AP
- y3: ATP
- y4: ATPL
- y5: ATPLV
- y7: APV
- y8: AAPV
- y9: AAPLV
- y10: AAPLVQ
- y11: AAPLVQY
- y12: AAPLVQYL
- y13: AAPLVQYLS

Raw file: 20180707_MaS_A375SR_ML_proteome_2_29
 Scan: 7148 Method: FTMS; HCD Score: 96.03 m/z: 466.79 Gene names: FAM11A;TMEM185A;TMEM185B

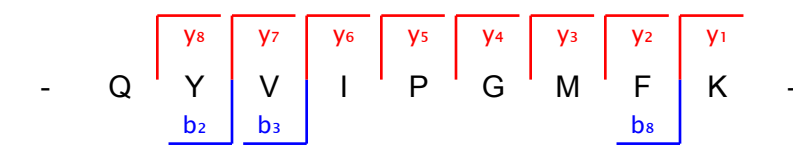
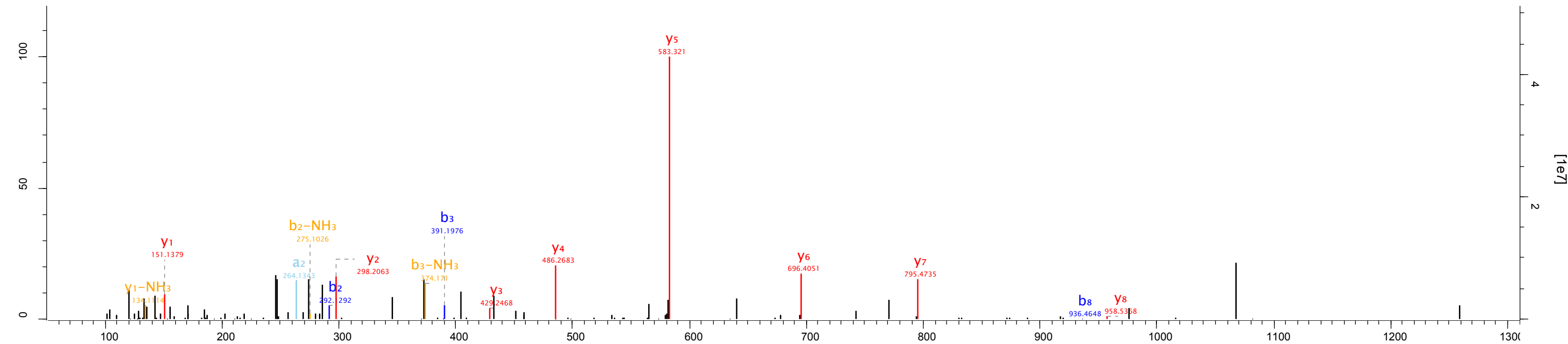




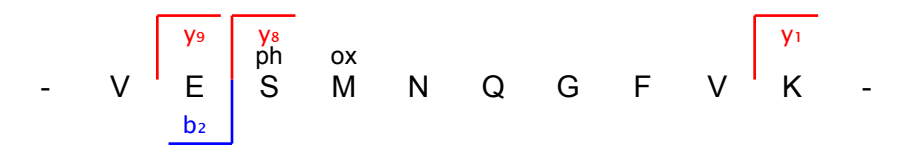
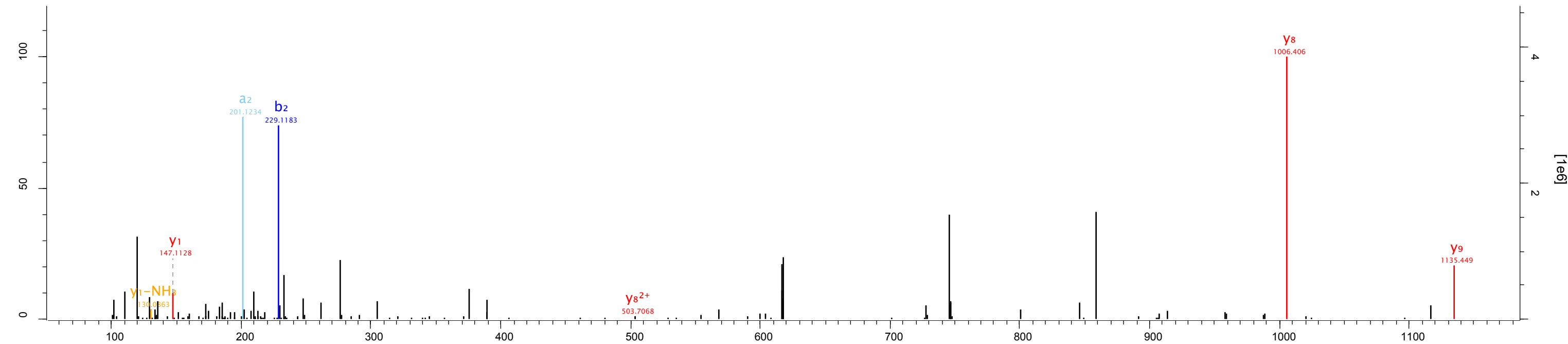
Raw file: 20180707_MaS_A375SR_ML_proteome_2_30
 Scan: 12548 Method: FTMS; HCD Score: 145.46 m/z: 578.79 Gene names: TMEM254



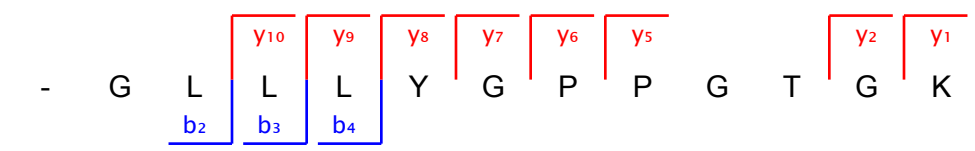
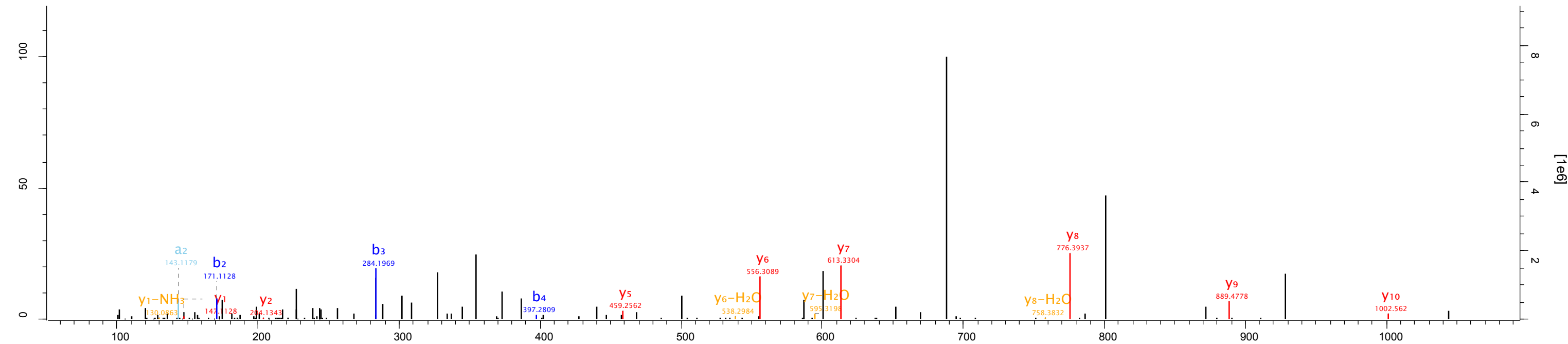
Raw file: 20180707_MaS_A375SR_ML_proteome_20
 Scan: 25488 Method: FTMS; HCD Score: 70.82 m/z: 543.8 Gene names: ACO1



Raw file 20180707_MaS_A375SR_ML_proteome_21 Scan 18388 Method FTMS; HCD Score 54.98 m/z 617.76

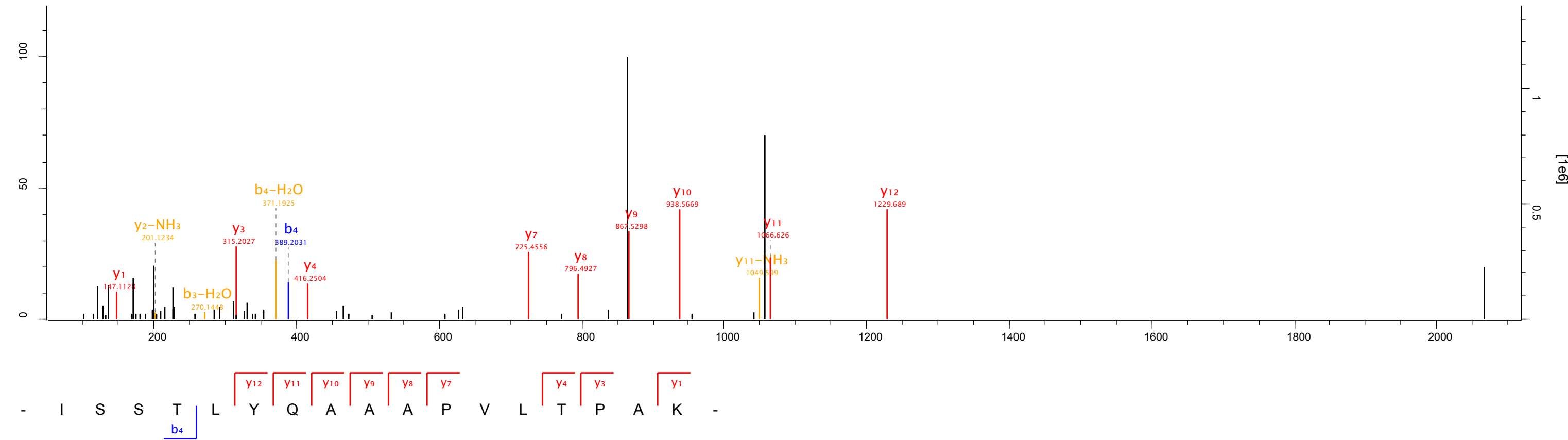


Raw file 20180707_MaS_A375SR_ML_proteome_21 Scan 22078 Method FTMS; HCD Score 39.73 m/z 587.33 Gene names KATNAL2

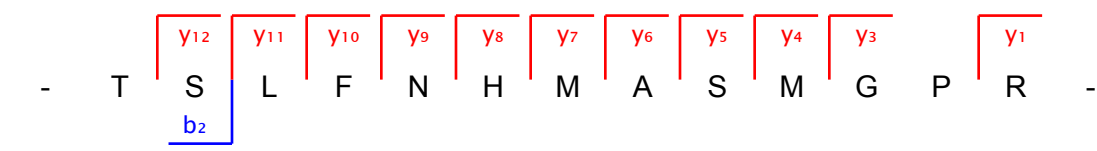
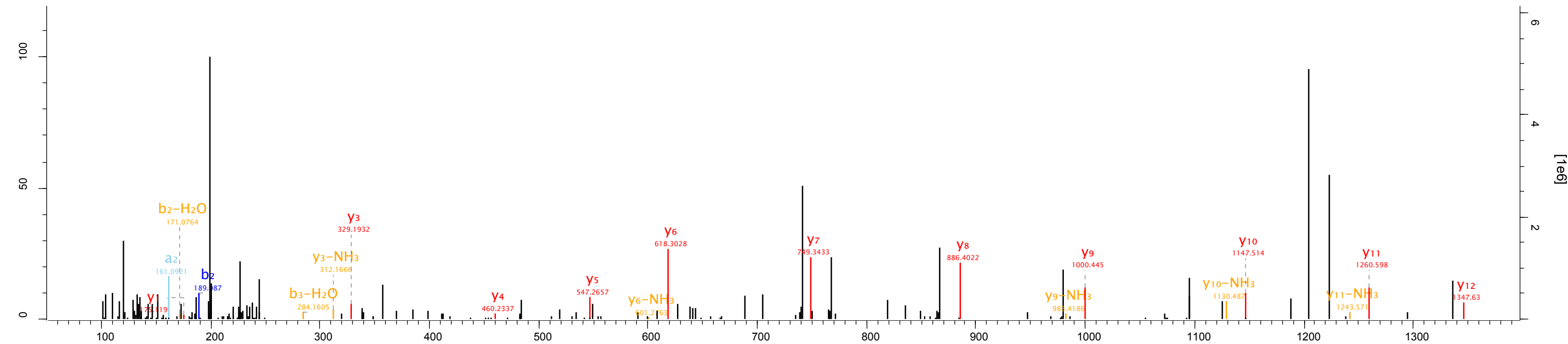


Raw file
20180707_MaS_A375SR_ML_proteome_23

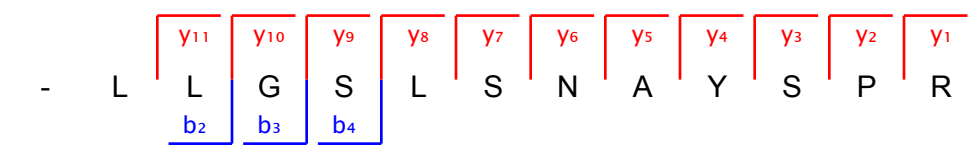
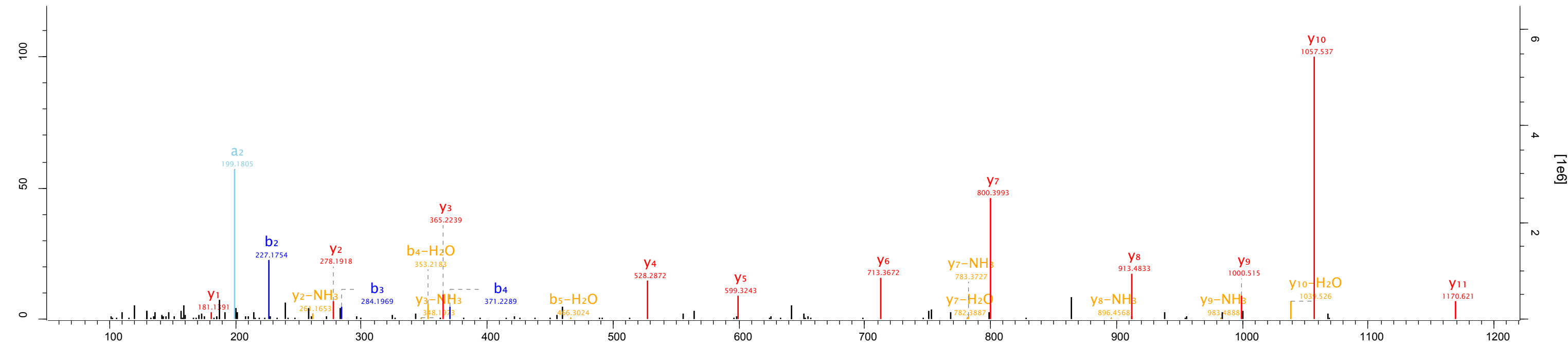
Scan 22908 Method FTMS; HCD Score 38.78 m/z 865.99 Gene names KRTCAP2



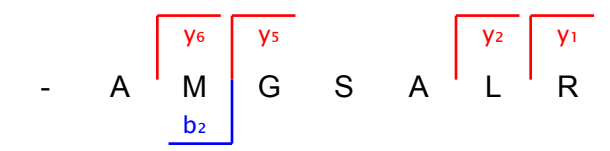
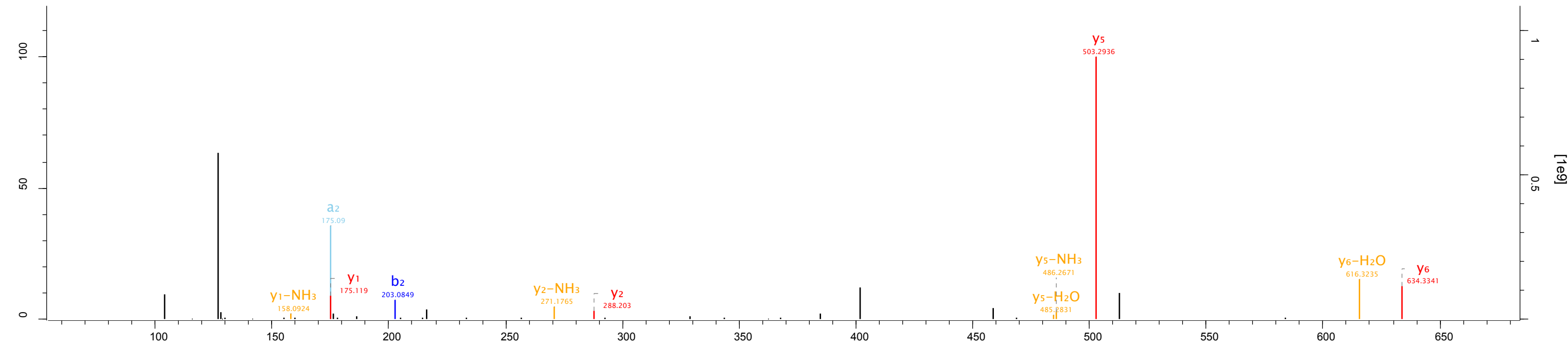
Raw file: 20180707_MaS_A375SR_ML_proteome_24
 Scan: 18418 Method: FTMS; HCD Score: 61.17 m/z: 483.97 Gene names: TMEM39B



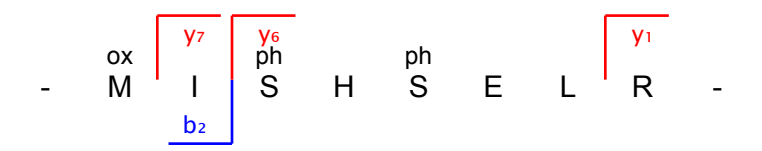
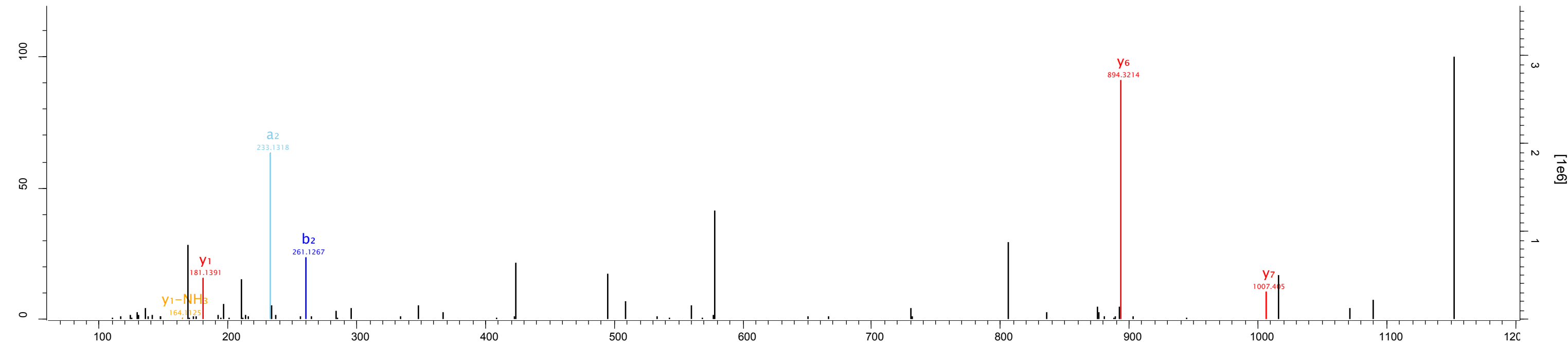
Raw file 20180707_MaS_A375SR_ML_proteome_24 Scan 18478 Method FTMS; HCD Score 95.42 m/z 642.36 Gene names ALG14



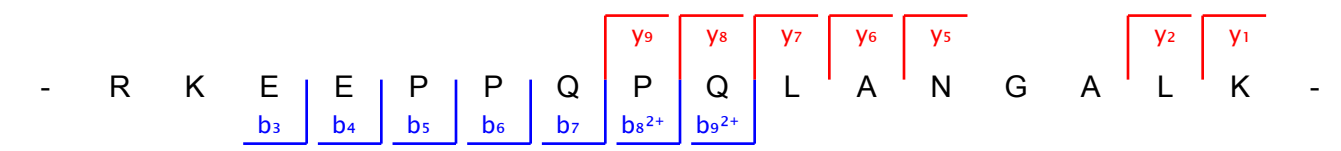
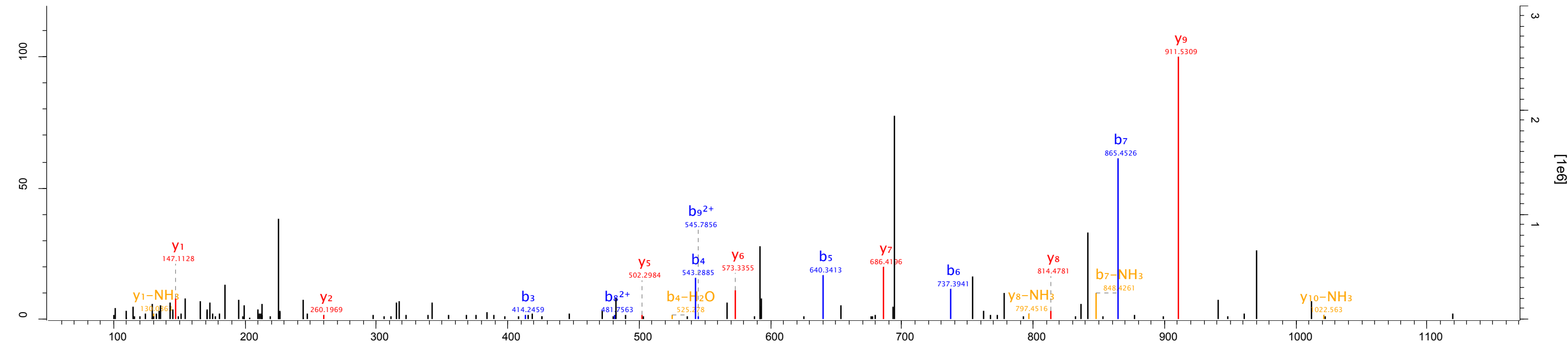
Raw file 20180707_MaS_A375SR_ML_proteome_24 Scan 6148 Method FTMS; HCD Score 79.45 m/z 353.19



Raw file 20180707_MaS_A375SR_ML_proteome_24 Scan 6468 Method FTMS; HCD Score 46.43 m/z 577.72 Gene names PSPHP1



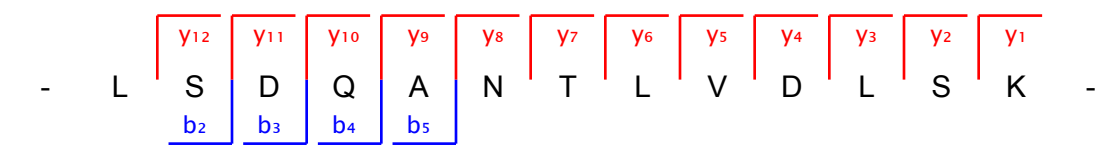
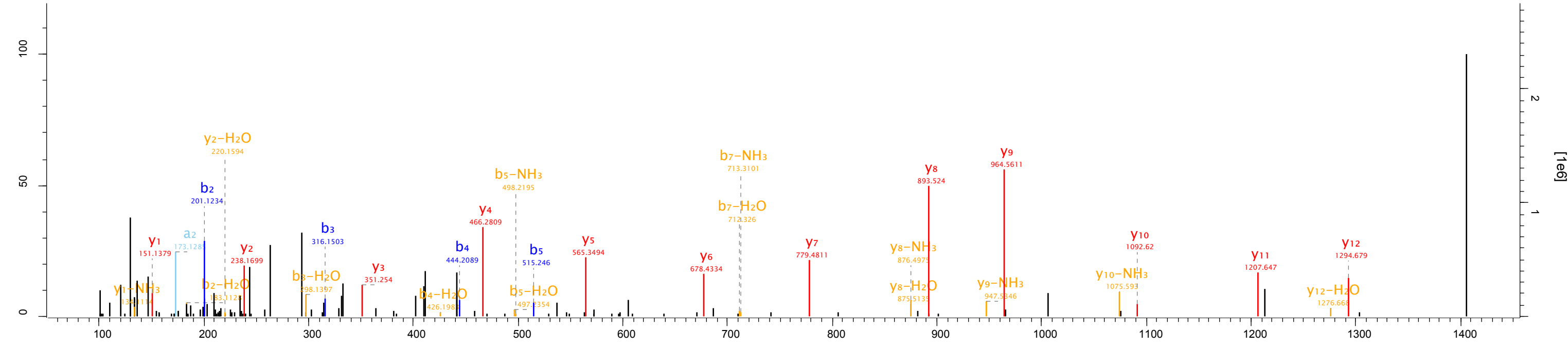
Raw file 20180707_MaS_A375SR_ML_proteome_25 Scan 9718 Method FTMS; HCD Score 36.58 m/z 593 Gene names C20orf24



Raw file

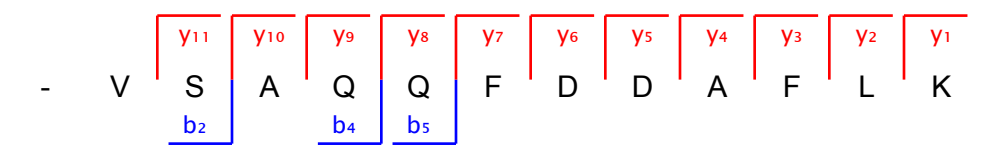
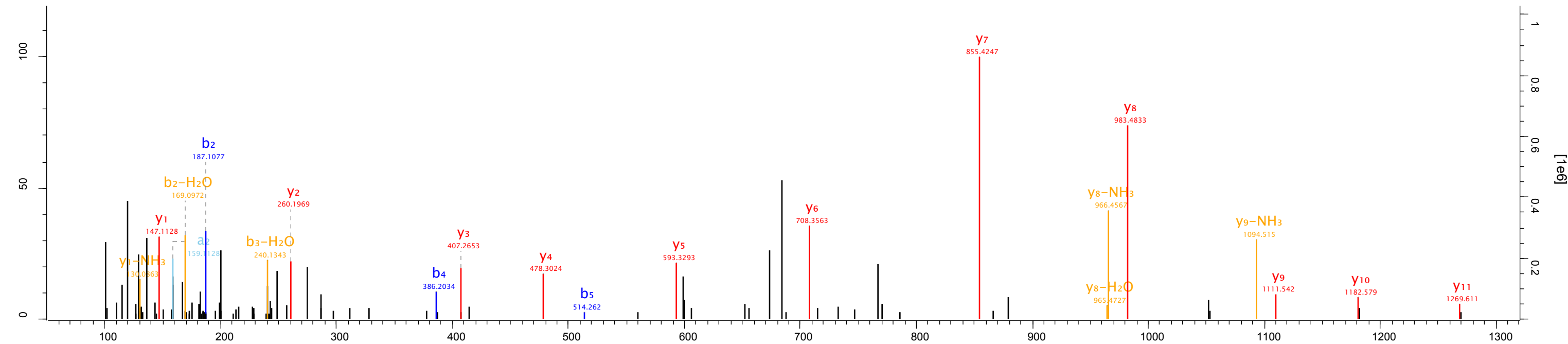
20180707_MaS_A375SR_ML_proteome_26

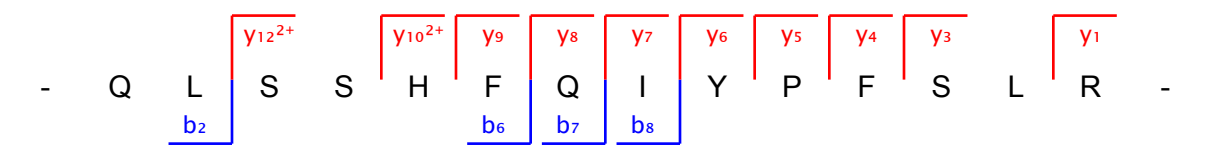
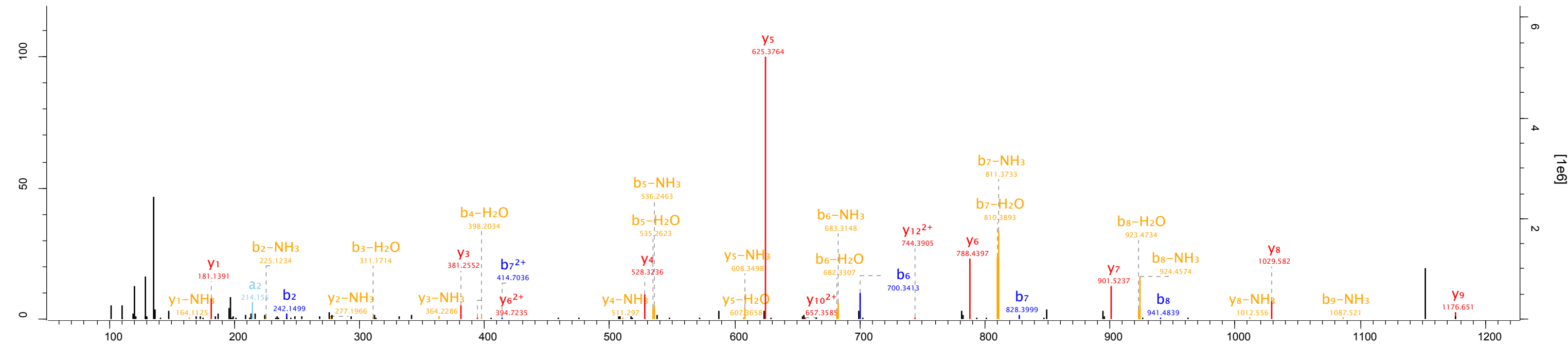
Scan	Method	Score	m/z	Gene names
18698	FTMS; HCD	109.83	704.38	KCNN3



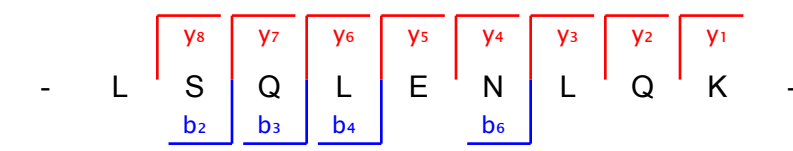
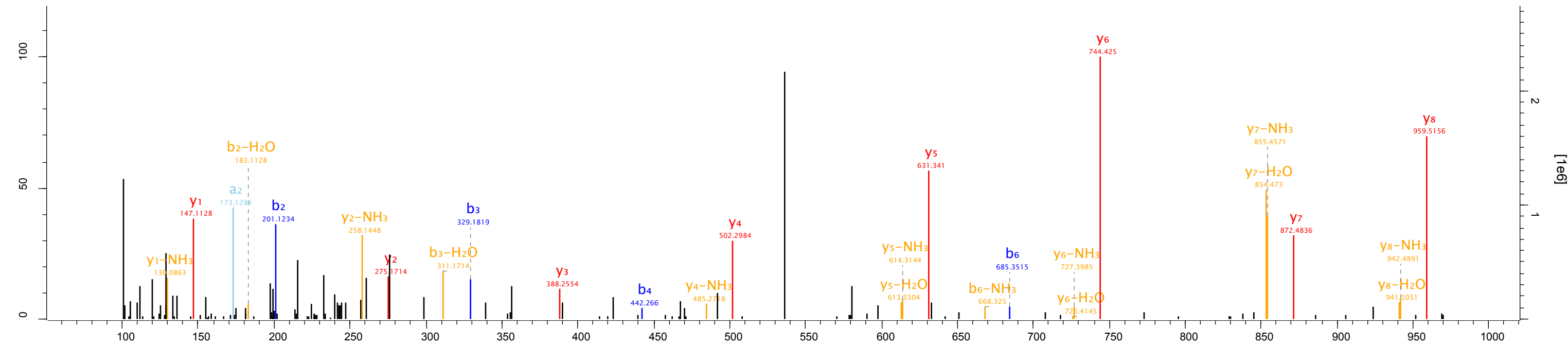
Raw file
20180707_MaS_A375SR_ML_proteome_26

Scan 24028 Method FTMS; HCD Score 92.86 m/z 684.84 Gene names PIGN

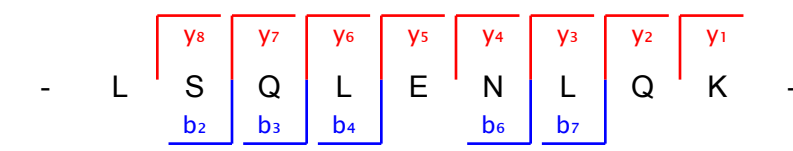
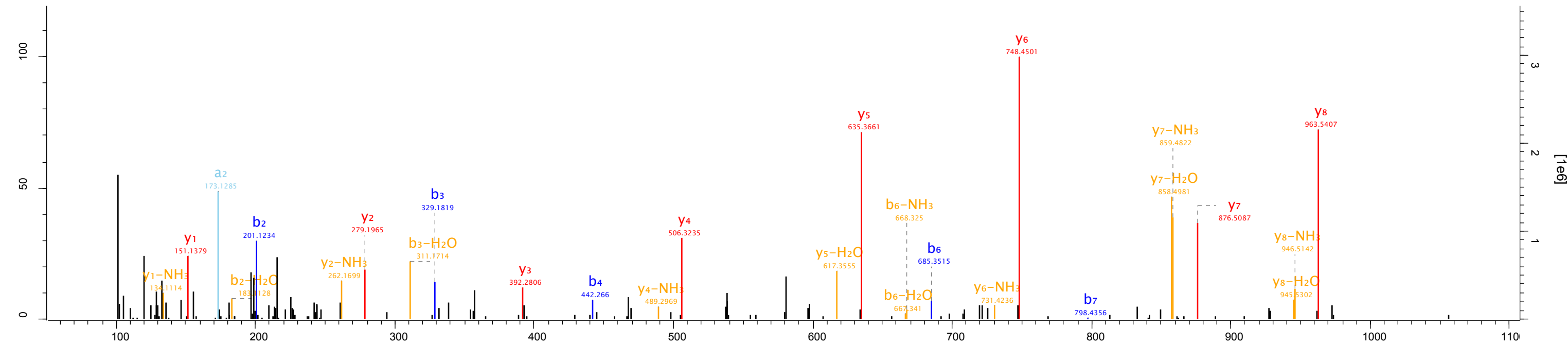




Raw file 20180707_MaS_A375SR_ML_proteome_27 Scan 11888 Method FTMS; HCD Score 182.39 m/z 536.8 Gene names ATP5S

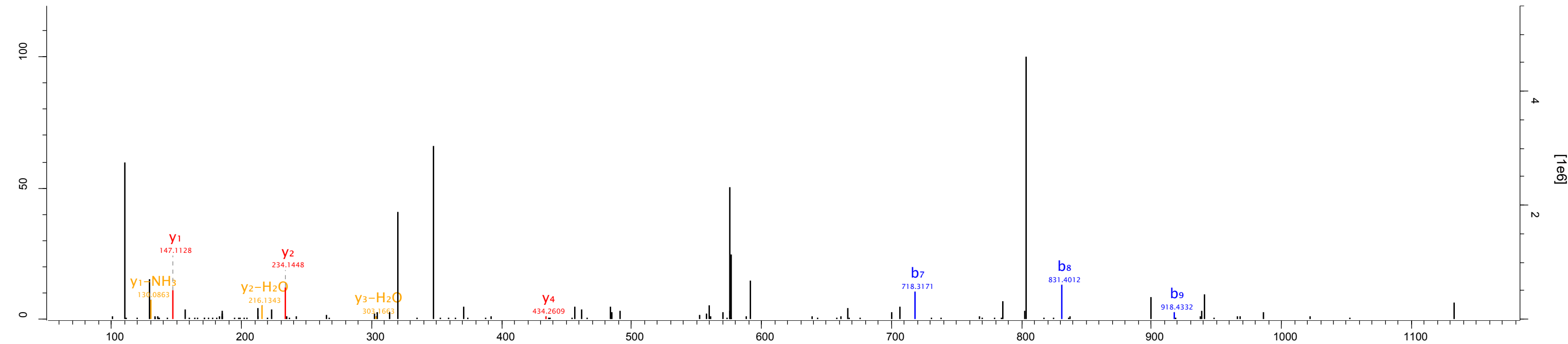


Raw file: 20180707_MaS_A375SR_ML_proteome_27
 Scan: 11898 Method: FTMS; HCD Score: 150.61 m/z: 538.82 Gene names: ATP5S



Raw file
20180707_MaS_A375SR_ML_proteome_27

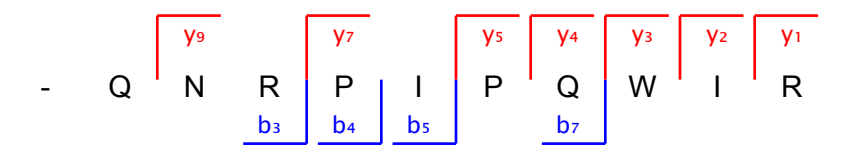
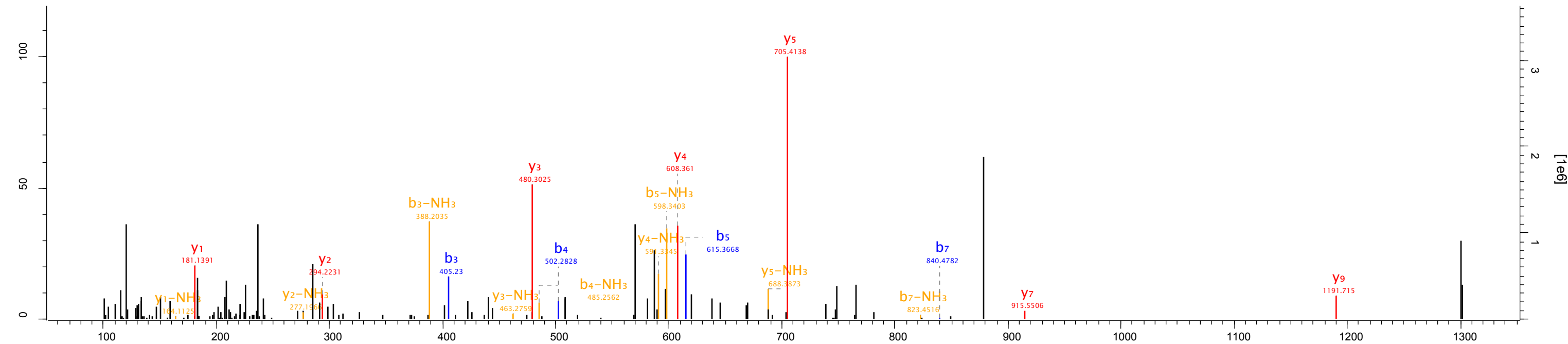
Scan 7788 Method FTMS; HCD Score 48.28 m/z 576.29



- ph S S G V I P P L S S K -

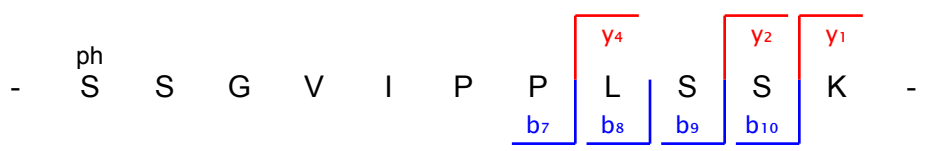
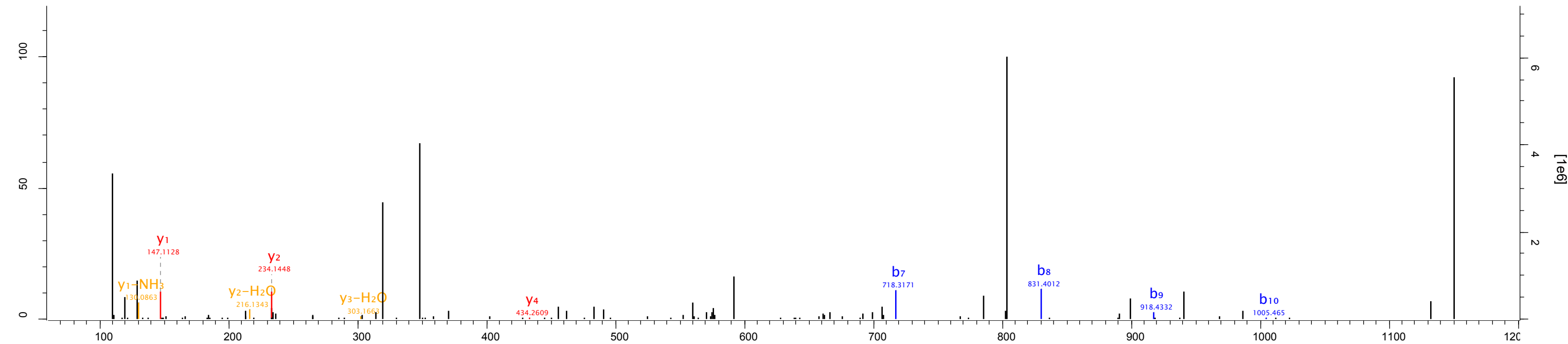
Fragmentation mapping:
- b7 [P] b8 [L] b9 [S] y4 [L S] y2 [S] y1 [K] -

Raw file 20180707_MaS_A375SR_ML_proteome_28 Scan 15408 Method FTMS; HCD Score 100.25 m/z 440.6 Gene names RPL39P5;RPL39

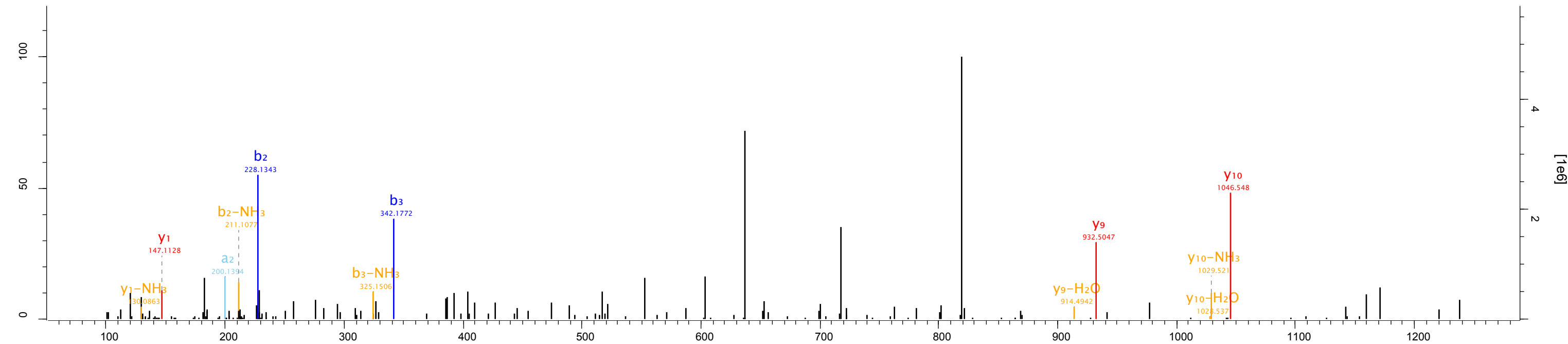


Raw file
20180707_MaS_A375SR_ML_proteome_28

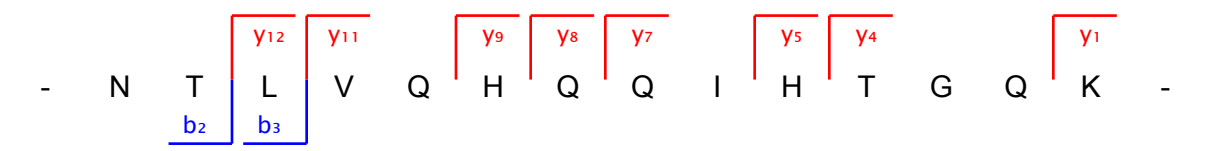
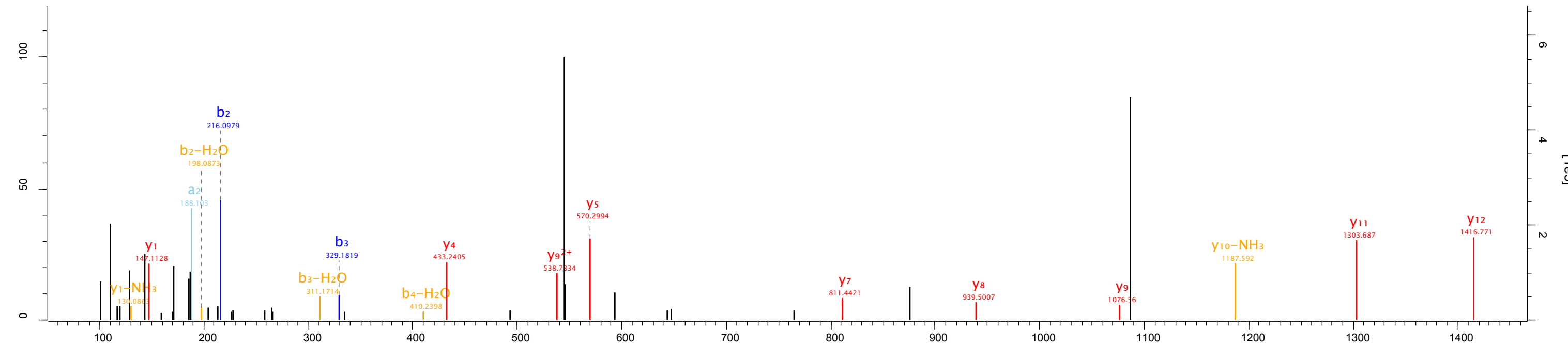
Scan 7648 Method FTMS; HCD Score 47.89 m/z 576.29



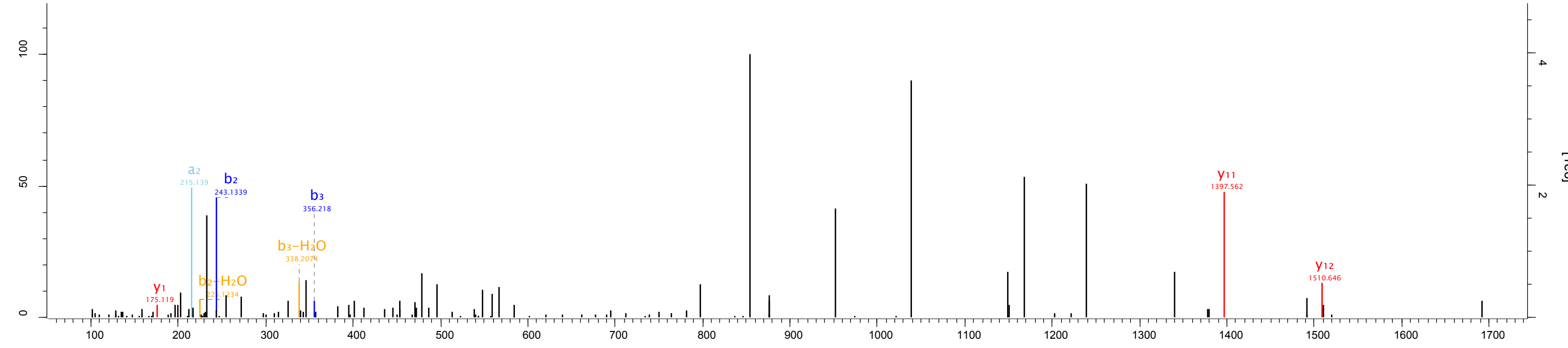
Raw file: 20180707_MaS_A375SR_ML_proteome_29
 Scan: 12788 Method: FTMS; HCD Score: 63.62 m/z: 637.34

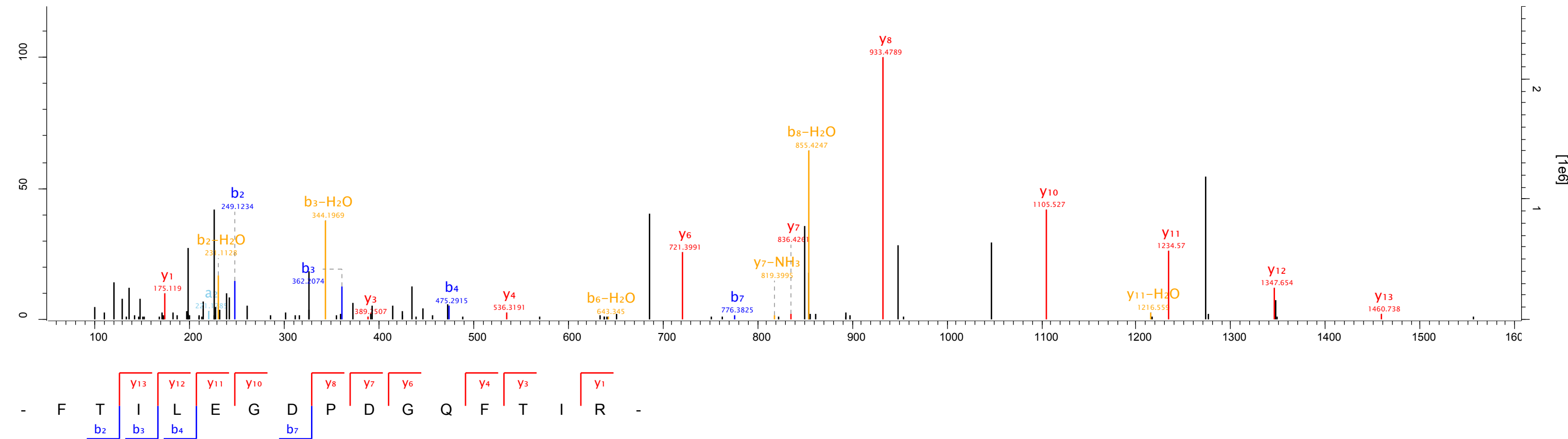


Raw file 20180707_MaS_A375SR_ML_proteome_29 Scan 4628 Method FTMS; HCD Score 61.41 m/z 544.96 Gene names ZNF551

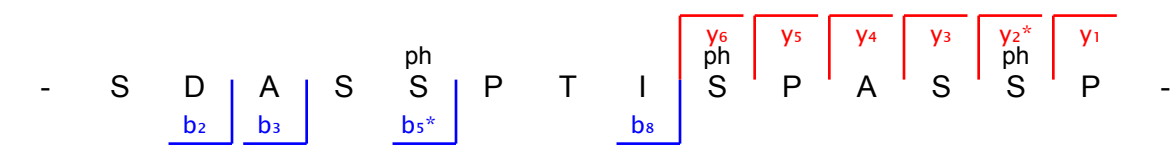
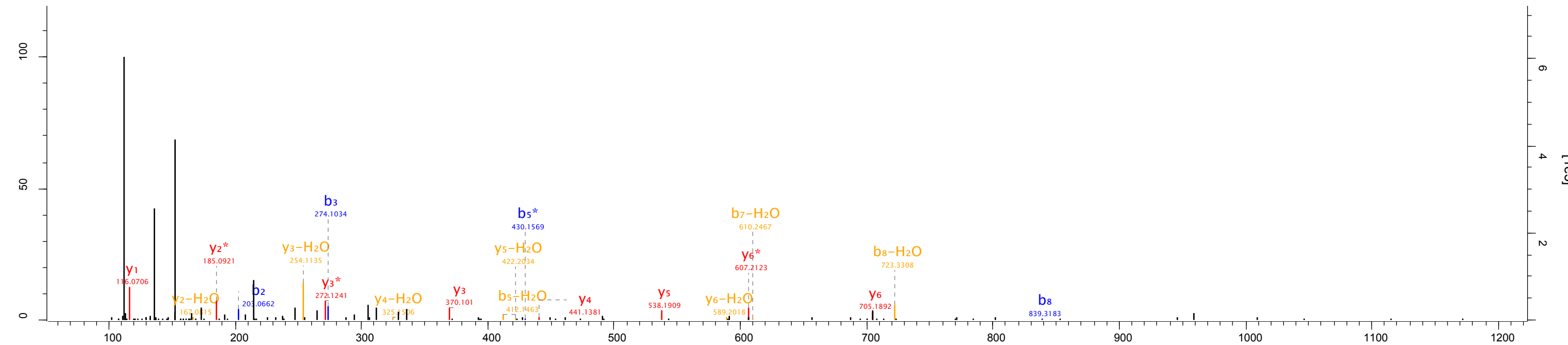


Raw file 20180707_MaS_A375SR_ML_proteome_30 Scan 20548 Method FTMS; HCD Score 46.88 m/z 876.89

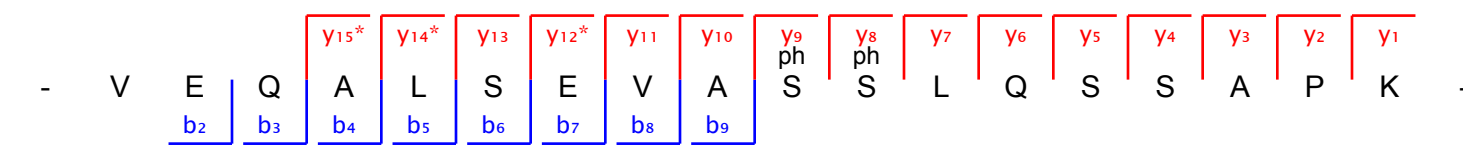
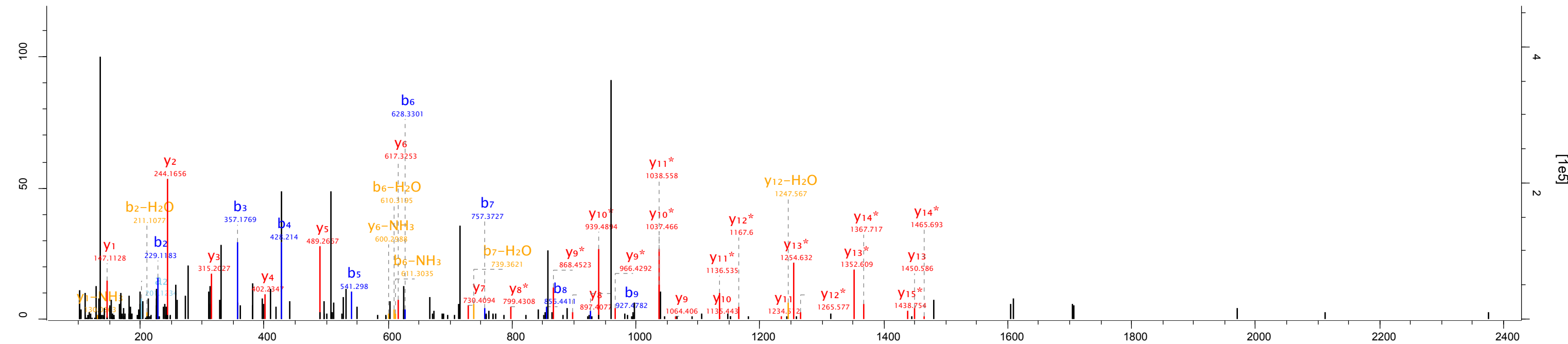




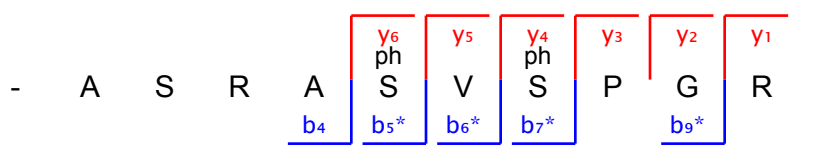
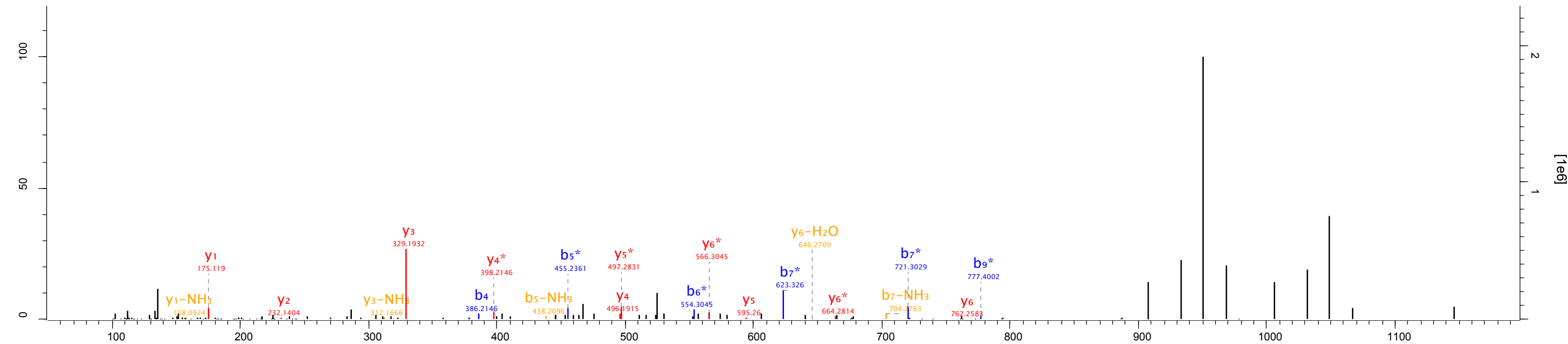
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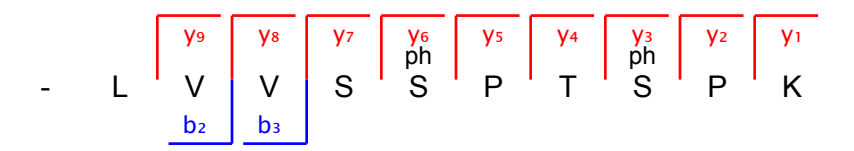
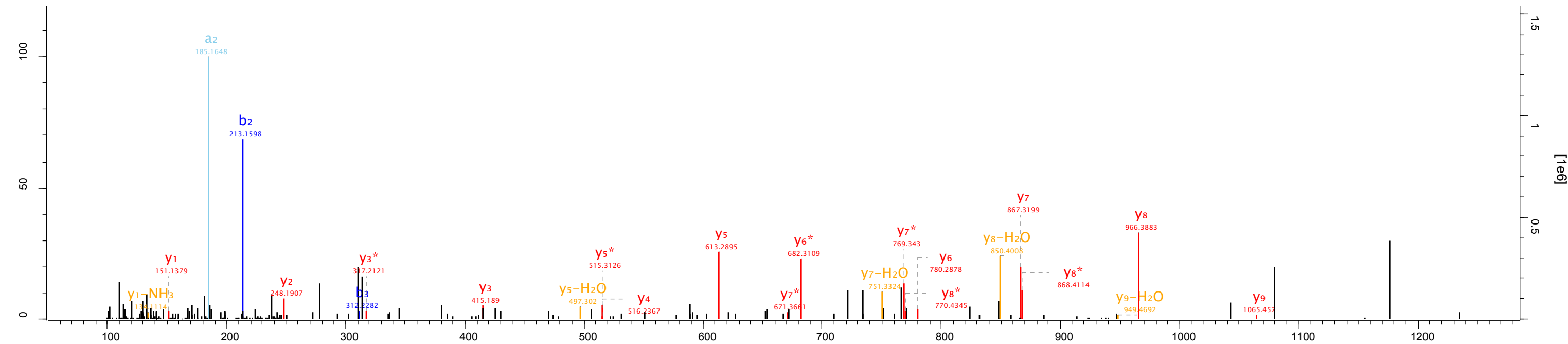
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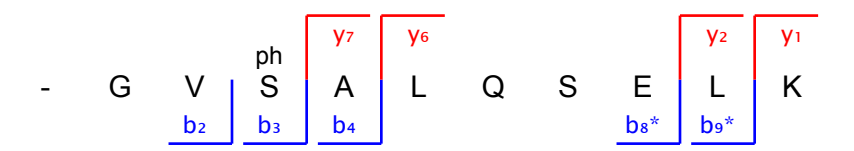
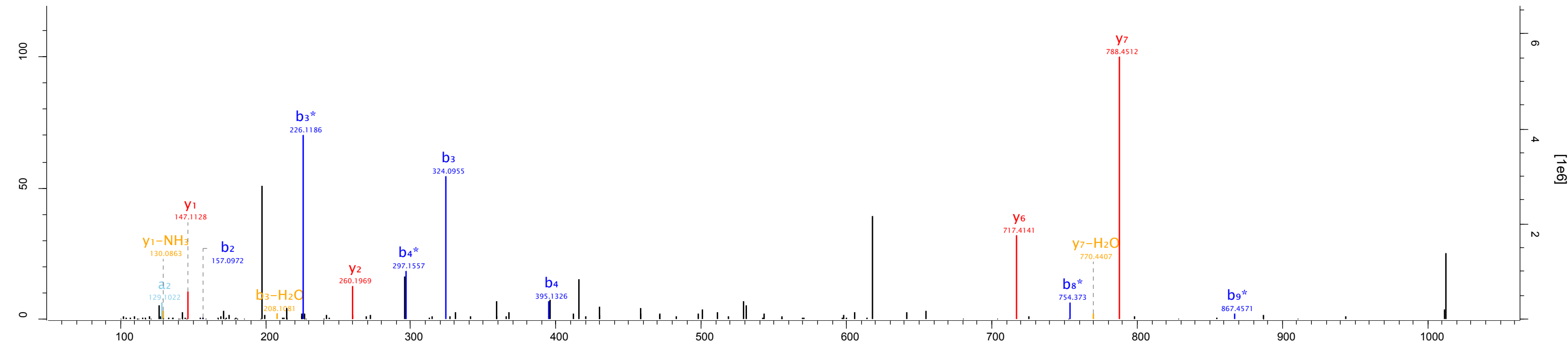
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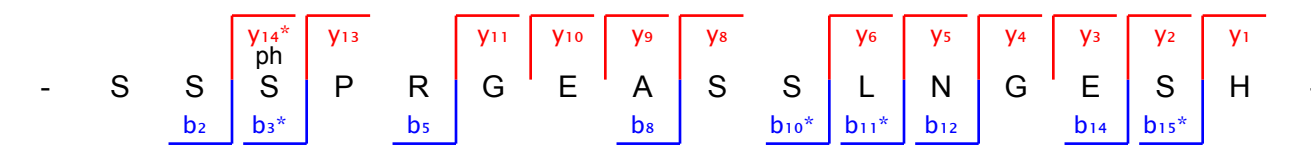
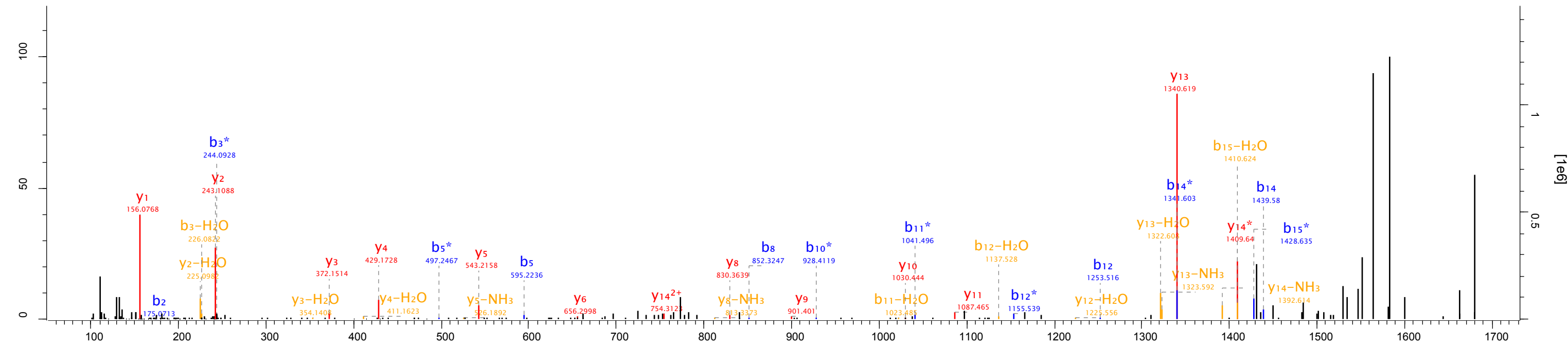
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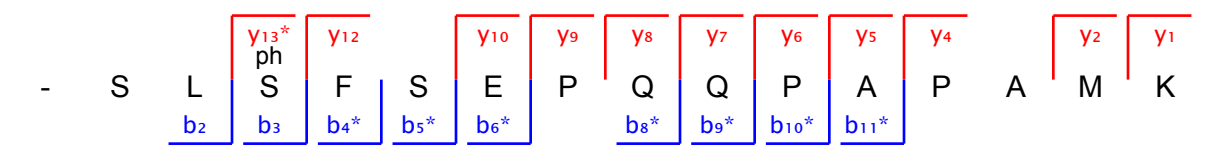
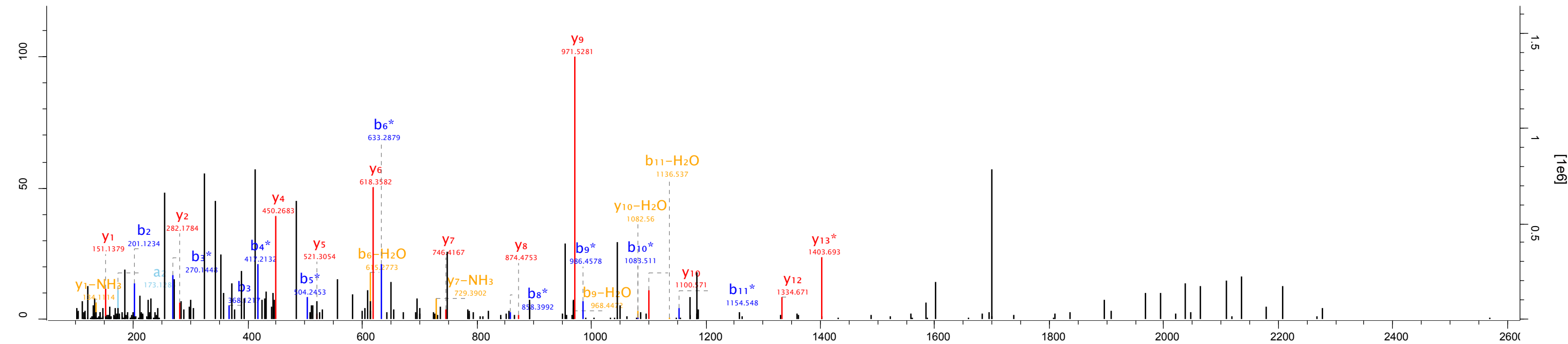
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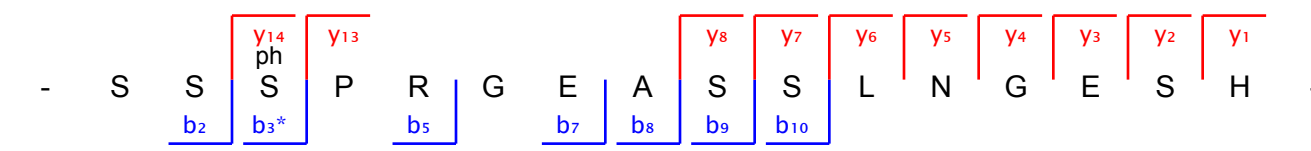
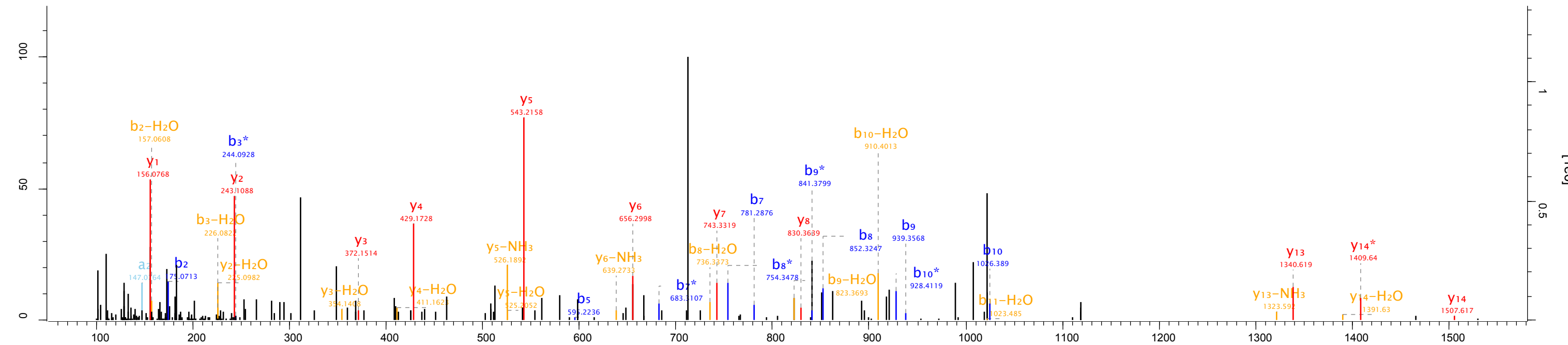
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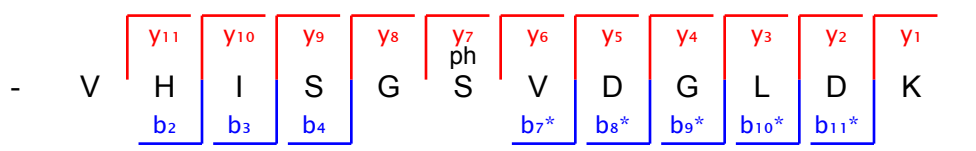
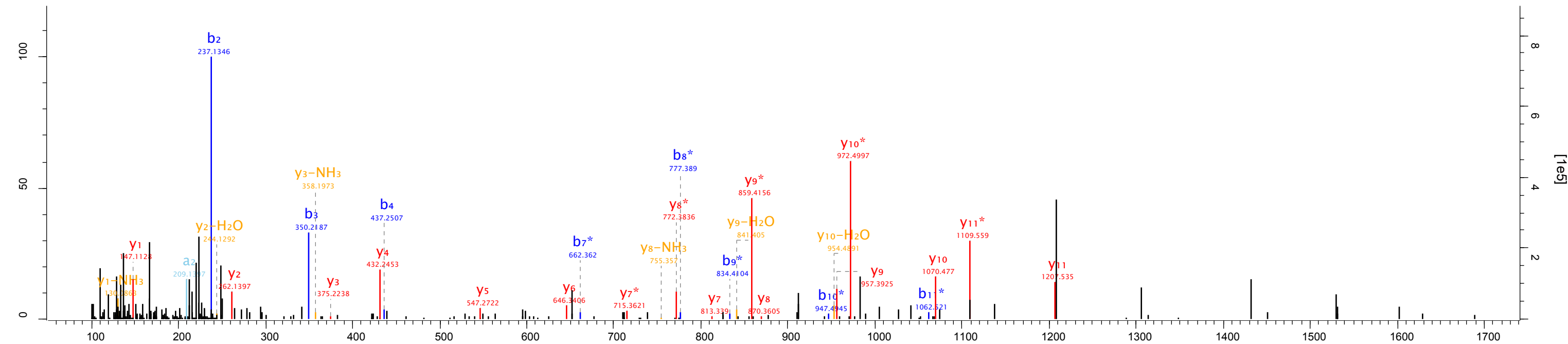
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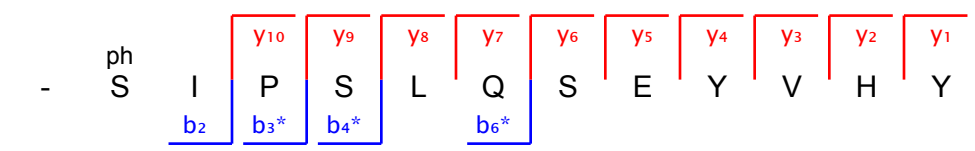
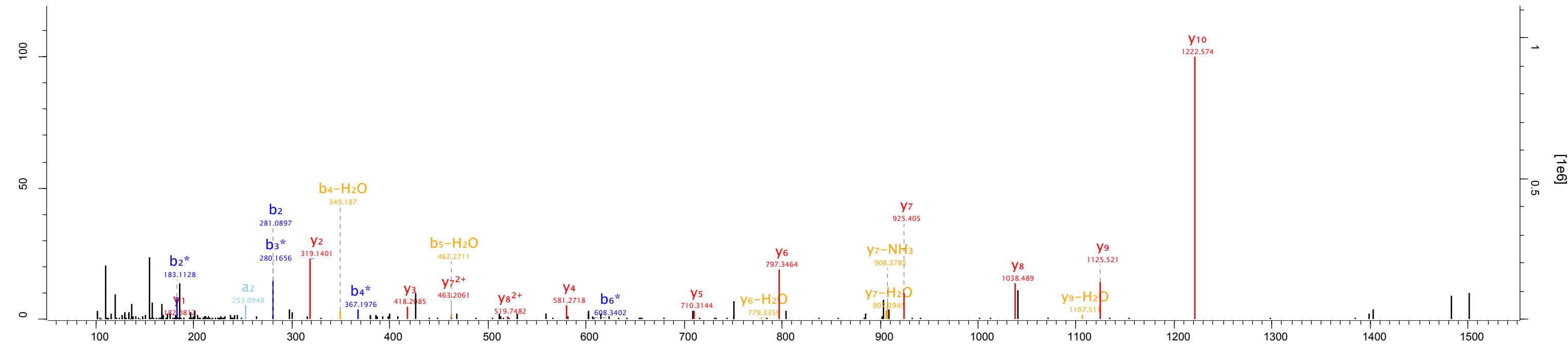
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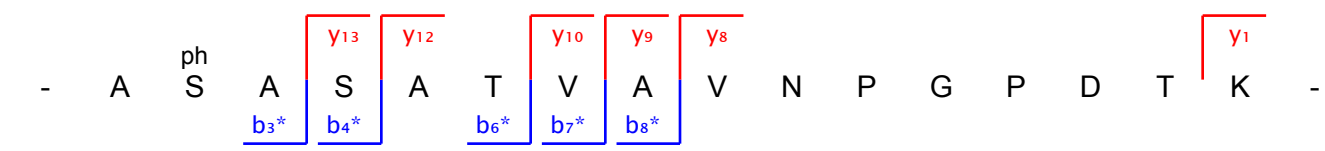
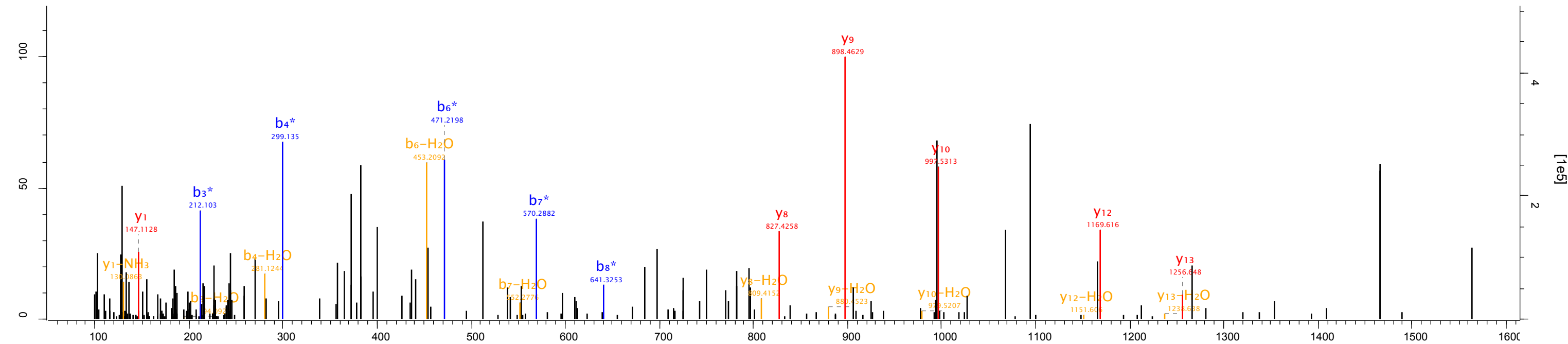
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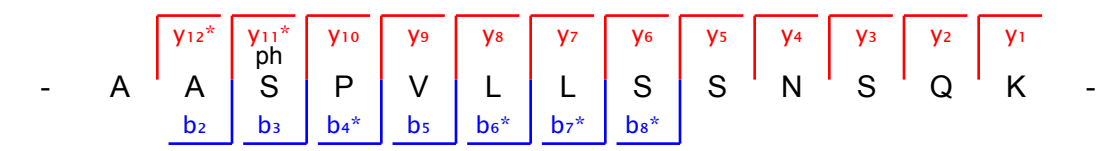
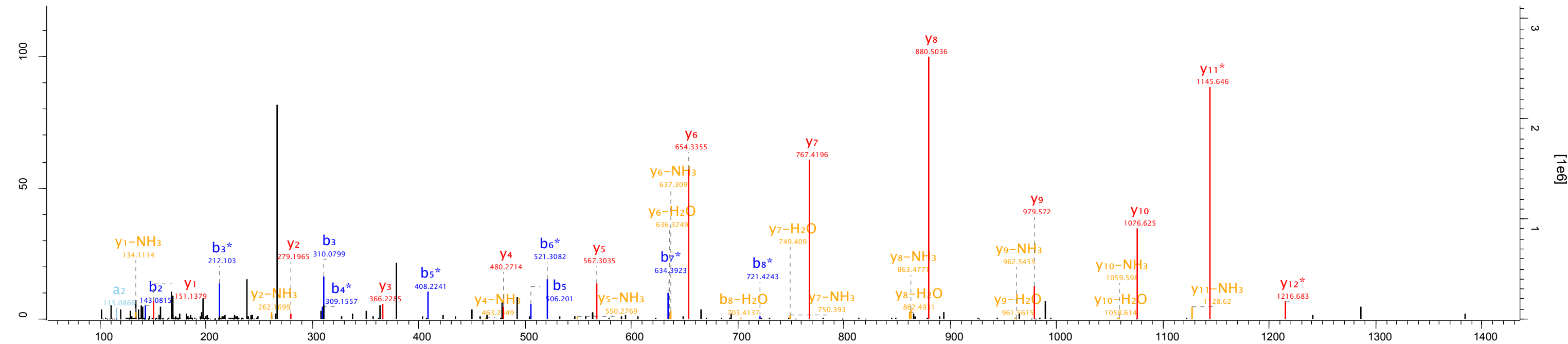
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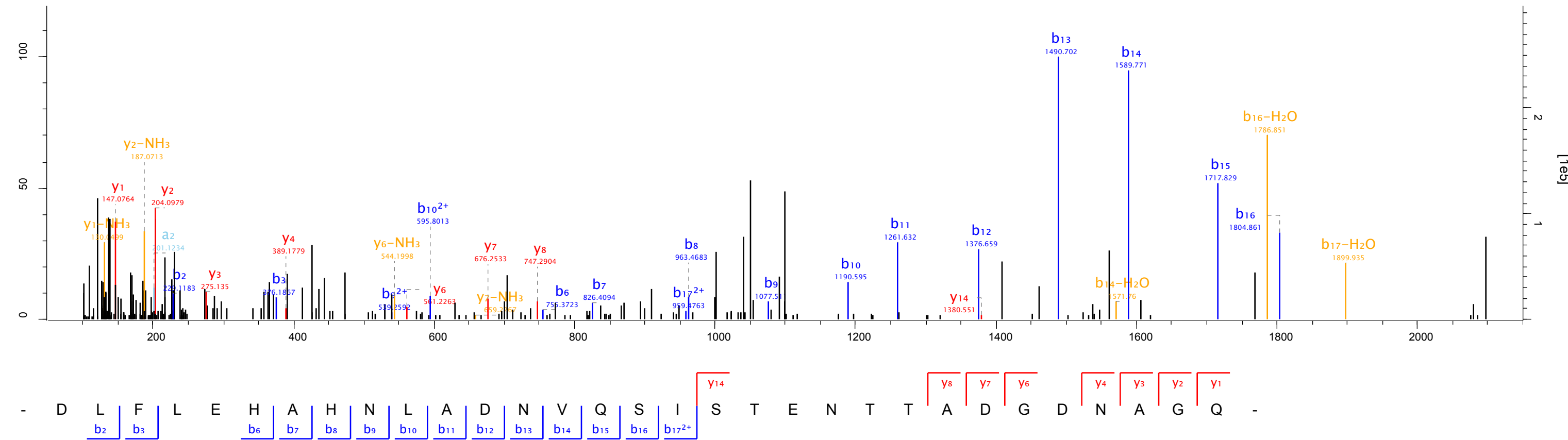
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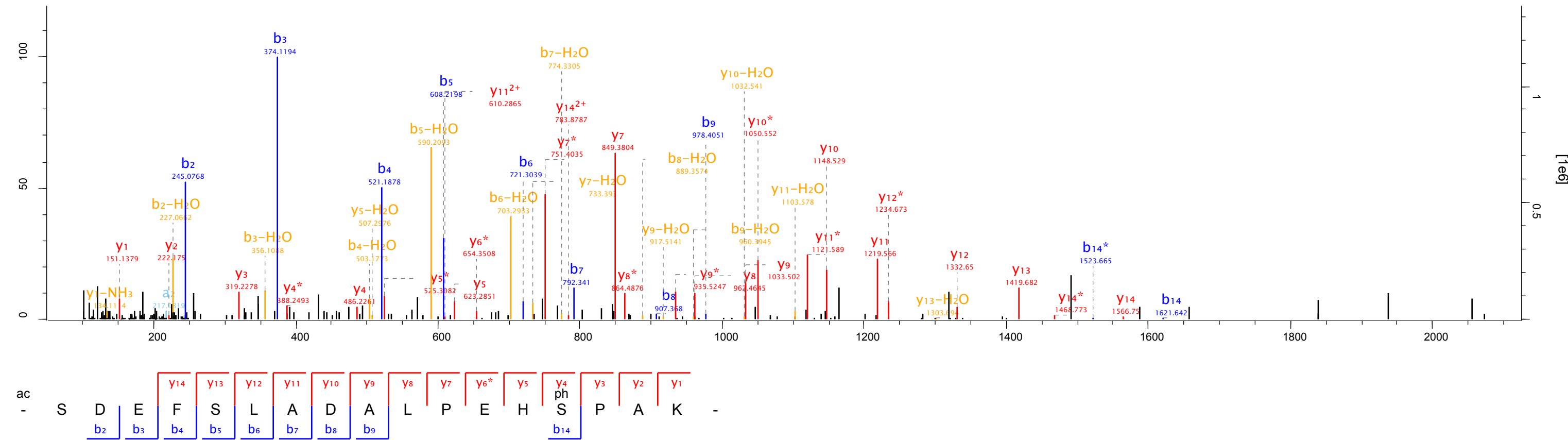
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 Scan: 11839 Method: FTMS; HCD Score: 142.19 m/z: 693.86 Gene names: ELK3



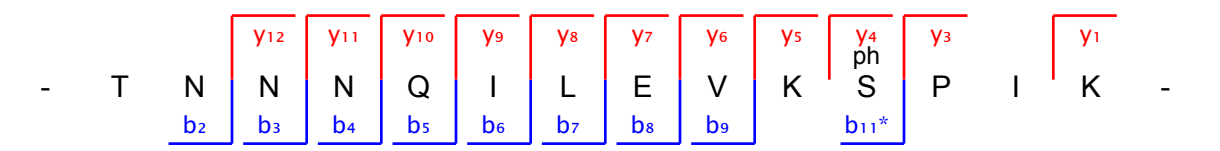
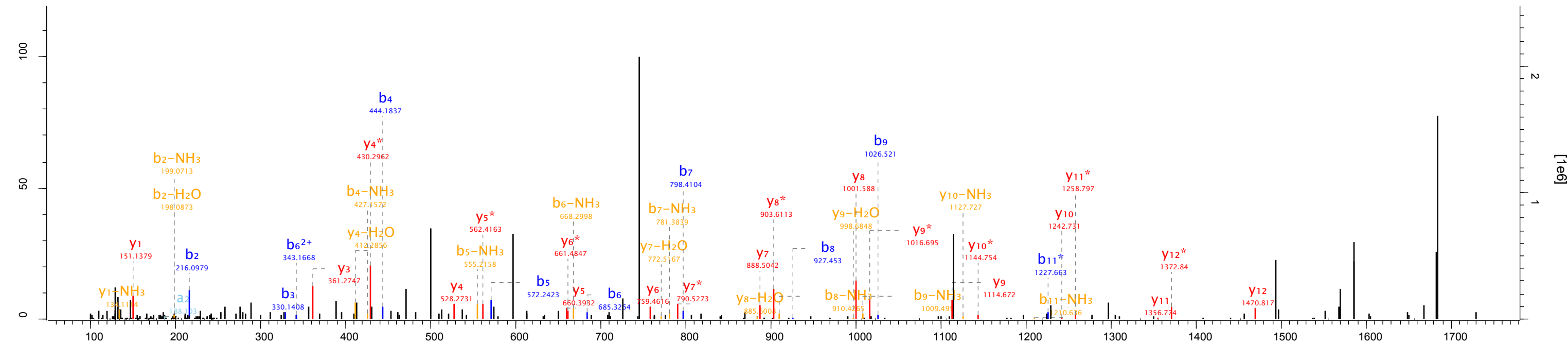
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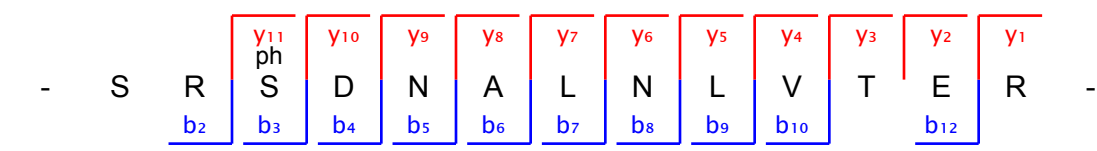
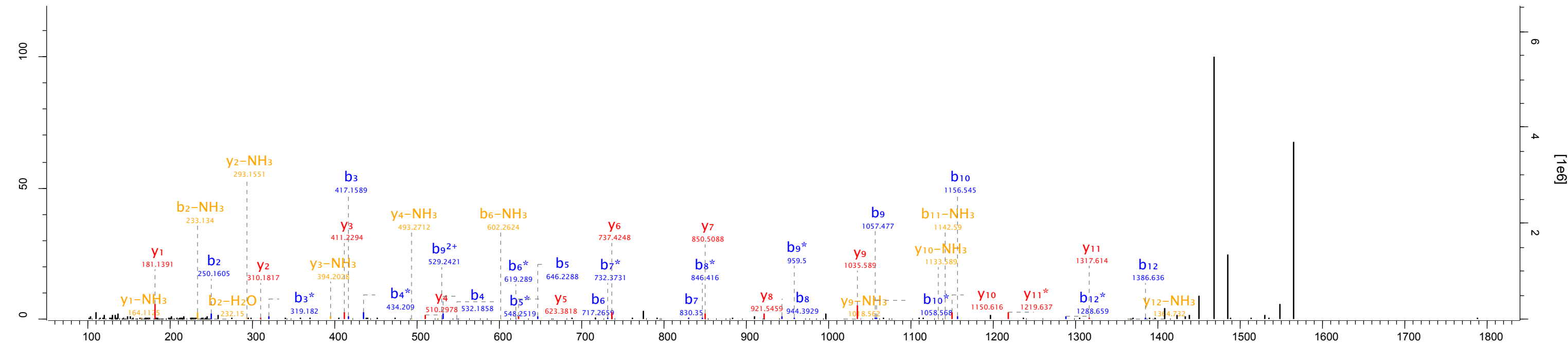
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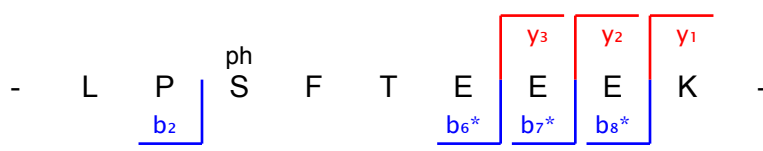
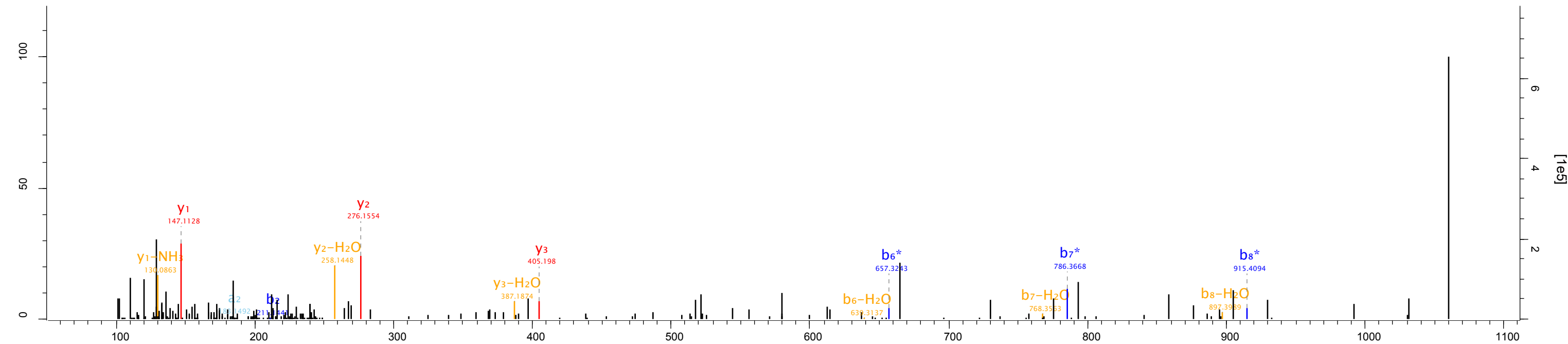
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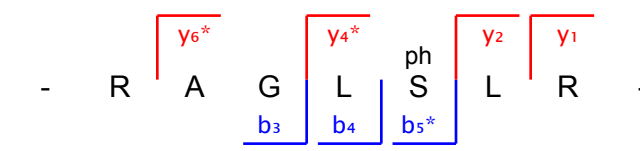
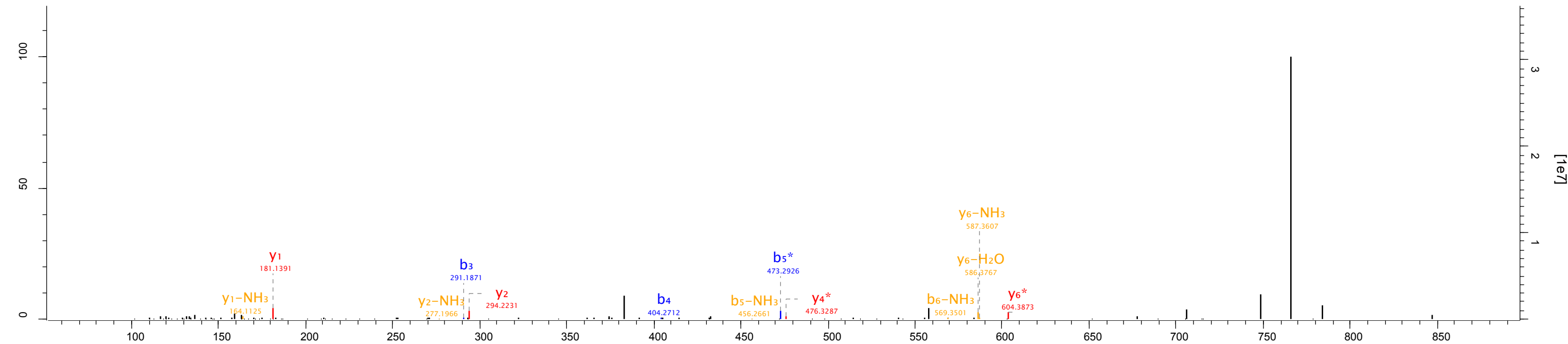
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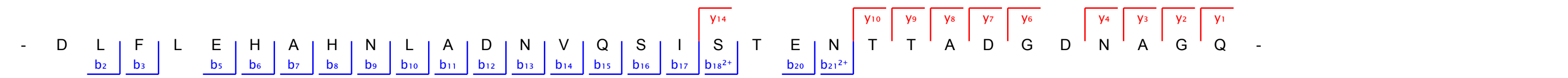
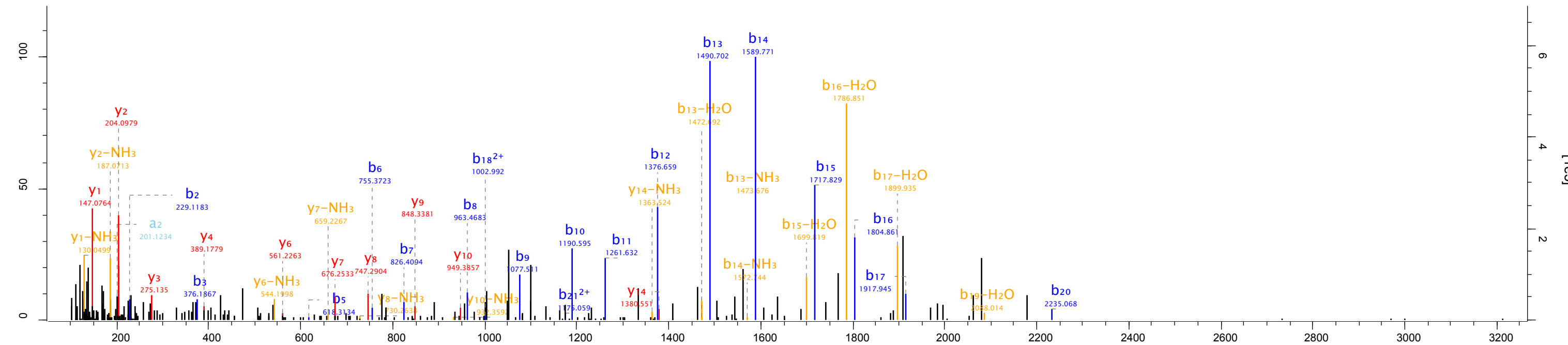
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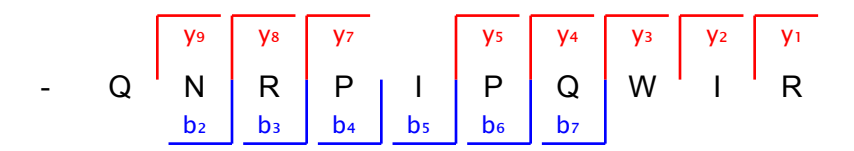
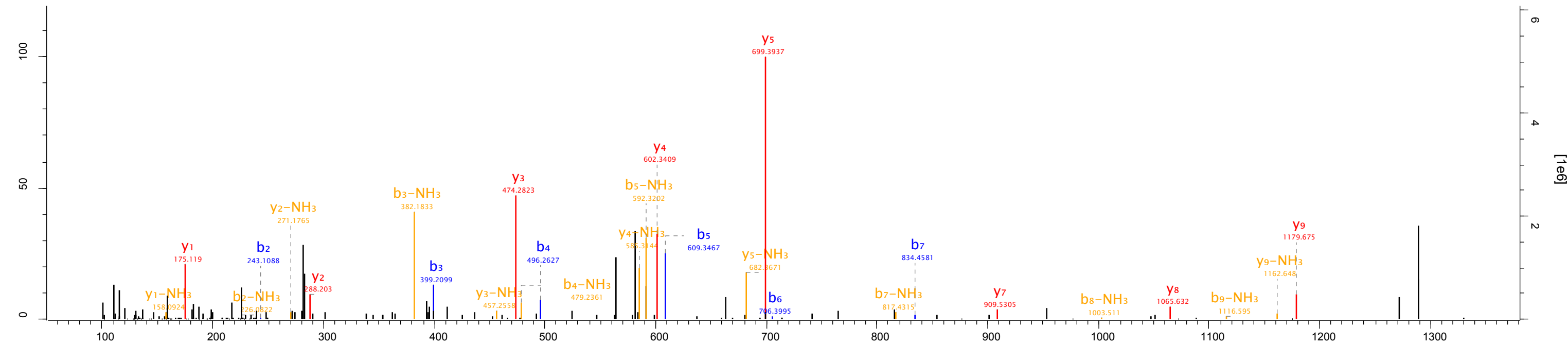
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20150812_A375SR_Phospho_BR1_07
Scan 7029 Method FTMS; HCD Score 51.95 m/z 432.75



Raw file: 20150812_A375SR_Phospho_BR1_08
 Scan: 22459 Method: FTMS; HCD Score: 128.03 m/z: 1100.17 Gene names: CEBPG

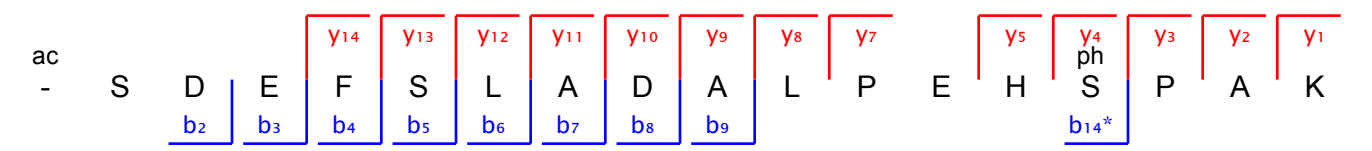
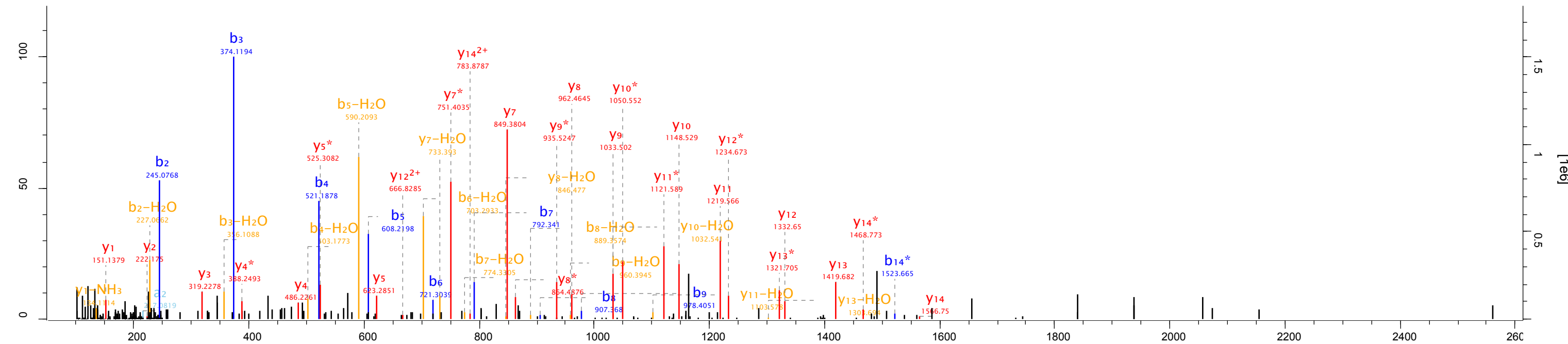


Raw file: 20150812_A375SR_Phospho_BR1_09
 Scan: 13489 Method: FTMS; HCD Score: 144.77 m/z: 436.58 Gene names: RPL39P5;RPL39

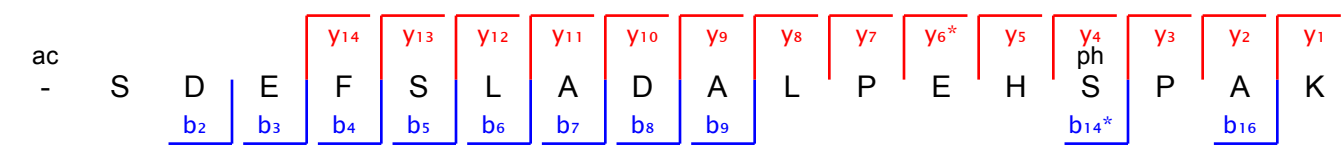
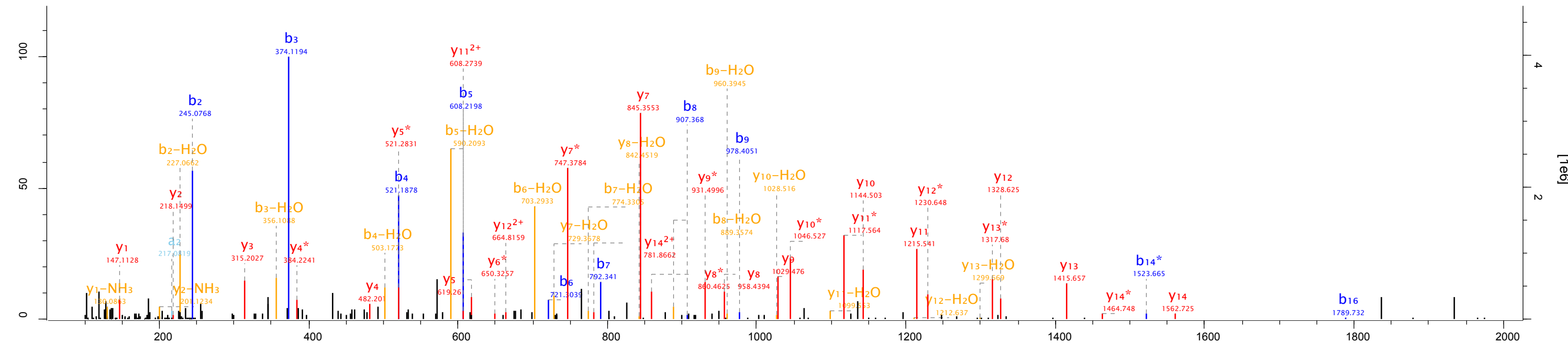


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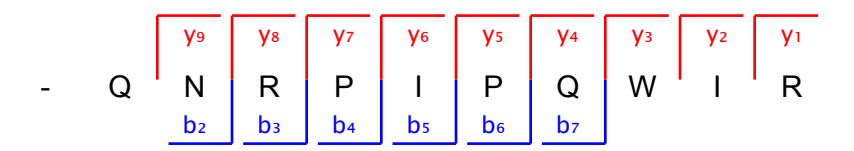
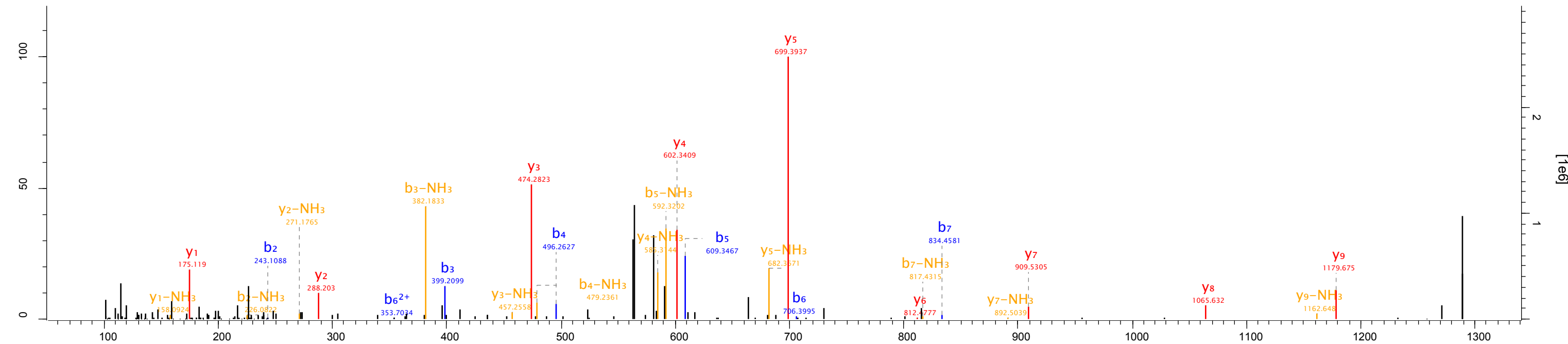
Scan 24029 Method FTMS; HCD Score 207.67 m/z 970.94 Gene names MAPK11P1L



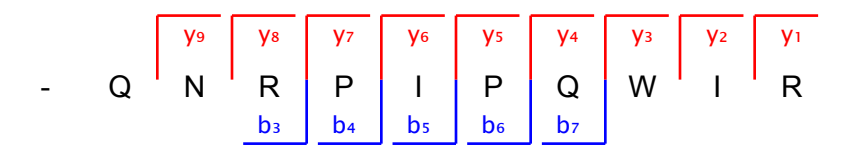
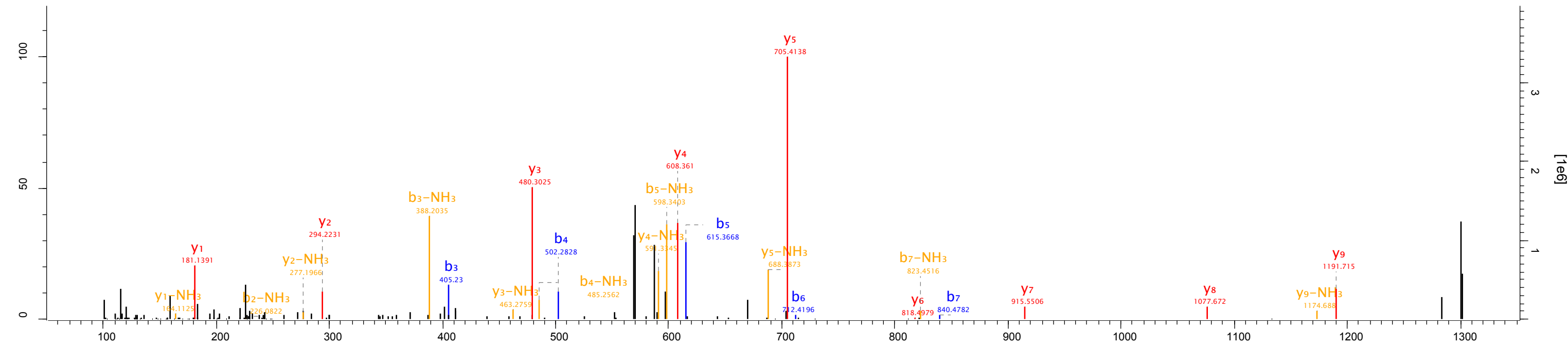
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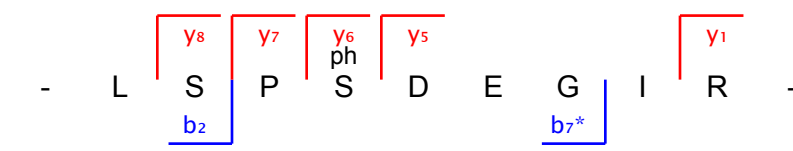
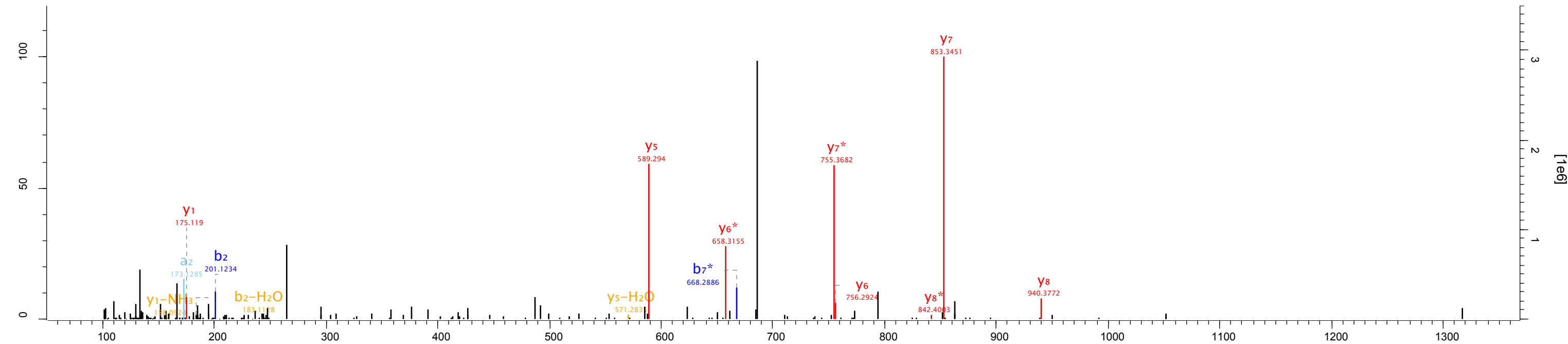
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Raw file: 20150812_A375SR_Phospho_BR1_10
 Scan: 13769 Method: FTMS; HCD Score: 162.88 m/z: 440.6 Gene names: RPL39P5;RPL39

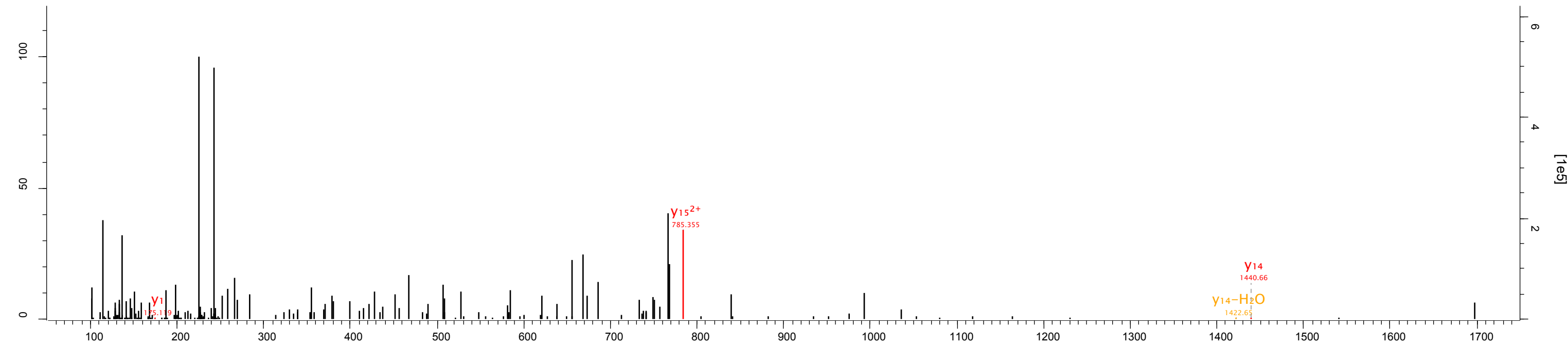


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 Scan 4849 Method FTMS; HCD Score 40.77 m/z 527.23



Raw file
20150814_A375SR_Phospho_BR2_02

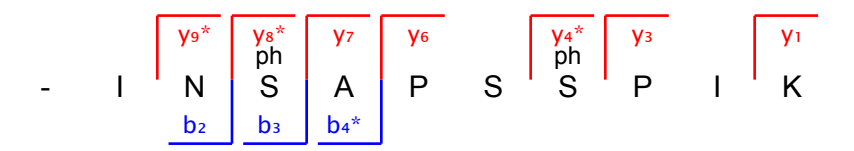
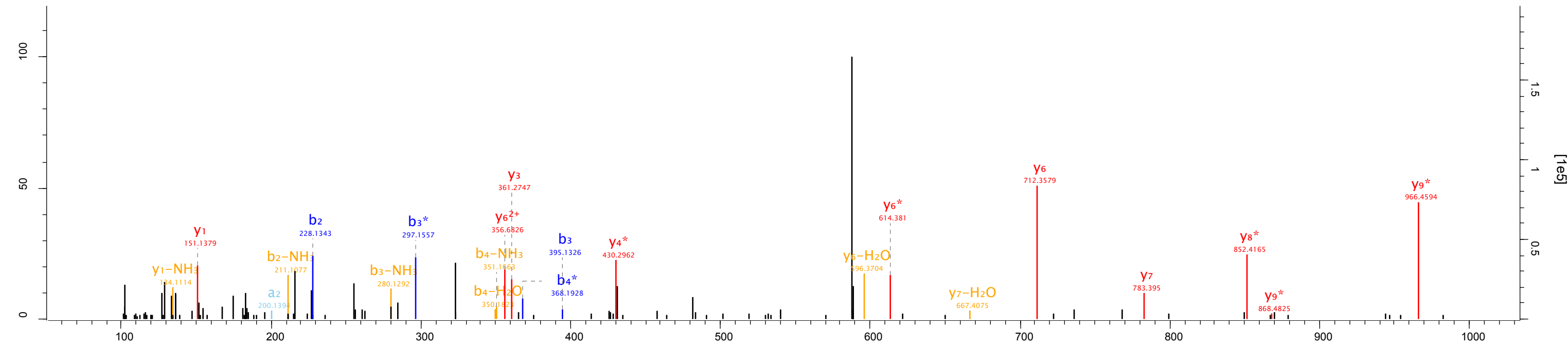
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14899	FTMS; HCD	2.8	674.33	FAM214B



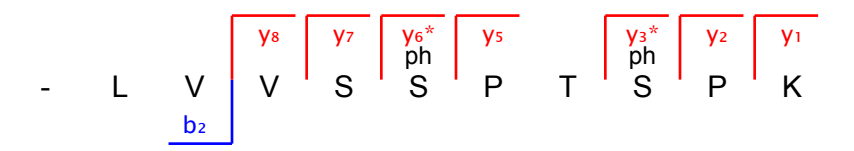
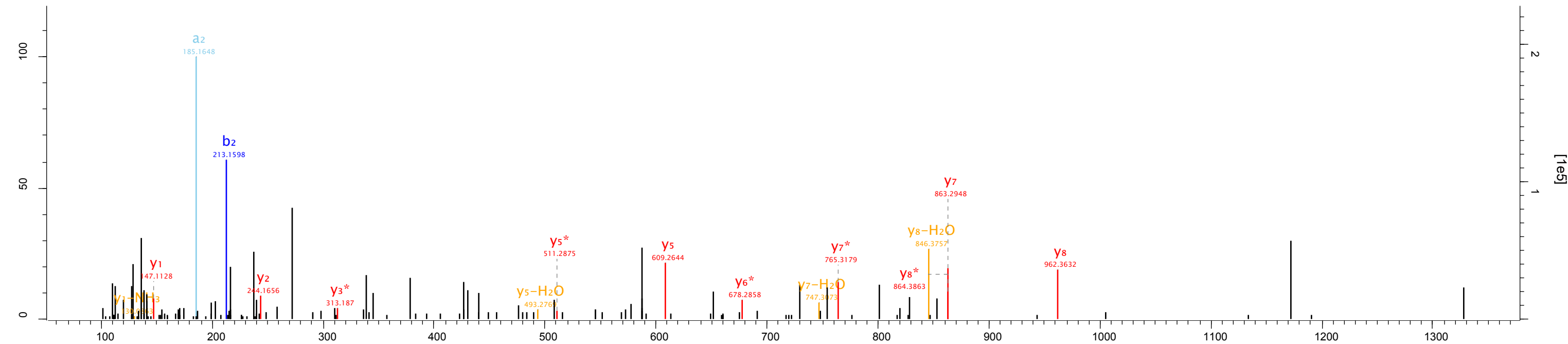
- L L P A G E A P D V S S E E E G P A P R -

Annotations: y_{15}^{2+} above E, y_{14} above A, y_1 above R.

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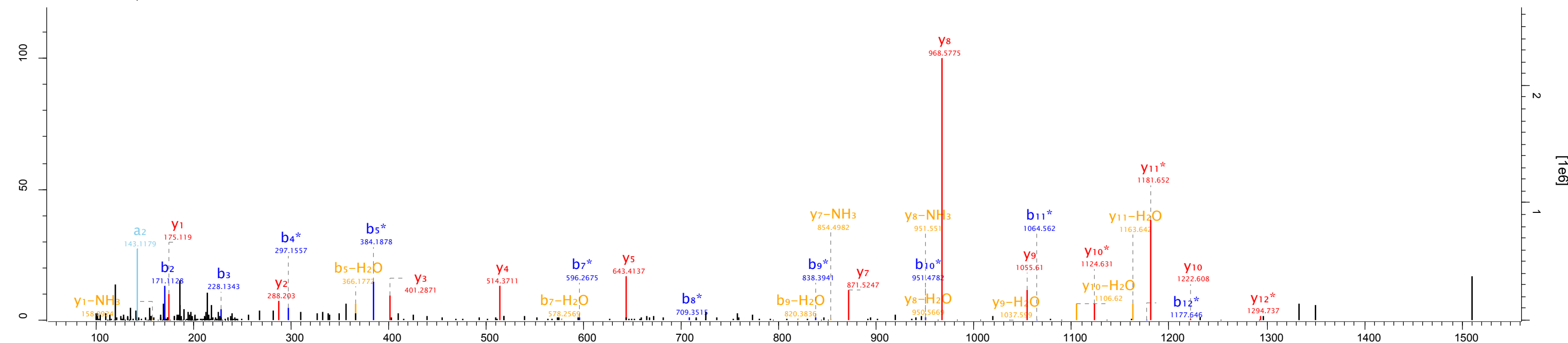


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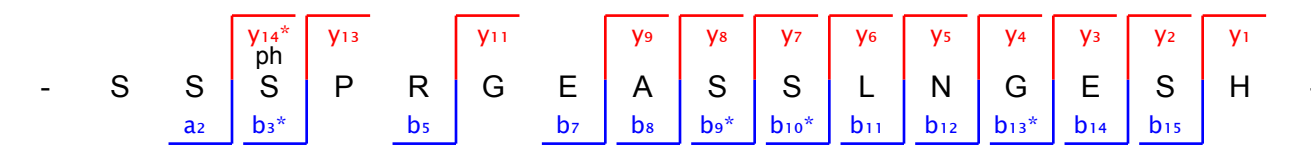
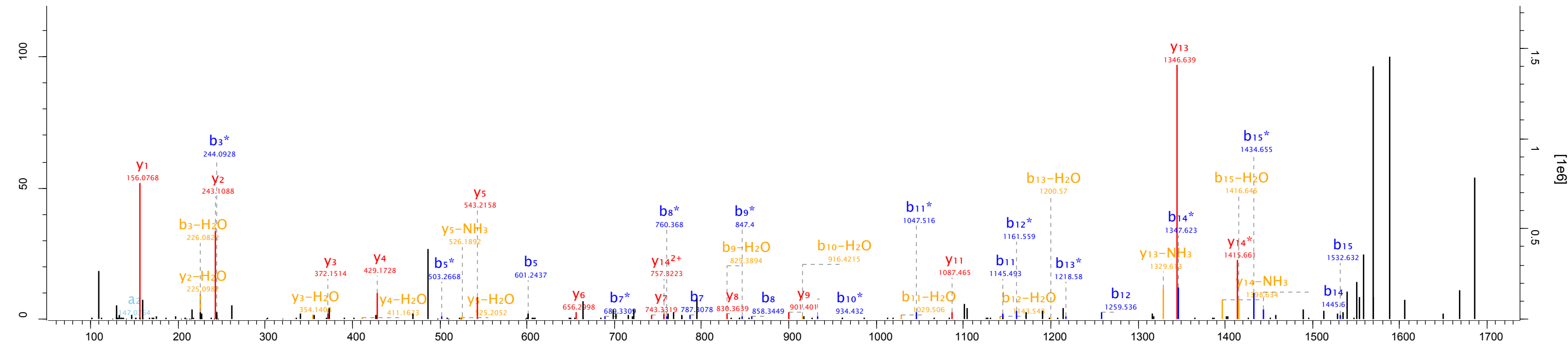
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20150814_A375SR_Phospho_BR2_03

Scan Method Score m/z Gene names
28639 FTMS; HCD 125.67 725.37 SLC35C2

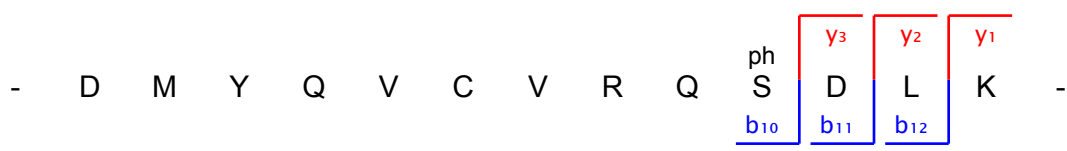
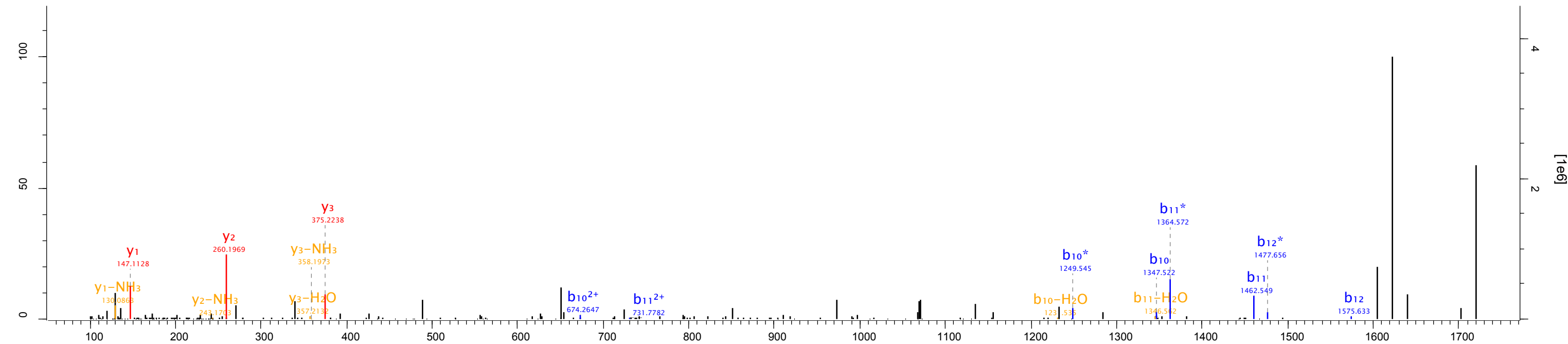


- G -
L G S S P D L E L L L R -
b2 b3 b4* b5* b7* b8* b9* b10* b11* b12*

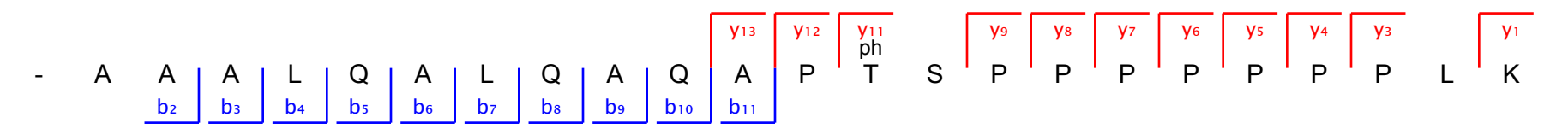
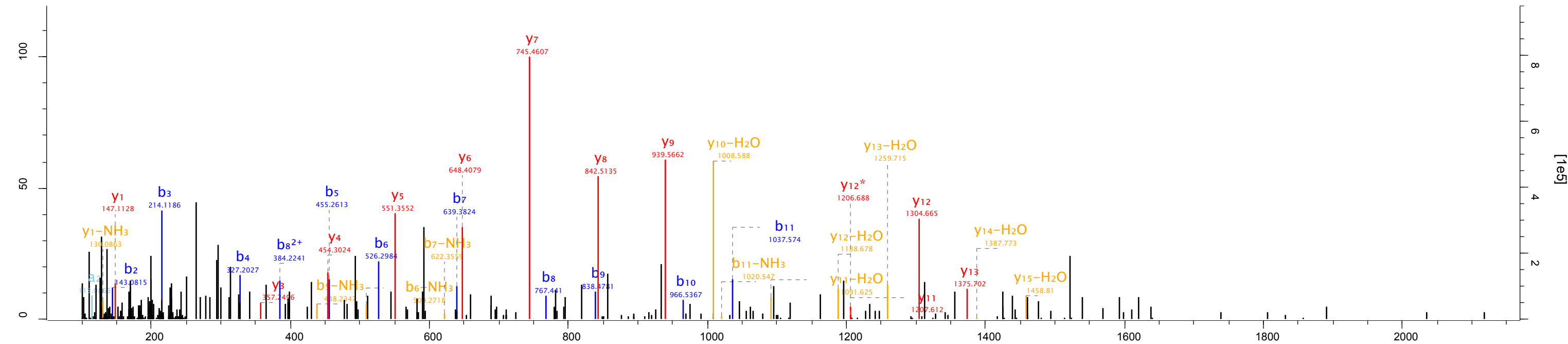
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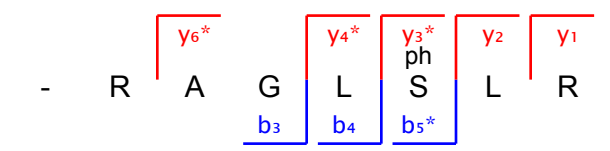
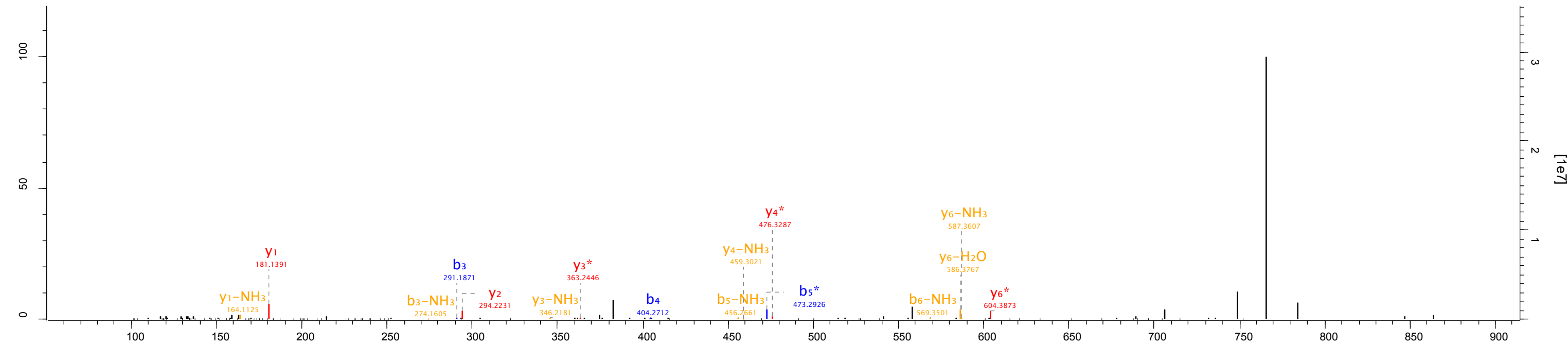
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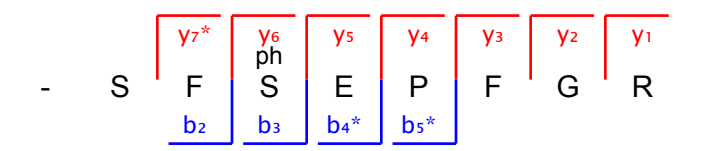
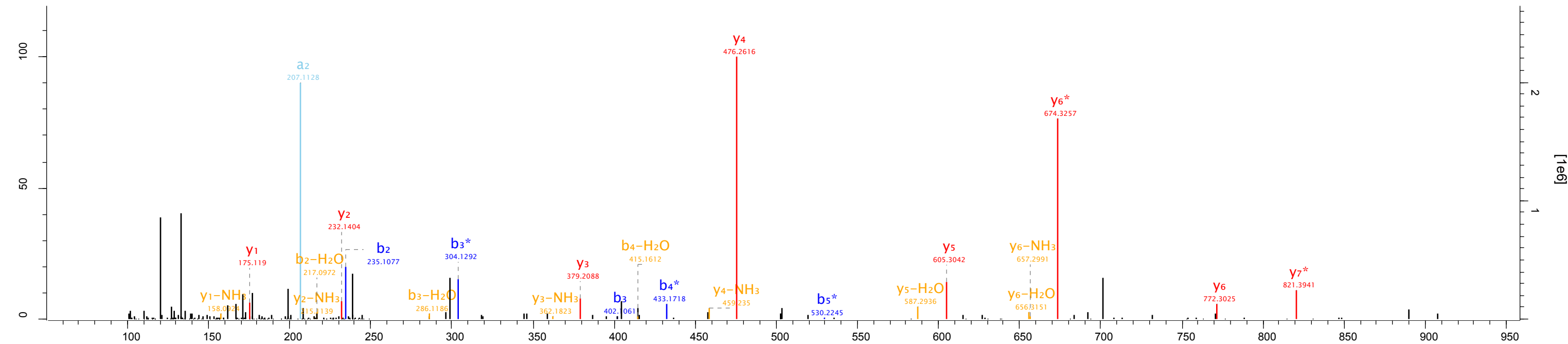
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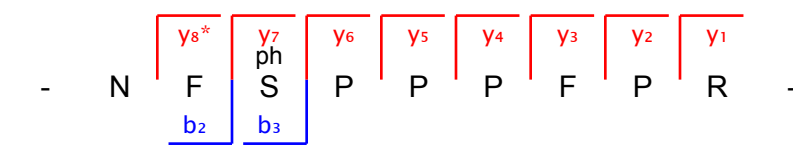
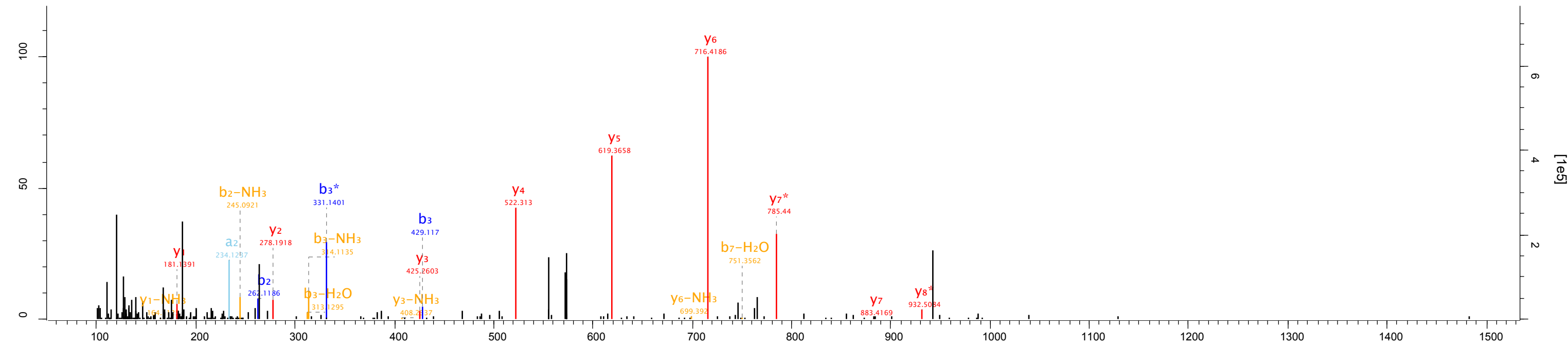
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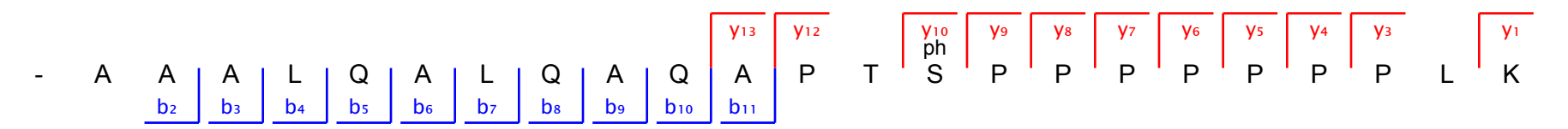
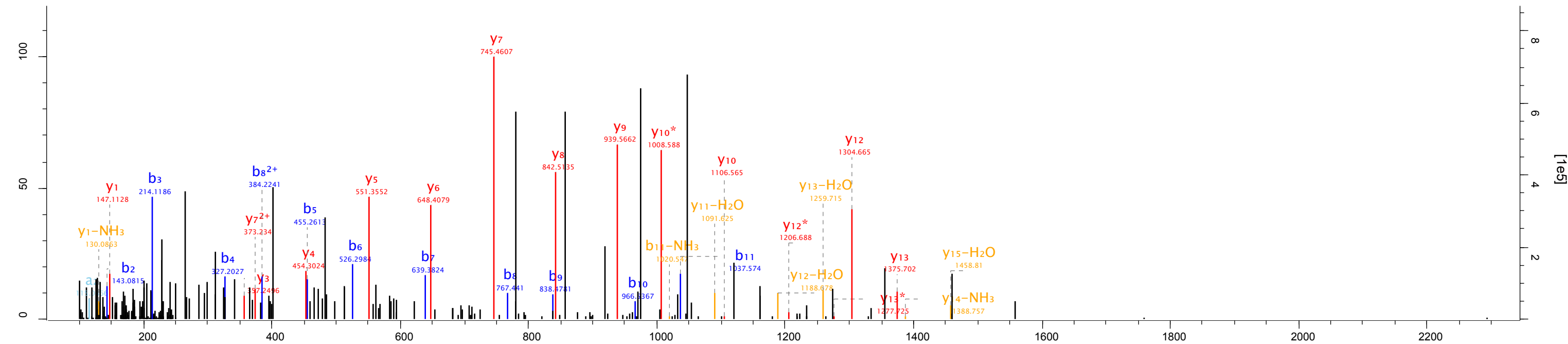
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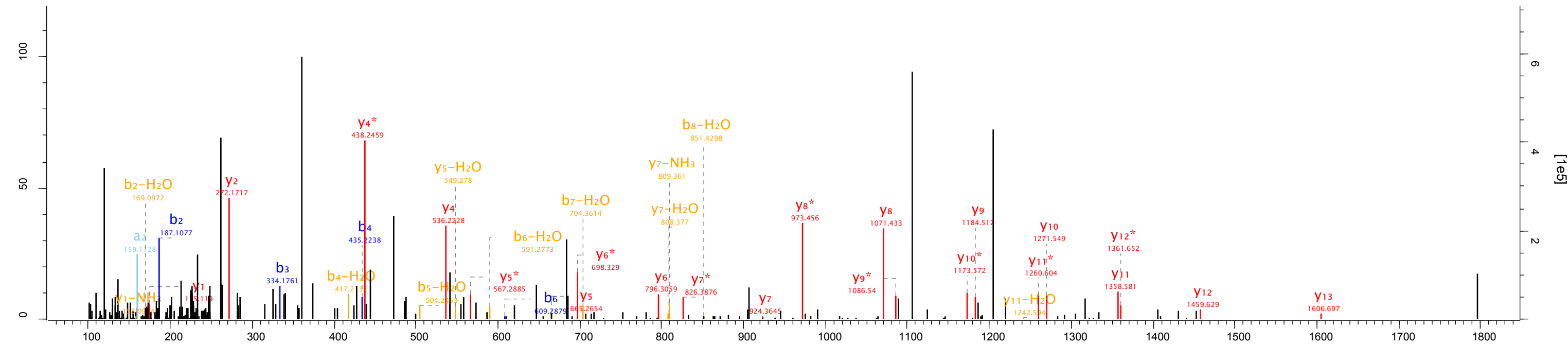
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 Scan: 19499 Method: FTMS; HCD Score: 66.27 m/z: 573.27 Gene names: CCDC125



Raw file: 20150814_A375SR_Phospho_BR2_05
 Scan: 20869 Method: FTMS; HCD Score: 67.5 m/z: 781.08 Gene names: ZNF579



Raw file
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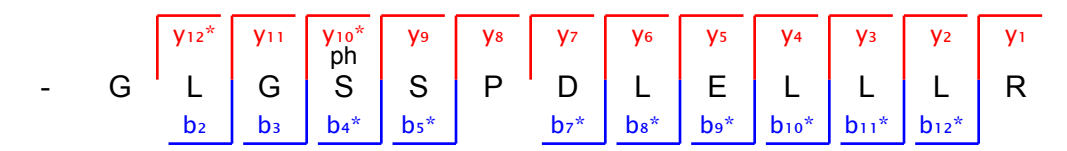
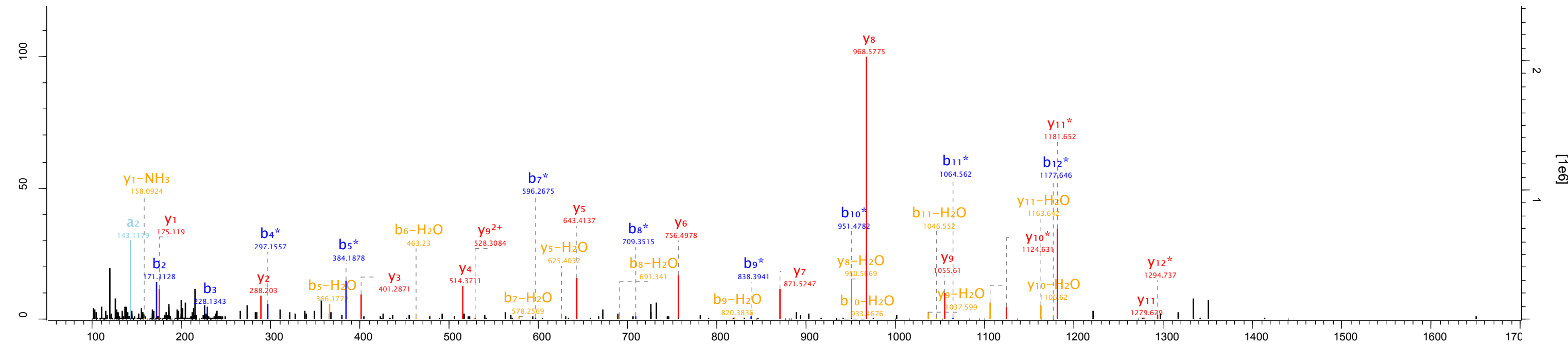


- S V F T S S L F Q M E P S P R -

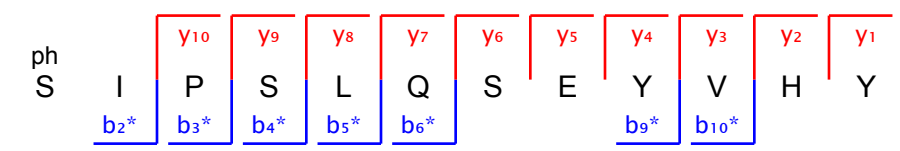
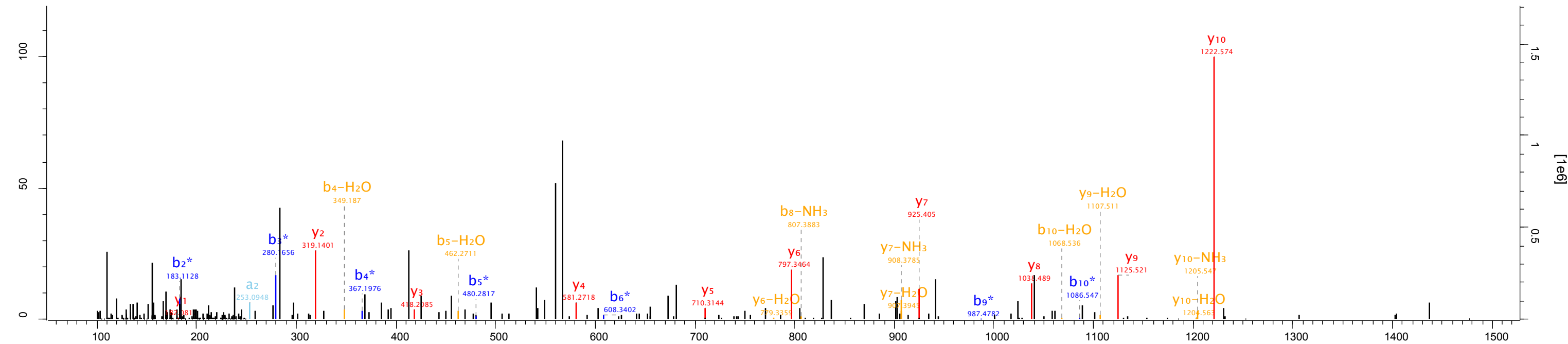
Fragmentation mapping:

- b₂ (V-F)
- b₃ (F-T)
- b₄ (T-S)
- b₆ (S-S)
- y₁ (P-R)
- y₂ (S-P)
- y₄ (E-P)
- y₅ (M-E)
- y₆ (Q-M)
- y₇ (F-Q)
- y₈ (L-F)
- y₉ (S-L)
- y₁₀ (S-S)
- y₁₁ (S-T)
- y₁₂ (T-F)
- y₁₃ (F-V)

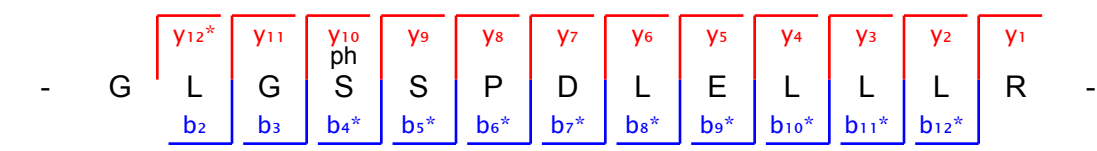
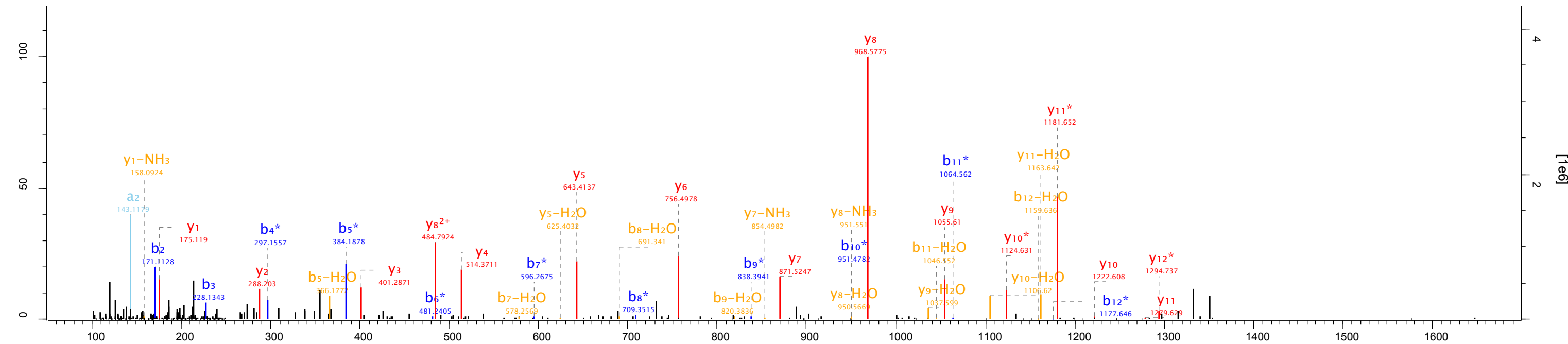
Raw file Scan Method Score m/z Gene names
 20150814_A375SR_Phospho_BR2_05 28769 FTMS; HCD 130.23 725.37 SLC35C2



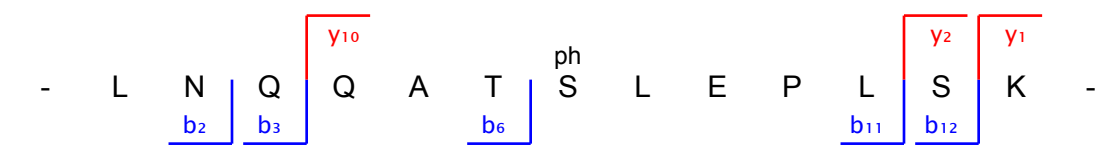
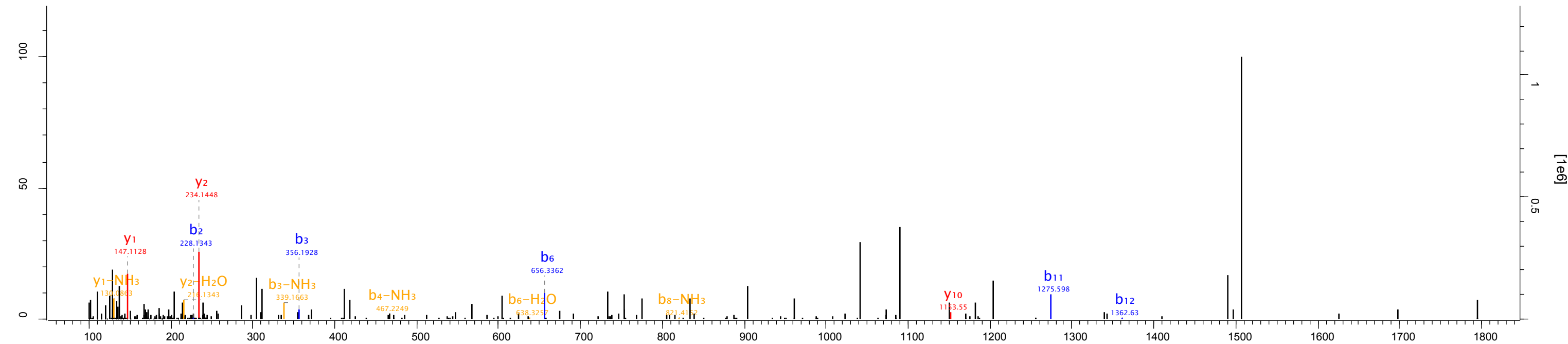
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 Scan: 21679 Method: FTMS; HCD Score: 62.04 m/z: 751.83 Gene names: CDC14A



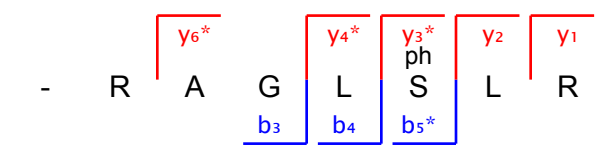
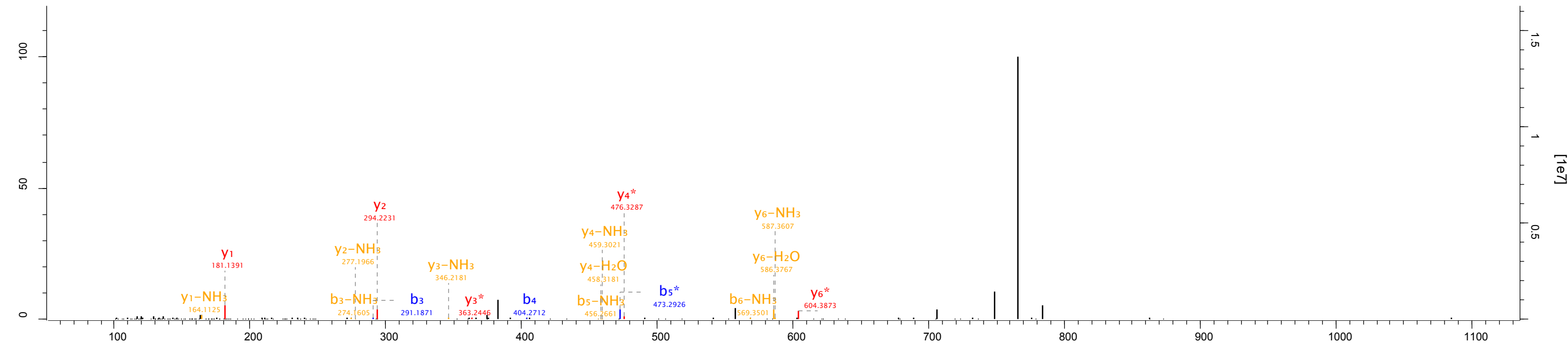
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 Scan: 28699 Method: FTMS; HCD Score: 166.04 m/z: 725.37 Gene names: SLC35C2



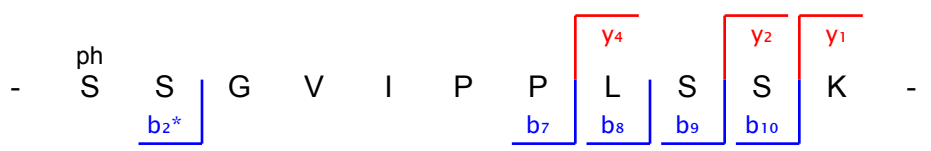
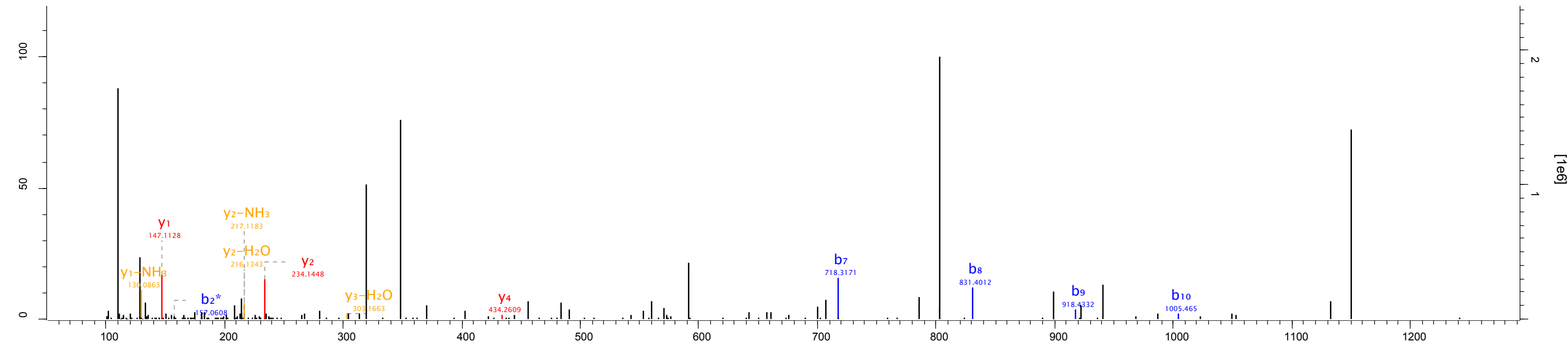
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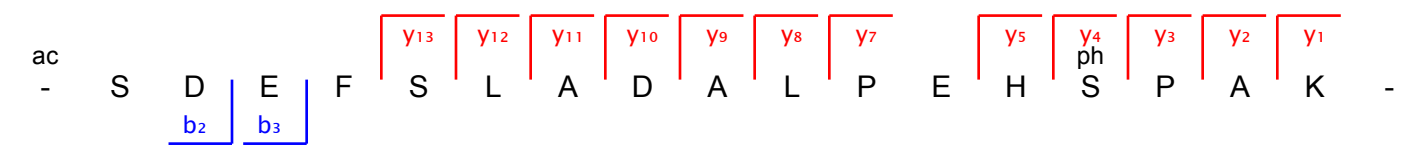
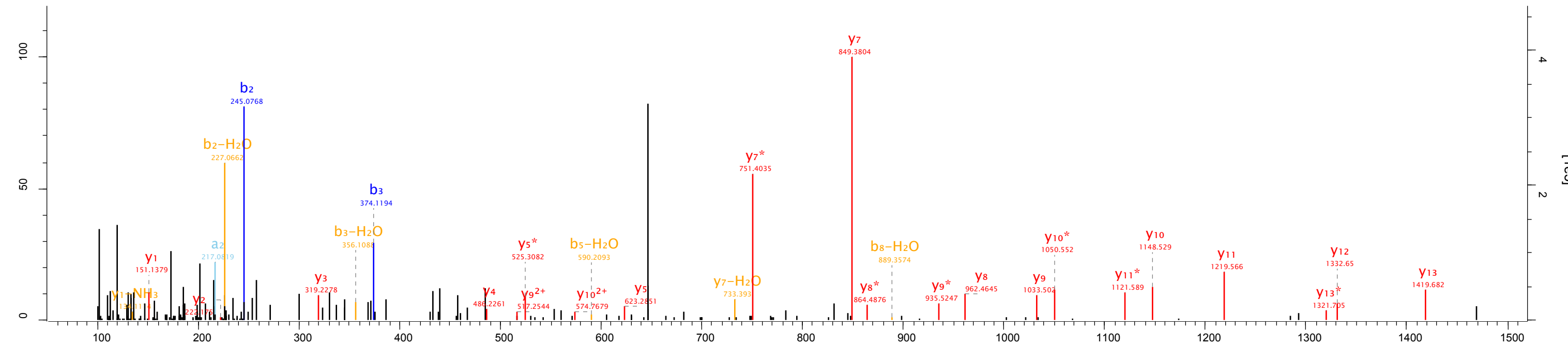
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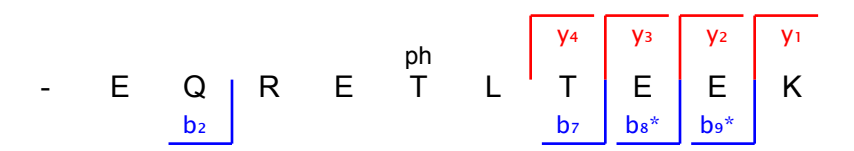
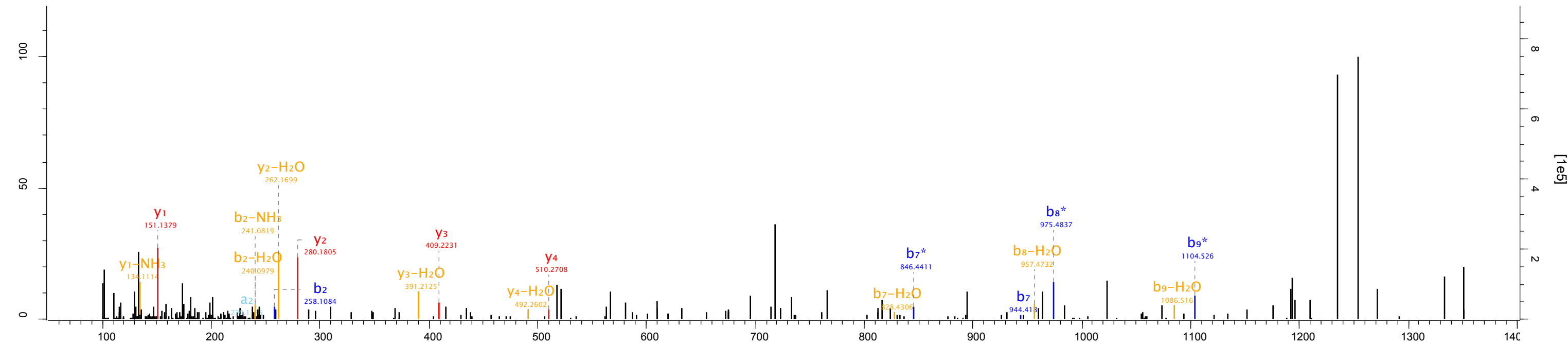
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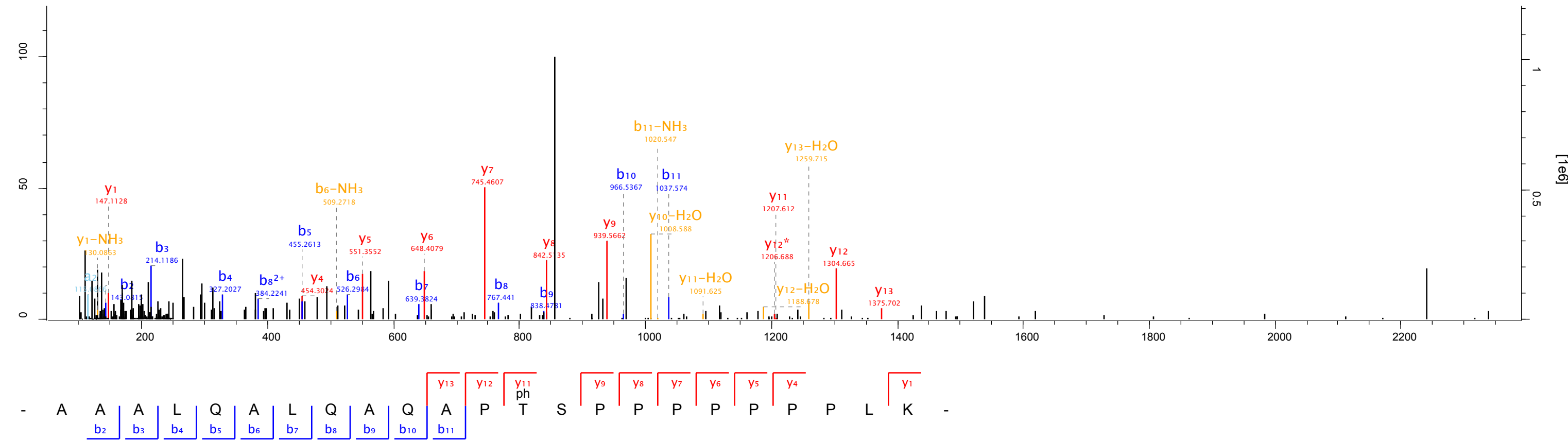
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 Scan: 24069 Method: FTMS; HCD Score: 88.09 m/z: 647.63 Gene names: MAPK11P1L



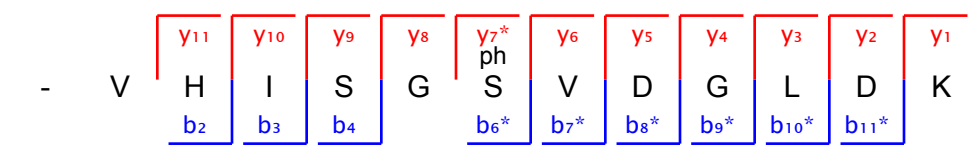
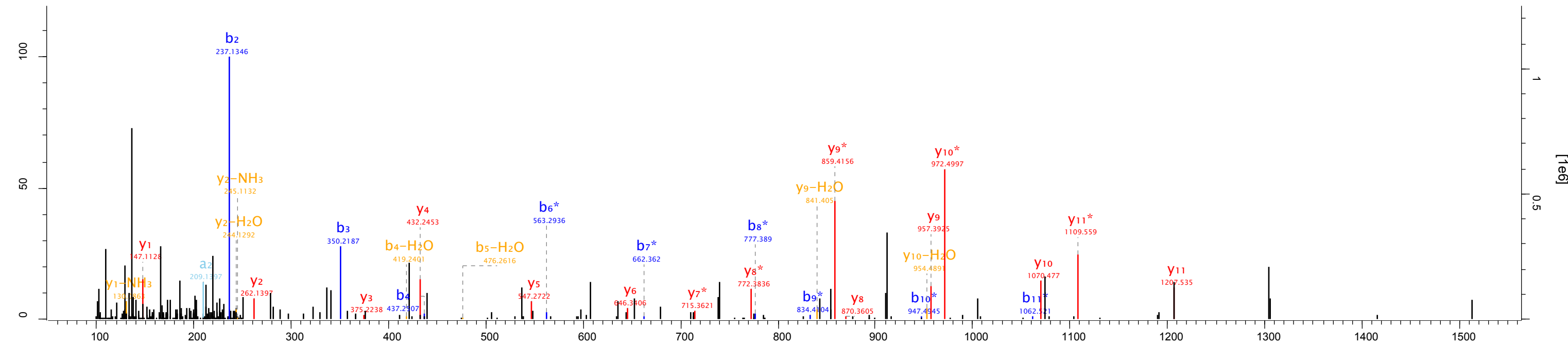
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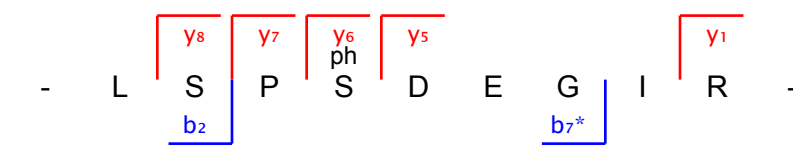
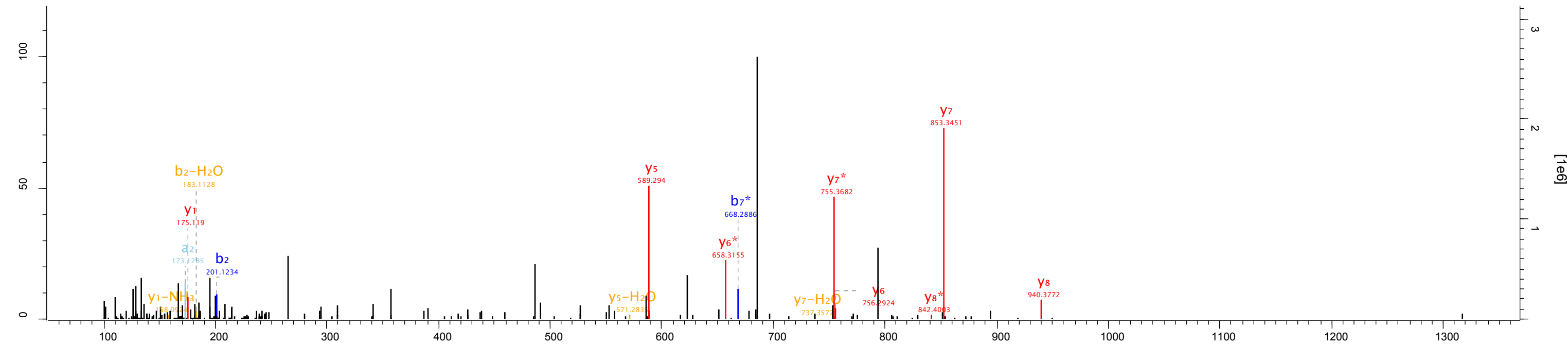
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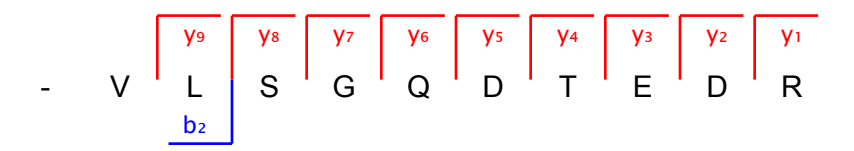
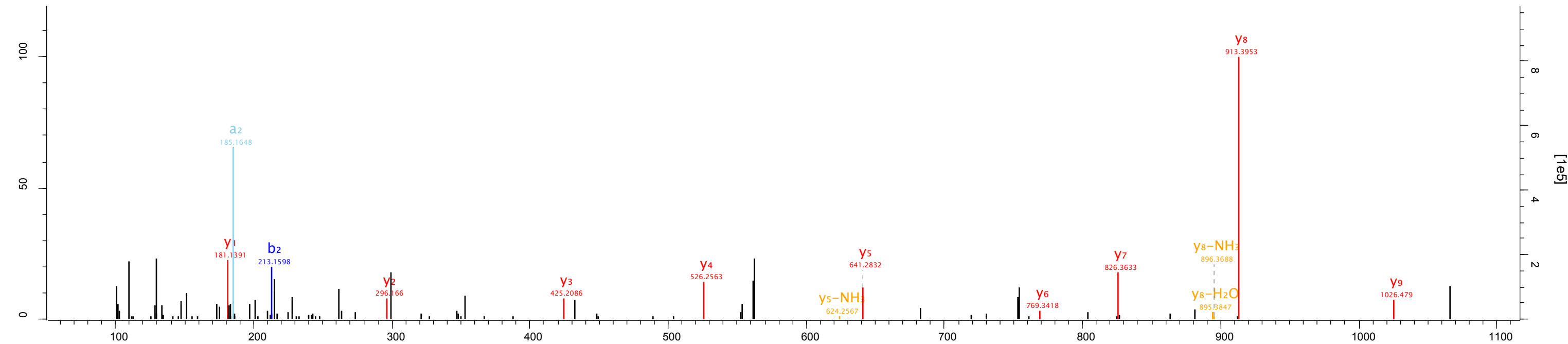
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 Scan: 10999 Method: FTMS; HCD Score: 76.15 m/z: 653.81 Gene names: PHACTR2



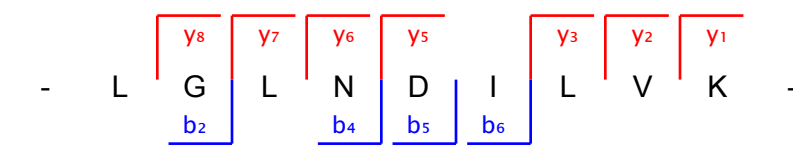
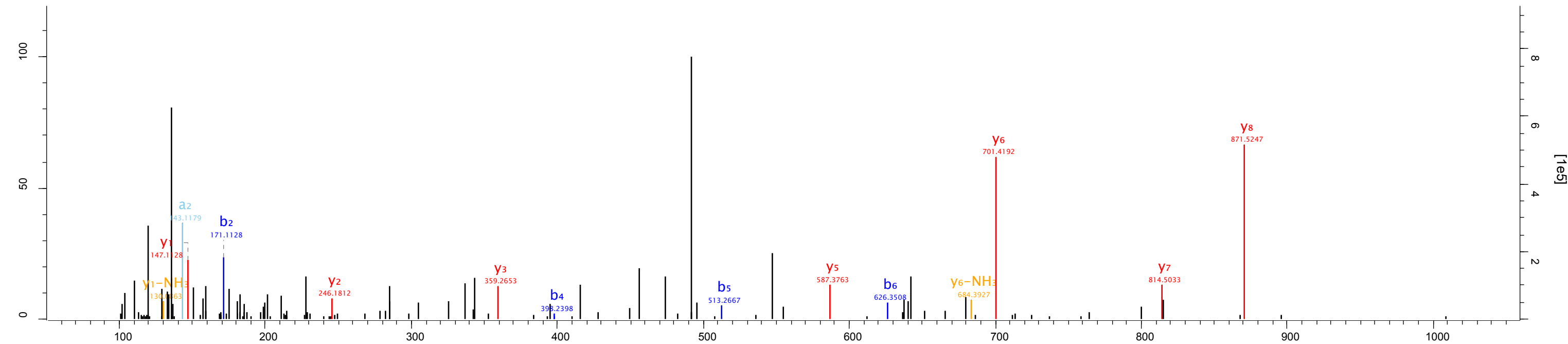
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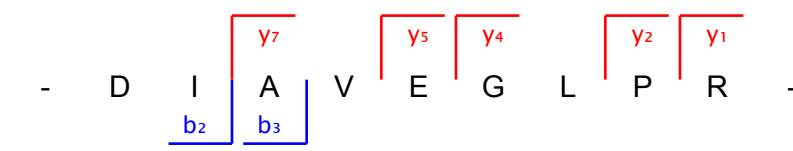
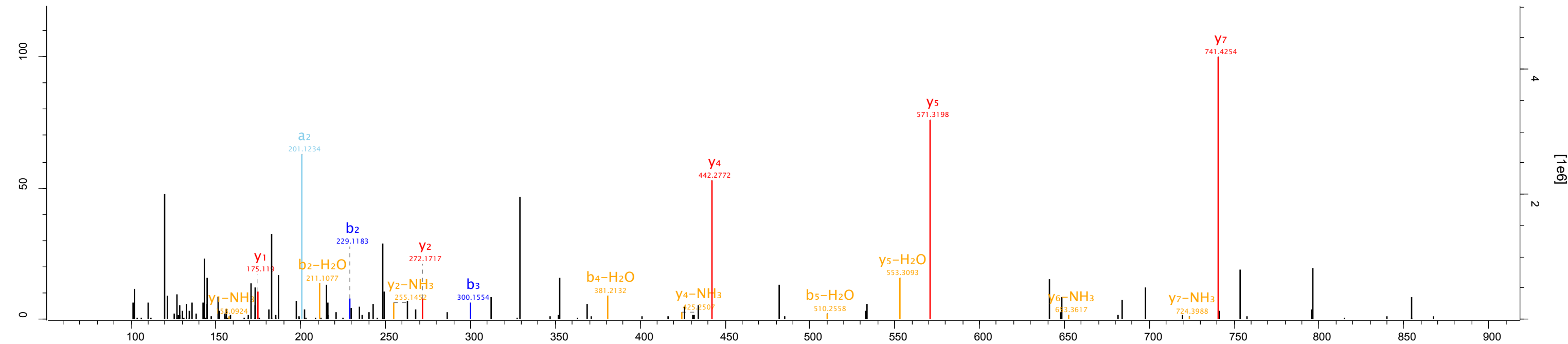
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 Scan: 5159 Method: FTMS; HCD Score: 52.25 m/z: 563.28 Gene names: SFT2D2



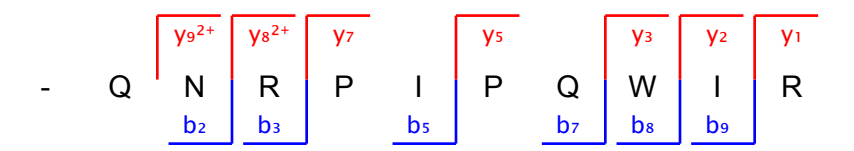
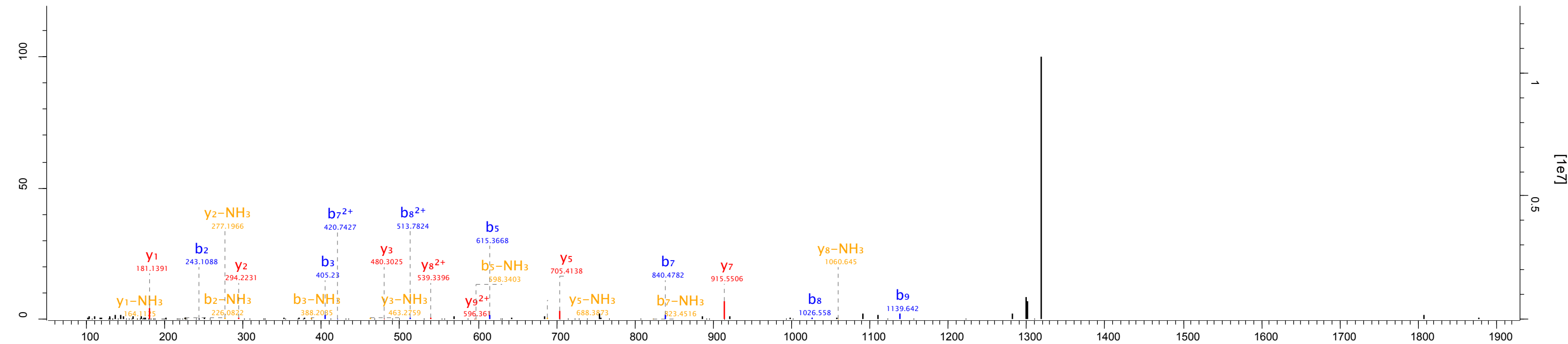
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 Scan: 71869 Method: FTMS; HCD Score: 50.19 m/z: 492.81 Gene names: STON2



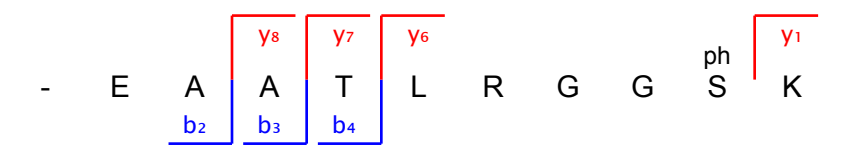
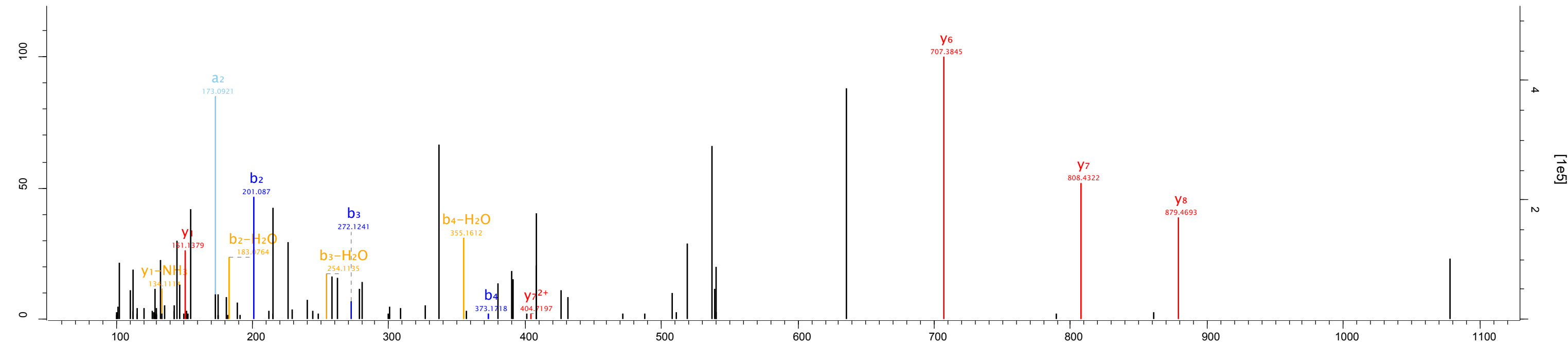
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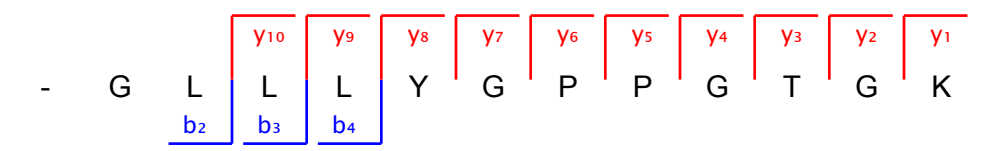
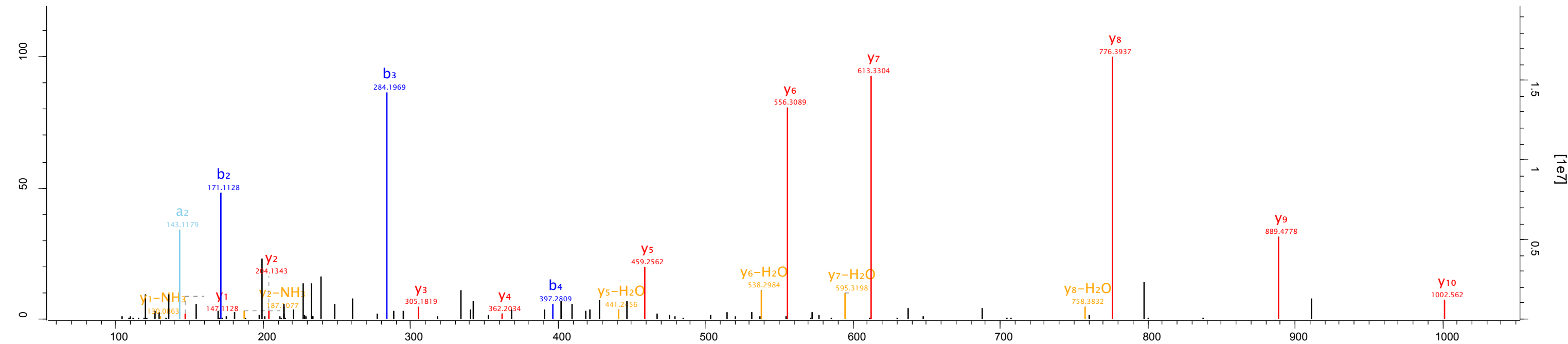
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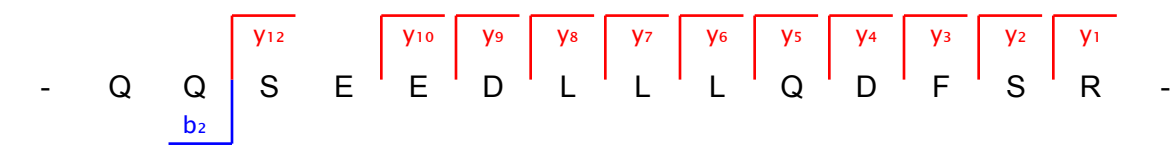
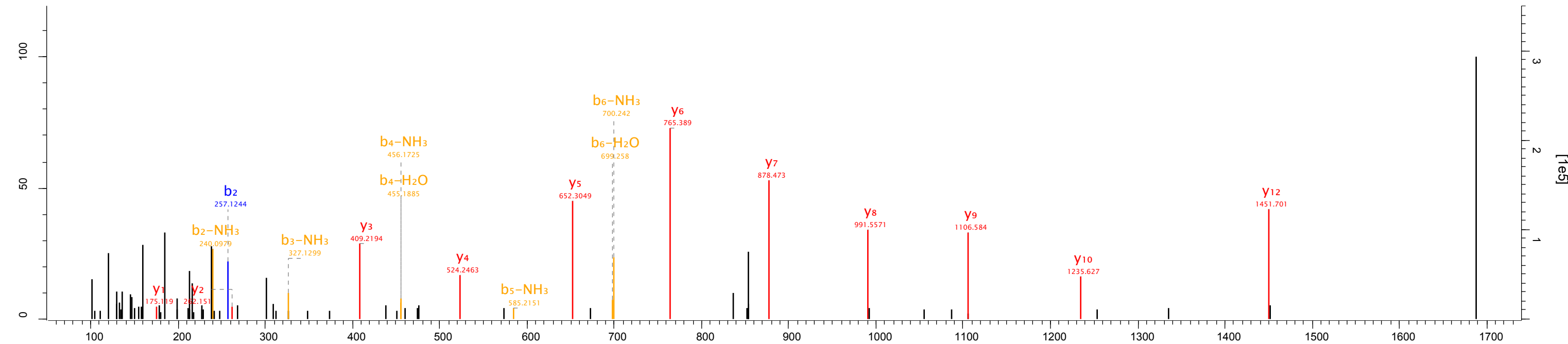
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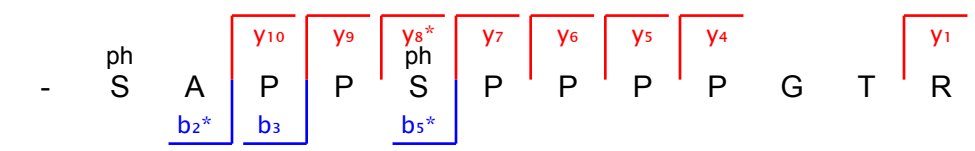
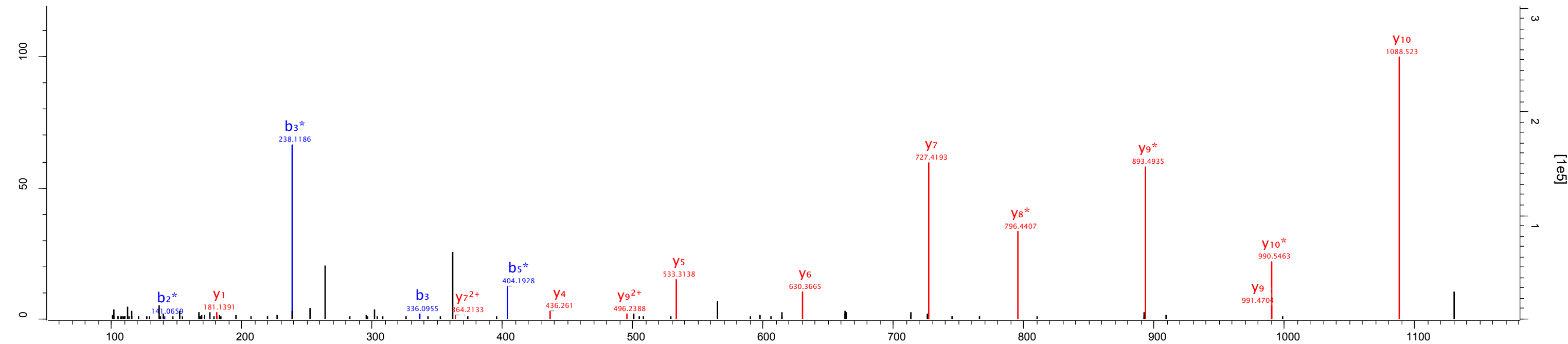
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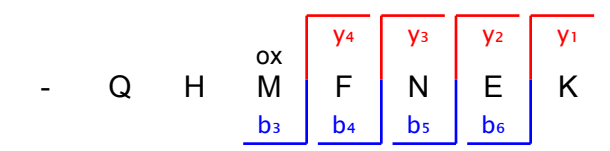
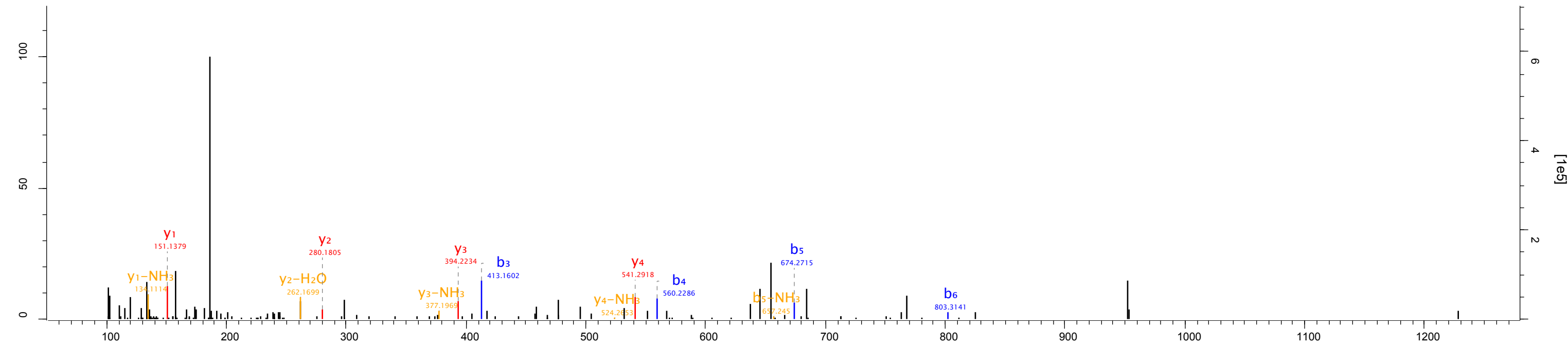
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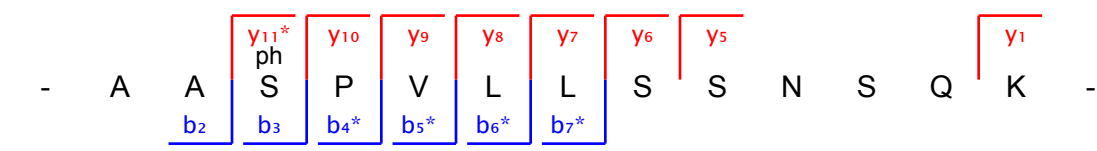
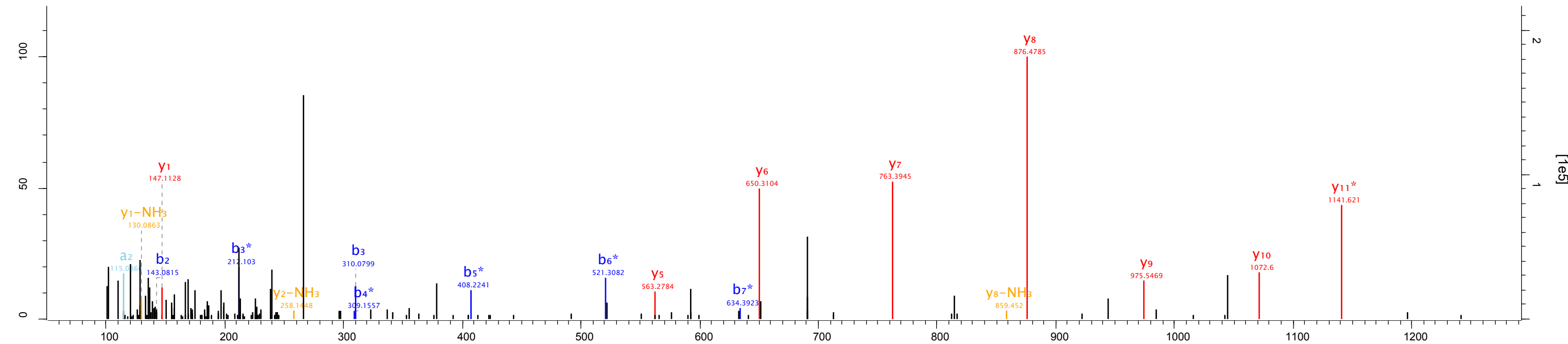
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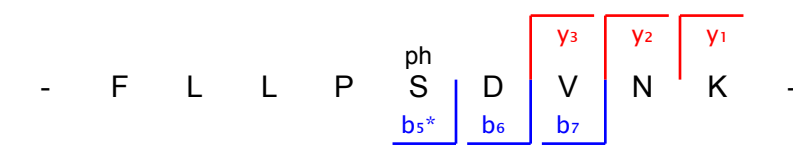
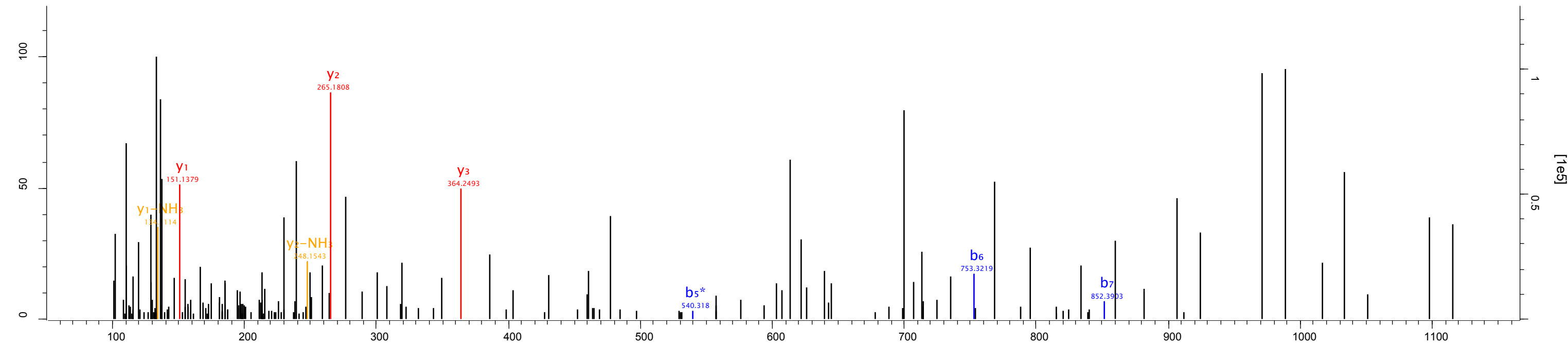
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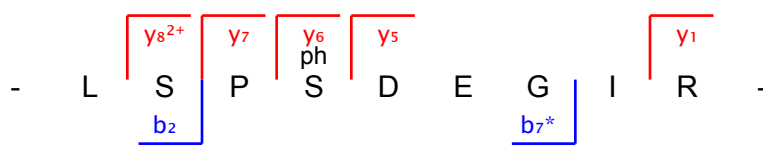
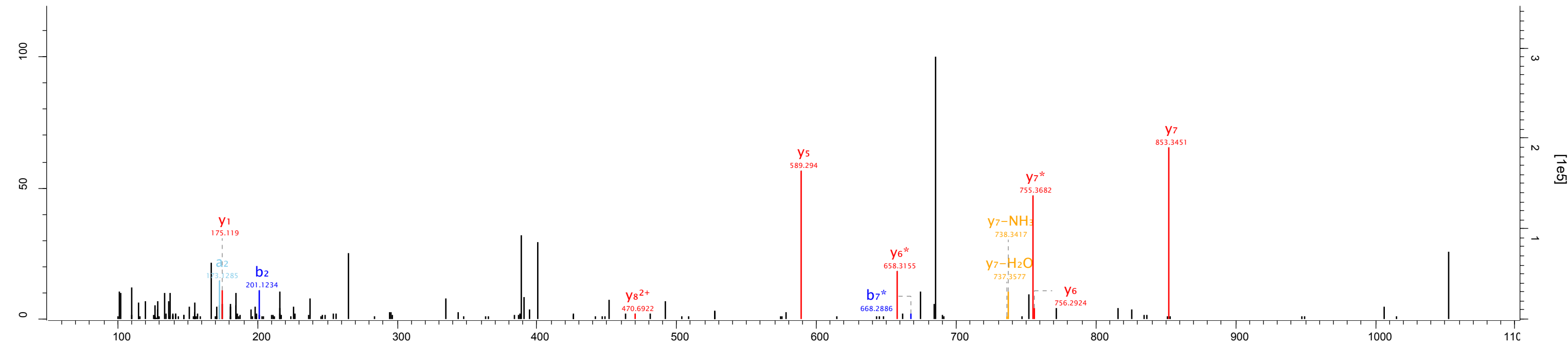
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 Scan: 10919 Method: FTMS; HCD Score: 53.56 m/z: 691.34 Gene names: ELK3



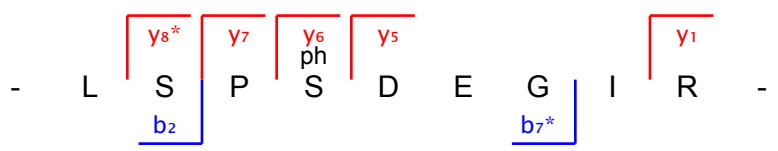
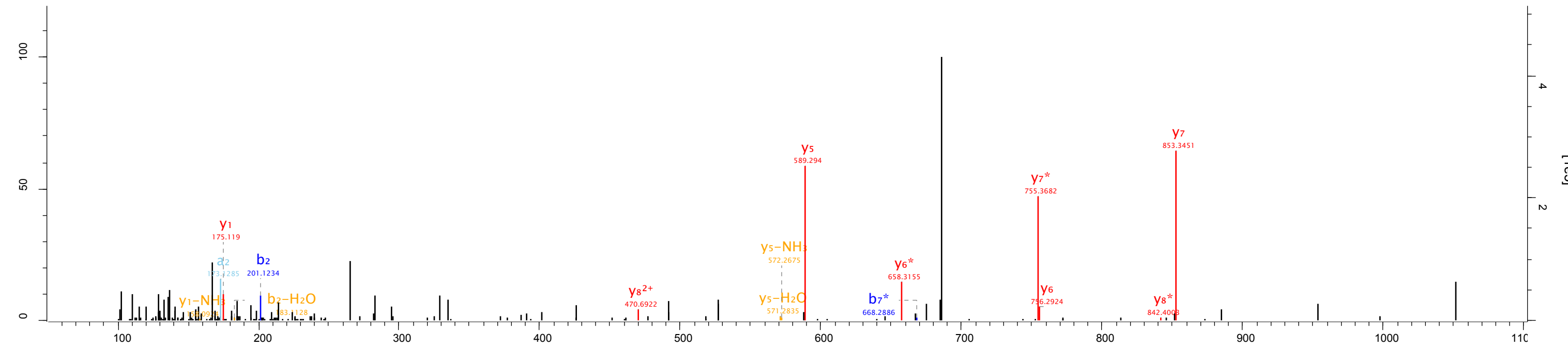
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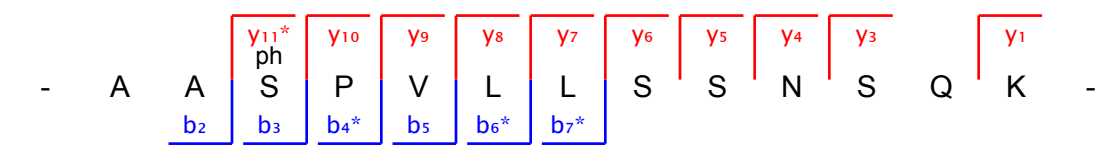
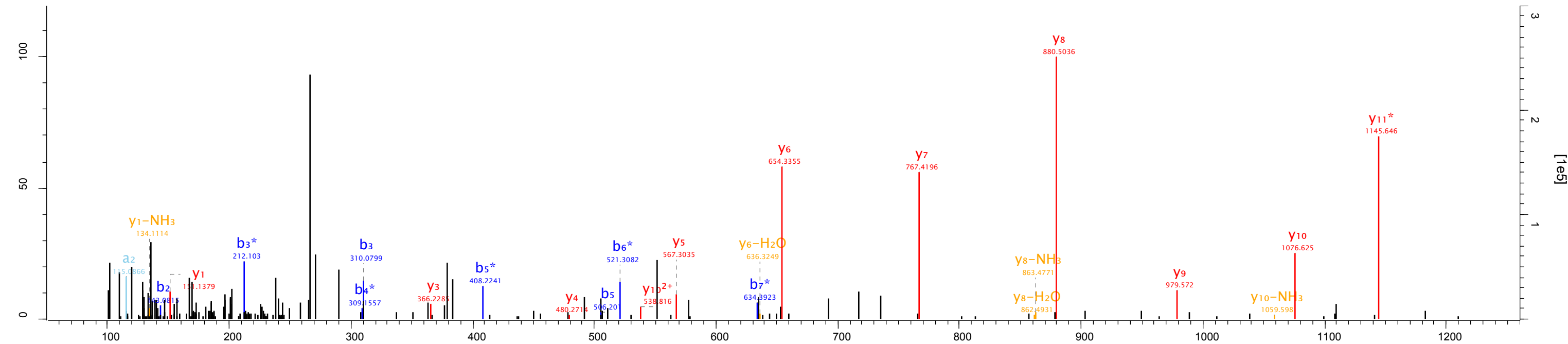
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 Scan: 5219 Method: FTMS; HCD Score: 44.61 m/z: 527.23



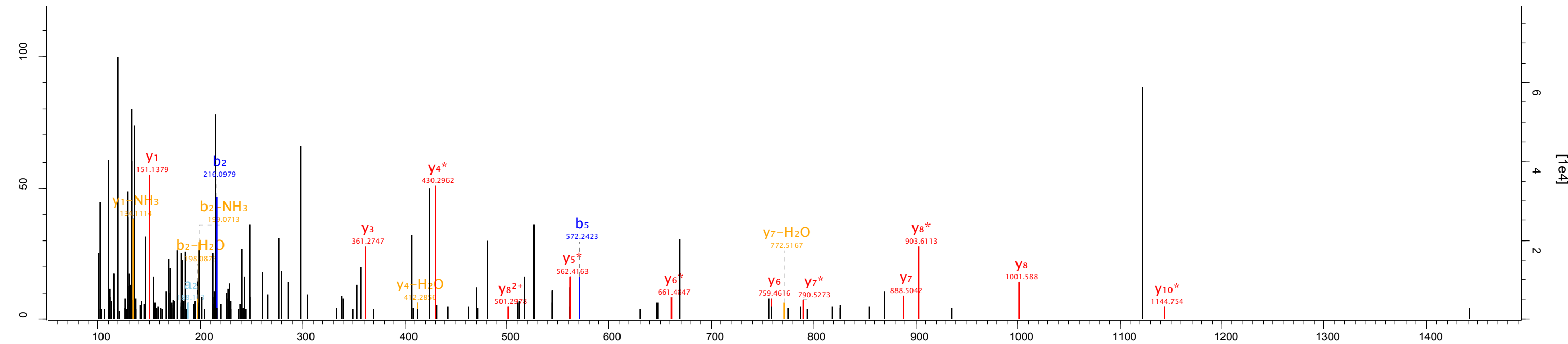
Raw file 20150822_A375SR_Phospho_BR3_07 Scan 5159 Method FTMS; HCD Score 50.79 m/z 527.23



Raw file: 20150822_A375SR_Phospho_BR3_08
 Scan: 11769 Method: FTMS; HCD Score: 60.54 m/z: 693.35 Gene names: ELK3



Raw file 20150822_A375SR_Phospho_BR3_08 Scan 14029 Method FTMS; HCD Score 55.44 m/z 562.64 Gene names MLLT3

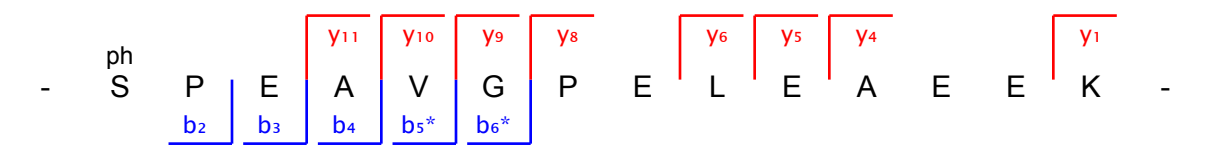
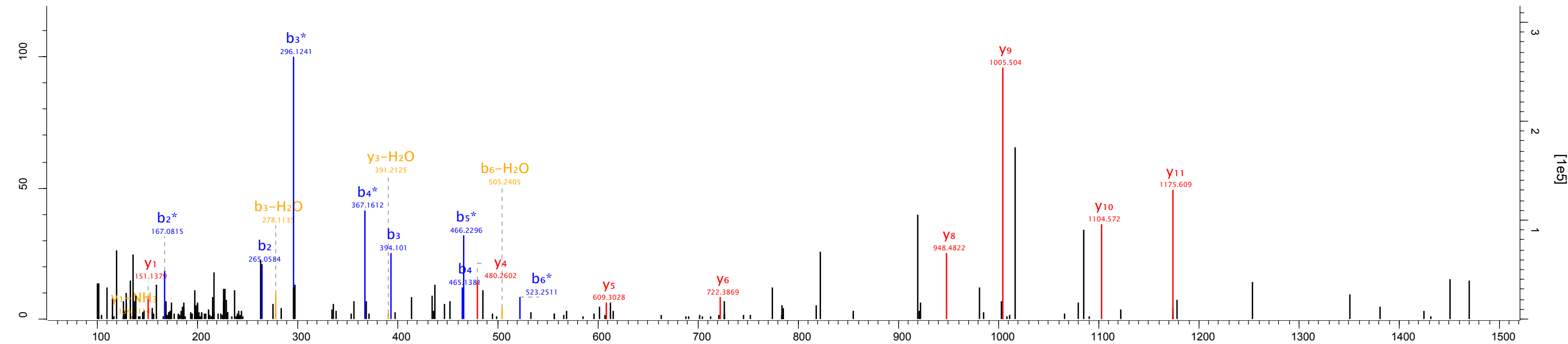


- T N N Q I L E V K S P I K -

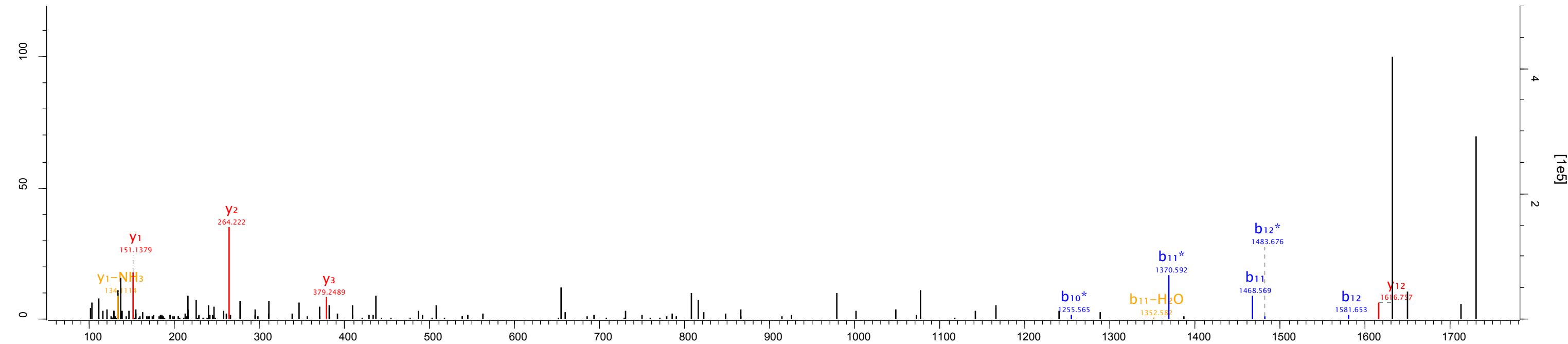
Fragmentation regions are indicated by brackets below the amino acid sequence:

- Blue brackets: b₂ (under N), b₅ (under Q)
- Red brackets: y₁₀^{*} (under Q), y₈ (under L), y₇ (under E), y₆ (under V), y₅^{*} (under K), y₄^{*} (under S), y₃ (under P), y₁ (under I)

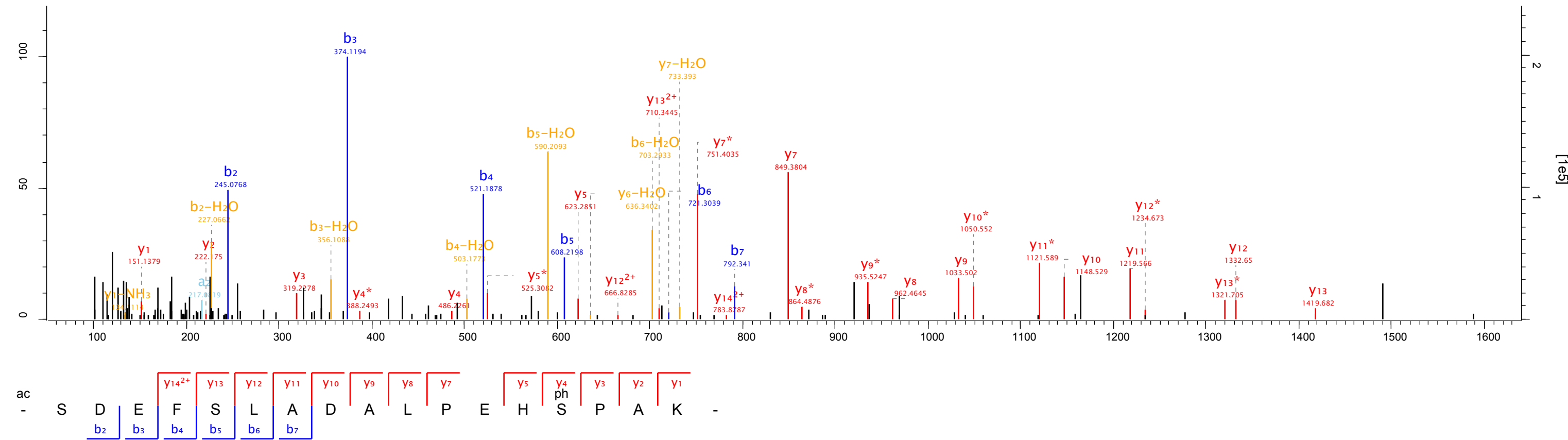
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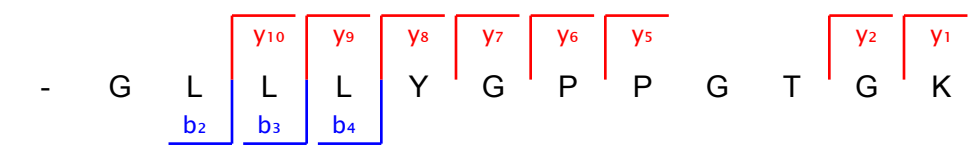
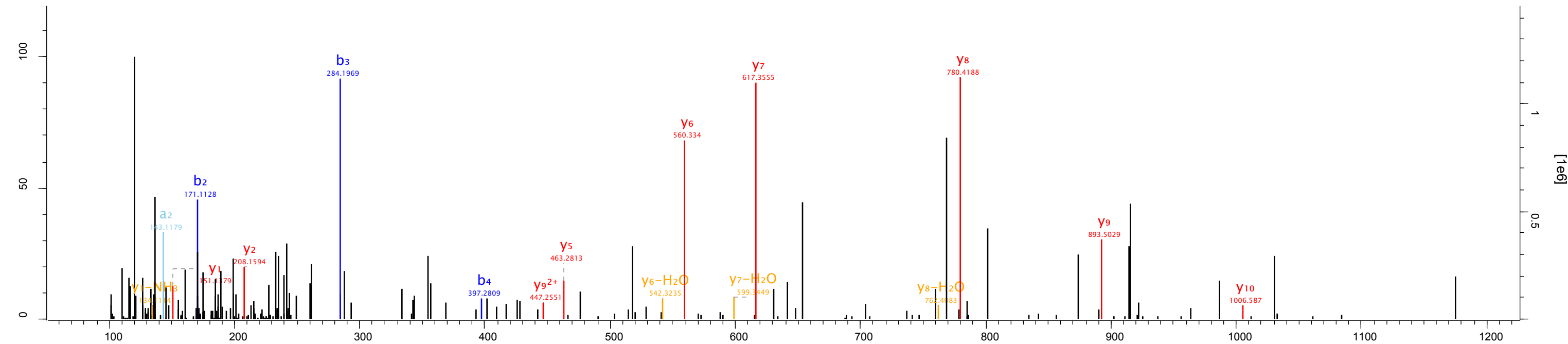
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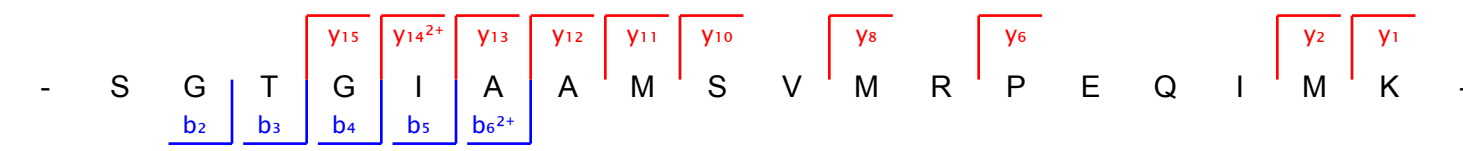
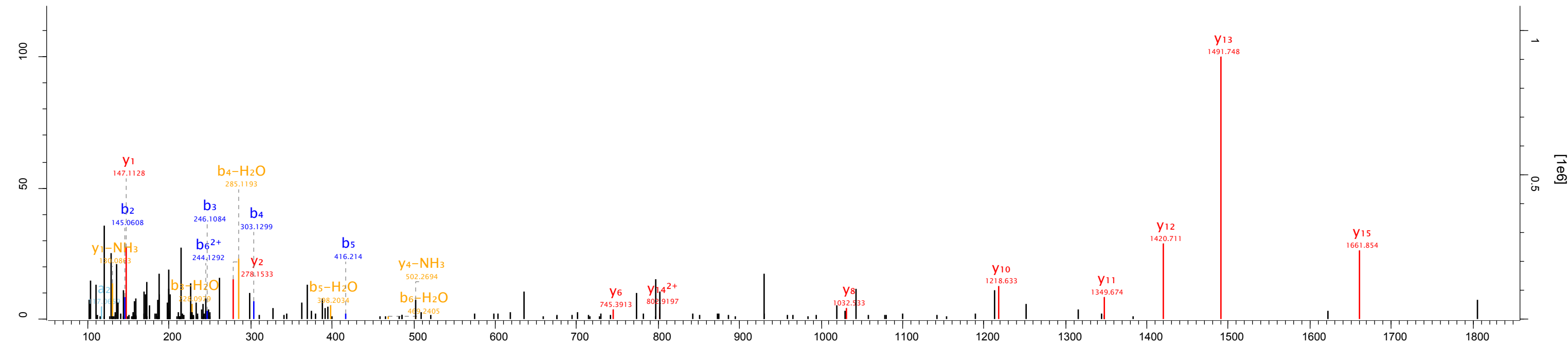
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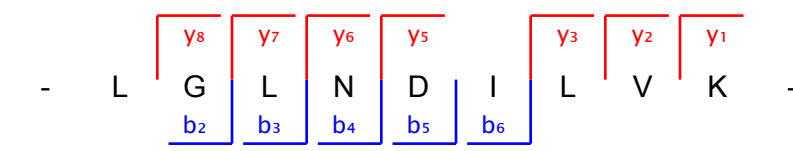
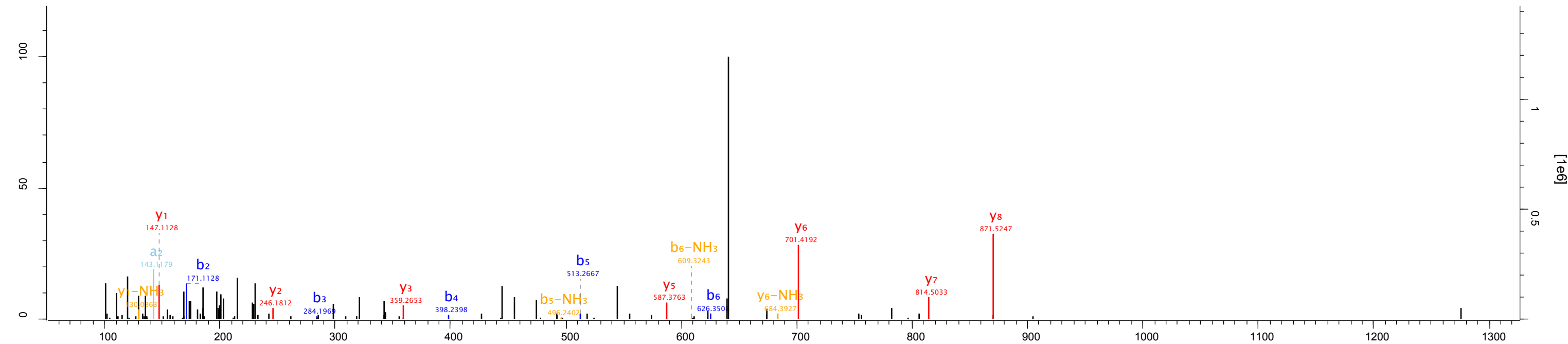
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Raw file: 20150822_A375SR-Proteome_BR3
 Scan: 71739 Method: FTMS; HCD Score: 35.63 m/z: 636.66 Gene names: ATP6V0C

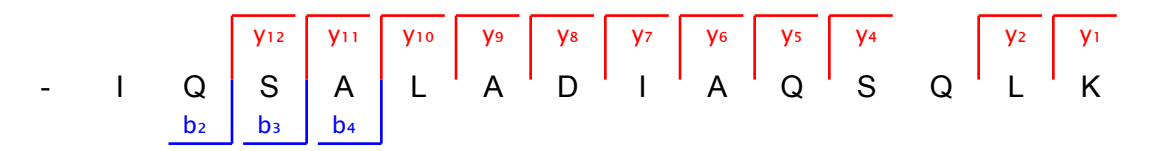
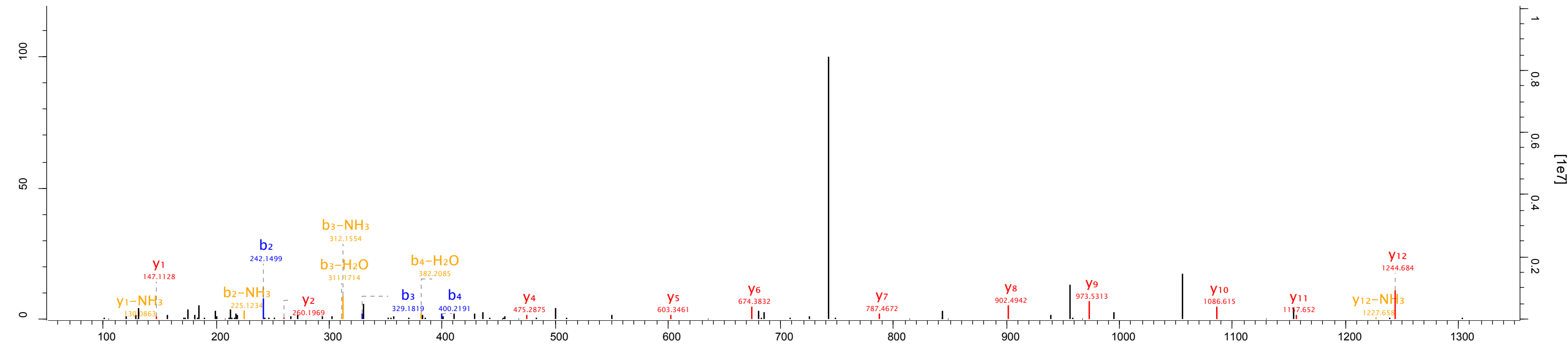


Raw file: 20150822_A375SR-Proteome_BR3
 Scan: 75229 Method: FTMS; HCD Score: 60.06 m/z: 492.81 Gene names: STON2



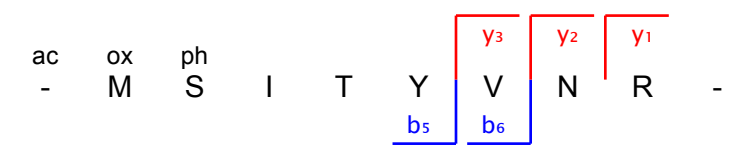
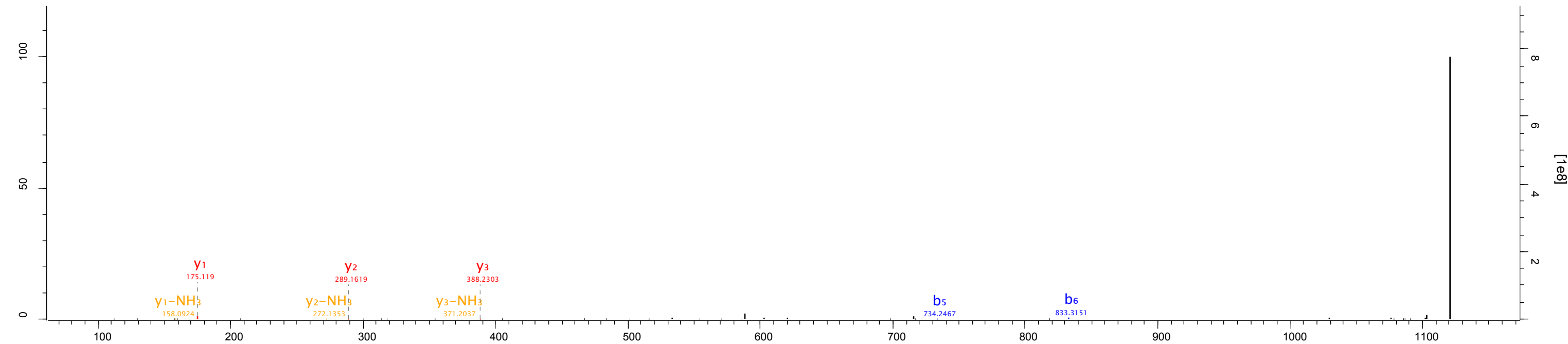
Raw file
20180707_MaS_A375SR_LM_proteome_01

Scan 20859 Method FTMS; HCD Score 64.52 m/z 743.42 Gene names MED21

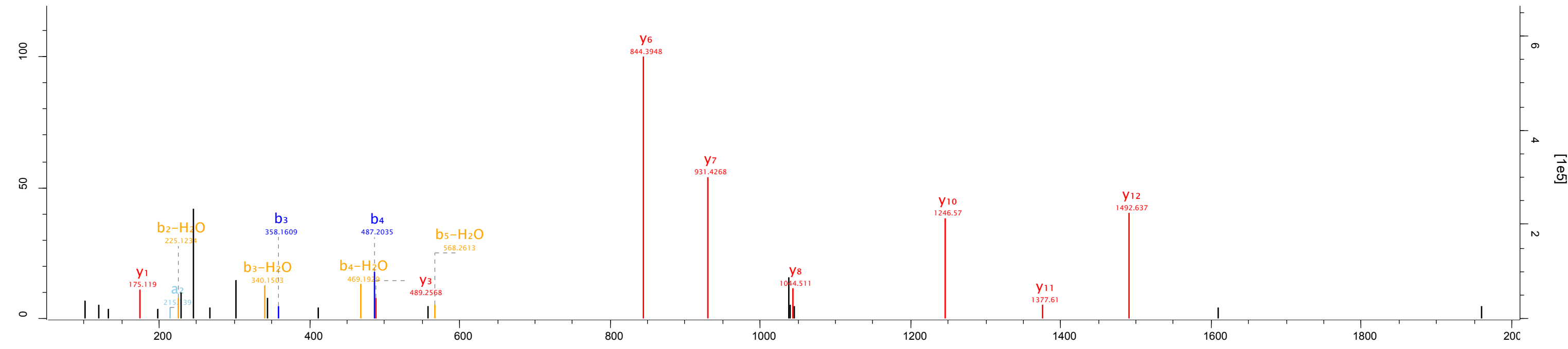


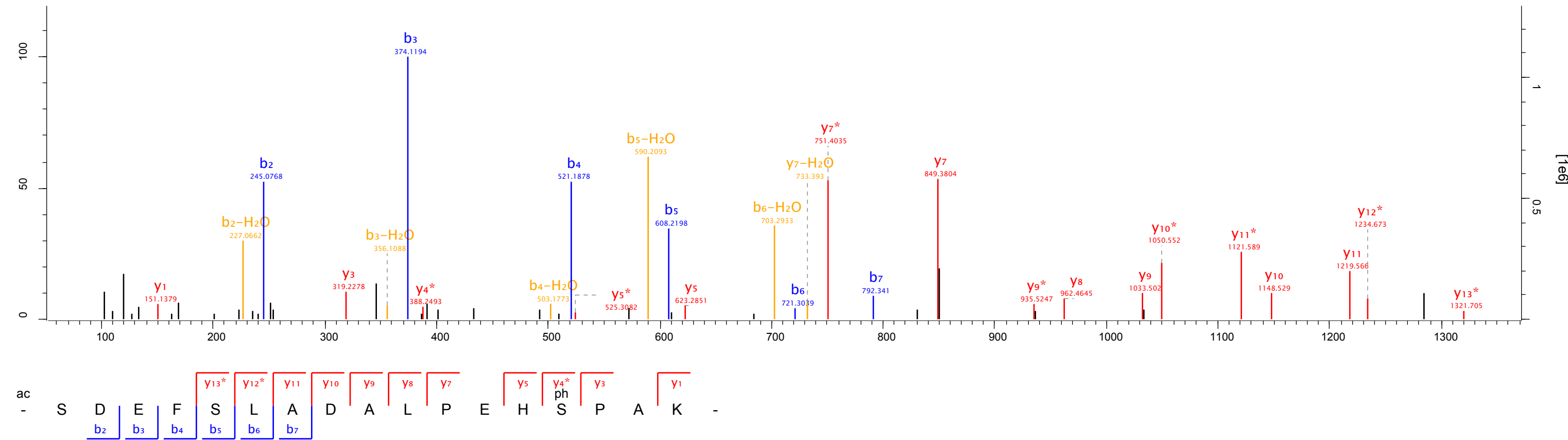
Raw file
20180707_MaS_A375SR_LM_proteome_02

Scan	Method	Score	m/z
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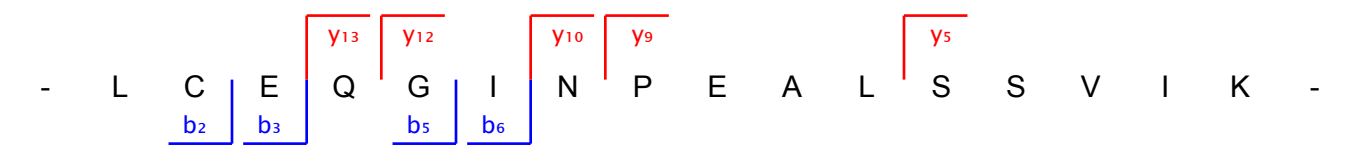
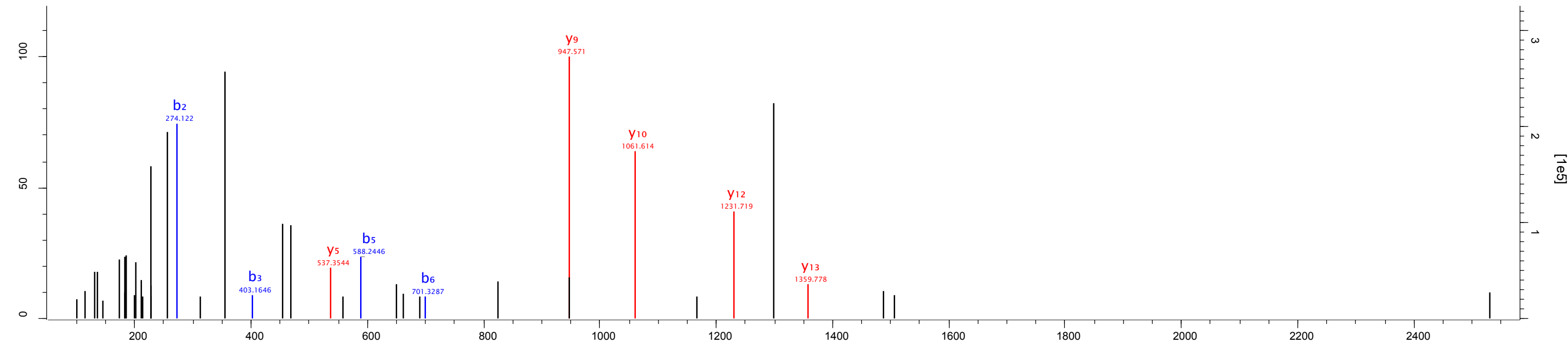
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 Scan: 26369 Method: FTMS; HCD Score: 54.28 m/z: 1039.96 Gene names: RNF121





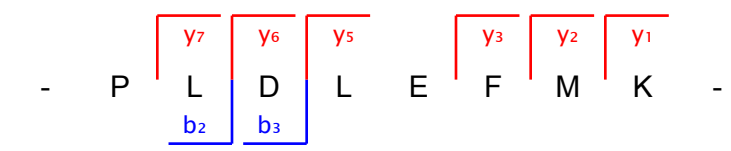
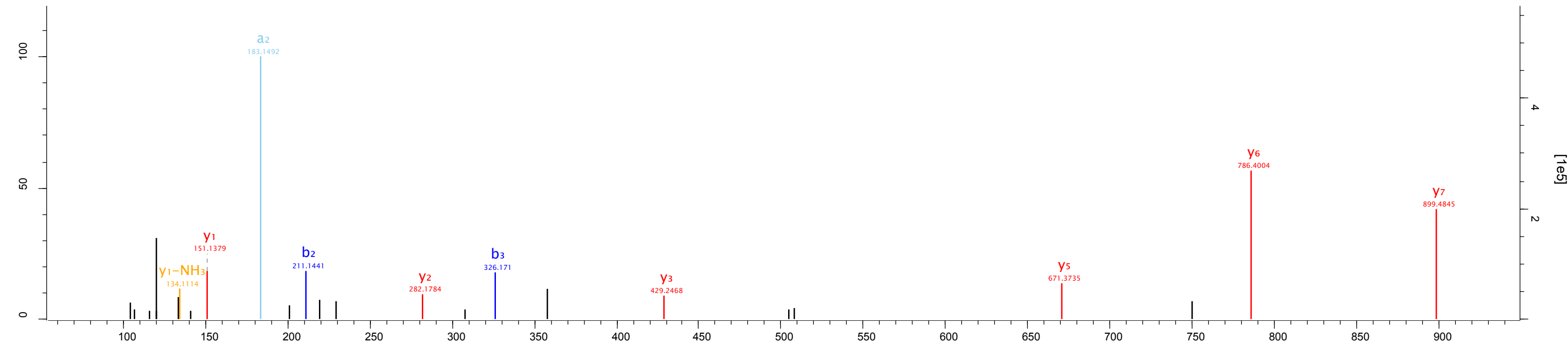
Raw file
20180707_MaS_A375SR_LM_proteome_06

Scan: 26169
Method: FTMS; HCD
Score: 29.58
m/z: 881.47
Gene names: MZT1

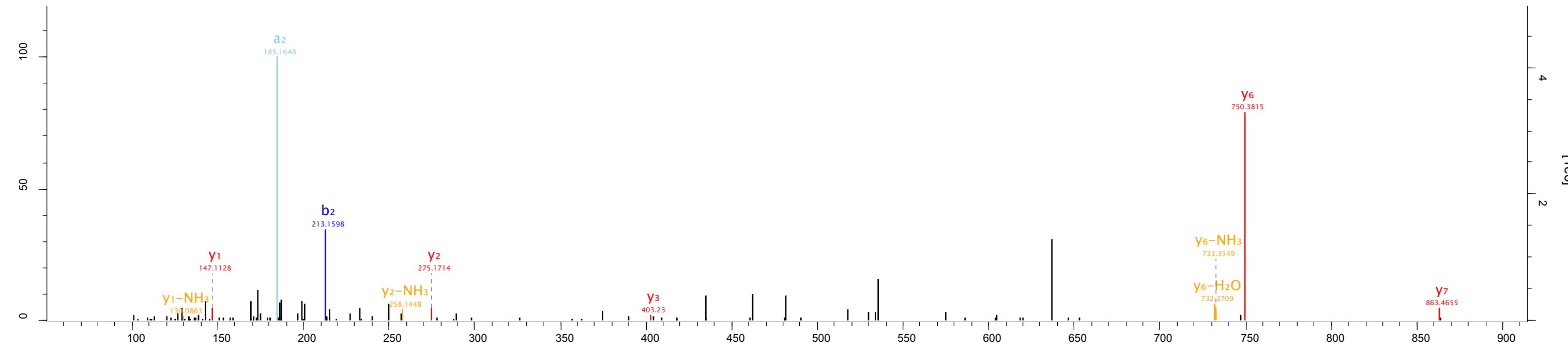


Raw file
20180707_MaS_A375SR_LM_proteome_07

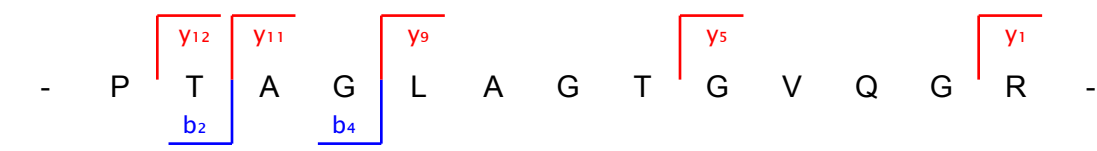
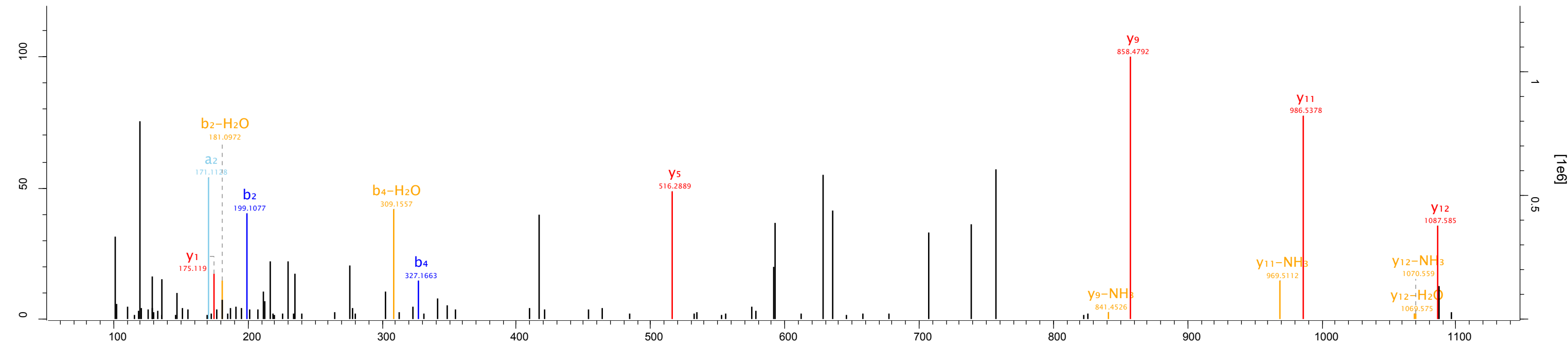
Scan: 24659
Method: FTMS; HCD
Score: 62.55
m/z: 498.77
Gene names: SEPT3



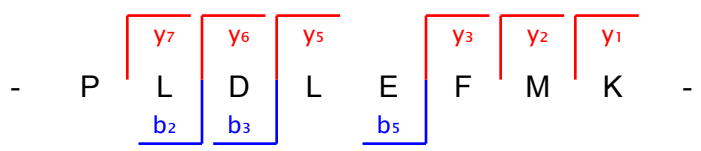
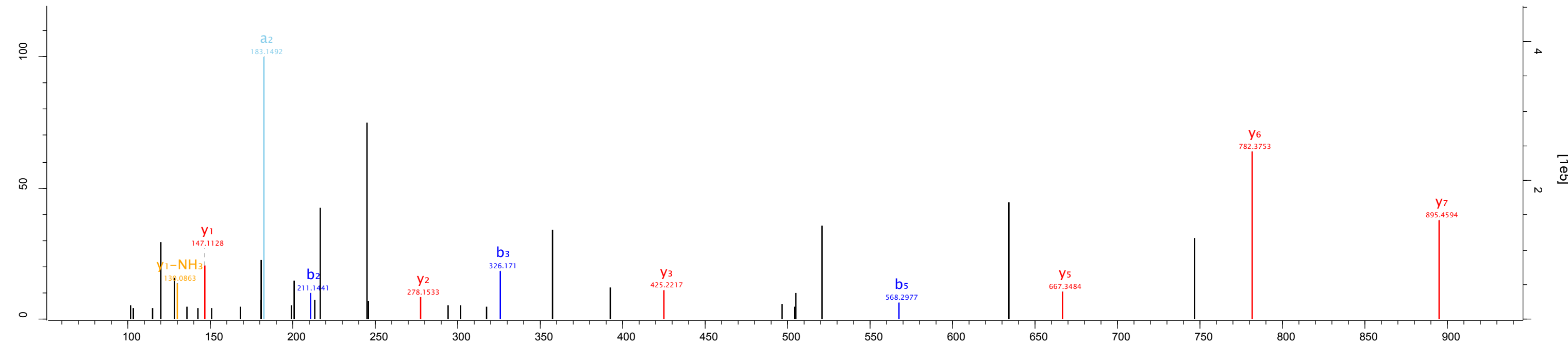
Raw file 20180707_MaS_A375SR_LM_proteome_13 Scan 8849 Method FTMS; HCD Score 54.16 m/z 481.77 Gene names CAPN6

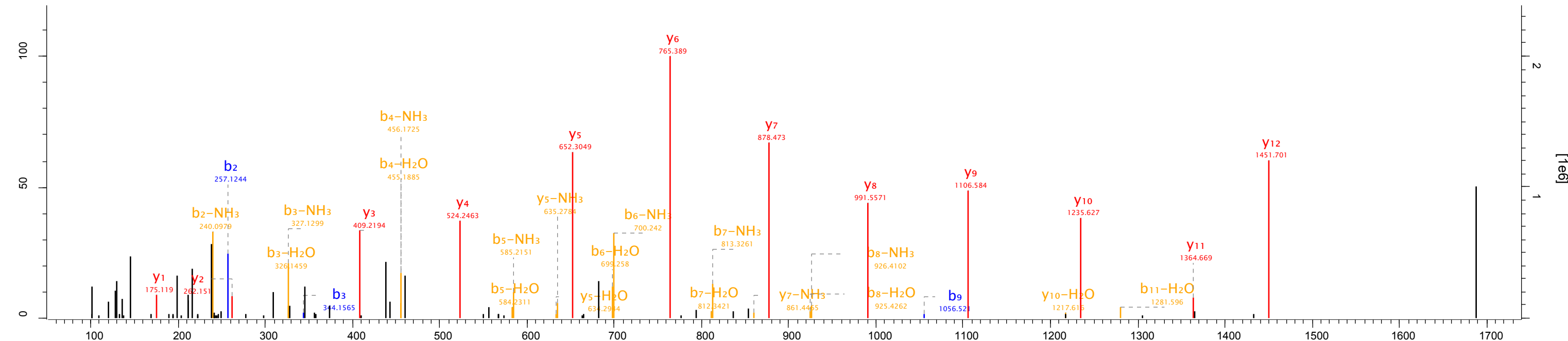


Raw file 20180707_MaS_A375SR_LM_proteome_18 Scan 8649 Method FTMS; HCD Score 65.18 m/z 592.83



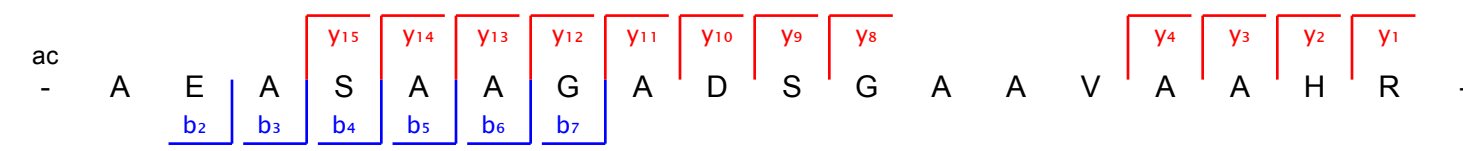
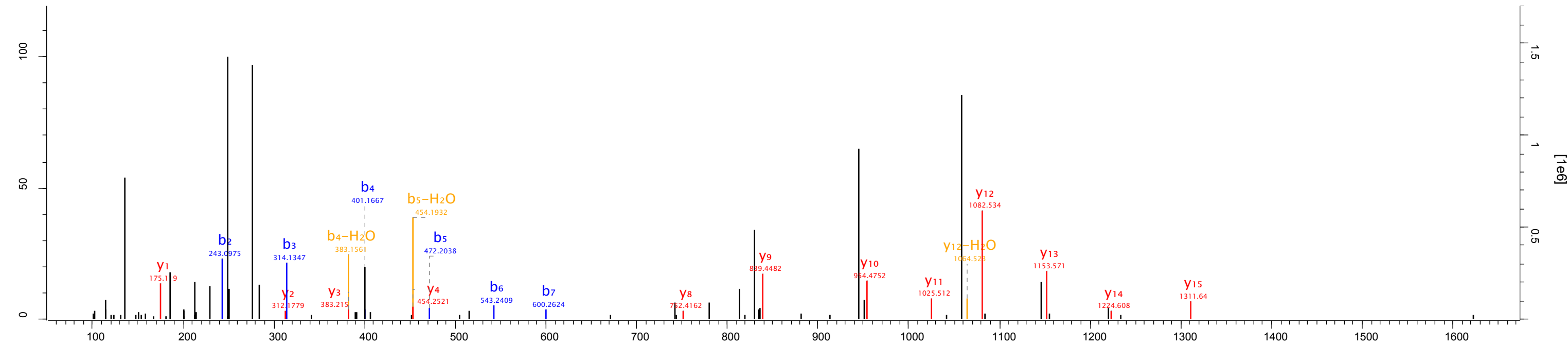
Raw file 20180707_MaS_A375SR_LM_proteome_21 Scan 25089 Method FTMS; HCD Score 58.98 m/z 496.76 Gene names SEPT3





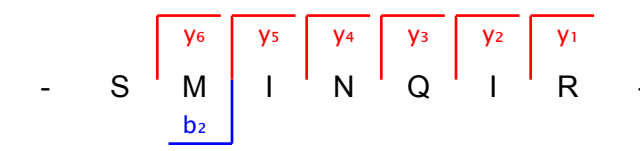
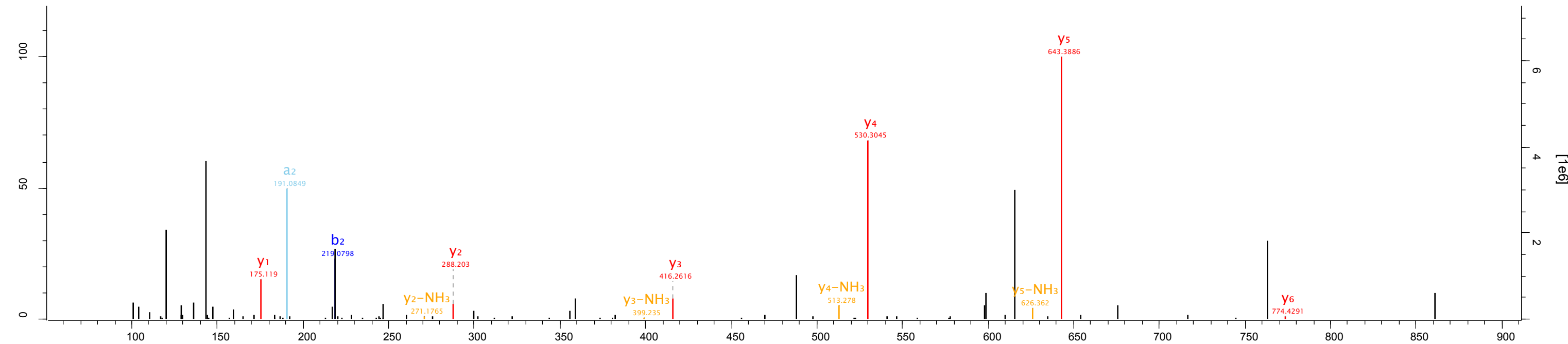
- Q Q S E E D L L L Q D F S R -
b₂ b₃ b₉

Raw file: 20180707_MaS_A375SR_LM_proteome_24
 Scan: 10909 Method: FTMS; HCD Score: 84.38 m/z: 813.39 Gene names: RNF115



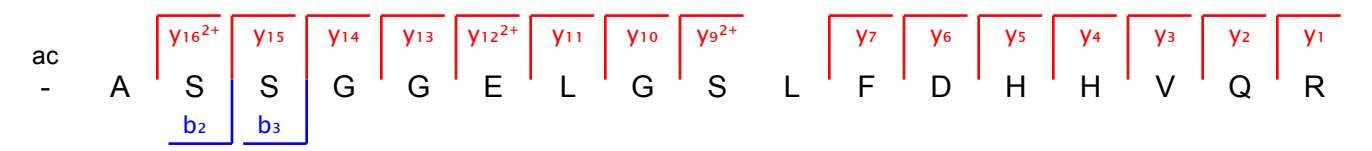
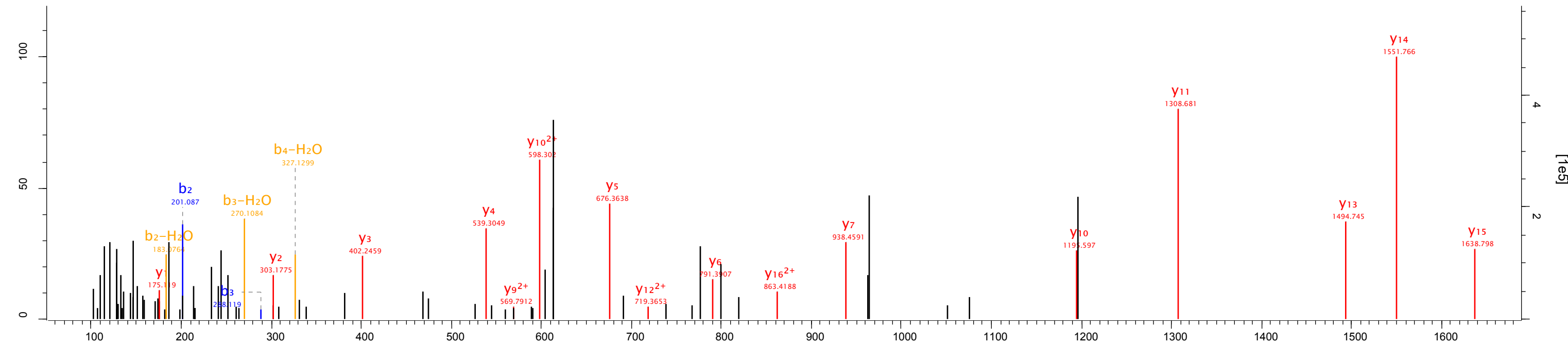
Raw file
20180707_MaS_A375SR_ML_proteome_01

Scan 10849 Method FTMS; HCD Score 81.38 m/z 431.23



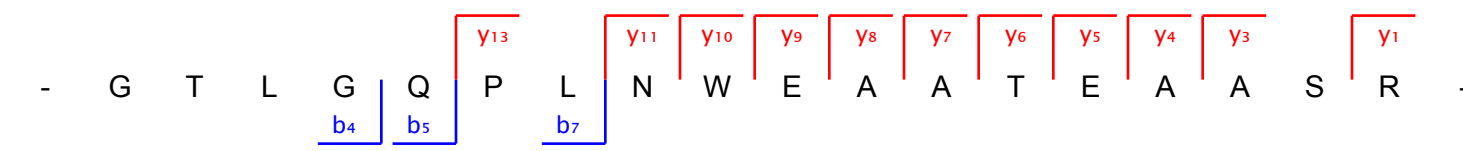
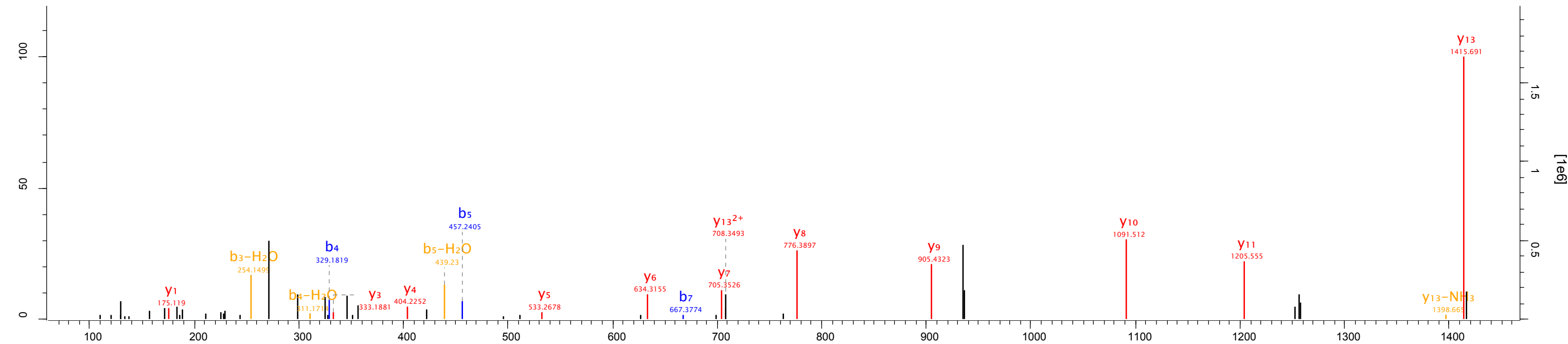
Raw file
20180707_MaS_A375SR_ML_proteome_01

Scan Method Score m/z Gene names
21199 FTMS; HCD 58.25 613.63 RBM48

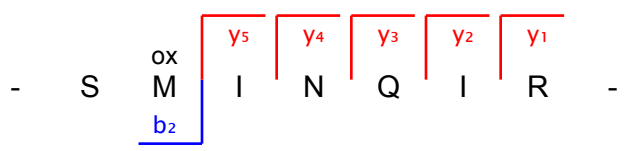
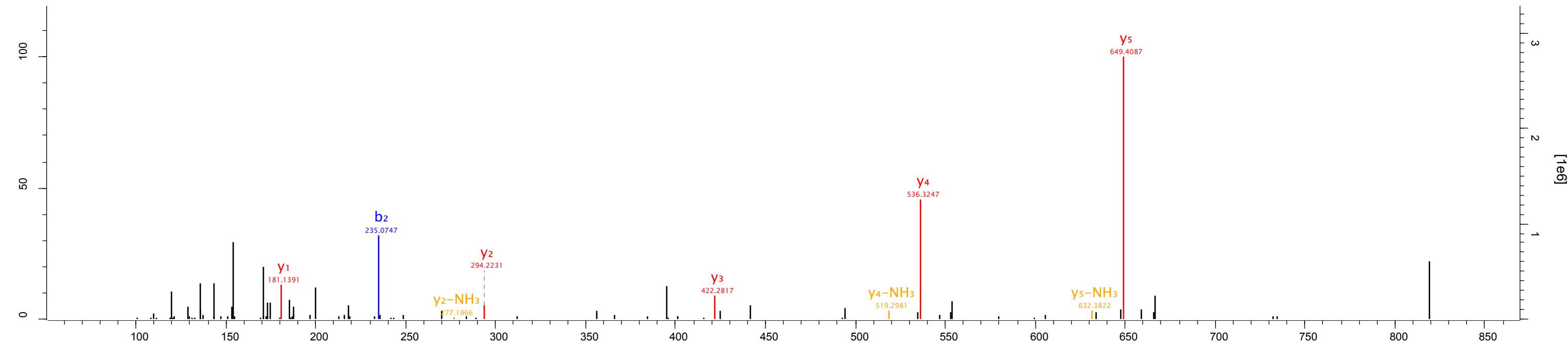


Raw file
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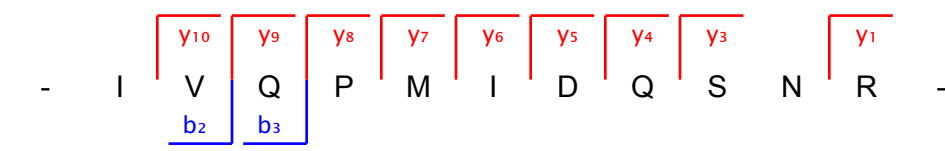
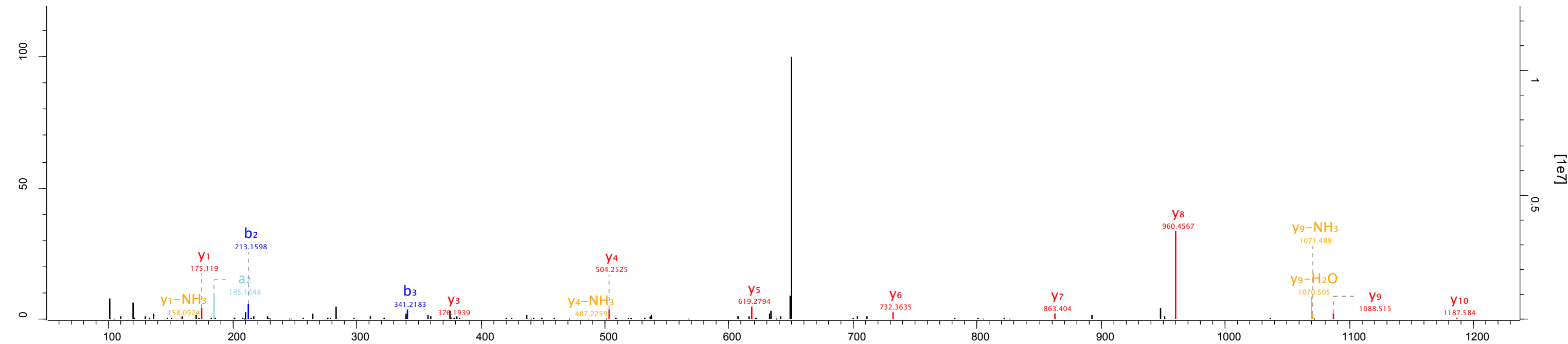
Scan 23599 Method FTMS; HCD Score 47.73 m/z 936.97 Gene names SIRT7

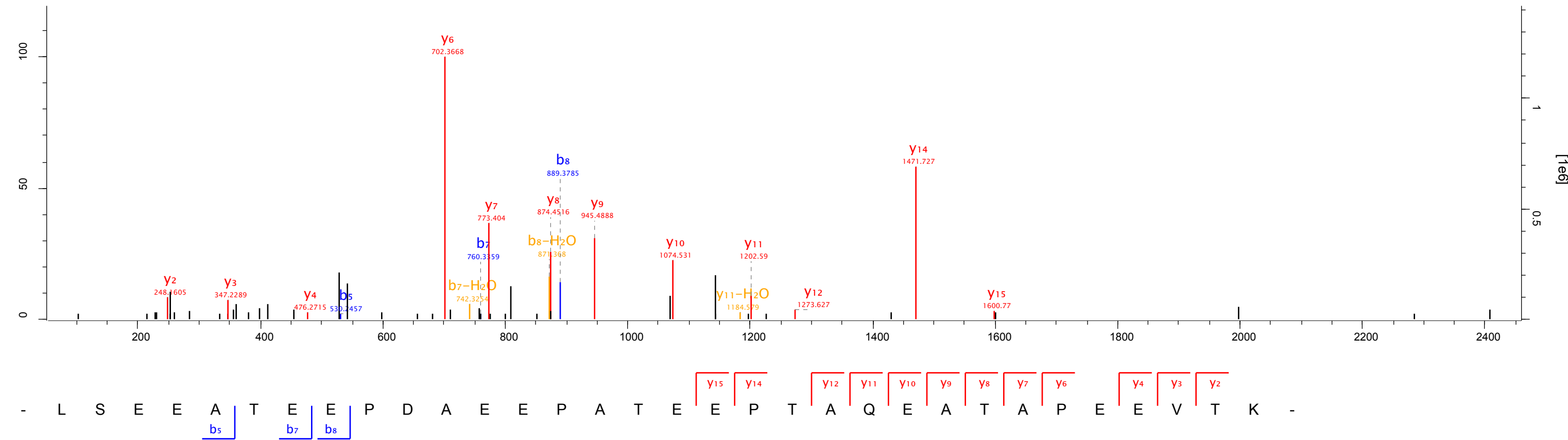


Raw file 20180707_MaS_A375SR_ML_proteome_01 Scan 5859 Method FTMS; HCD Score 55.44 m/z 442.24

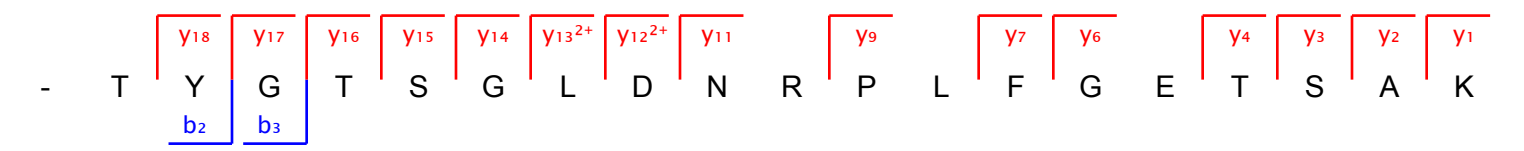
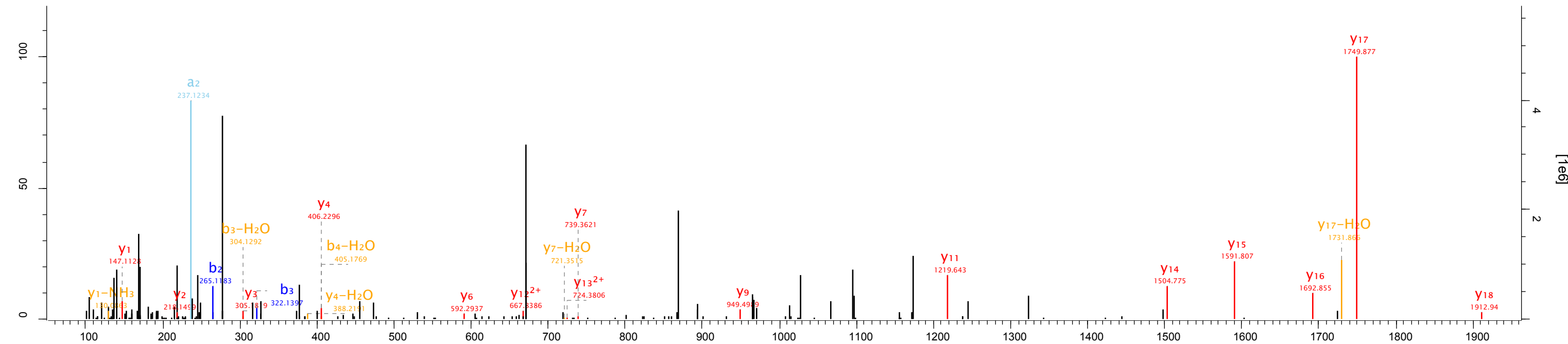


Raw file: 20180707_MaS_A375SR_ML_proteome_02
 Scan: 10899 Method: FTMS; HCD Score: 74.61 m/z: 650.84 Gene names: MEIS2;MEIS3;MEIS1;MEIS3P1

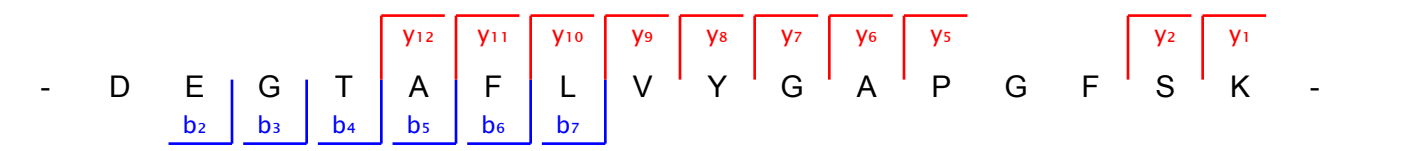
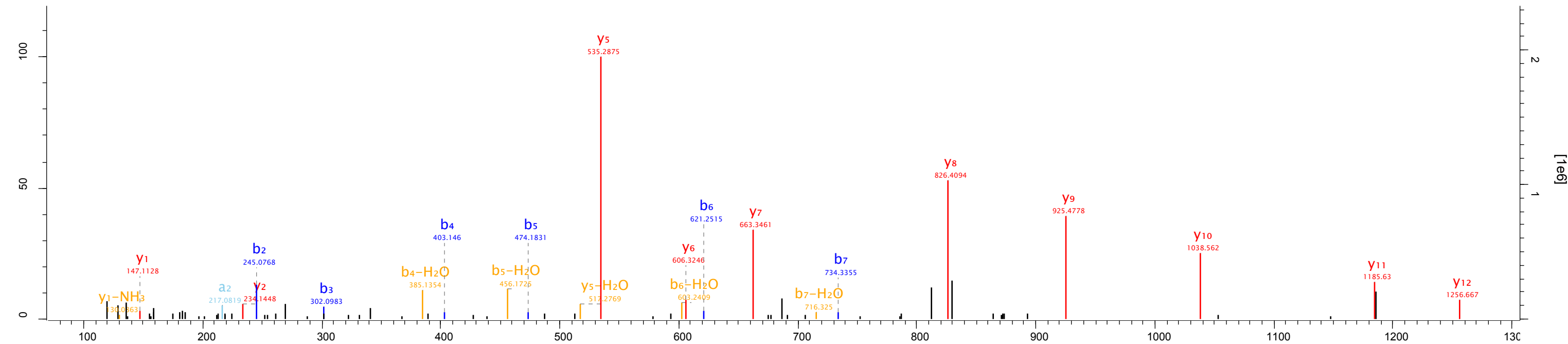


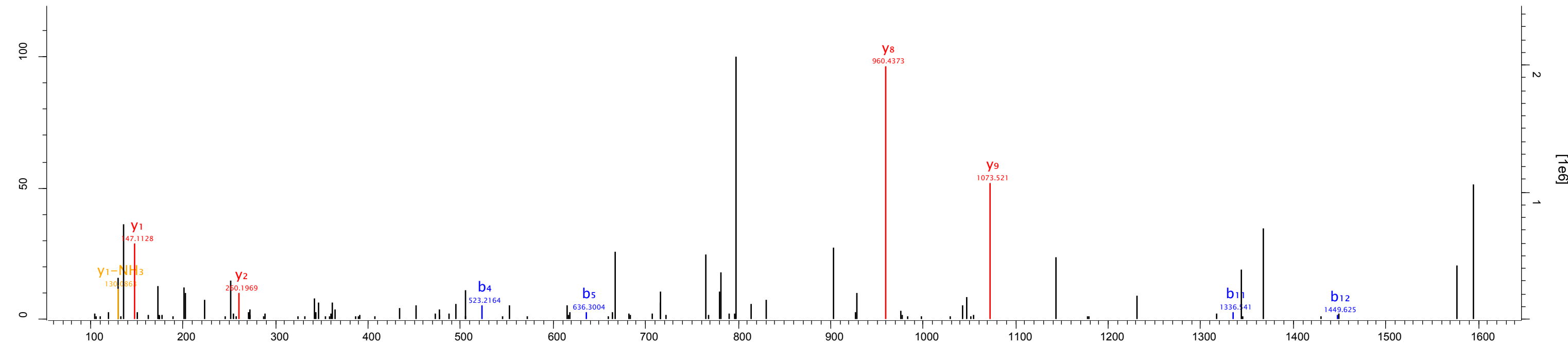


Raw file 20180707_MaS_A375SR_ML_proteome_02 Scan 15689 Method FTMS; HCD Score 33.66 m/z 672 Gene names TMEM243



Raw file: 20180707_MaS_A375SR_ML_proteome_03
 Scan: 23679 Method: FTMS; HCD Score: 109.79 m/z: 830.41 Gene names: BCHE





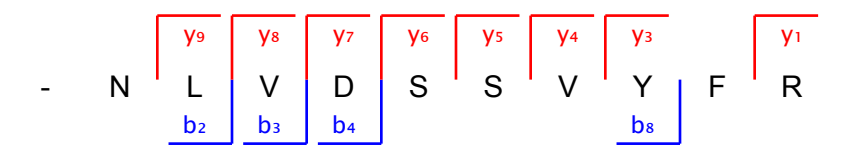
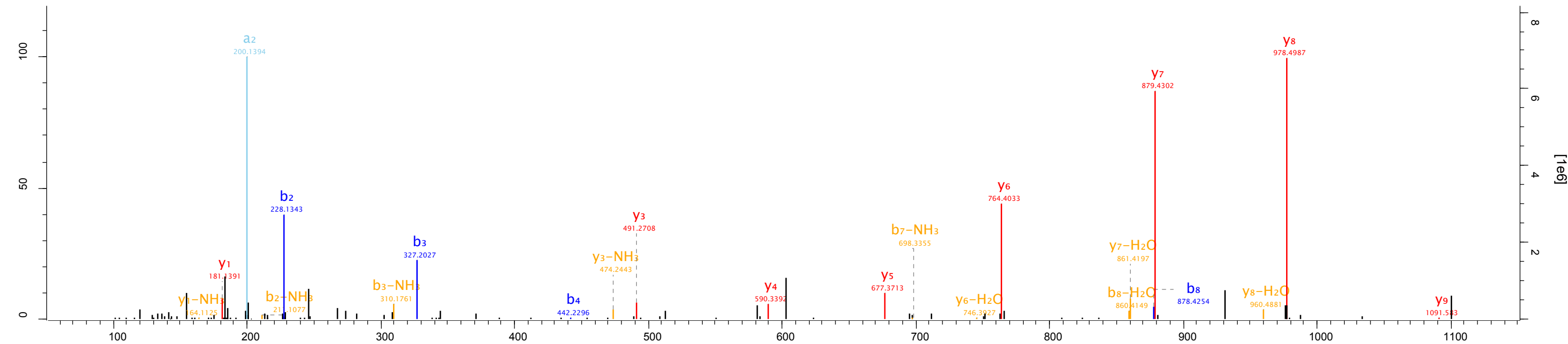
- S L I E L P H S A P M L K -

Fragmentation labels (b and y ions) are shown below the corresponding amino acids:

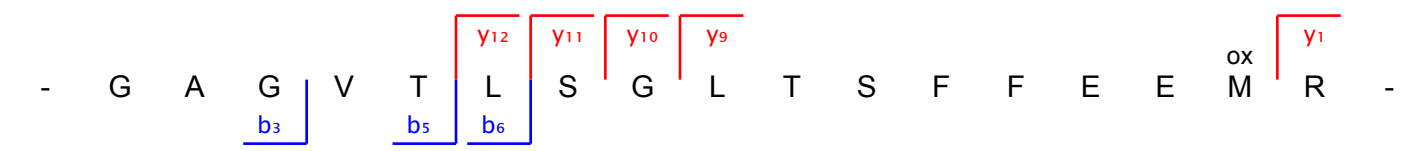
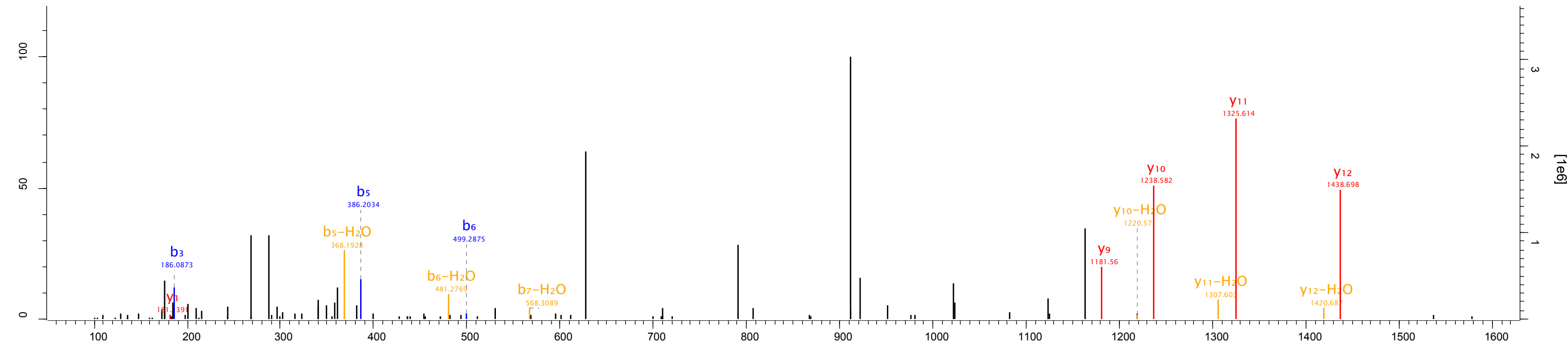
- b_4 (under E)
- b_5 (under L)
- b_{11} (under M)
- b_{12} (under L)
- y_9 (over E)
- y_8 (over P)
- y_2 (over L)
- y_1 (over K)

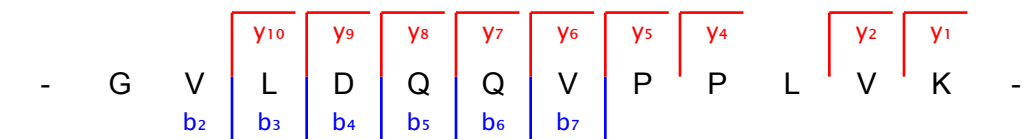
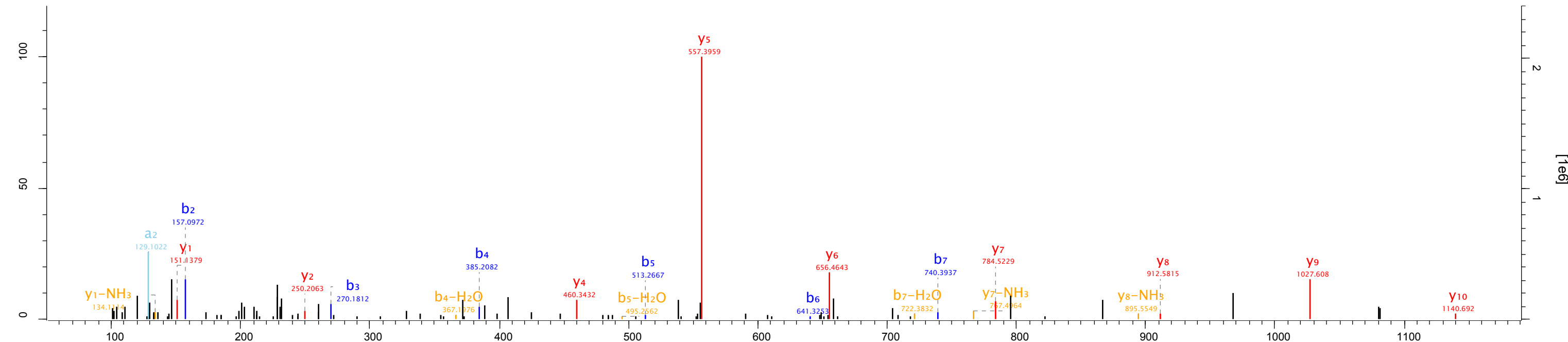
Raw file
20180707_MaS_A375SR_ML_proteome_04

Scan 22049 Method FTMS; HCD Score 99.28 m/z 603.32 Gene names MEF2BNB

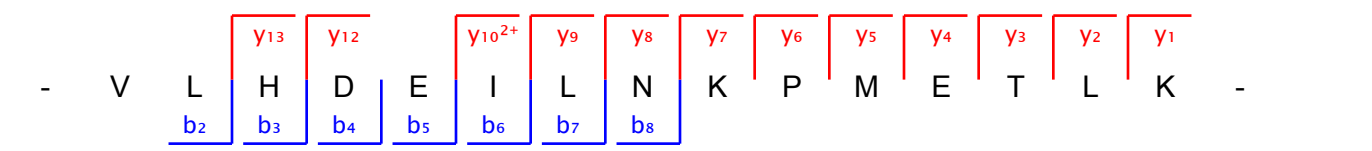
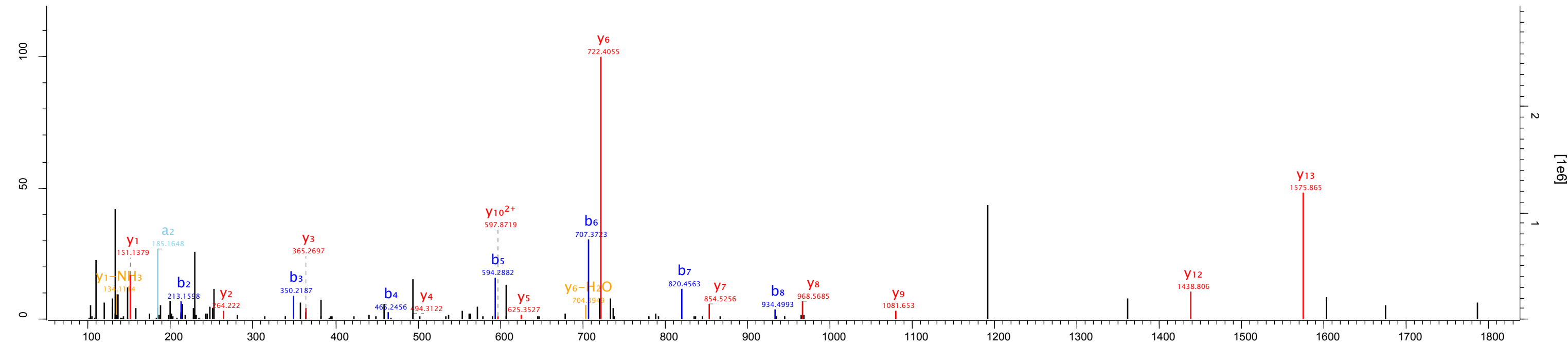


Raw file 20180707_MaS_A375SR_ML_proteome_05 Scan 22139 Method FTMS; HCD Score 42.95 m/z 912.45

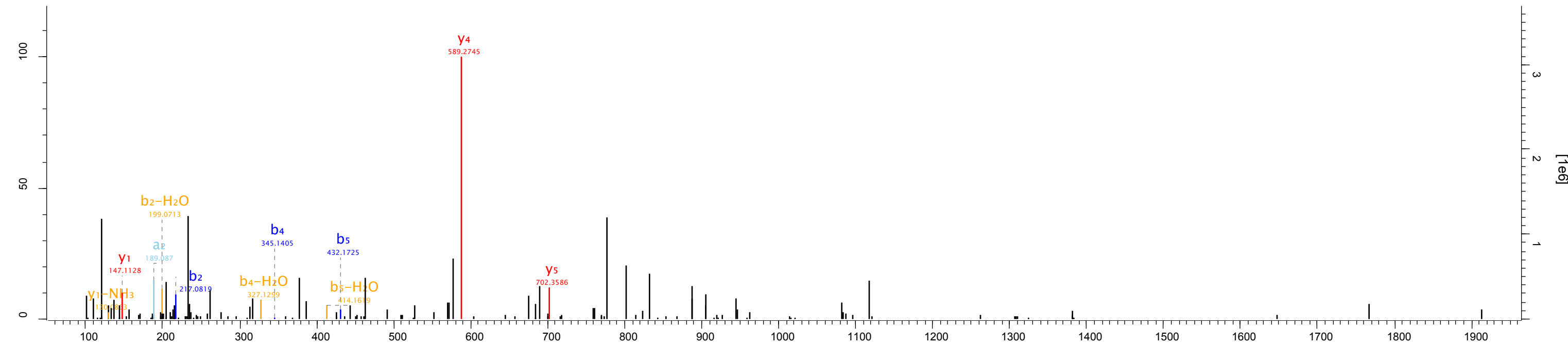




Raw file: 20180707_MaS_A375SR_ML_proteome_06
 Scan: 17289 Method: FTMS; HCD Score: 76.82 m/z: 597.01 Gene names: SLC35A3



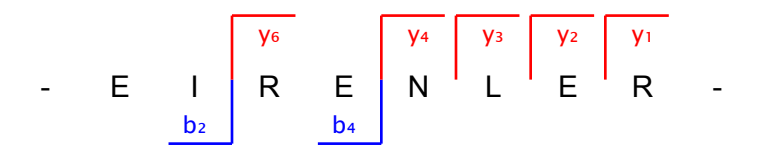
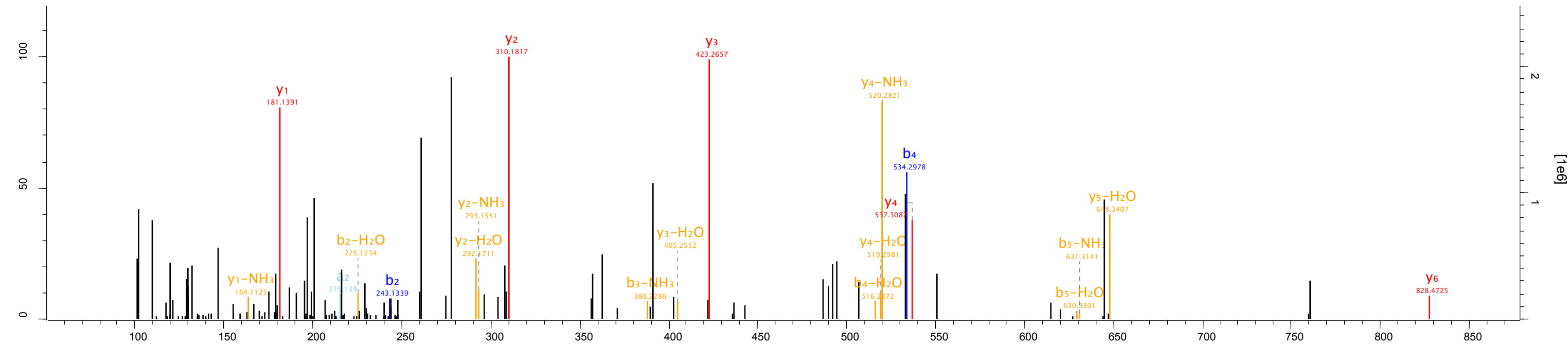
Raw file 20180707_MaS_A375SR_ML_proteome_06 Scan 24929 Method FTMS; HCD Score 42.31 m/z 676.99 Gene names AIM1L



- D T A G S K N F Q S H G P I F S K K -

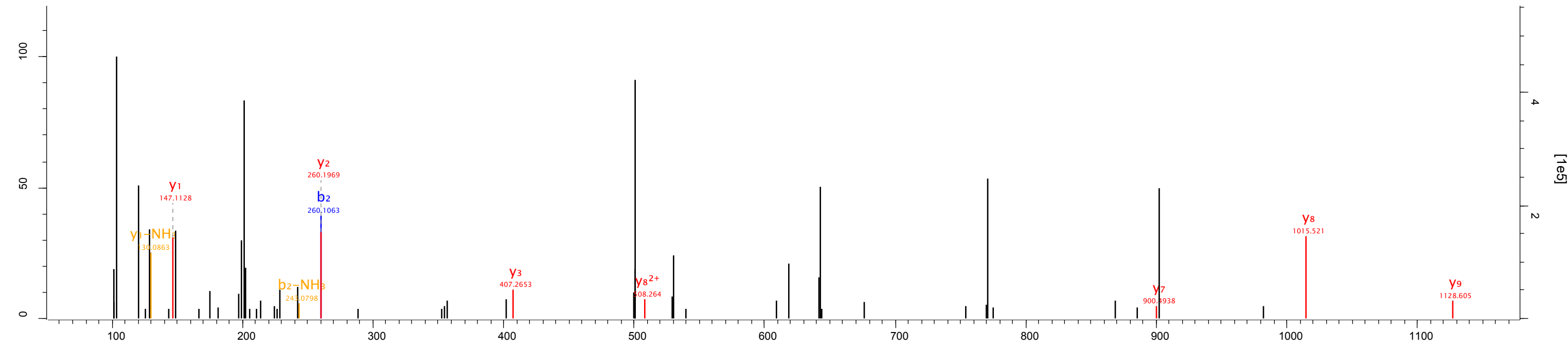
Fragmentation sites are indicated by brackets below the sequence: b2 (under T), b4 (under G), b5 (under S), y5 (under I), y4 (under F), and y1 (under K).

Raw file: 20180707_MaS_A375SR_ML_proteome_06
 Scan: 8989 Method: FTMS; HCD Score: 93.47 m/z: 357.54 Gene names: DACH2



Raw file
20180707_MaS_A375SR_ML_proteome_08

Scan Method Score m/z Gene names
25649 FTMS; HCD 26.75 500.93 DET1



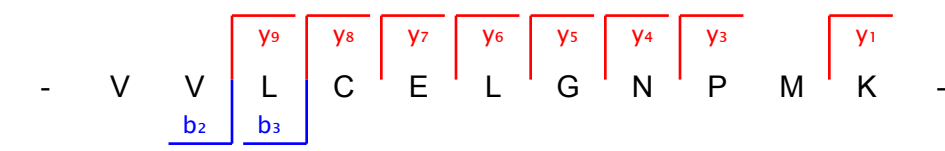
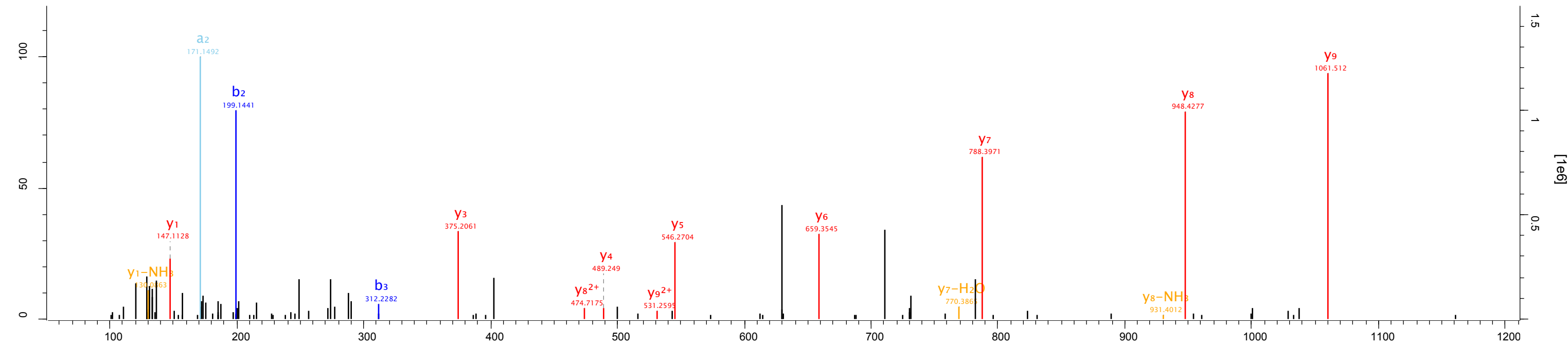
- M Q L L D E N H L F I K -

b₂ (under Q)

y₉ (over L), y₈ (over D), y₇ (over E)

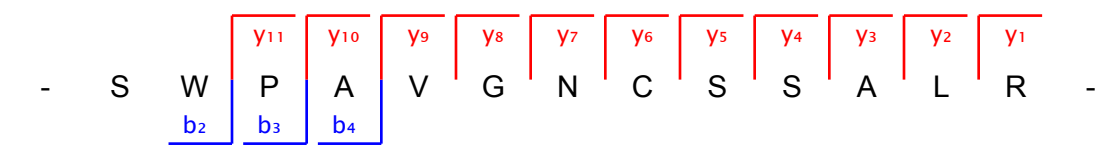
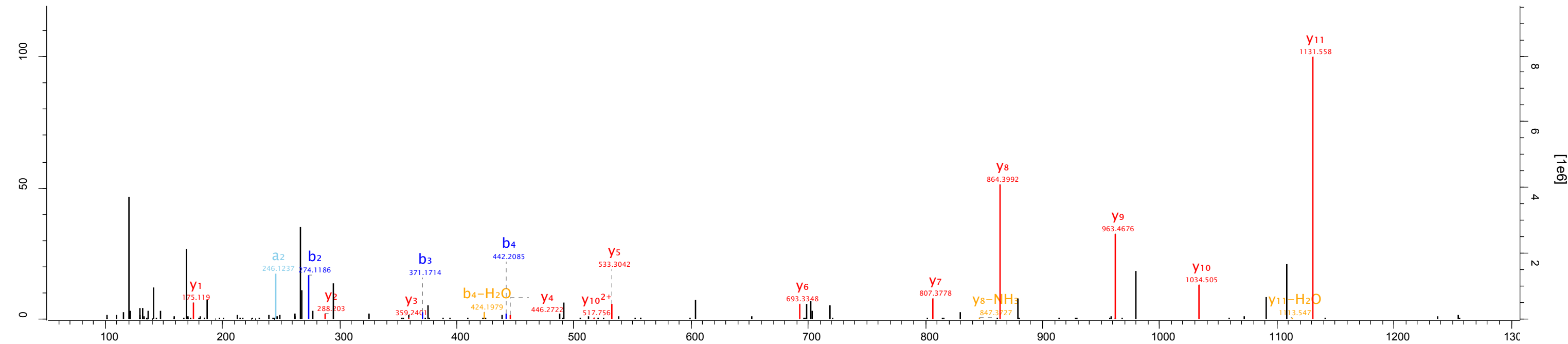
y₃ (over F), y₂ (over I), y₁ (over K)

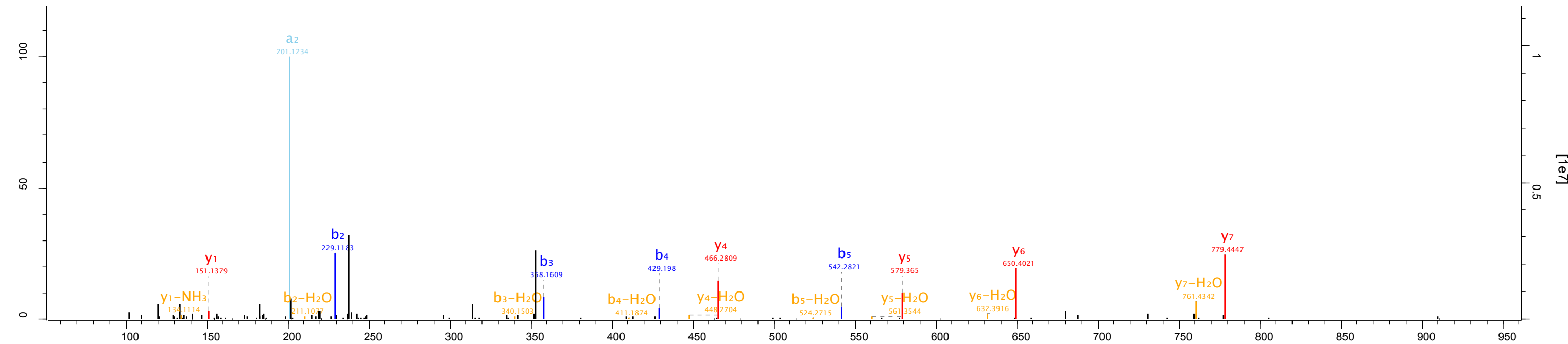
Raw file: 20180707_MaS_A375SR_ML_proteome_09
 Scan: 19899 Method: FTMS; HCD Score: 94.69 m/z: 630.33 Gene names: ITGA2B



Raw file
20180707_MaS_A375SR_ML_proteome_11

Scan Method Score m/z Gene names
18169 FTMS; HCD 59.25 702.84 HPX



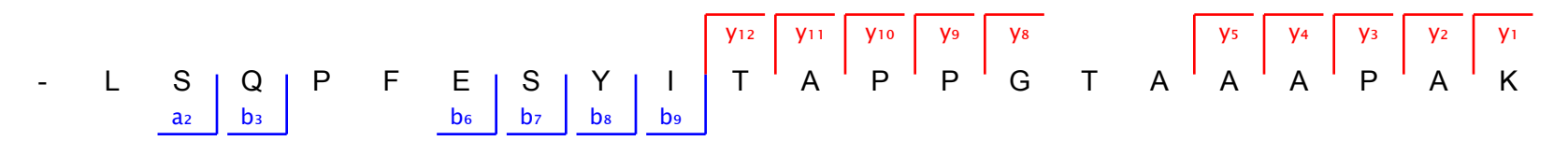
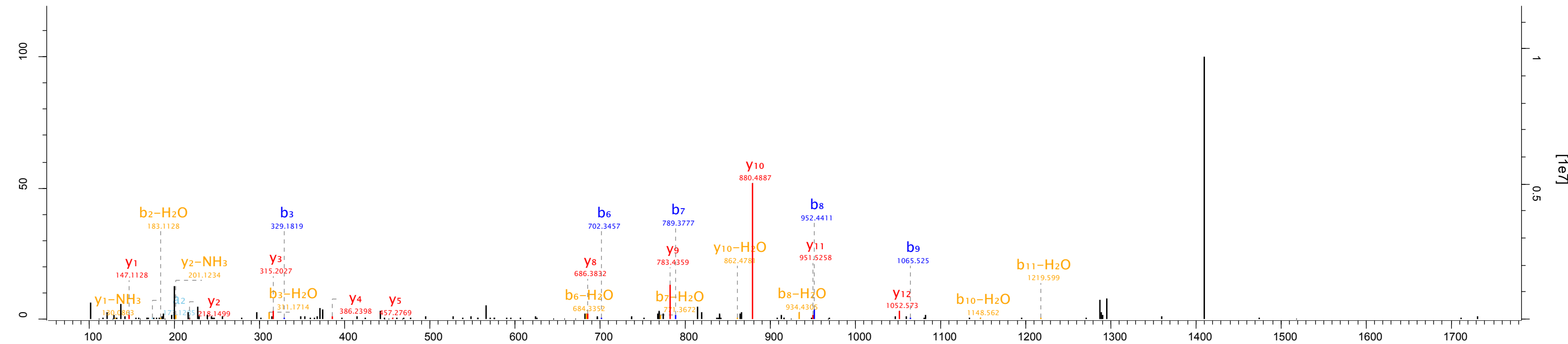


- D L E A L V T D K -

Fragmentation scheme showing b and y ions for the peptide sequence: D L E A L V T D K. The b ions (blue) are b2, b3, b4, and b5. The y ions (red) are y1, y4, y5, y6, and y7.

Raw file
20180707_MaS_A375SR_ML_proteome_11

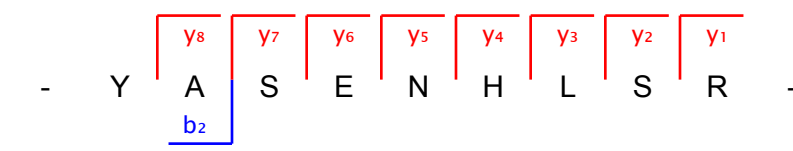
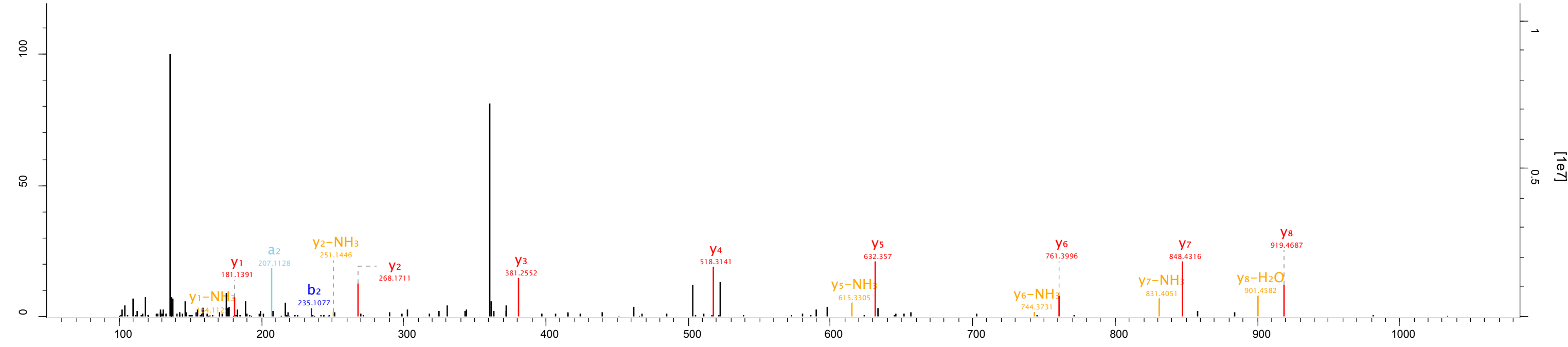
Scan 25649 Method FTMS; HCD Score 25.61 m/z 706.37 Gene names TMEM261



Raw file

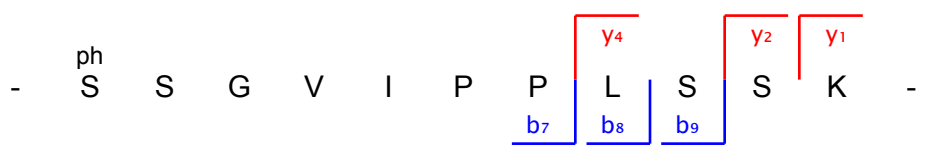
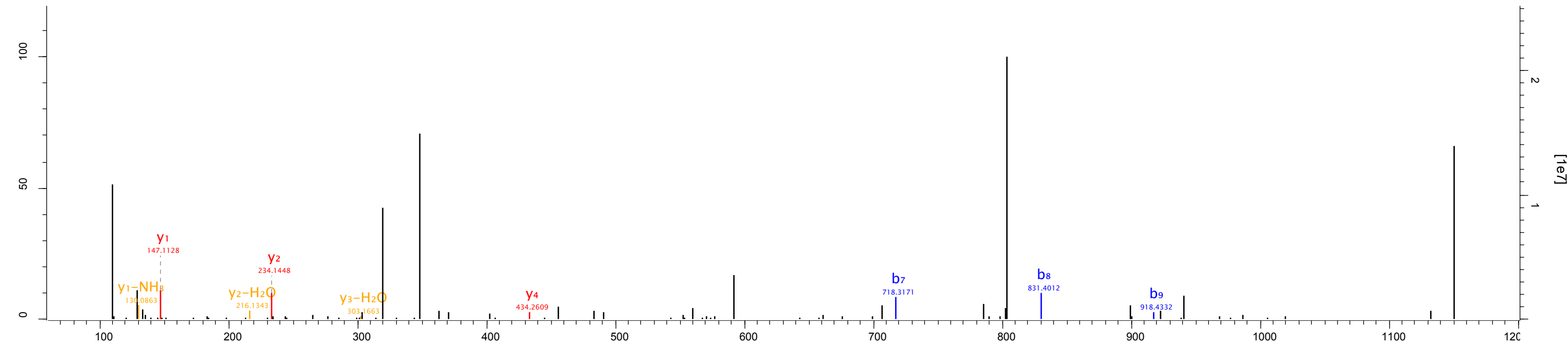
20180707_MaS_A375SR_ML_proteome_11

Scan 3159 Method FTMS; HCD Score 90.15 m/z 361.51 Gene names TM4SF1



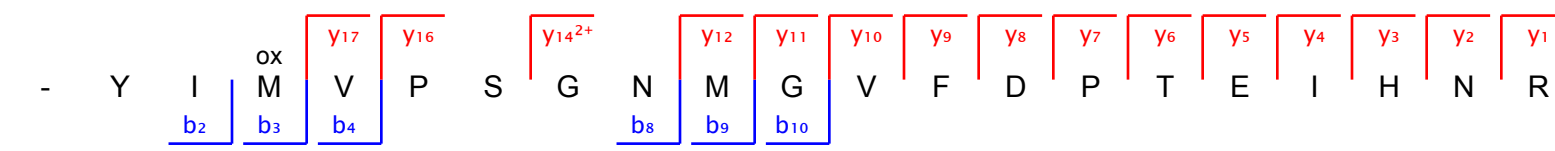
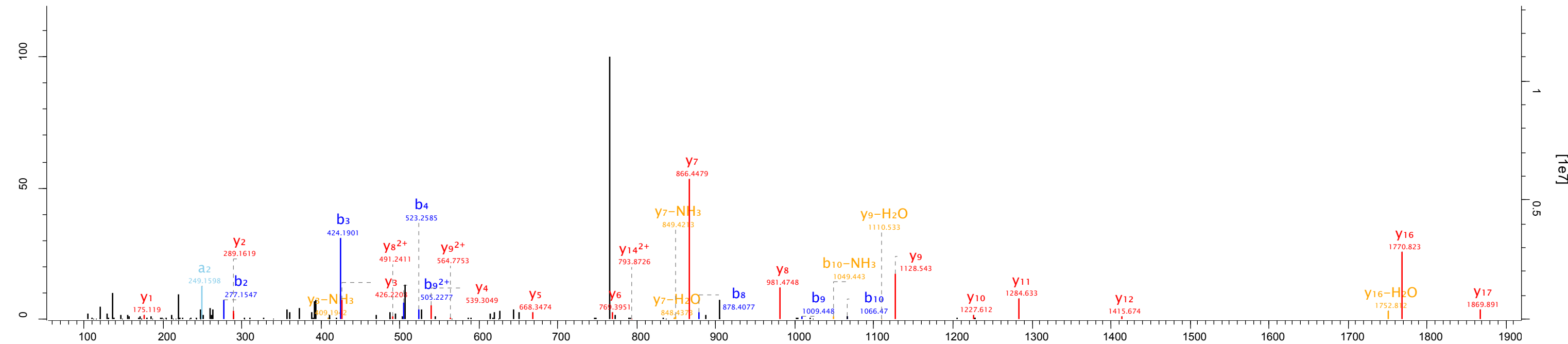
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20180707_MaS_A375SR_ML_proteome_12

Scan 8279 Method FTMS; HCD Score 48.28 m/z 576.29

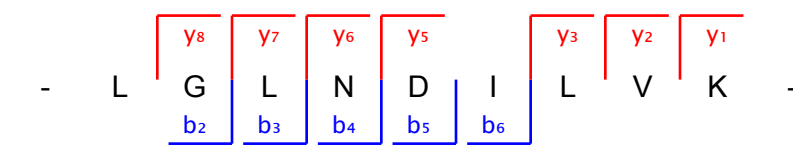
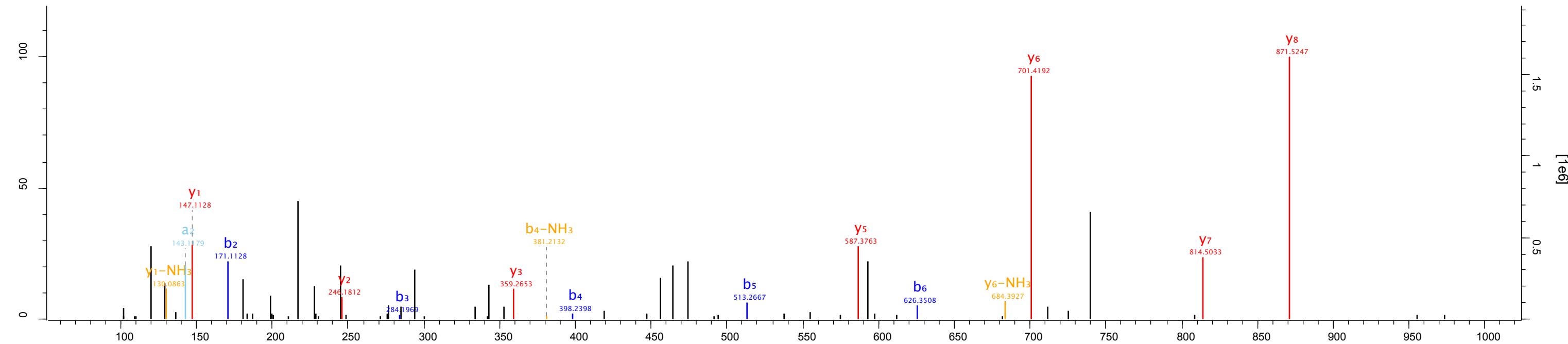


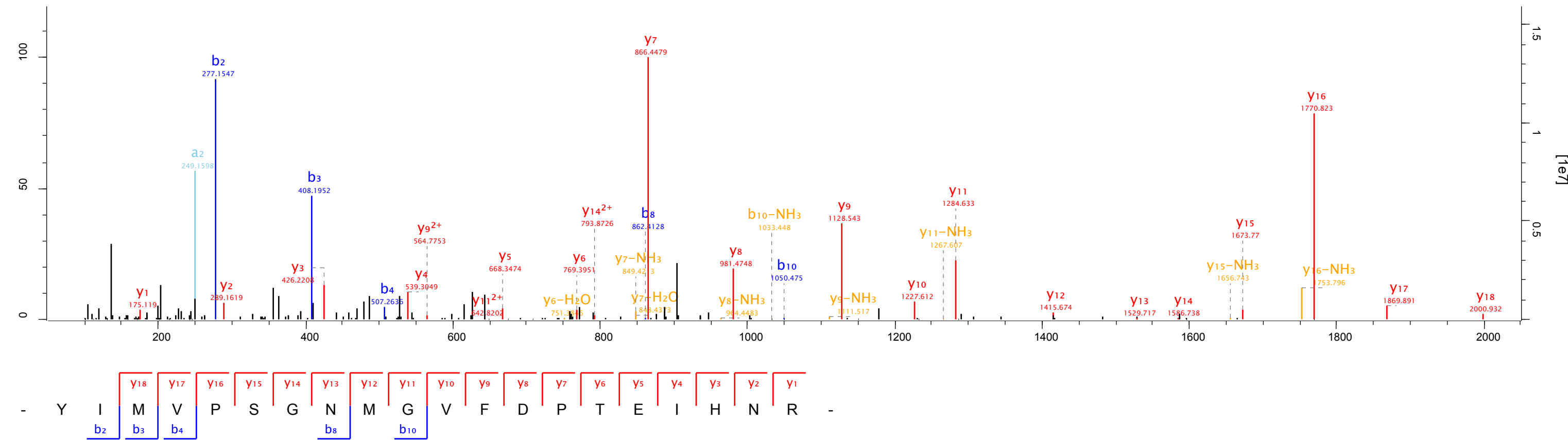
Raw file
20180707_MaS_A375SR_ML_proteome_13

Scan 25349 Method FTMS; HCD Score 114.55 m/z 765.36 Gene names CNIH4

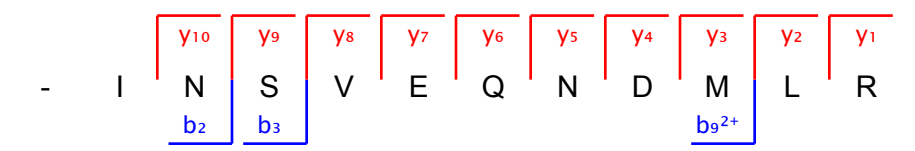
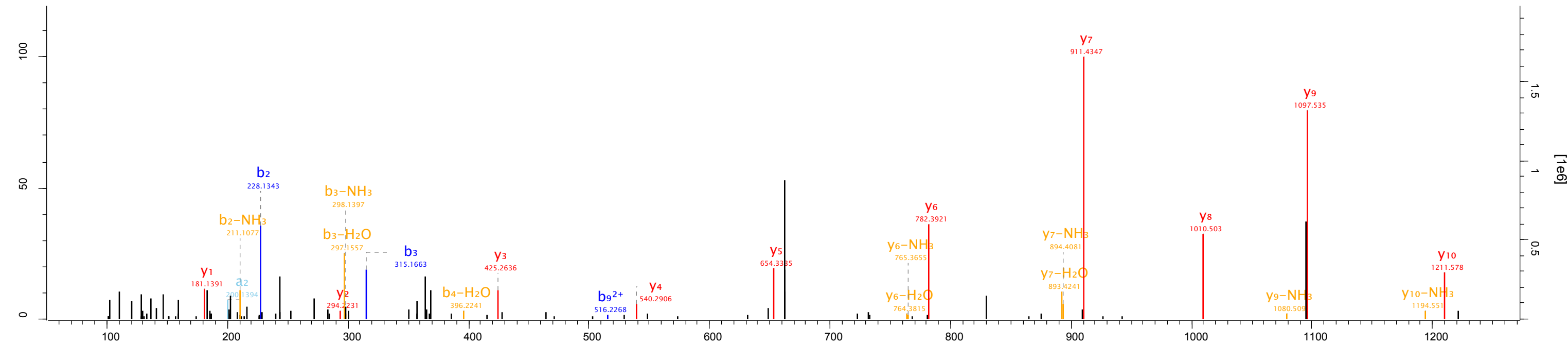


Raw file 20180707_MaS_A375SR_ML_proteome_13 Scan 26269 Method FTMS; HCD Score 78.1 m/z 492.81 Gene names STON2

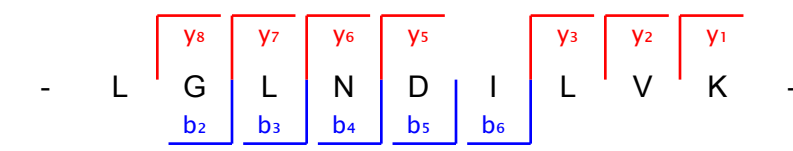
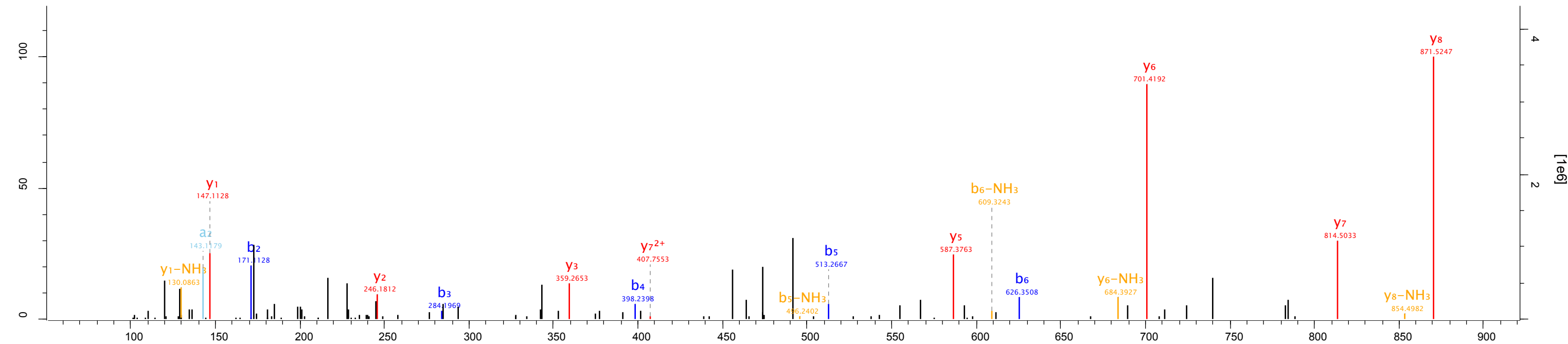




Raw file: 20180707_MaS_A375SR_ML_proteome_14
 Scan: 12909 Method: FTMS; HCD Score: 124.42 m/z: 662.84 Gene names: SLC9A7

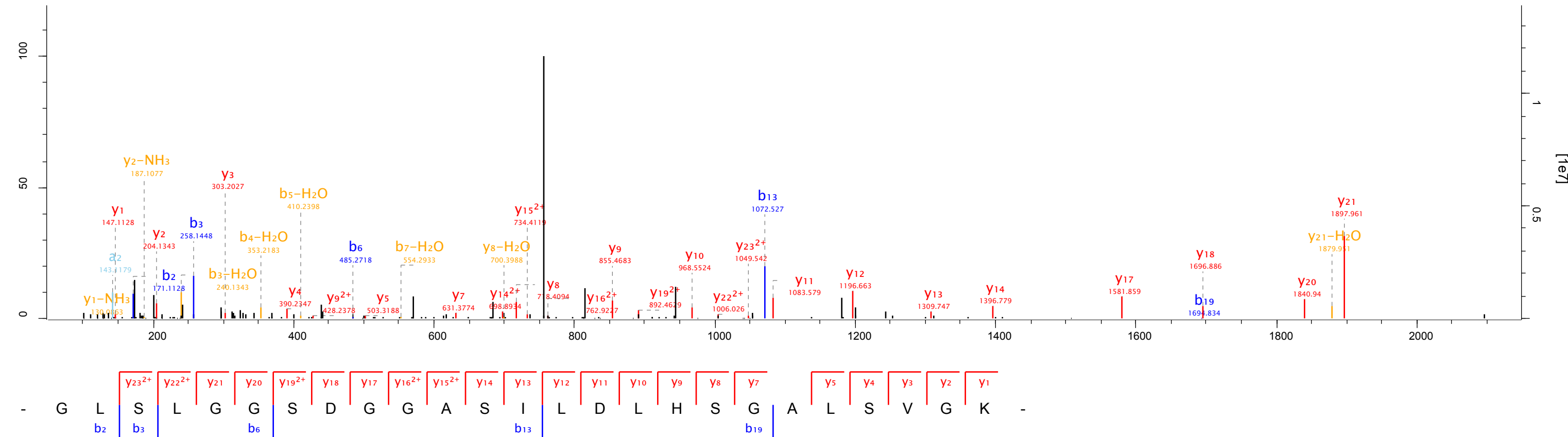


Raw file: 20180707_MaS_A375SR_ML_proteome_14
 Scan: 25629 Method: FTMS; HCD Score: 97.57 m/z: 492.81 Gene names: STON2



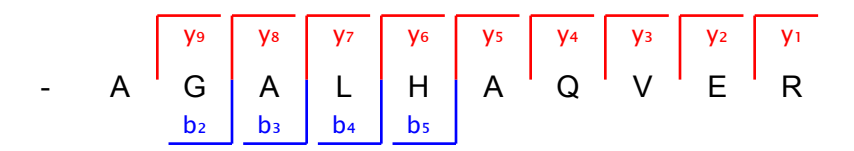
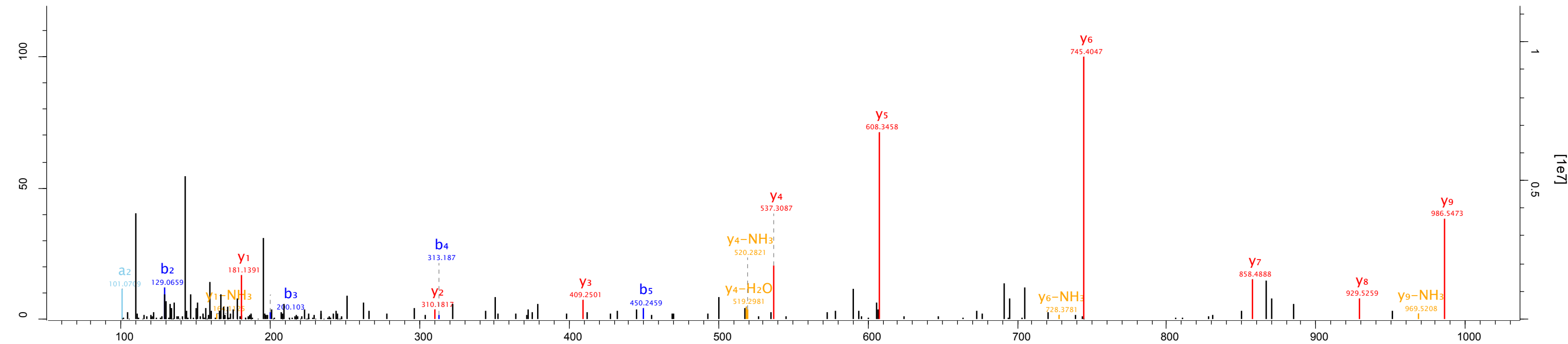
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20180707_MaS_A375SR_ML_proteome_14

Scan Method Score m/z Gene names
26569 FTMS; HCD 107.75 757.07 OGFOD3

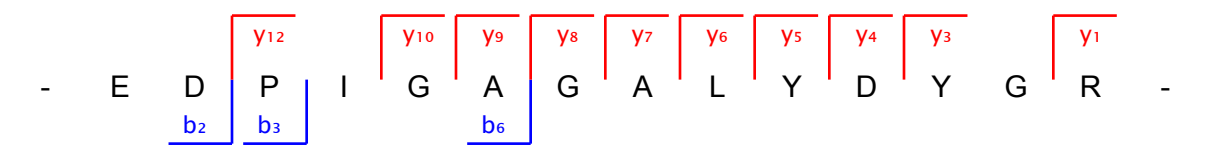
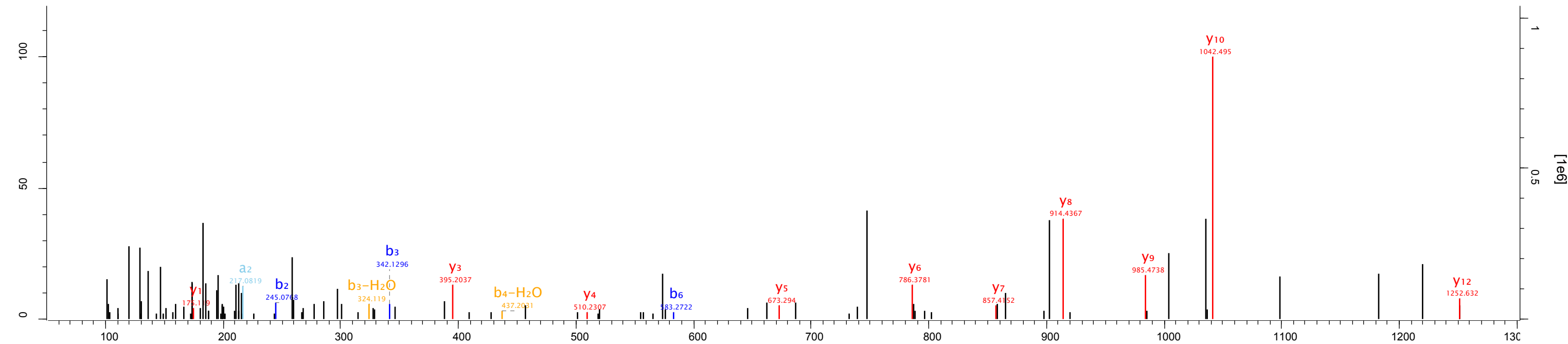


Raw file
20180707_MaS_A375SR_ML_proteome_14

Scan 4639 Method FTMS; HCD Score 70.41 m/z 353.2 Gene names MYBBP1A

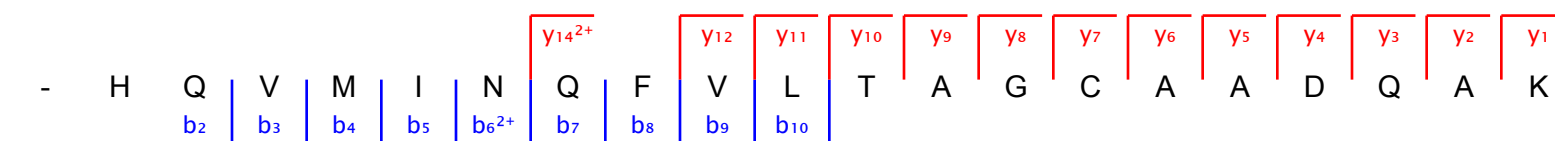
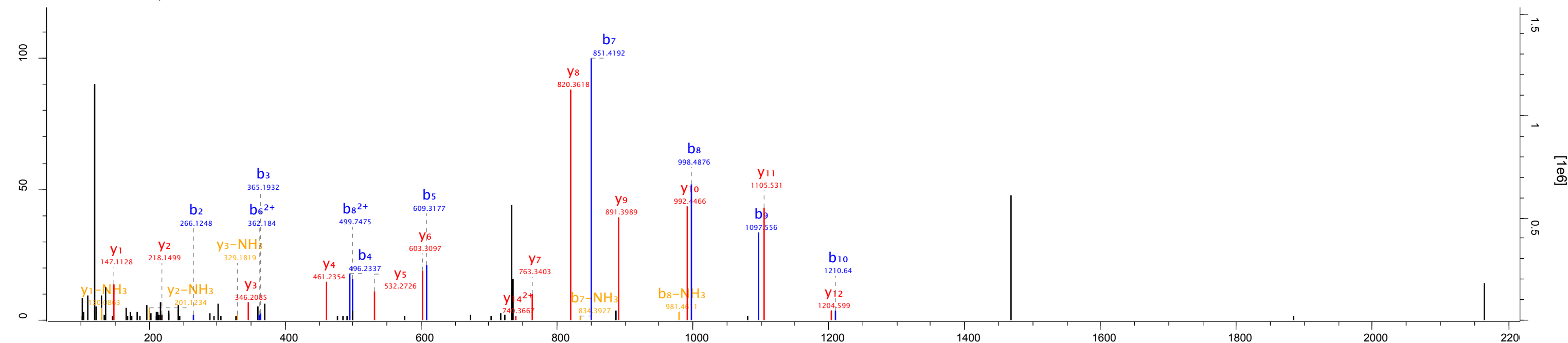


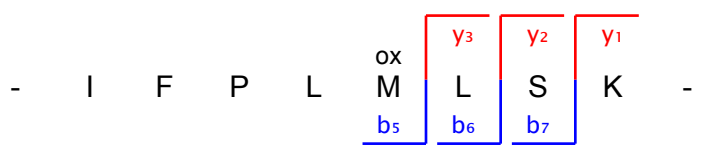
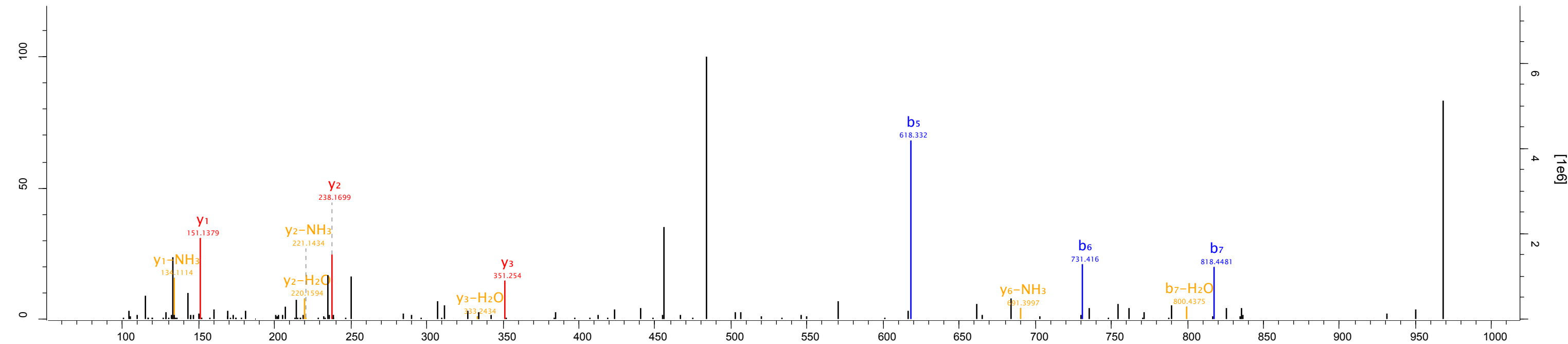
Raw file: 20180707_MaS_A375SR_ML_proteome_16
 Scan: 22569 Method: FTMS; HCD Score: 49.19 m/z: 748.86 Gene names: MT-ND6

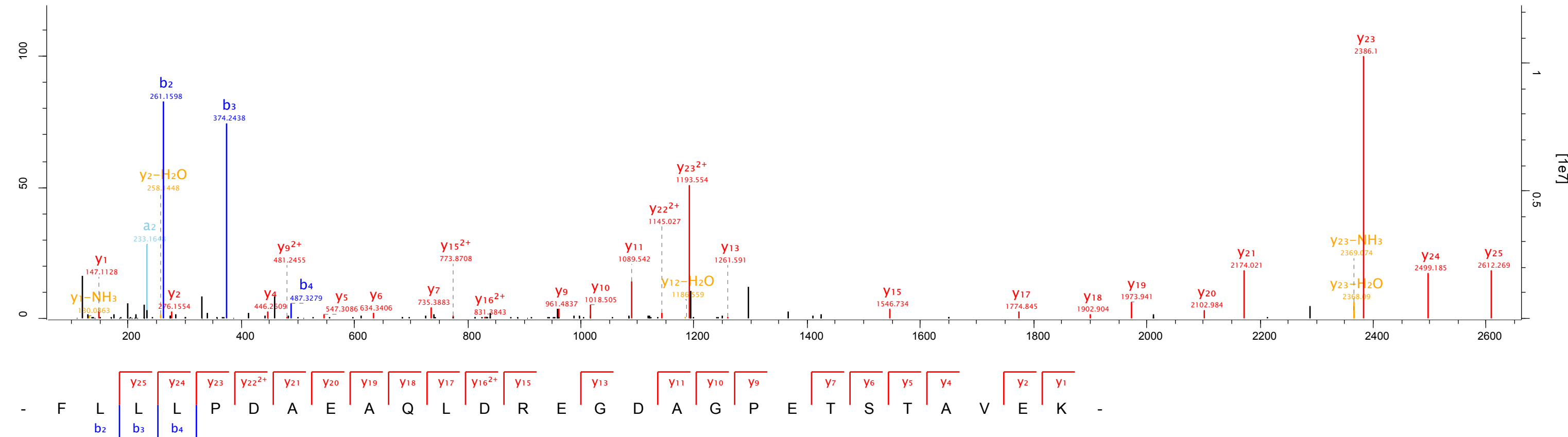


Raw file
20180707_MaS_A375SR_ML_proteome_16

Scan 24309 Method FTMS; HCD Score 74.03 m/z 735.03 Gene names UBALD1

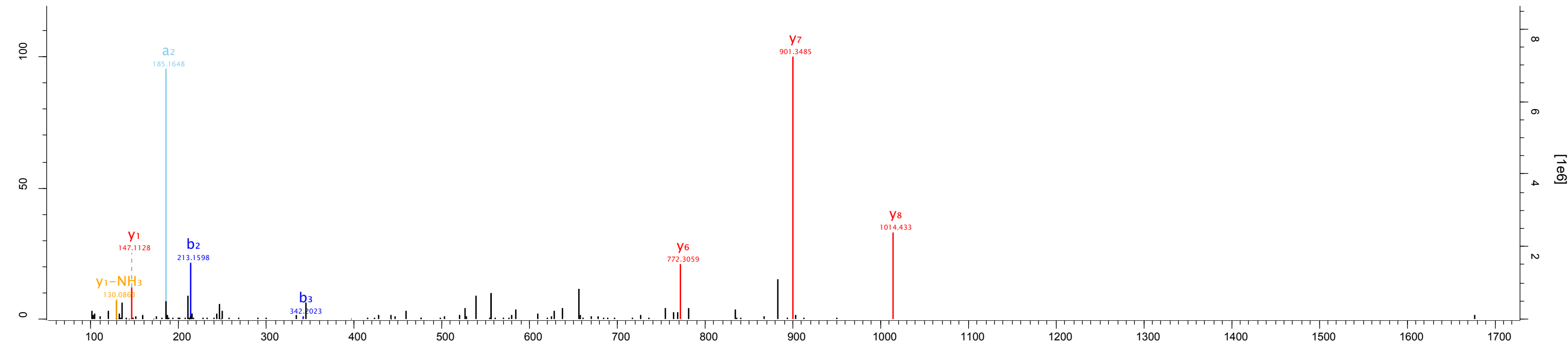






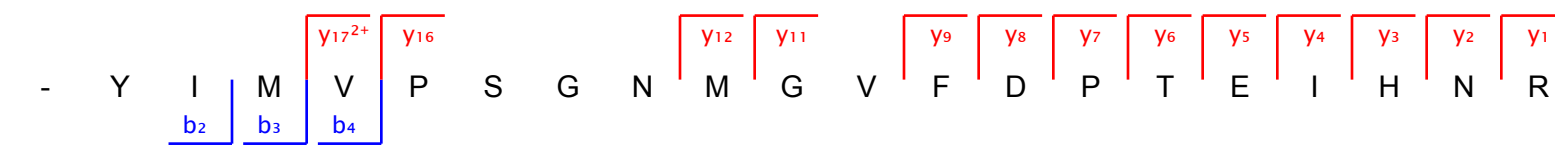
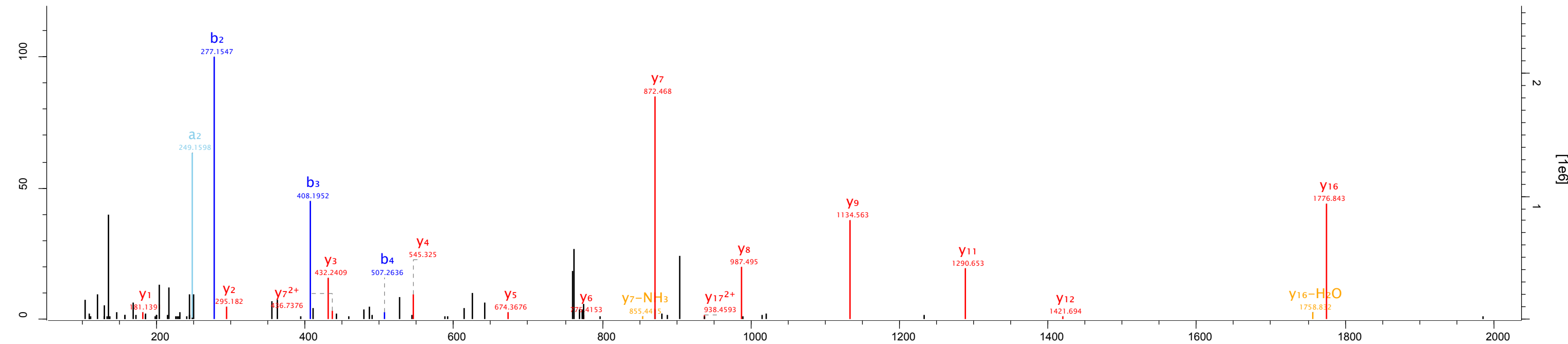
Raw file
20180707_MaS_A375SR_ML_proteome_19

Scan 12779 Method FTMS; HCD Score 57.59 m/z 557.25



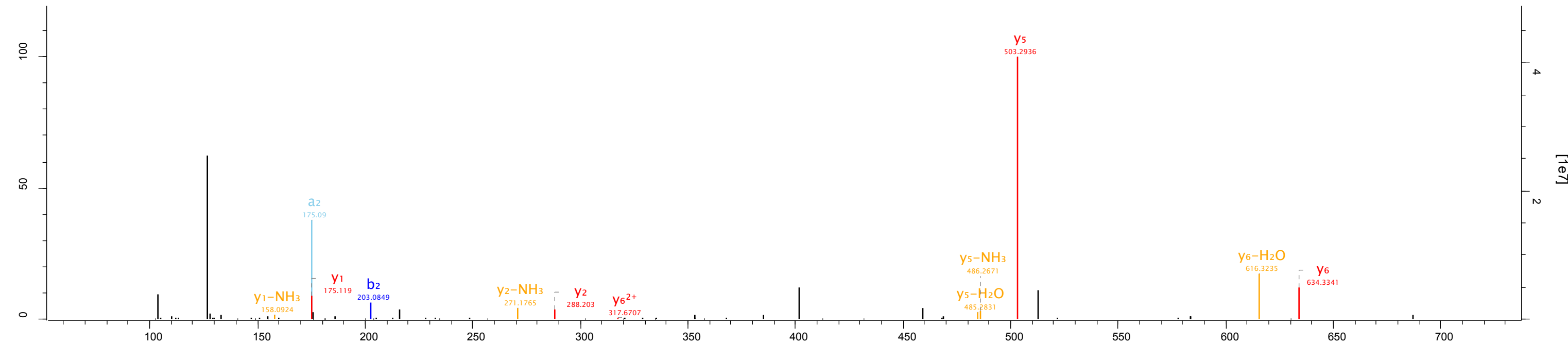
Raw file
20180707_MaS_A375SR_ML_proteome_2_01

Scan 26179 Method FTMS; HCD Score 51.94 m/z 762.04 Gene names CNIH4



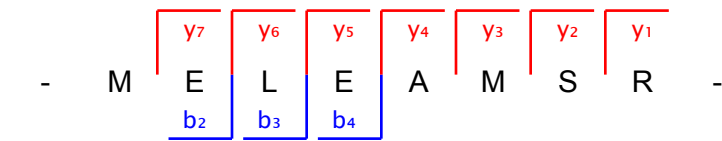
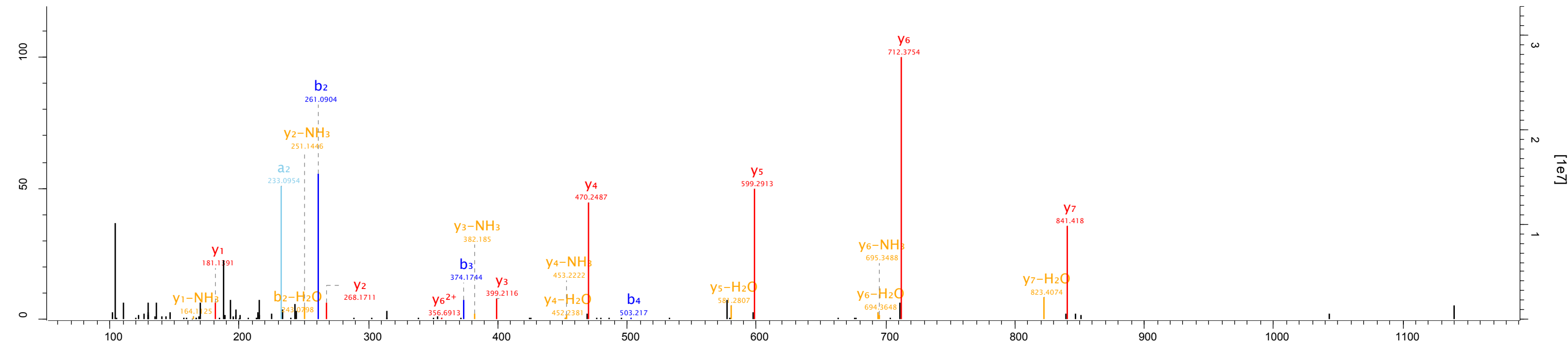
Raw file
20180707_MaS_A375SR_ML_proteome_2_01

Scan 6139 Method FTMS; HCD Score 92.69 m/z 353.19

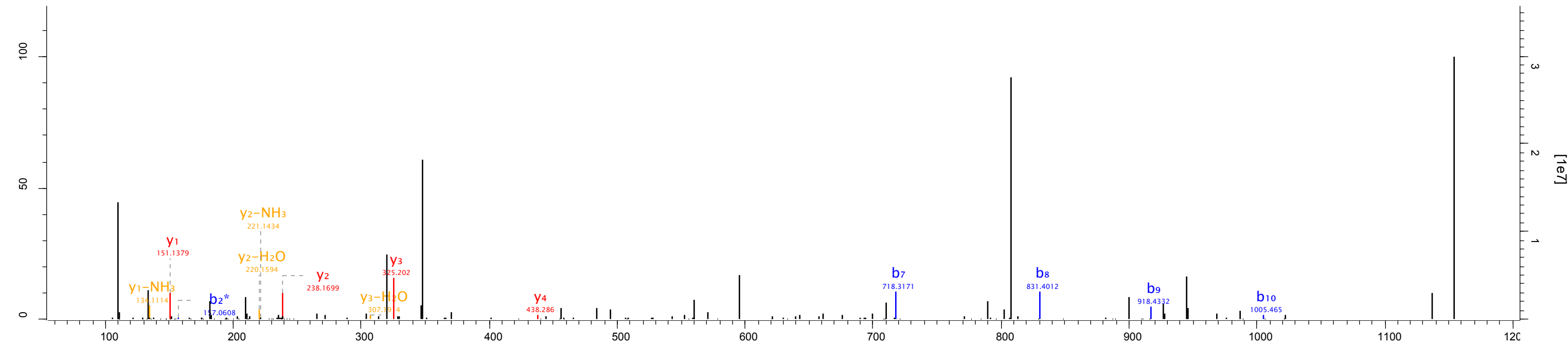


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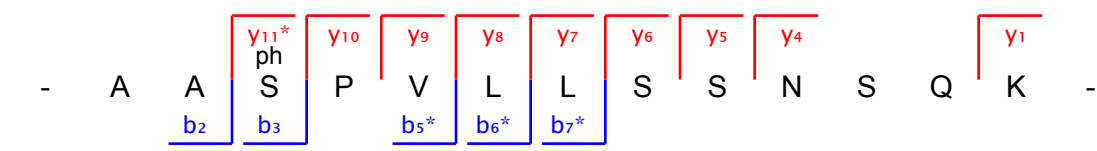
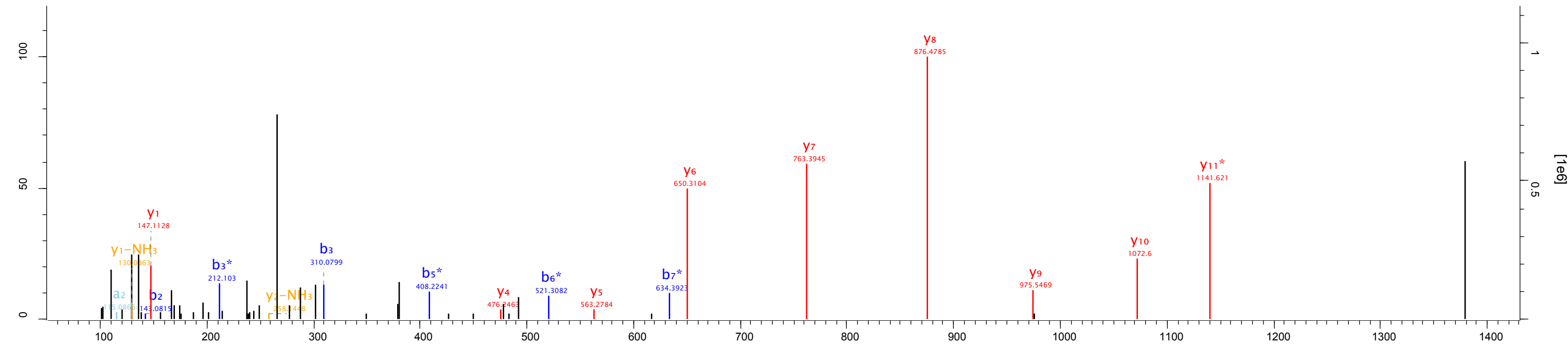
Scan 14039 Method FTMS; HCD Score 120.87 m/z 486.73 Gene names TMEM258



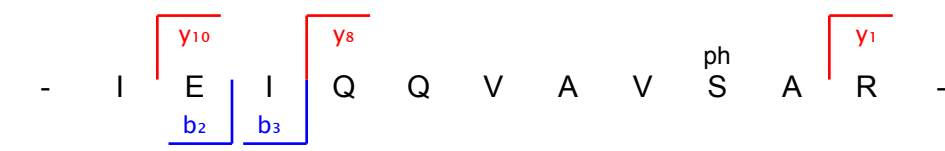
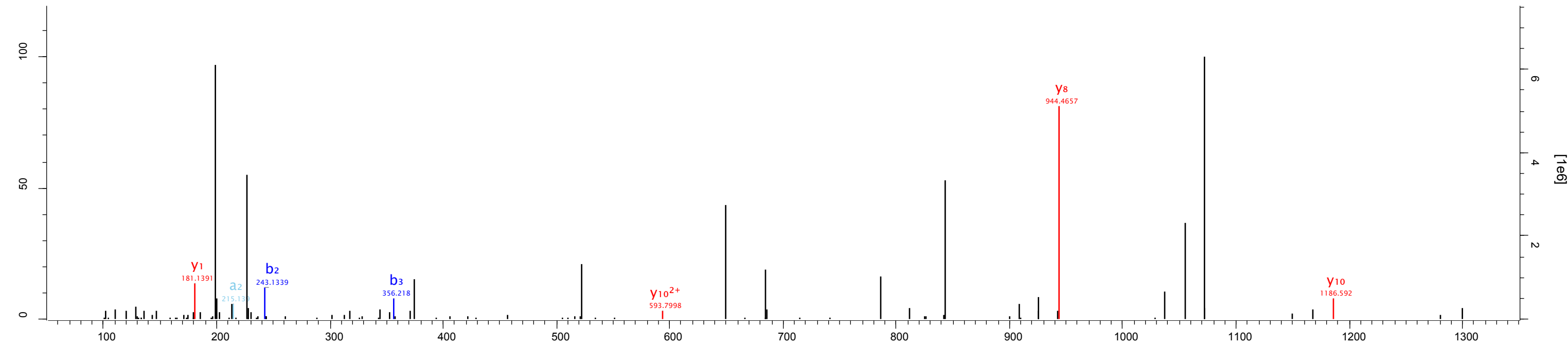
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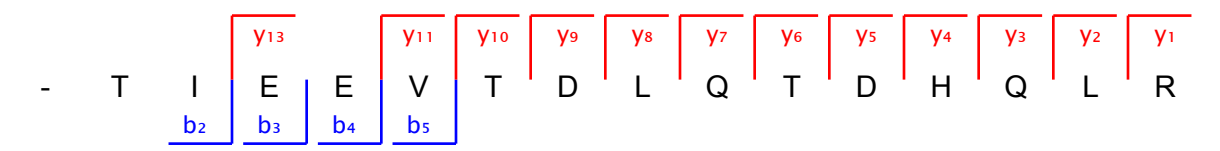
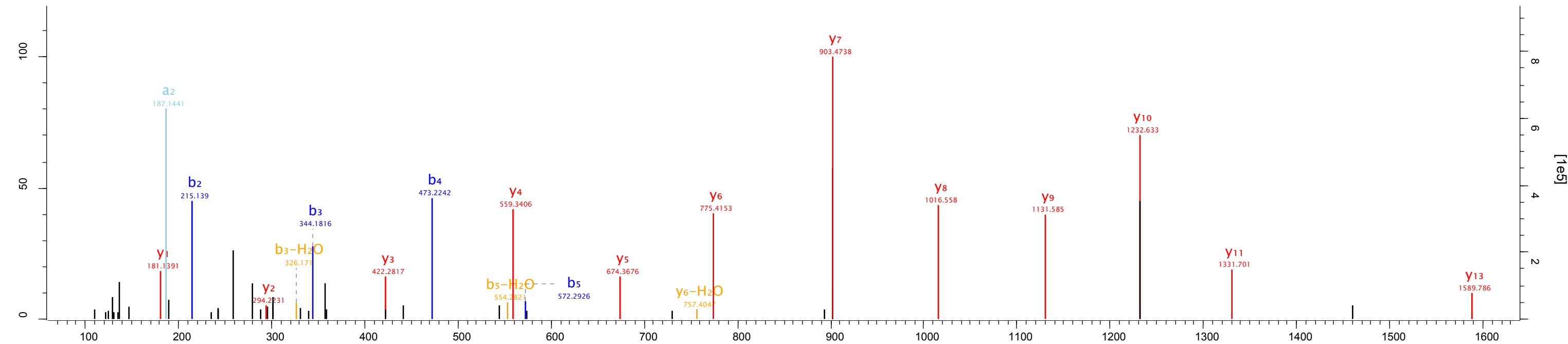
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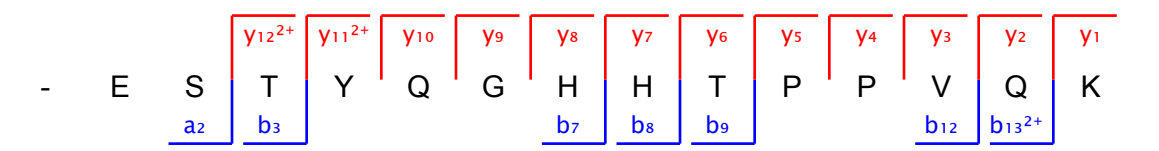
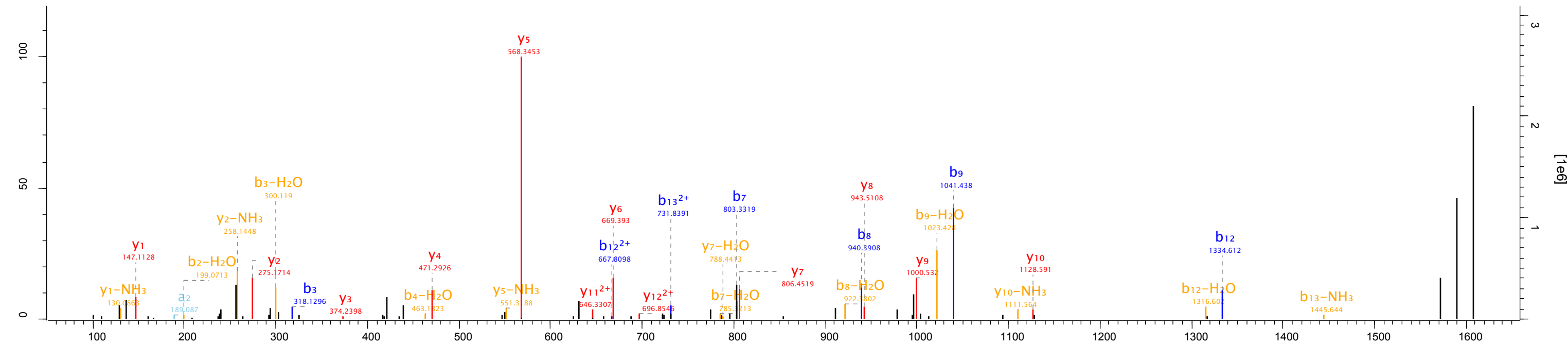
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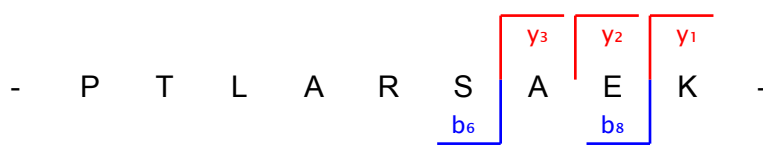
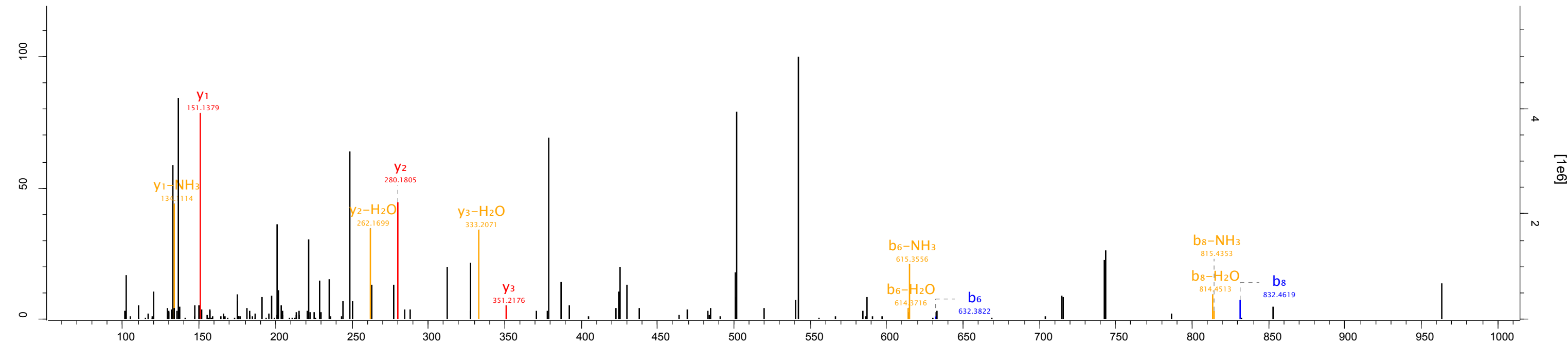
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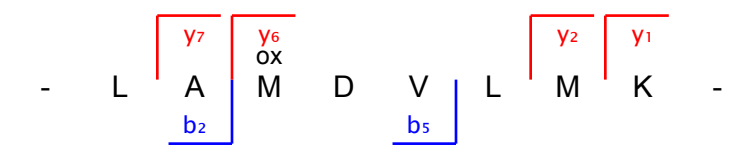
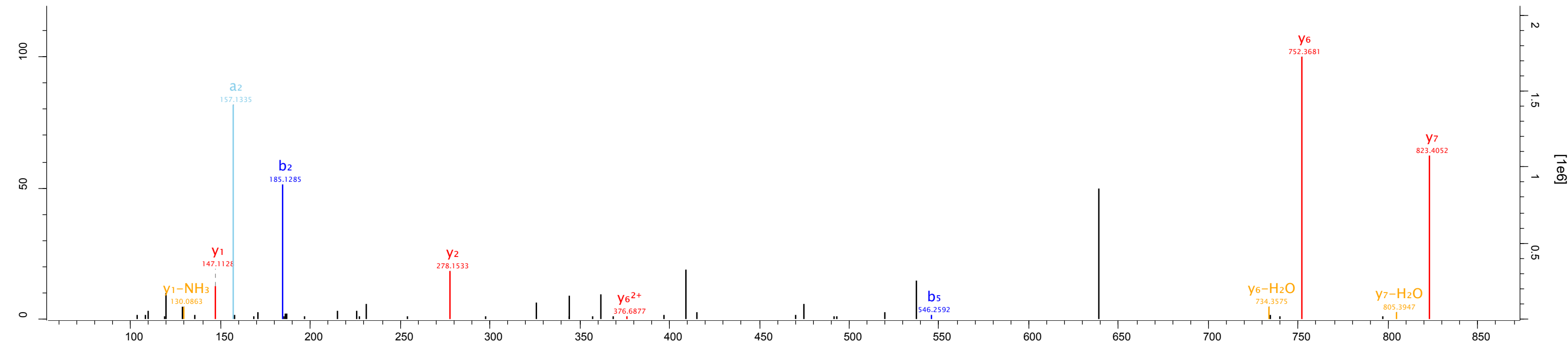
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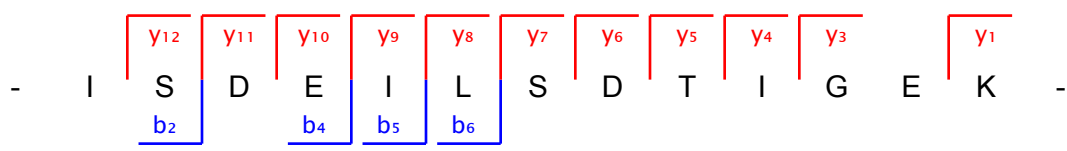
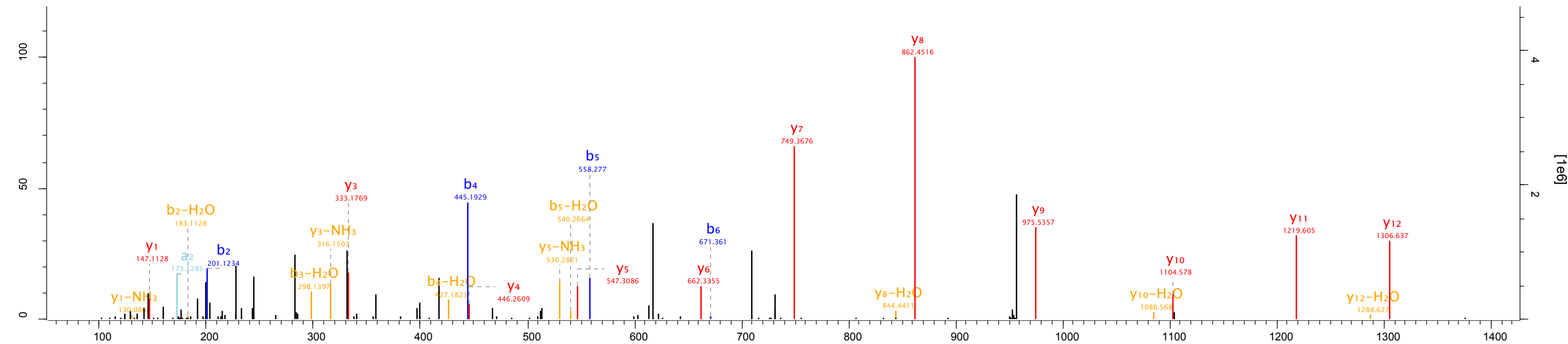


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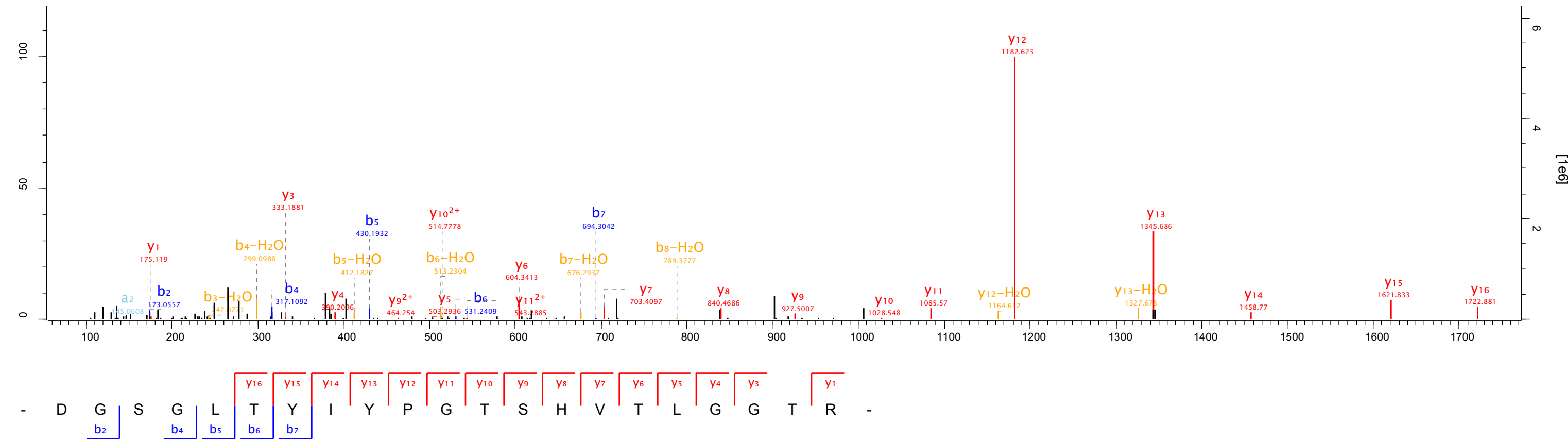
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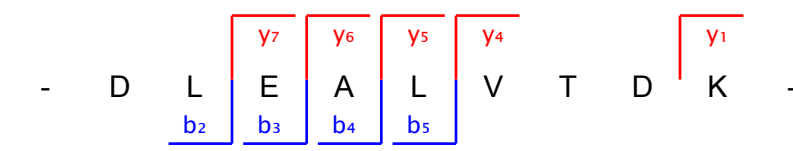
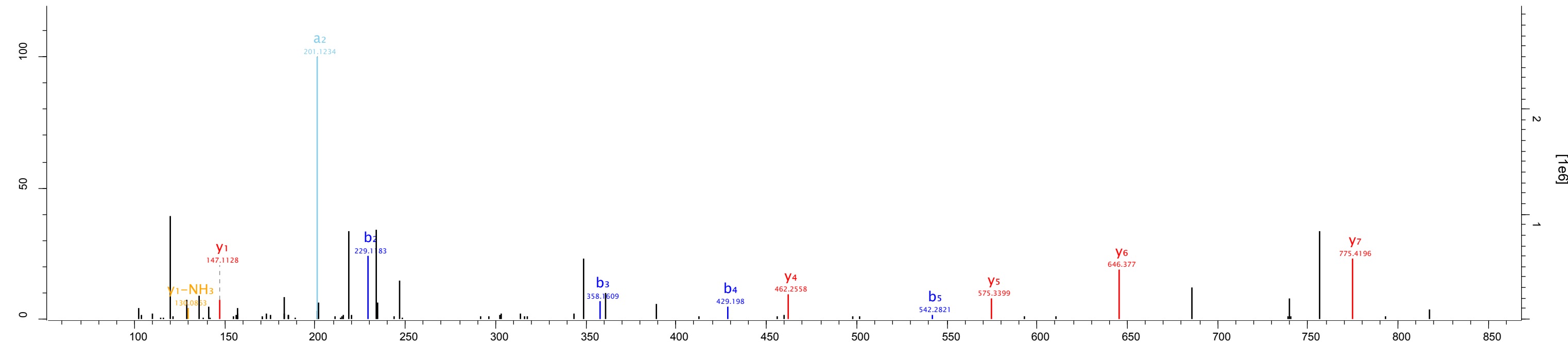


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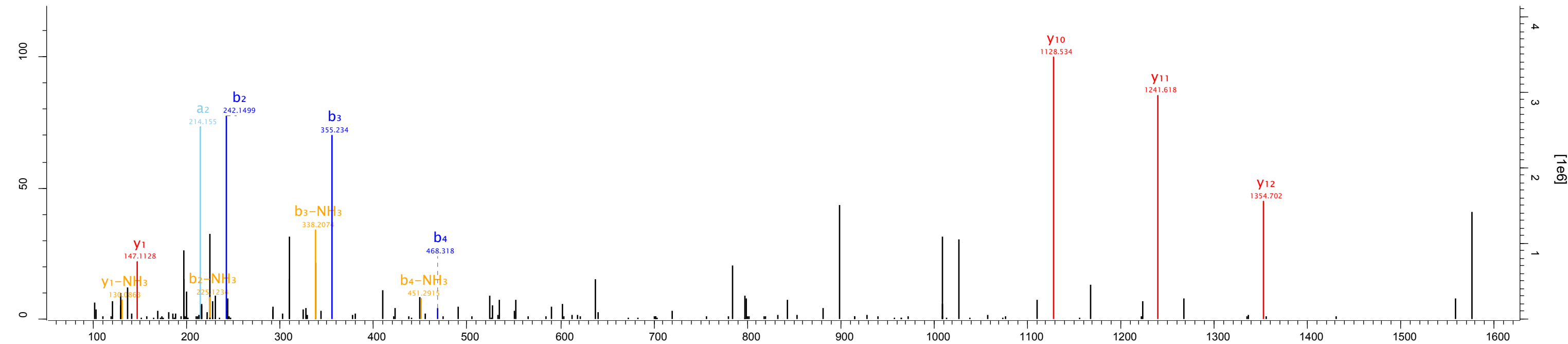
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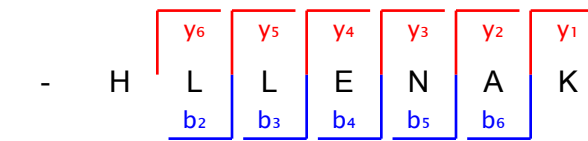
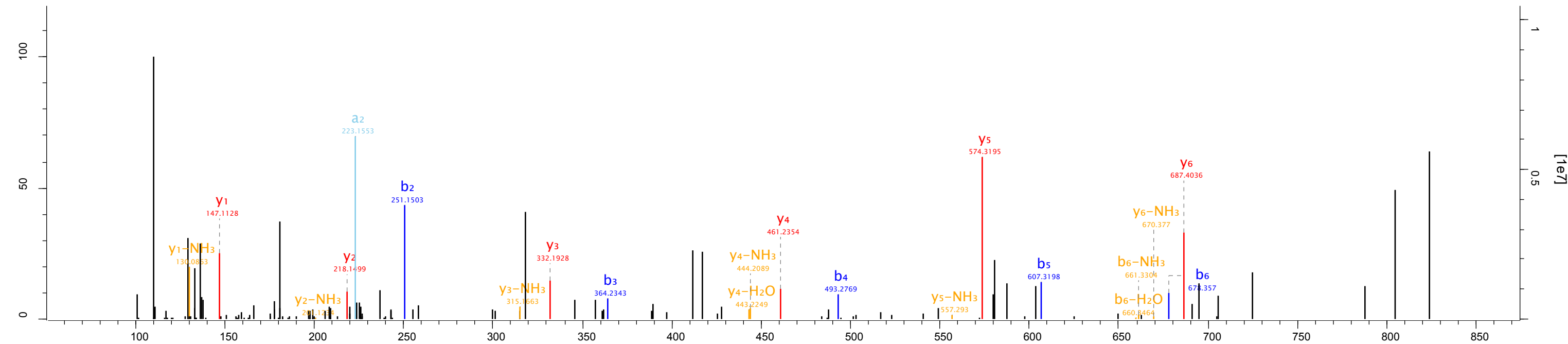
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22749Method
FTMS; HCDScore
82.63m/z
718.36Gene names
DDO

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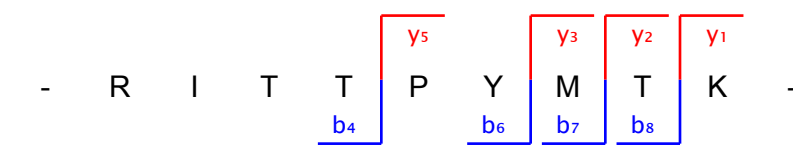
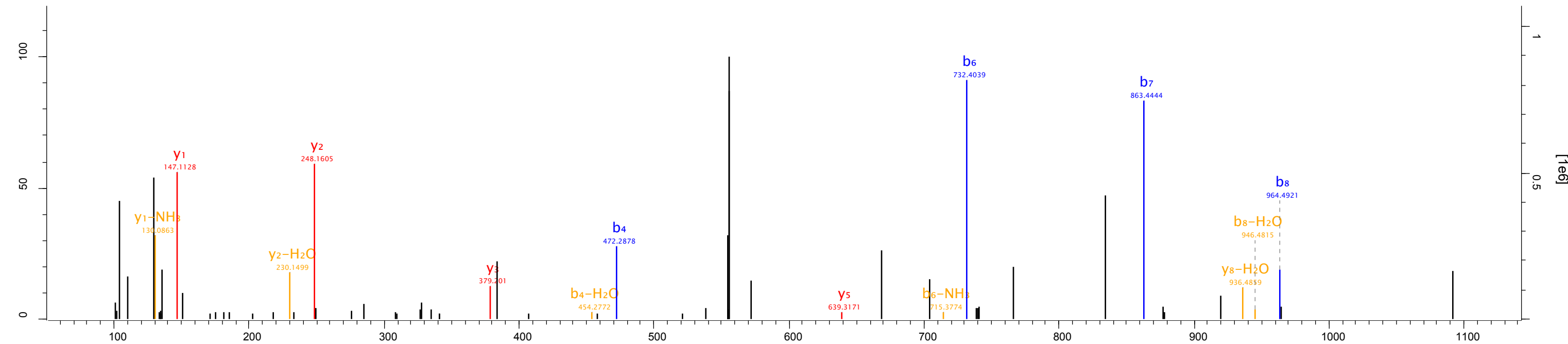


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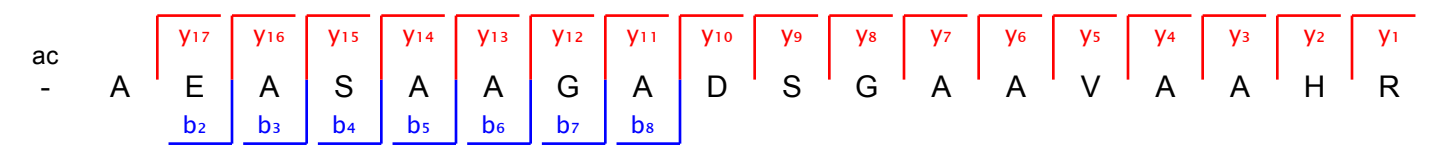
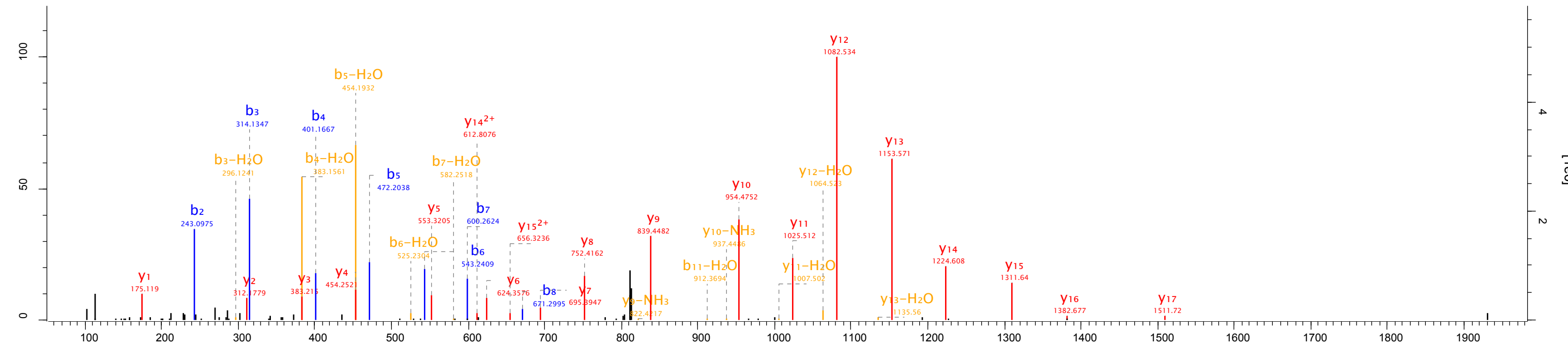


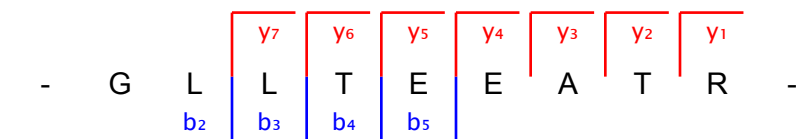
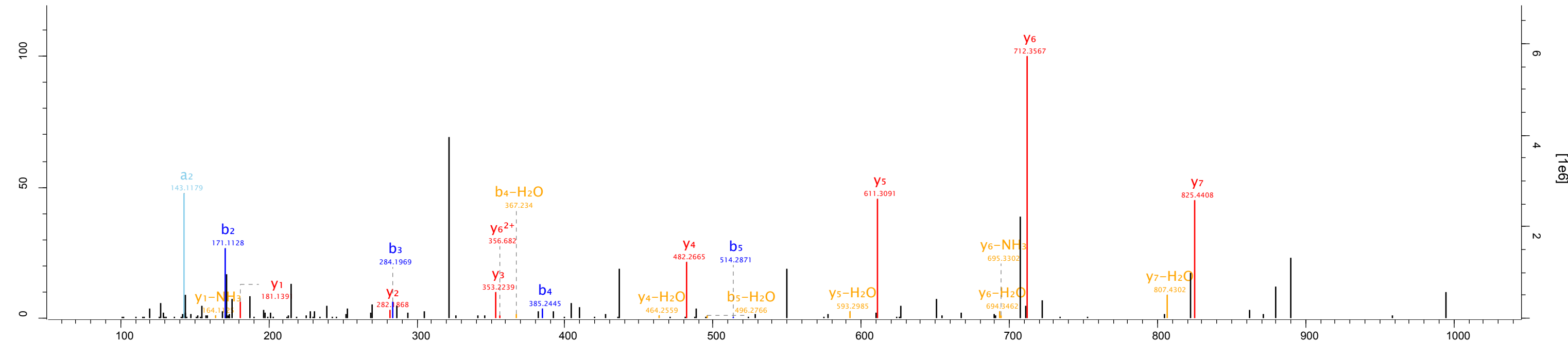


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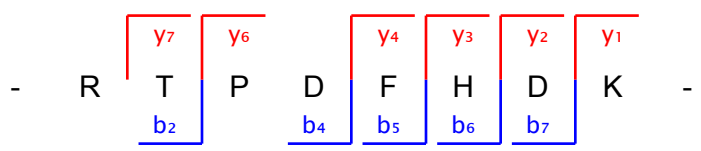
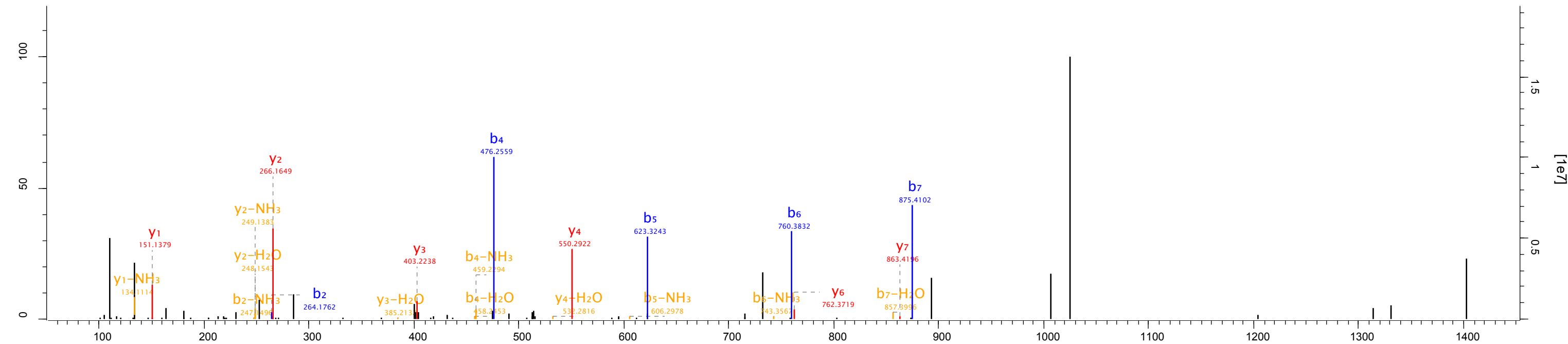
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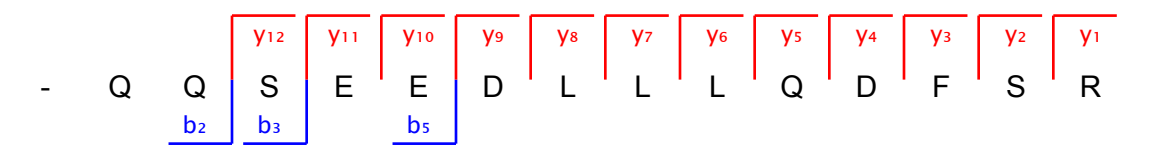
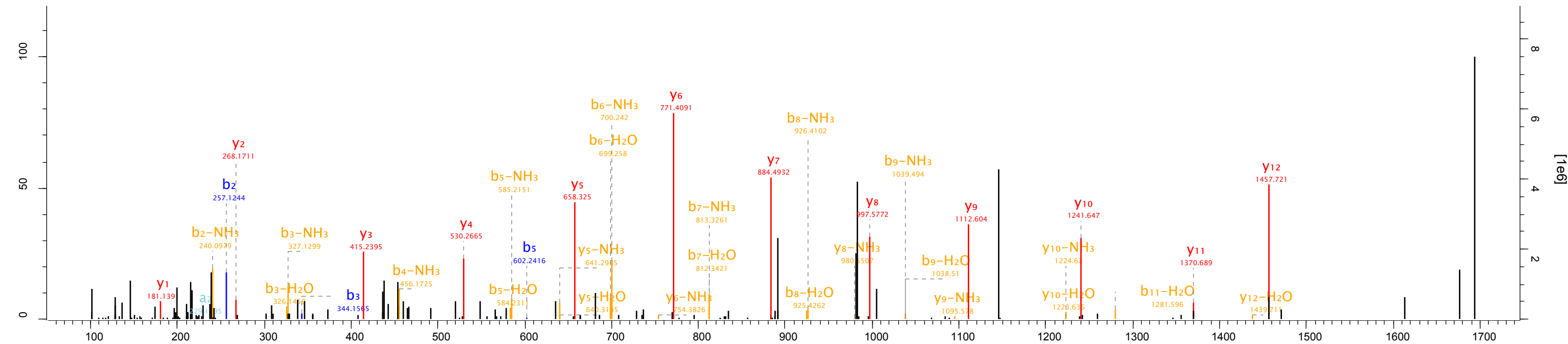


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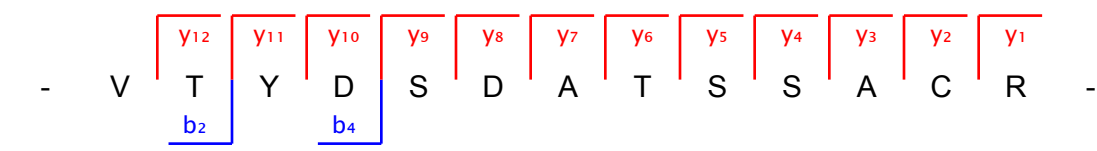
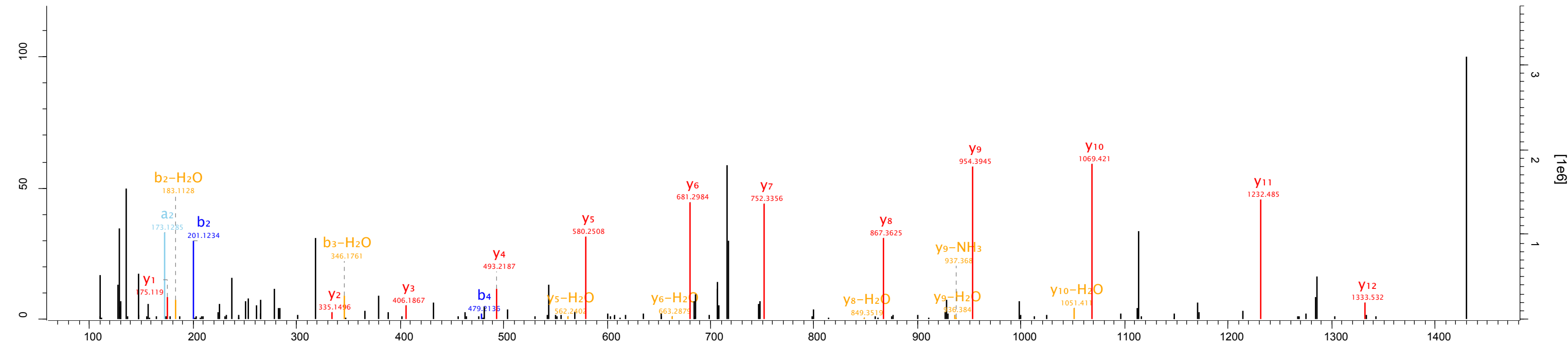
Scan 3309 Method FTMS; HCD Score 117.01 m/z 513.27 Gene names COX7B



Raw file 20180707_MaS_A375SR_ML_proteome_2_08 Scan 27819 Method FTMS; HCD Score 105.58 m/z 857.42 Gene names SSR3

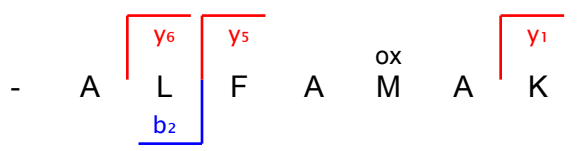
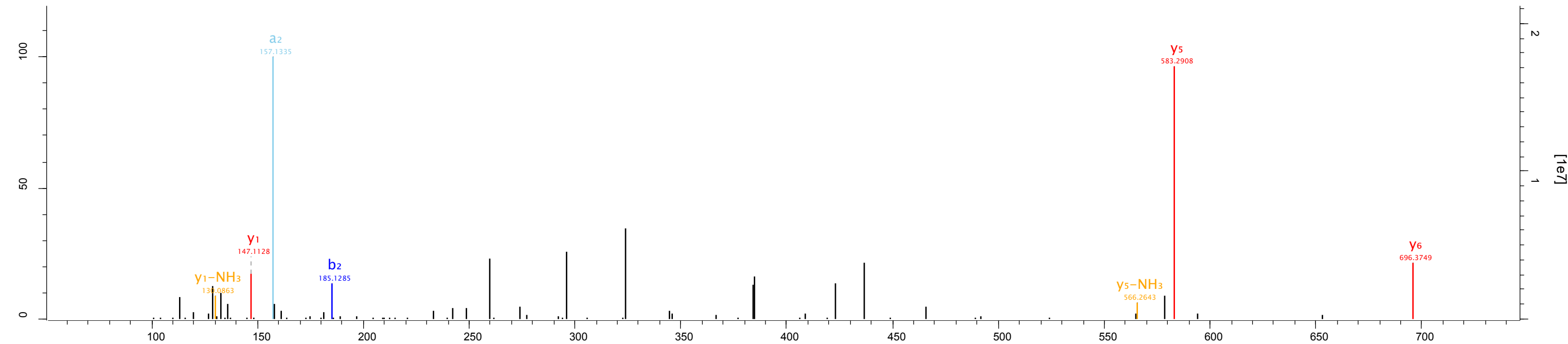


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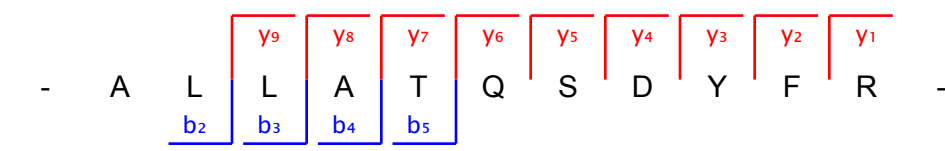
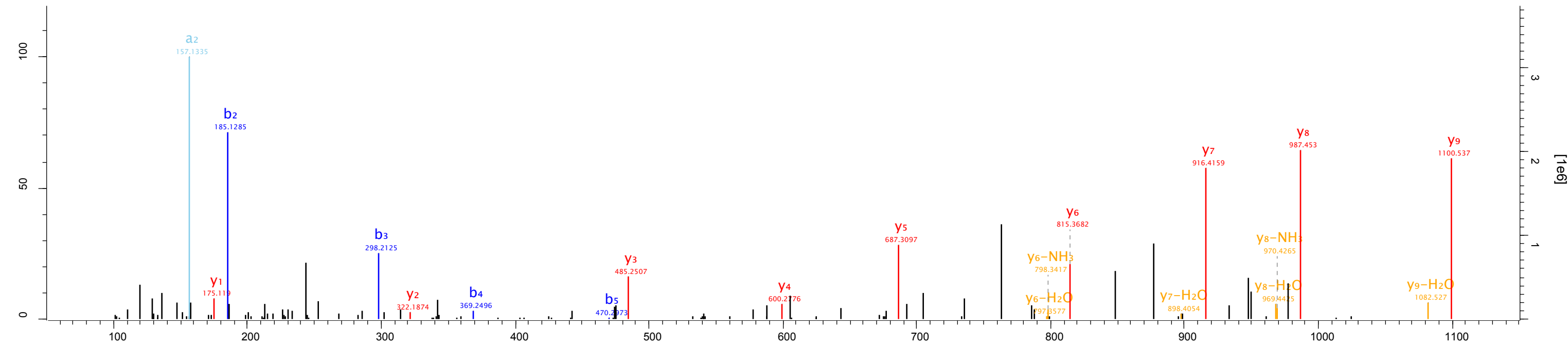


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20180707_MaS_A375SR_ML_proteome_2_09

Scan 12559 Method FTMS; HCD Score 44.97 m/z 384.21 Gene names RASD1

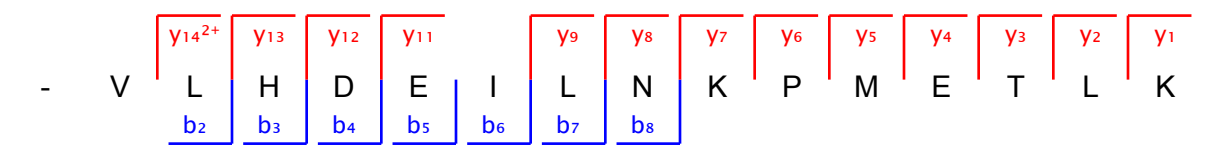
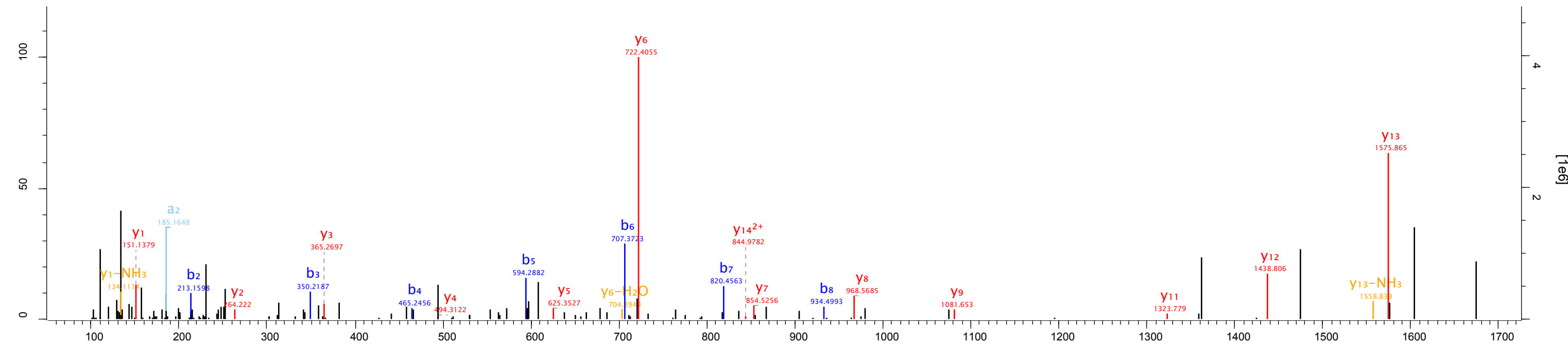


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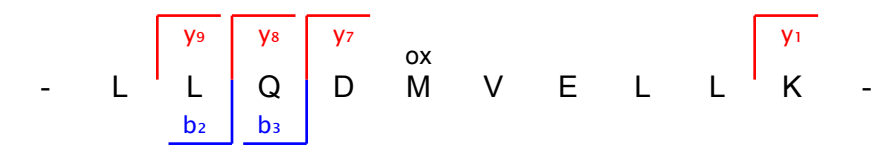
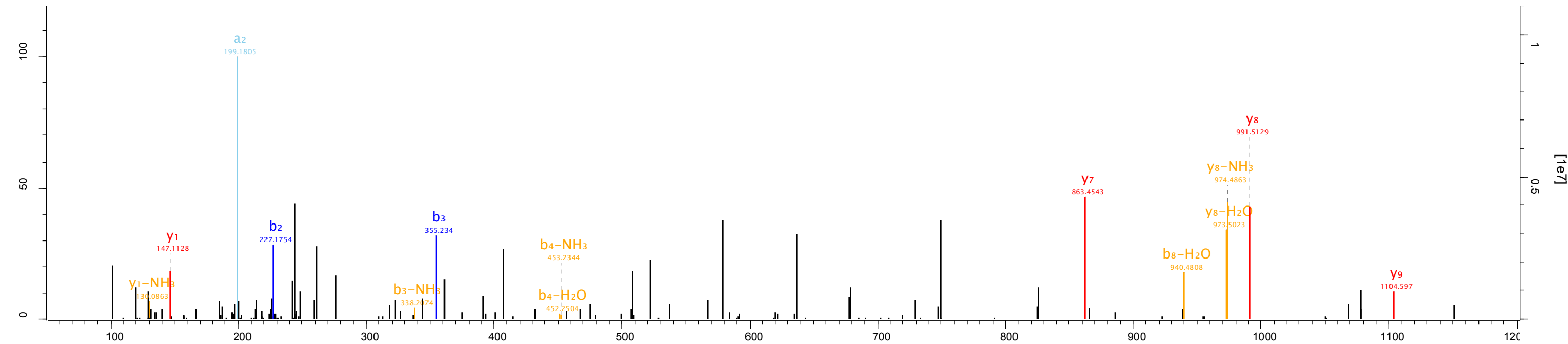


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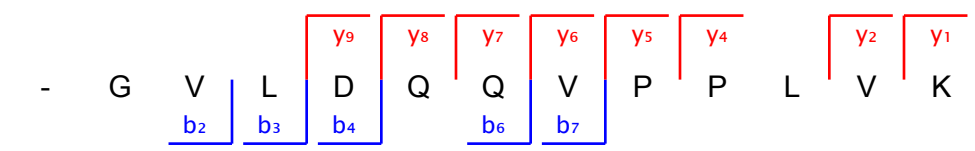
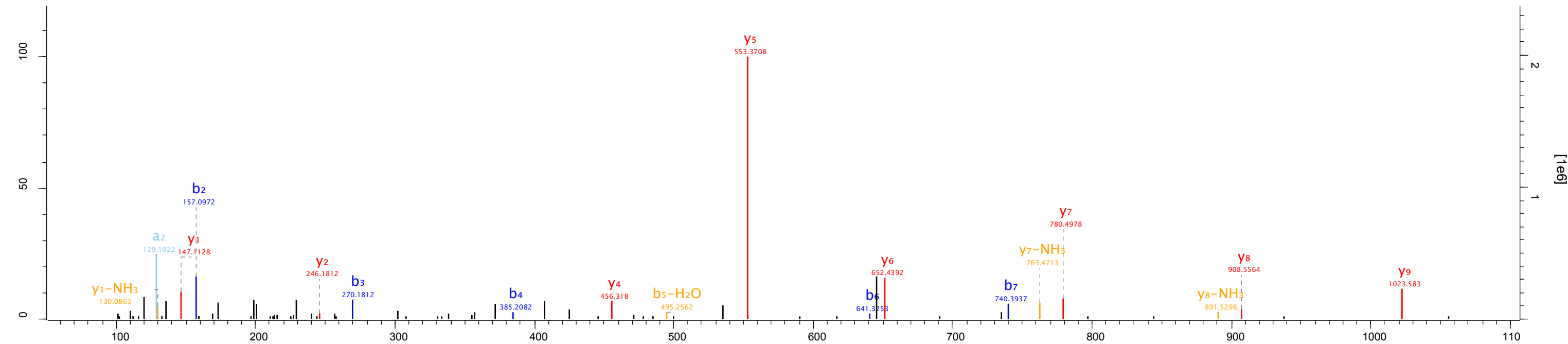


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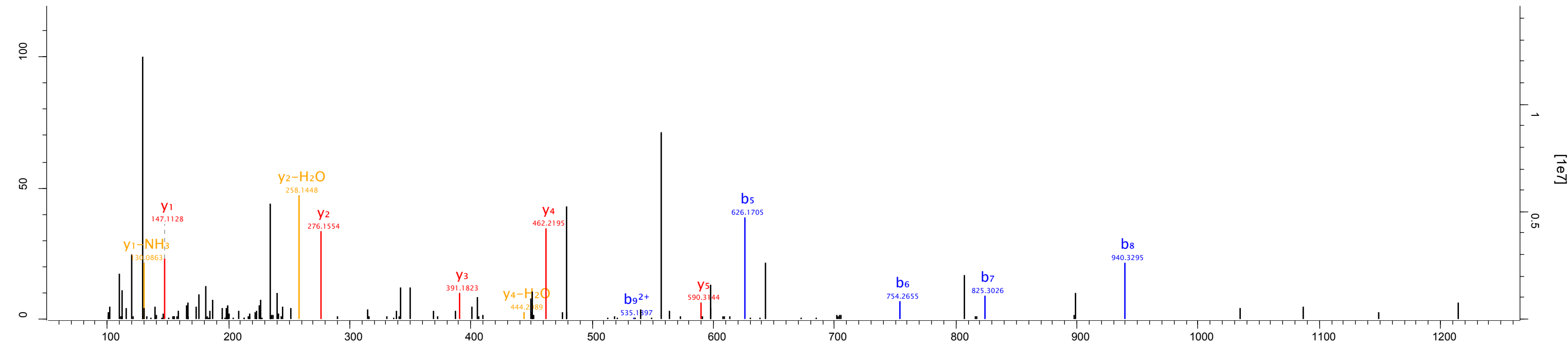
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Scan 25769 Method FTMS; HCD Score 105.46 m/z 646.88 Gene names HFE



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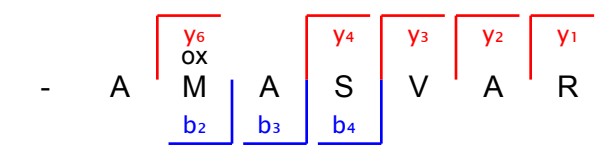
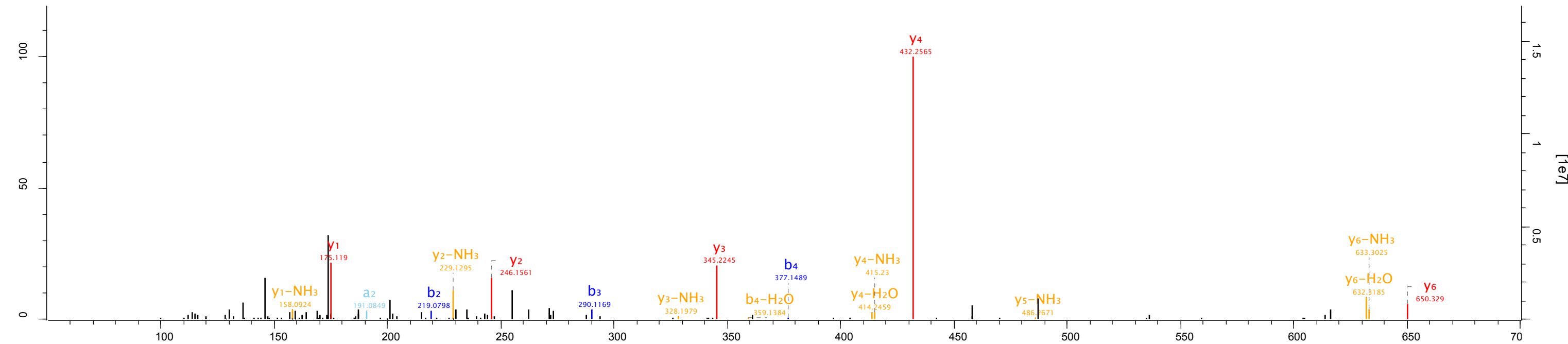
Scan 8489 Method FTMS; HCD Score 72.2 m/z 405.83 Gene names HIVEP3



- E E E A -
ph S
b₅ b₆ b₇ b₈ b₉²⁺ K
y₅ y₄ y₃ y₂ y₁
K A D E K

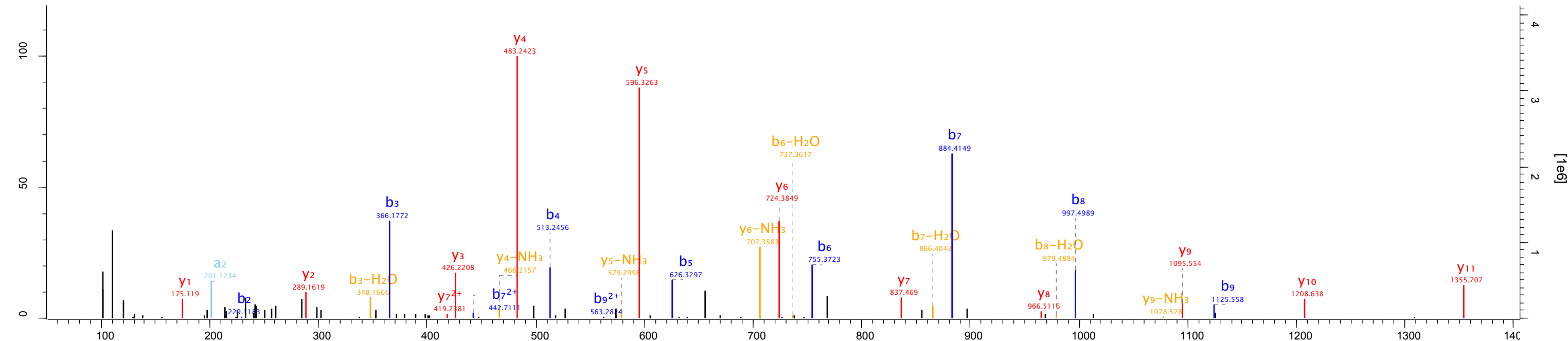
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Scan 9719 Method FTMS; HCD Score 101.72 m/z 361.19 Gene names ART4



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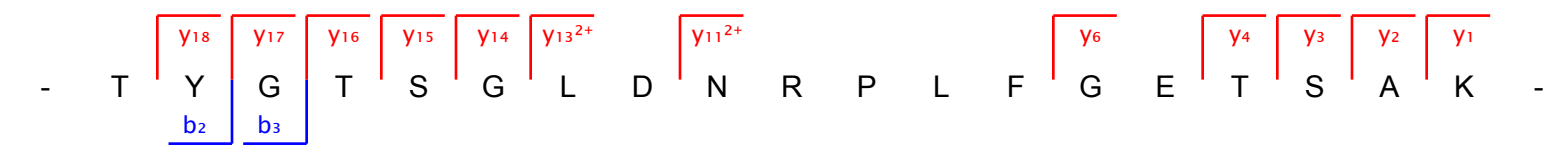
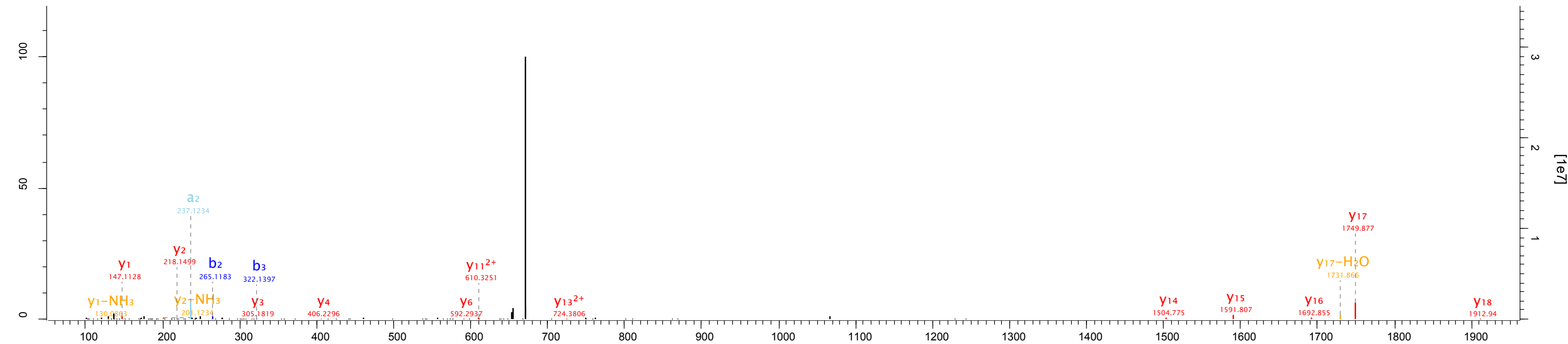
25789 FTMS; HCD 175.74 574.3 IGFALS



- D L H F L E E L Q L G H N R -

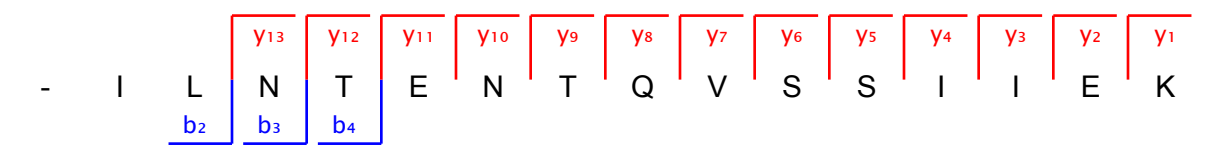
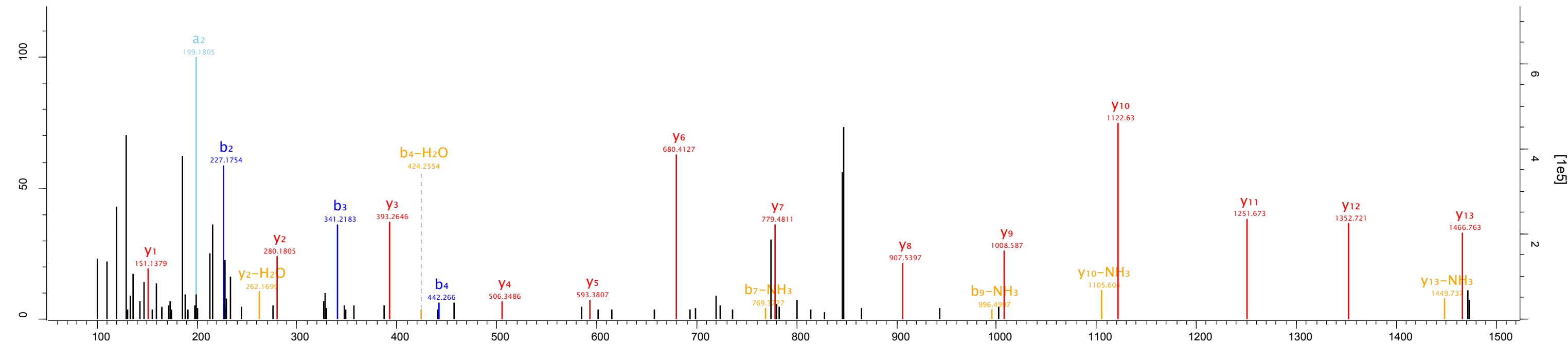
Fragmentation scheme showing b and y ions for the peptide sequence: D L H F L E E L Q L G H N R. The b ions are labeled b2 through b9, and the y ions are labeled y1 through y11.

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 Scan: 18289 Method: FTMS; HCD Score: 46.49 m/z: 672 Gene names: TMEM243



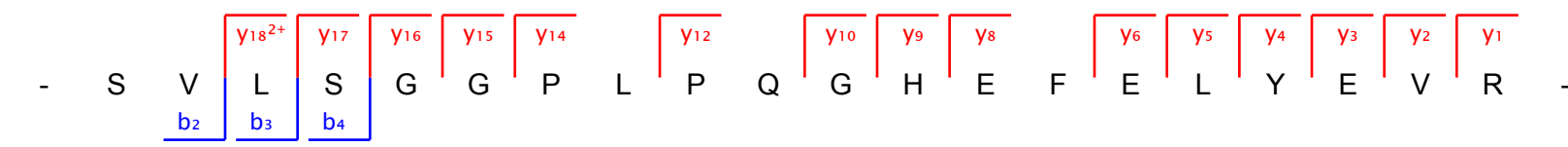
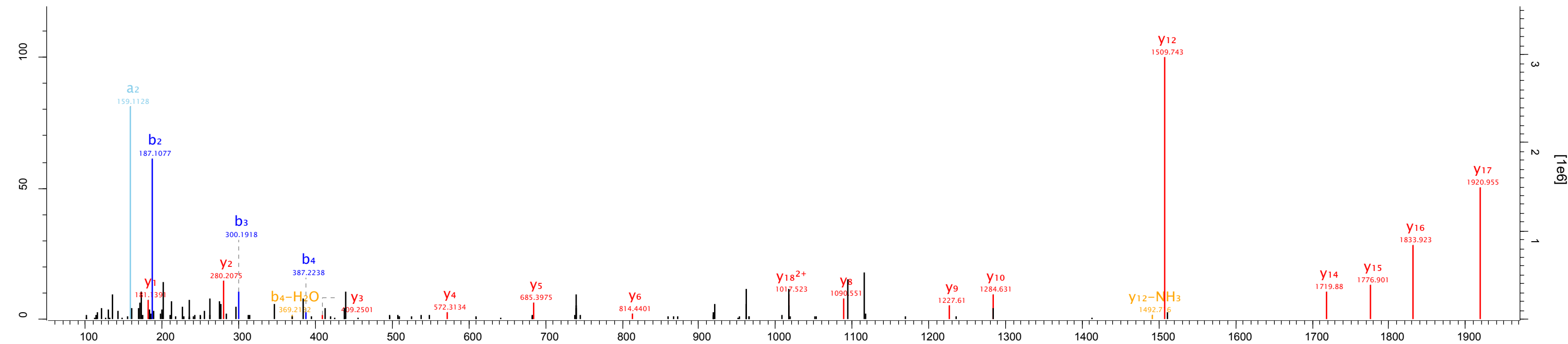
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Scan 20309 Method FTMS; HCD Score 92.38 m/z 846.97 Gene names GRIK2

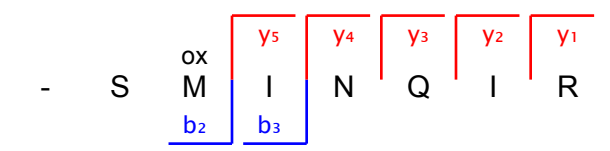
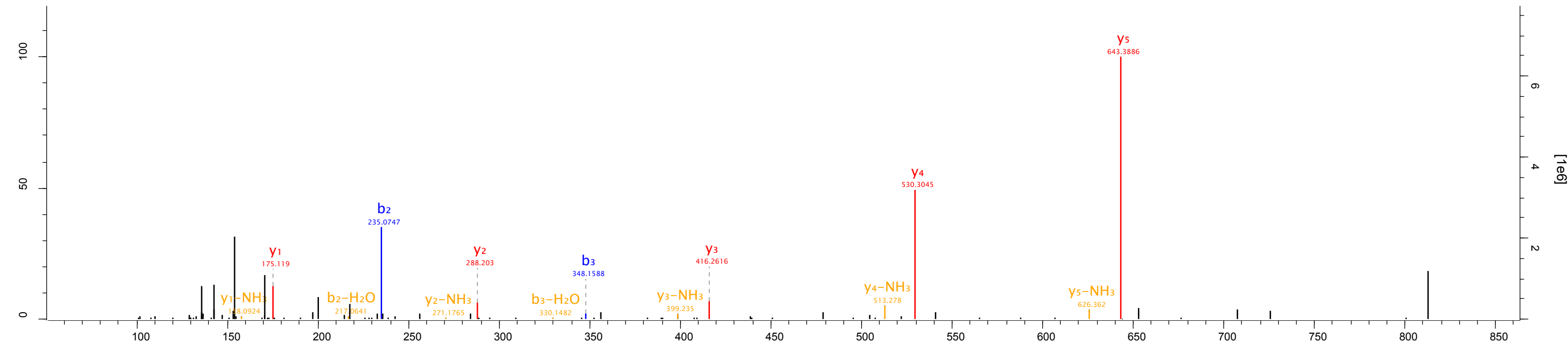


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Scan 26509 Method FTMS; HCD Score 66.64 m/z 741.05 Gene names CA8

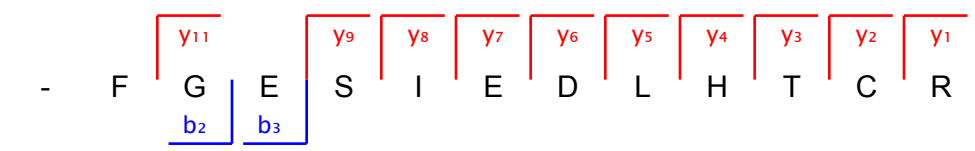
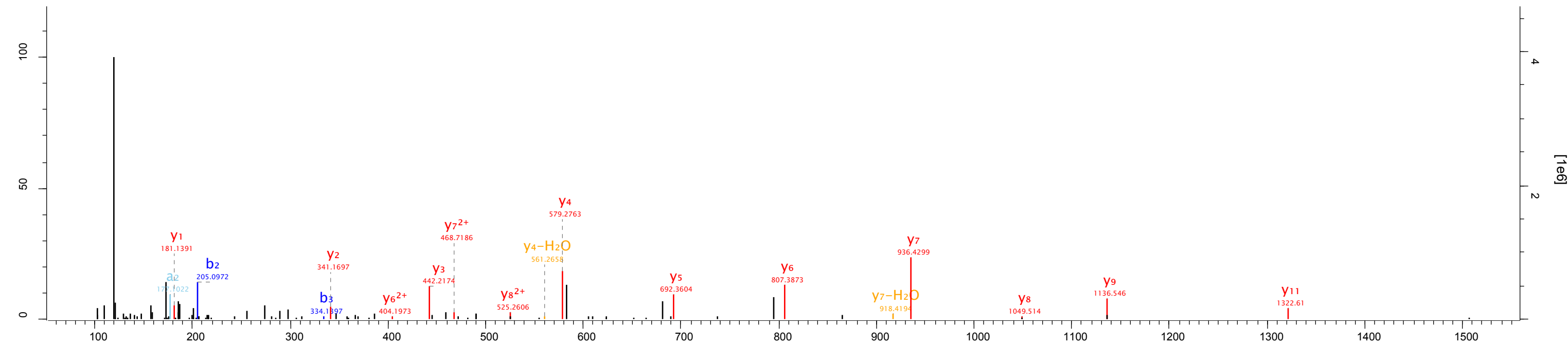


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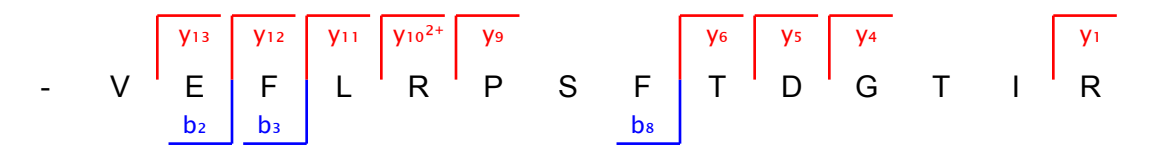
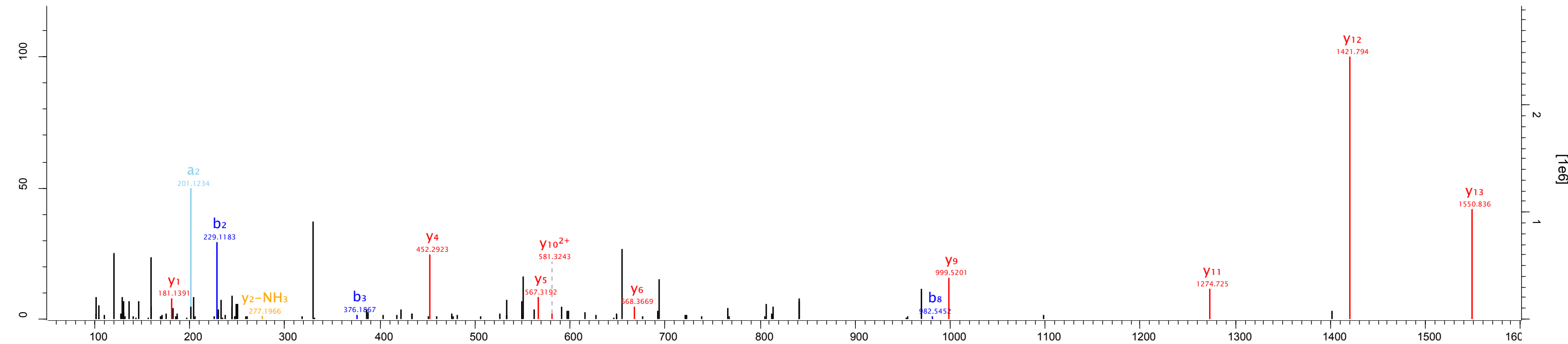


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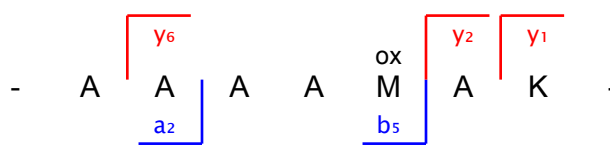
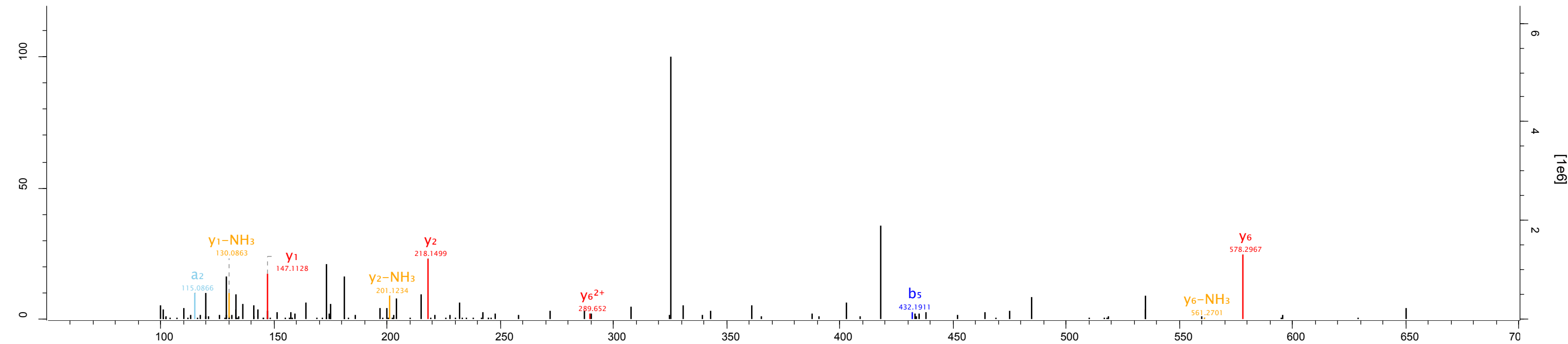
Scan 14999 Method FTMS; HCD Score 78.32 m/z 490.56 Gene names PIGX



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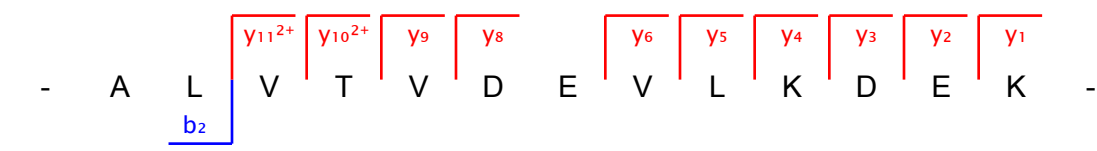
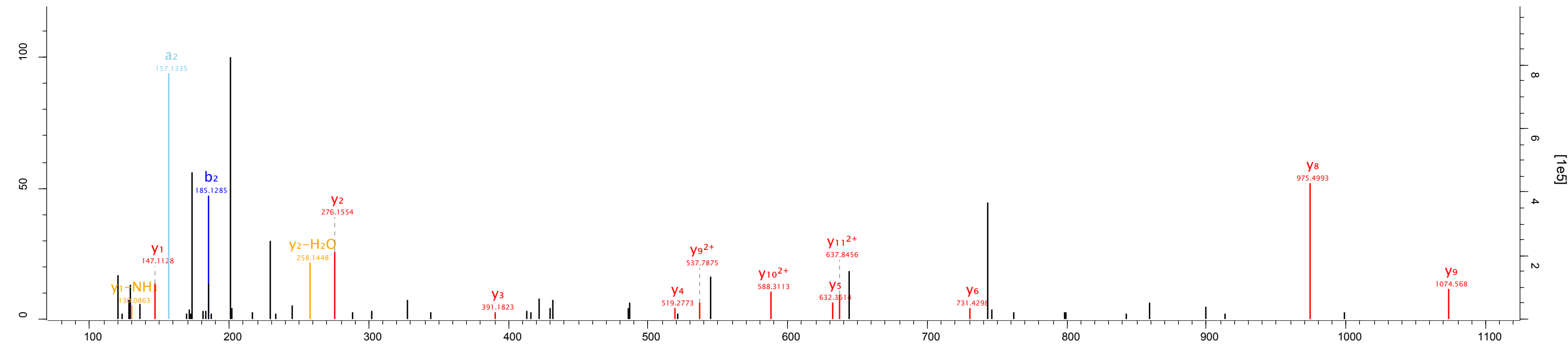


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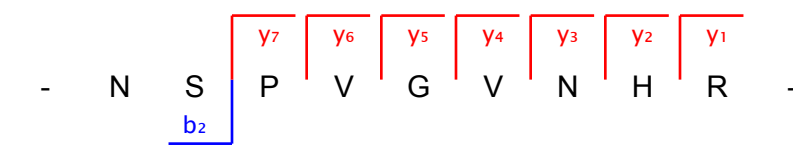
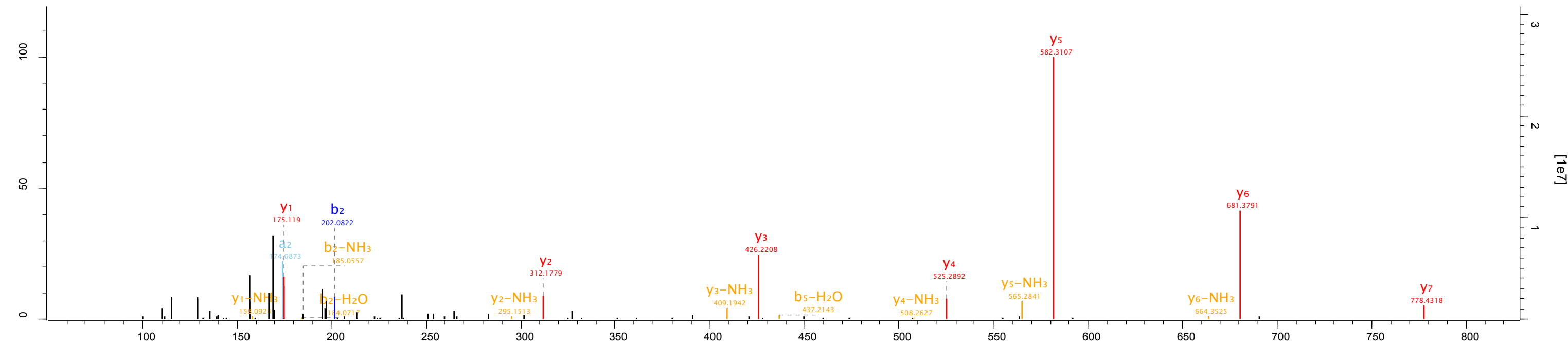
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Scan 21819 Method FTMS; HCD Score 60.16 m/z 486.94 Gene names WFIKKN2



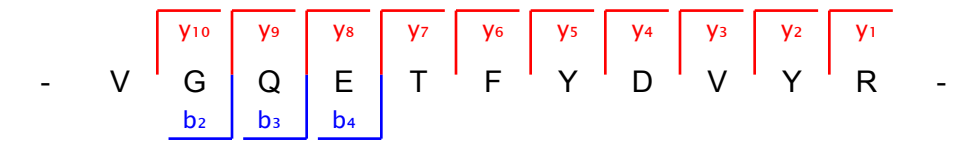
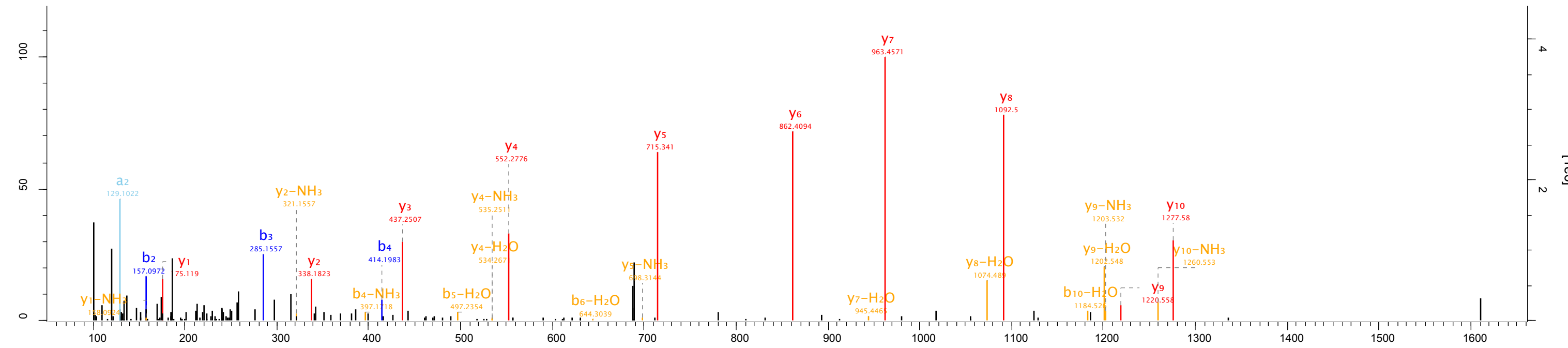
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Scan 2549 Method FTMS; HCD Score 77.73 m/z 327.17 Gene names TIMM17A



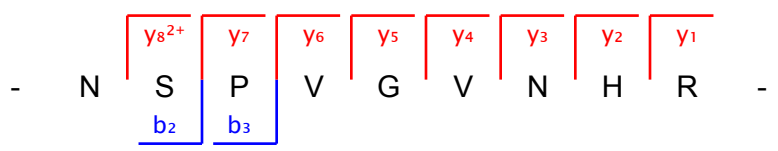
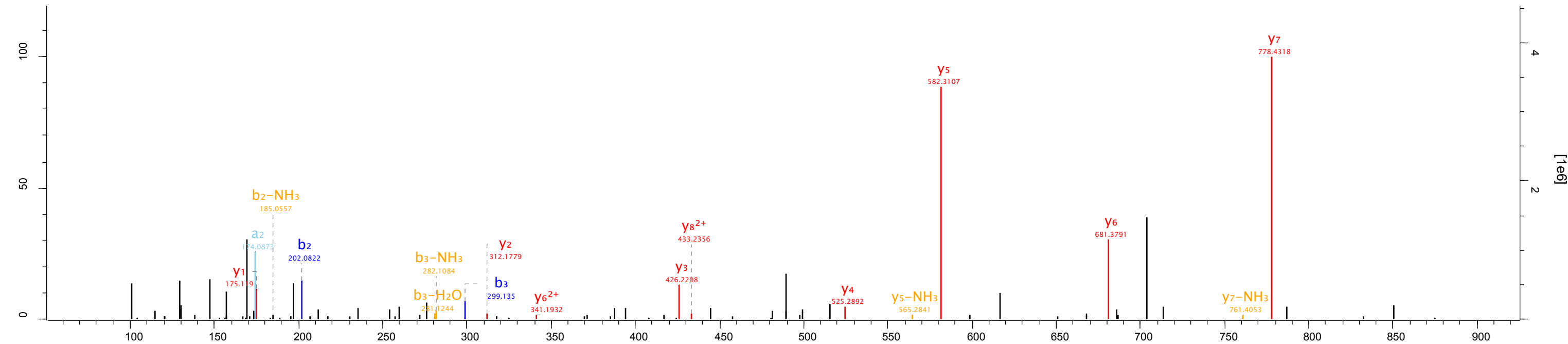
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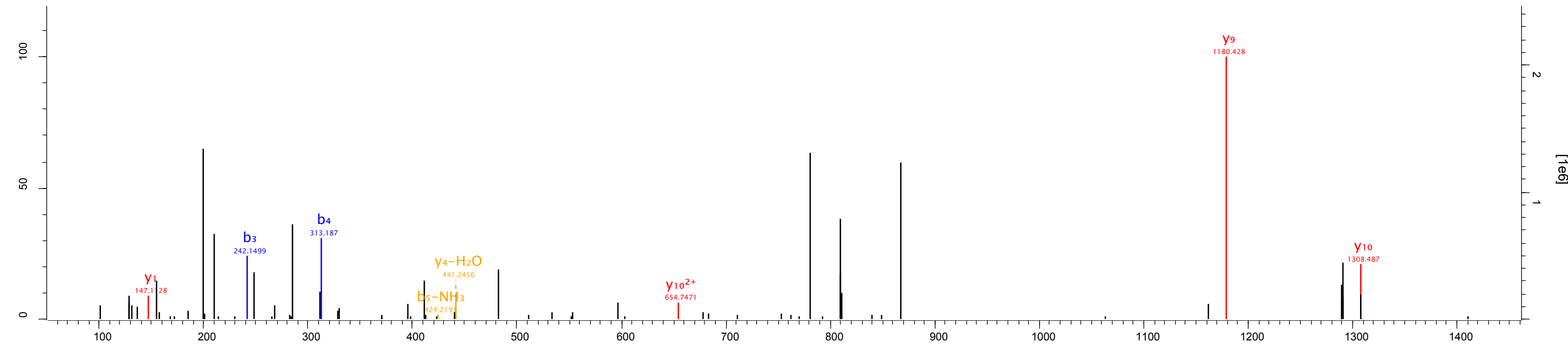


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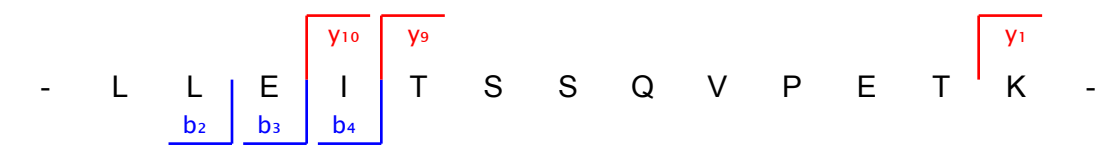
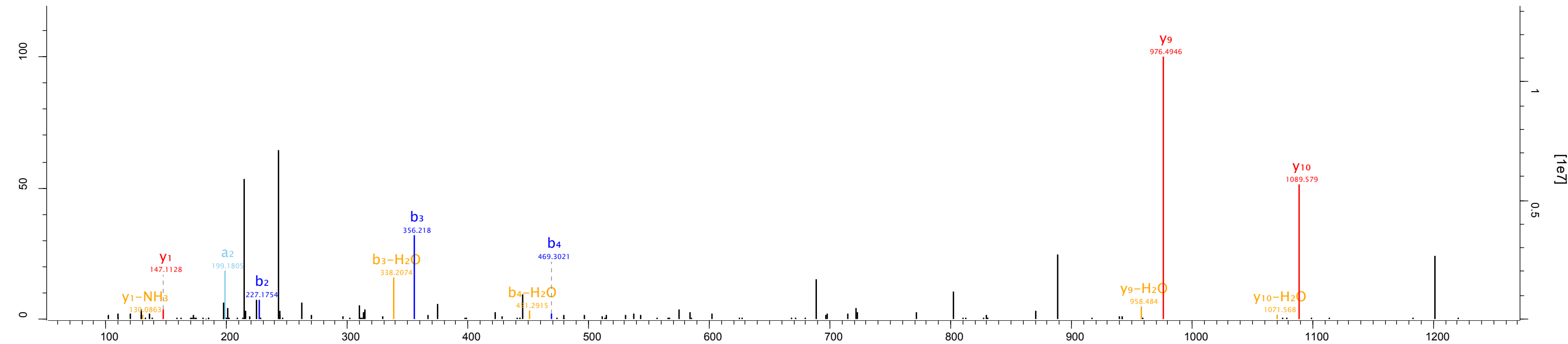
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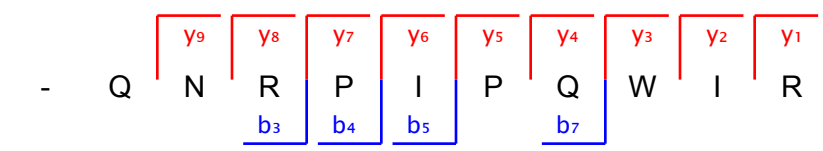
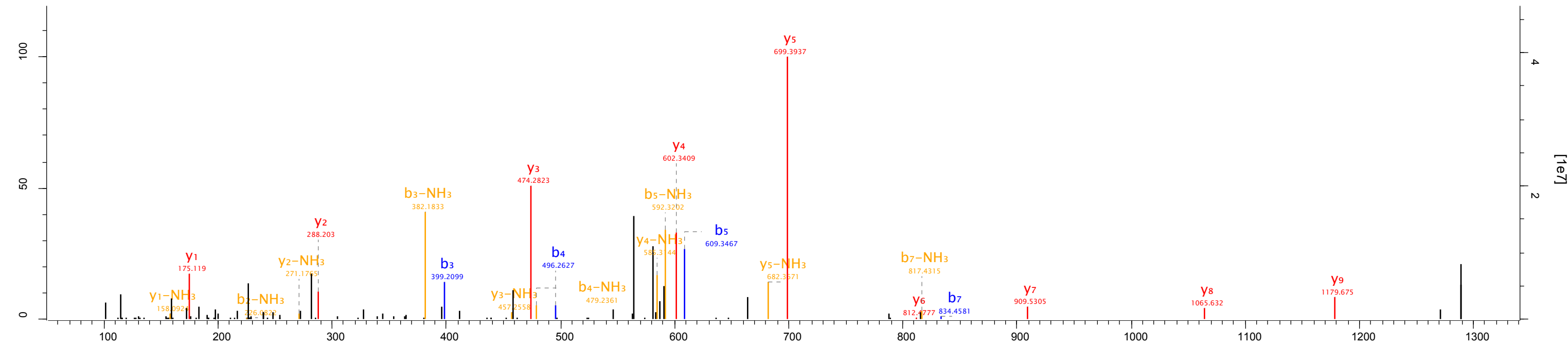
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Fragmentation labels: b_3 , b_4 , y_{10} , y_9 , y_1

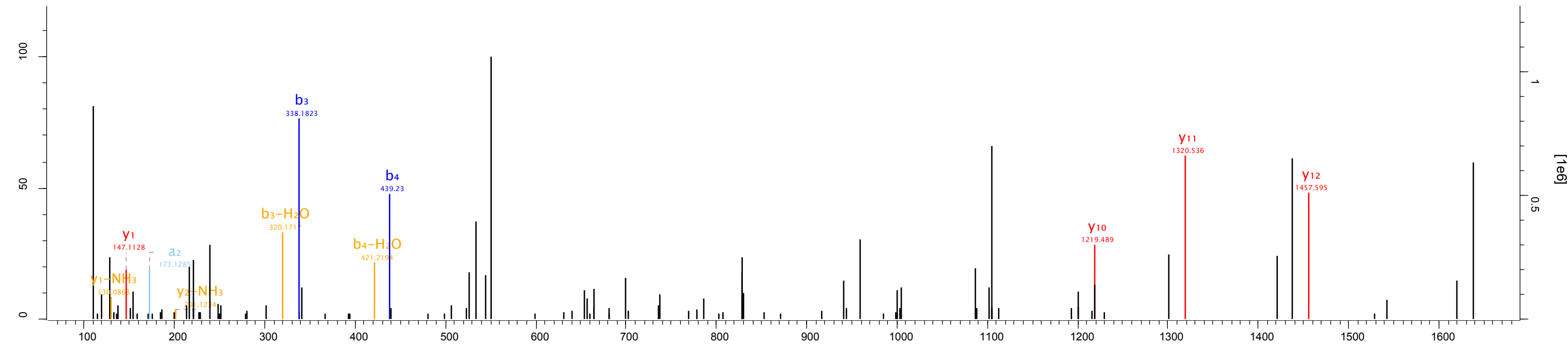
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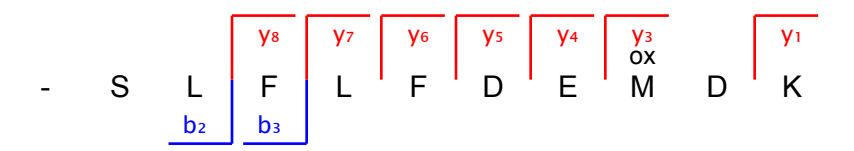
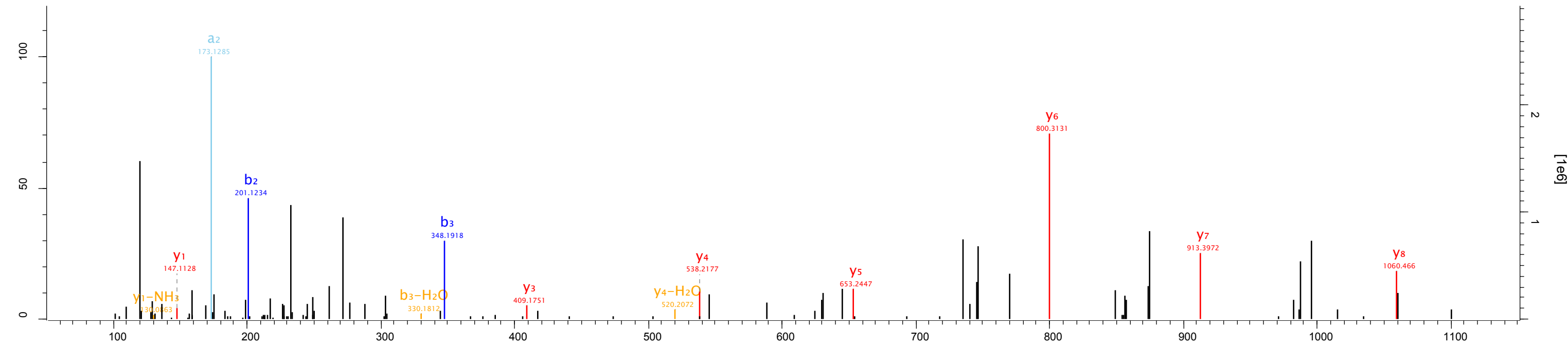
Raw file: 20180707_MaS_A375SR_ML_proteome_2_23
 Scan: 16699 Method: FTMS; HCD Score: 140.83 m/z: 436.58 Gene names: RPL39P5;RPL39



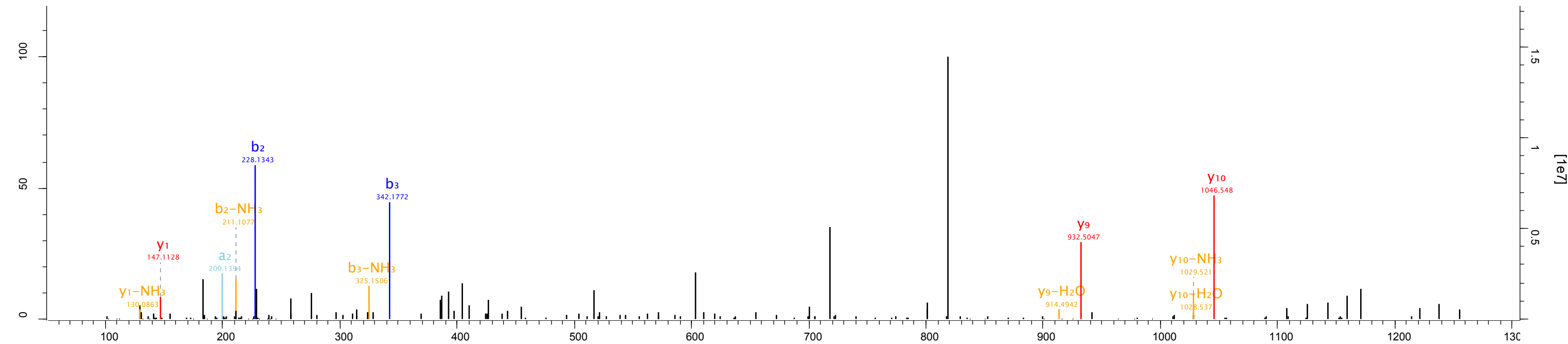
Raw file 20180707_MaS_A375SR_ML_proteome_2_23 Scan 23449 Method FTMS; HCD Score 61.11 m/z 829.36 Gene names HIF3A



Raw file 20180707_MaS_A375SR_ML_proteome_2_23 Scan 27459 Method FTMS; HCD Score 54.26 m/z 630.8 Gene names TOR2A

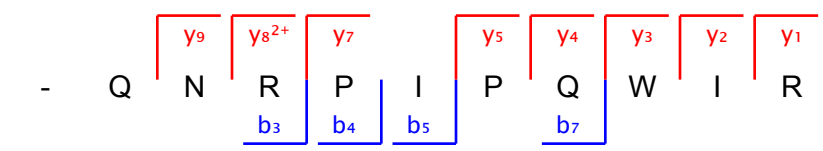
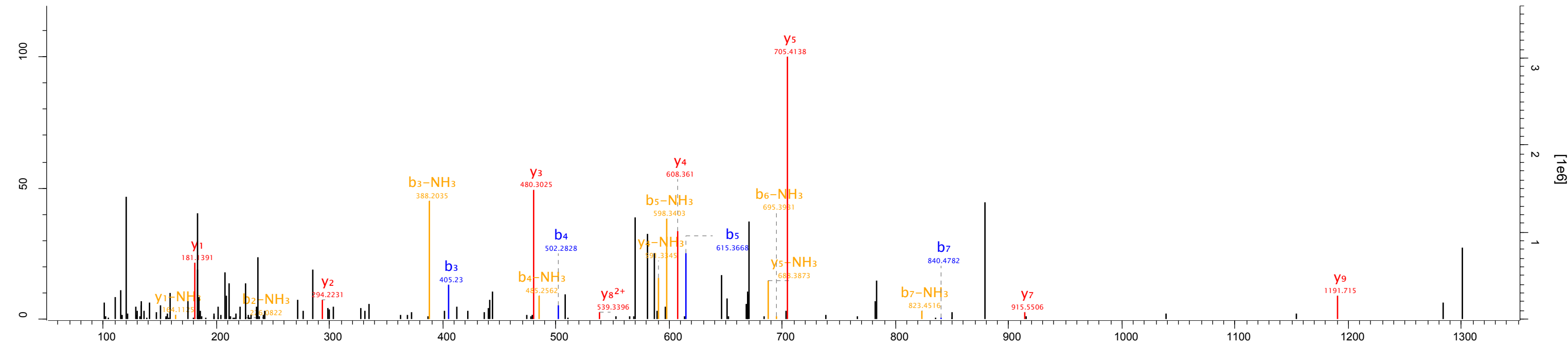


Raw file 20180707_MaS_A375SR_ML_proteome_2_26 Scan 12219 Method FTMS; HCD Score 63.62 m/z 637.34

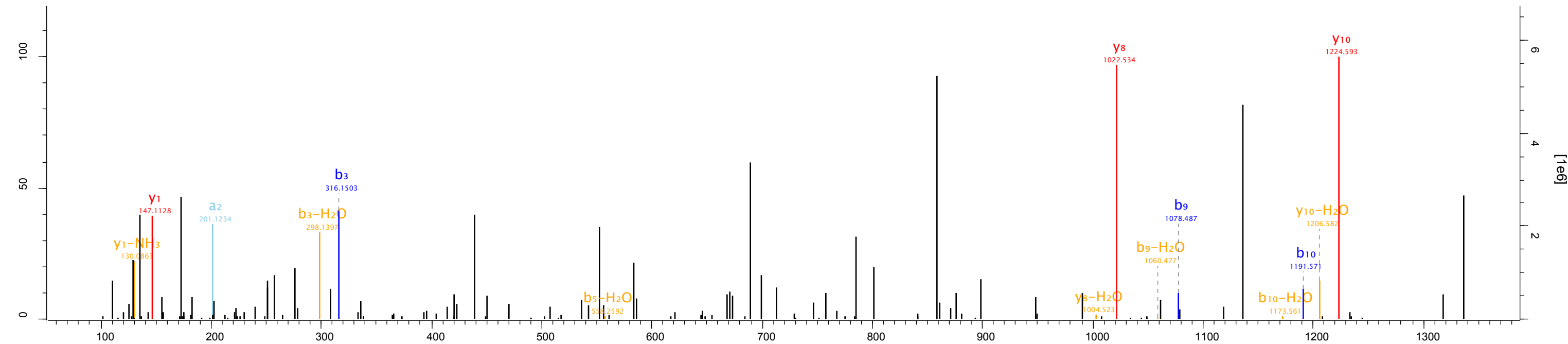


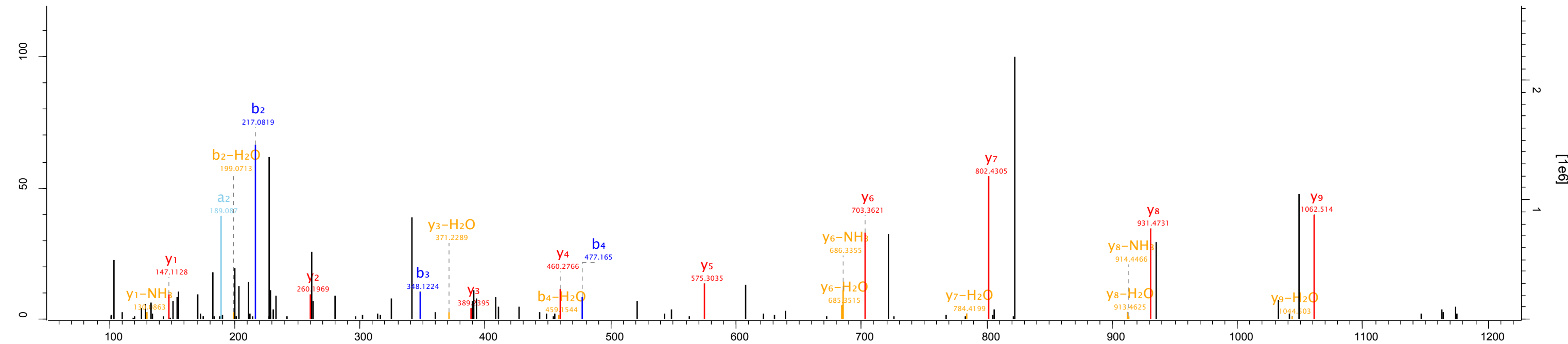
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20180707_MaS_A375SR_ML_proteome_2_26

Scan 15489 Method FTMS; HCD Score 101.46 m/z 440.6 Gene names RPL39P5;RPL39



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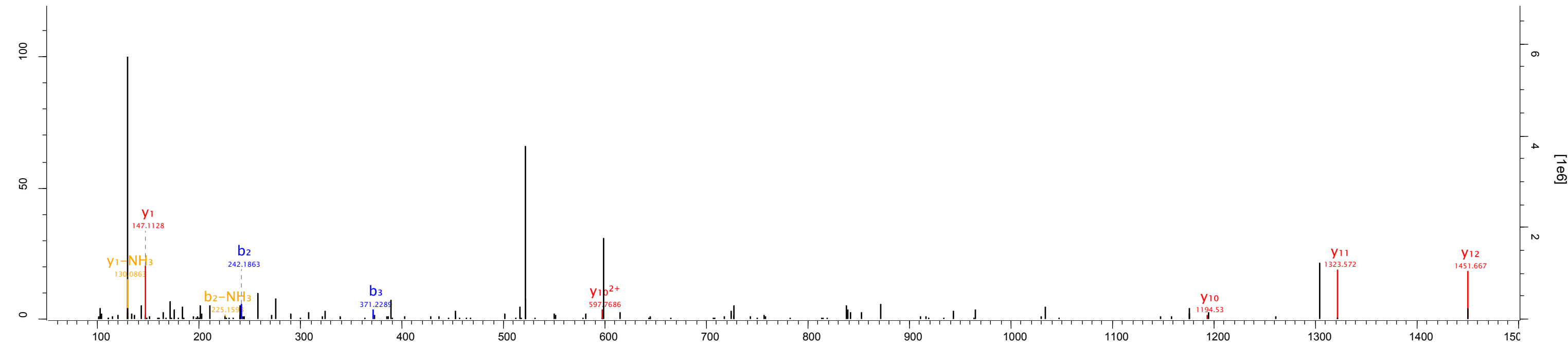


- S E M E V Q D A E L K -

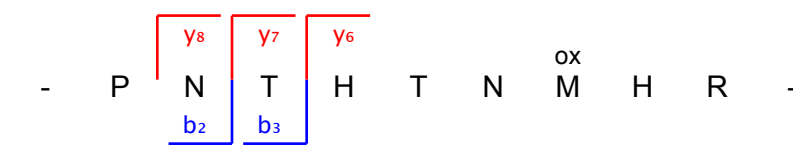
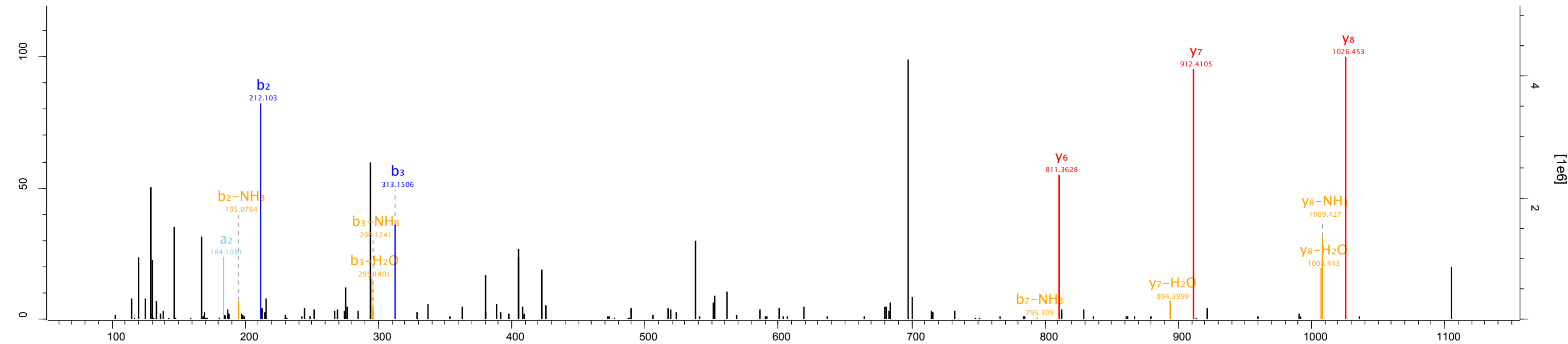
b₂ b₃ b₄ y₉ y₈ y₇ y₆ y₅ y₄ y₃ y₂ y₁

Raw file
20180707_MaS_A375SR_ML_proteome_2_27

Scan 7789 Method FTMS; HCD Score 56.2 m/z 522.26

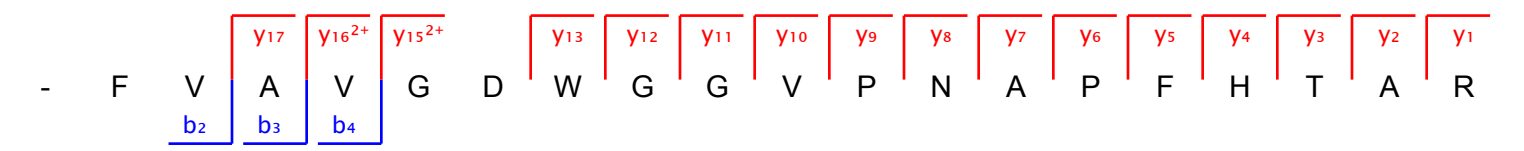
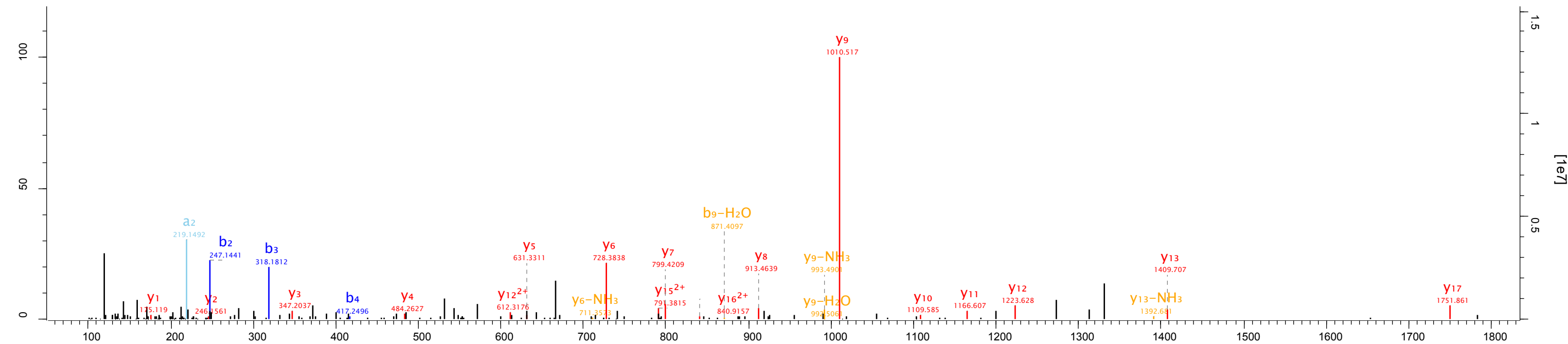


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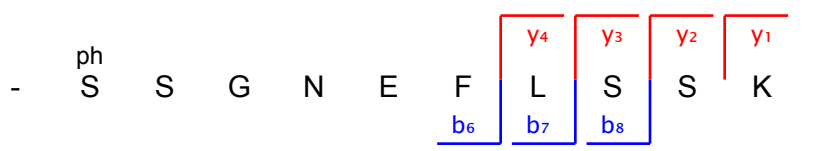
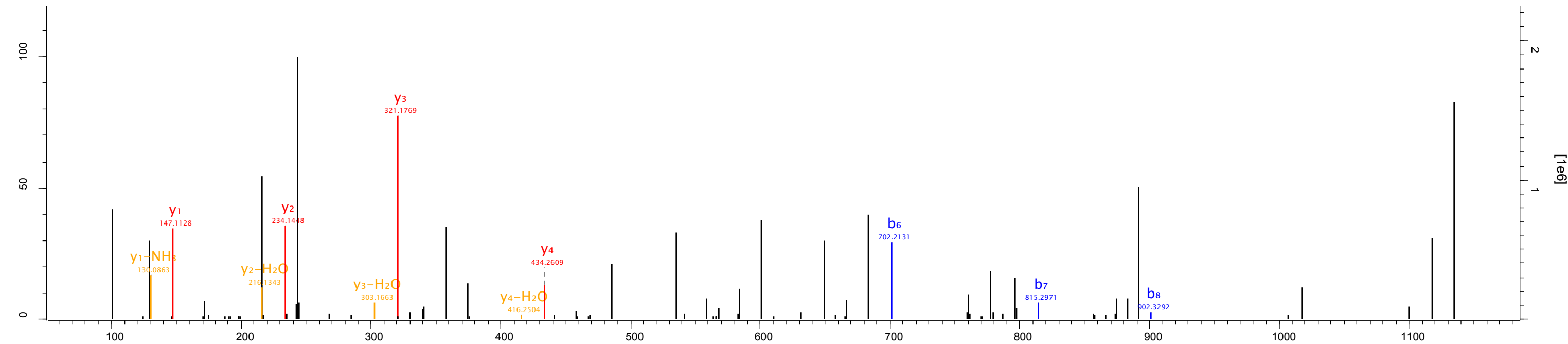


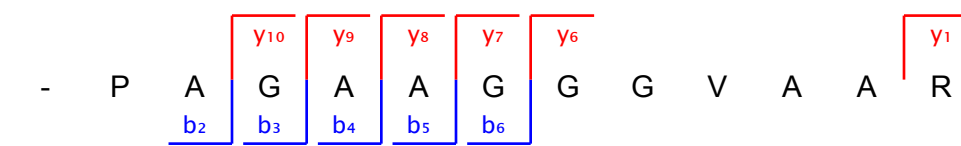
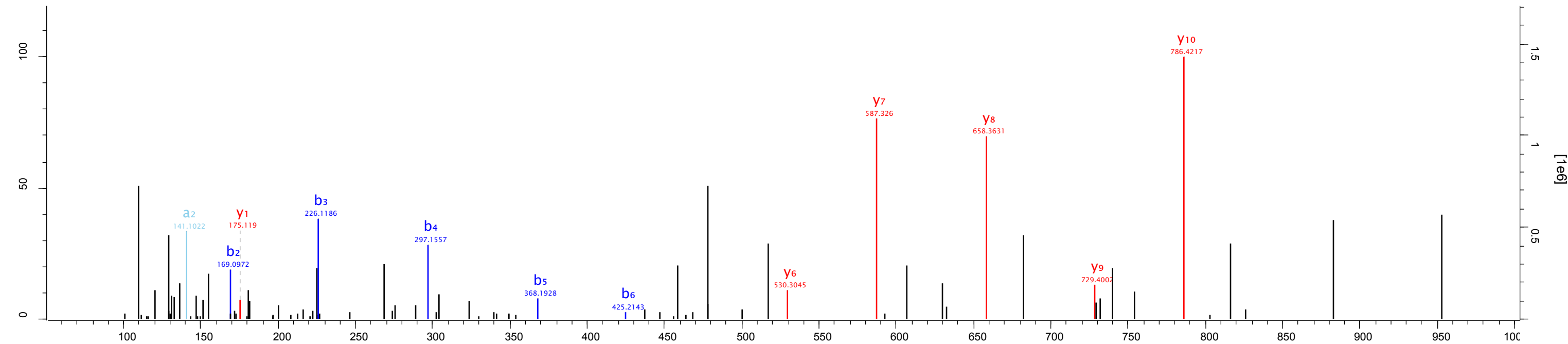
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20180707_MaS_A375SR_ML_proteome_2_28

Scan 24439 Method FTMS; HCD Score 87.68 m/z 667.01 Gene names ACP5

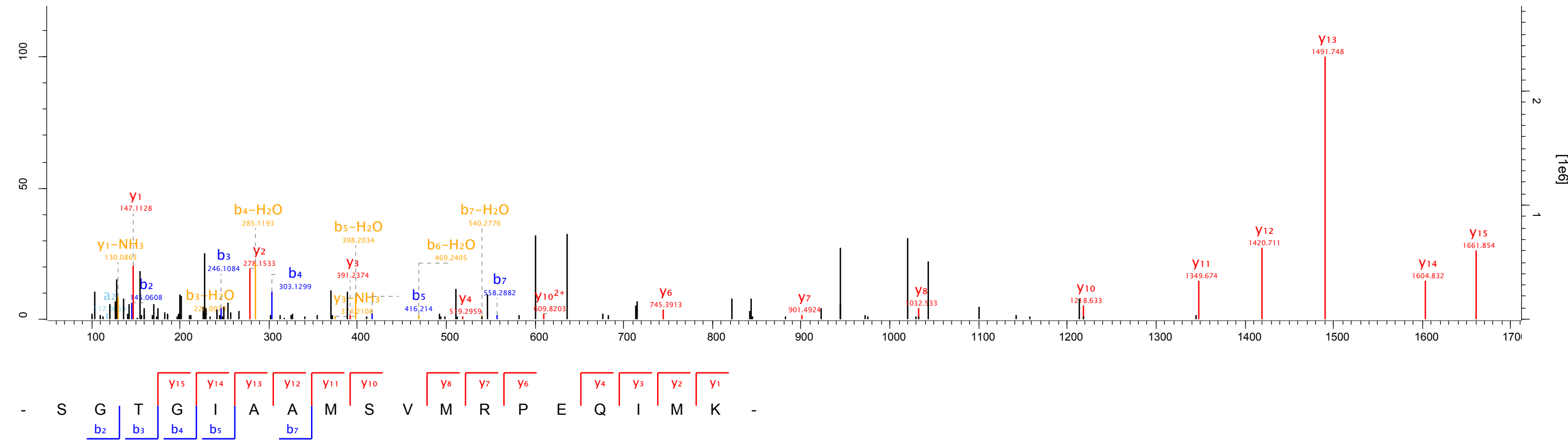


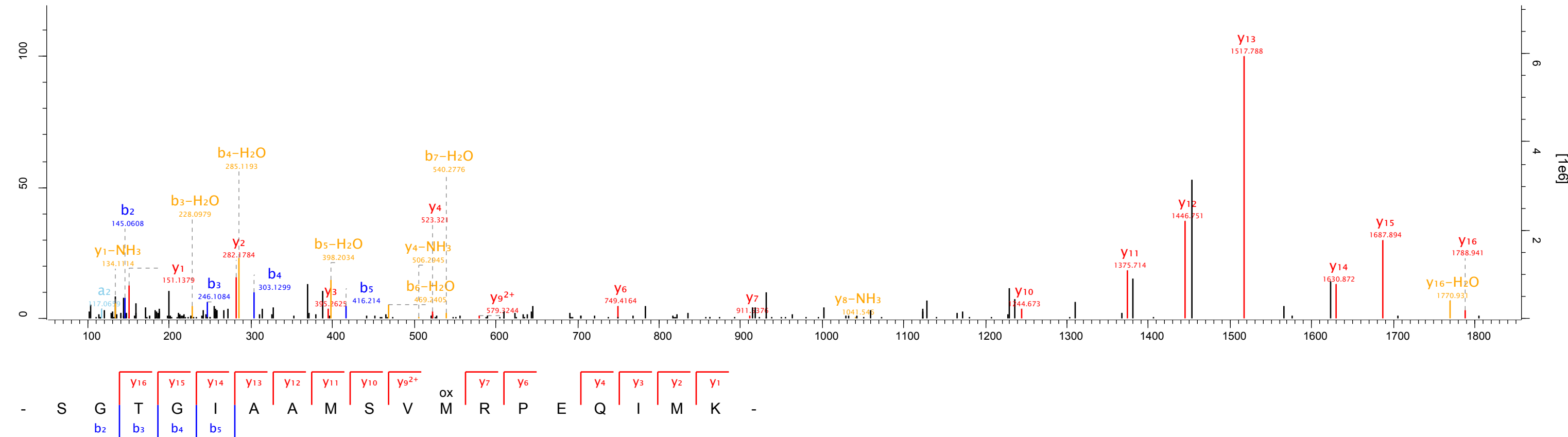
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 Scan 3449 Method FTMS; HCD Score 85.53 m/z 568.24 Gene names MAP3K19



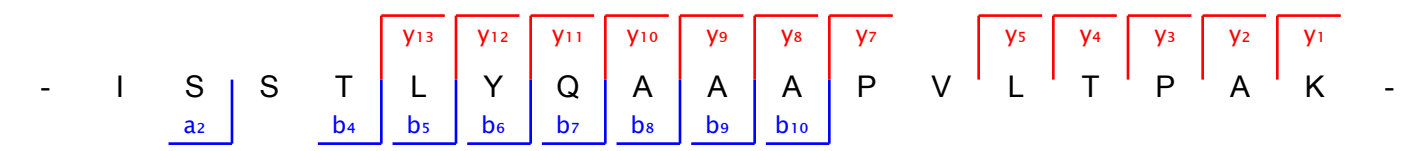
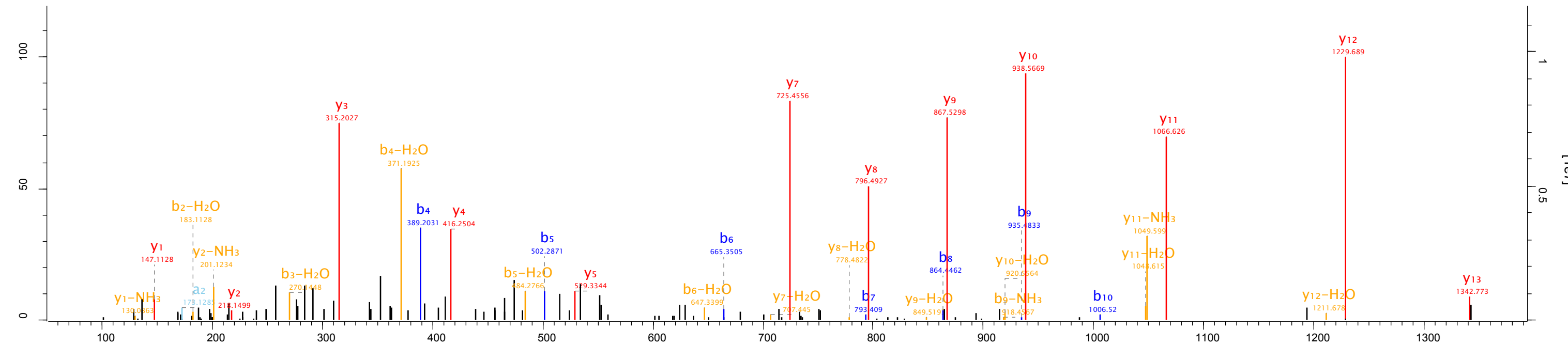


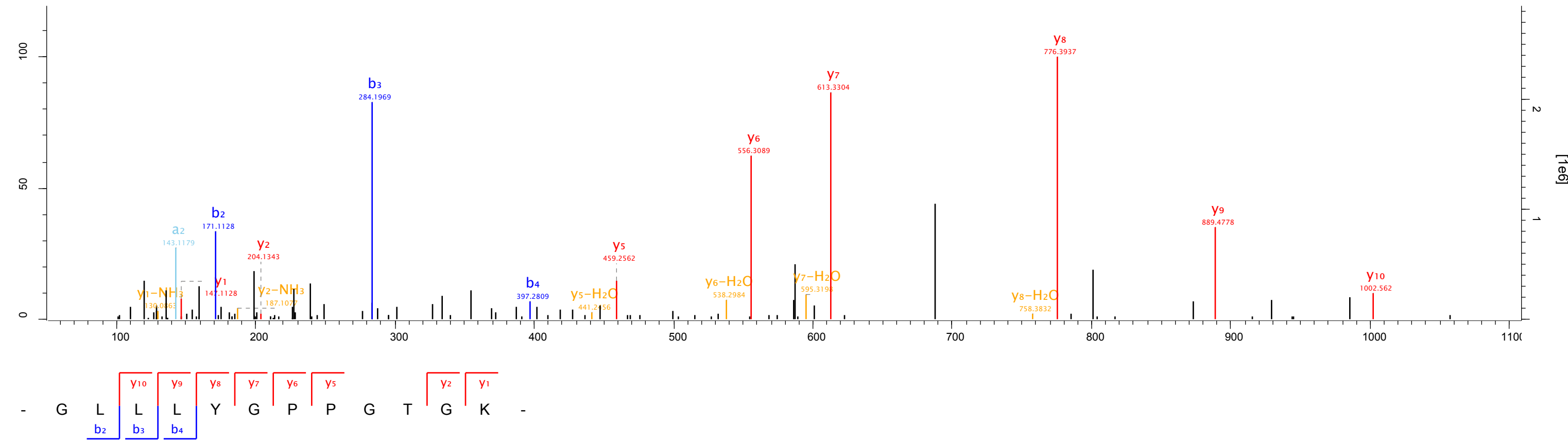
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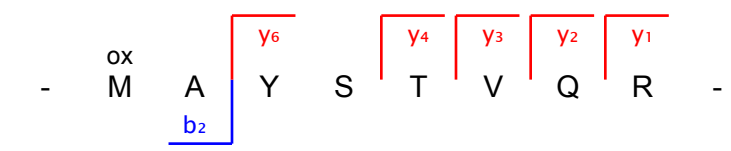
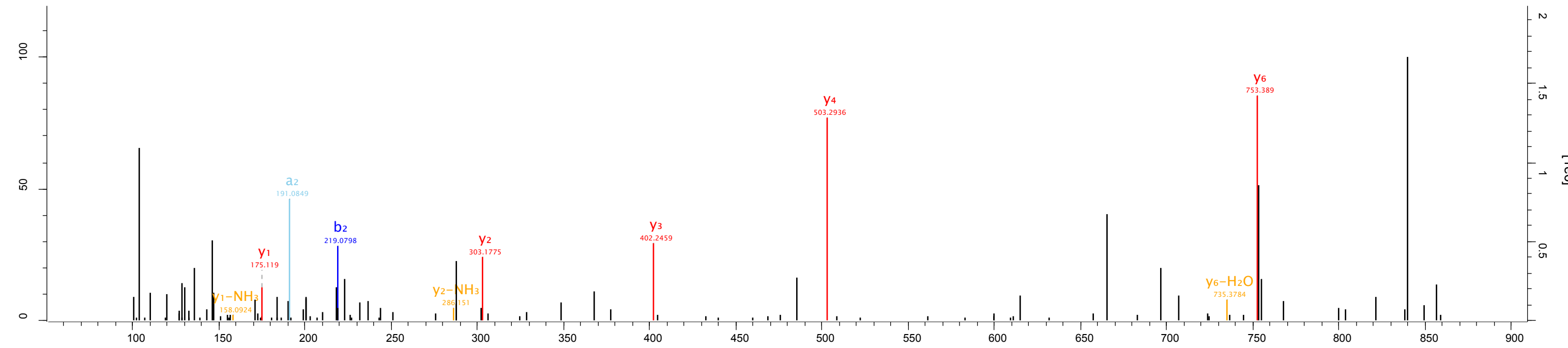


Raw file 20180707_MaS_A375SR_ML_proteome_22 Scan 22549 Method FTMS; HCD Score 122.14 m/z 865.99 Gene names KRTCAP2

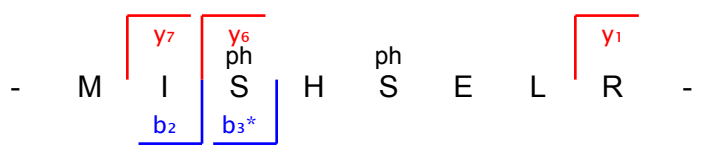
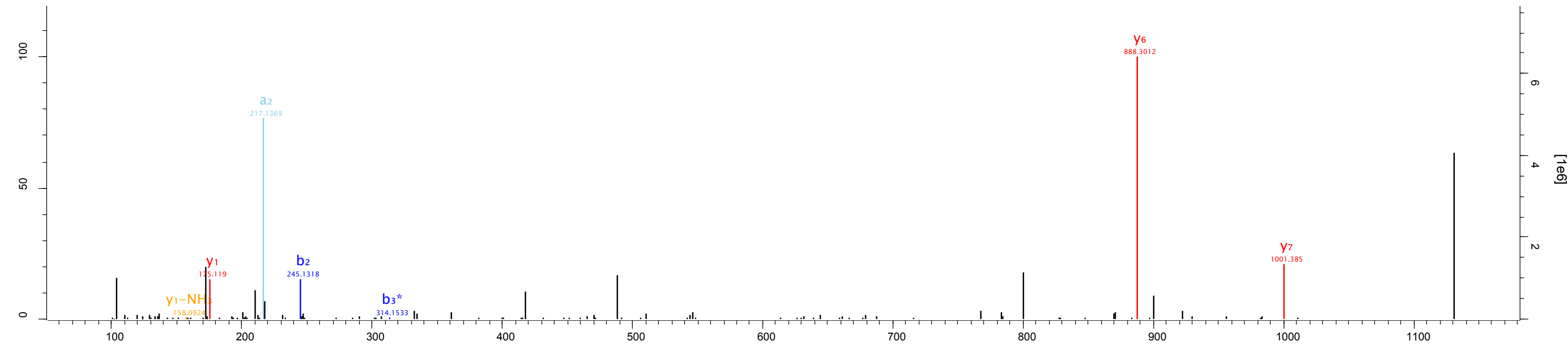




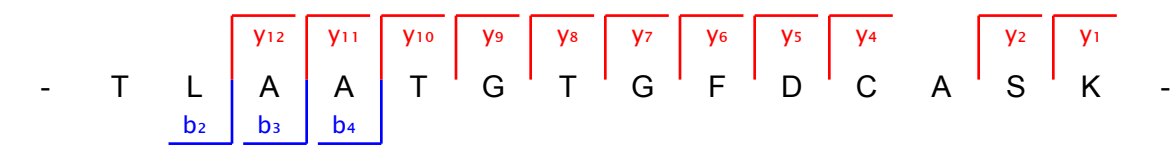
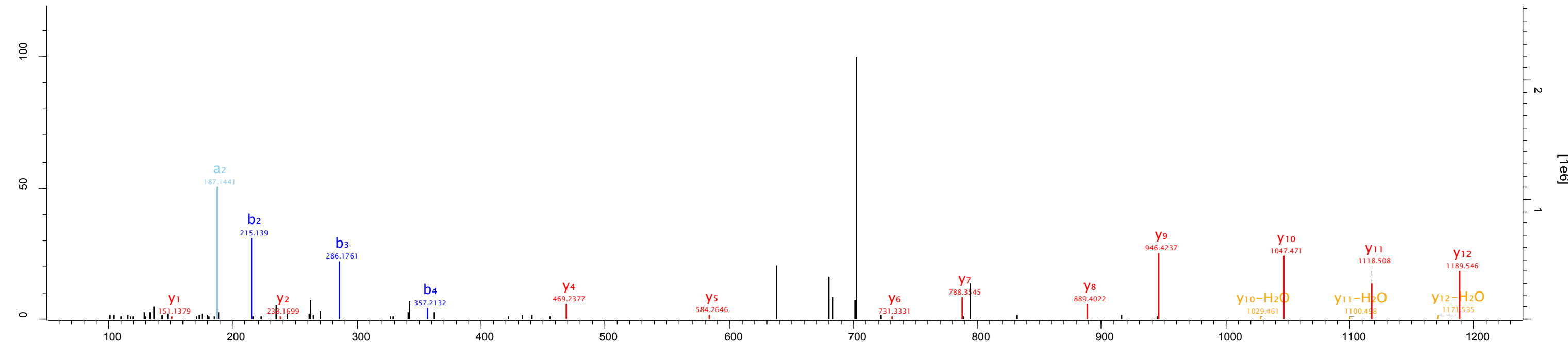
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 Scan: 7239 Method: FTMS; HCD Score: 41.43 m/z: 486.23 Gene names: RIC3



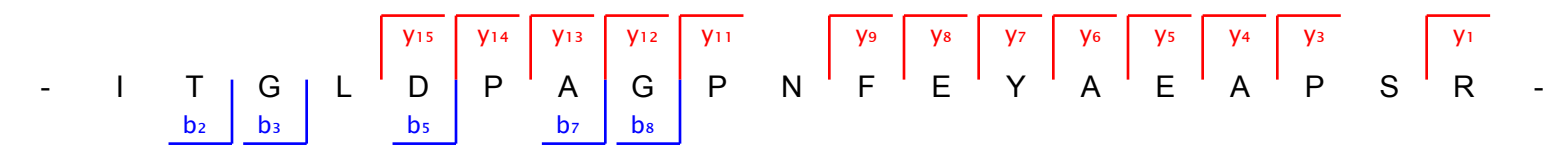
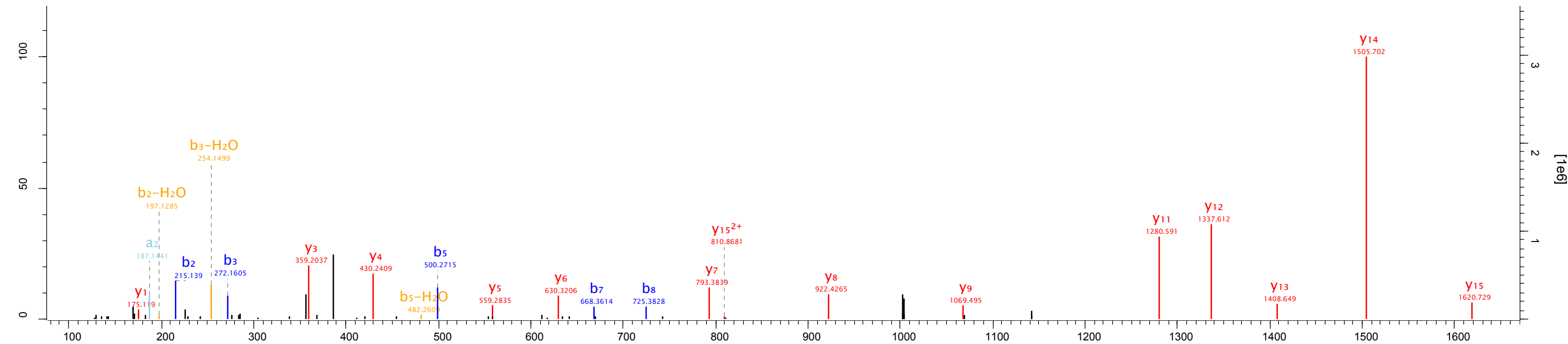
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 Scan: 8129 Method: FTMS; HCD Score: 46.43 m/z: 566.72 Gene names: PSPHP1



Raw file 20180707_MaS_A375SR_ML_proteome_24 Scan 12399 Method FTMS; HCD Score 73.83 m/z 702.34 Gene names ODC1

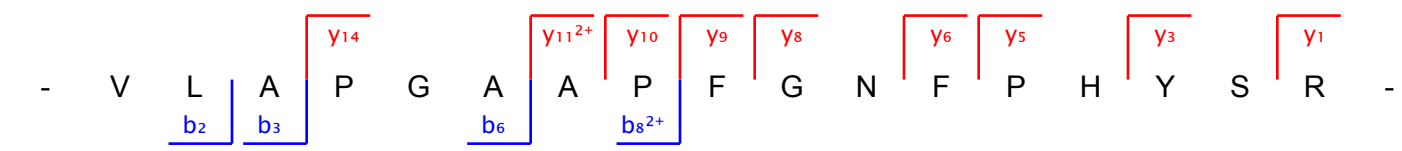
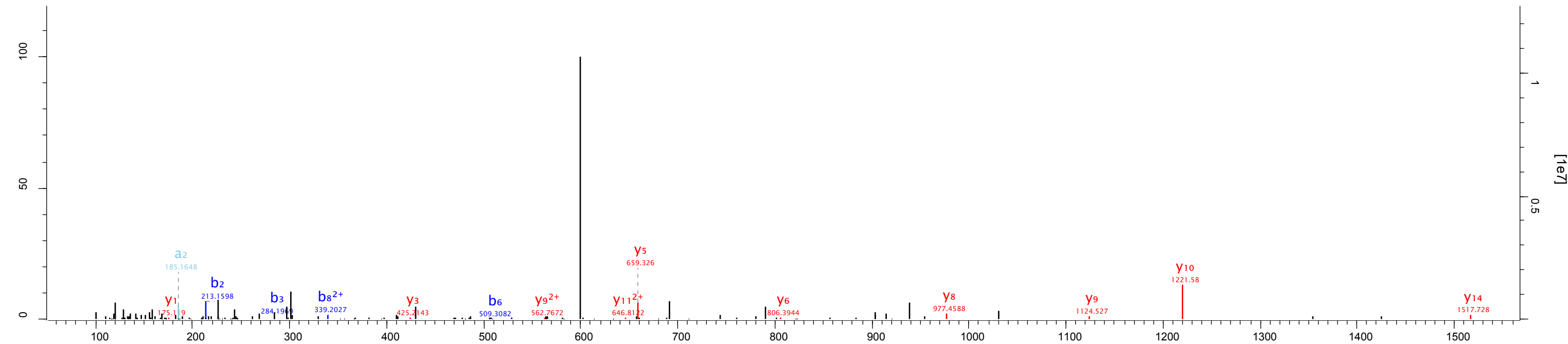


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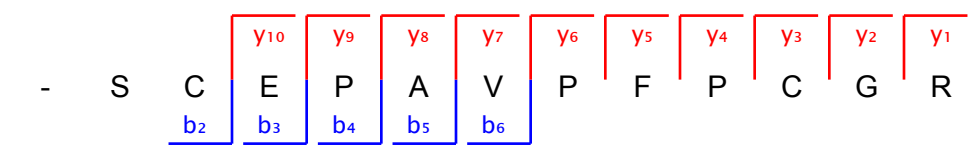
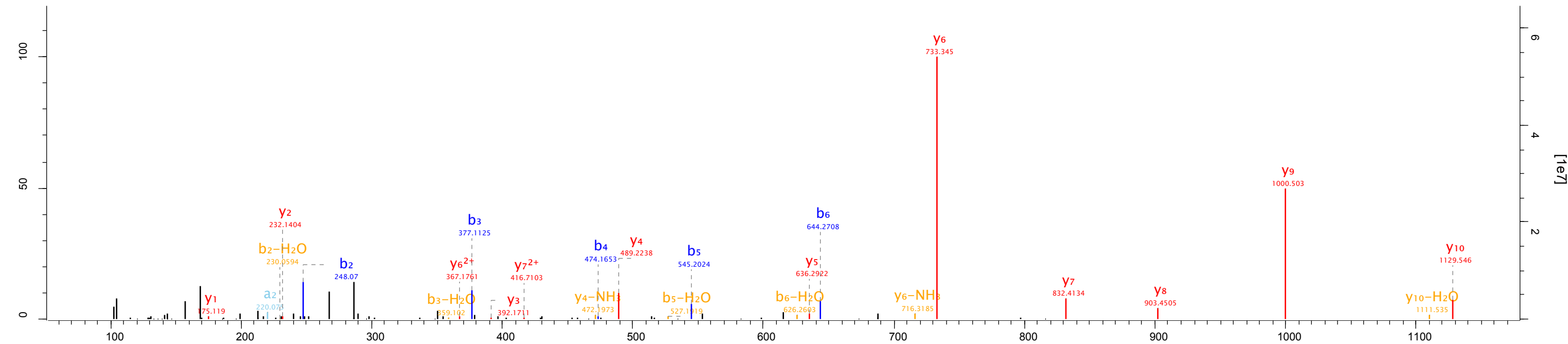


Raw file
20180707_MaS_A375SR_ML_proteome_25

Scan 22879 Method FTMS; HCD Score 27.71 m/z 600.98 Gene names BCDIN3D

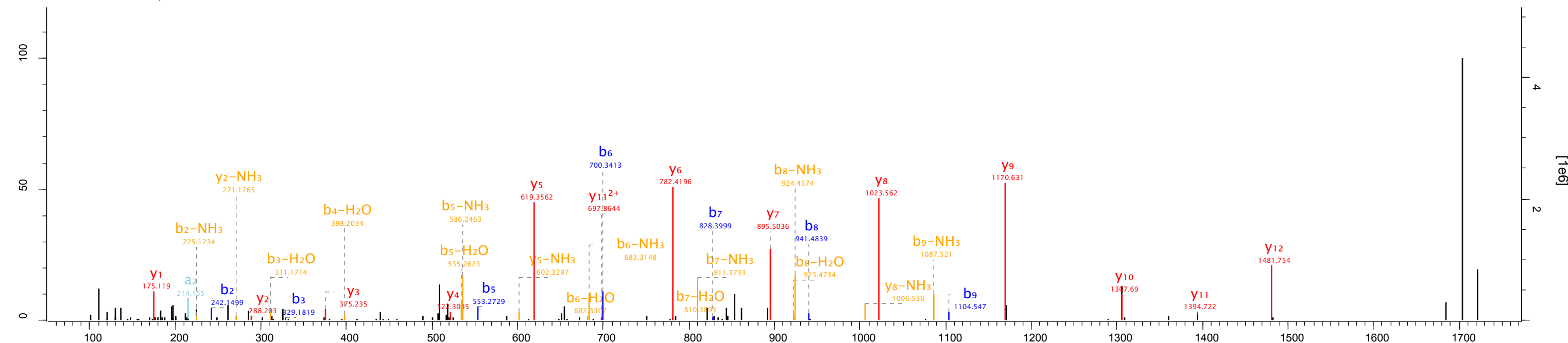


Raw file: 20180707_MaS_A375SR_ML_proteome_26
 Scan: 17329 Method: FTMS; HCD Score: 105.2 m/z: 688.81 Gene names: F9



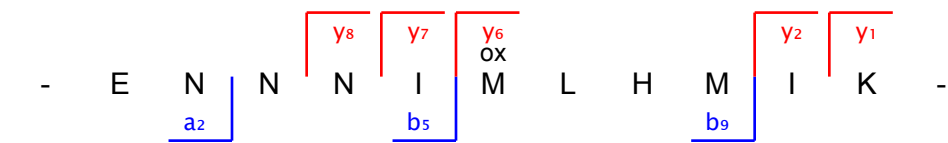
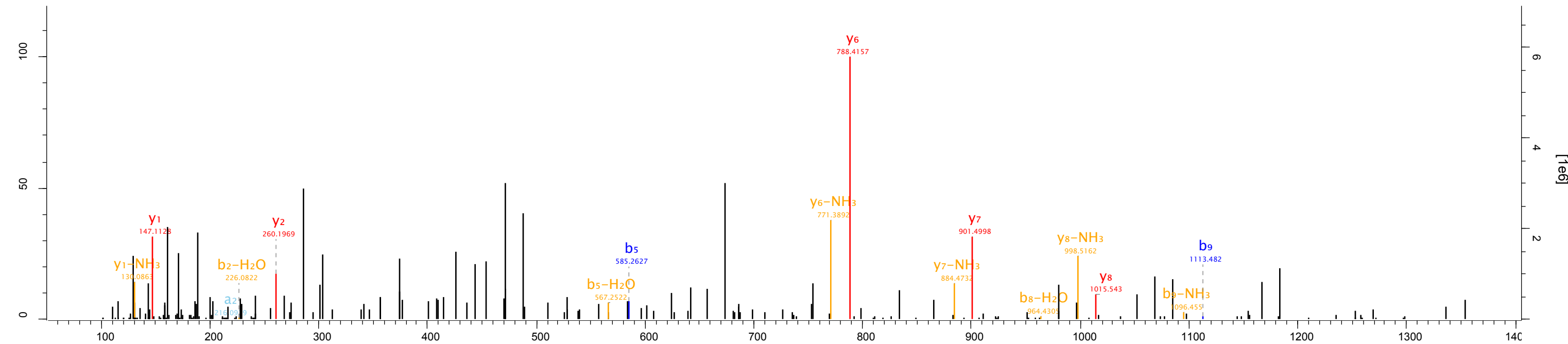
Raw file
20180707_MaS_A375SR_ML_proteome_26

Scan 27229 Method FTMS; HCD Score 155.57 m/z 862.45 Gene names EPT1



- Q L S S H F Q I Y P F S L R -

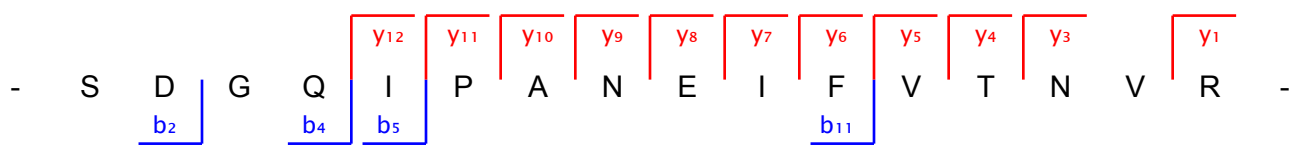
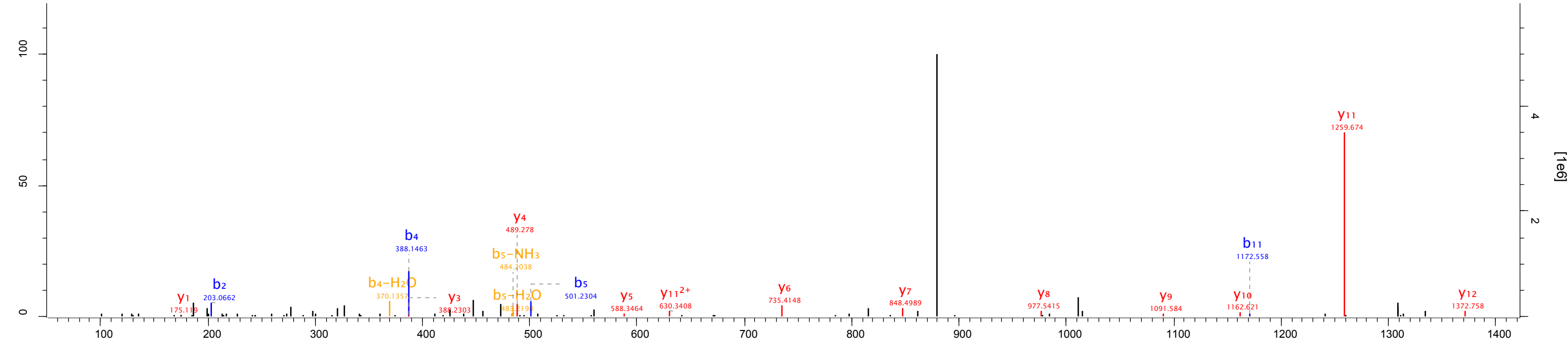
Fragmentation mapping:
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b2 b3 b5 b6 b7 b8 b9



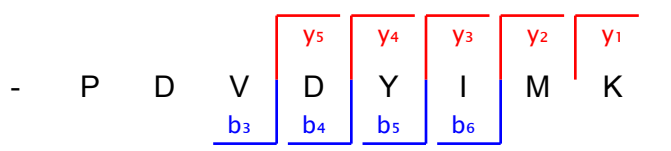
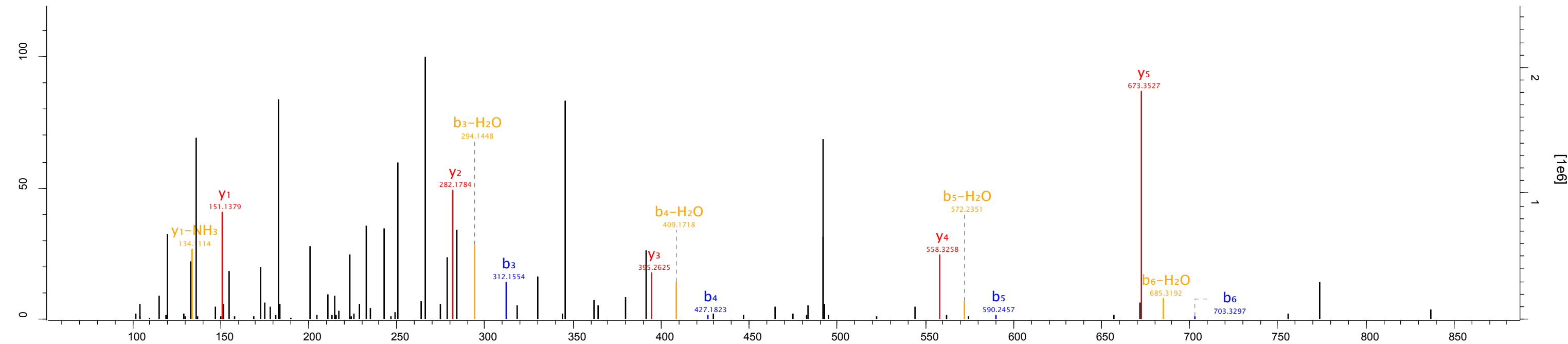
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20180707_MaS_A375SR_ML_proteome_27

Scan	Method	Score	m/z	Gene names
23689	FTMS; HCD	64.45	880.45	SERTAD4

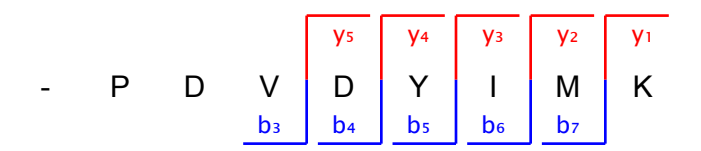
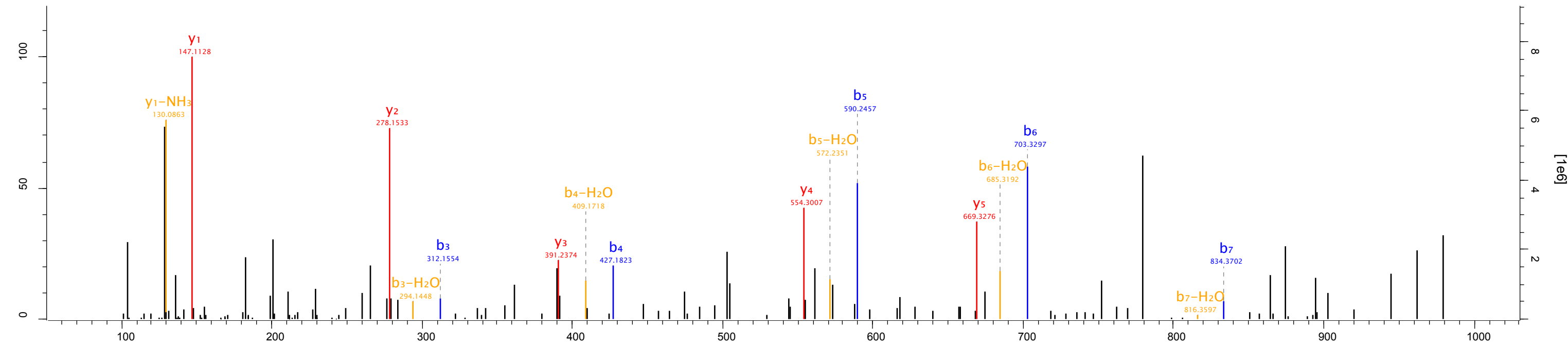


Raw file 20180707_MaS_A375SR_ML_proteome_27 Scan 23829 Method FTMS; HCD Score 68.38 m/z 492.75

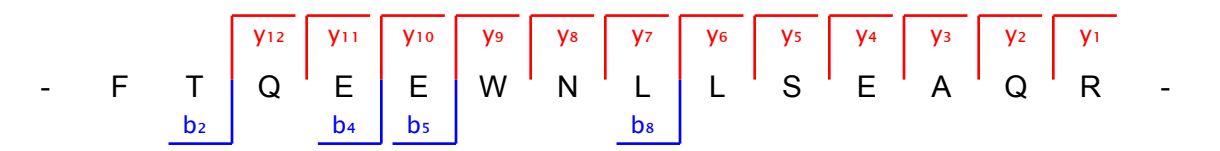
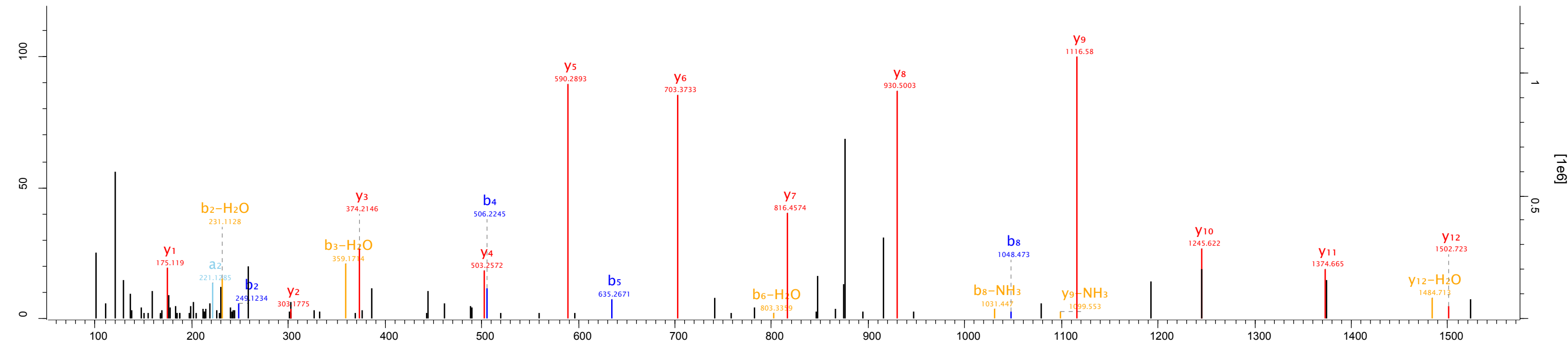


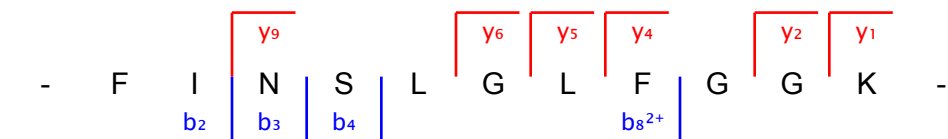
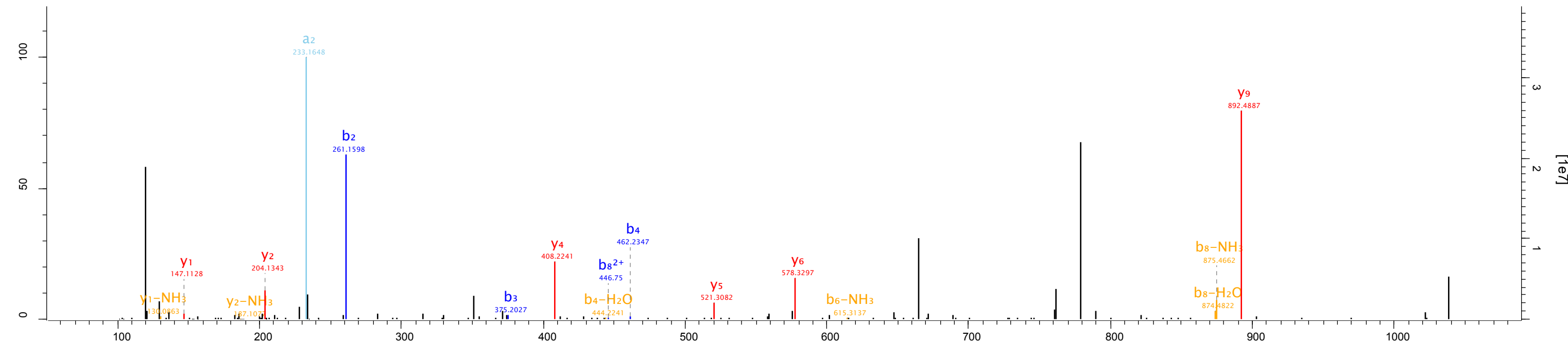
Raw file
20180707_MaS_A375SR_ML_proteome_27

Scan	Method	Score	m/z
25479	FTMS; HCD	106.04	490.74



Raw file: 20180707_MaS_A375SR_ML_proteome_27
 Scan: 26279 Method: FTMS; HCD Score: 87.52 m/z: 876.43 Gene names: ZNF552;ZNF587B

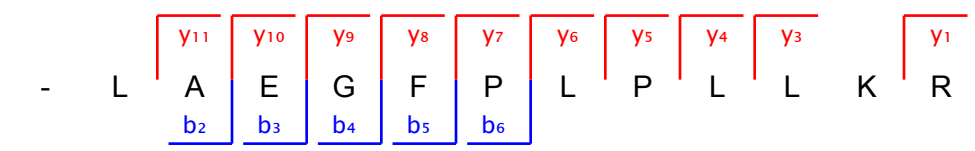
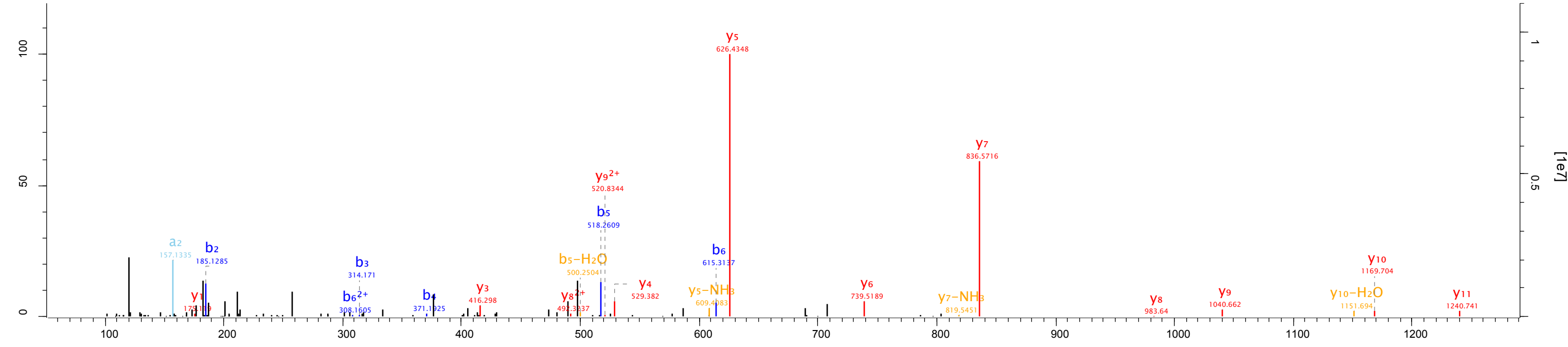




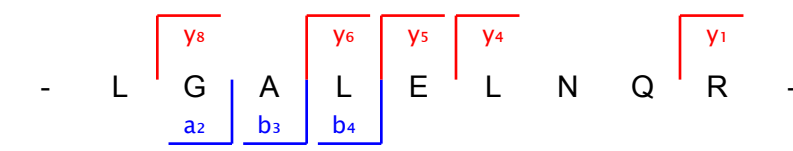
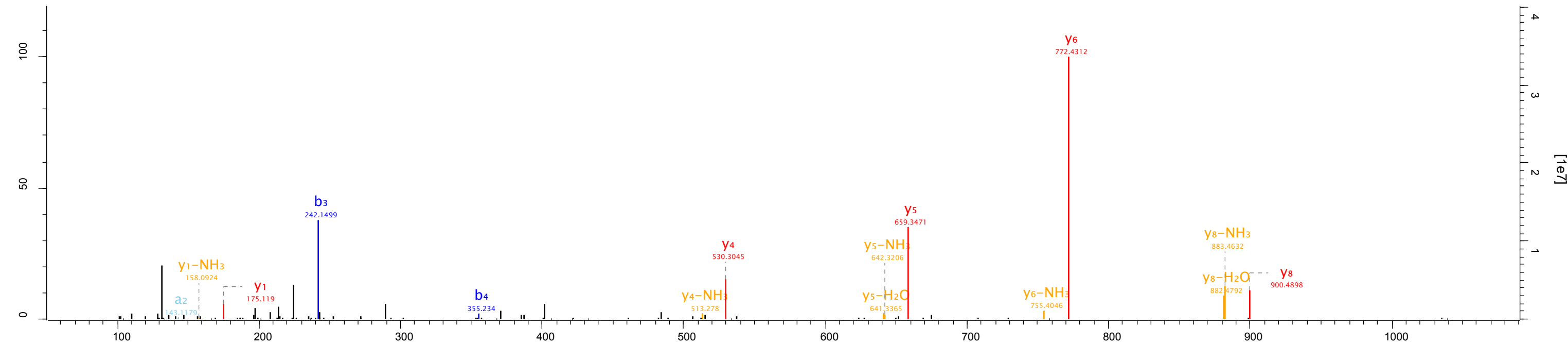
Raw file

20180707_MaS_A375SR_ML_proteome_27

Scan	Method	Score	m/z	Gene names
27389	FTMS; HCD	92.61	451.95	LBP



Raw file: 20180707_MaS_A375SR_ML_proteome_29
 Scan: 13639 Method: FTMS; HCD Score: 103.74 m/z: 507.29 Gene names: TBC1D30



Raw file 20180707_MaS_A375SR_ML_proteome_29 Scan 7719 Method FTMS; HCD Score 93.35 m/z 595.83

