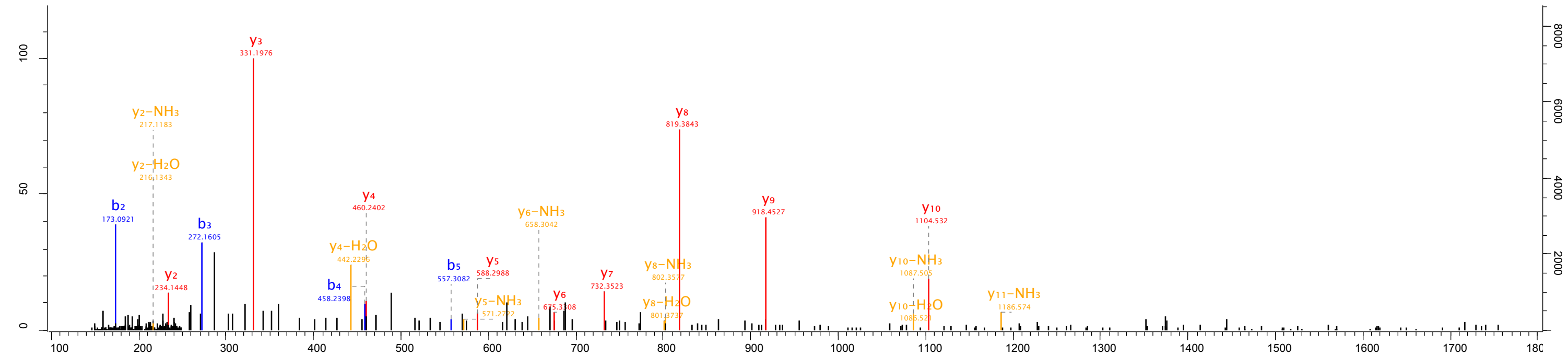


Raw file 20150307_Hepa1_Top_opt_D1_01_1671 Scan 24207 Method TOF; CID Score 89.23 m/z 688.34 Gene names Procr

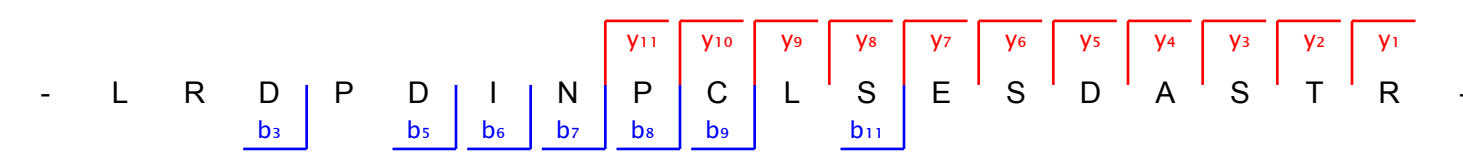
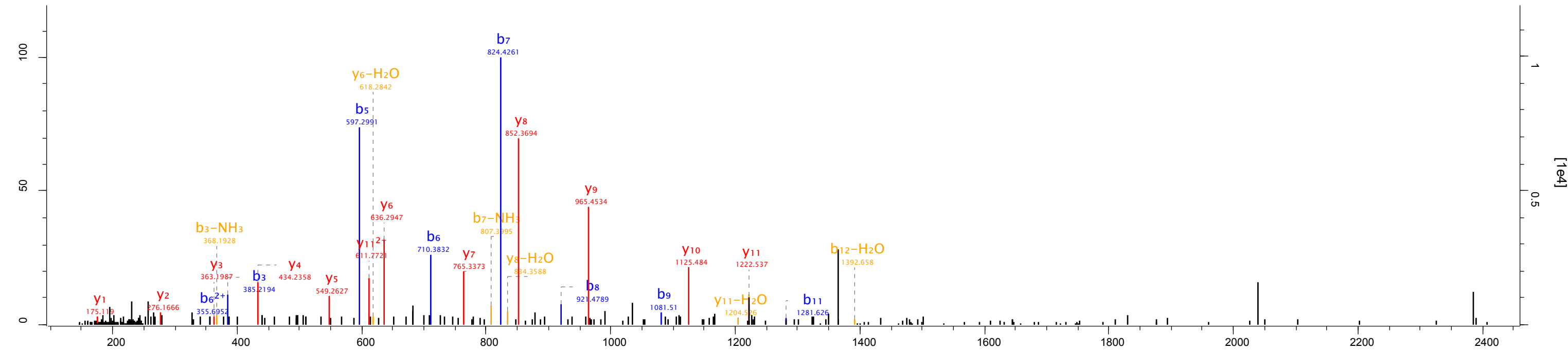


- T A V W V S G S Q E P S K -

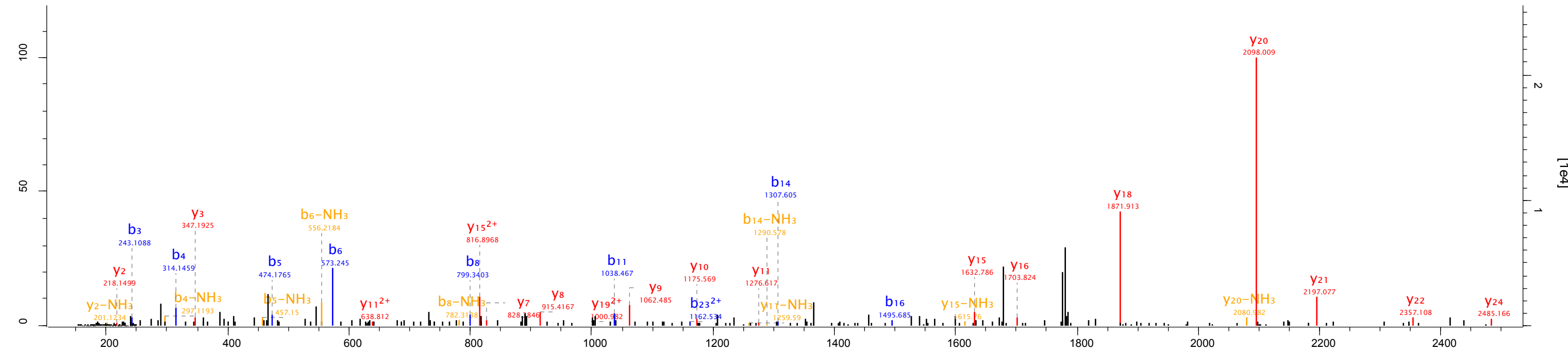
Fragmentation mapping (b and y ions):

- b₂ (A)
- b₃ (V)
- b₄ (W)
- b₅ (V)
- y₂ (S)
- y₃ (P)
- y₄ (E)
- y₅ (Q)
- y₆ (S)
- y₇ (G)
- y₈ (S)
- y₉ (V)
- y₁₀ (W)

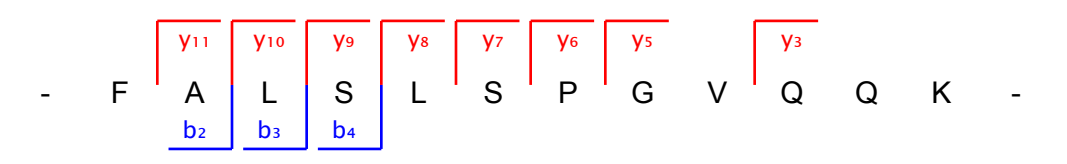
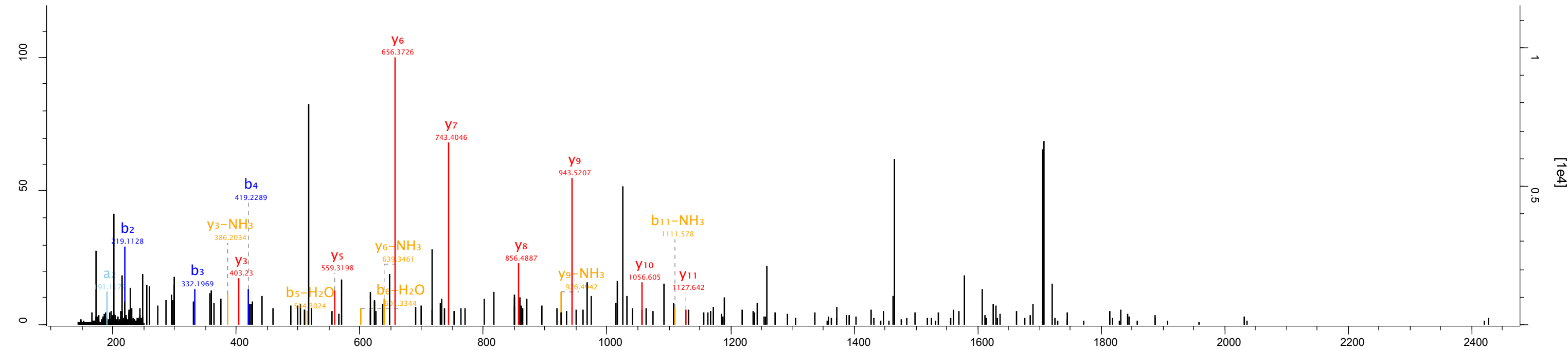
Raw file 20150307_Hepa1_Top_opt_D1_01_1671 Scan 28943 Method TOF; CID Score 83.42 m/z 682.65 Gene names Chchd7



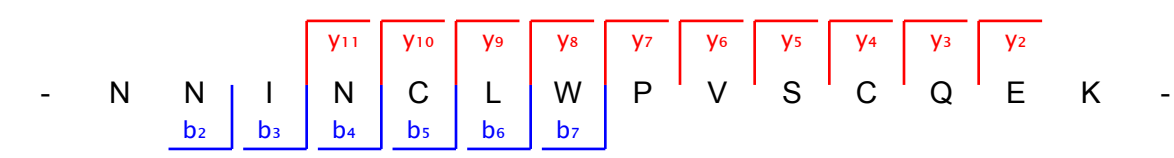
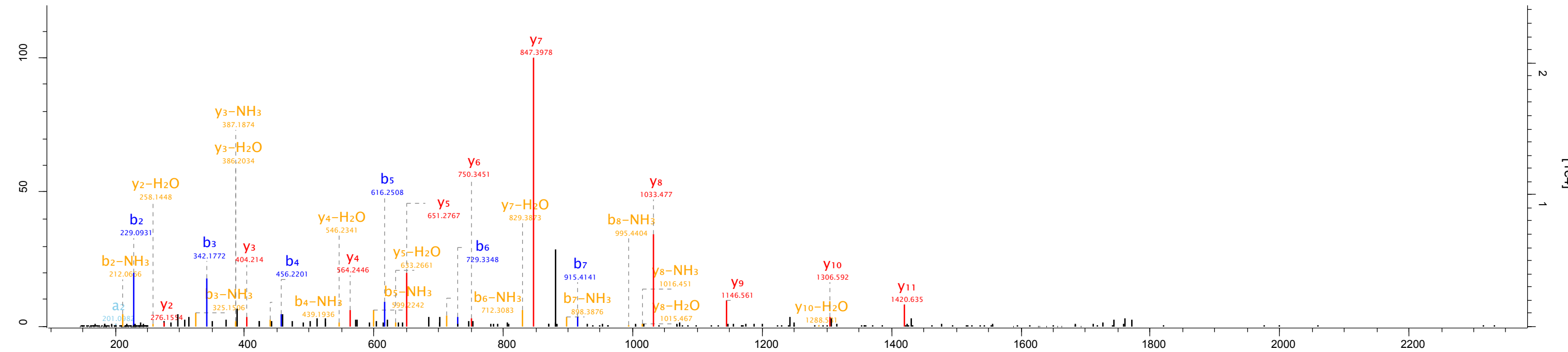
Raw file 20150307_Hepa1_Top_opt_D1_01_1671 Scan 40501 Method TOF; CID Score 82.48 m/z 891.08 Gene names Igfbp1



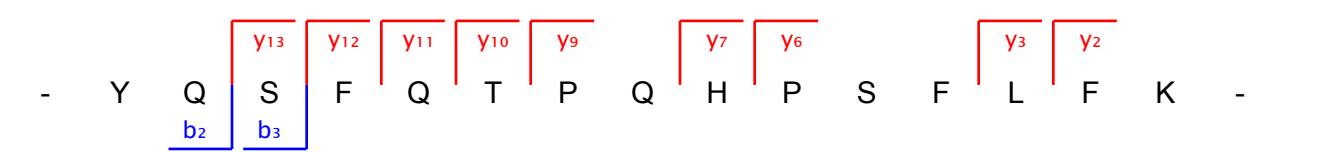
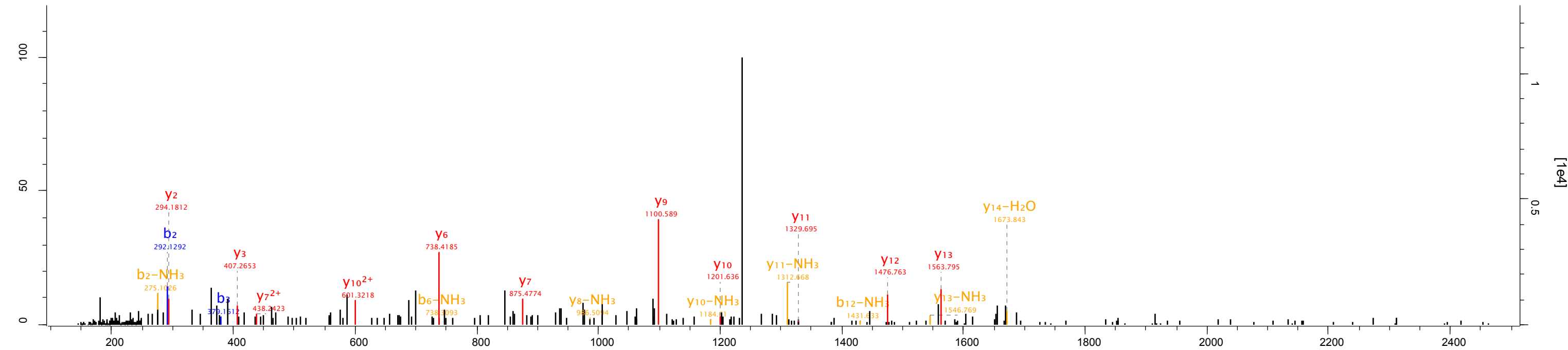
Raw file 20150307_Hepa1_Top_opt_D1_01_1671 Scan 45109 Method TOF; CID Score 62.69 m/z 638.33 Gene names Myd88



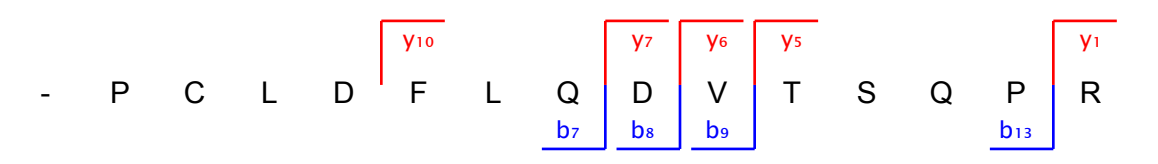
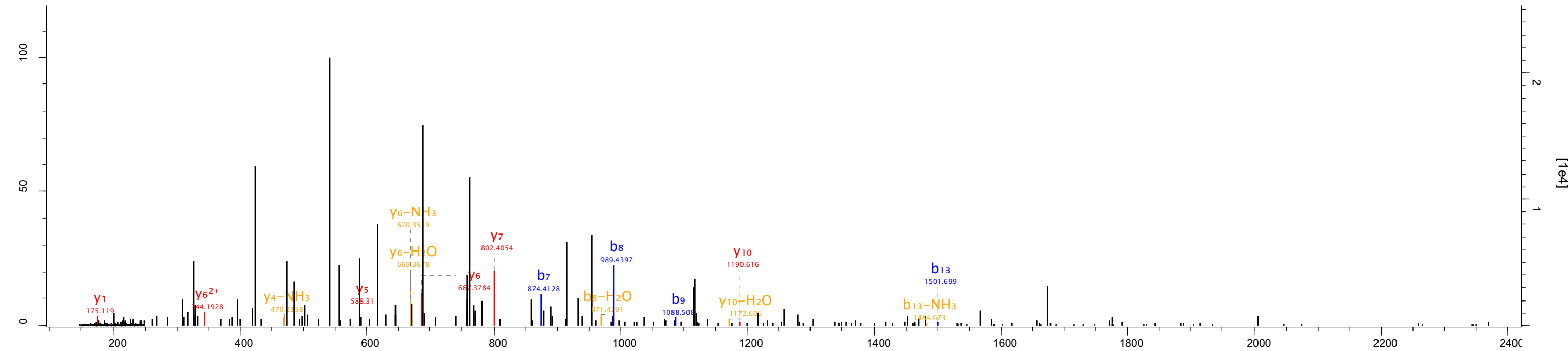
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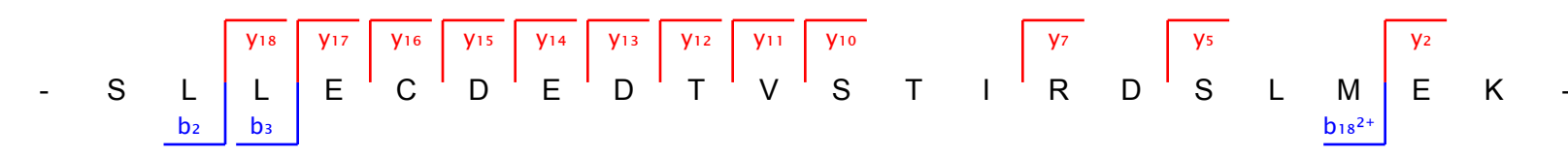
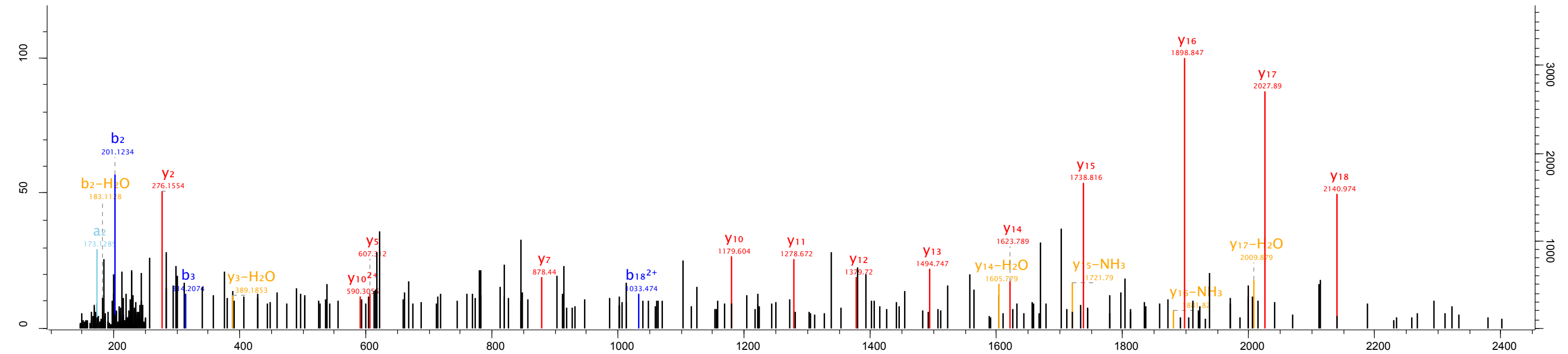
Raw file 20150307_Hepa1_Top_opt_D1_01_1671 Scan 47165 Method TOF; CID Score 50.3 m/z 619.31 Gene names Lgals3bp



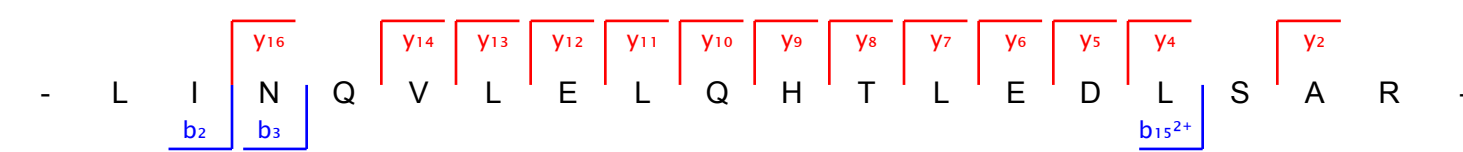
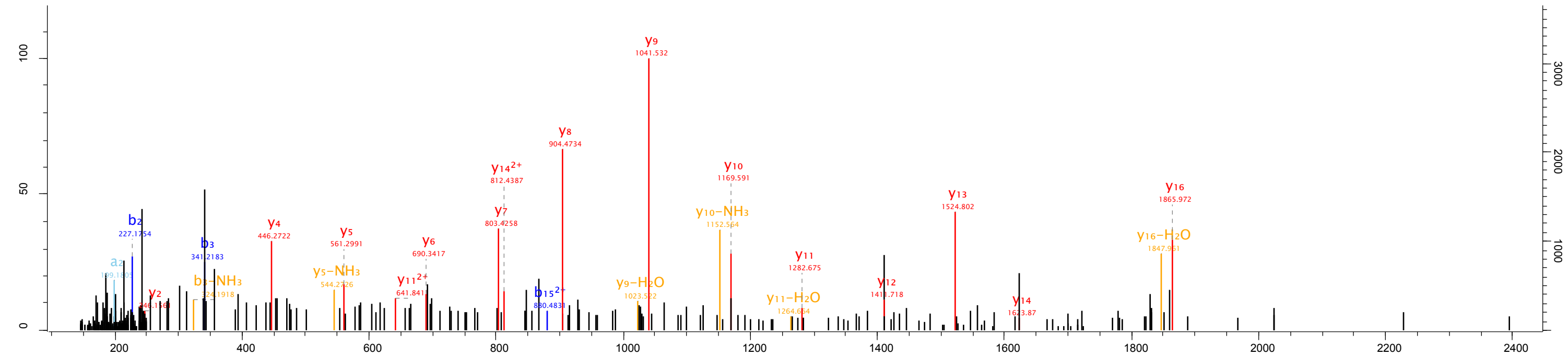
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Raw file Scan Method Score m/z Gene names
 20150307_Hepa1_Top_opt_D1_01_1671 58244 TOF; CID 76.3 781.37 Stc1

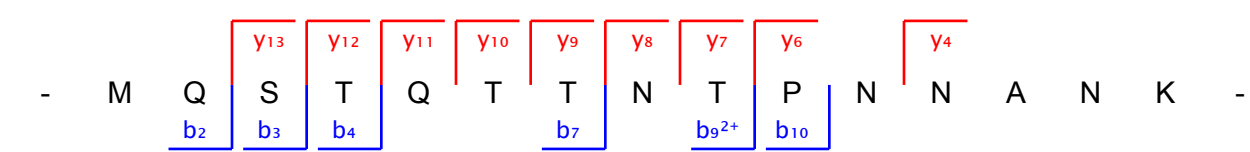
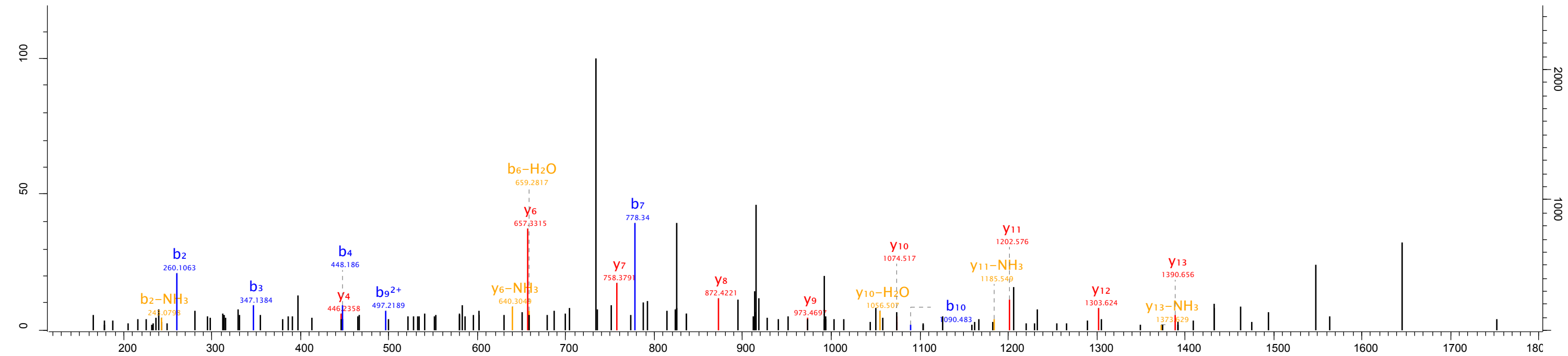


Raw file 20150307_Hepa1_Top_opt_D1_01_1671 Scan 69497 Method TOF; CID Score 91.4 m/z 698.38 Gene names Scoc



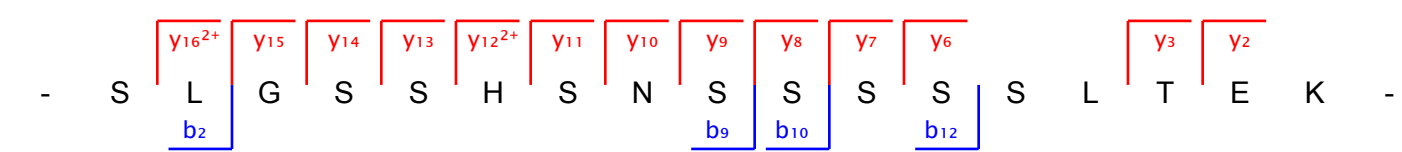
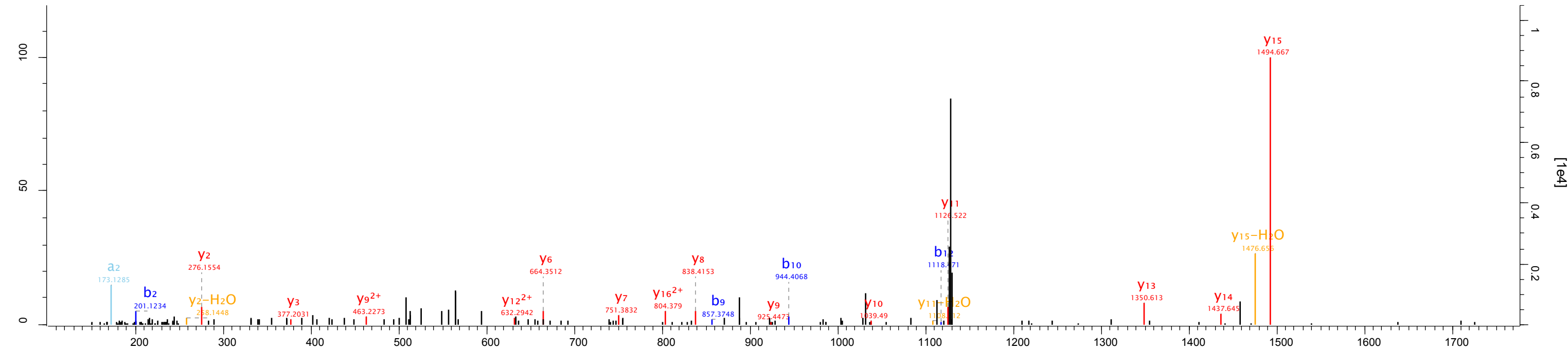
Raw file
20150307_Hepa1_Top_opt_D1_01_1683

Scan Method Score m/z Gene names
5405 TOF; CID 72.32 825.37 Papd5

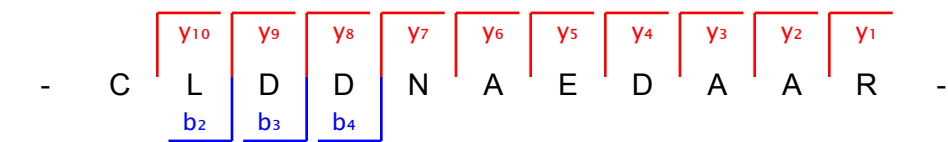
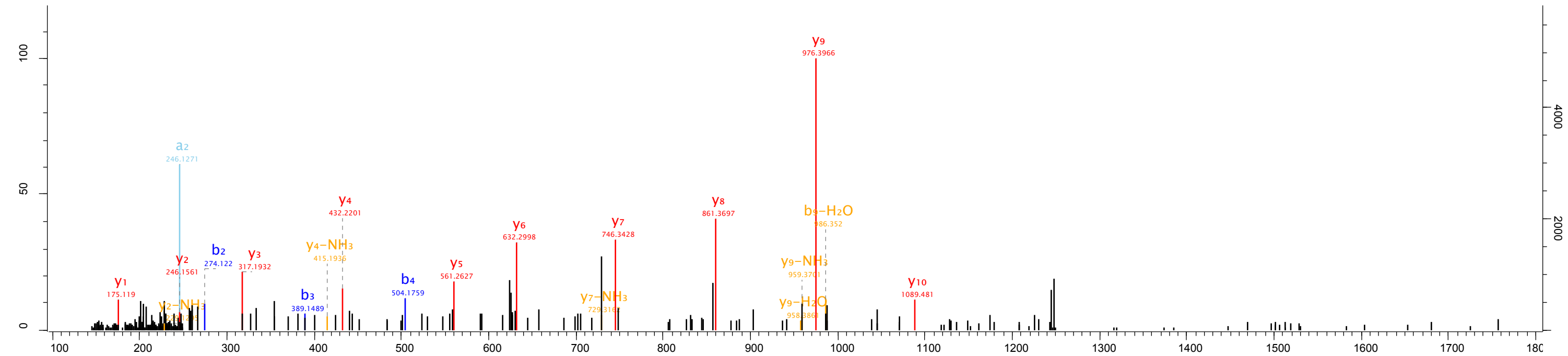


Raw file
20150307_Hepa1_Top_opt_D1_01_1683

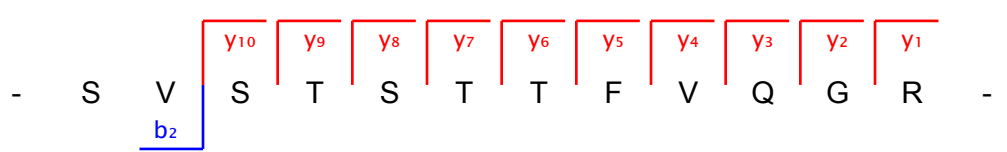
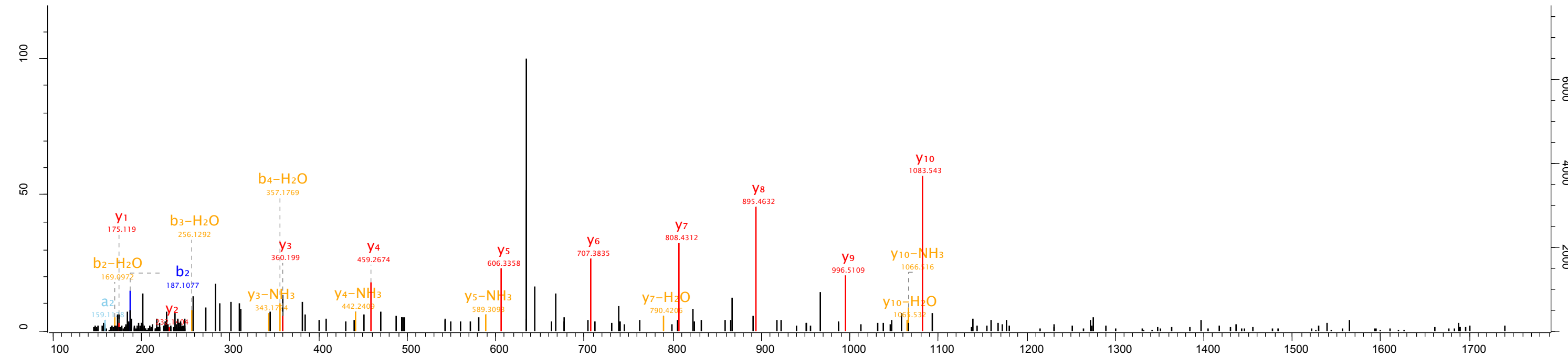
Scan 8227 Method TOF; CID Score 54.25 m/z 565.6 Gene names Fam76b



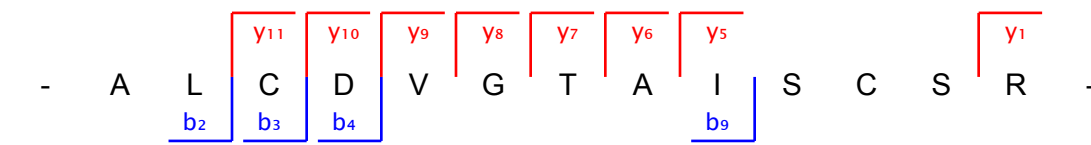
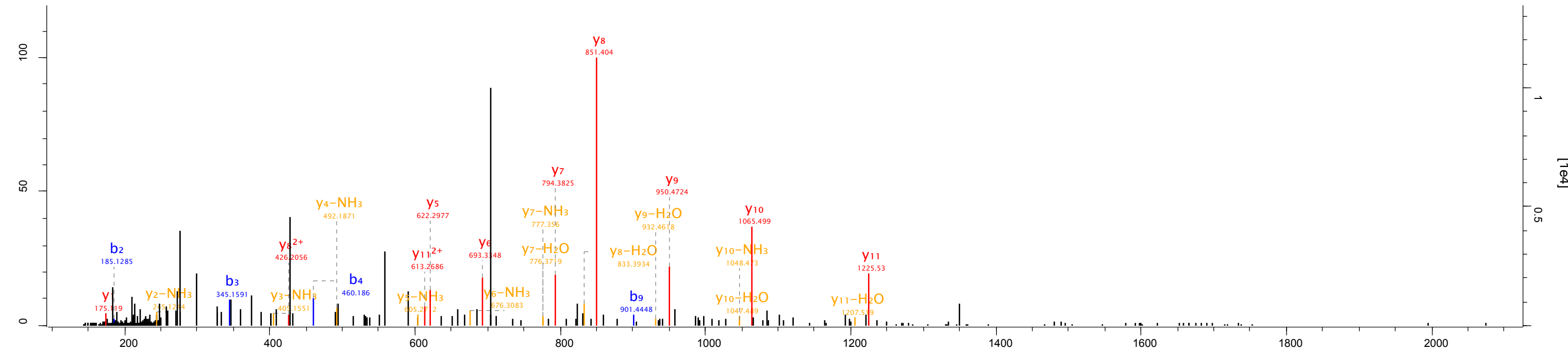
Raw file 20150307_Hepa1_Top_opt_D1_01_1683 Scan 13304 Method TOF; CID Score 73.44 m/z 625.26 Gene names Coa6



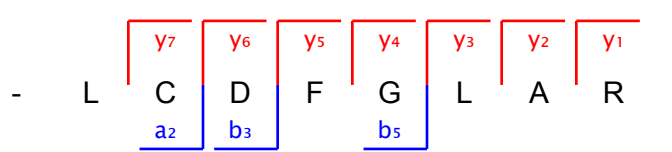
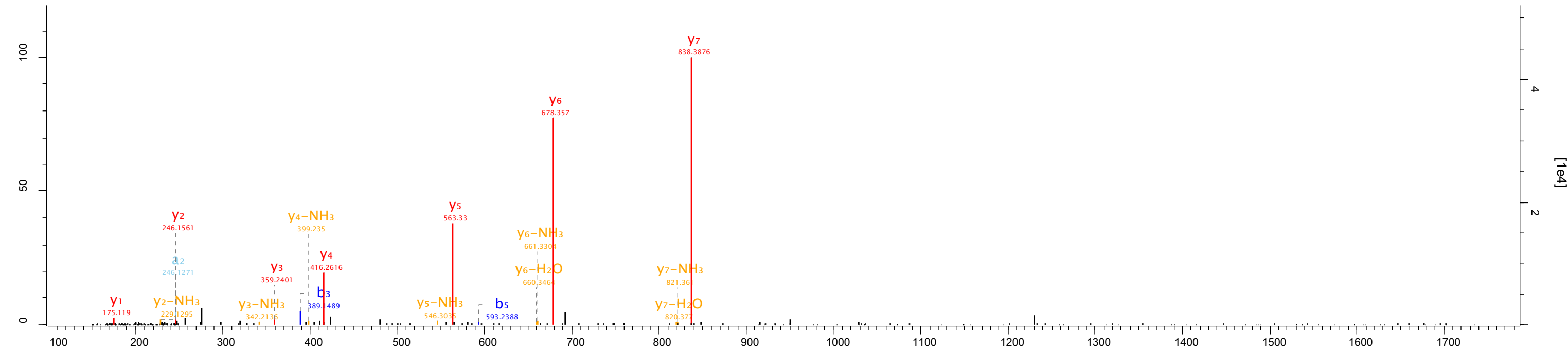
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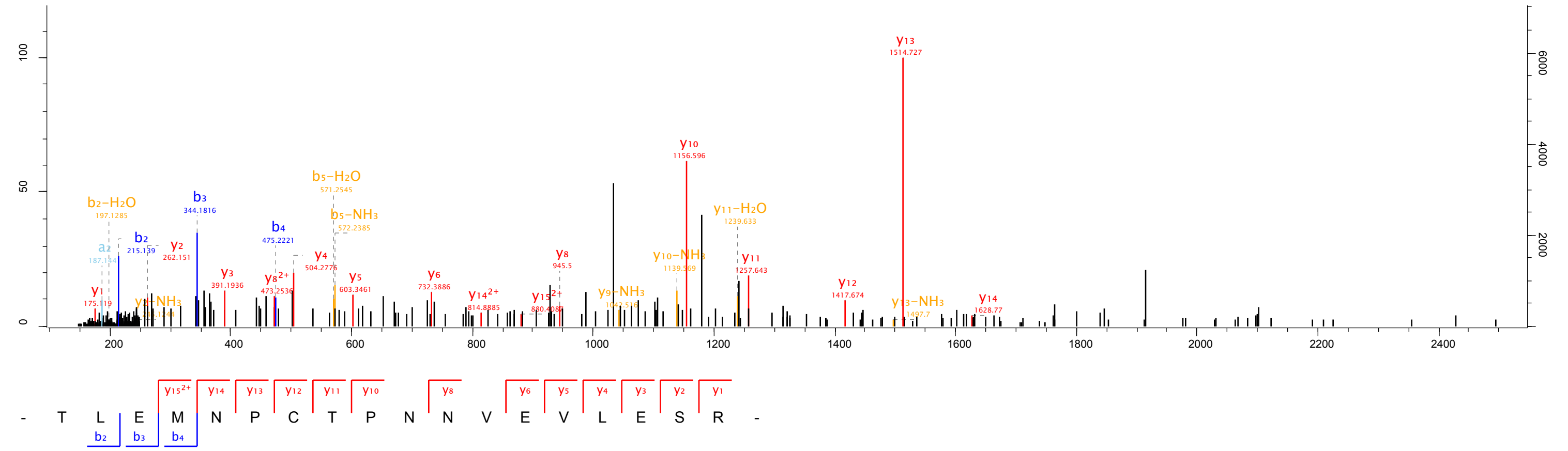
Raw file: 20150307_Hepa1_Top_opt_D1_01_1683
 Scan: 31253 Method: TOF; CID Score: 77.28 m/z: 705.33 Gene names: Vkorc1



Raw file: 20150307_Hepa1_Top_opt_D1_01_1683
 Scan: 35469 Method: TOF; CID Score: 161.11 m/z: 476.24 Gene names: Mapk15

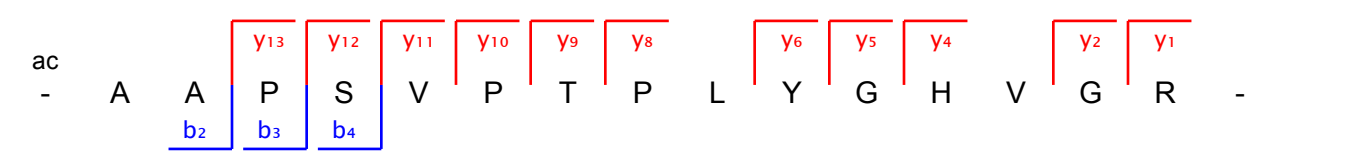
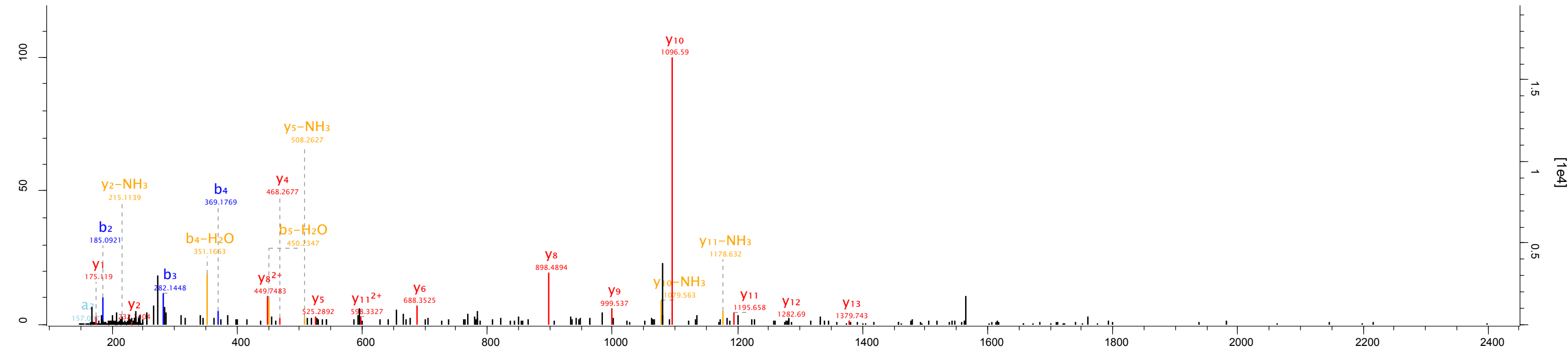


Raw file 20150307_Hepa1_Top_opt_D1_01_1683 Scan 46496 Method TOF; CID Score 75.68 m/z 1052.49 Gene names Lifr

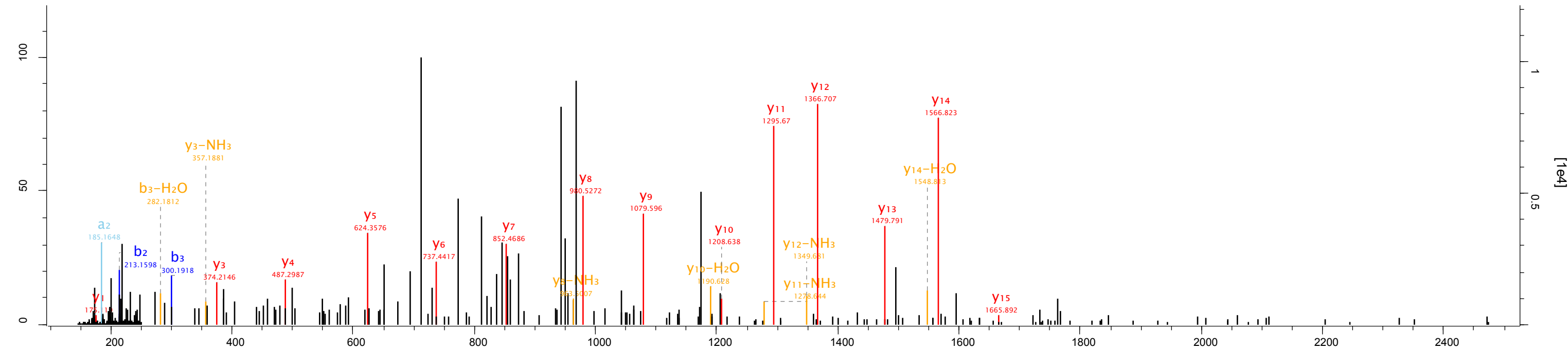


Raw file
20150307_Hepa1_Top_opt_D1_01_1683

Scan 47202 Method TOF; CID Score 84.75 m/z 782.41 Gene names N6amt1

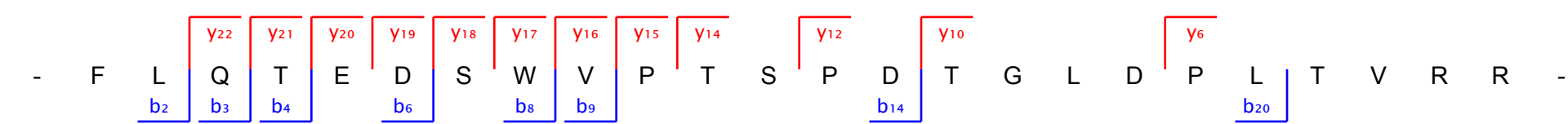
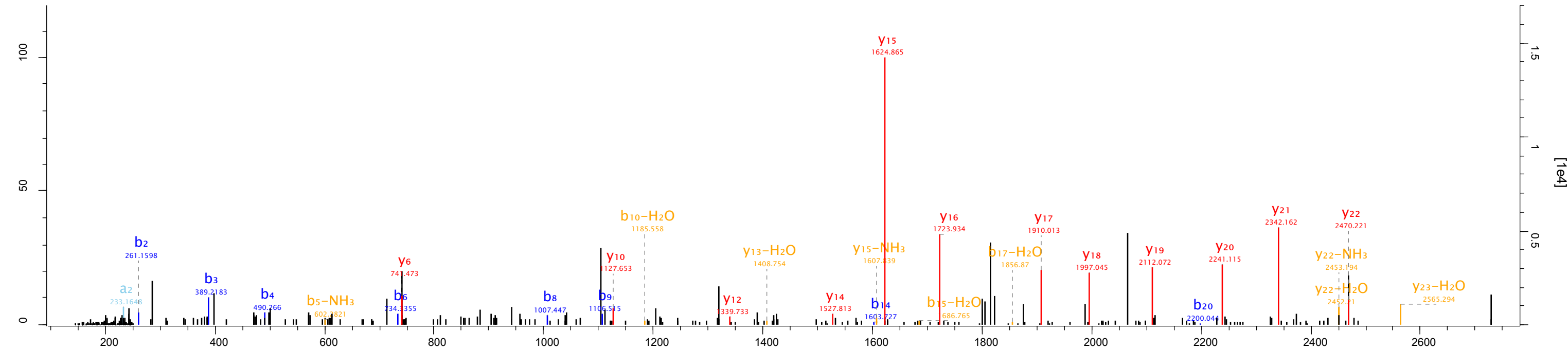


Raw file 20150307_Hepa1_Top_opt_D1_01_1683 Scan 54707 Method TOF; CID Score 120.7 m/z 594.33 Gene names Mboat7

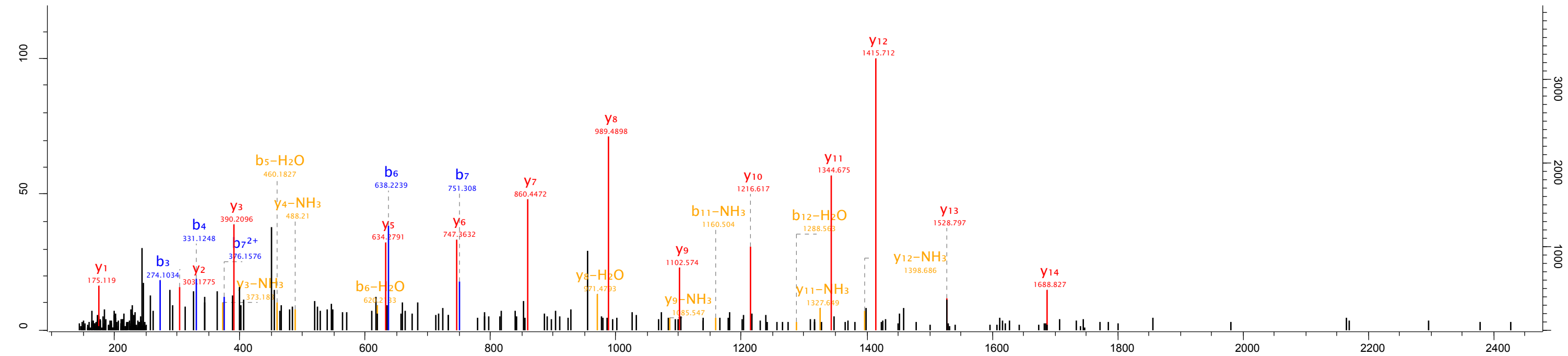


- L V S L A S E V Q D L H L A Q R -
 b2 b3

Raw file 20150307_Hepa1_Top_opt_D1_01_1683 Scan 61410 Method TOF; CID Score 72.3 m/z 911.12 Gene names Rpp25l



Raw file 20150307_Hepa1_Top_opt_D1_01_1683 Scan 63543 Method TOF; CID Score 94.28 m/z 1084.01 Gene names Ly6c2;Ly6c1

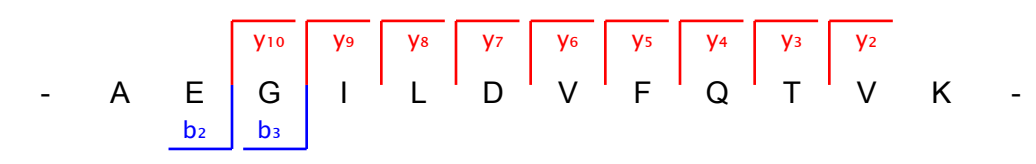
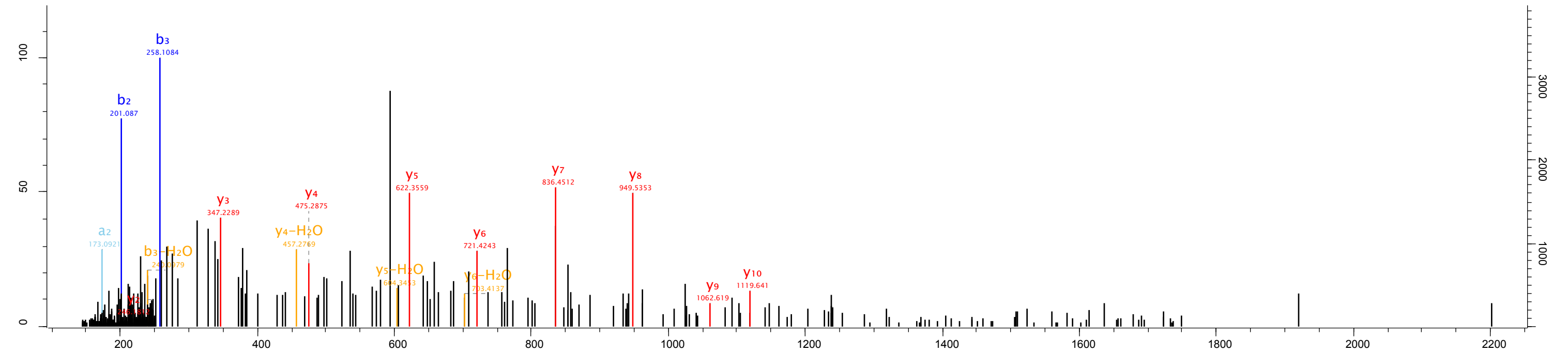


- A S D G F C I A Q N I E L I E D S Q R -

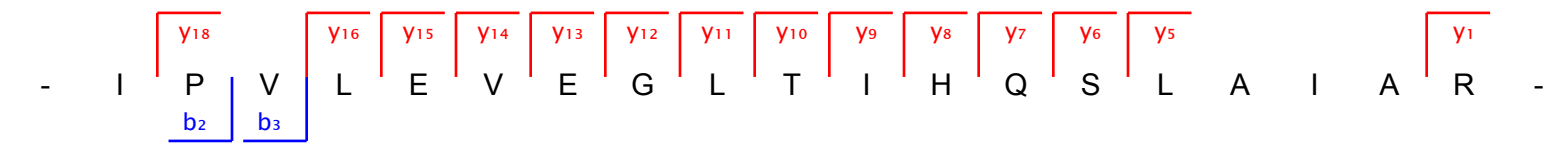
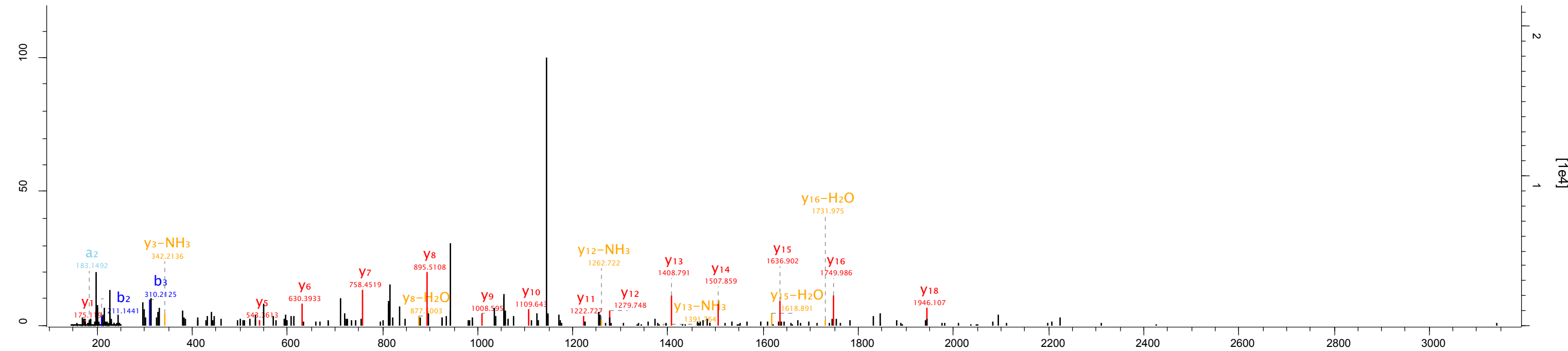
Fragmentation mapping (b and y ions):

- b₃ (D), b₄ (G)
- b₆ (C), b₇ (I)
- y₁ (R), y₂ (Q), y₃ (S)
- y₅ (E), y₆ (I), y₇ (L), y₈ (E), y₉ (I), y₁₀ (N), y₁₁ (Q), y₁₂ (A), y₁₃ (I), y₁₄ (C)

Raw file 20150307_Hepa1_Top_opt_D1_01_1683 Scan 64066 Method TOF; CID Score 69.03 m/z 660.36 Gene names Ptpa

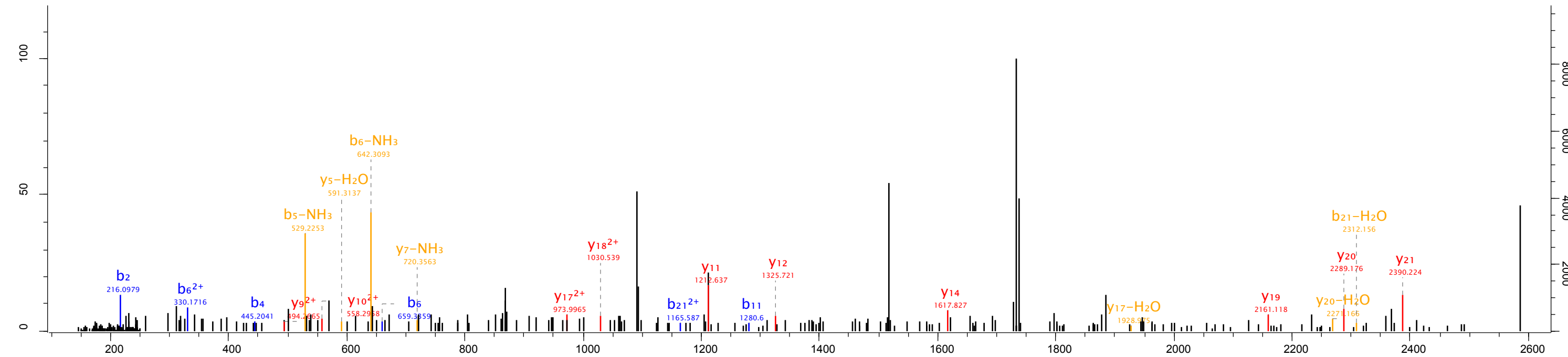


Raw file 20150307_Hepa1_Top_opt_D1_01_1683 Scan 64551 Method TOF; CID Score 47.69 m/z 687.4 Gene names Hpgds



Raw file
20150307_Hepa1_Top_opt_D1_01_1683

Scan 64751 Method TOF; CID Score 38.27 m/z 869.44 Gene names Als2

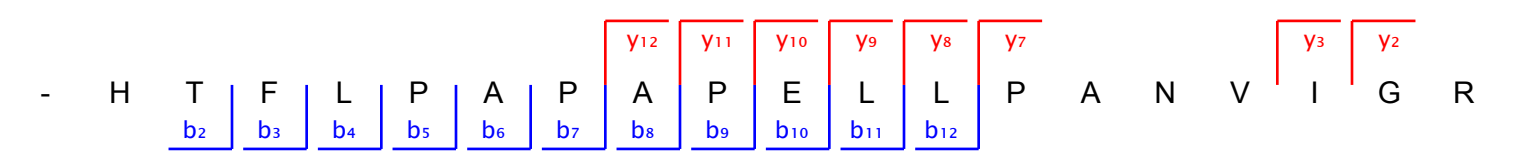
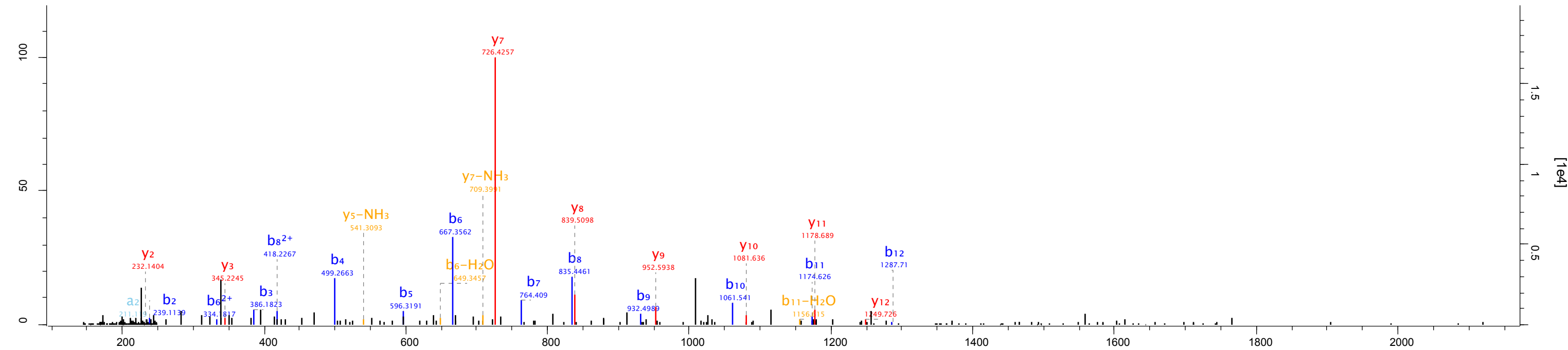


- S Q T Q T L E S L E Y I P Q H I G A F S V E K -

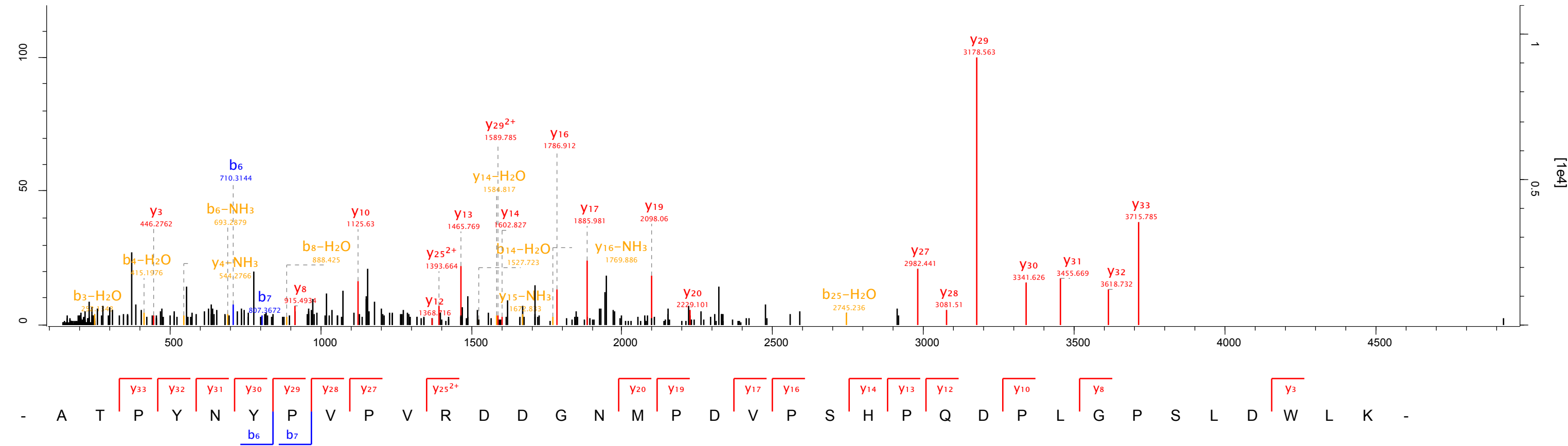
Fragmentation scheme showing b-ions (blue) and y-ions (red) corresponding to the peptide sequence. Brackets indicate the charge state of the ions.

- b₂ (Q-T)
- b₄ (Q-T)
- b₆ (L-E)
- b₁₁ (Y-I)
- b₂₁²⁺ (V-E)
- y₉²⁺ (T-L)
- y₁₀²⁺ (L-E)
- y₁₂ (I-P)
- y₁₁ (P-Q)
- y₁₄ (L-E)
- y₁₇²⁺ (T-L)
- y₁₈²⁺ (L-E)
- y₁₉ (T-L)
- y₂₀ (Q-T)
- y₂₁ (S-Q)

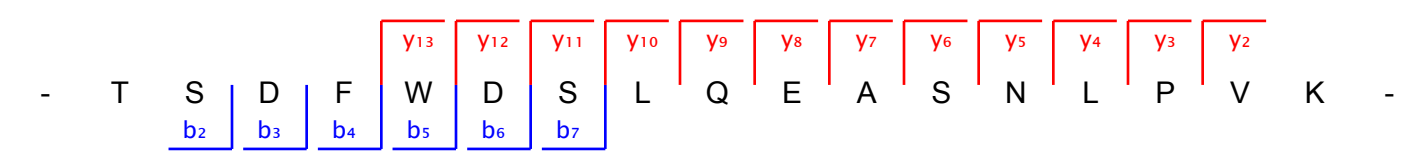
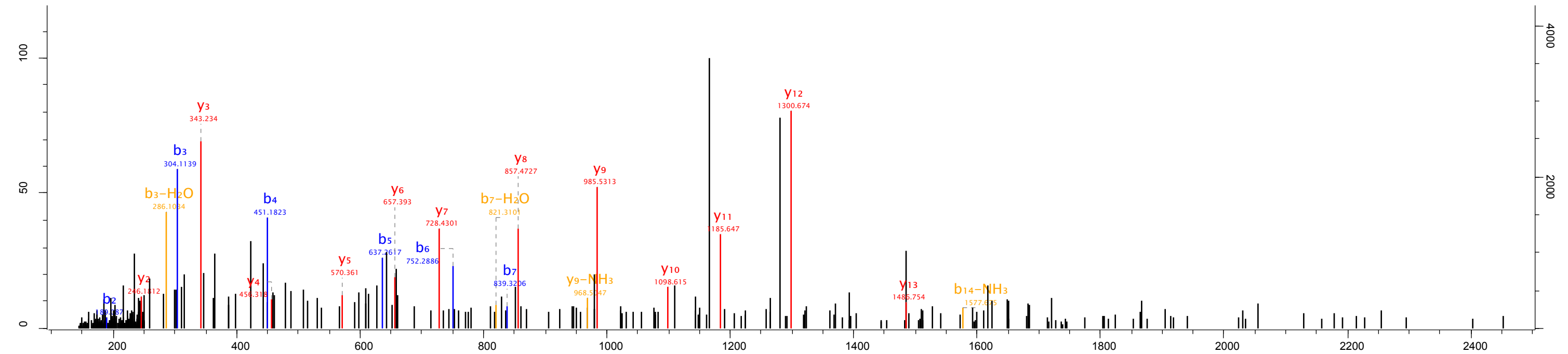
Raw file 20150307_Hepa1_Top_opt_D1_01_1683 Scan 65230 Method TOF; CID Score 91.4 m/z 672.05 Gene names Tsen54



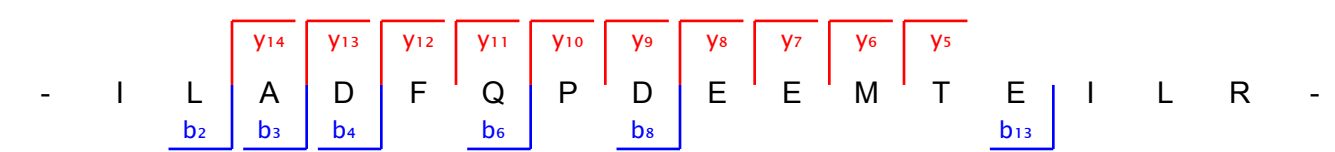
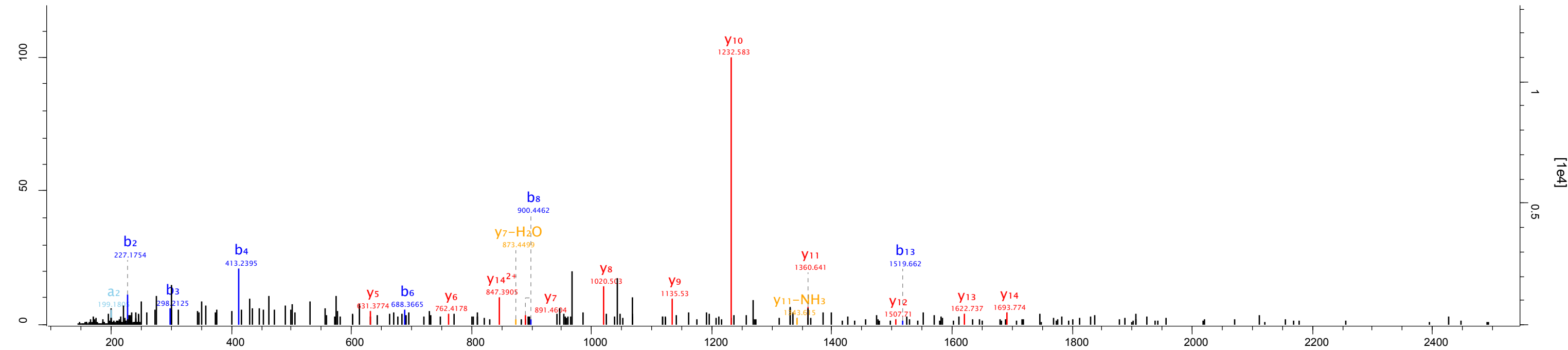
Raw file 20150307_Hepa1_Top_opt_D1_01_1683 Scan 65233 Method TOF; CID Score 34.99 m/z 973.47 Gene names Ndufa3



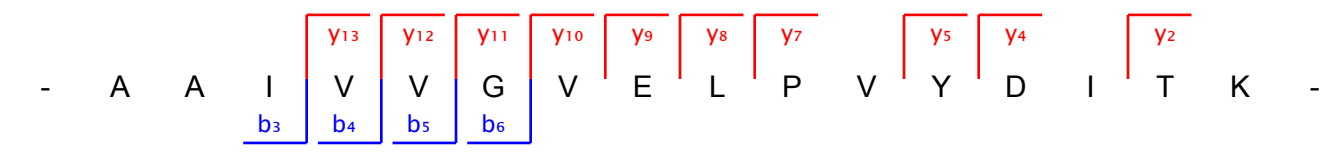
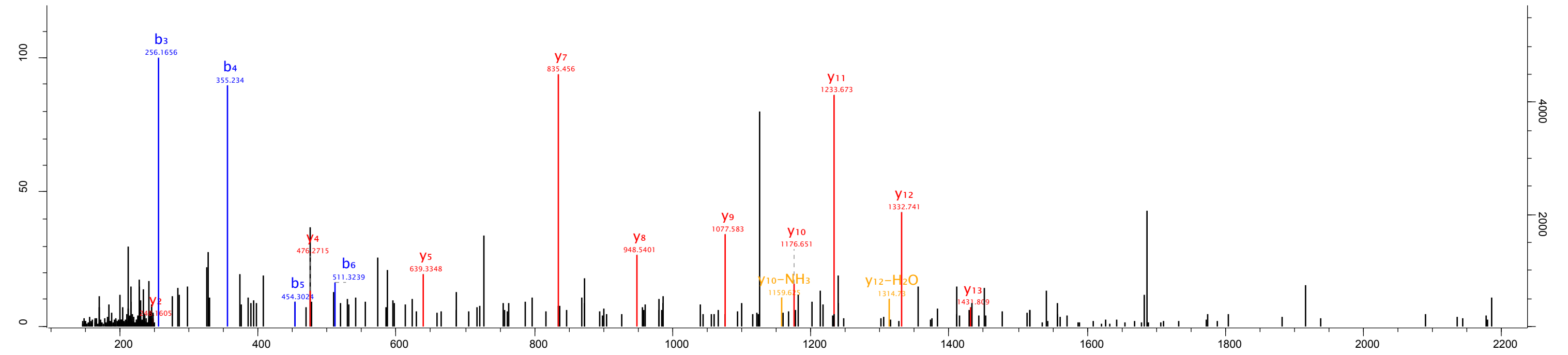
Raw file 20150307_Hepa1_Top_opt_D1_01_1683 Scan 66257 Method TOF; CID Score 86.49 m/z 969.47 Gene names Enpep



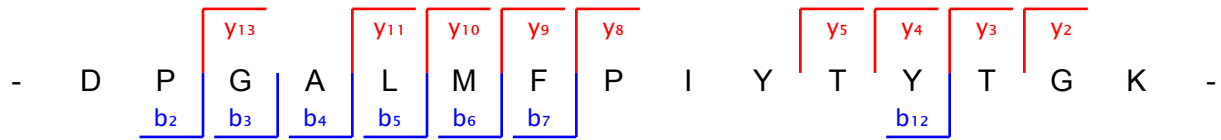
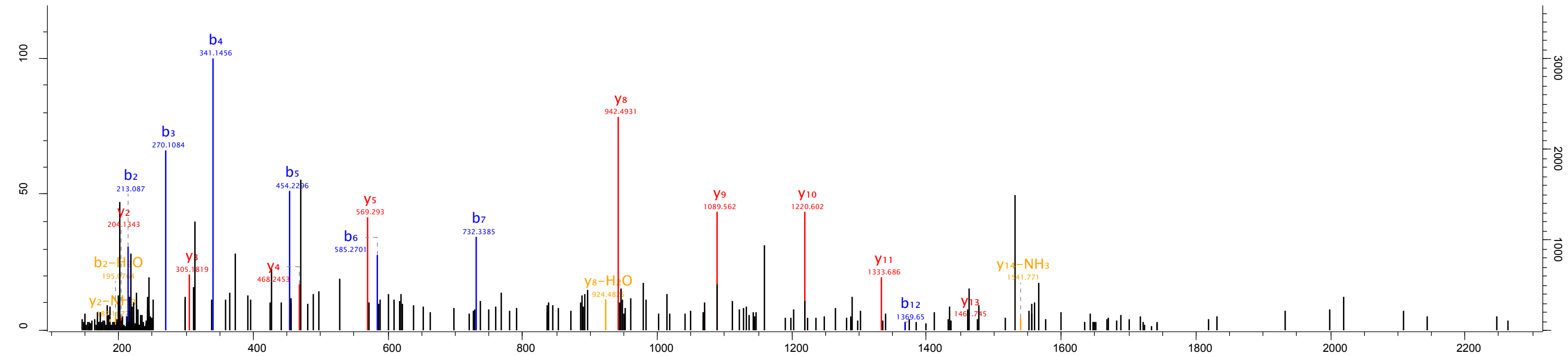
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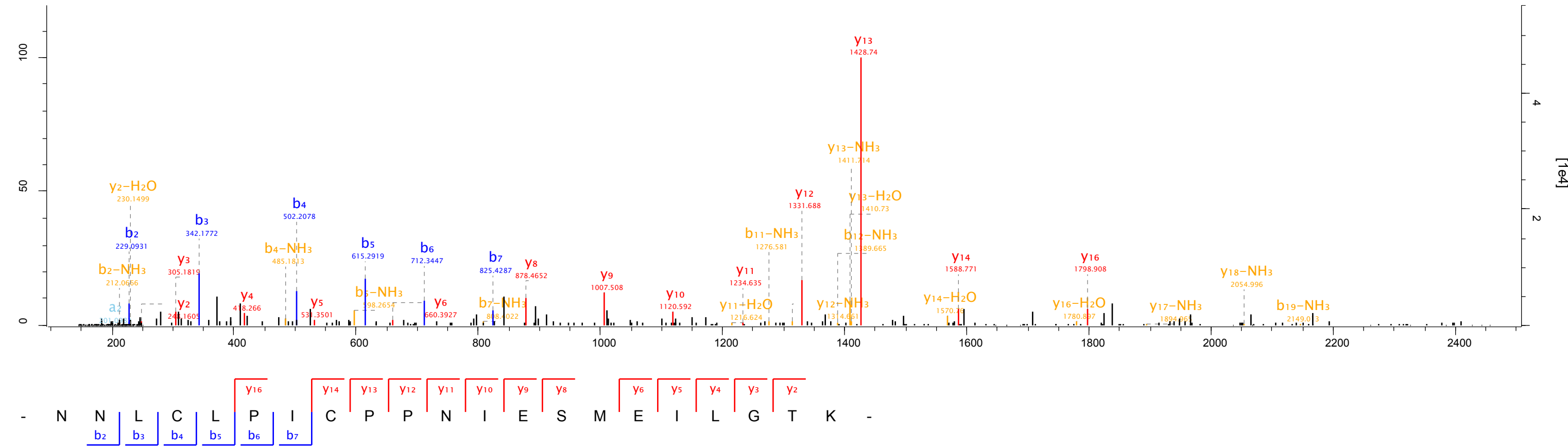


Raw file: 20150307_Hepa1_Top_opt_D1_01_1683
 Scan: 68708 Method: TOF; CID Score: 62.06 m/z: 843.98 Gene names: Slc25a30;Slc25a14

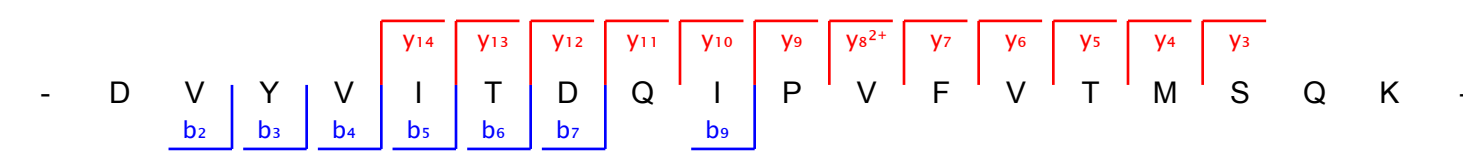
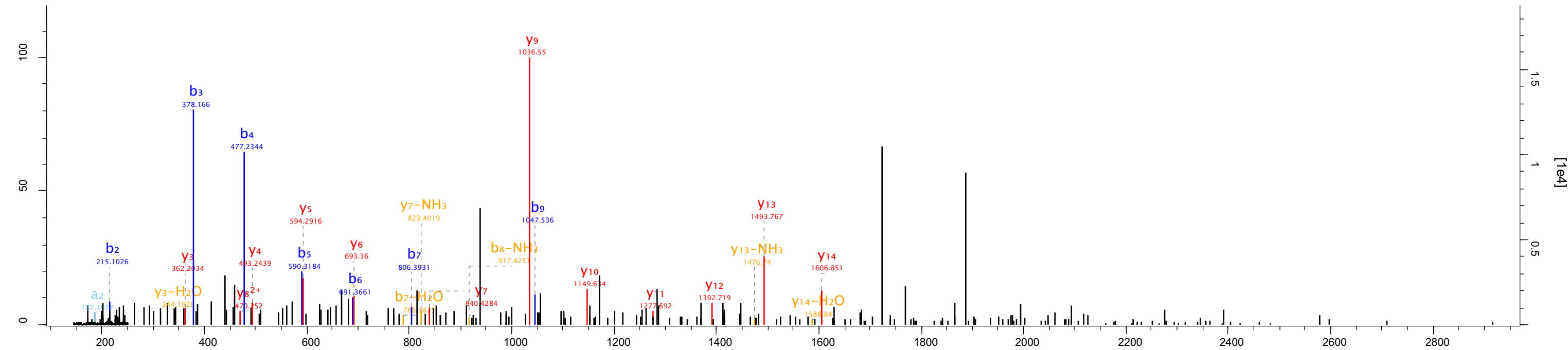


Raw file 20150307_Hepa1_Top_opt_D1_01_1683 Scan 68775 Method TOF; CID Score 52.17 m/z 837.41 Gene names Mmp13

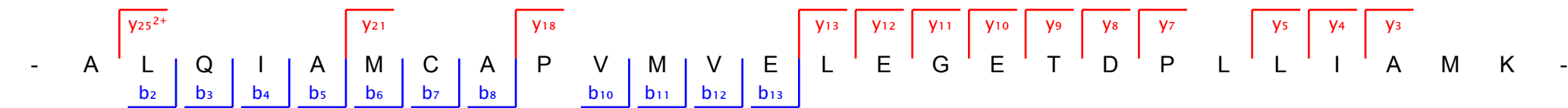
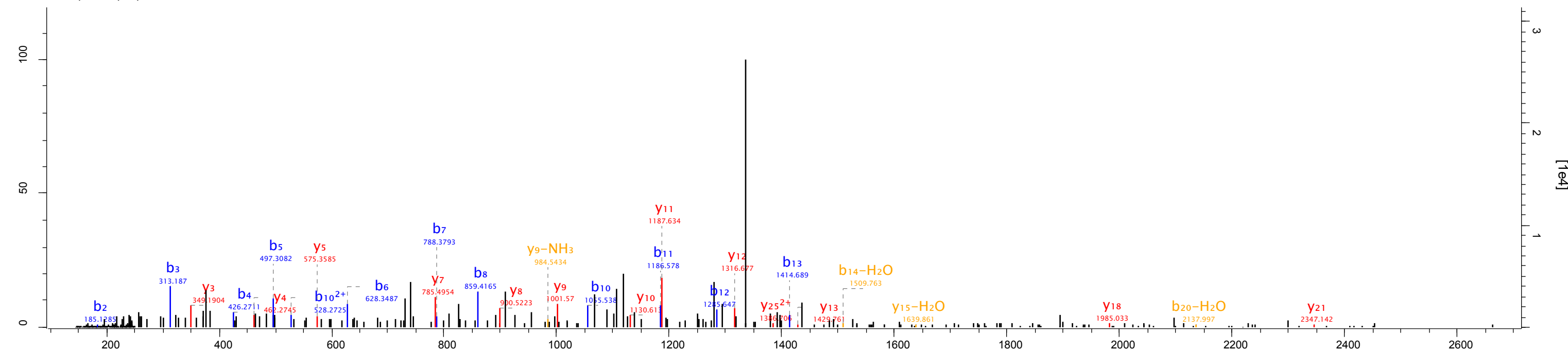




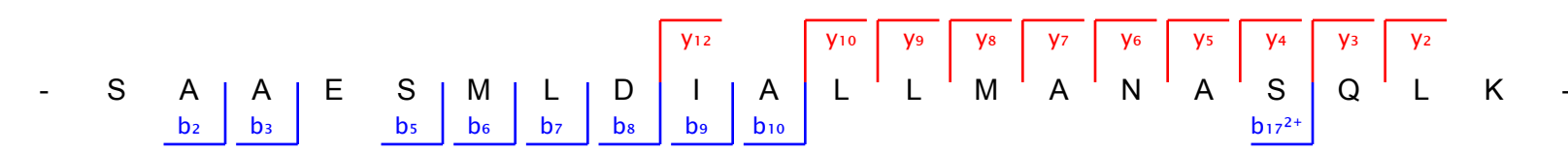
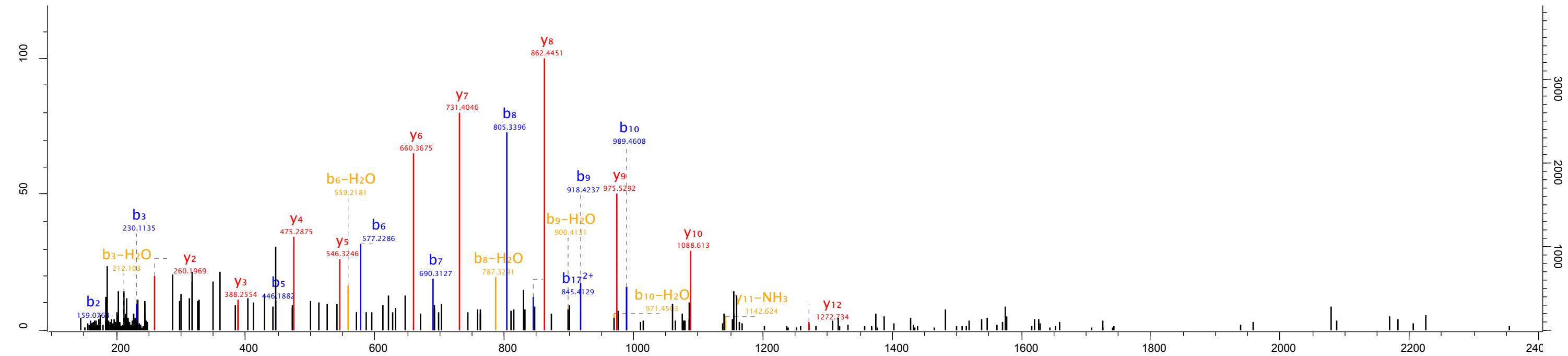
Raw file 20150307_Hepa1_Top_opt_D1_01_1683 Scan 71086 Method TOF; CID Score 65.02 m/z 1042.54 Gene names Gpnmb



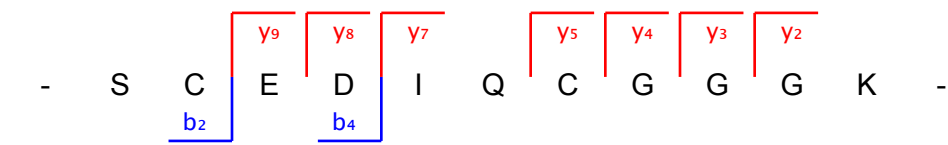
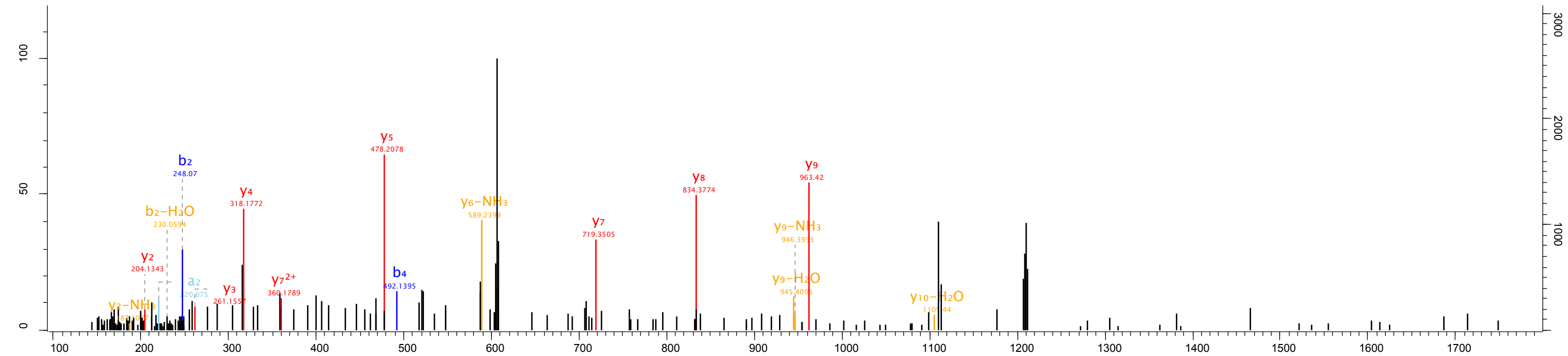
Raw file 20150307_Hepa1_Top_opt_D1_01_1683 Scan 71898 Method TOF; CID Score 62.03 m/z 948.48 Gene names Polr2f



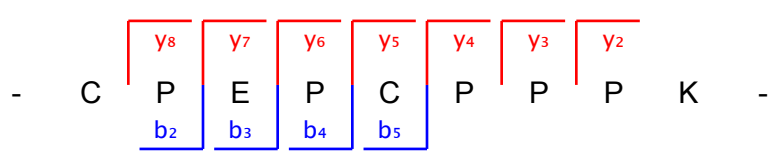
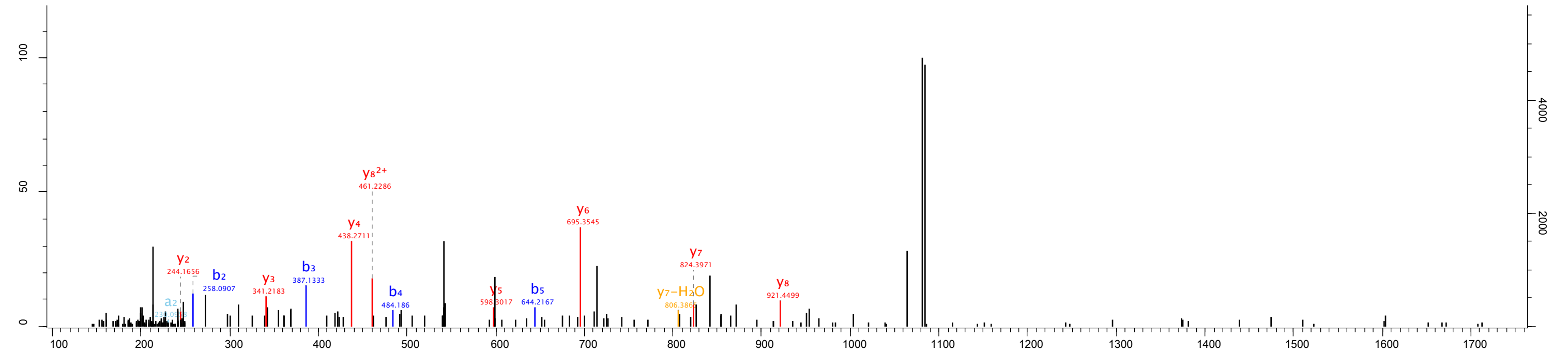
Raw file: 20150307_Hepa1_Top_opt_D1_01_1683
 Scan: 72128 Method: TOF; CID Score: 68.64 m/z: 693.35 Gene names: Ninj1



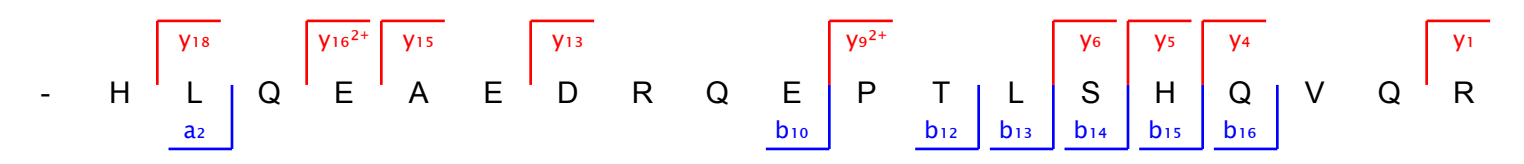
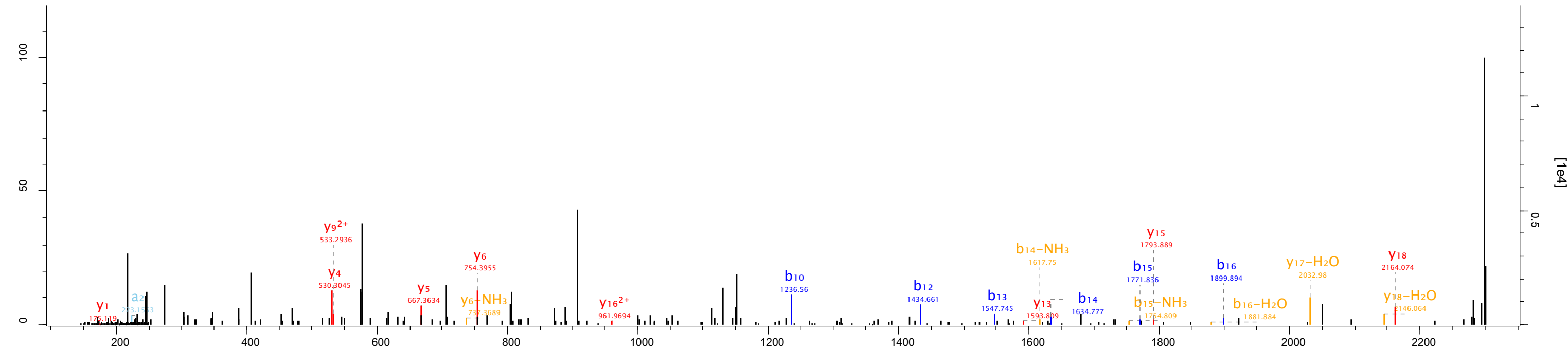
Raw file 20150307_Hepa2_Top_opt_D2_01_1673 Scan 6252 Method TOF; CID Score 73.5 m/z 605.74 Gene names Fst



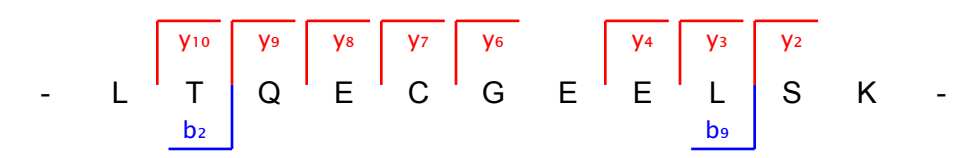
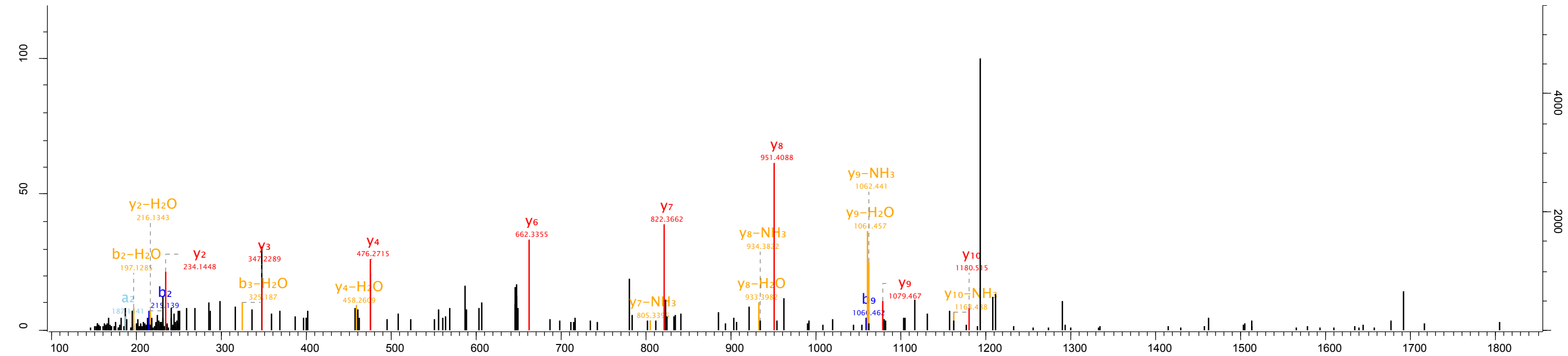
Raw file: 20150307_Hepa2_Top_opt_D2_01_1673
 Scan: 10356 Method: TOF; CID Score: 83.95 m/z: 541.74 Gene names: Sprr2k;Sprr2b;Sprr2g;Sprr2d;Sprr2h



Raw file 20150307_Hepa2_Top_opt_D2_01_1673 Scan 13469 Method TOF; CID Score 67.42 m/z 576.28 Gene names Gm17296

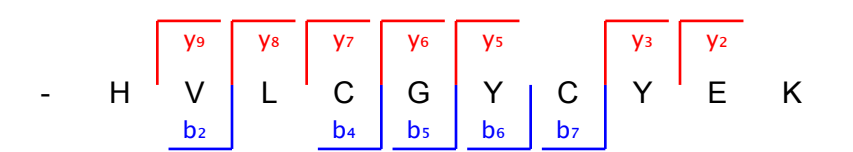
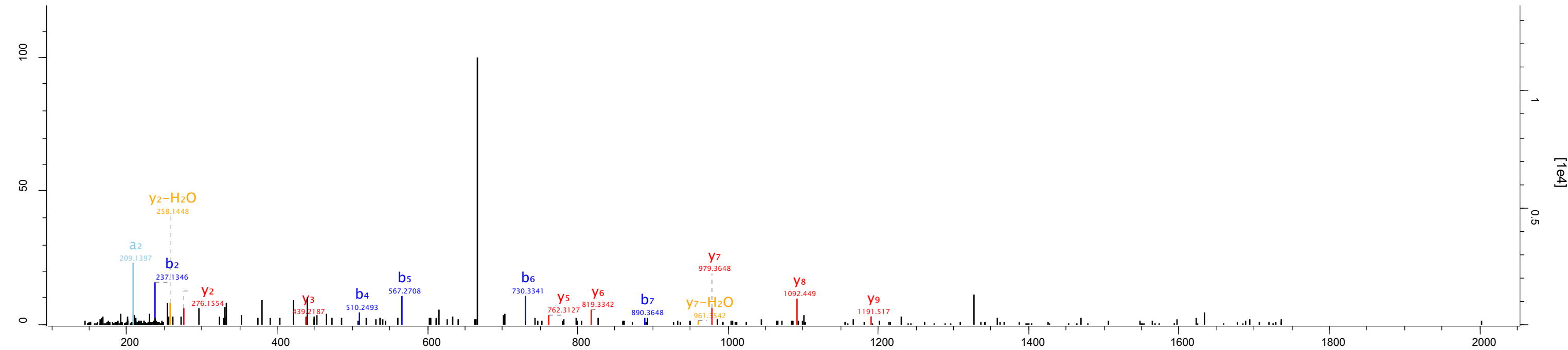


Raw file 20150307_Hepa2_Top_opt_D2_01_1673 Scan 13493 Method TOF; CID Score 85.92 m/z 647.3 Gene names Polr3e



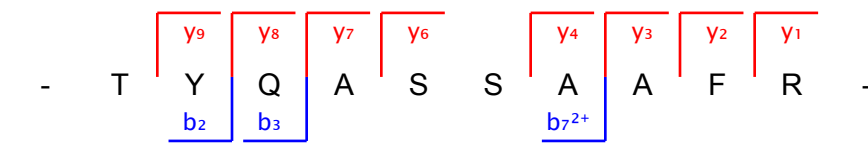
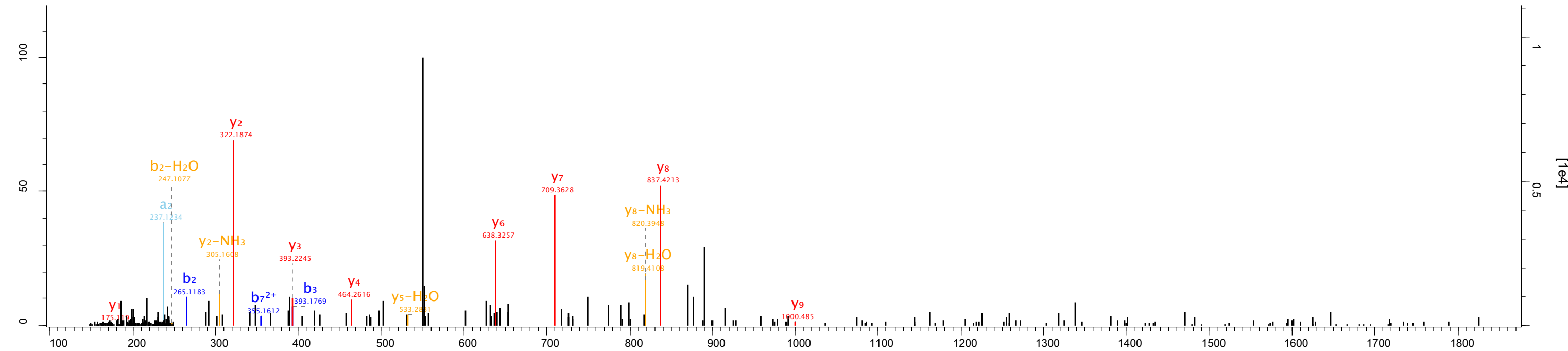
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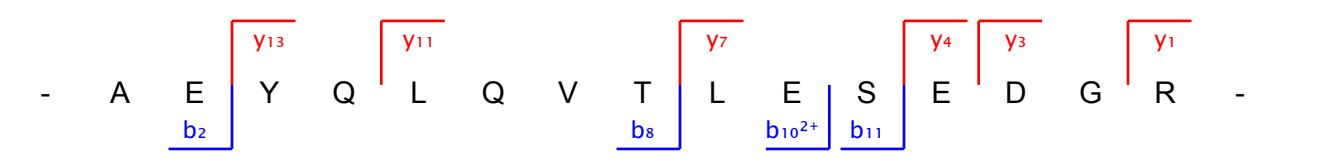
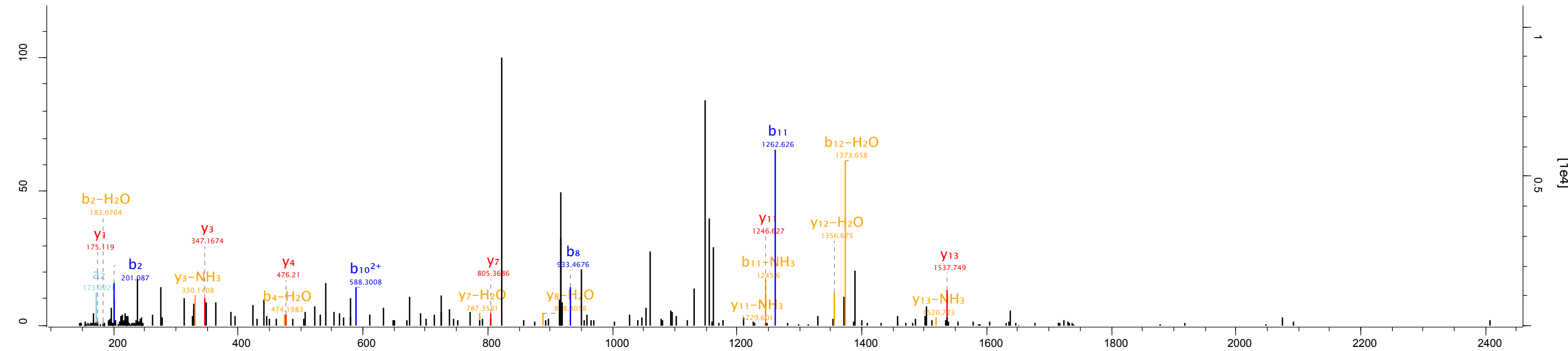


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Scan 18658 Method TOF; CID Score 73.5 m/z 551.27 Gene names Fam168a

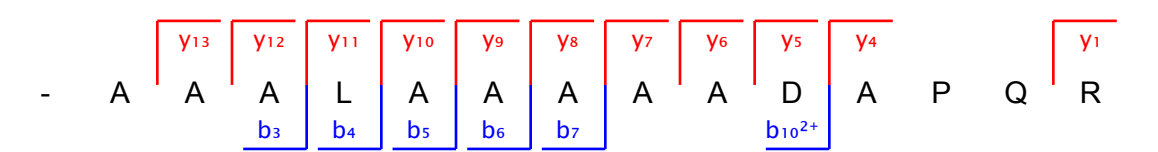
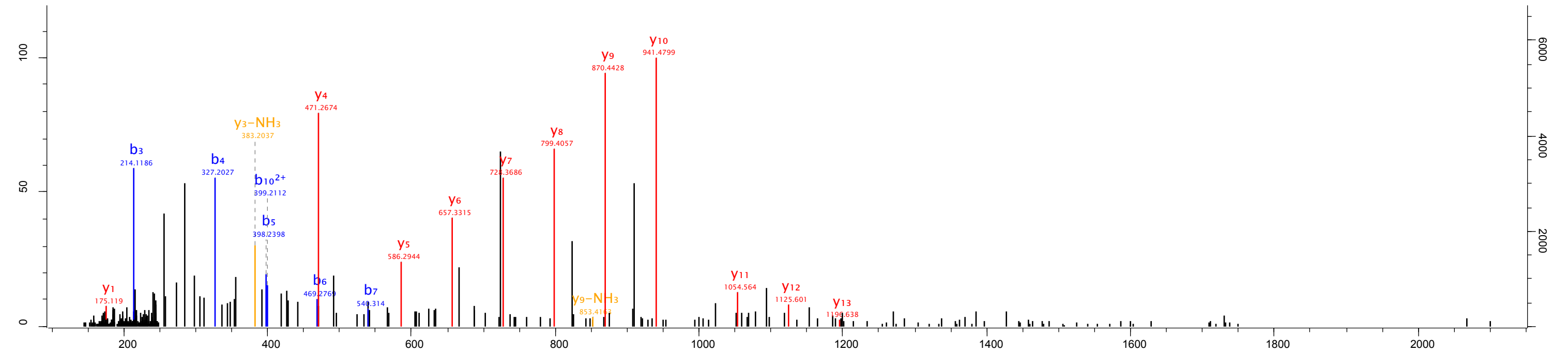


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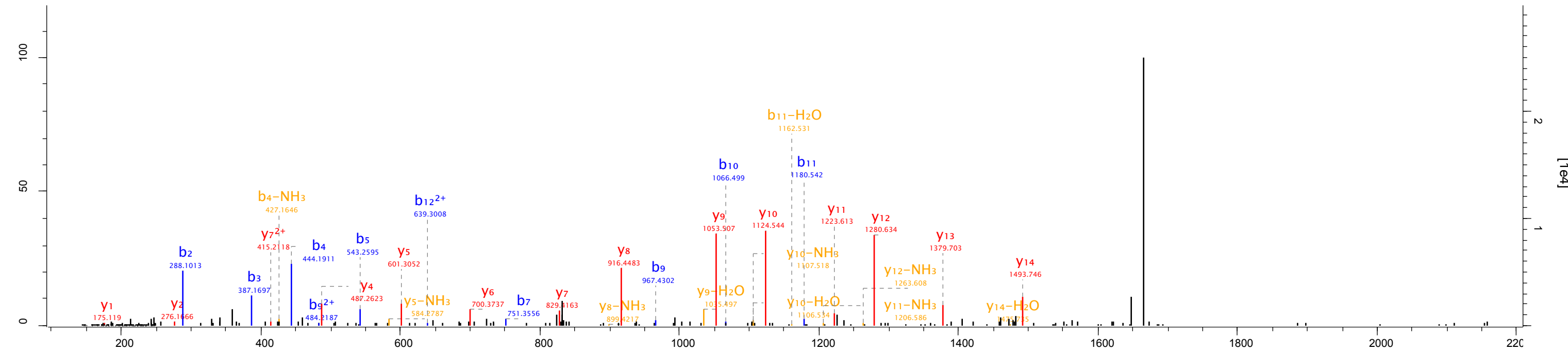
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Scan 23176 Method TOF; CID Score 60.55 m/z 634.33 Gene names Ndfip2



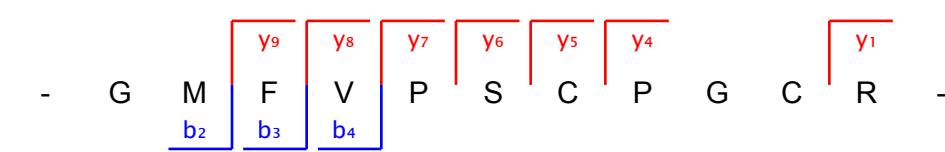
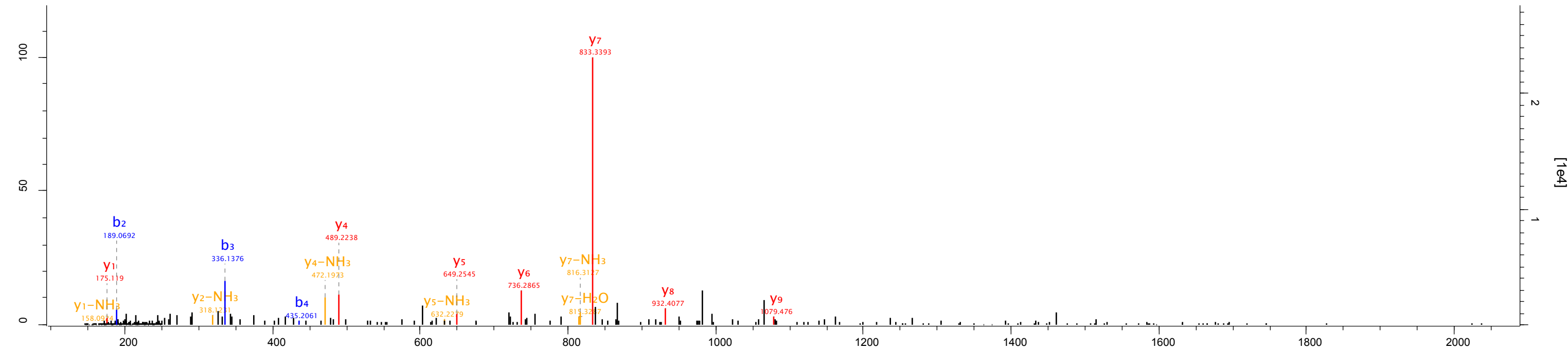
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Scan 30900 Method TOF; CID Score 130.29 m/z 834.4 Gene names Ormdl2;Ormdl1

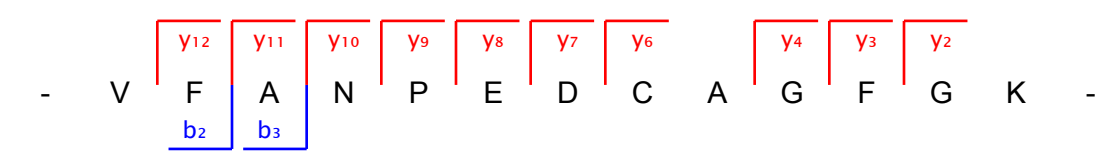
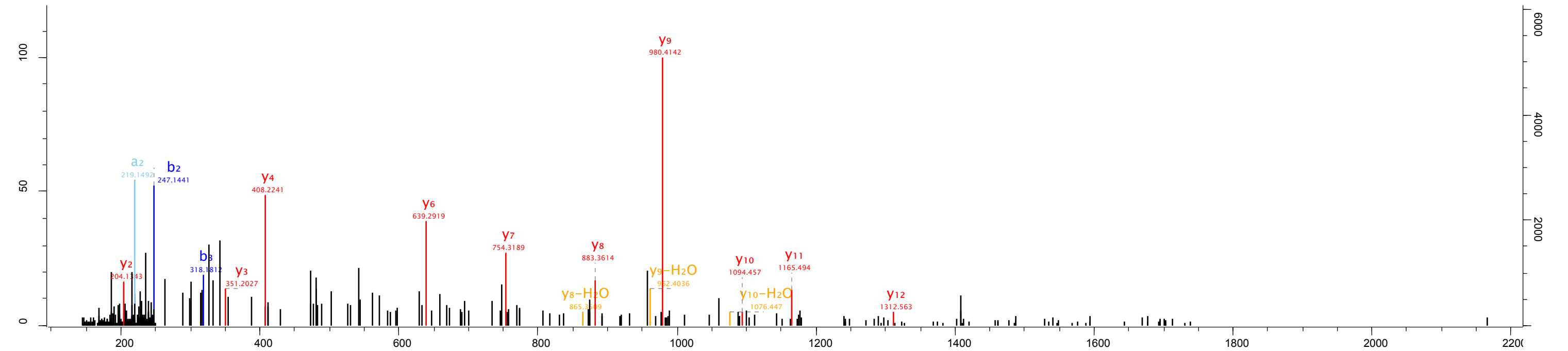


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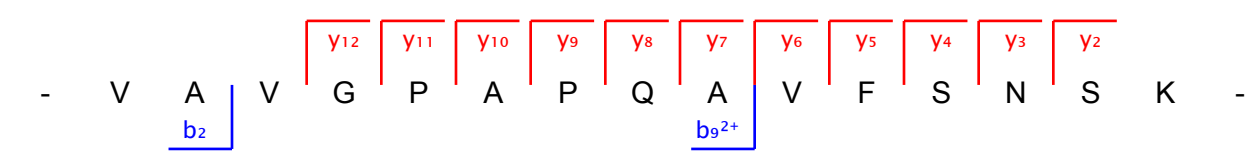
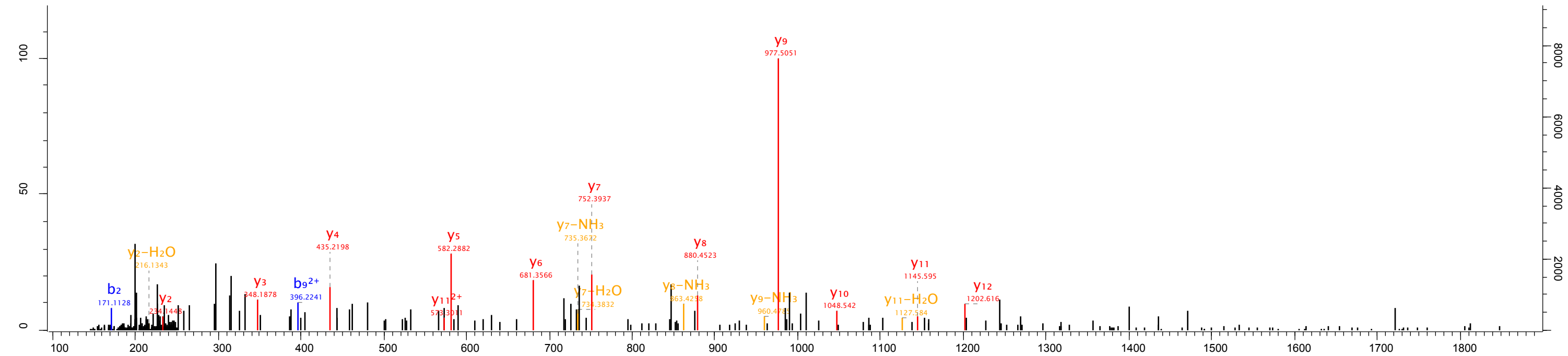
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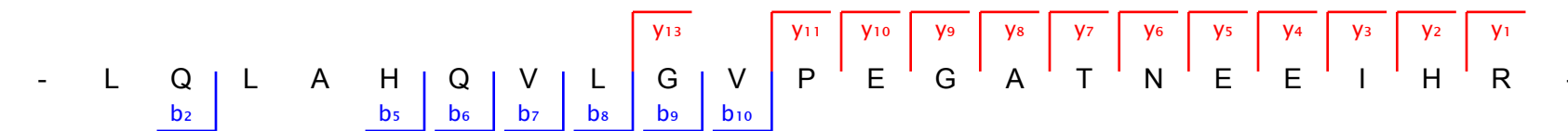
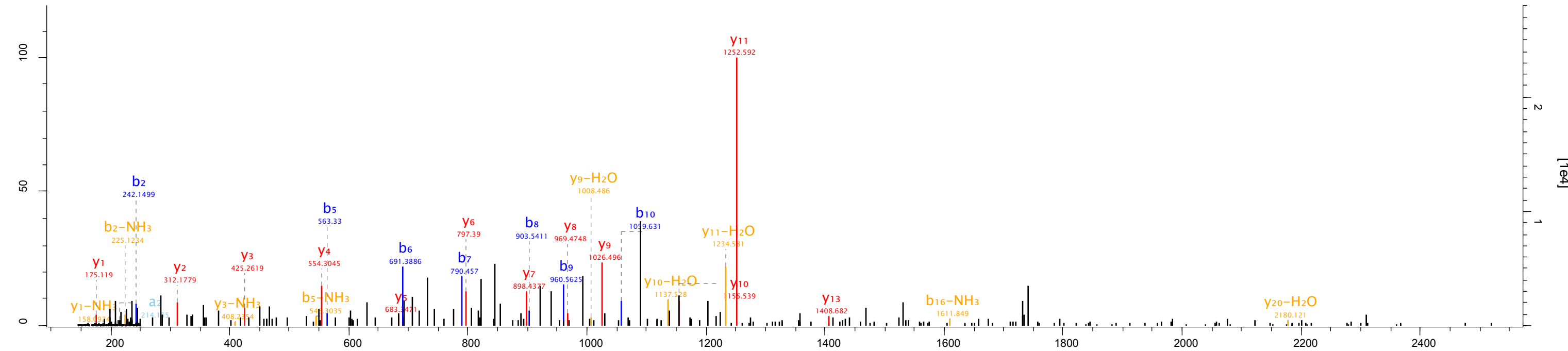


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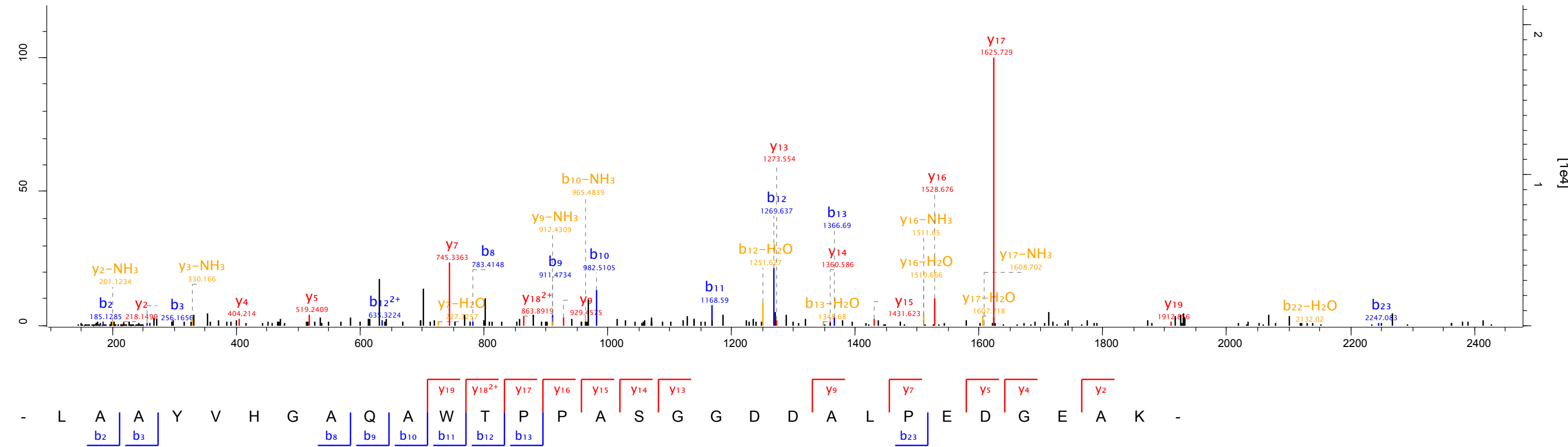


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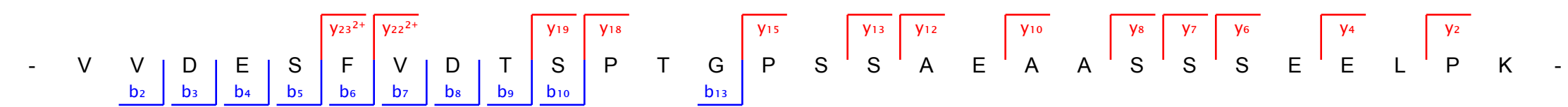
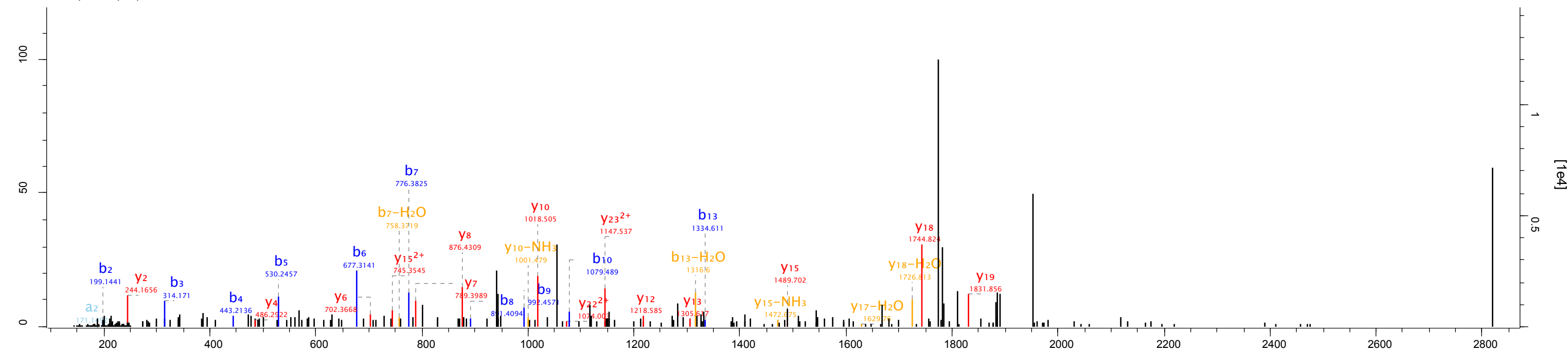




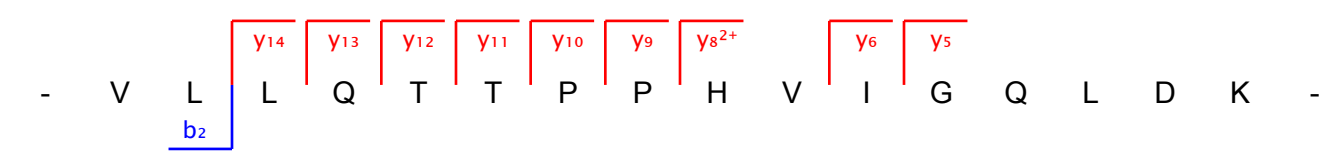
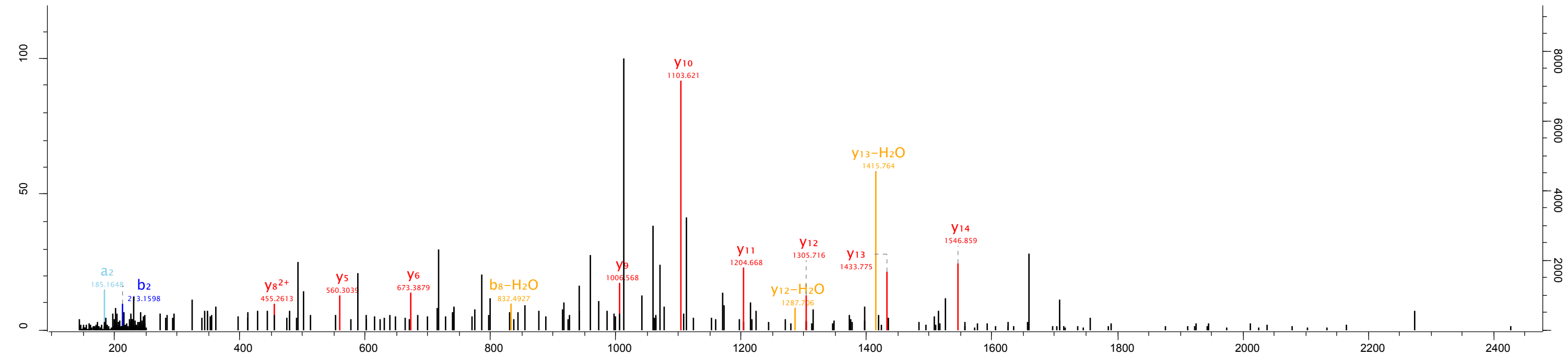
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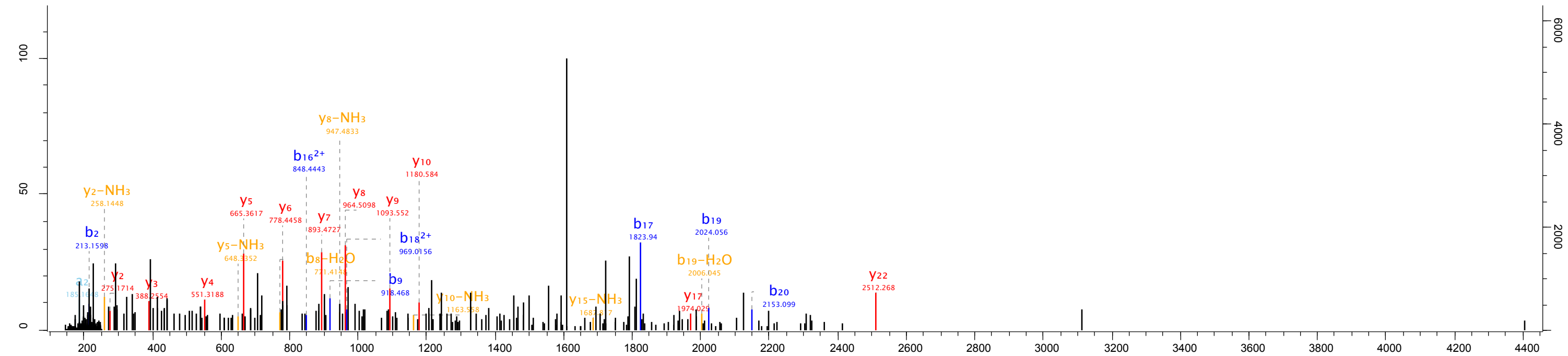
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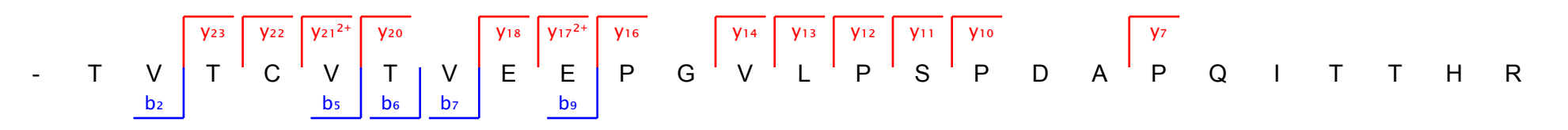
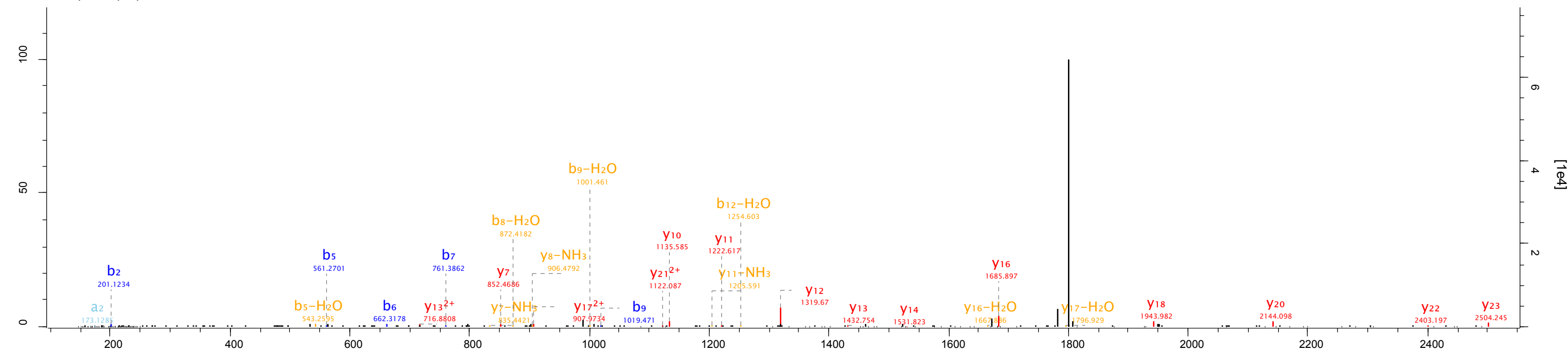


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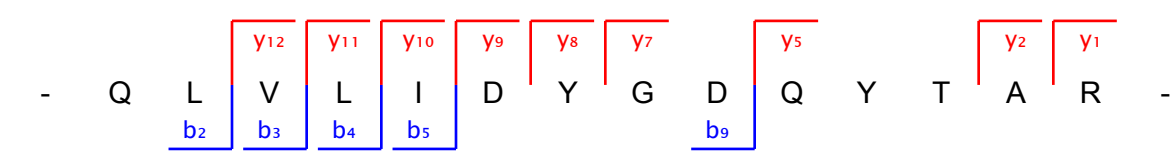
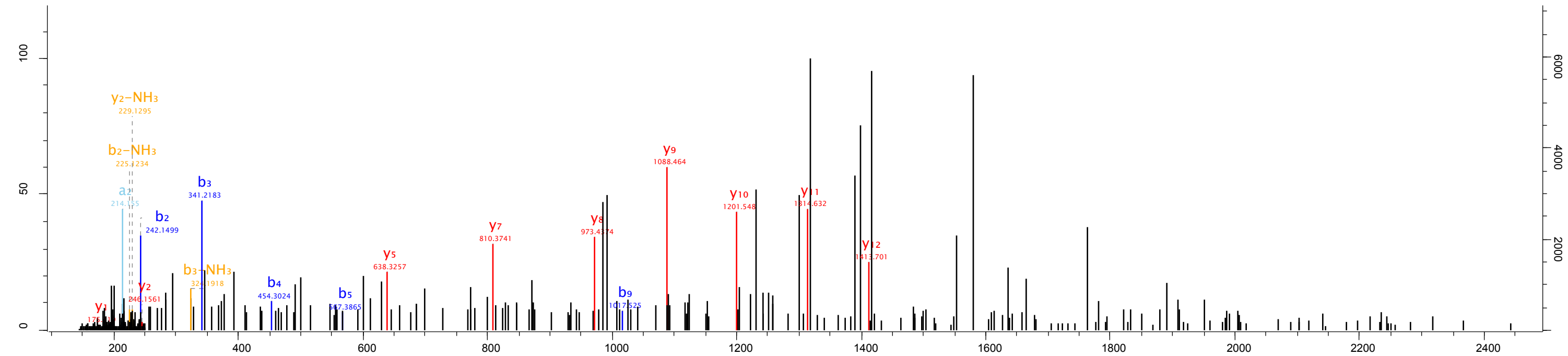


Raw file
20150307_Hepa2_Top_opt_D2_01_1673

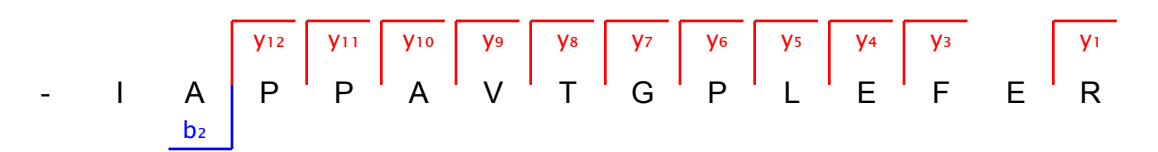
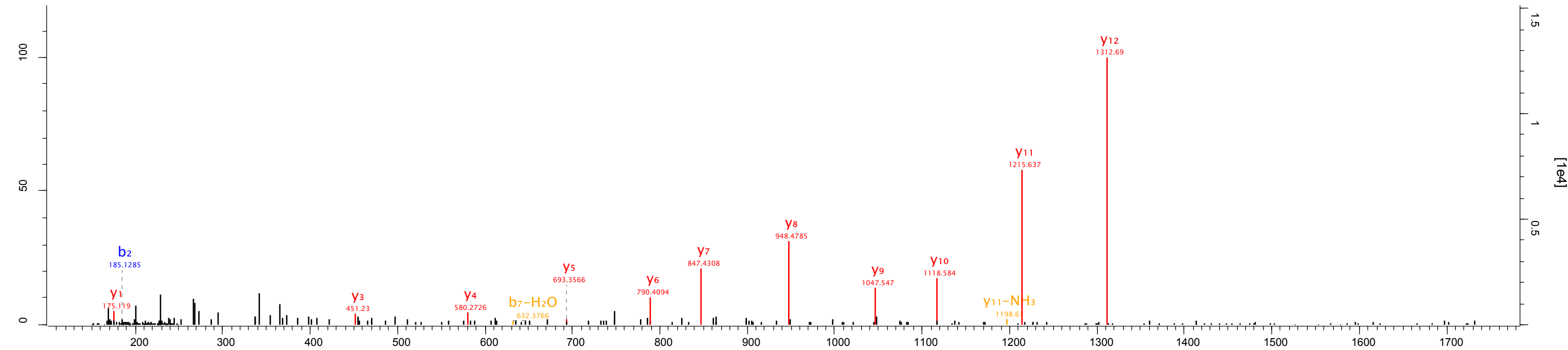
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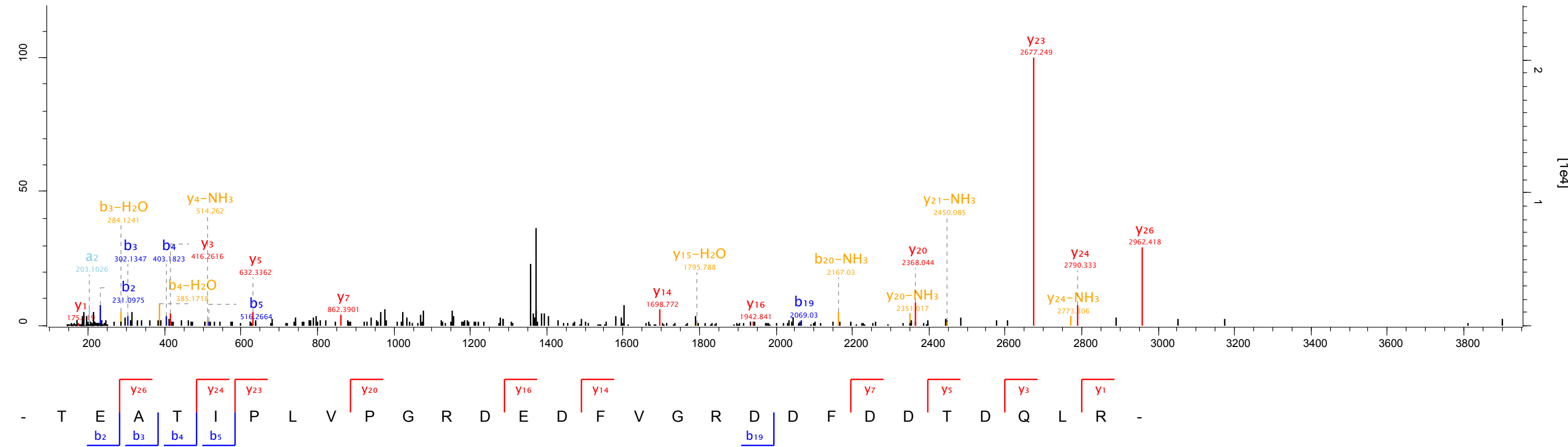


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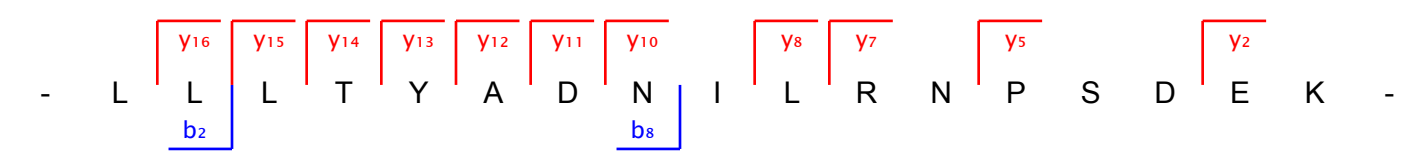
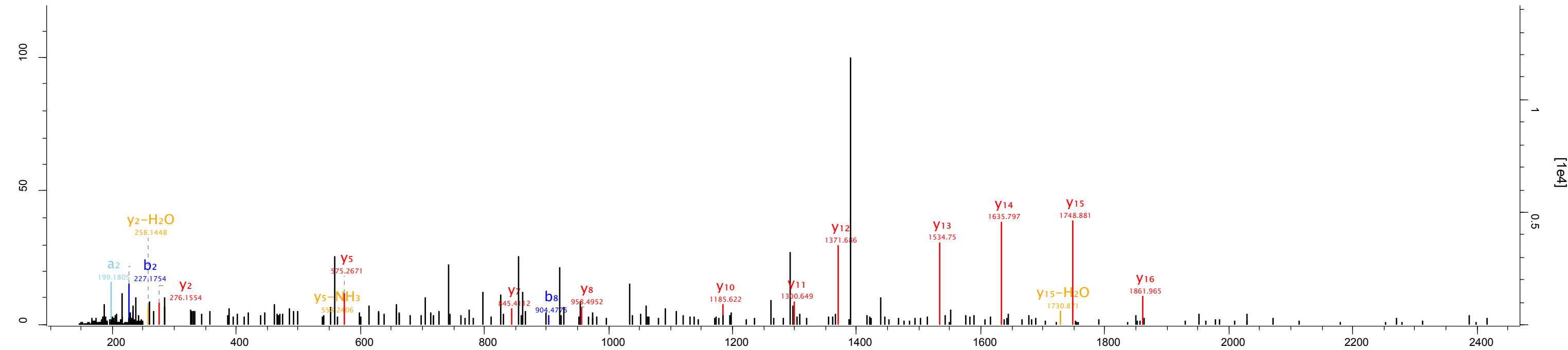


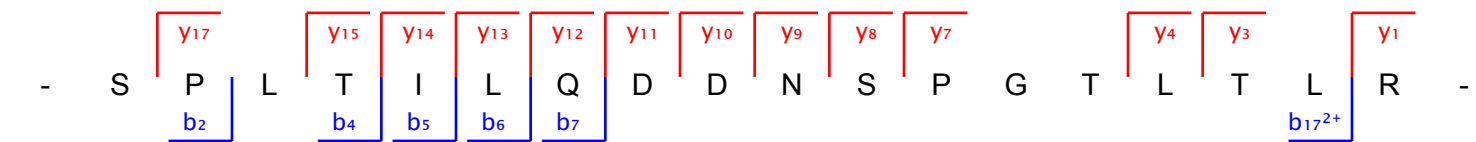
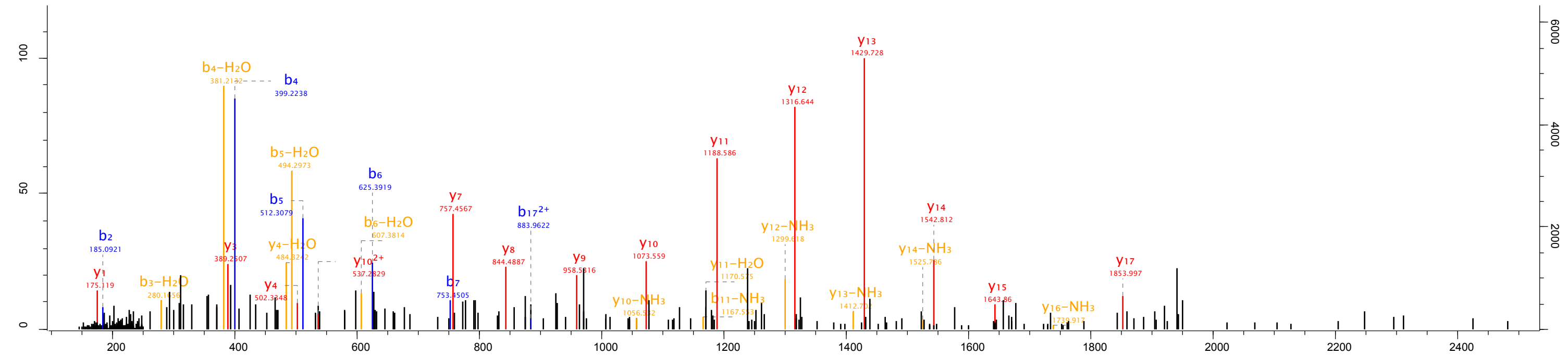
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20150307_Hepa2_Top_opt_D2_01_1673

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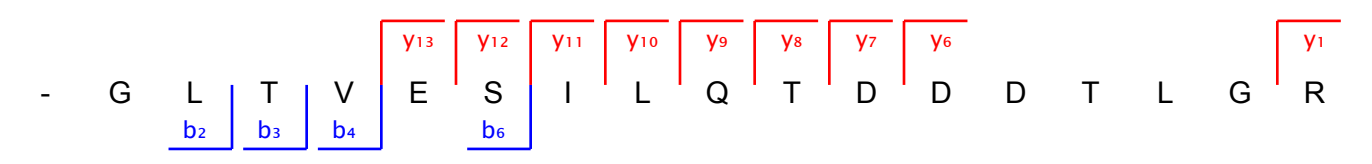
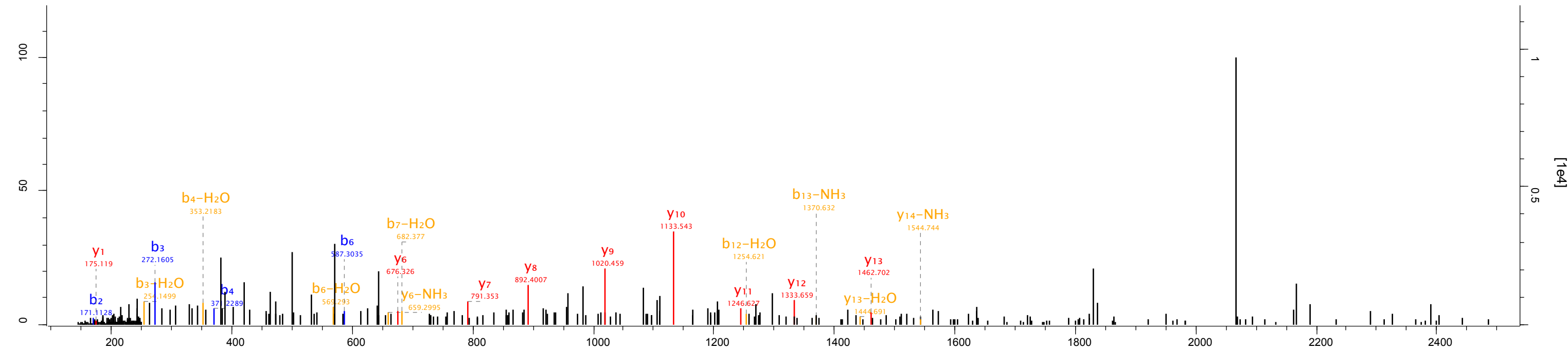


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 Scan: 54029 Method: TOF; CID Score: 56.12 m/z: 659.35 Gene names: Ngly1

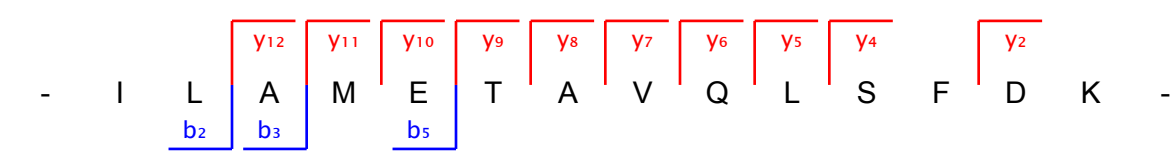
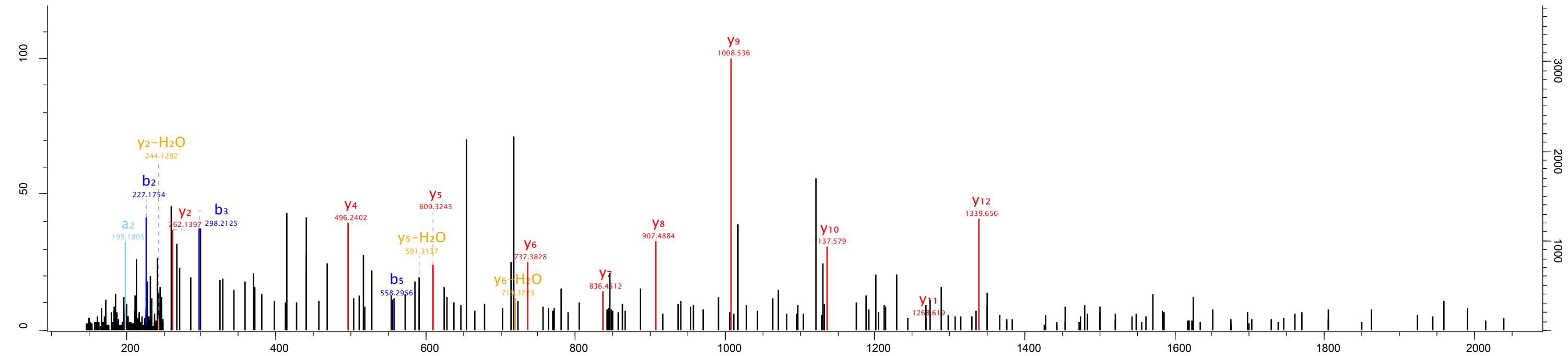




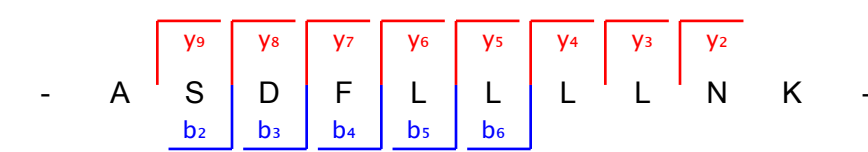
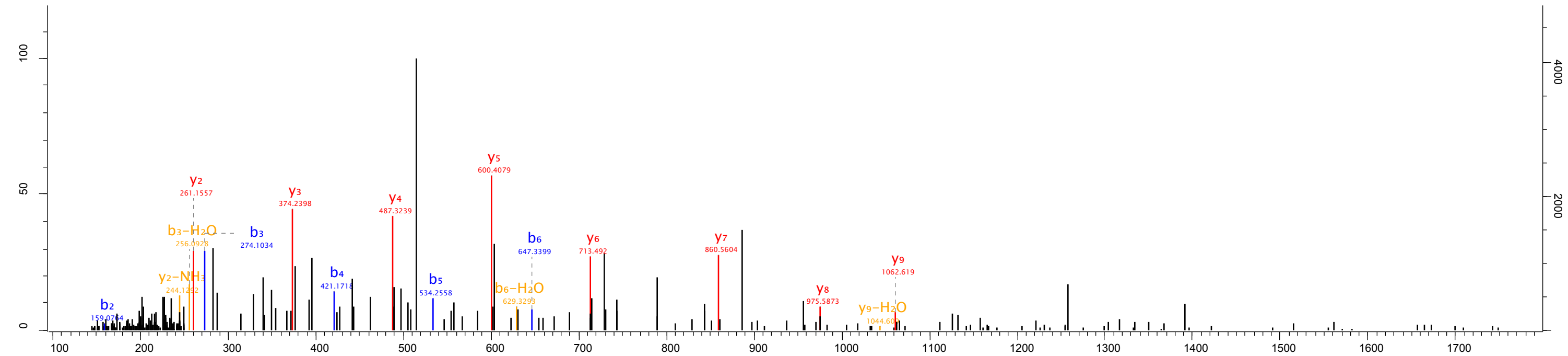
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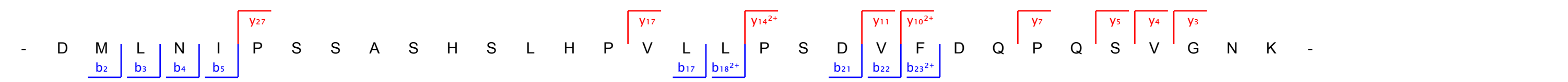
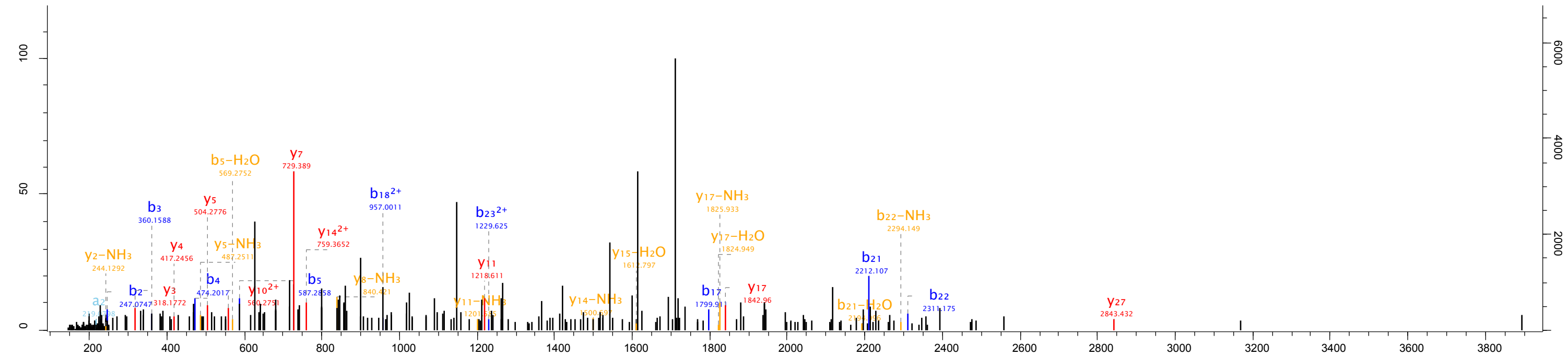
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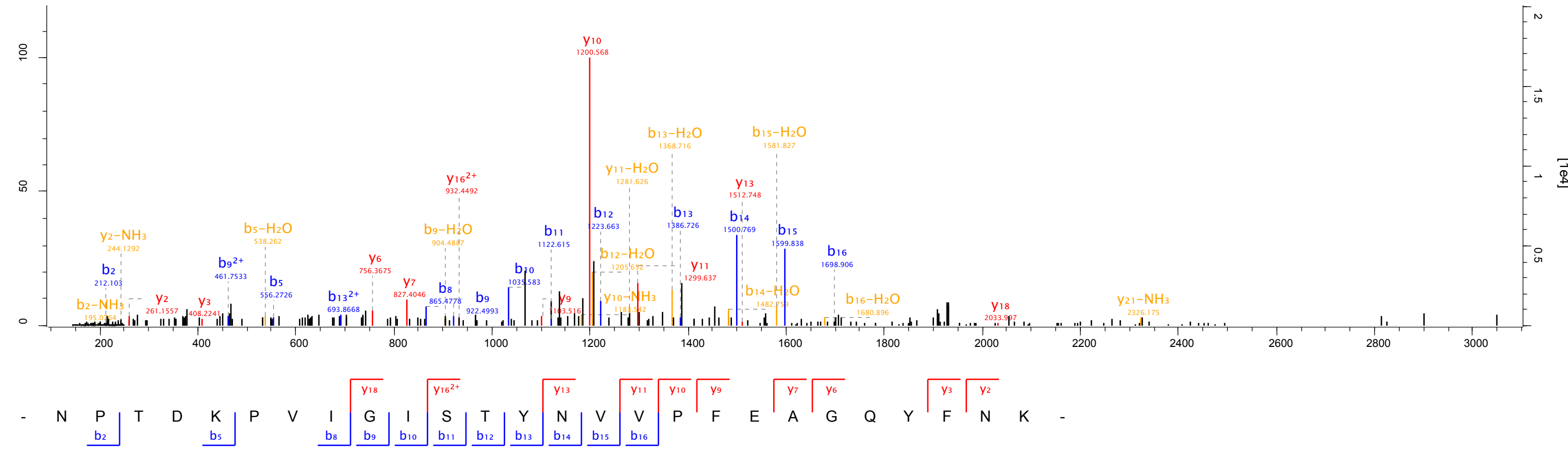
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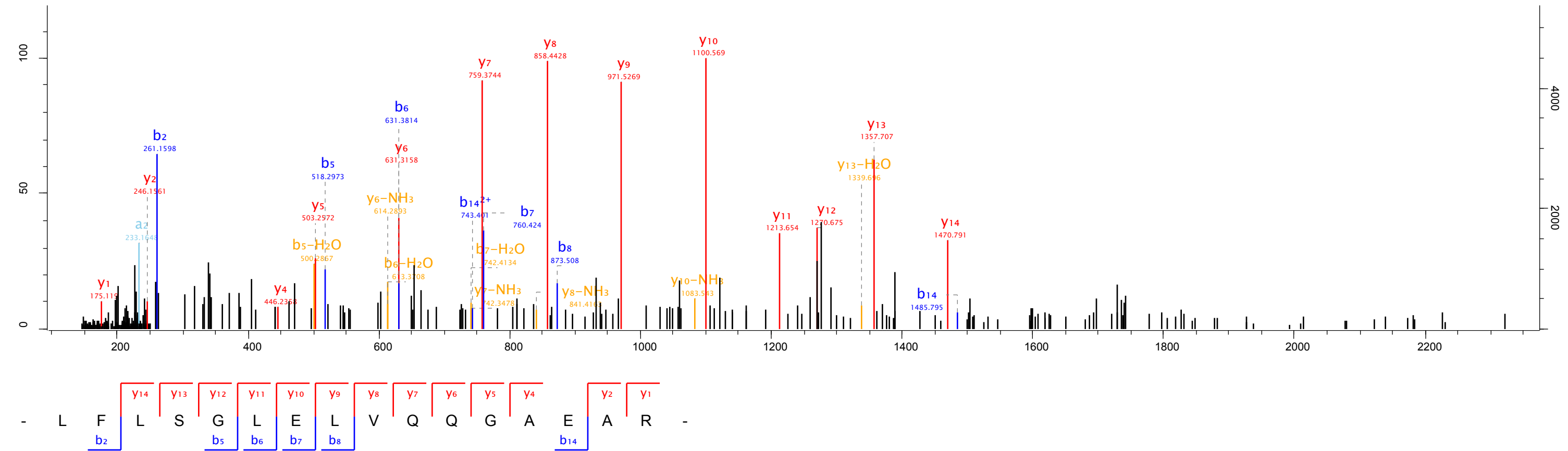


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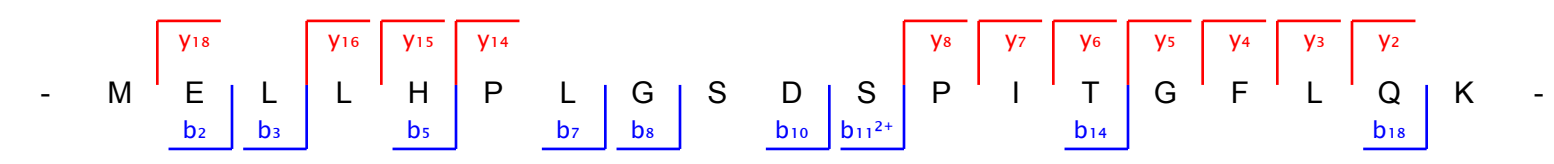
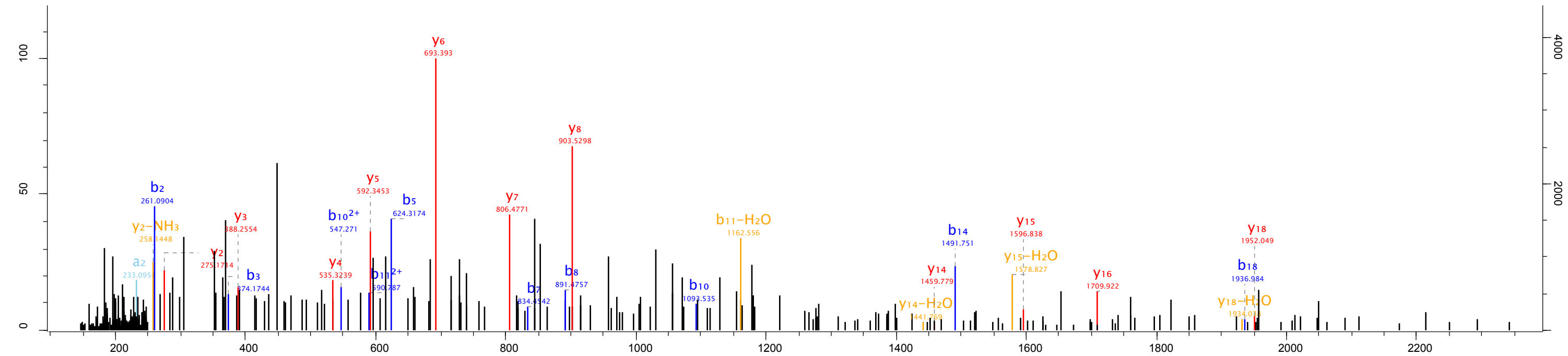


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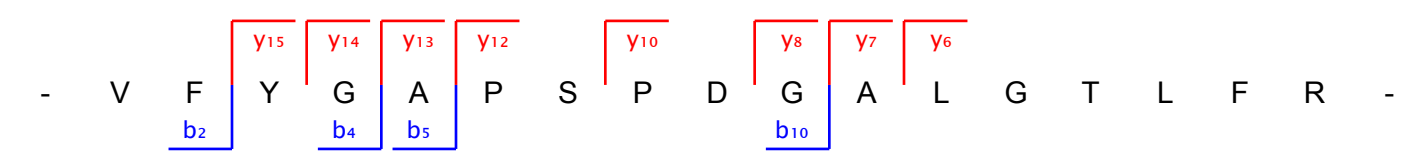
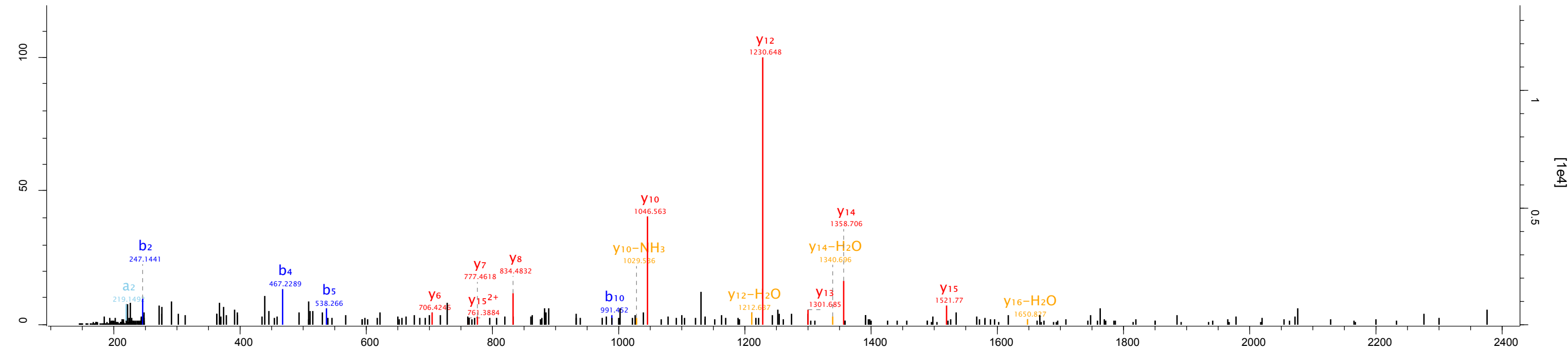


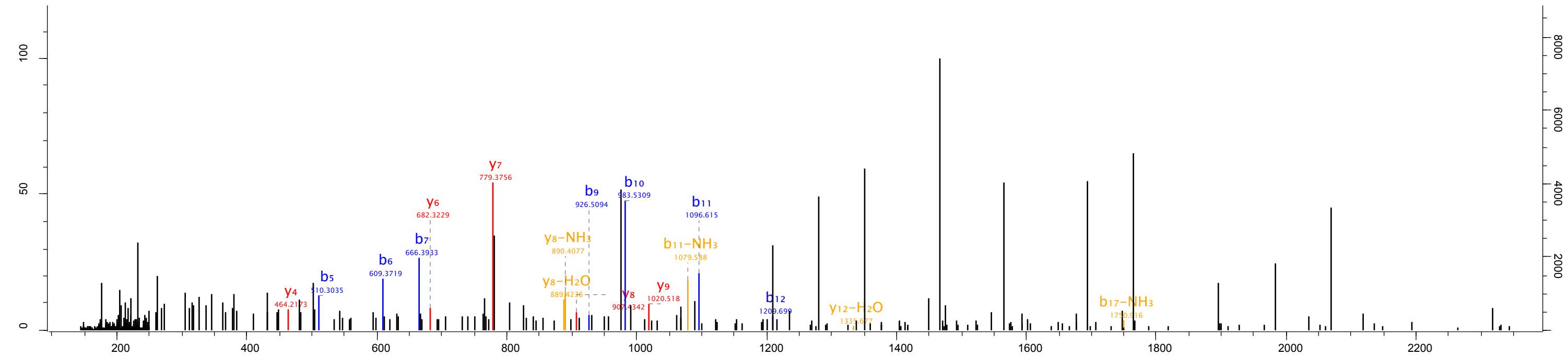


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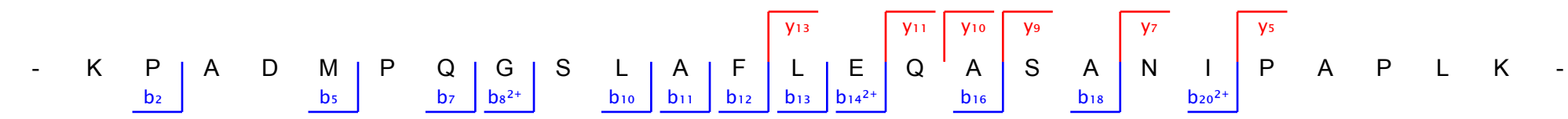
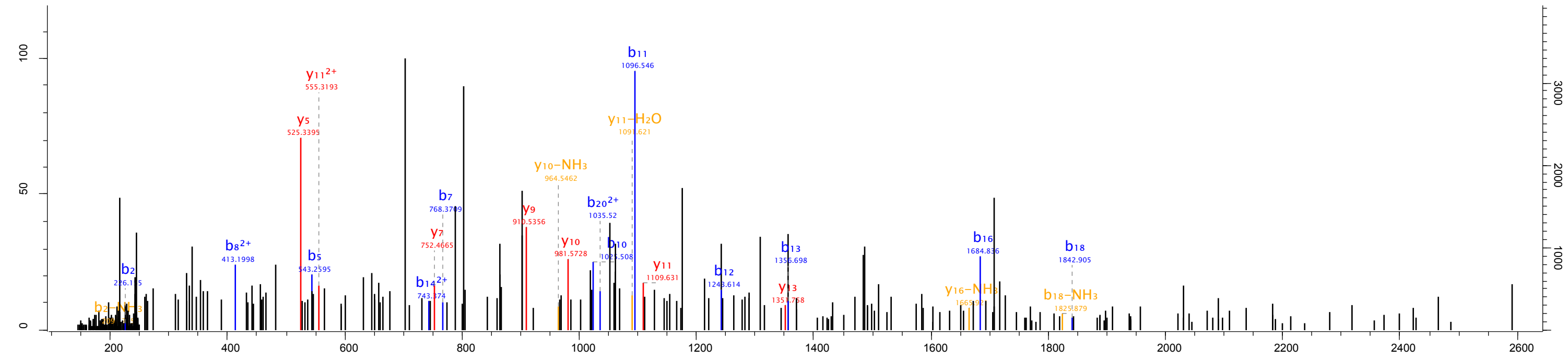


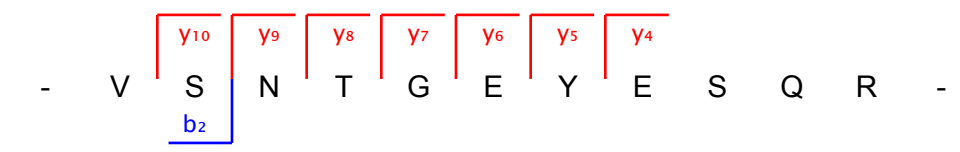
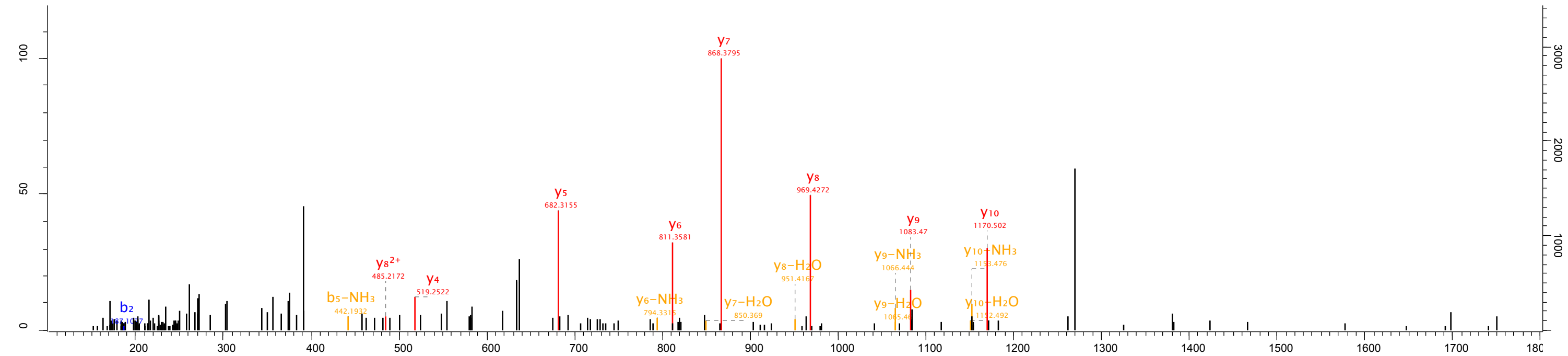
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Fragmentation sites are indicated by brackets below the sequence:

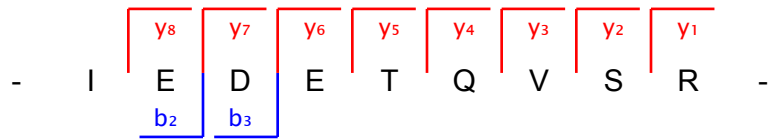
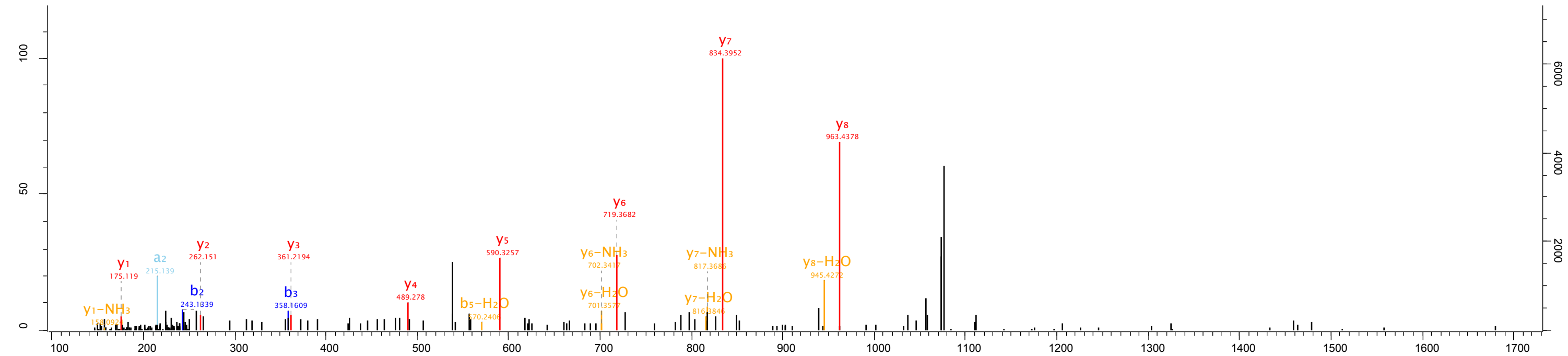
- Blue brackets (b-series): I-V, V-G, G-P, Y-G, G-I, I-L, L-Q, Q-P, P-F, F-A, A-D, D-A, A-M, M-K.
- Red brackets (y-series): I-L, L-Q, Q-P, P-F, F-A, A-D.

Raw file 20150307_Hepa2_Top_opt_D2_01_1673 Scan 67886 Method TOF; CID Score 37.53 m/z 865.45 Gene names Med28



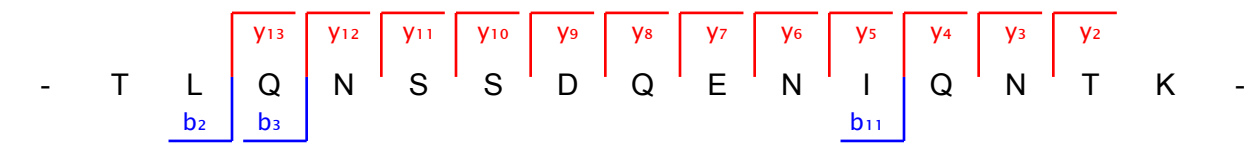
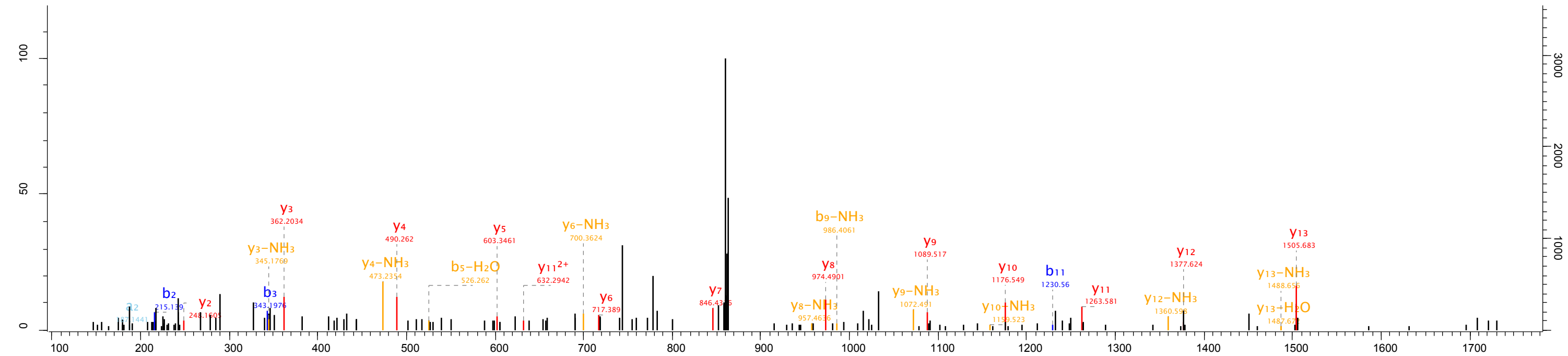


Raw file 20150307_Hepa2_Top_opt_D2_01_1686 Scan 10335 Method TOF; CID Score 86.9 m/z 538.76 Gene names Med22

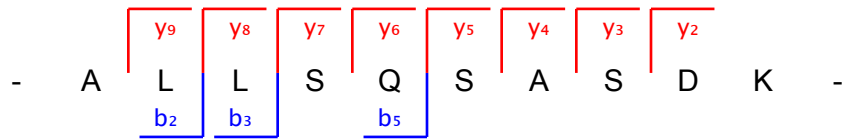
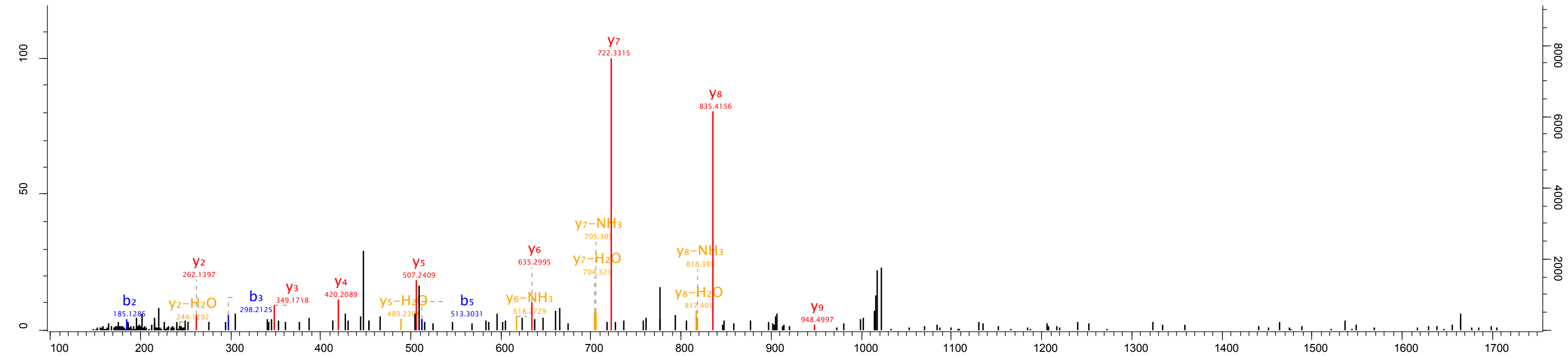


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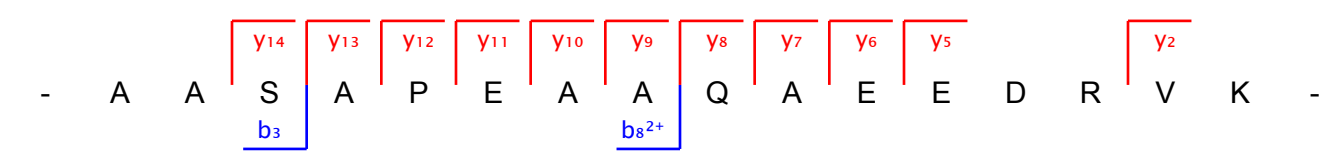
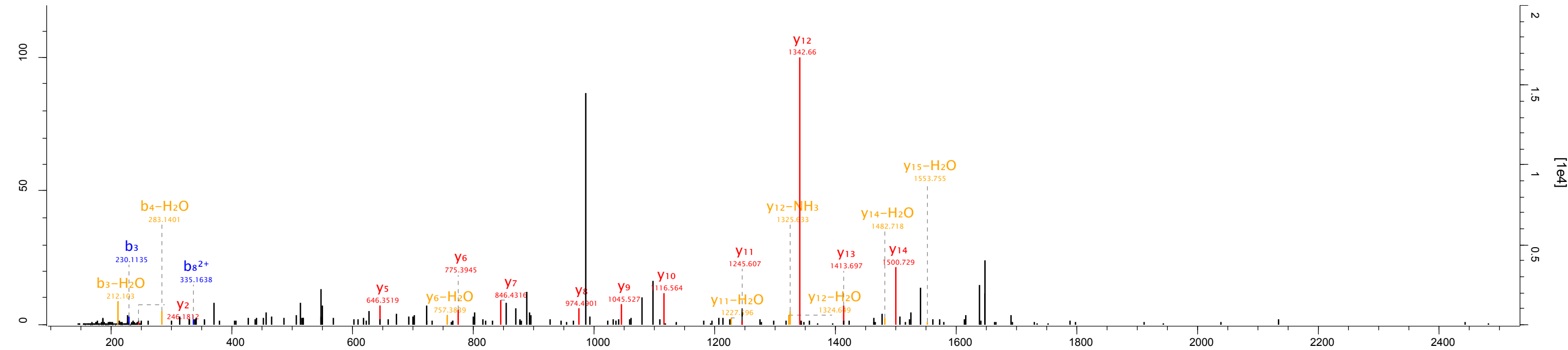
Scan 13137 Method TOF; CID Score 76.34 m/z 860.41 Gene names Sgol2



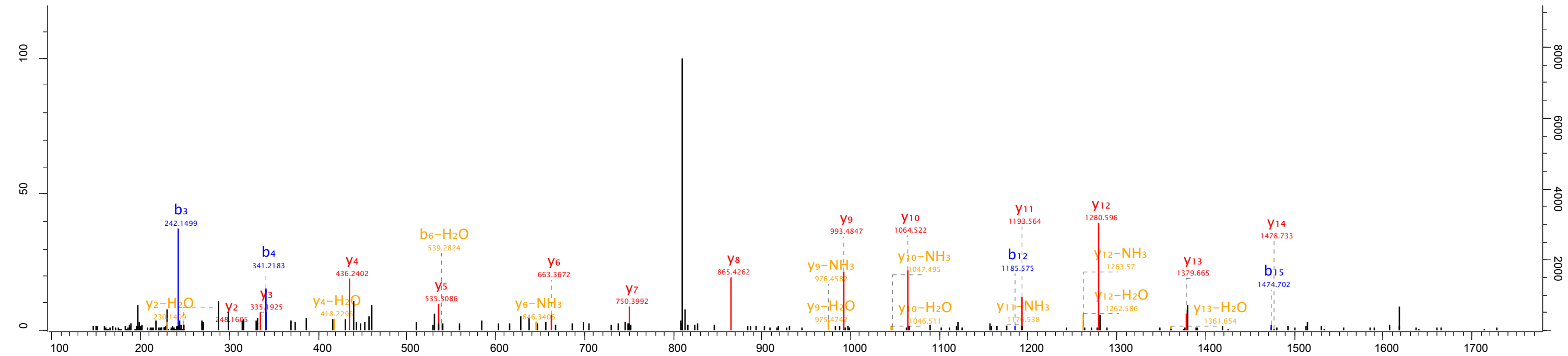
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Raw file 20150307_Hepa2_Top_opt_D2_01_1686 Scan 17330 Method TOF; CID Score 68.48 m/z 548.27 Gene names Tdp2



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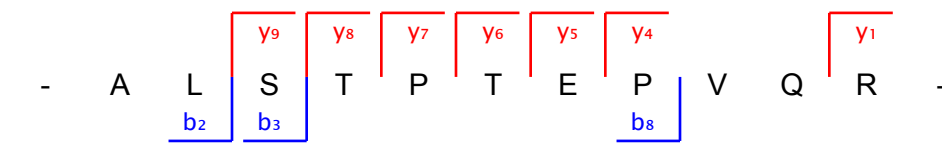
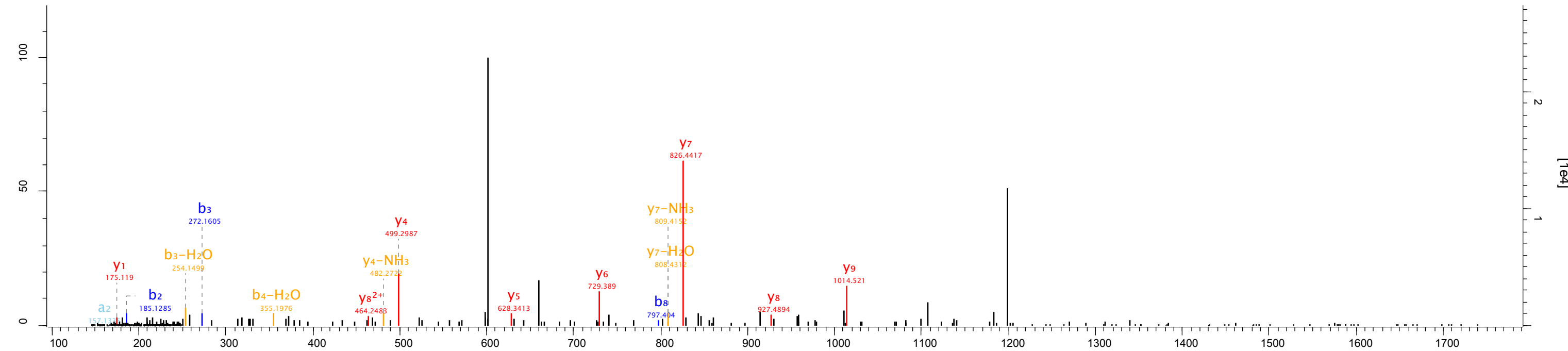


- A A V V S E A Q D S Q V T S T K -

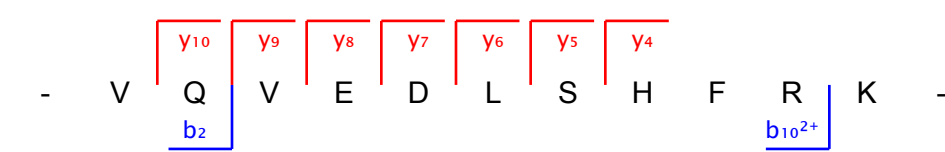
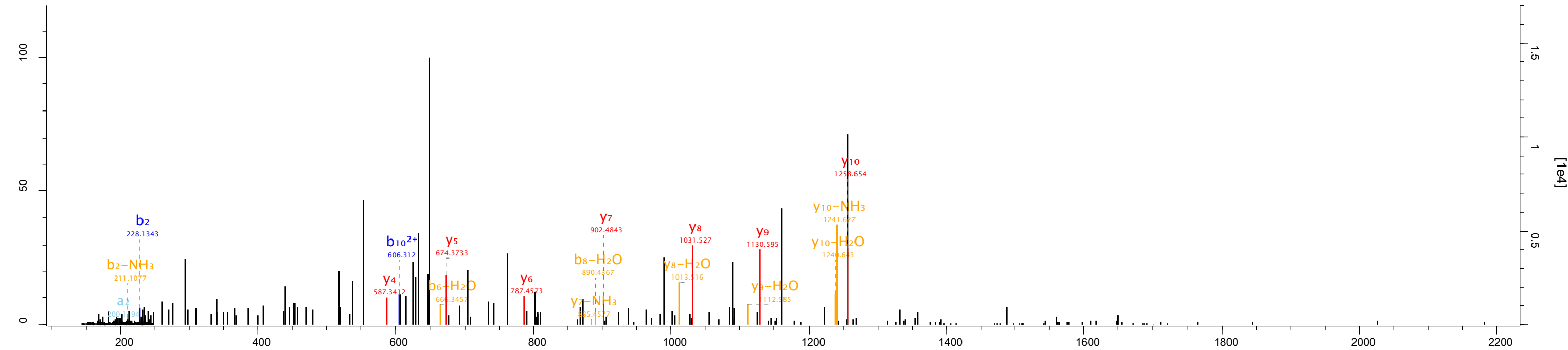
b₃ b₄ b₁₂ b₁₅

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

Raw file 20150307_Hepa2_Top_opt_D2_01_1686 Scan 21715 Method TOF; CID Score 79.66 m/z 599.82 Gene names Psmb10

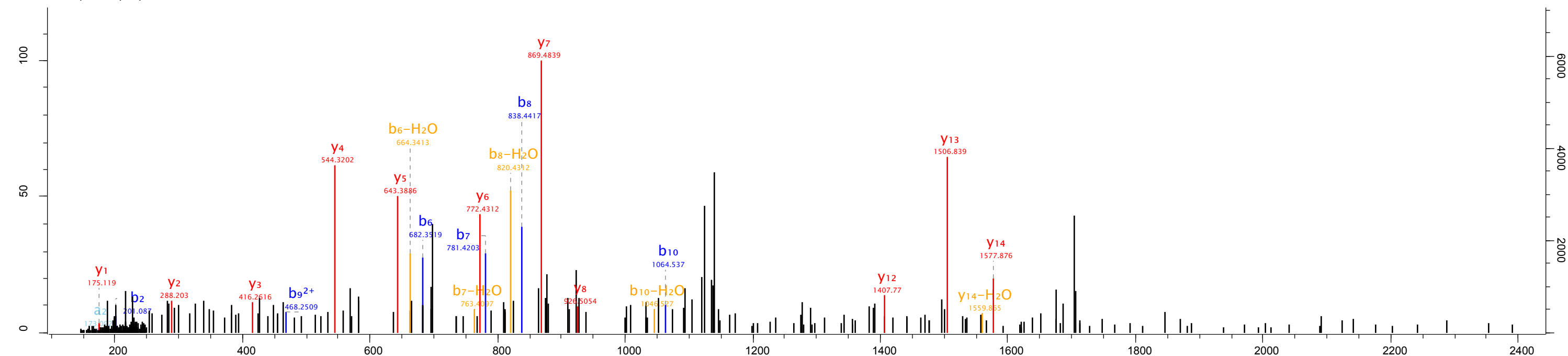


Raw file 20150307_Hepa2_Top_opt_D2_01_1686 Scan 26563 Method TOF; CID Score 60.26 m/z 453.24 Gene names Nsun4



Raw file
20150307_Hepa2_Top_opt_D2_01_1686

Scan Method Score m/z Gene names
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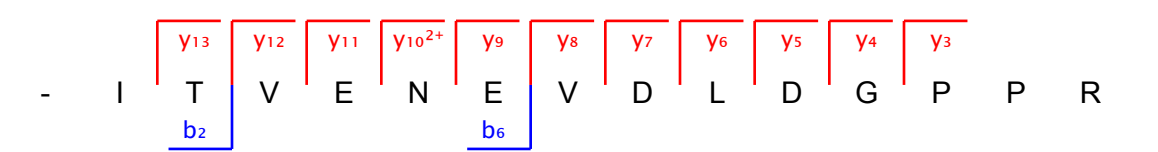
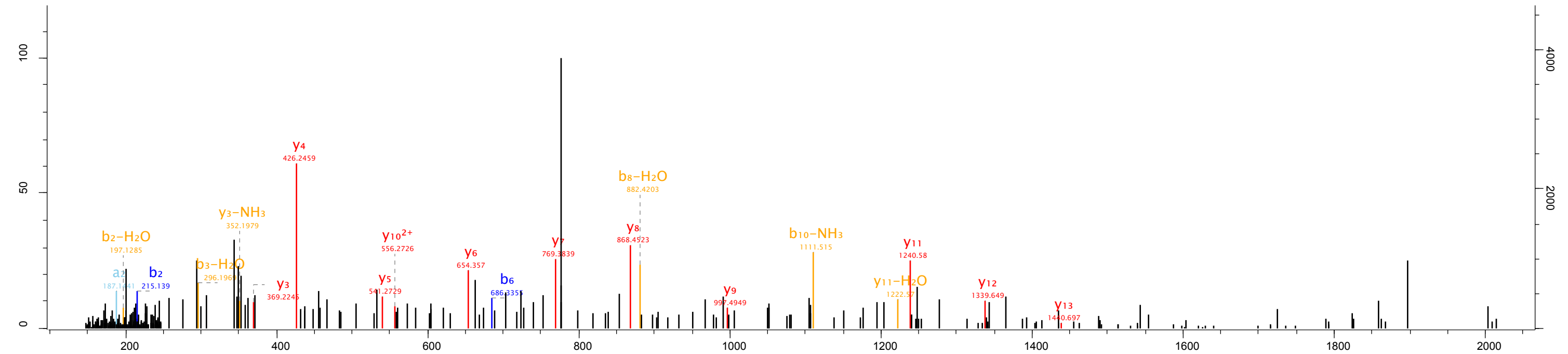


- E A V R P E V G P E V Q Q L R -

Fragmentation mapping (b and y ions):

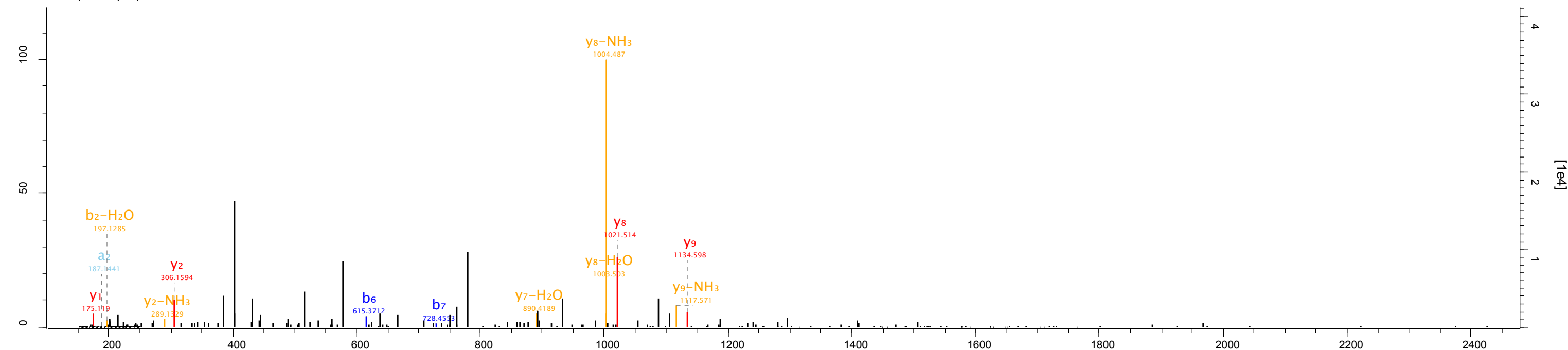
- Red boxes (y ions): y14 (A-V), y13 (V-R), y12 (R), y8 (G-P), y7 (P-E), y6 (E-V), y5 (V-Q), y4 (Q-Q), y3 (Q-L), y2 (L-R), y1 (R)
- Blue boxes (b ions): b2 (A), b6 (E-V), b7 (V-G), b8 (G-P), b9²⁺ (P-E), b10 (E-V)

Raw file 20150307_Hepa2_Top_opt_D2_01_1686 Scan 39518 Method TOF; CID Score 50.3 m/z 777.39 Gene names Suv39h1



Raw file
20150307_Hepa2_Top_opt_D2_01_1686

Scan 40103 Method TOF; CID Score 43.03 m/z 438.74 Gene names Grik5

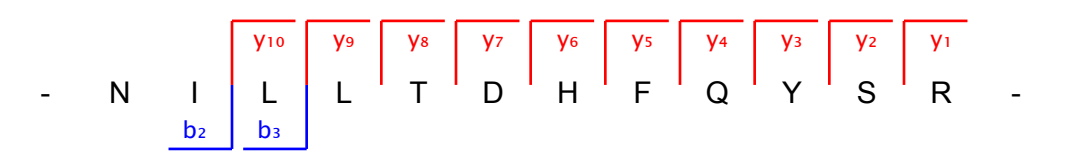
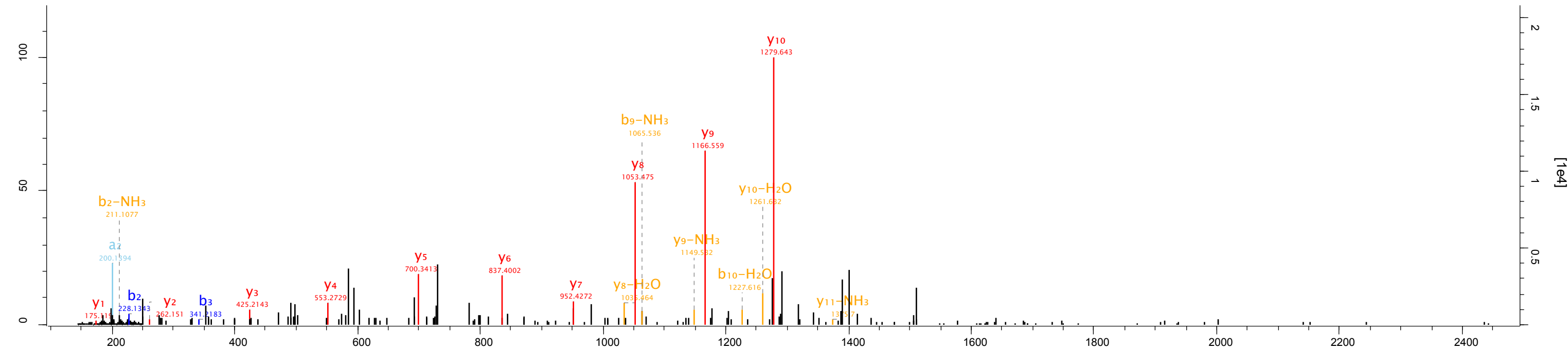


- T L V V T T I L E N P Y V M R -

Fragmentation mapping:
- a_2 (L)
- b_6 (T) - b_7 (I)
- y_9 (I) - y_8 (L)
- y_2 (M) - y_1 (R)

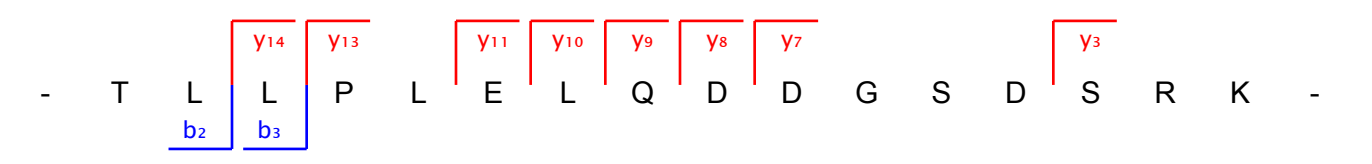
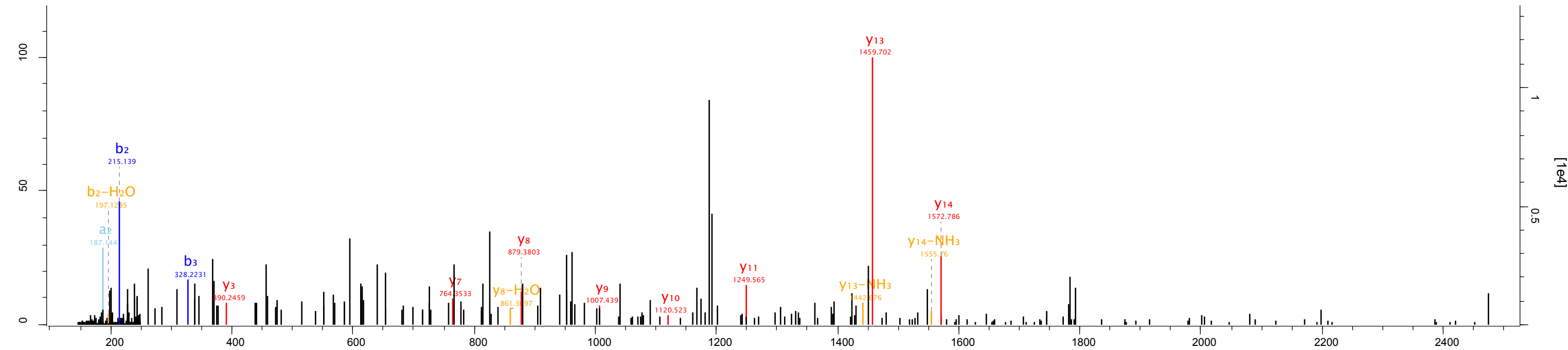
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Scan 42293 Method TOF; CID Score 66.99 m/z 503.26 Gene names Slc35e1

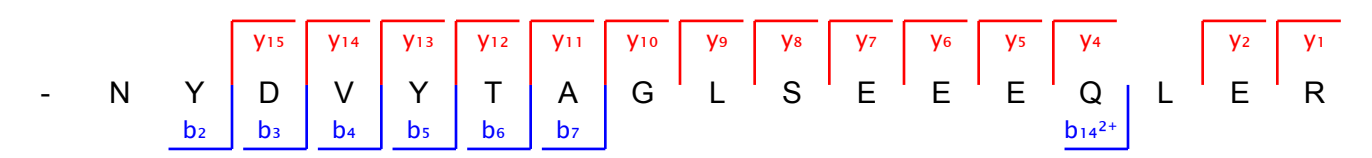
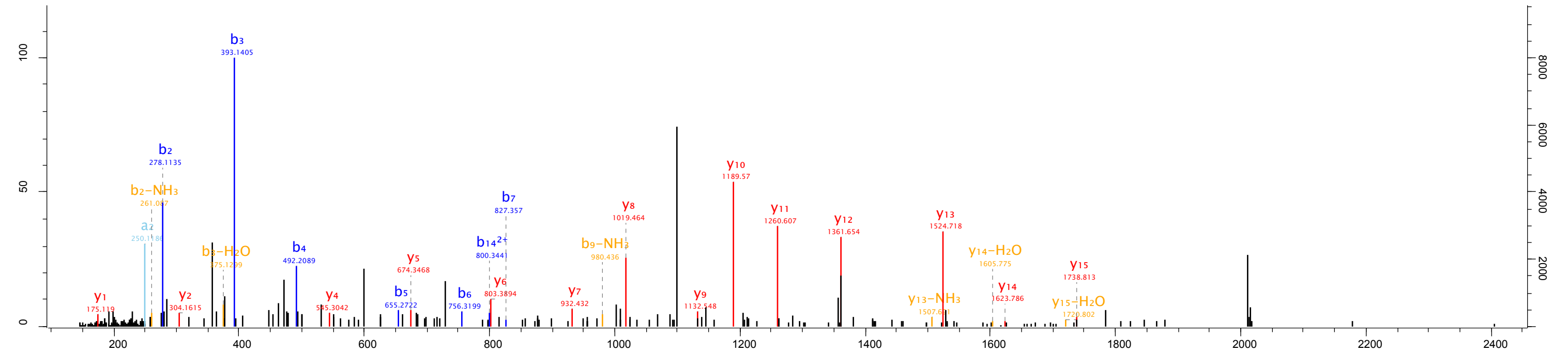


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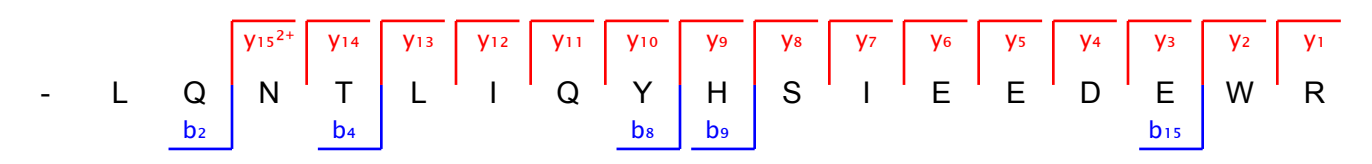
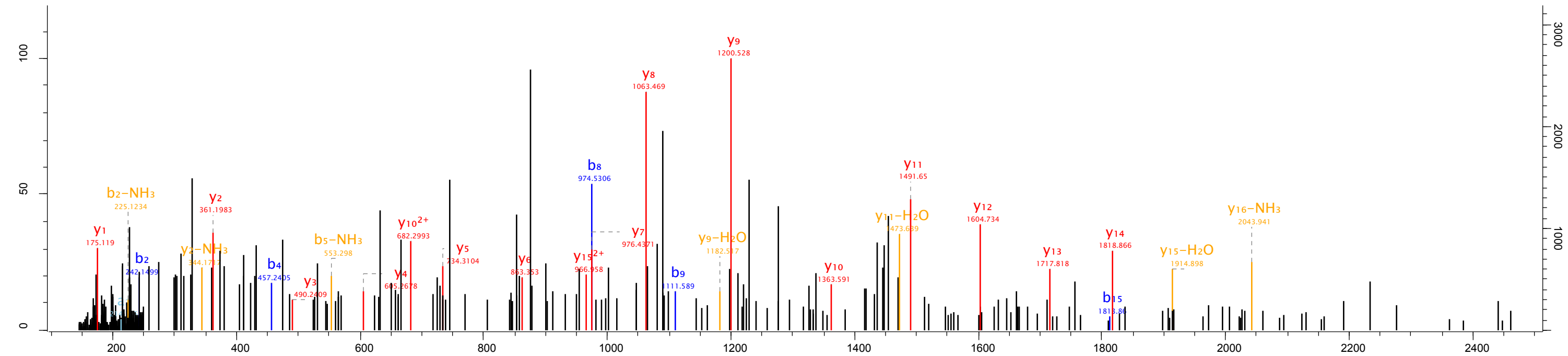
Scan 47373 Method TOF; CID Score 48.22 m/z 596.31 Gene names Vps72



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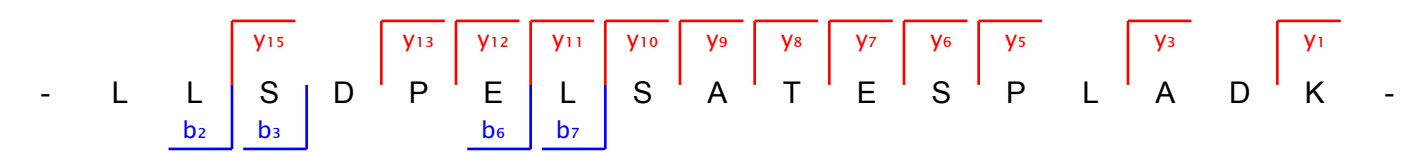
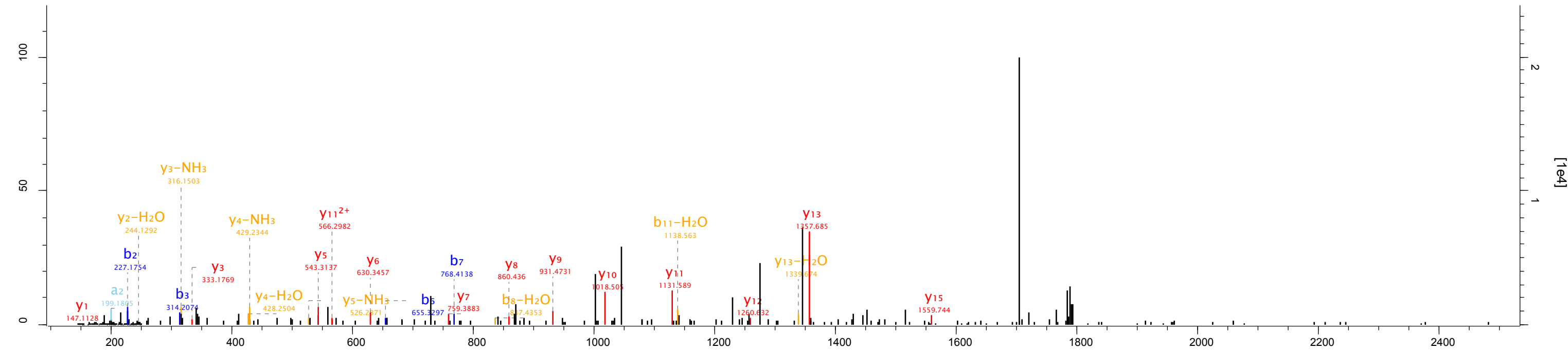


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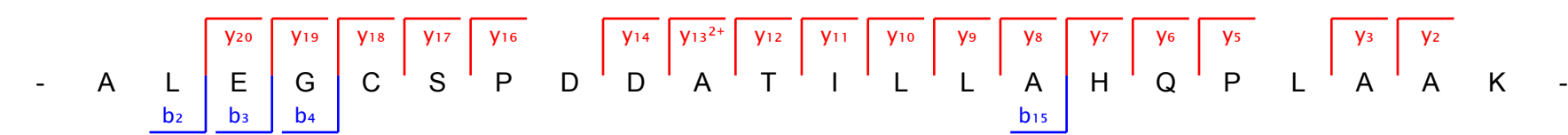
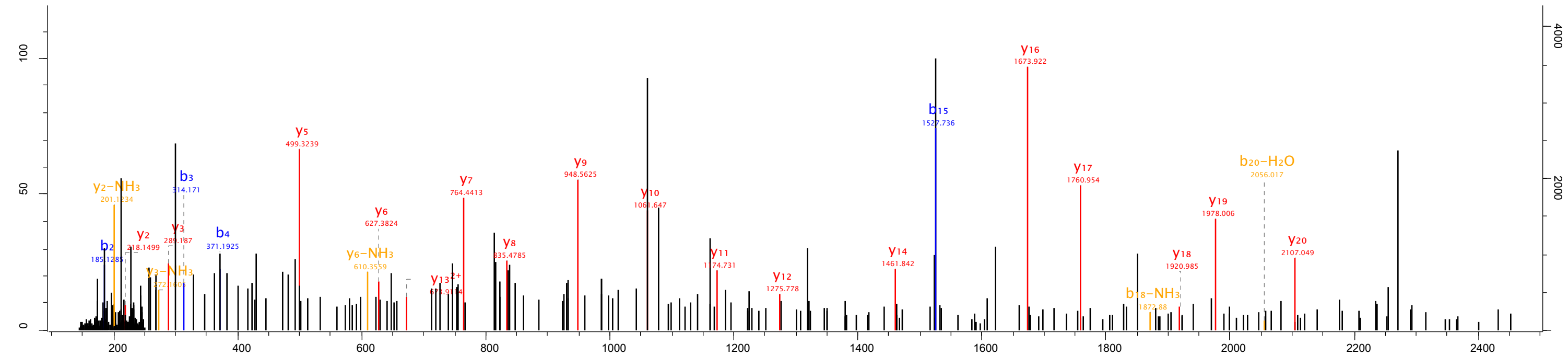


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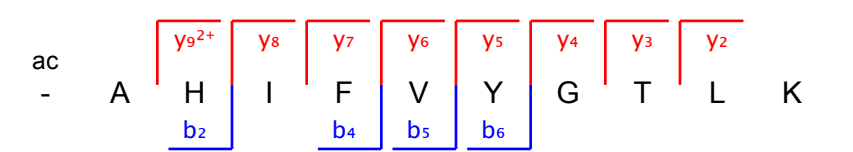
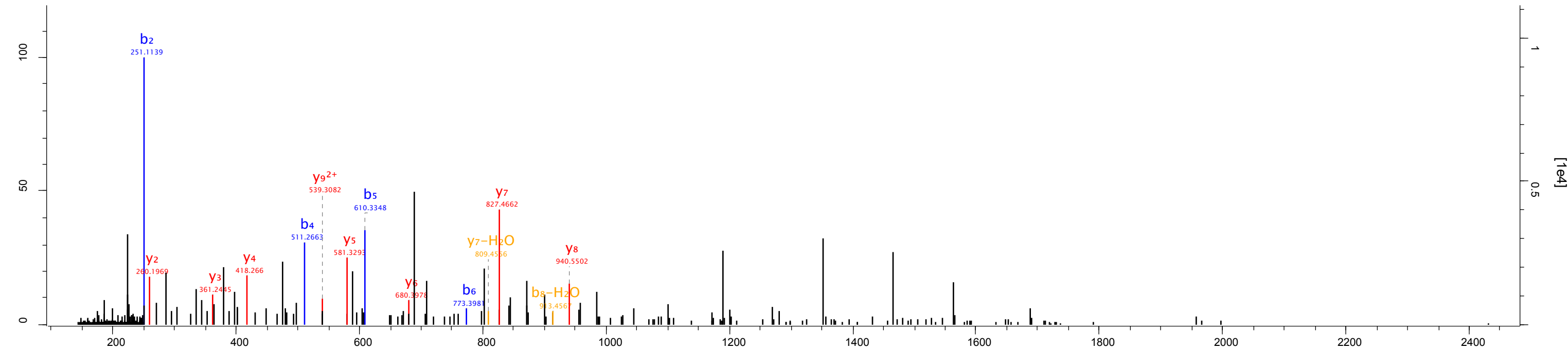
Scan 47804 Method TOF; CID Score 77.51 m/z 894.46 Gene names Biccl1

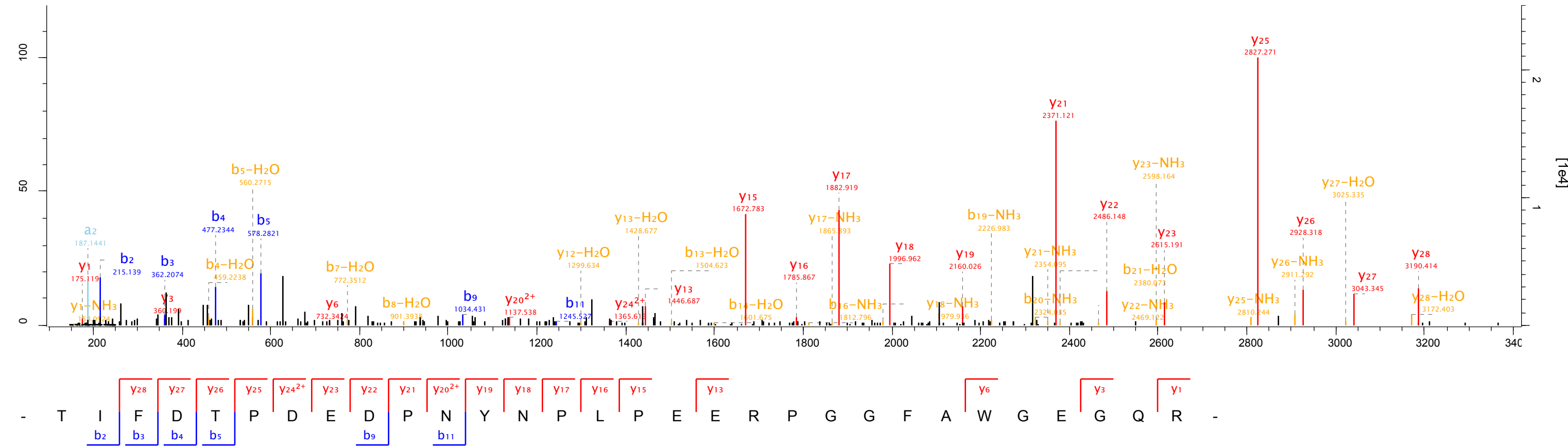


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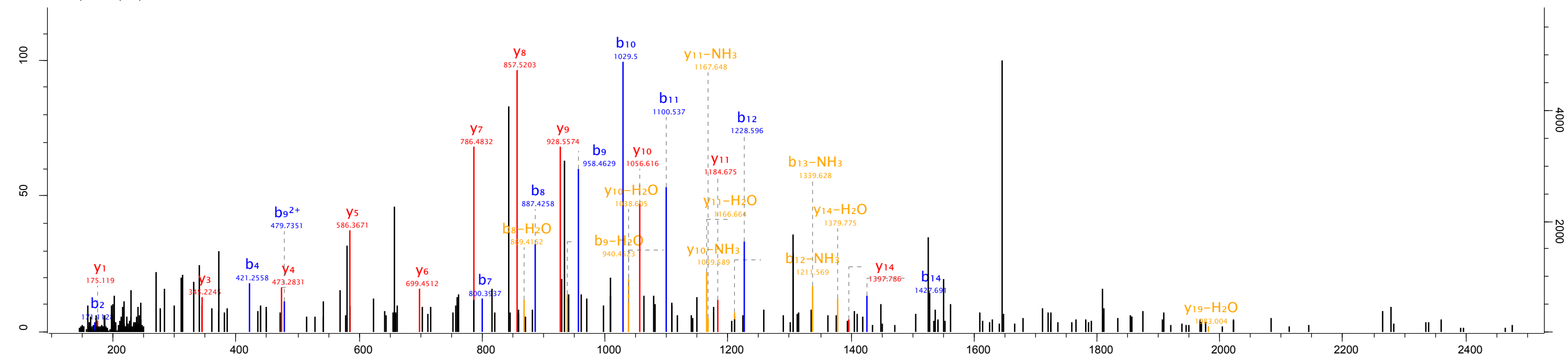
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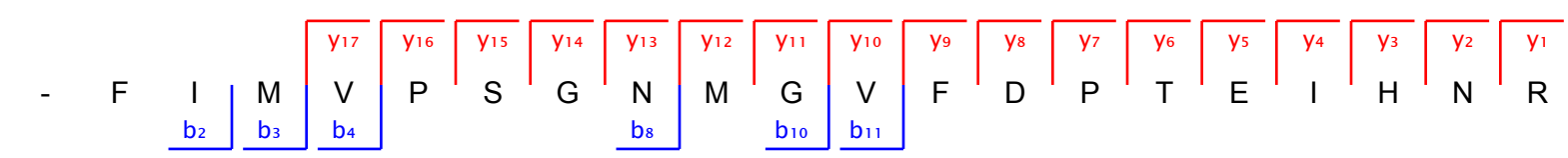
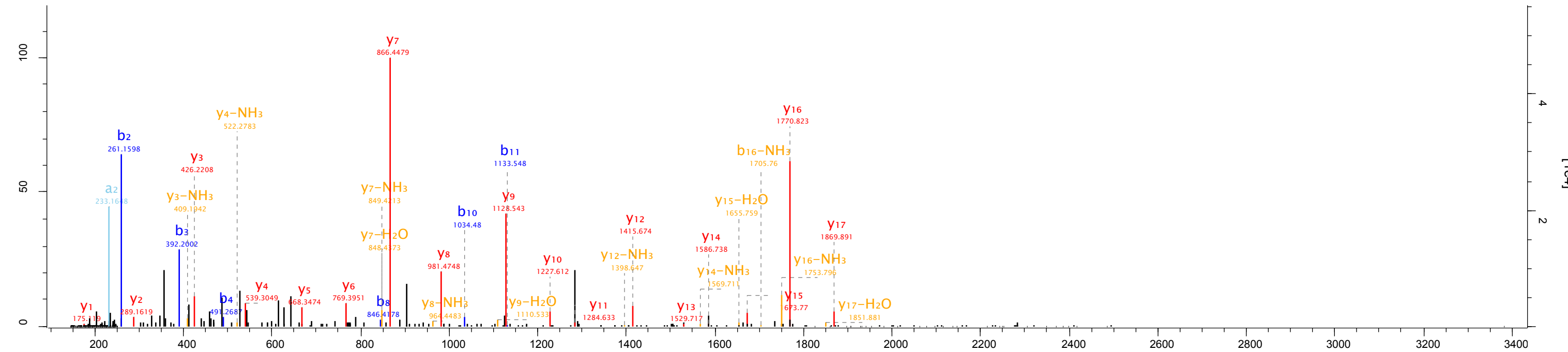
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Scan 61589 Method TOF; CID Score 77.47 m/z 762.4 Gene names Mthfsd



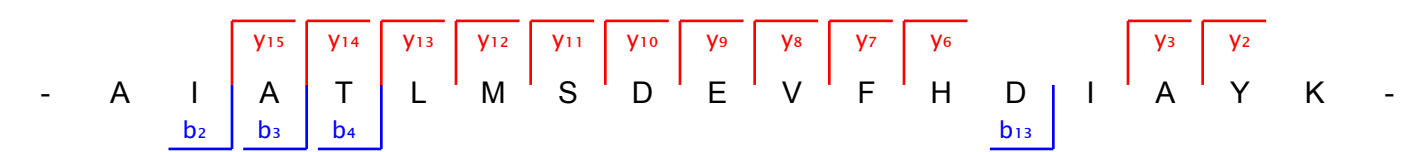
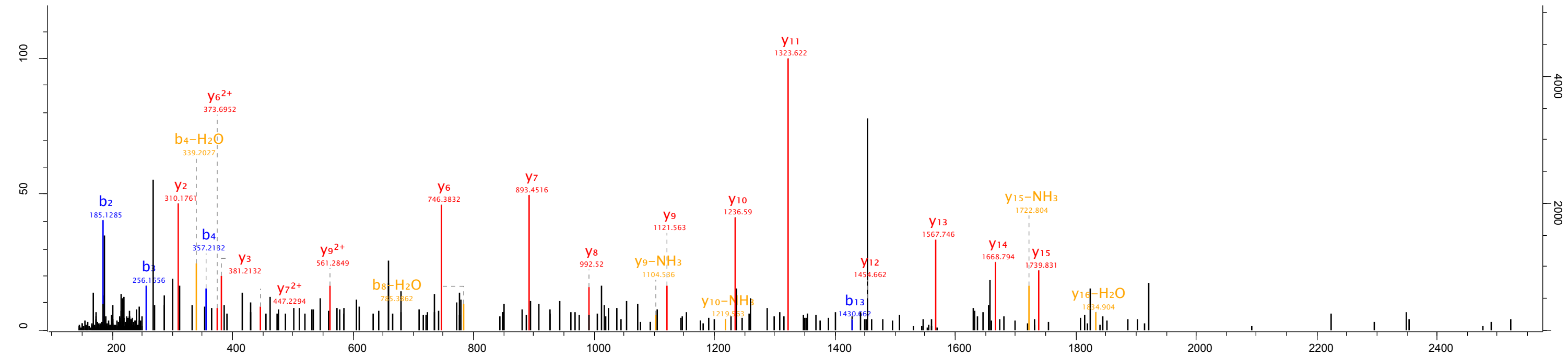
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 y₁₄ **y₁₁** **y₁₀** **y₉** **y₈** **y₇** **y₆** **y₅** **y₄** **y₃** **y₁**

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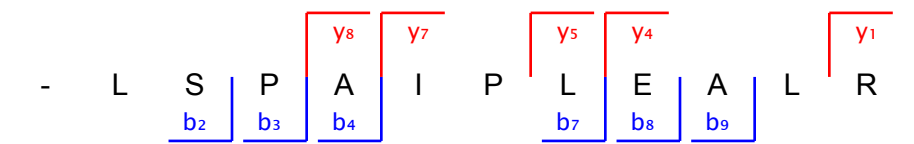
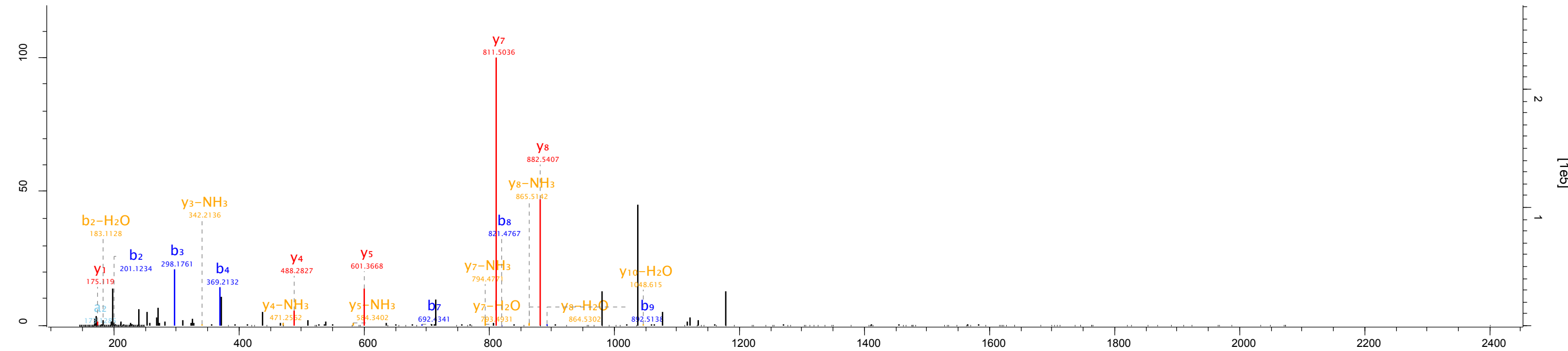


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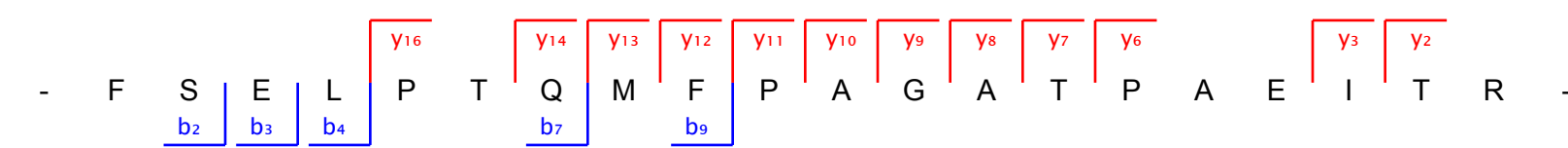
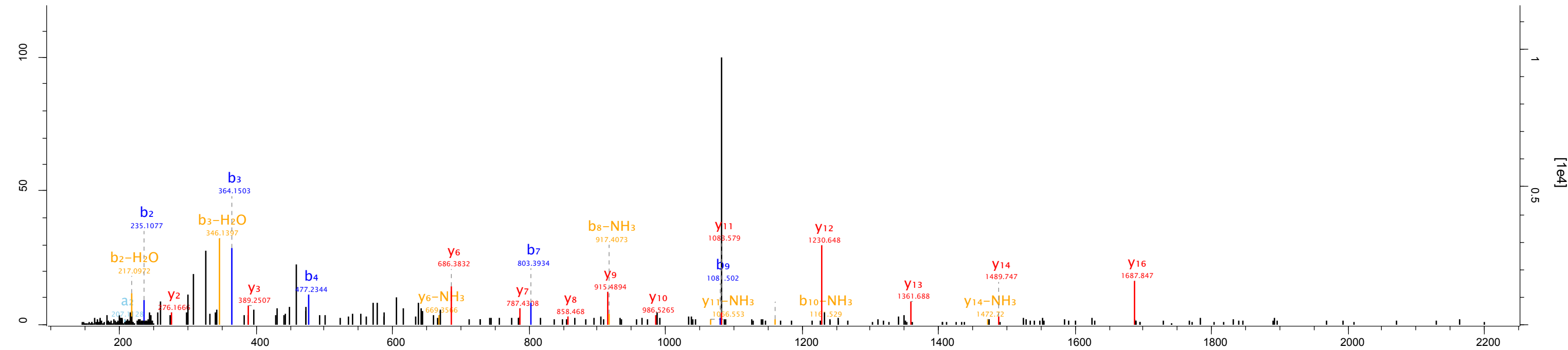
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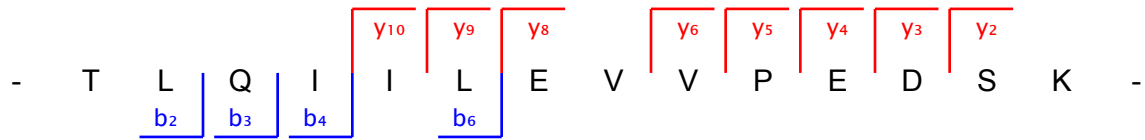
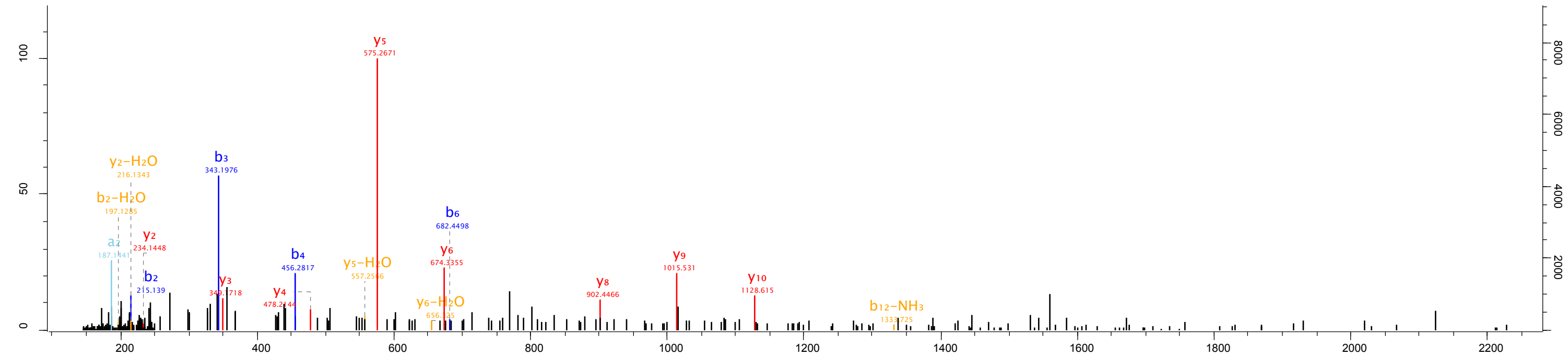
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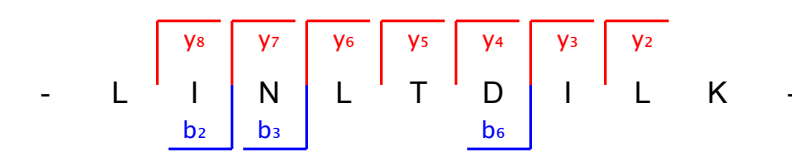
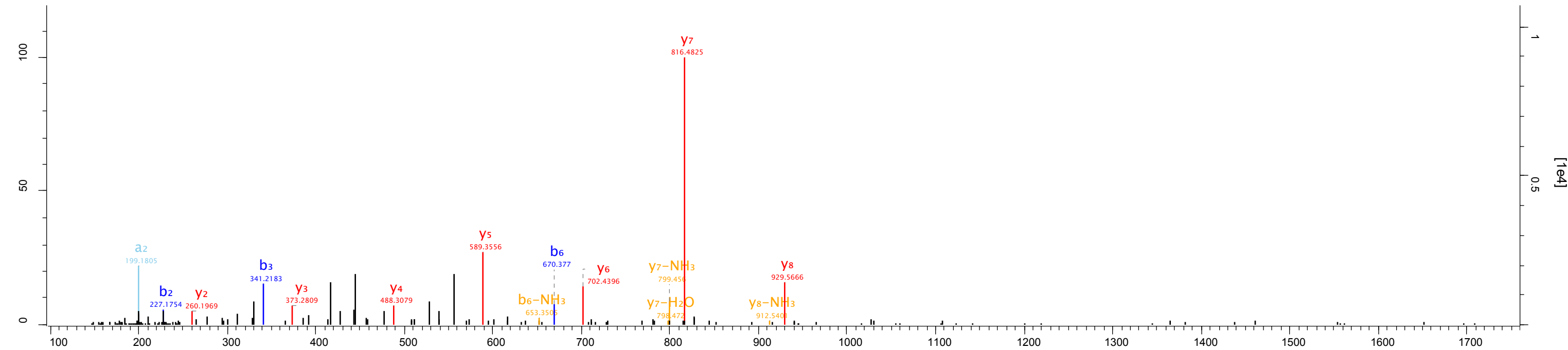


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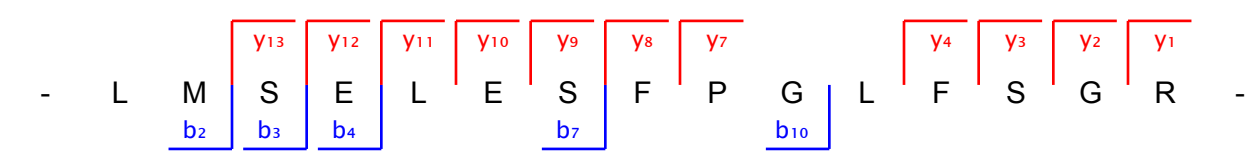
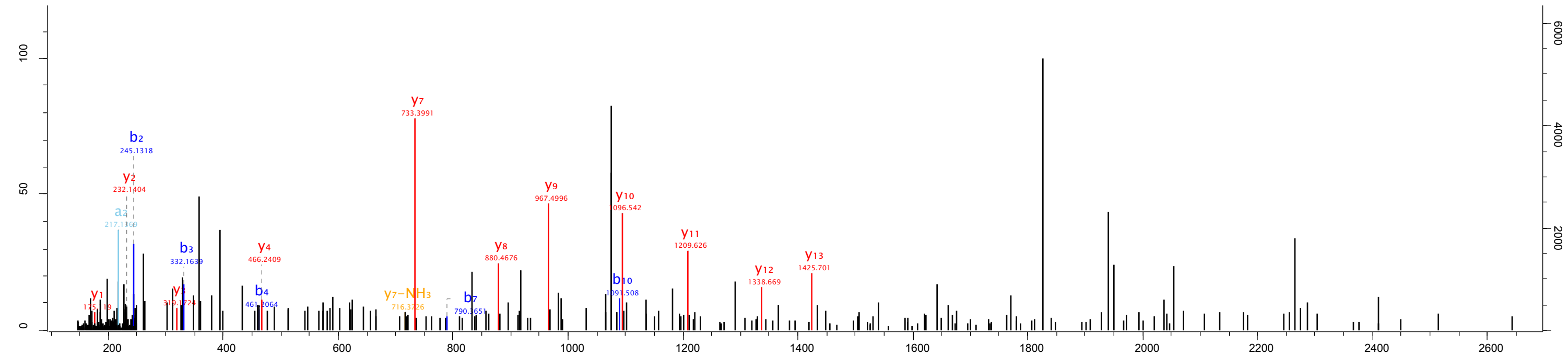
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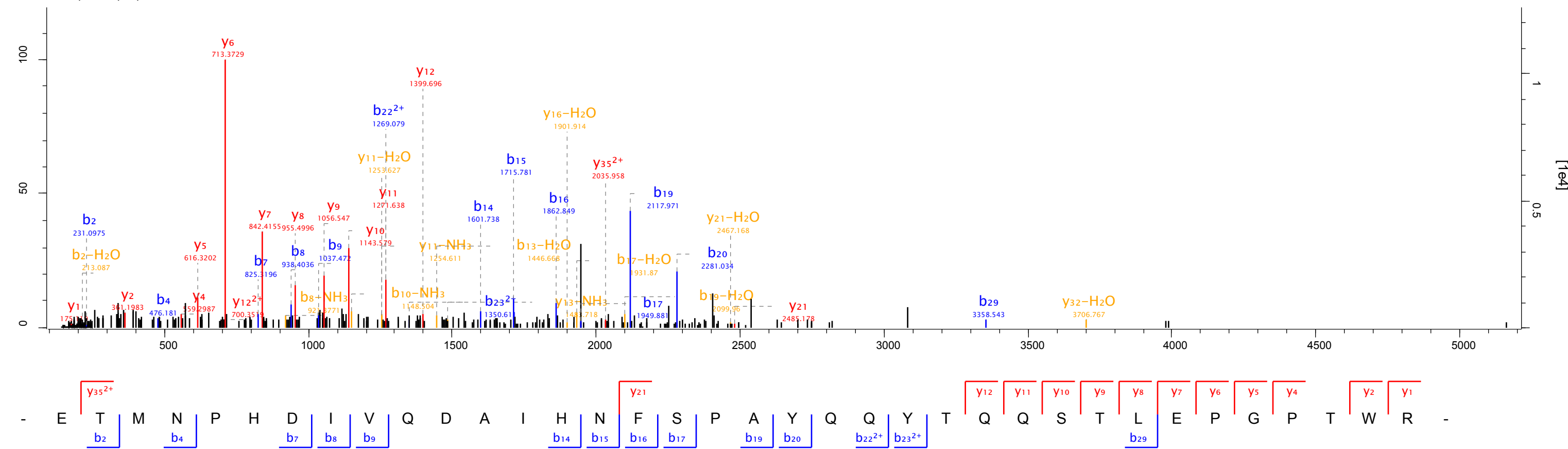
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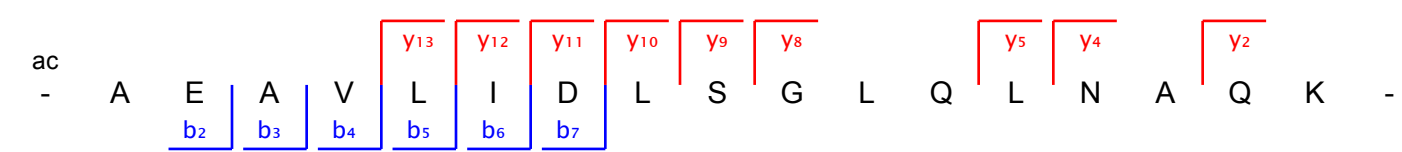
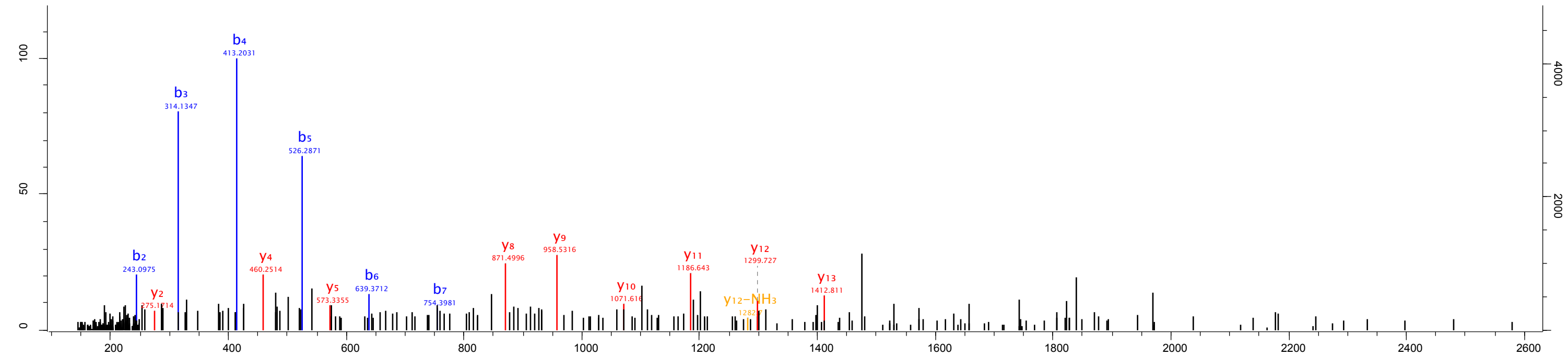


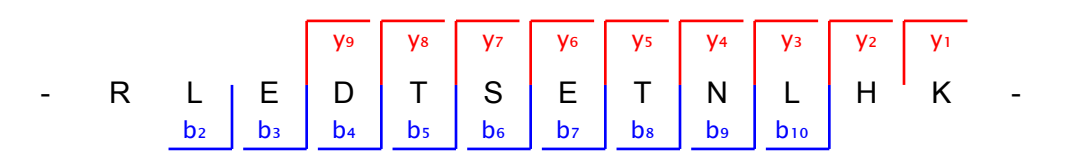
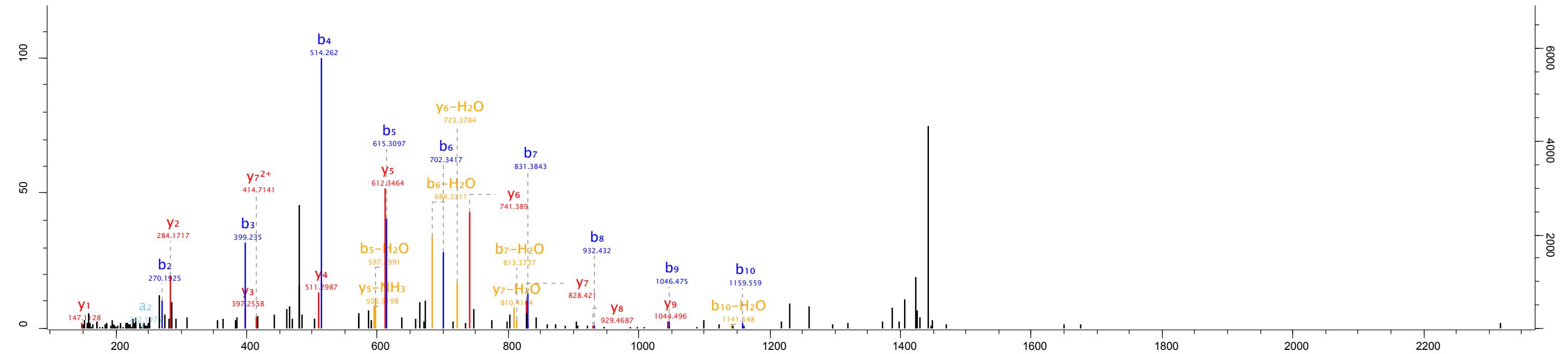
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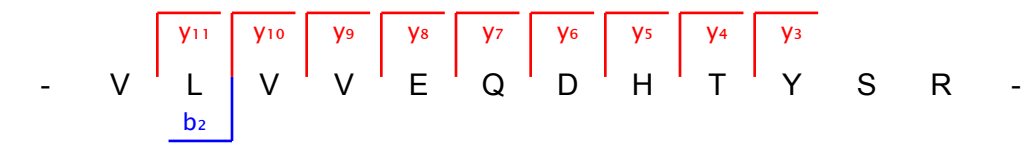
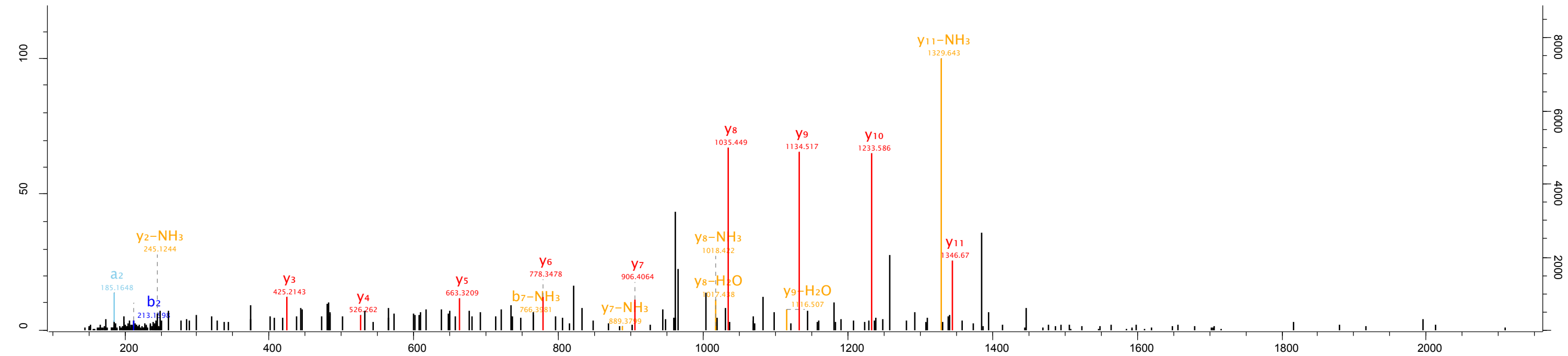
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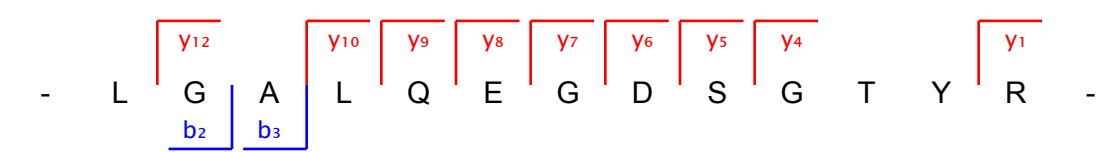
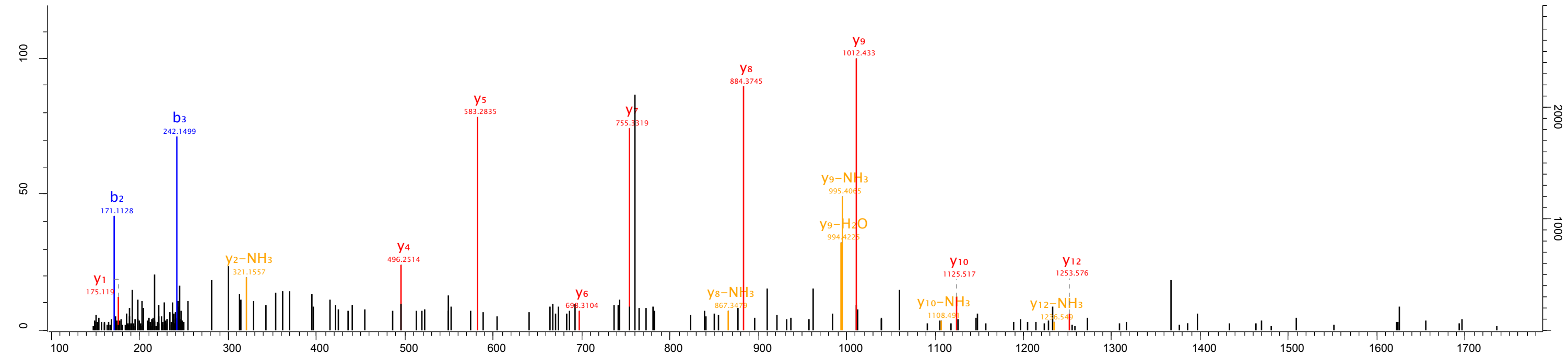
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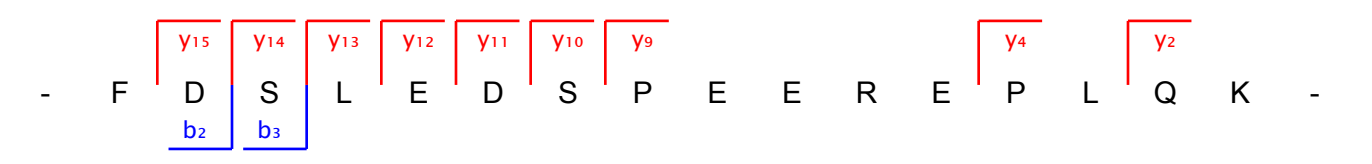
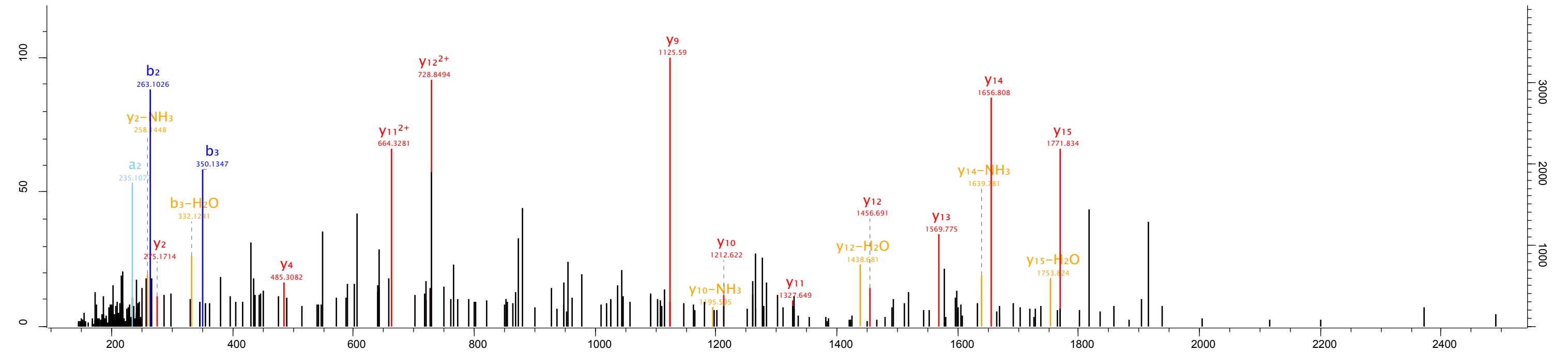
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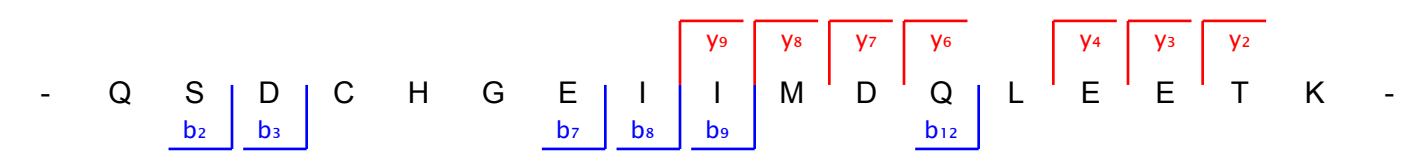
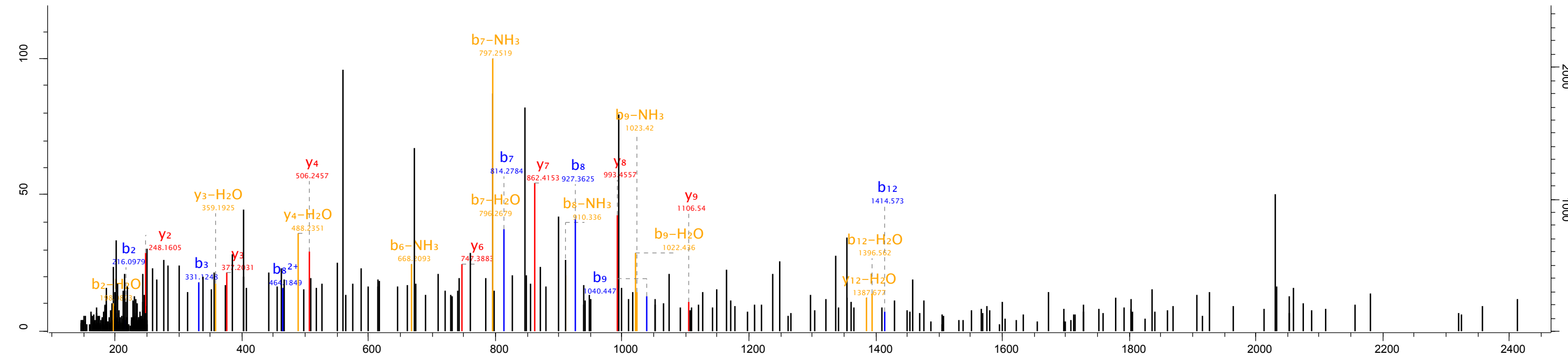
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Scan 22570 Method TOF; CID Score 58.32 m/z 683.83 Gene names Esam

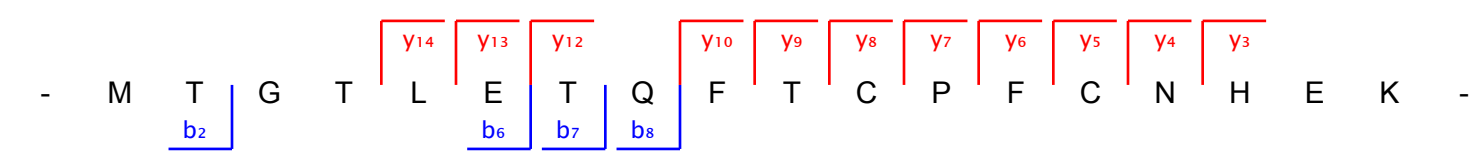
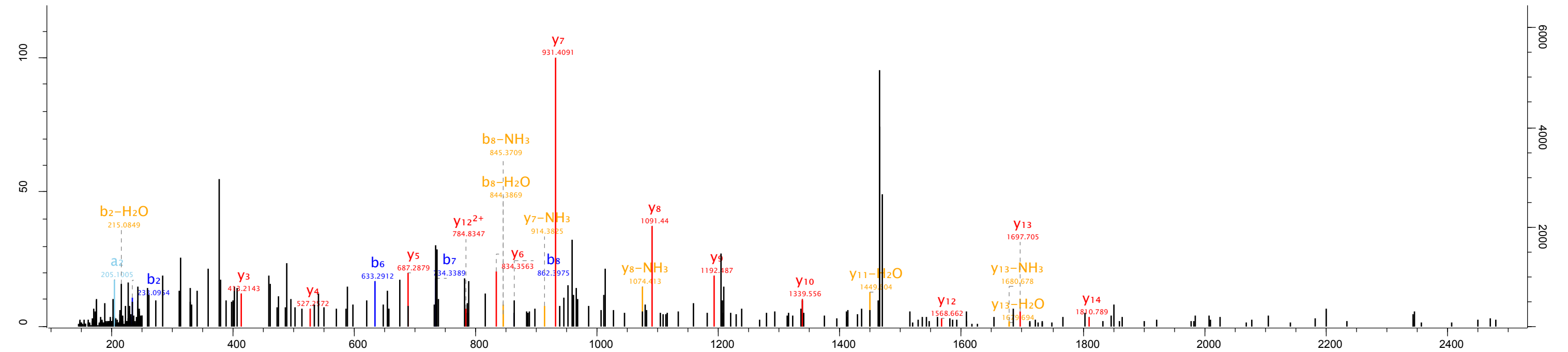




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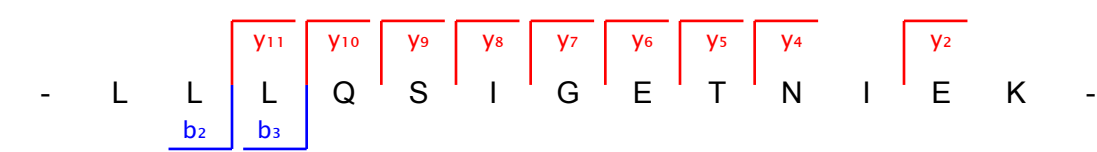
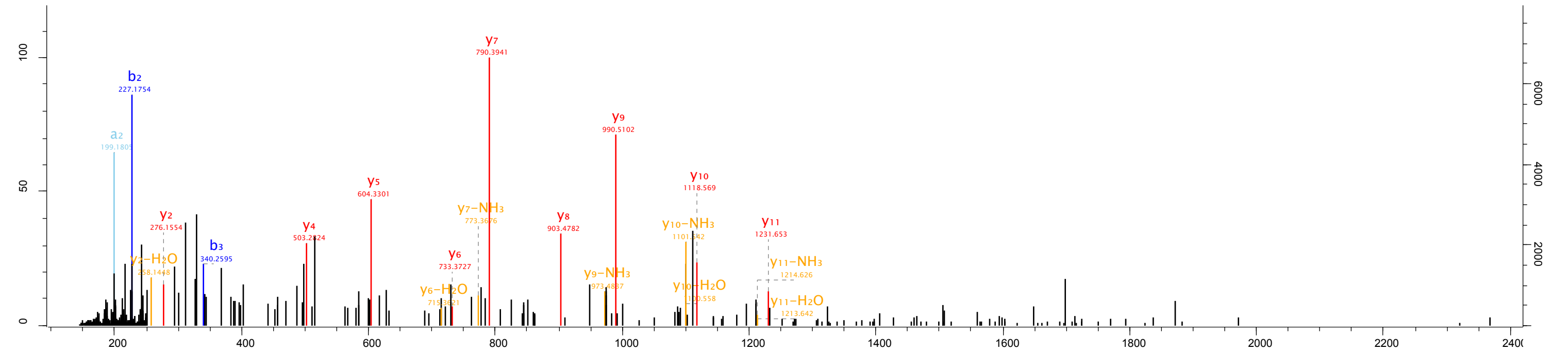


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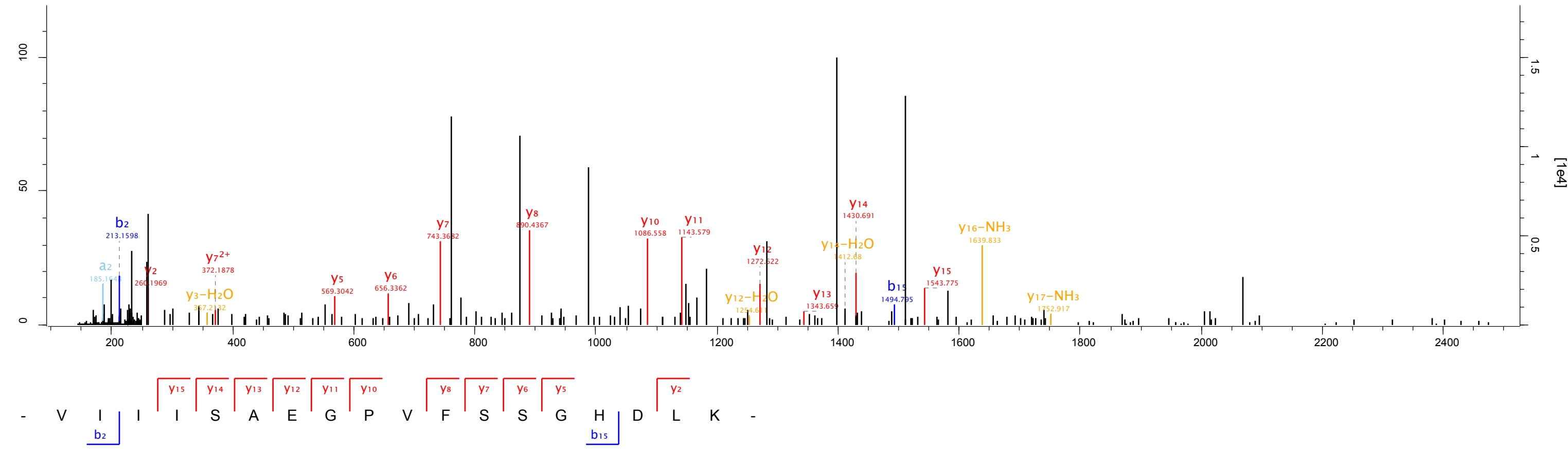


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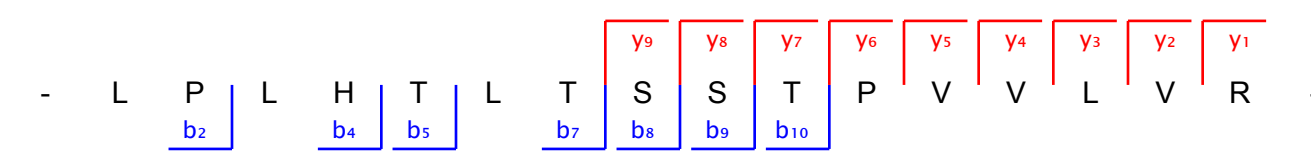
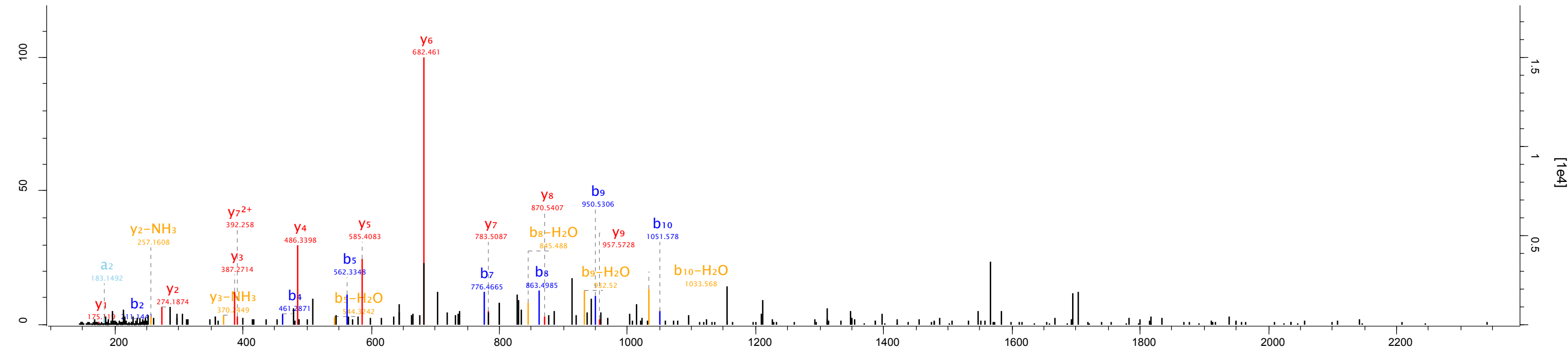
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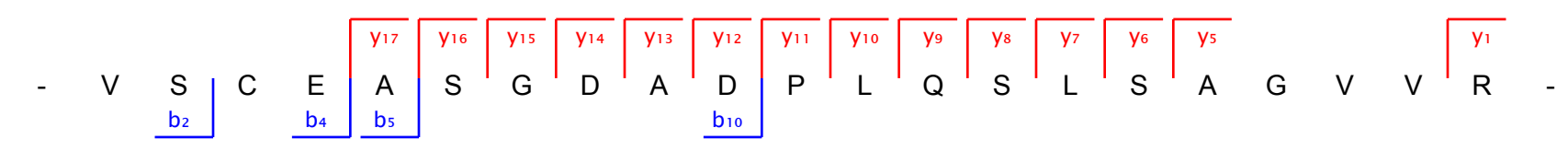
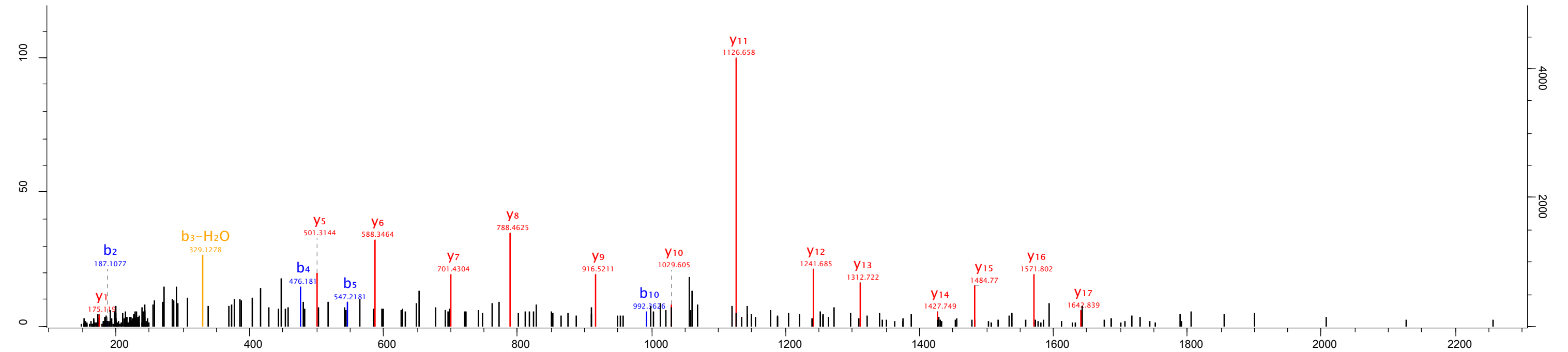
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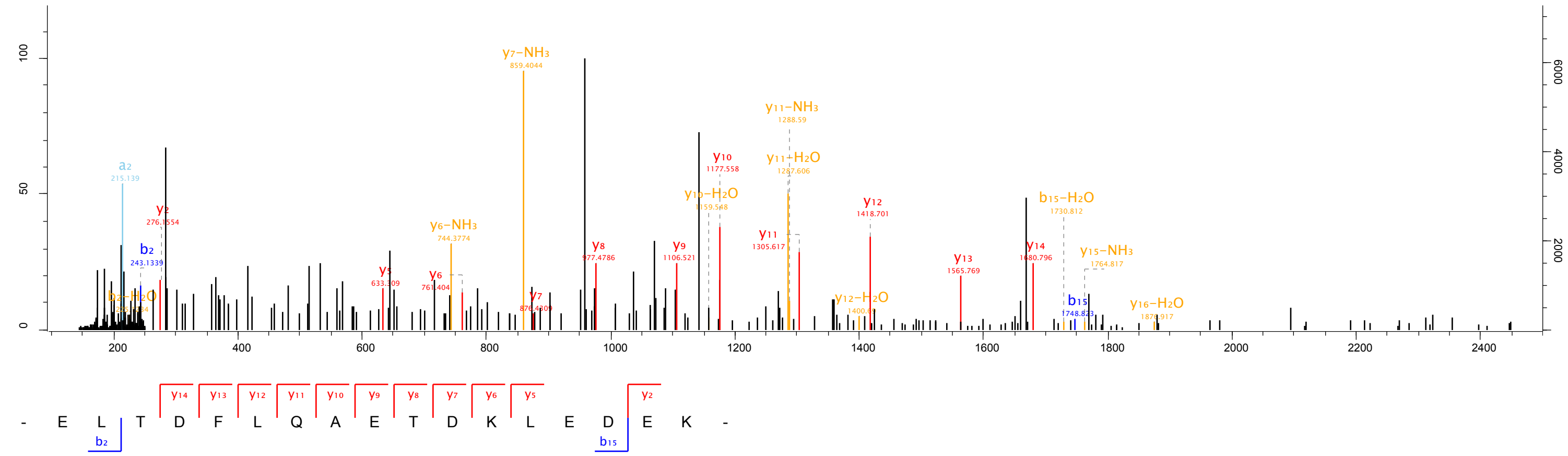
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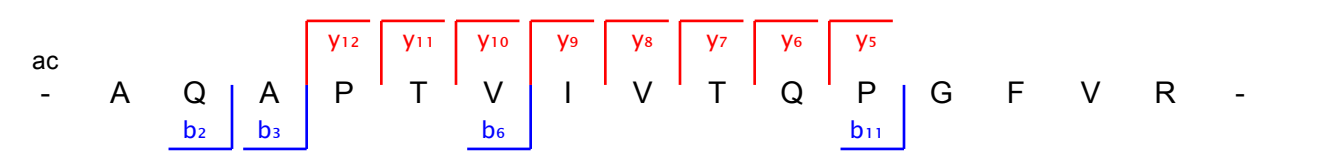
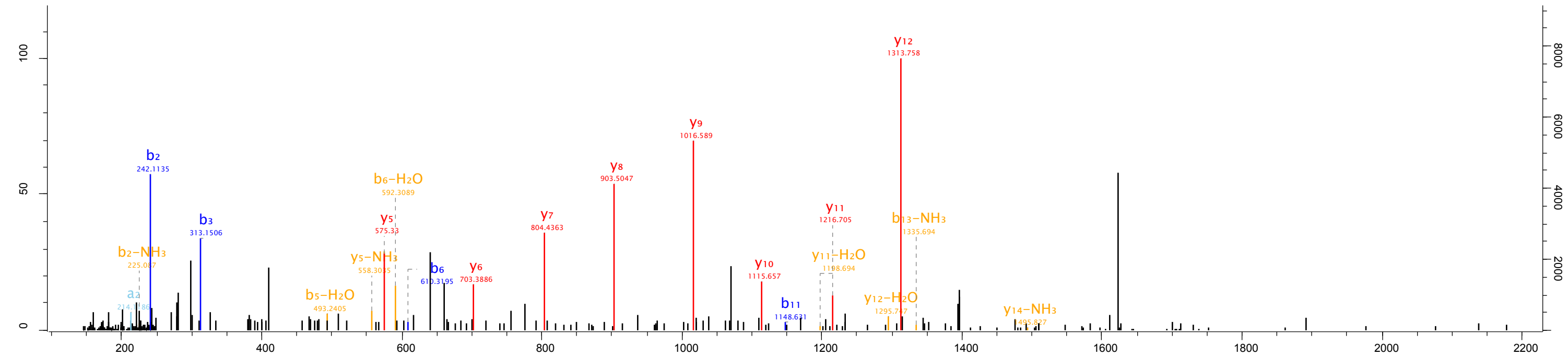
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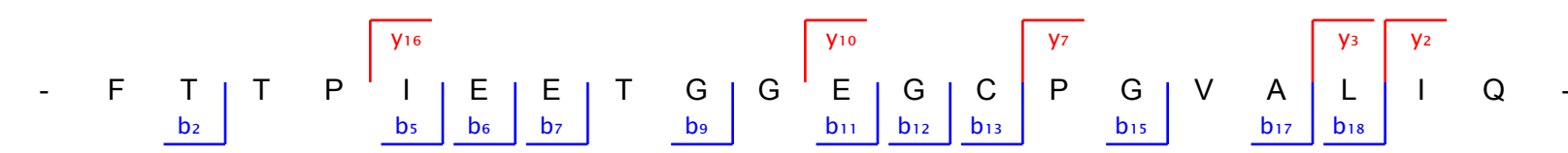
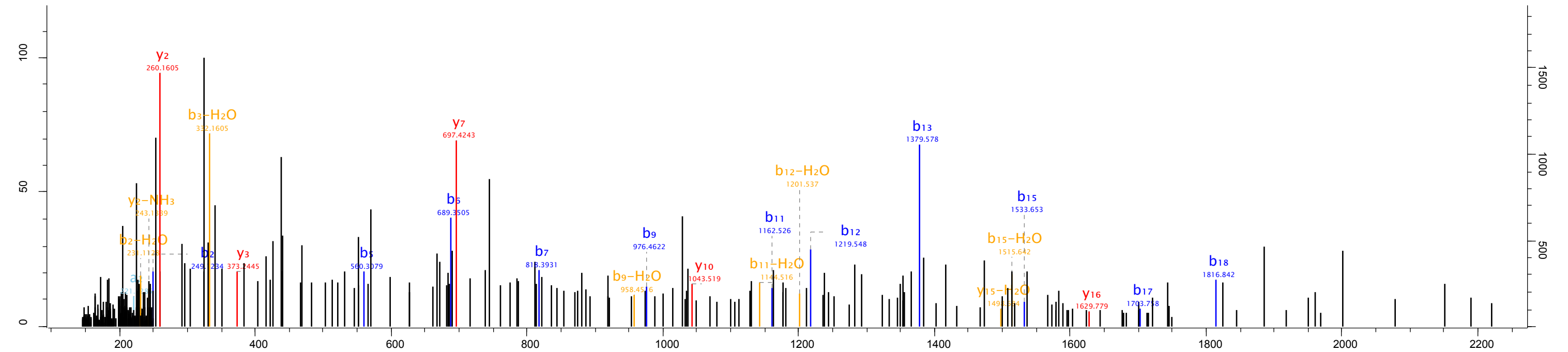
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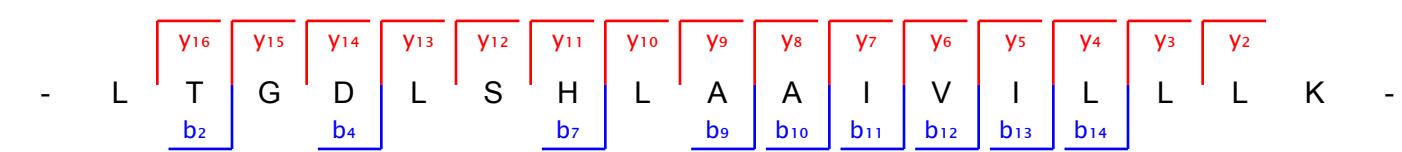
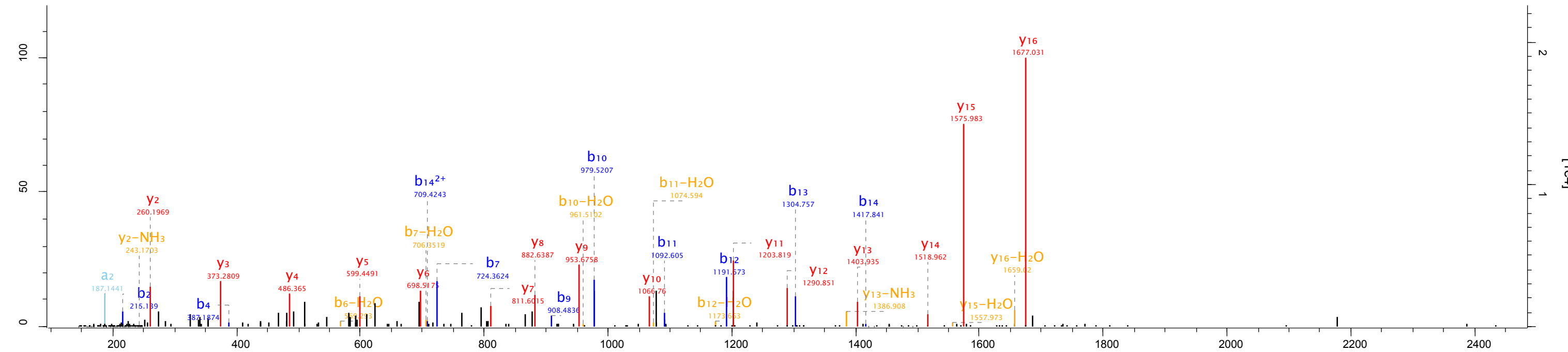
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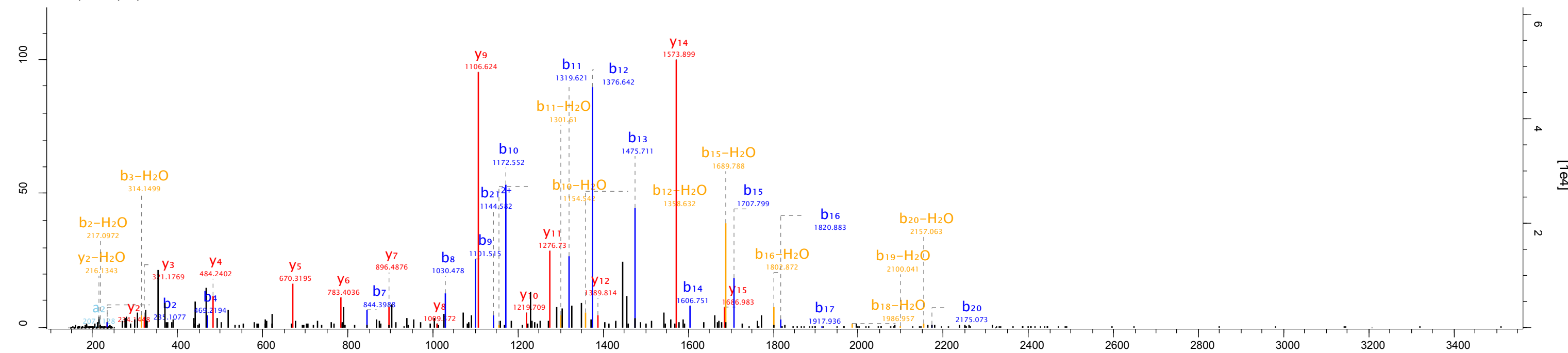


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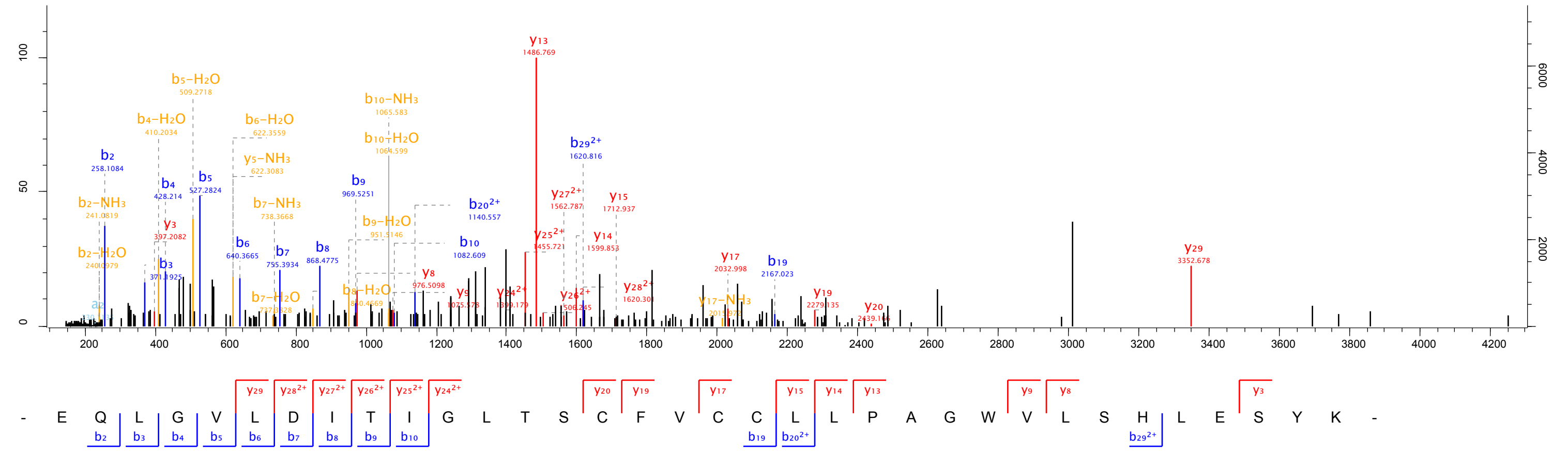
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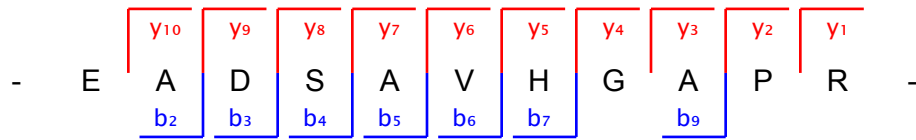
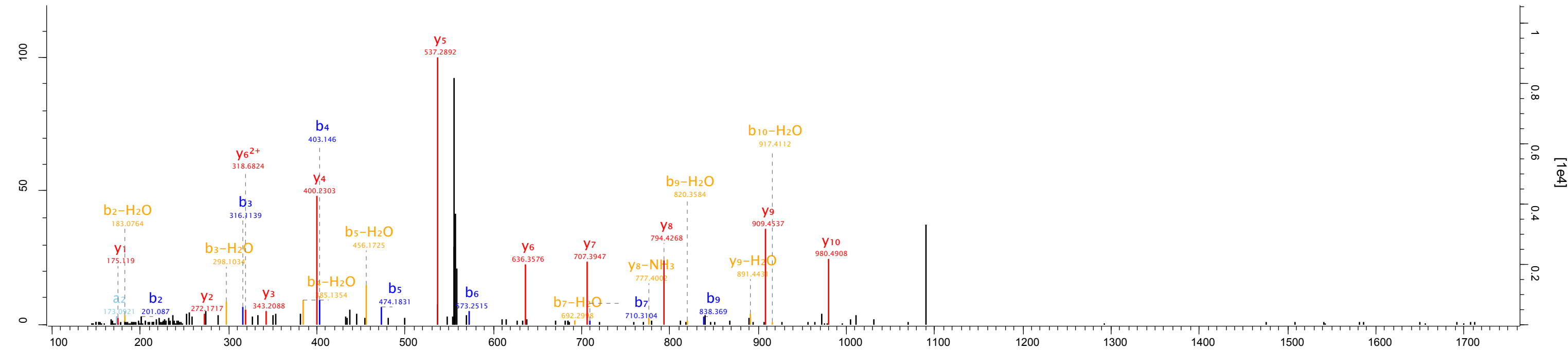
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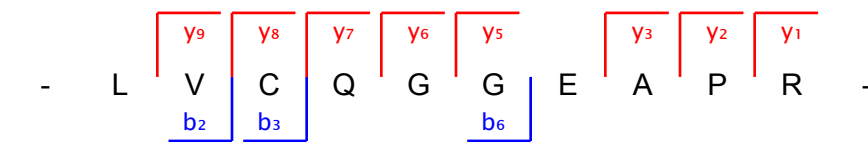
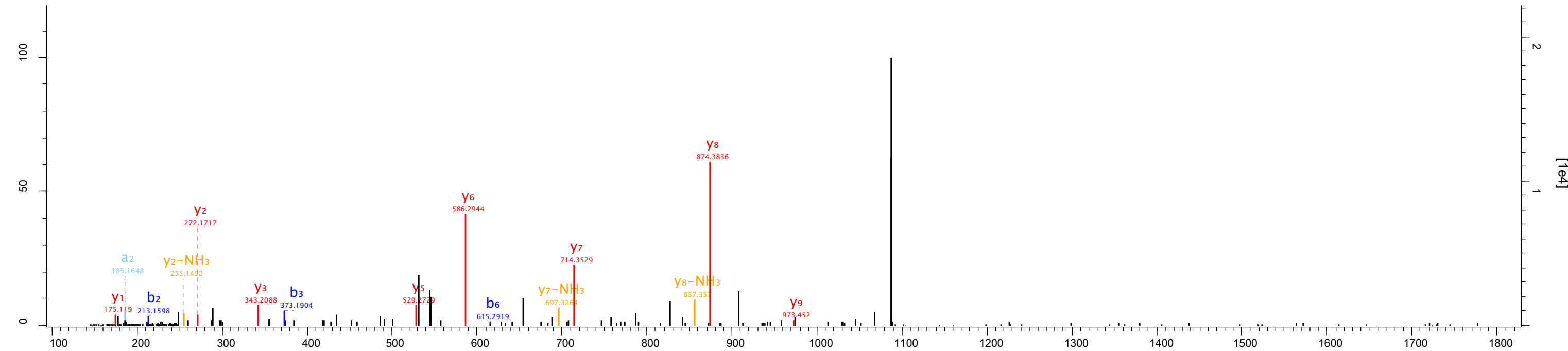
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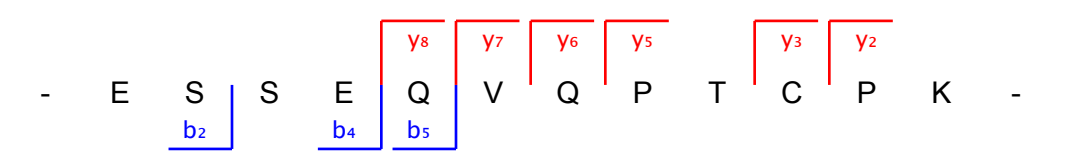
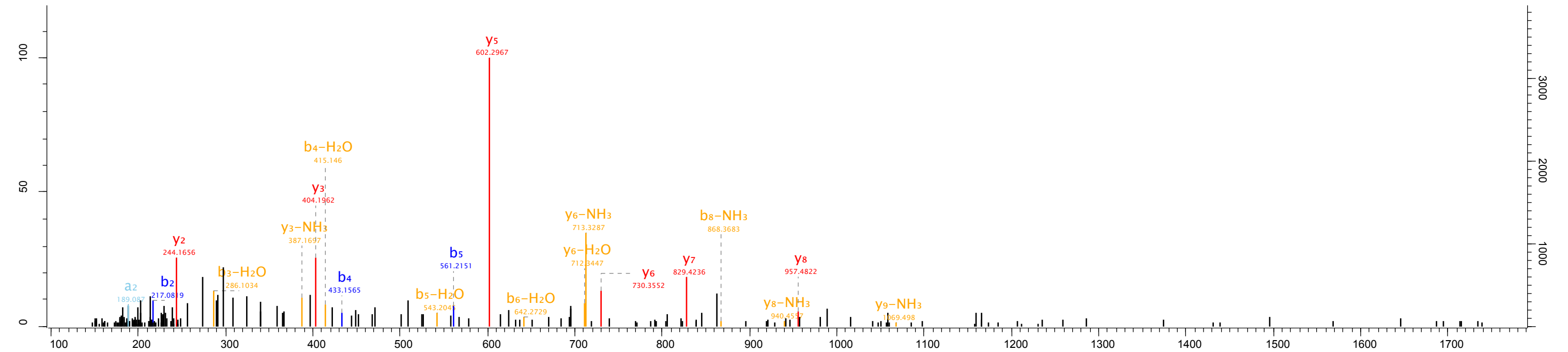


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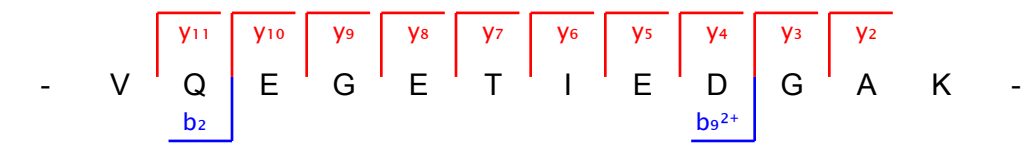
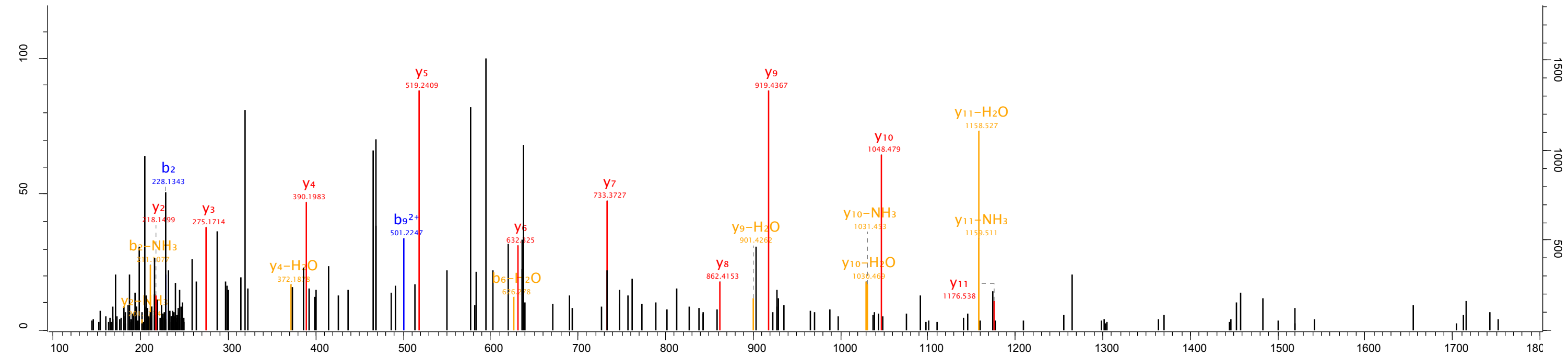
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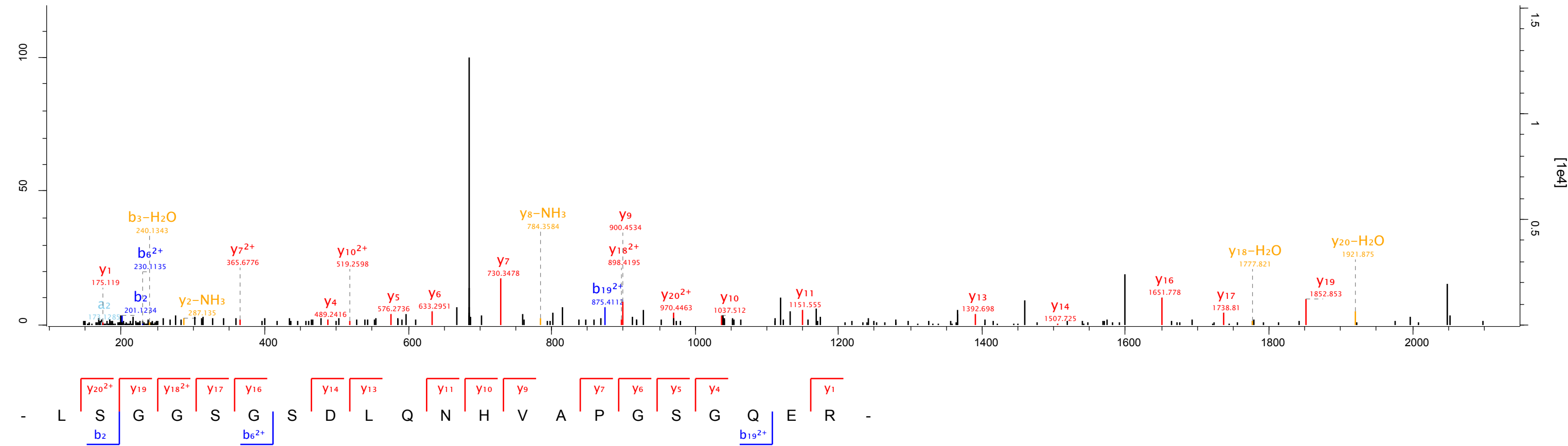
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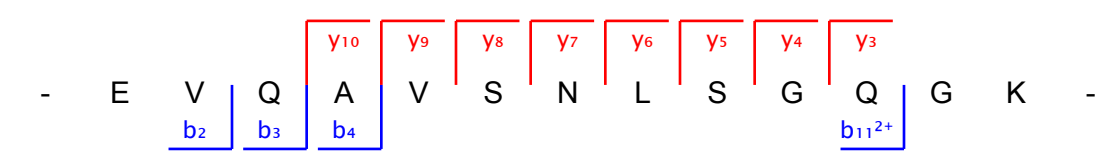
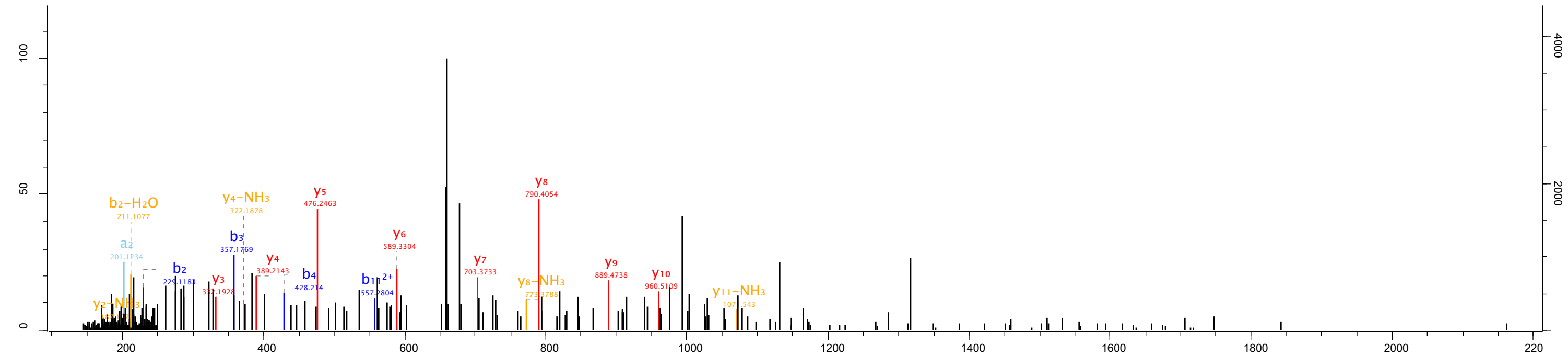
Raw file: 20150307_Hepa3_Top_opt_D3_01_1689
 Scan: 14054 Method: TOF; CID Score: 84.17 m/z: 638.3 Gene names: Nudt1



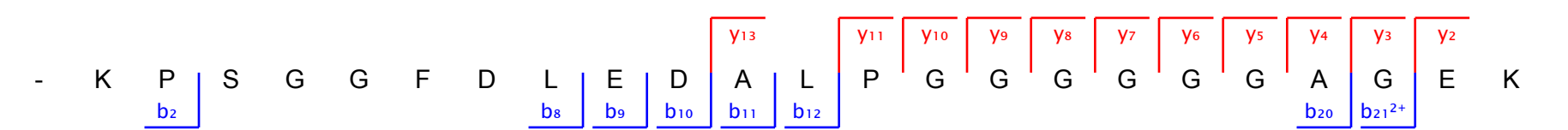
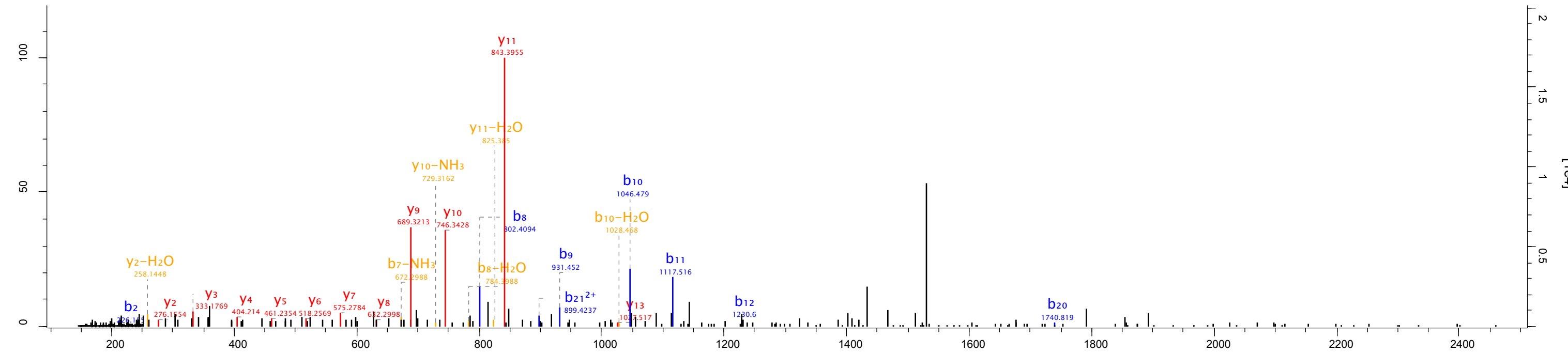
Raw file 20150307_Hepa3_Top_opt_D3_01_1689 Scan 18676 Method TOF; CID Score 40.72 m/z 685.33 Gene names Kmt2d



Raw file 20150307_Hepa3_Top_opt_D3_01_1689 Scan 20387 Method TOF; CID Score 56.57 m/z 658.84 Gene names Banp

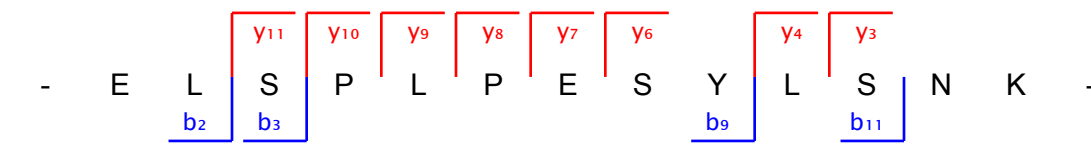
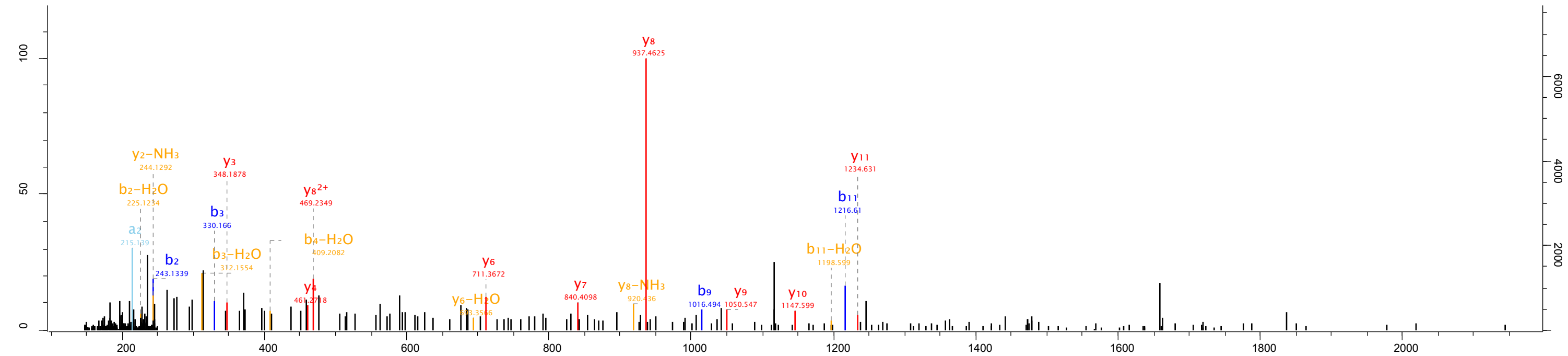


Raw file 20150307_Hepa3_Top_opt_D3_01_1689 Scan 45529 Method TOF; CID Score 42.56 m/z 692 Gene names Cd99

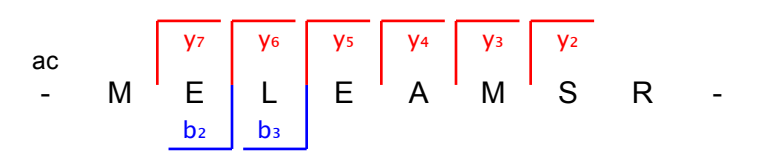
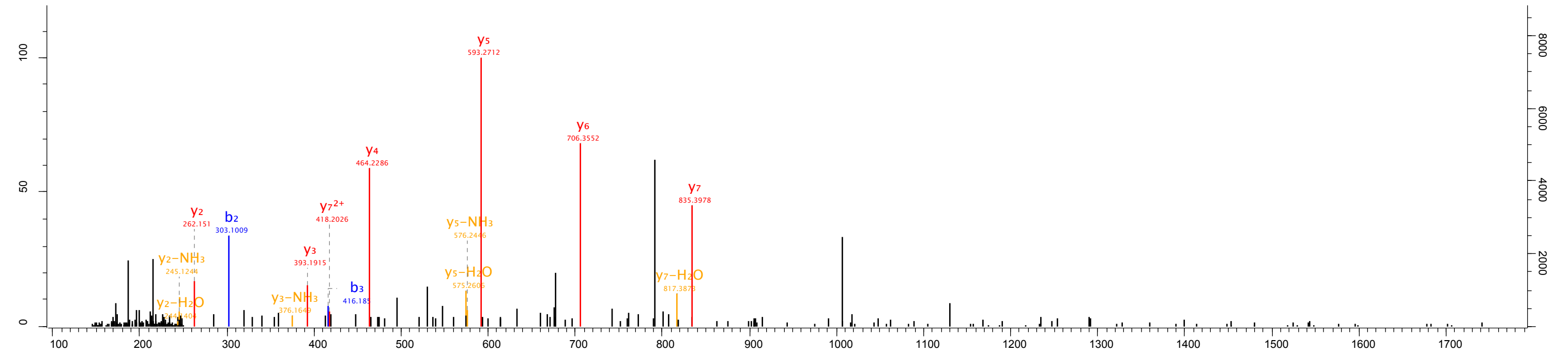


Raw file
20150307_Hepa3_Top_opt_D3_01_1689

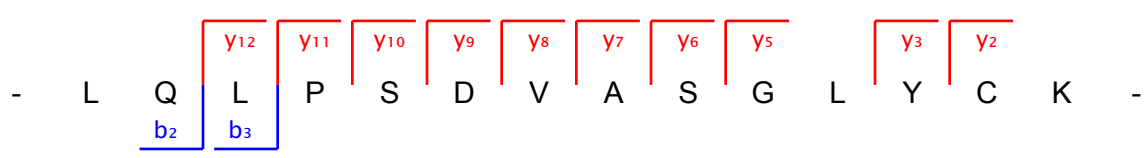
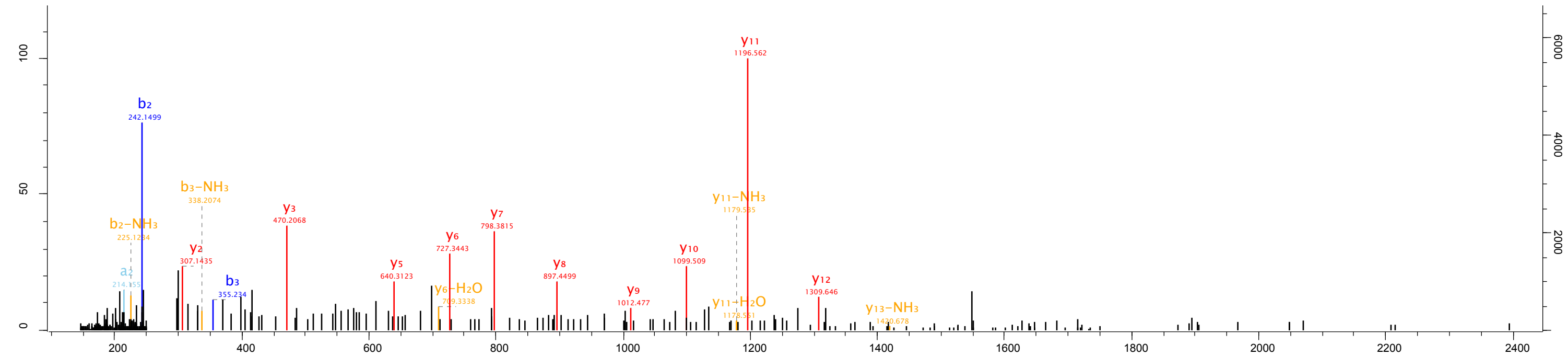
Scan 48369 Method TOF; CID Score 72.89 m/z 738.88 Gene names Fitm2

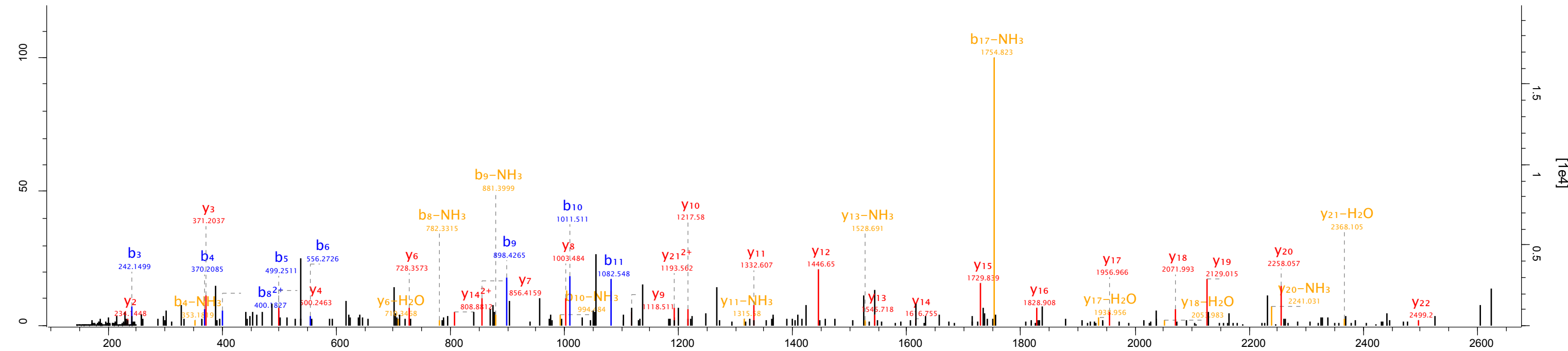


Raw file: 20150307_Hepa3_Top_opt_D3_01_1689
 Scan: 49165 Method: TOF; CID Score: 99.44 m/z: 504.72 Gene names: Tmem258



Raw file 20150307_Hepa3_Top_opt_D3_01_1689 Scan 51662 Method TOF; CID Score 66.22 m/z 775.89 Gene names Mbd1



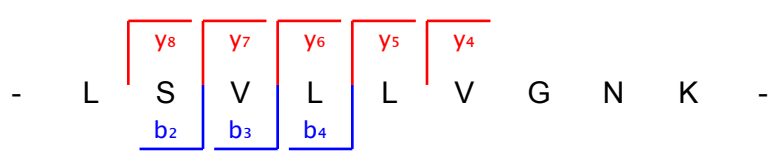
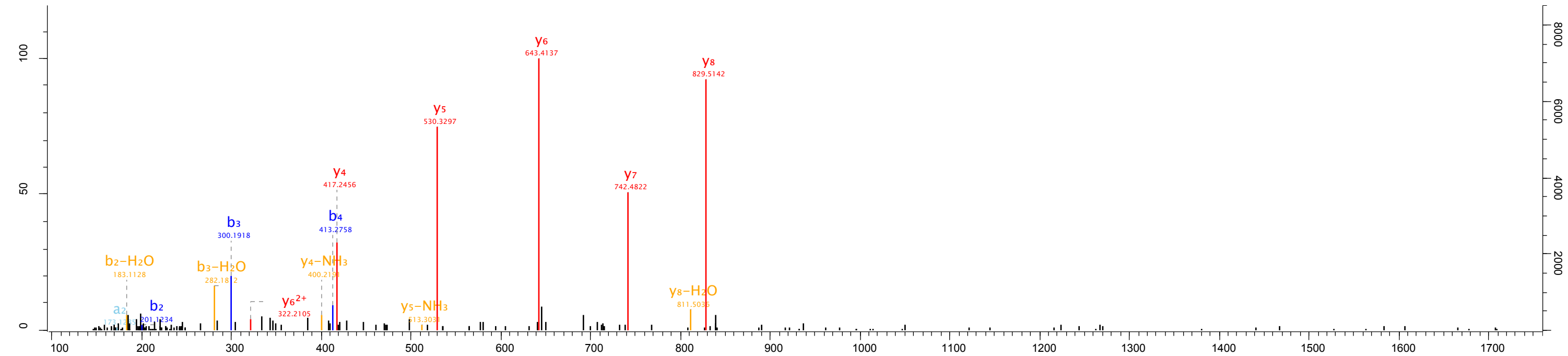


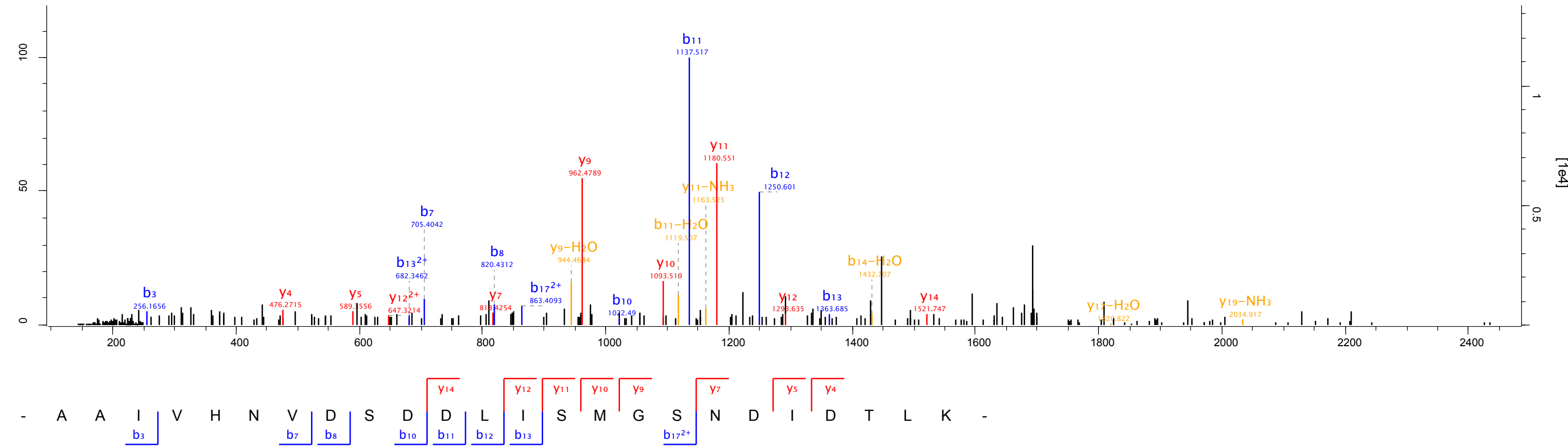
- A G L Q E G D Q V L A V N D V D F Q D I E H S K -

b3 b4 b5 b6 b8-2+ b9 b10 b11

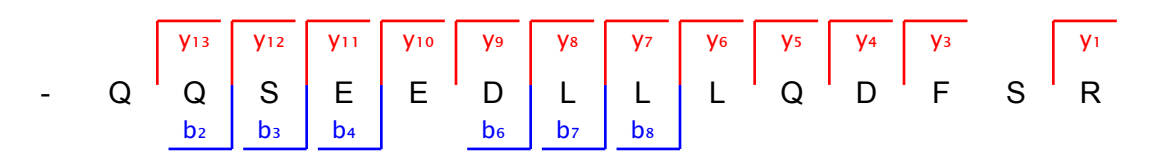
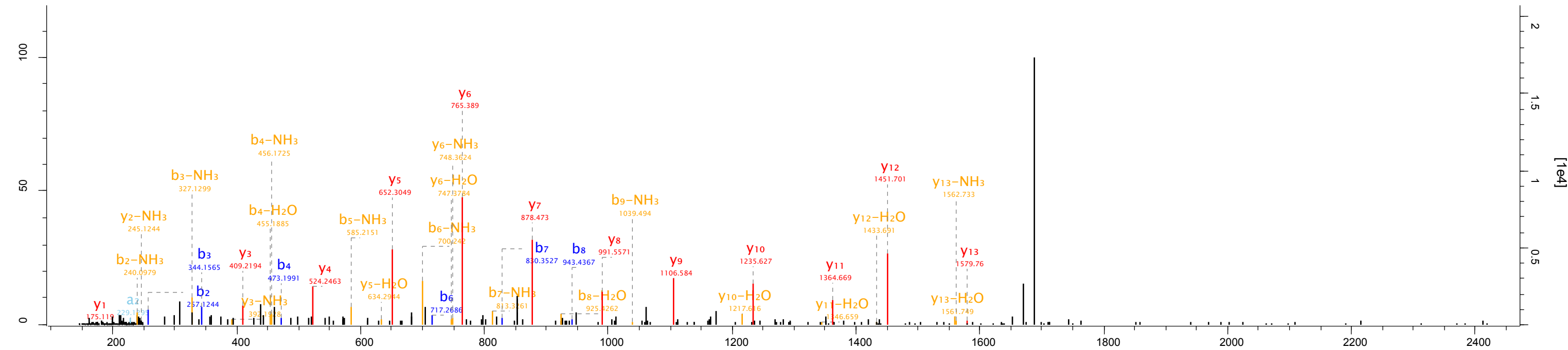
y22 y21-2+ y20 y19 y18 y17 y16 y15 y14 y13 y12 y11 y10 y9 y8 y7 y6 y4 y3 y2

Raw file: 20150307_Hepa3_Top_opt_D3_01_1689
 Scan: 54983 Method: TOF; CID Score: 80.17 m/z: 471.8 Gene names: Rhebl1



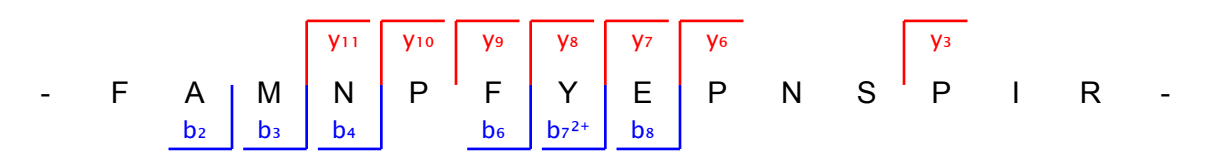
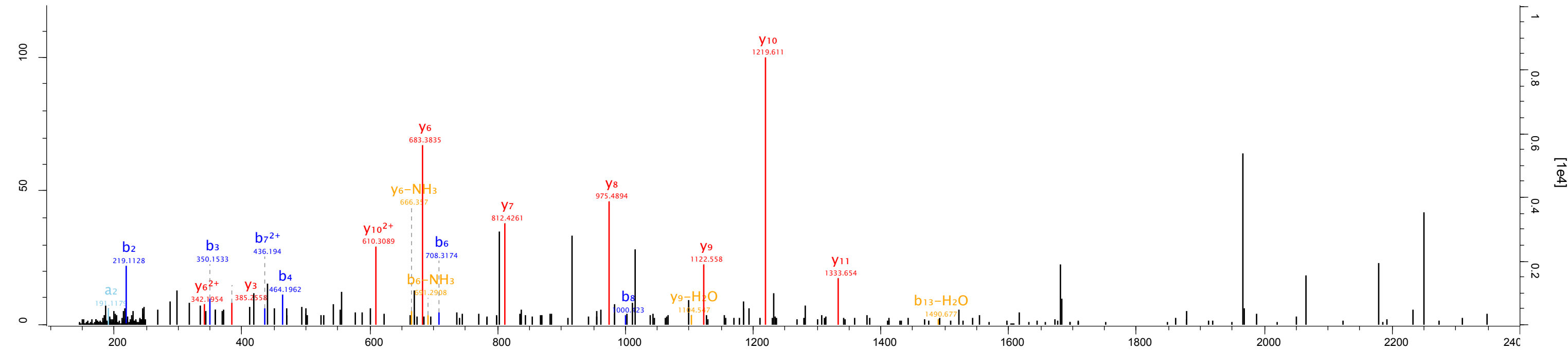


Raw file 20150307_Hepa3_Top_opt_D3_01_1689 Scan 57246 Method TOF; CID Score 147.56 m/z 854.91 Gene names Ssr3



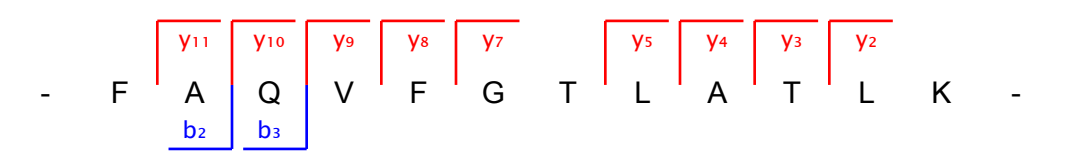
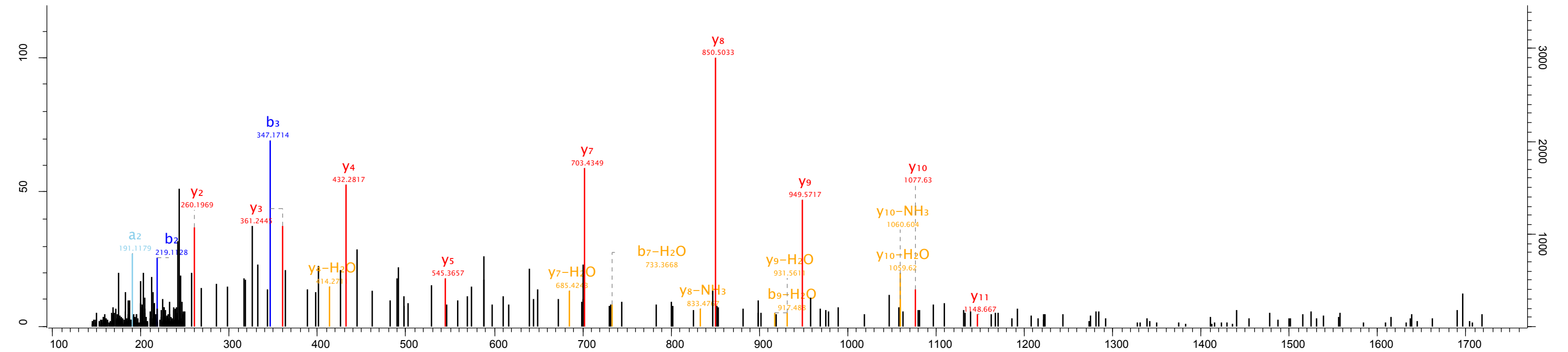
Raw file
20150307_Hepa3_Top_opt_D3_01_1689

Scan 58866 Method TOF; CID Score 76.73 m/z 842.4 Gene names Trappc2;0610009B22Rik

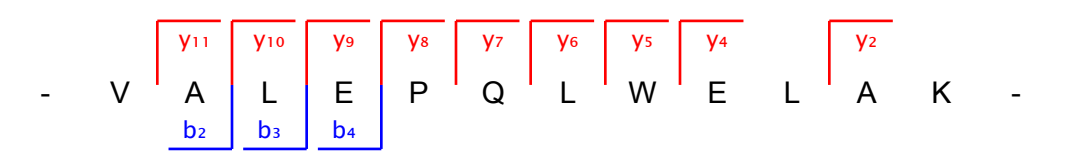
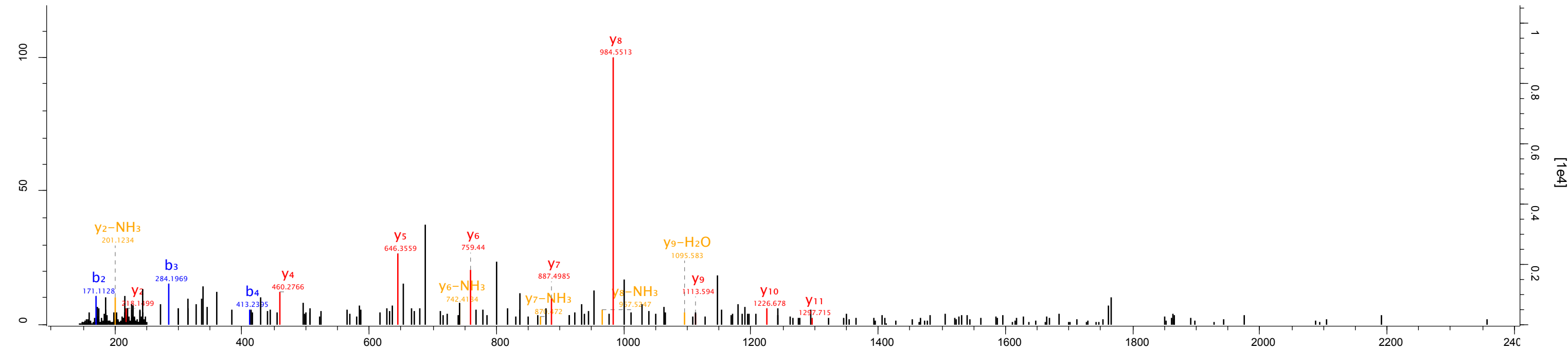


Raw file
20150307_Hepa3_Top_opt_D3_01_1689

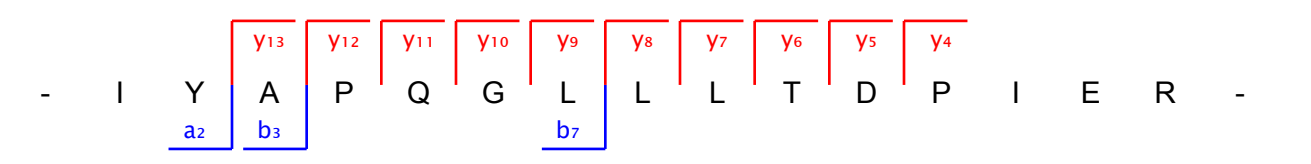
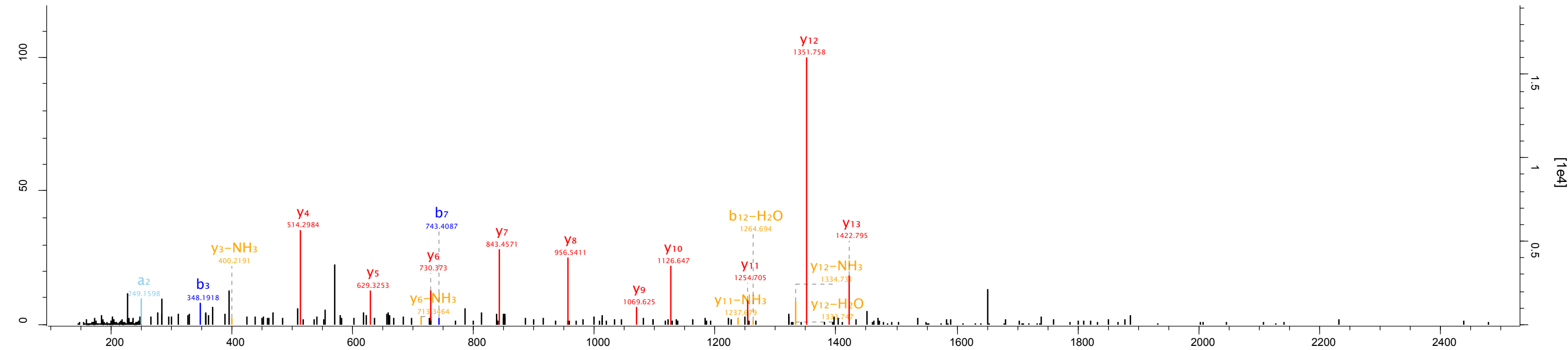
Scan 61263 Method TOF; CID Score 79.49 m/z 648.37 Gene names Tmem186



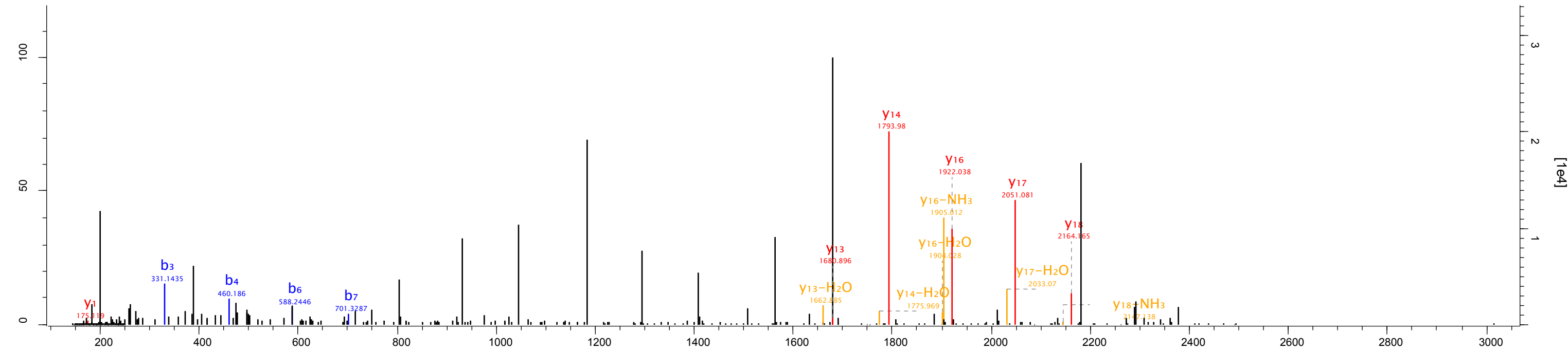
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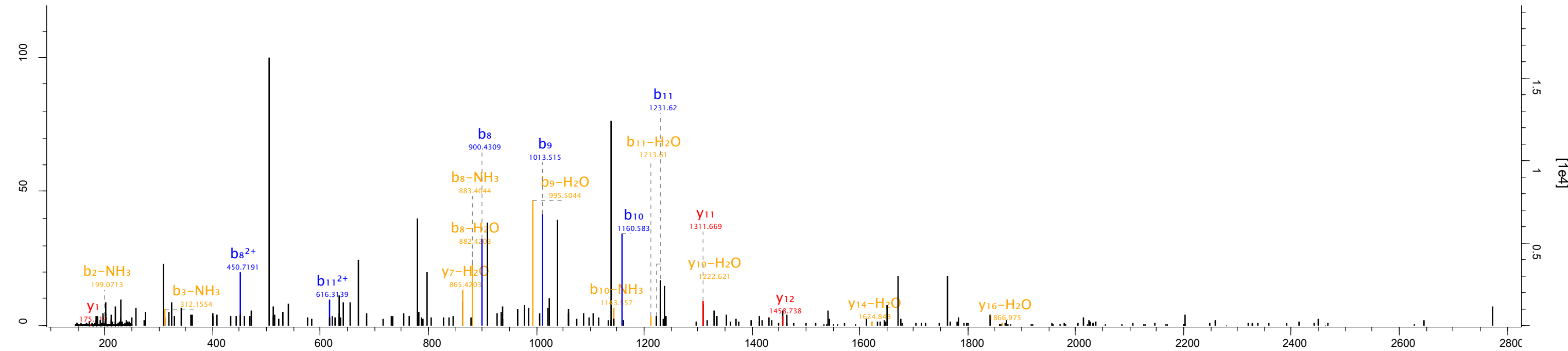


Raw file: 20150307_Hepa3_Top_opt_D3_01_1689
 Scan: 63733 Method: TOF; CID Score: 64.52 m/z: 850.47 Gene names: Golga7



Raw file 20150307_Hepa3_Top_opt_D3_01_1689 Scan 68743 Method TOF; CID Score 54.76 m/z 794.74 Gene names Nlrp1



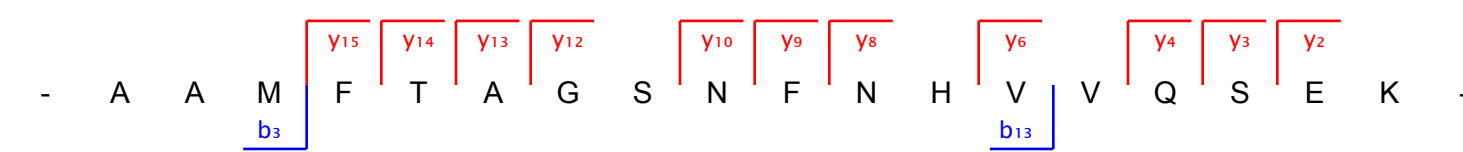
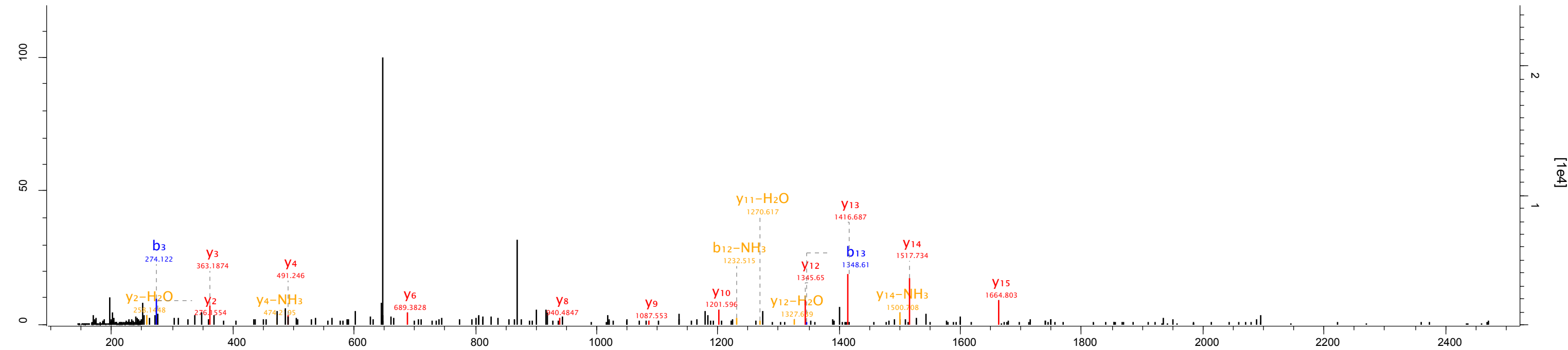


- S Q L E E L E A L F A K T Q Y P D V Y A R -

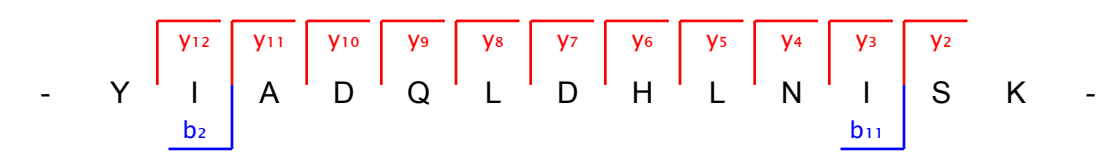
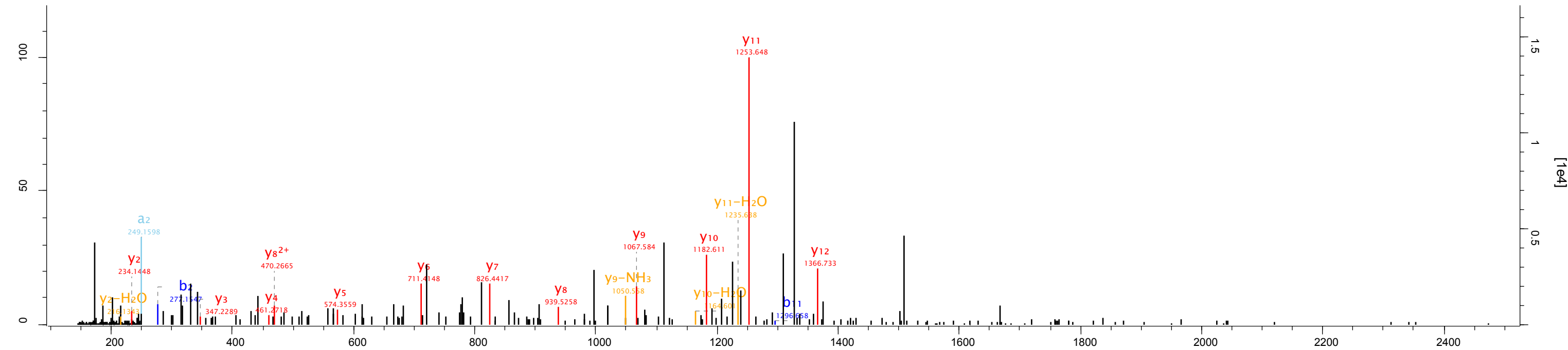
Fragmentation mapping:

- b8: A
- b9: L
- b10: F
- b11: A
- y12: F
- y11: A
- y1: R

Raw file 20150307_MEF1_Top_opt_E1_01_1677 Scan 38213 Method TOF; CID Score 39.9 m/z 646.97 Gene names Icmt

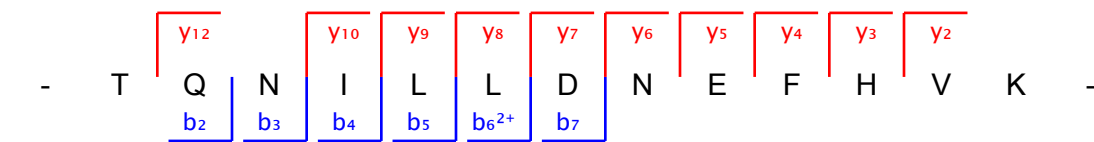
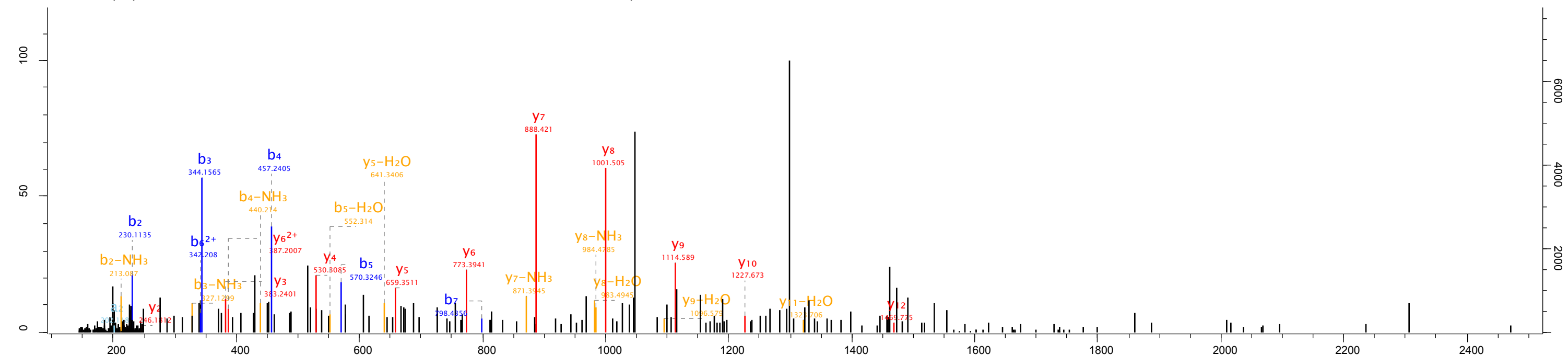


Raw file 20150307_MEF1_Top_opt_E1_01_1677 Scan 42047 Method TOF; CID Score 73.39 m/z 510.6 Gene names Mrpl57

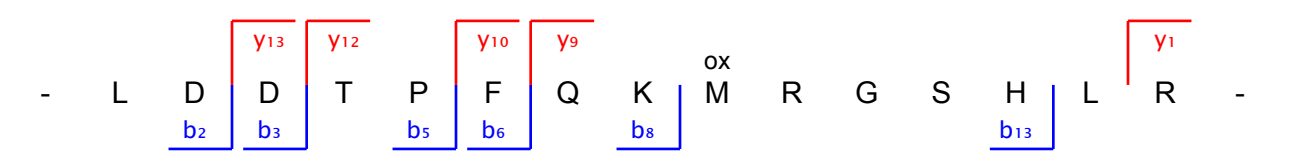
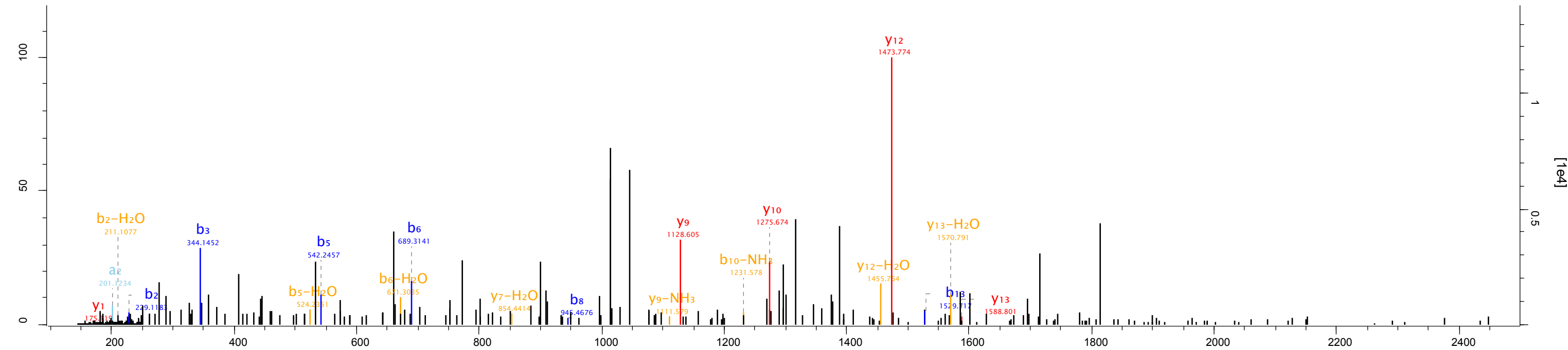


Raw file
20150307_MEF1_Top_opt_E1_01_1677

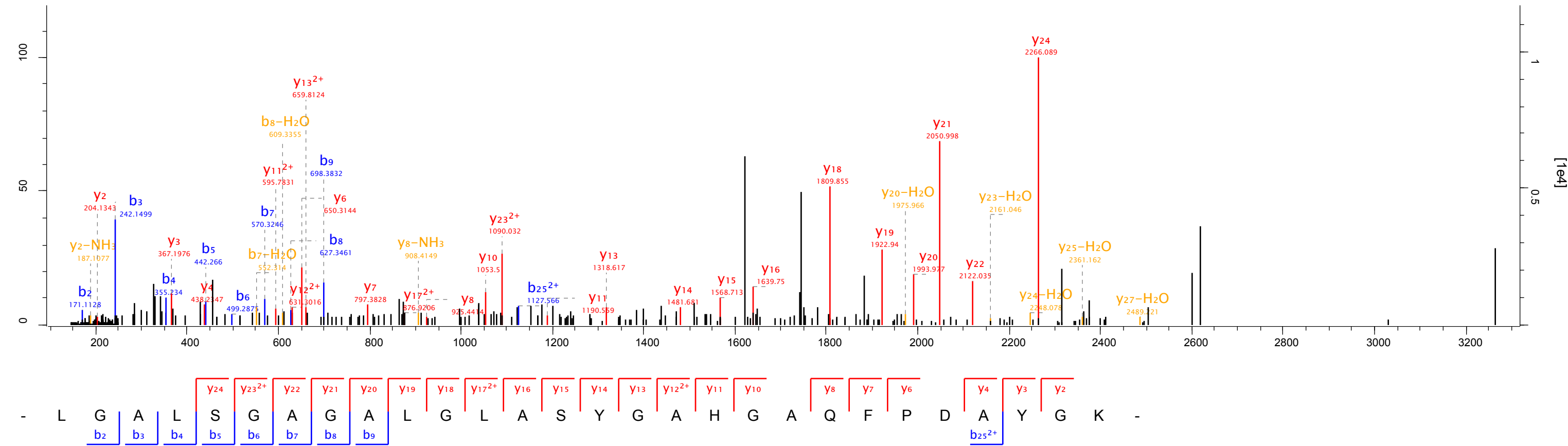
Scan 45288 Method TOF; CID Score 93.23 m/z 524.27 Gene names Ripk2



Raw file 20150307_MEF1_Top_opt_E1_01_1677 Scan 51804 Method TOF; CID Score 59.71 m/z 909.45 Gene names Tsr3

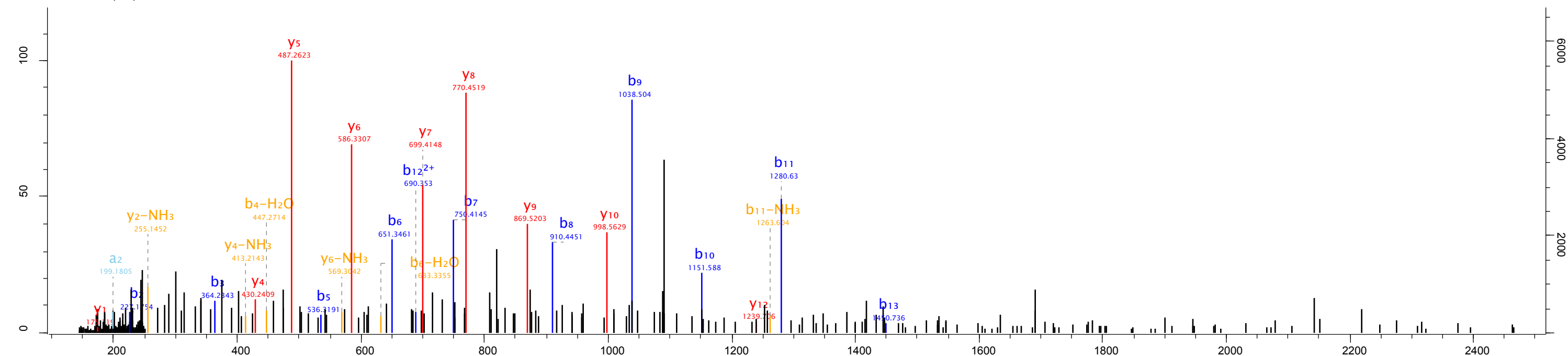


Raw file 20150307_MEF1_Top_opt_E1_01_1677 Scan 57749 Method TOF; CID Score 123.03 m/z 874.44 Gene names Tmem256



Raw file
20150307_MEF1_Top_opt_E1_01_1677

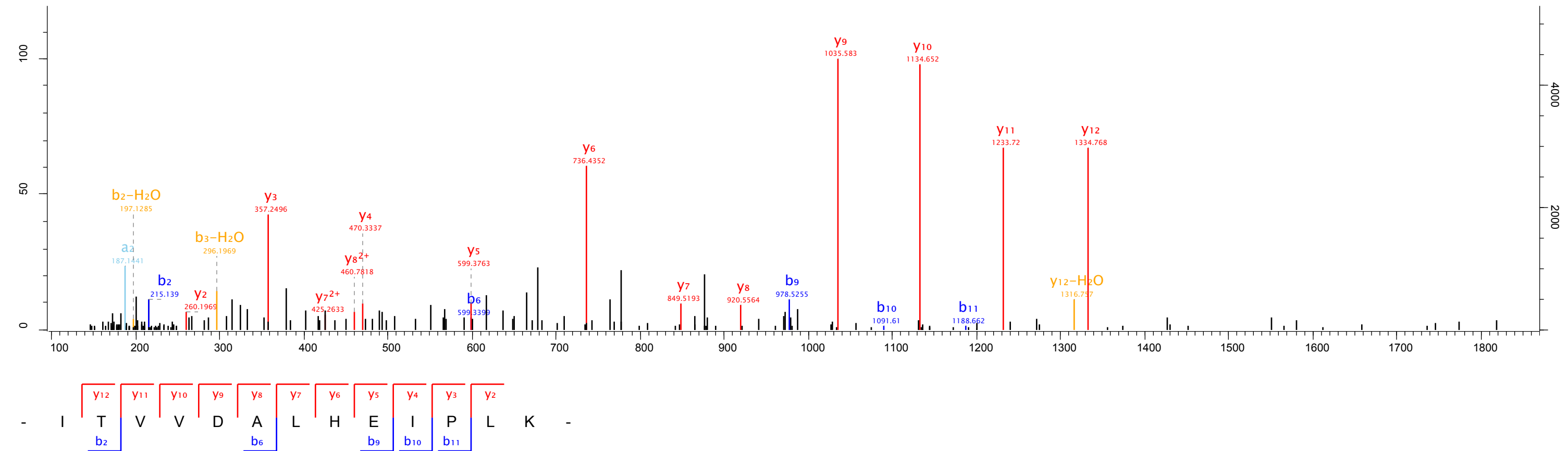
Scan 60484 Method TOF; CID Score 41.26 m/z 717.38 Gene names 0610031J06Rik



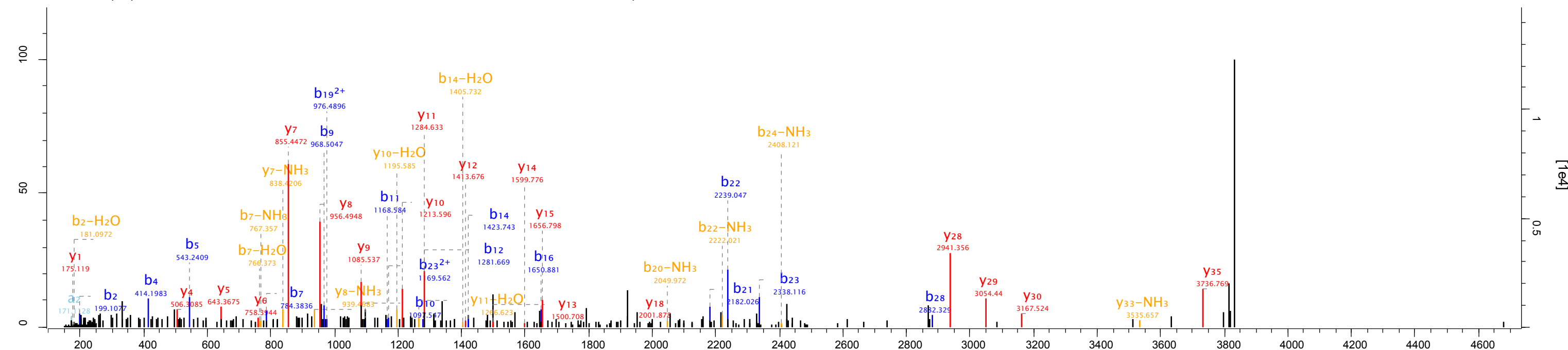
- L L H T A D V C Q L E V A L V G A S P R -

Fragmentation mapping (b and y ions):

- b2: L-L
- b3: L-H
- b5: A-D
- b6: D-V
- b7: V-C
- b8: C-Q
- b9: Q-L
- b10: L-E
- b11: E-V
- b12²⁺: V-A
- b13: A-L
- y1: R
- y4: A
- y5: G
- y6: V
- y7: L
- y8: A
- y9: V
- y10: E
- y12: P



Raw file 20150307_MEF1_Top_opt_E1_01_1677 Scan 65338 Method TOF; CID Score 84.89 m/z 960.45 Gene names Aebp1

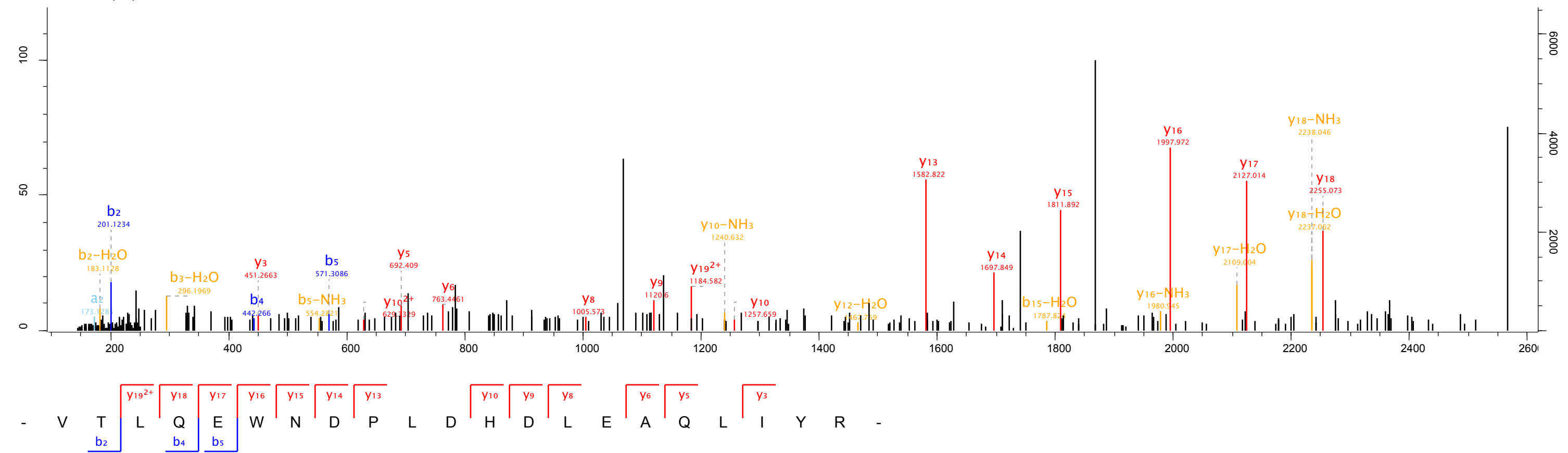


- T P S Q E Q L L A E A L A A A R G E D D D G V S E A Q E T P D H A I F R -

Fragmentation mapping: b₂ (P), b₄ (Q), b₅ (E), b₇ (L), b₉ (A), b₁₀ (E), b₁₁ (A), b₁₂ (L), b₁₄ (A), b₁₆ (R), b₁₉²⁺ (D), b₂₁ (D), b₂₂ (G), b₂₃ (V), b₂₈ (E), y₁ (R), y₄ (Q), y₅ (D), y₆ (H), y₇ (P), y₈ (T), y₉ (E), y₁₀ (A), y₁₁ (S), y₁₂ (E), y₁₃ (V), y₁₄ (G), y₁₅ (D), y₁₈ (E), y₂₈ (A), y₂₉ (L), y₃₀ (L), y₃₅ (P).

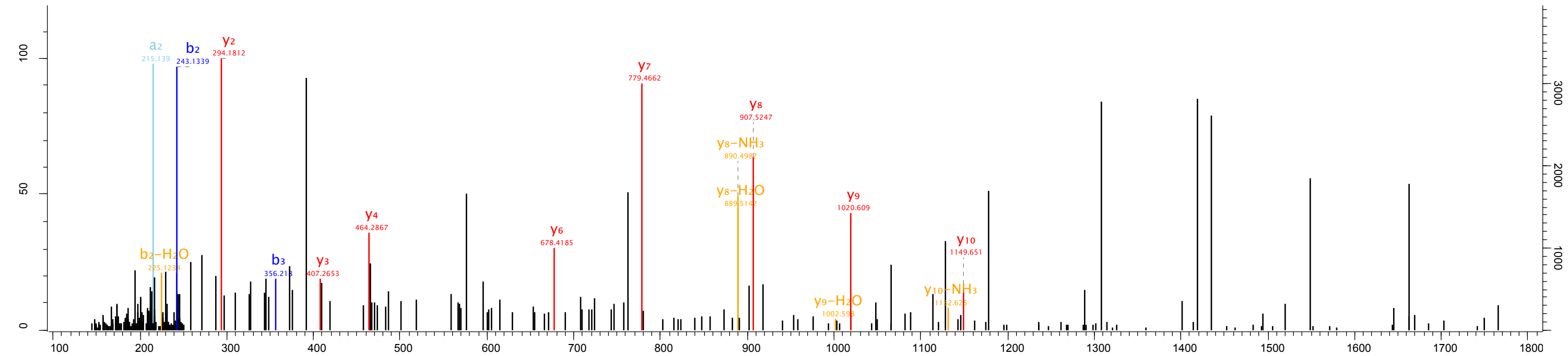
Raw file
20150307_MEF1_Top_opt_E1_01_1677

Scan 65612 Method TOF; CID Score 81.02 m/z 857.43 Gene names Rasa4



Raw file
20150307_MEF1_Top_opt_E1_01_1677

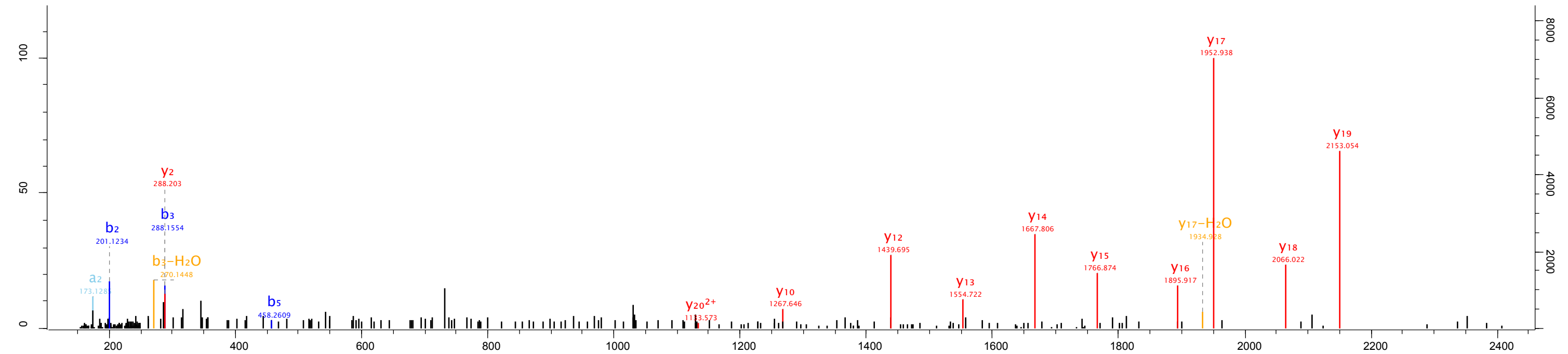
Scan 66367 Method TOF; CID Score 88.6 m/z 631.87 Gene names Casp6



- I E I Q T L T G L F K -
b₂ b₃ y₁₀ y₉ y₈ y₇ y₆ y₄ y₃ y₂

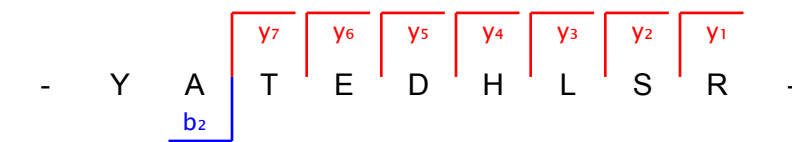
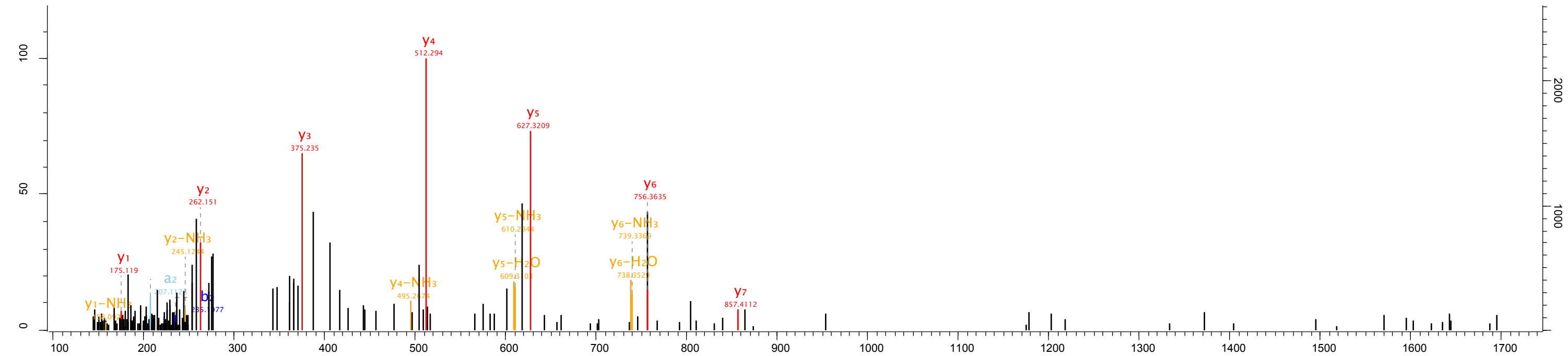
Raw file
20150307_MEF1_Top_opt_E1_01_1677

Scan 68185 Method TOF; CID Score 53.03 m/z 785.39 Gene names Tm9sf1



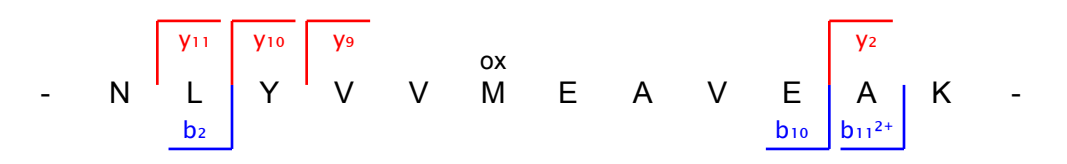
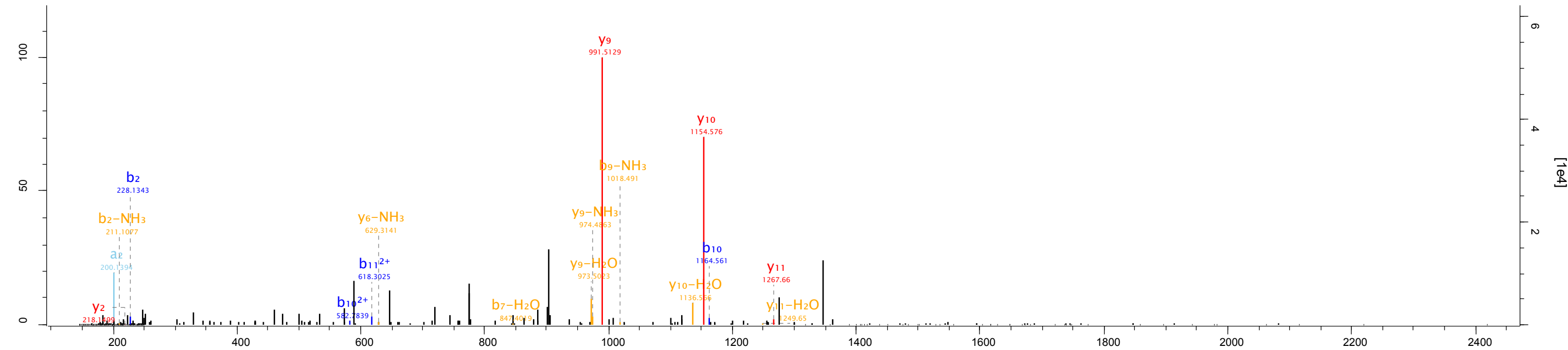
- S L S L G E V L D G D R M A E S L Y E I R -
b2 b3 b5 y20²⁺ y19 y18 y17 y16 y15 y14 y13 y12 y10 y2

Raw file 20150307_MEF1_Top_opt_E1_01_1684 Scan 8950 Method TOF; CID Score 71.61 m/z 364.51 Gene names Tm4sf1



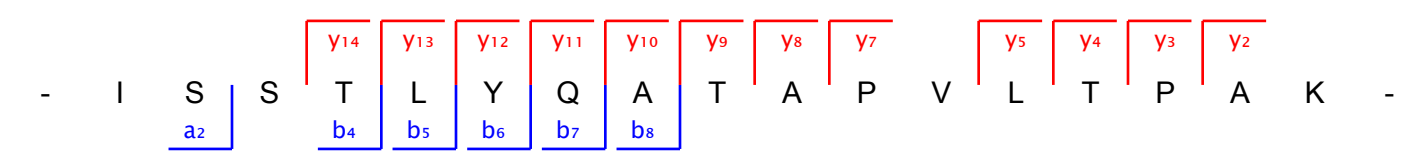
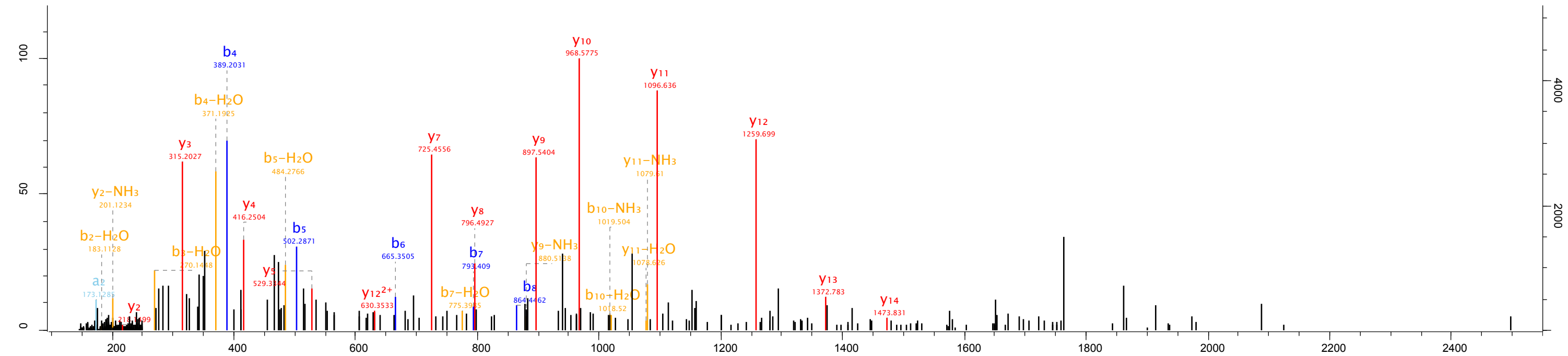
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20150307_MEF1_Top_opt_E1_01_1684

Scan 21987 Method TOF; CID Score 60.26 m/z 461.23 Gene names Gsdma3



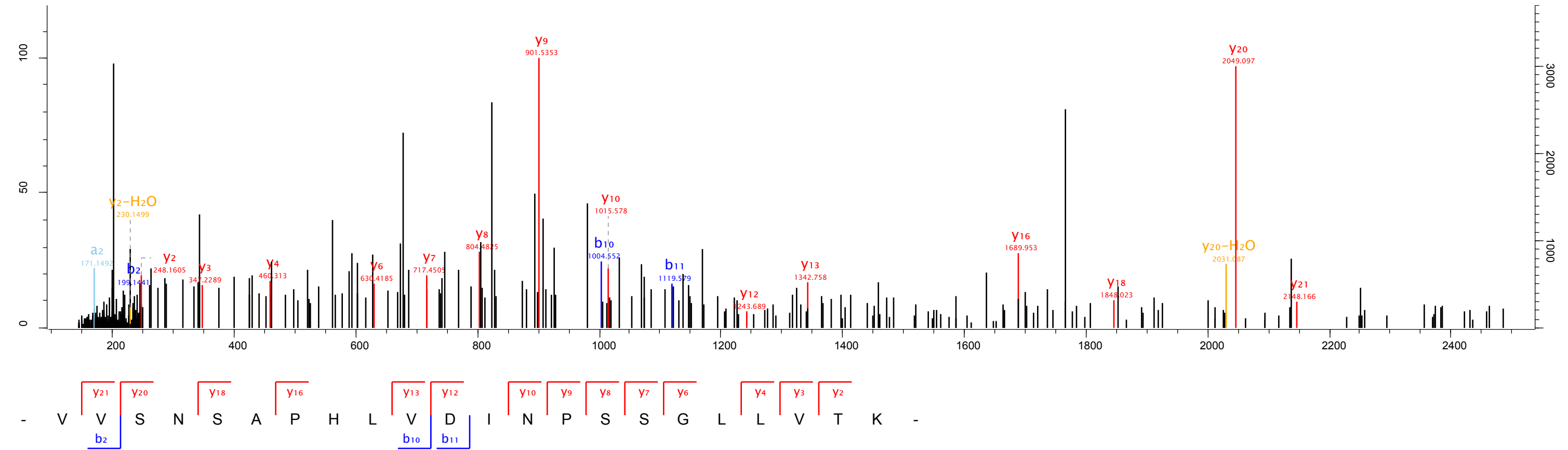
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20150307_MEF1_Top_opt_E1_01_1684

Scan 47497 Method TOF; CID Score 100.04 m/z 880.99 Gene names Krtcap2

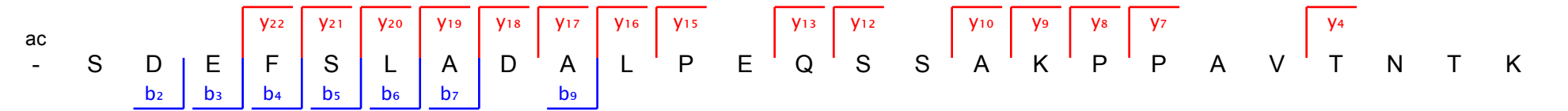
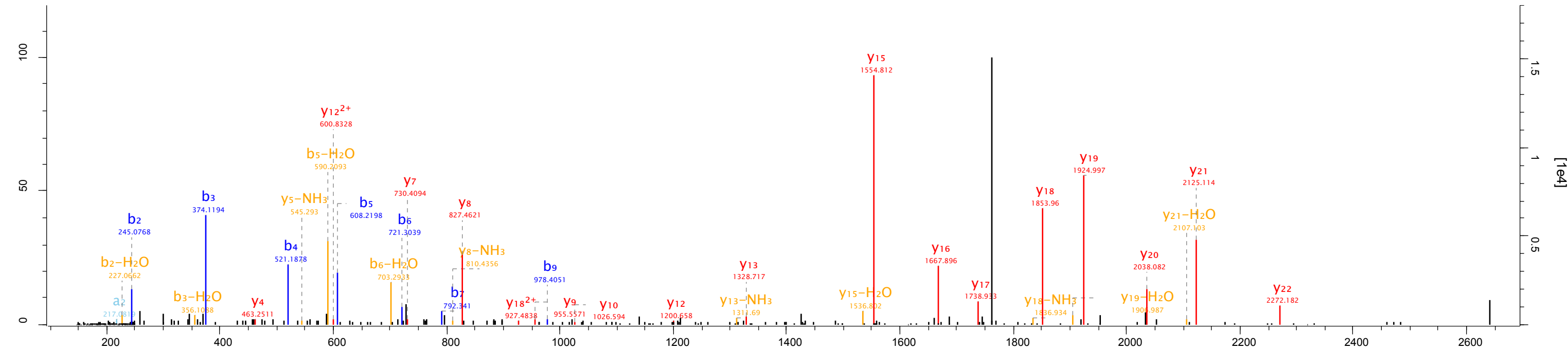


Raw file
20150307_MEF1_Top_opt_E1_01_1684

Scan	Method	Score	m/z	Gene names
51804	TOF; CID	35.81	750.08	Pcdh19

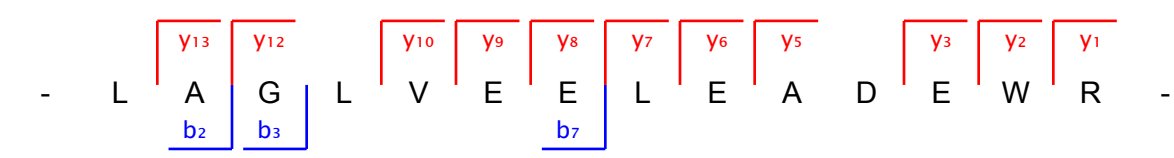
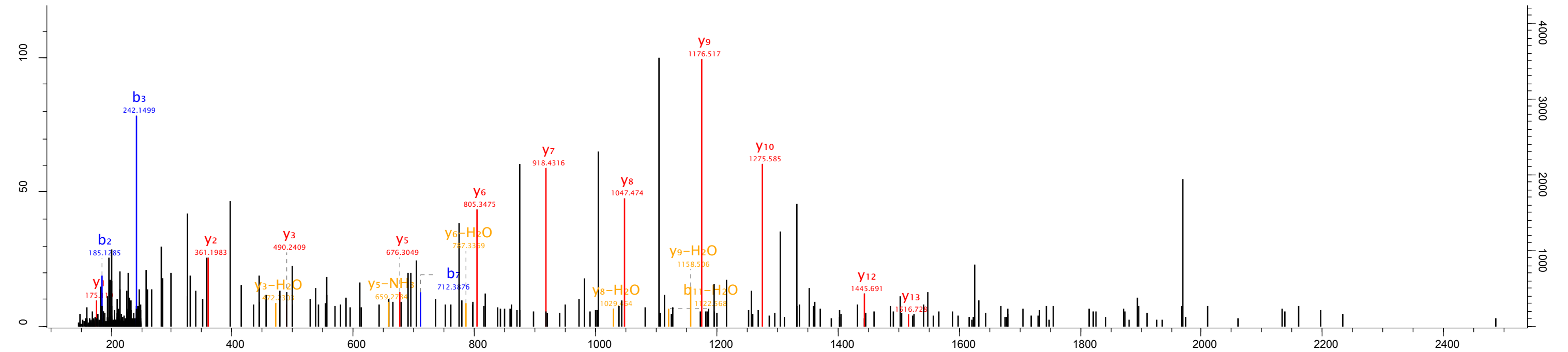


Raw file 20150307_MEF1_Top_opt_E1_01_1684 Scan 54948 Method TOF; CID Score 158.37 m/z 882.77 Gene names Mapk1ip1l



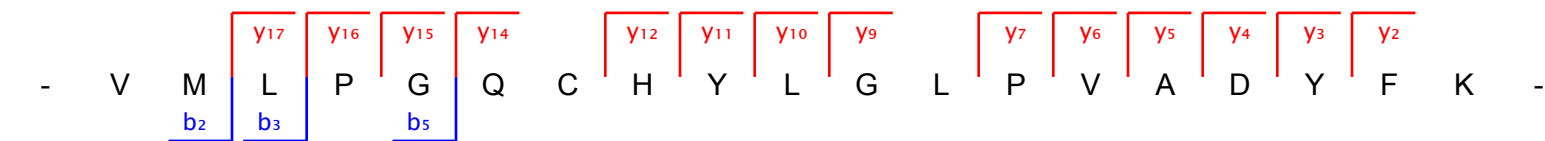
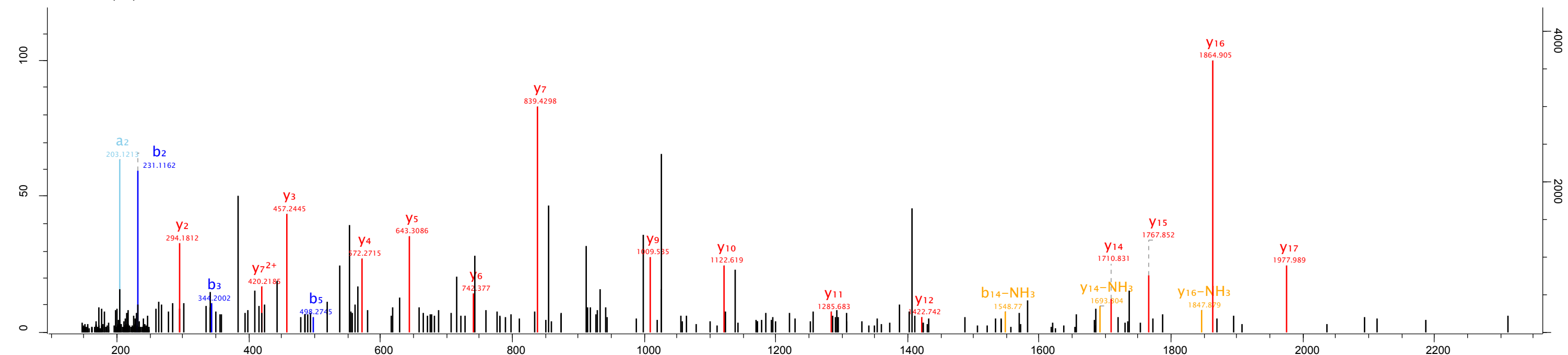
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20150307_MEF1_Top_opt_E1_01_1684

Scan 62588 Method TOF; CID Score 52.01 m/z 815.4 Gene names Anapc16

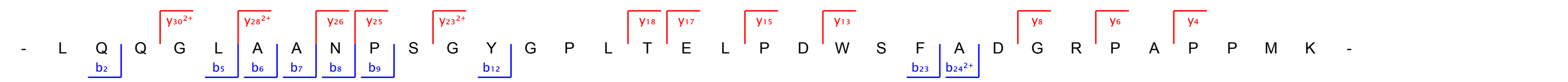
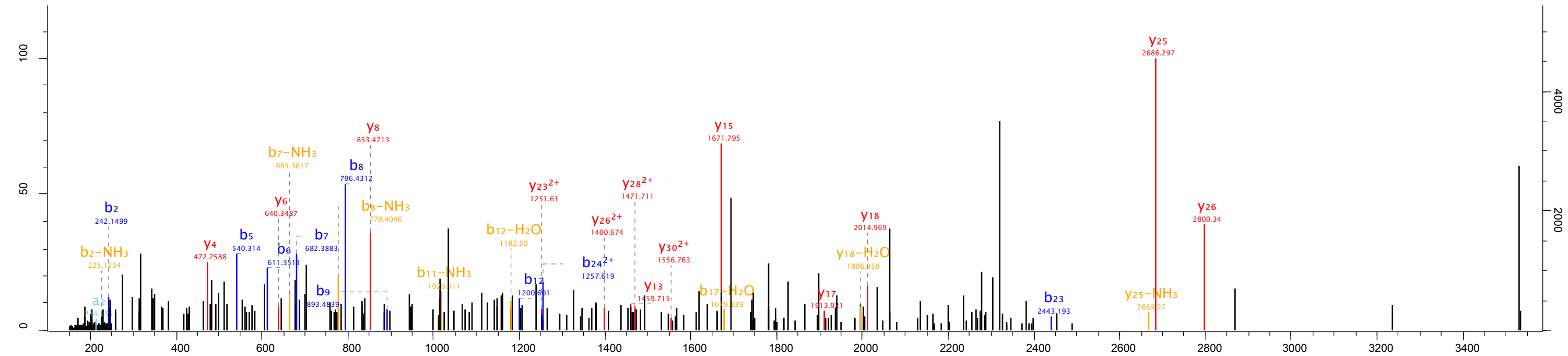


Raw file
20150307_MEF1_Top_opt_E1_01_1684

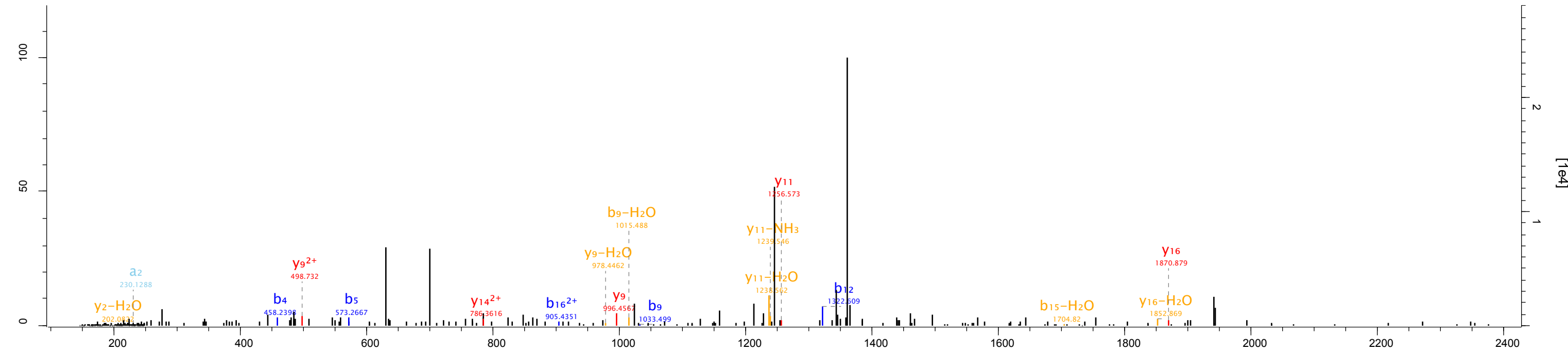
Scan 63743 Method TOF; CID Score 79.68 m/z 737.03 Gene names Eri3



Raw file 20150307_MEF1_Top_opt_E1_01_1684 Scan 66442 Method TOF; CID Score 42.73 m/z 1161.24 Gene names Mrpl52



Raw file 20150307_MEF2_Top_opt_E2_01_1679 Scan 15449 Method TOF; CID Score 40.24 m/z 486.23 Gene names 1700034J04Rik



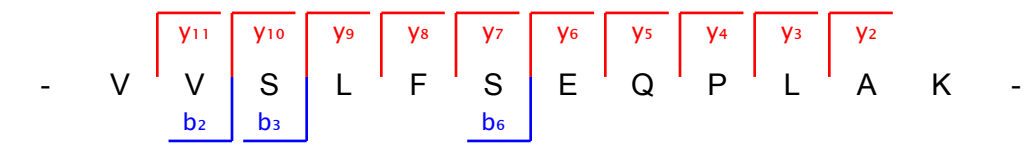
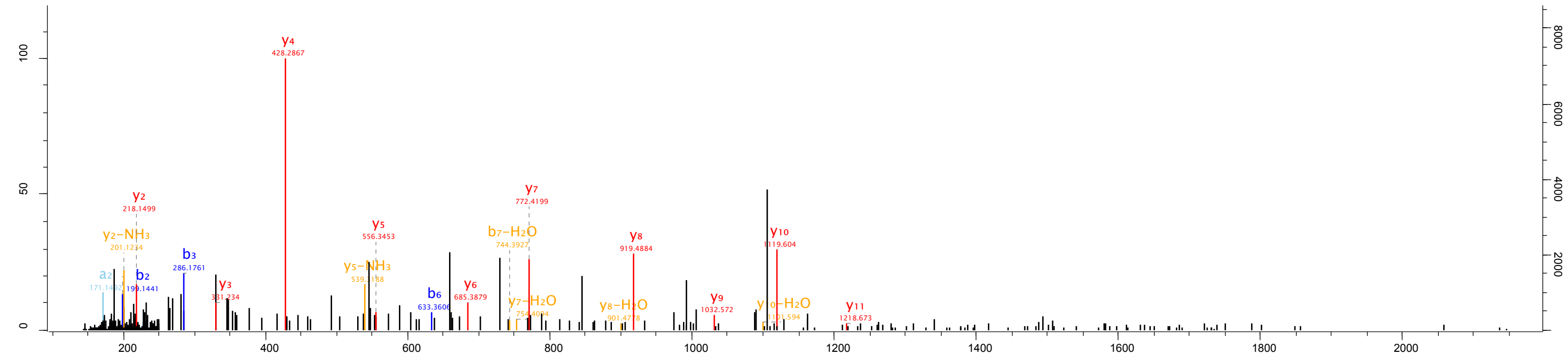
- A W L S D L Y P S S M A F P R S N -

Fragmentation mapping (red boxes): y16 (W), y14²⁺ (S), y11 (Y), y9 (S)

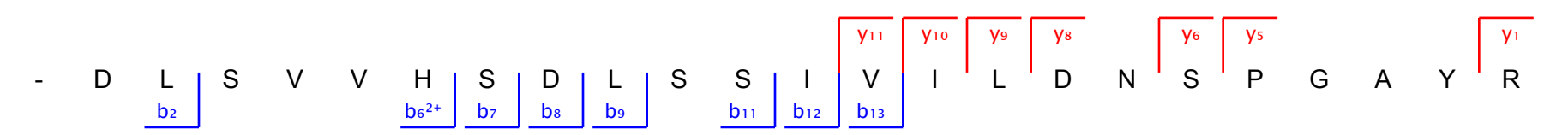
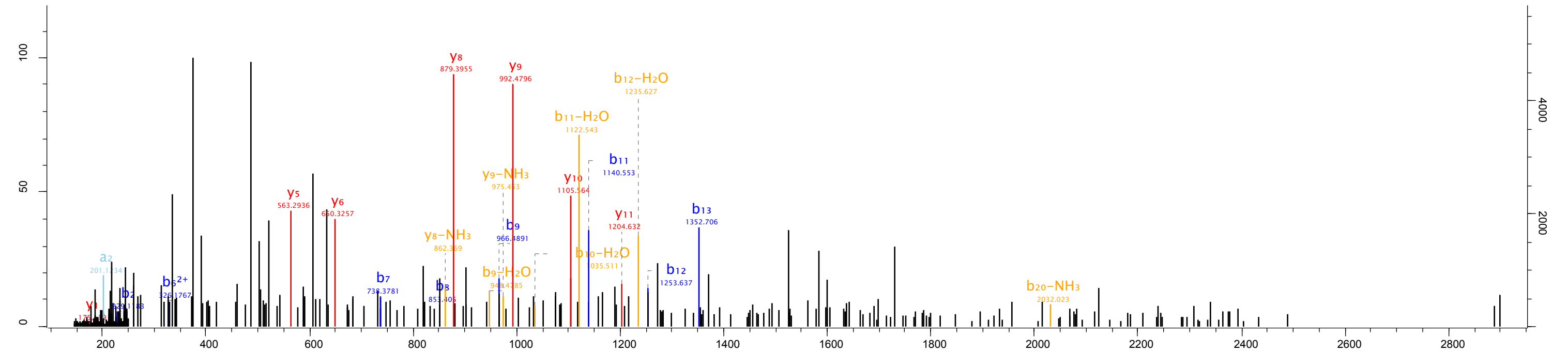
Fragmentation mapping (blue boxes): a2 (W), b4 (S), b5 (D), b9 (S), b12 (A), b16²⁺ (R)

Raw file
20150307_MEF2_Top_opt_E2_01_1679

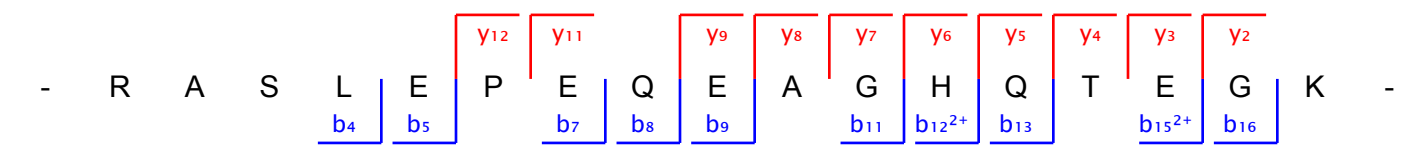
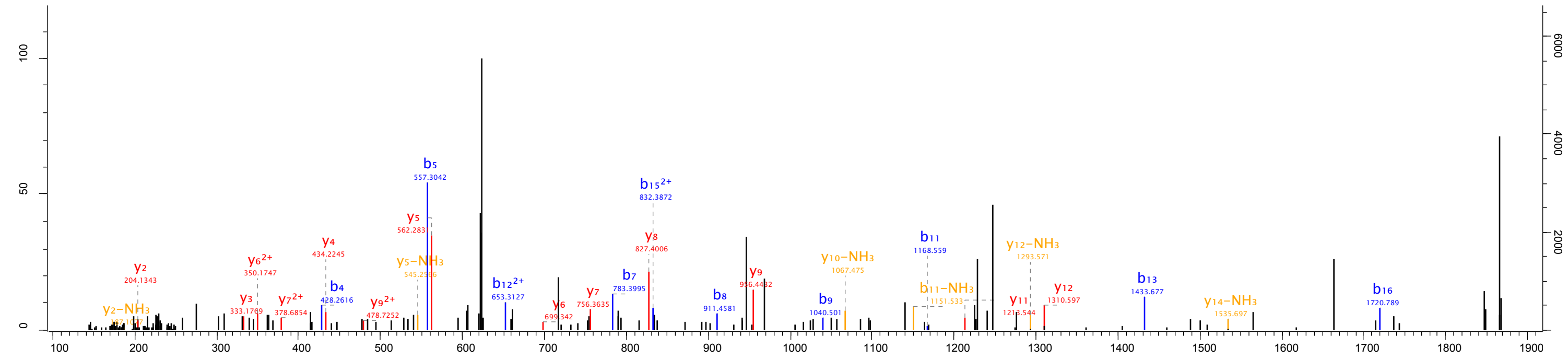
Scan 48023 Method TOF; CID Score 81.68 m/z 659.37 Gene names Mrps33



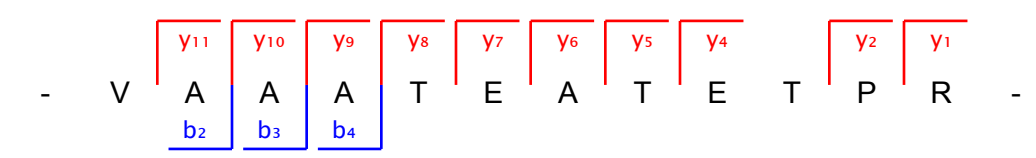
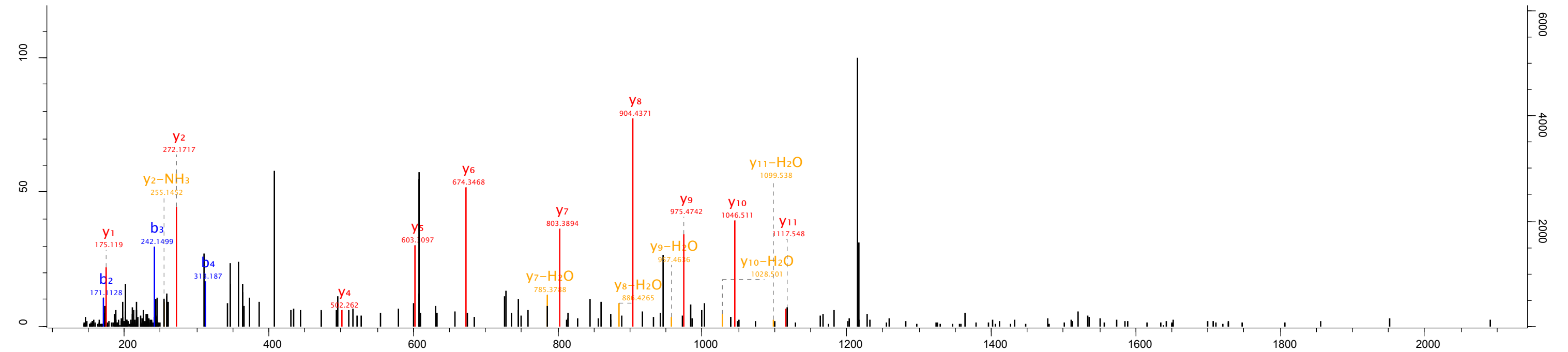
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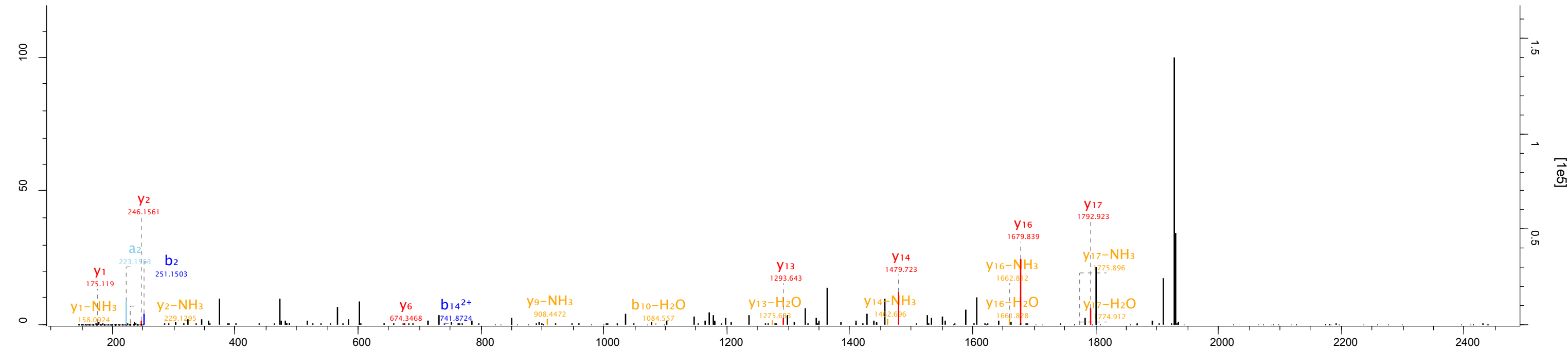


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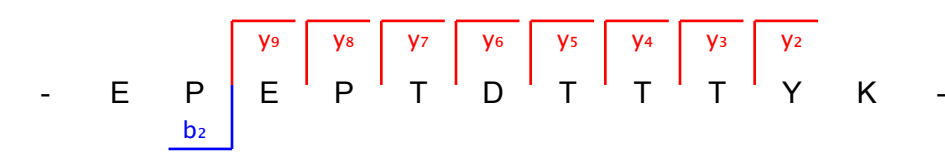
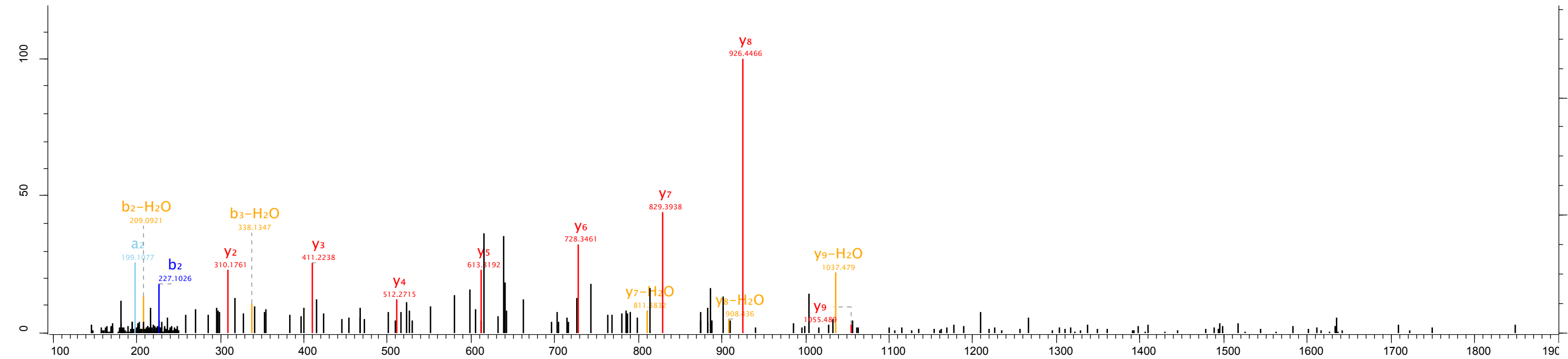
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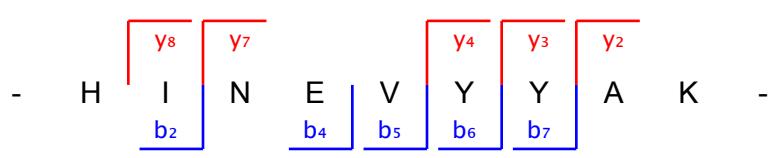
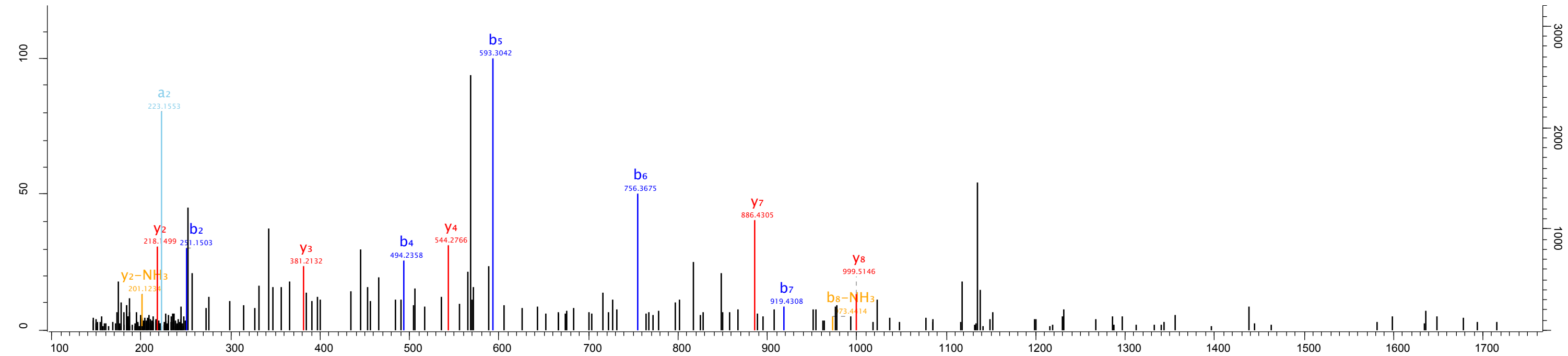


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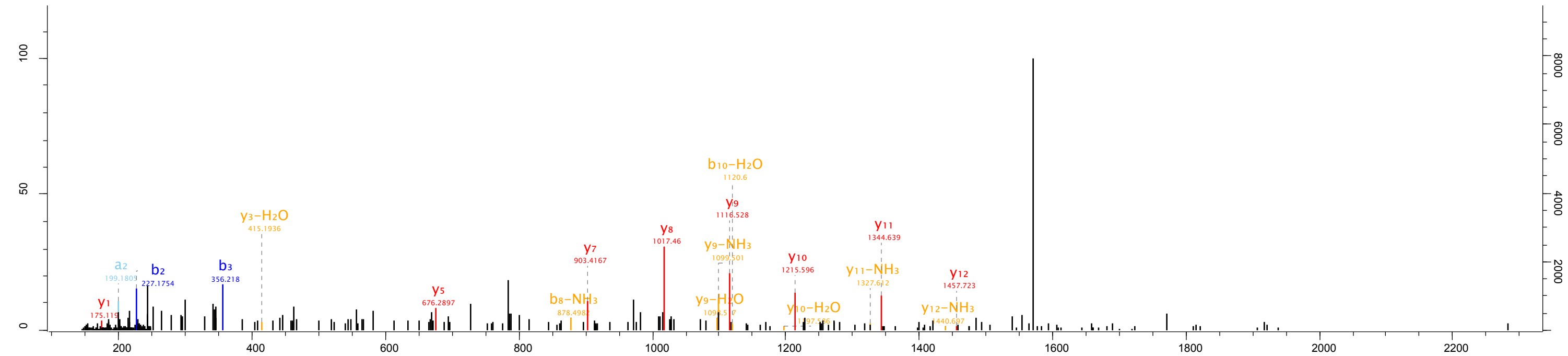


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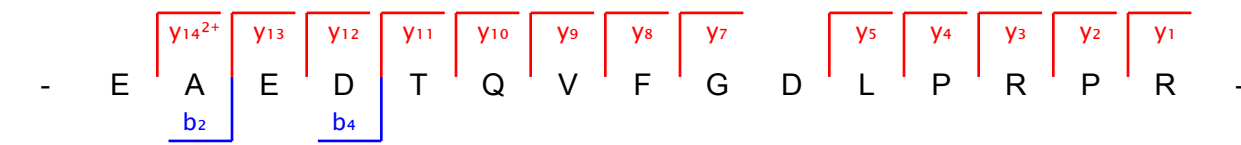
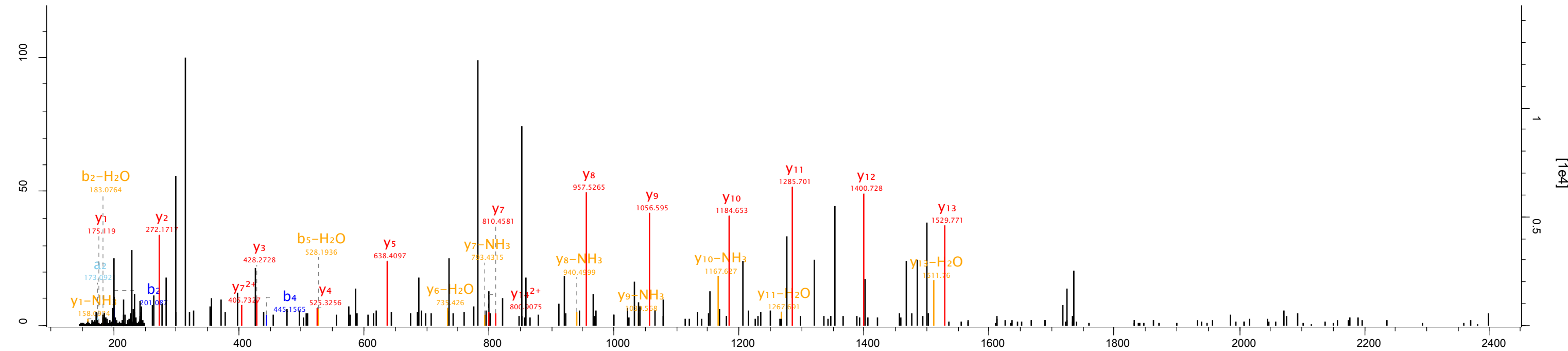
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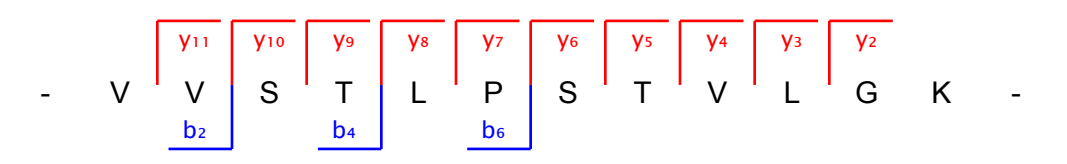
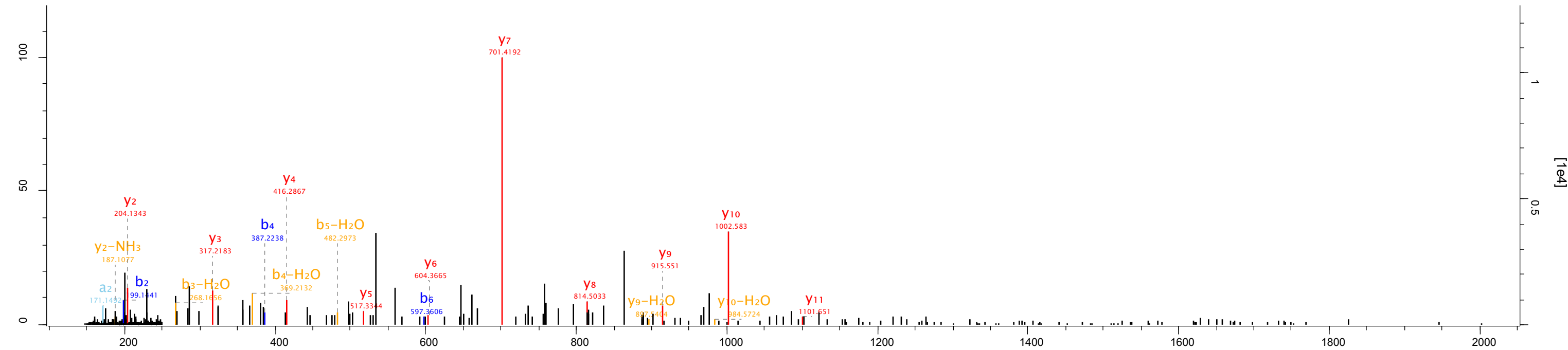


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b₂ b₃

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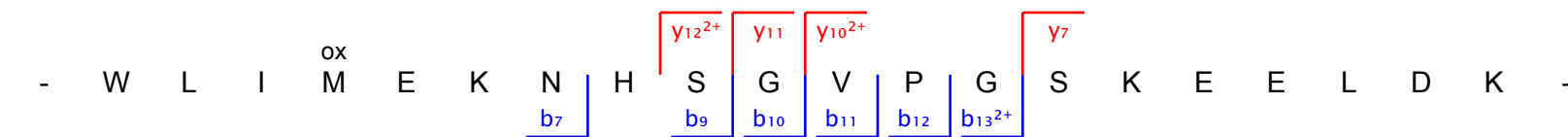
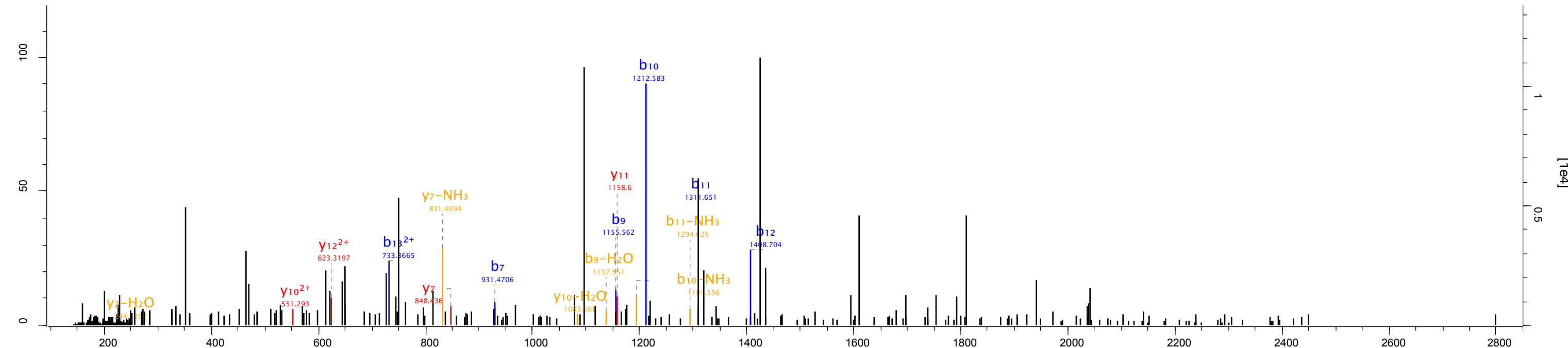


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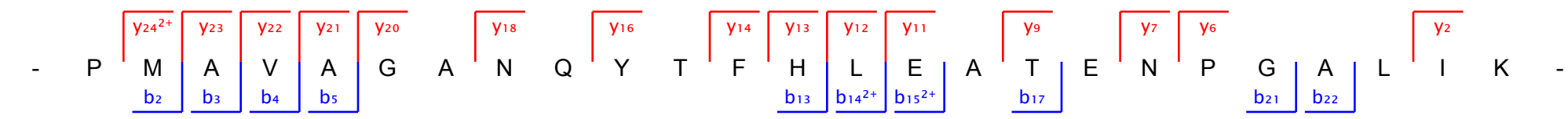
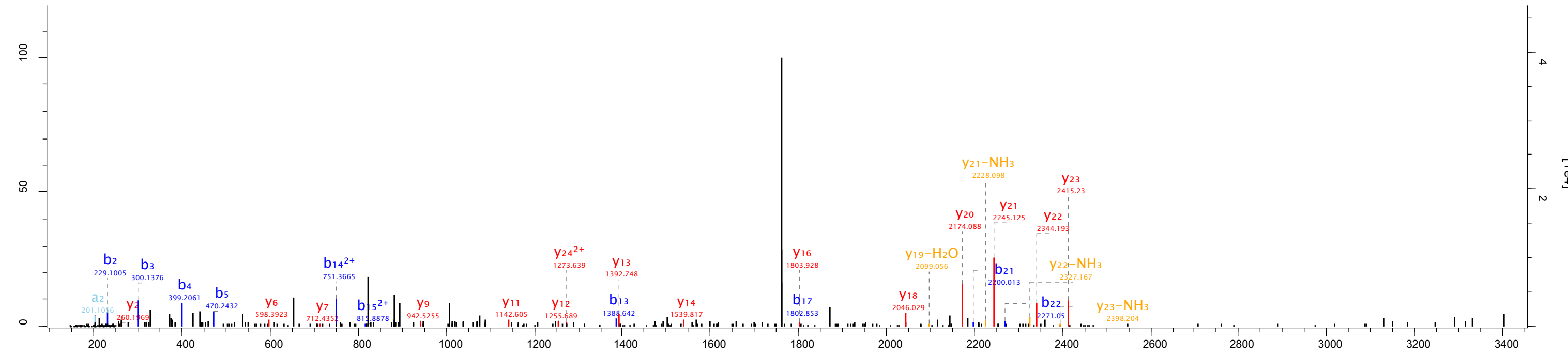


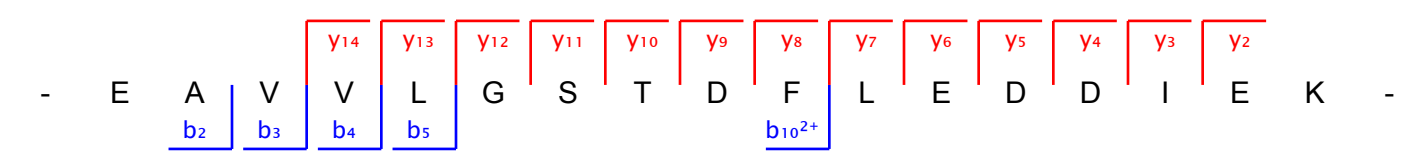
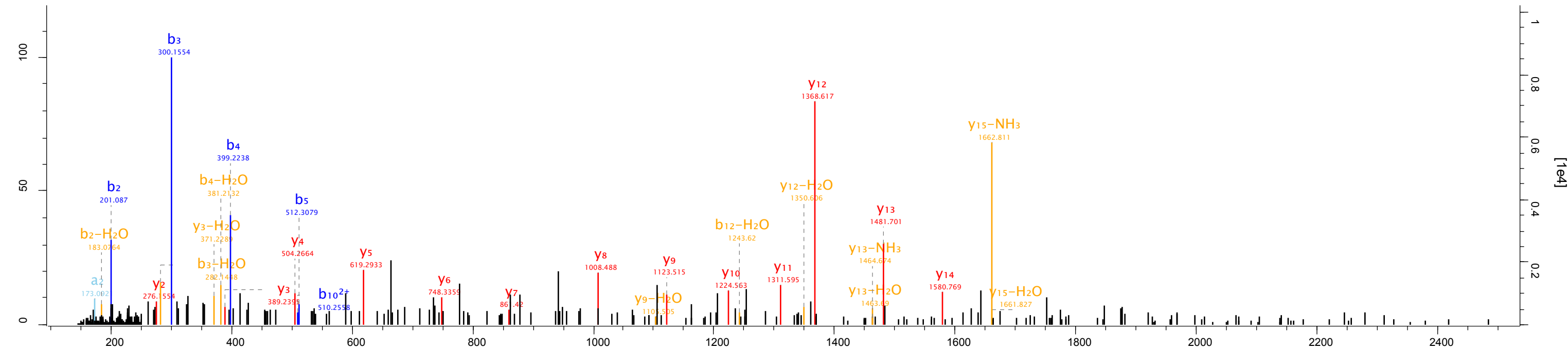
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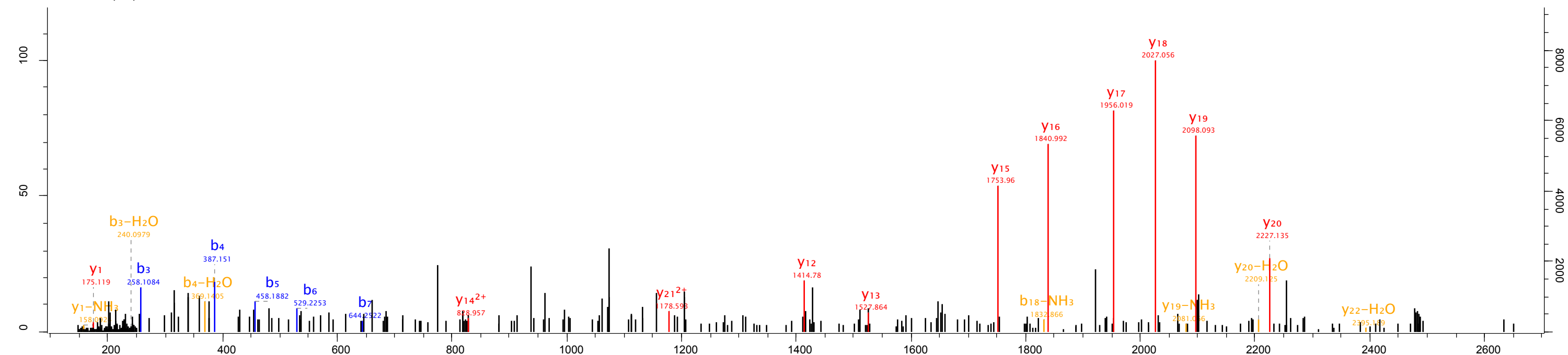


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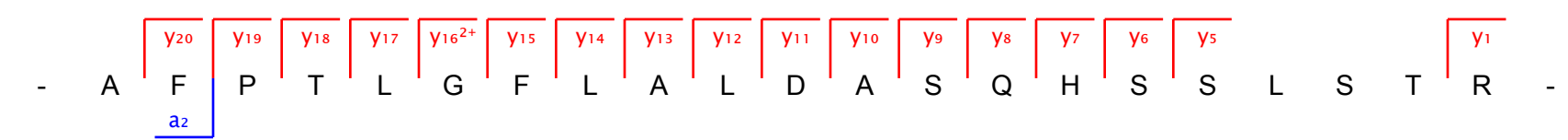
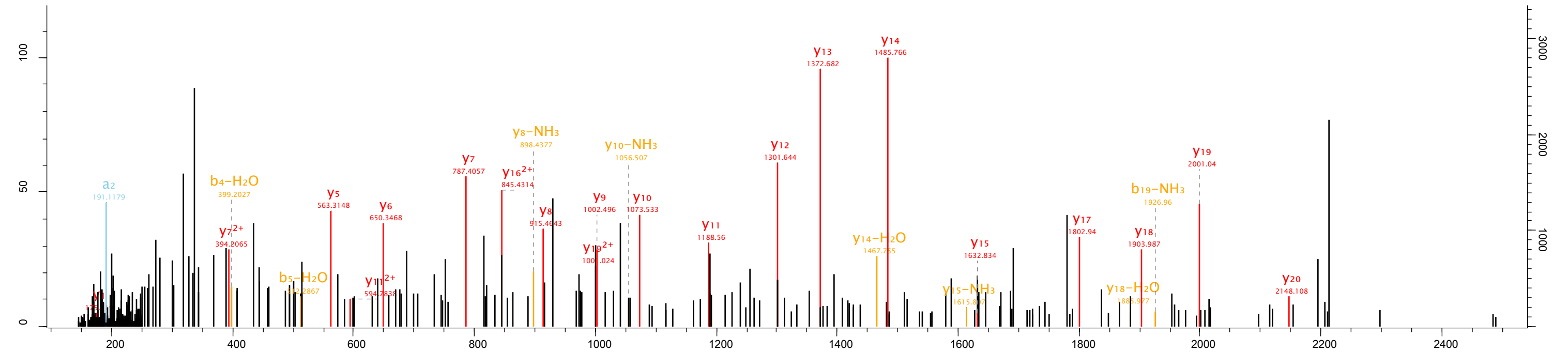


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y₂₁²⁺
y₂₀
y₁₉
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y₁

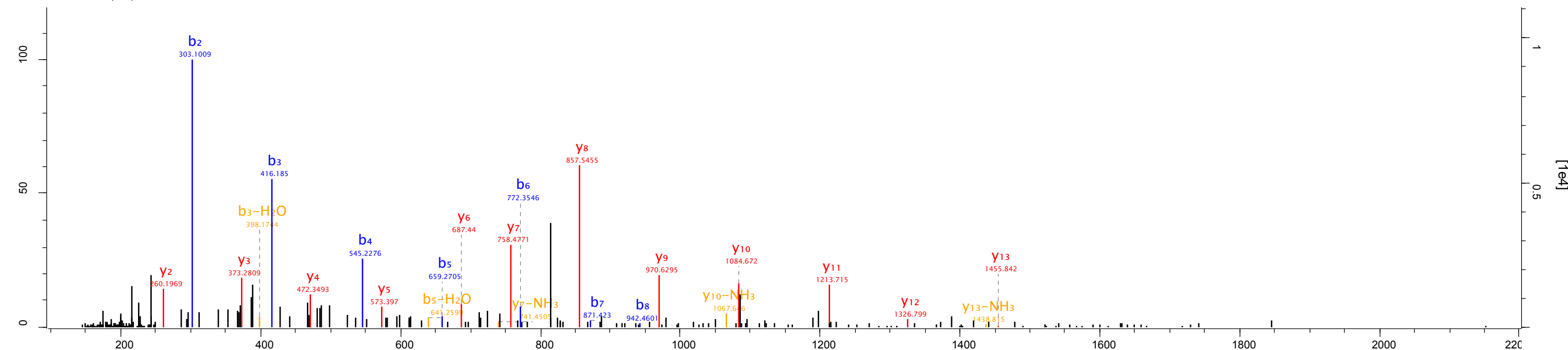
b₃
b₄
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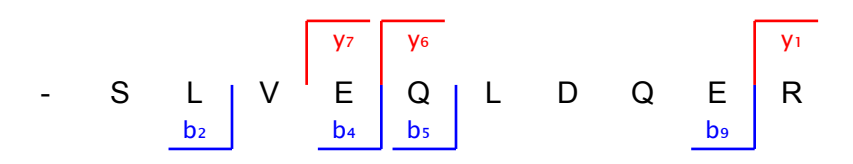
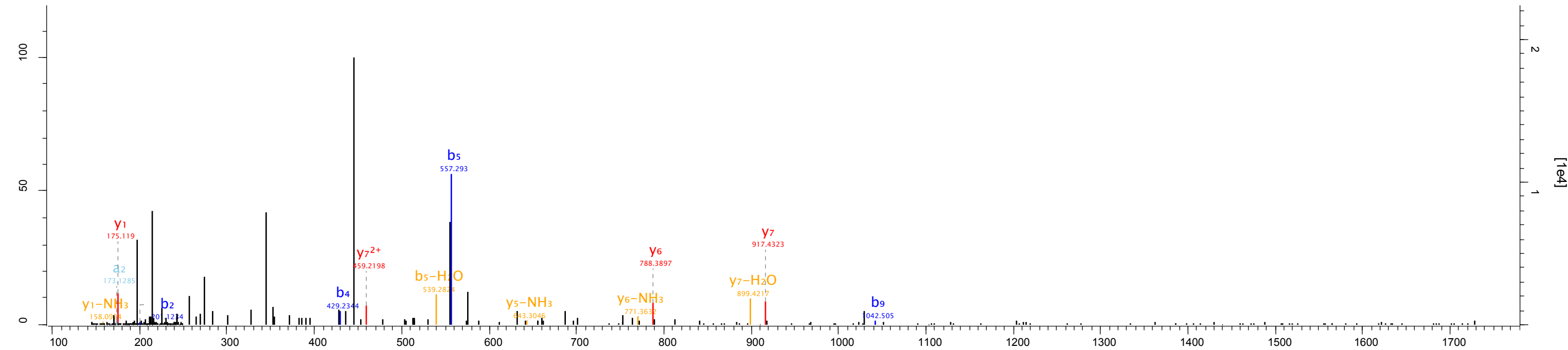
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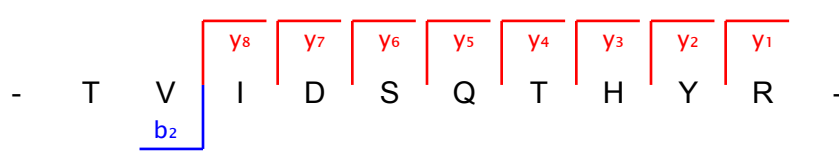
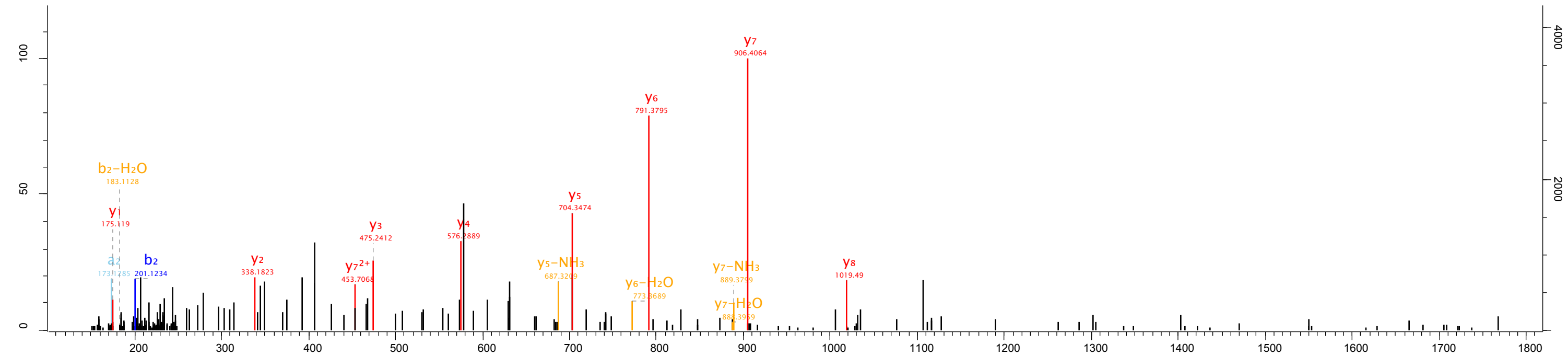
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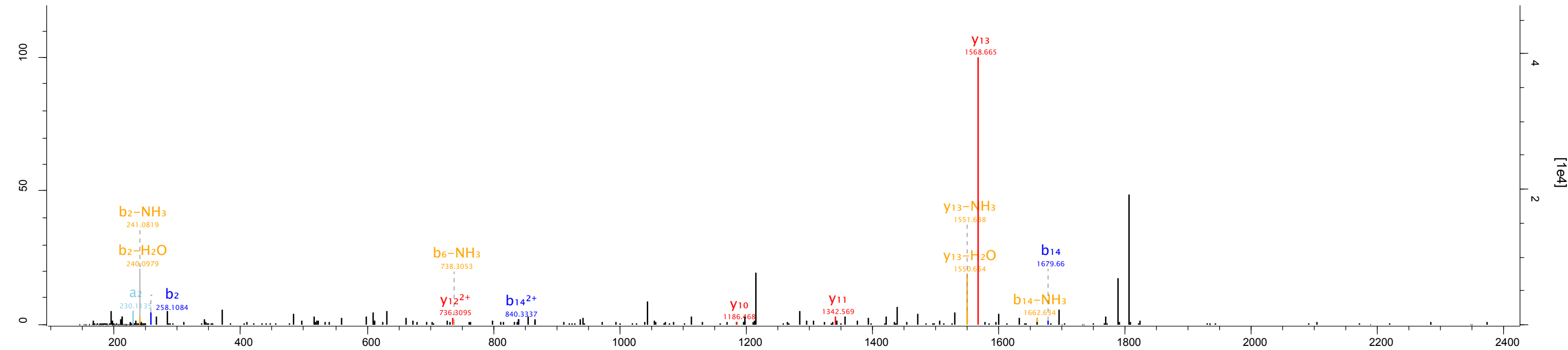


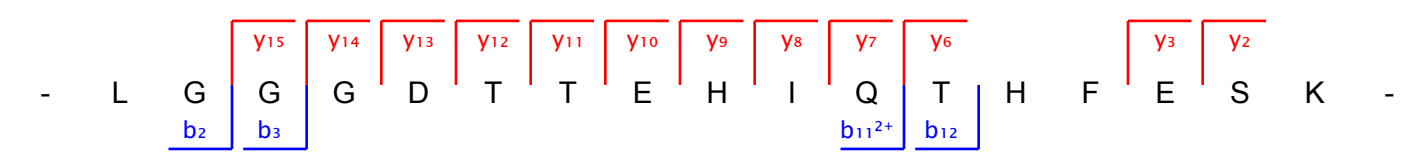
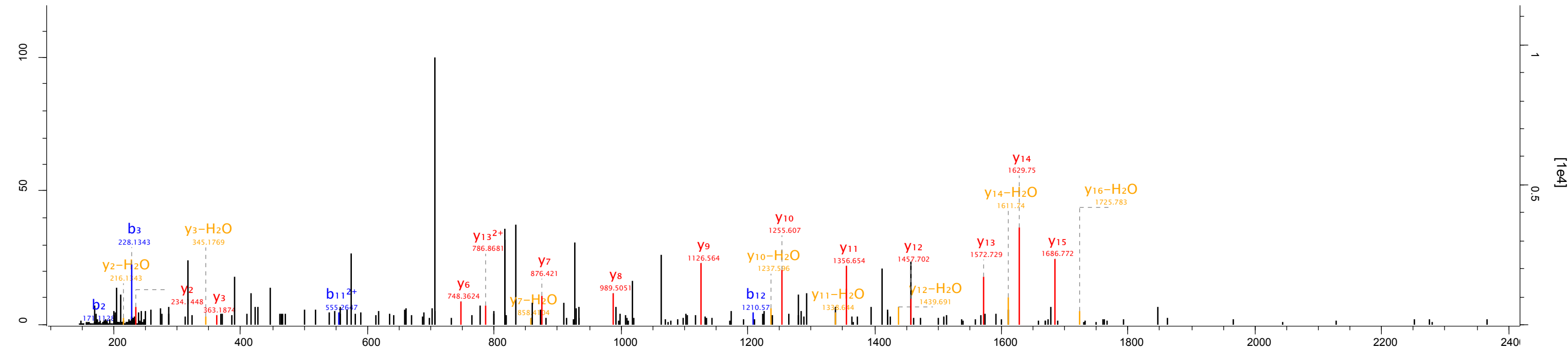
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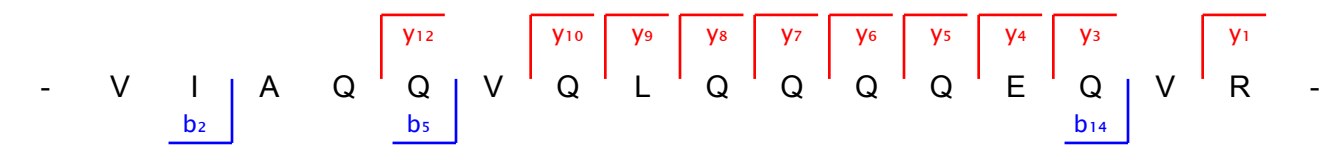
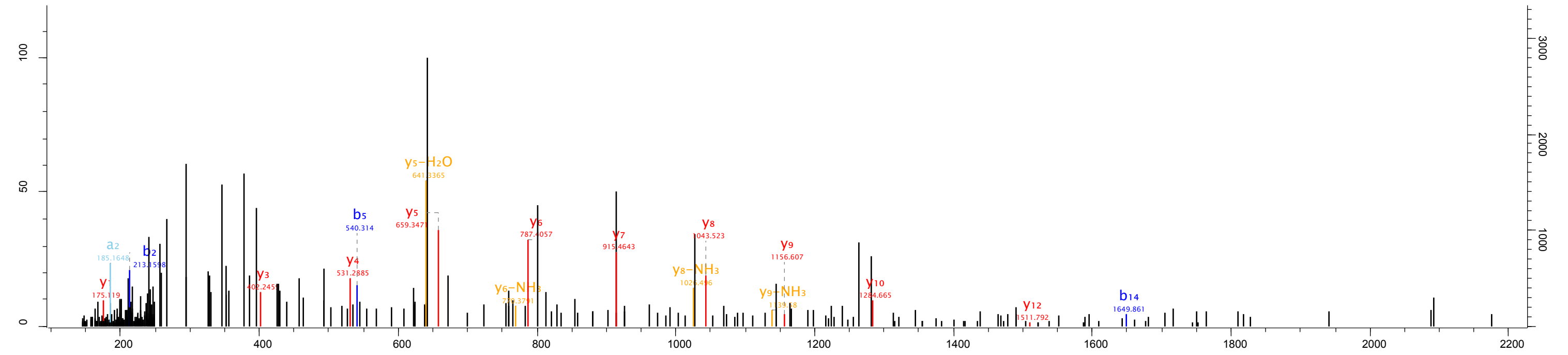
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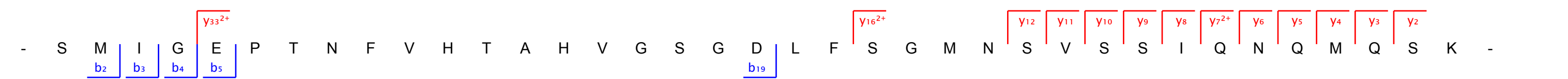
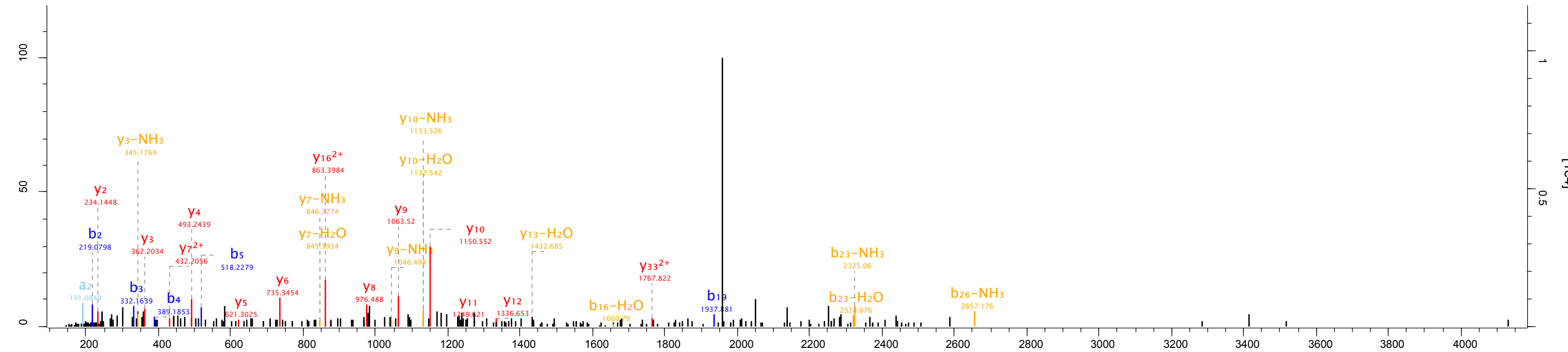


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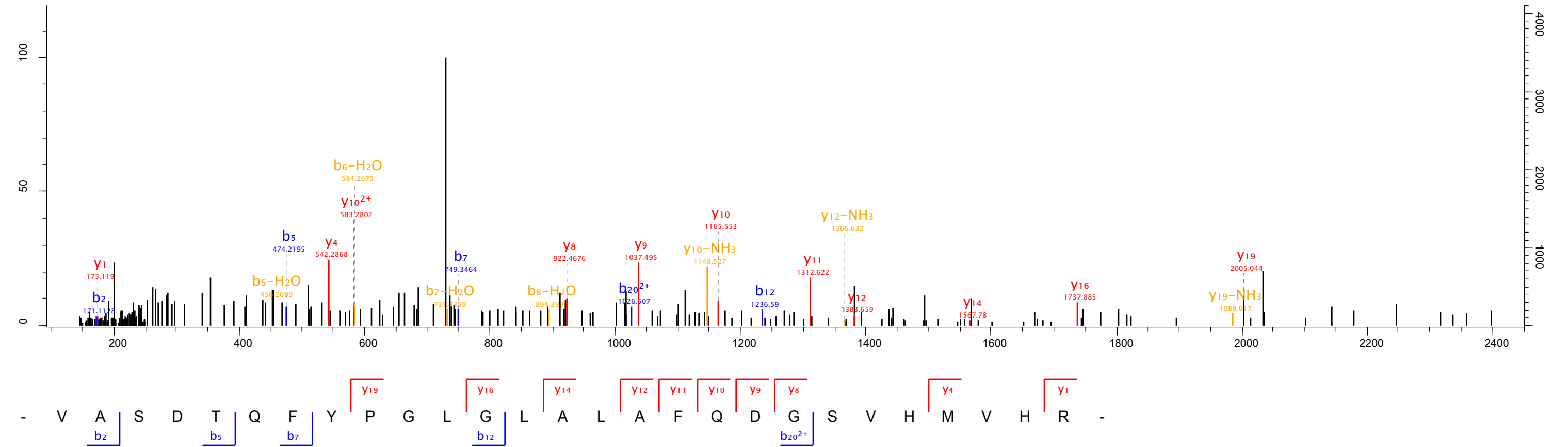
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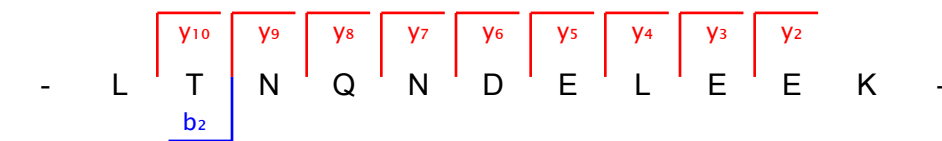
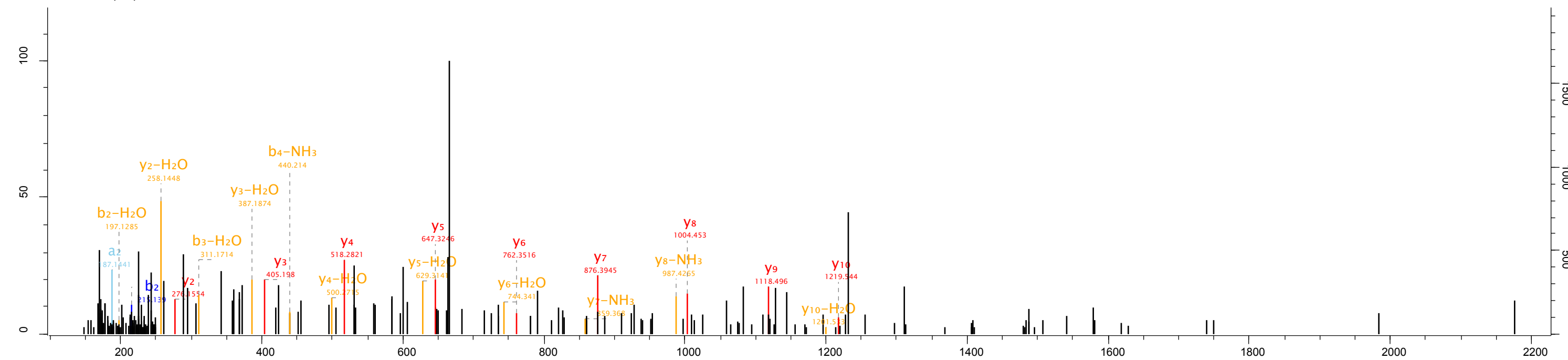
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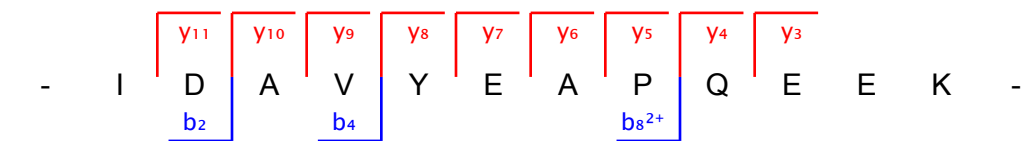
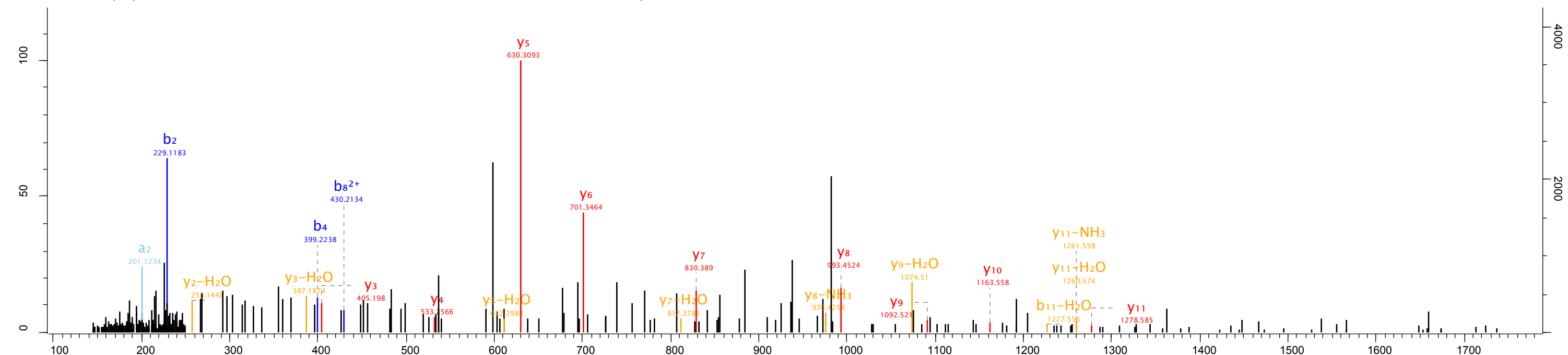


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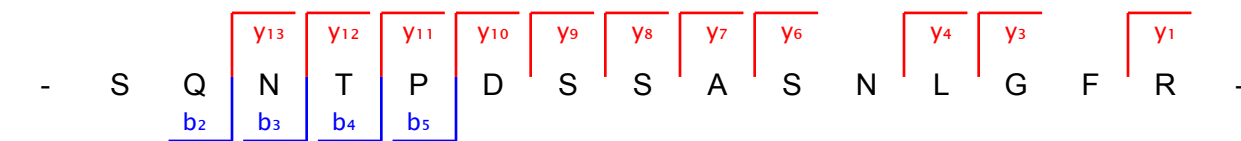
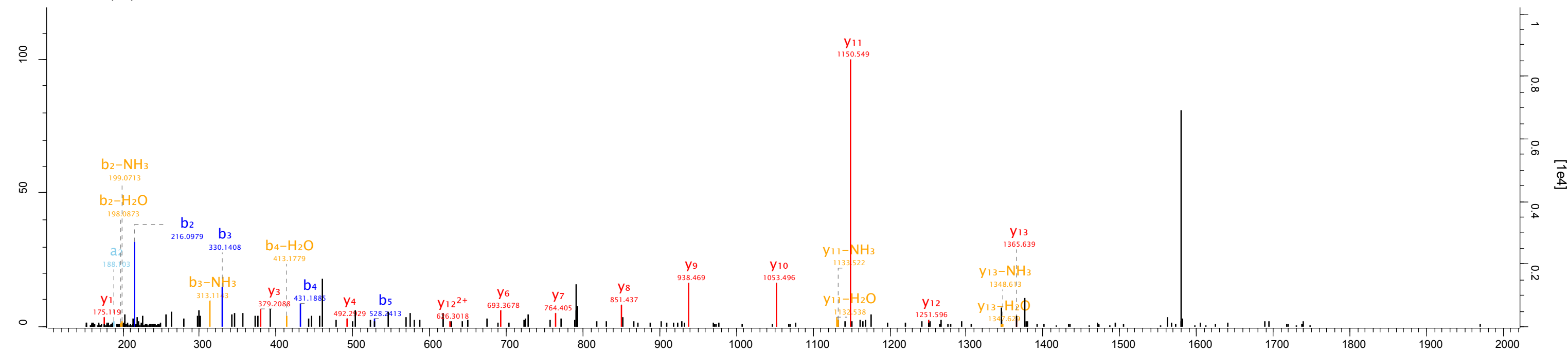
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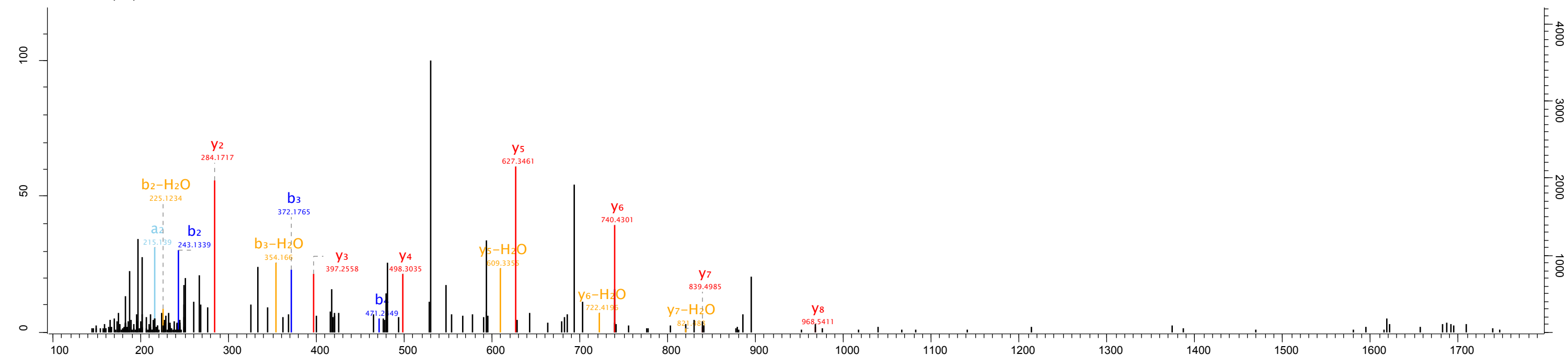


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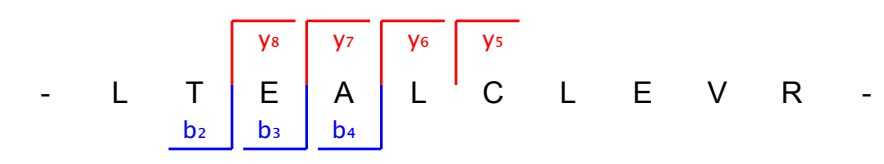
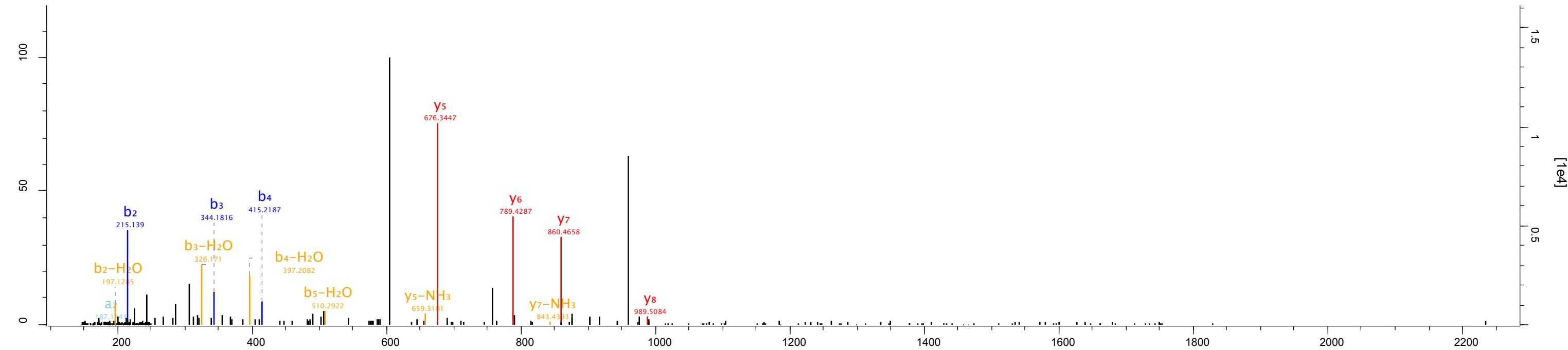
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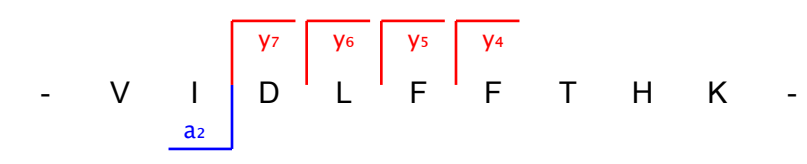
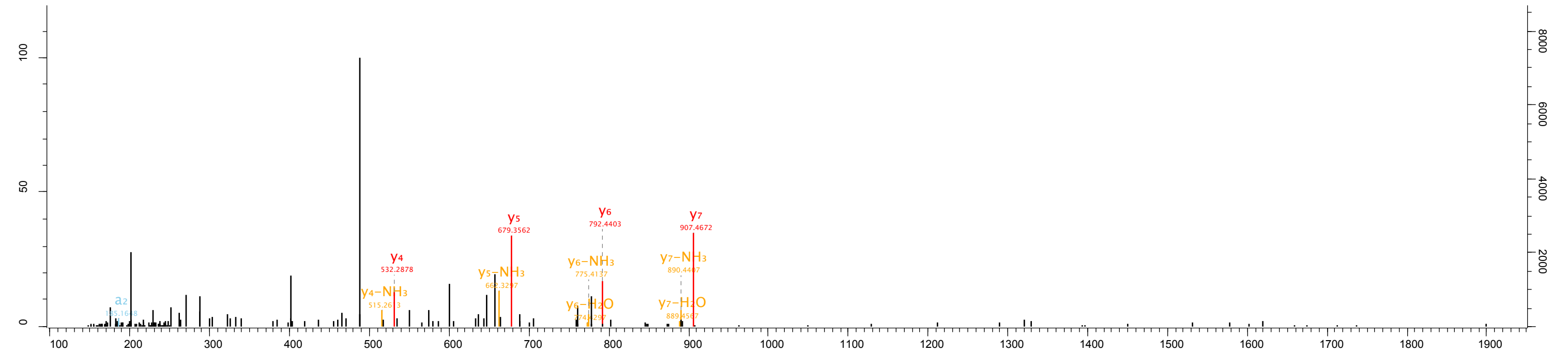
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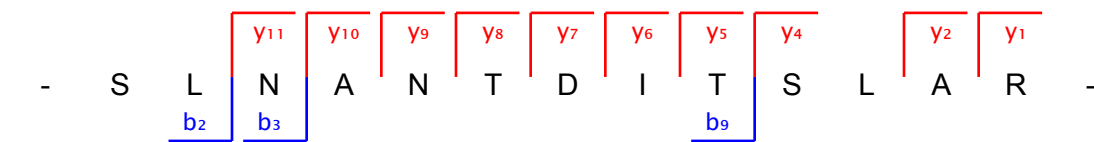
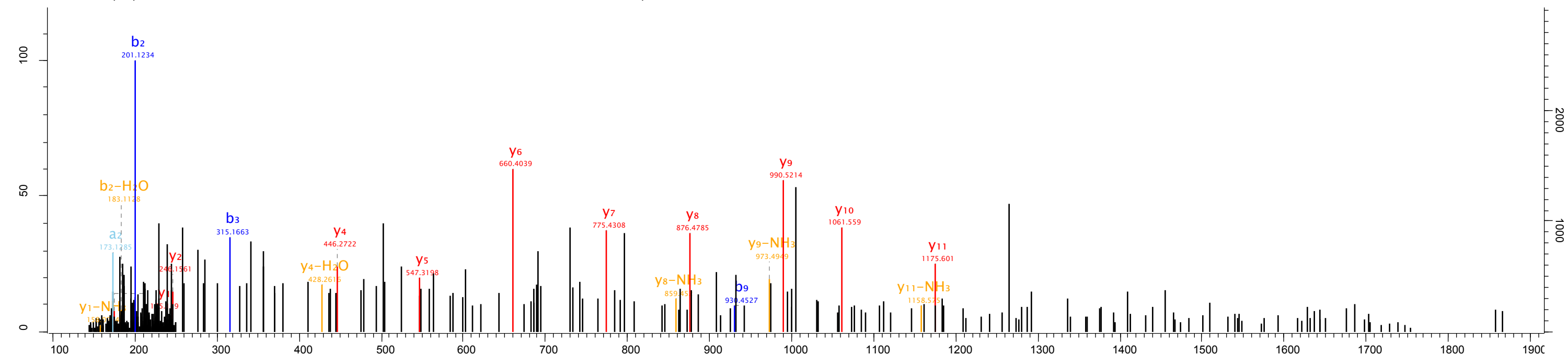
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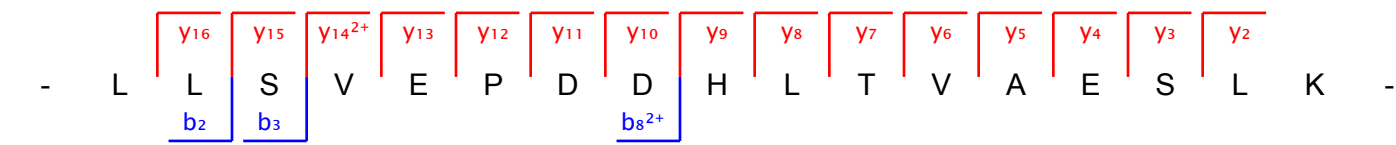
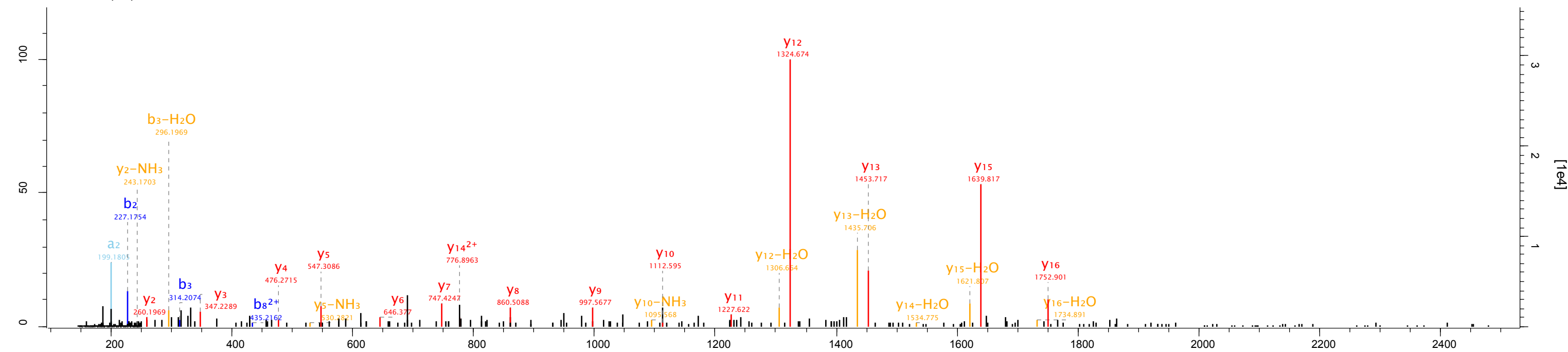


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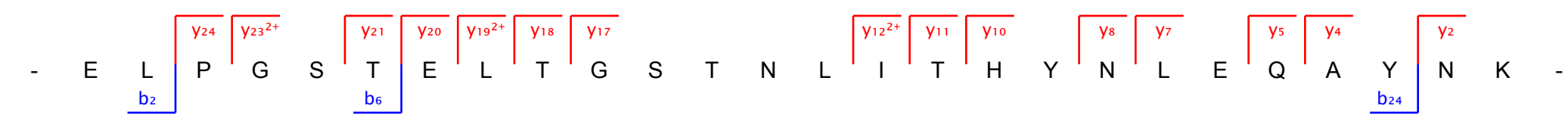
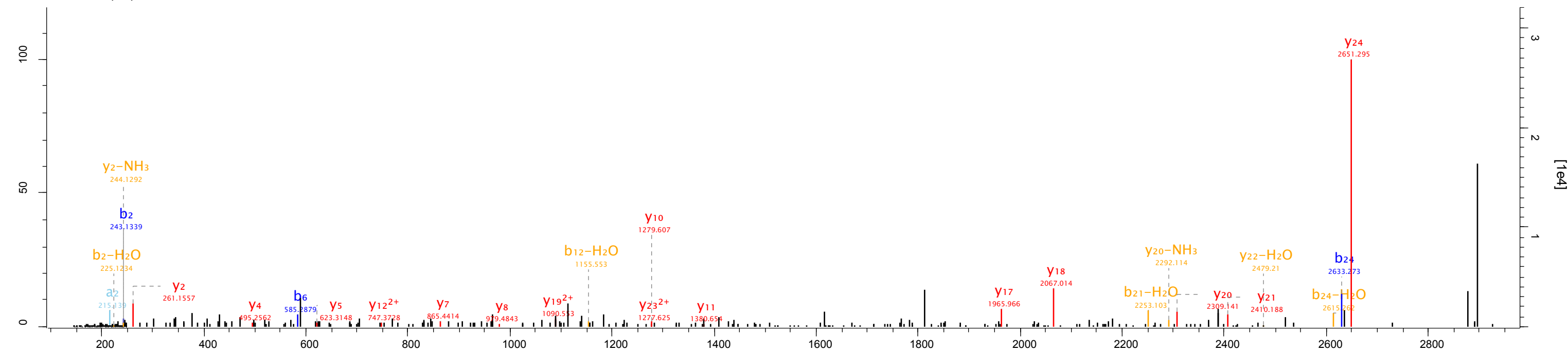


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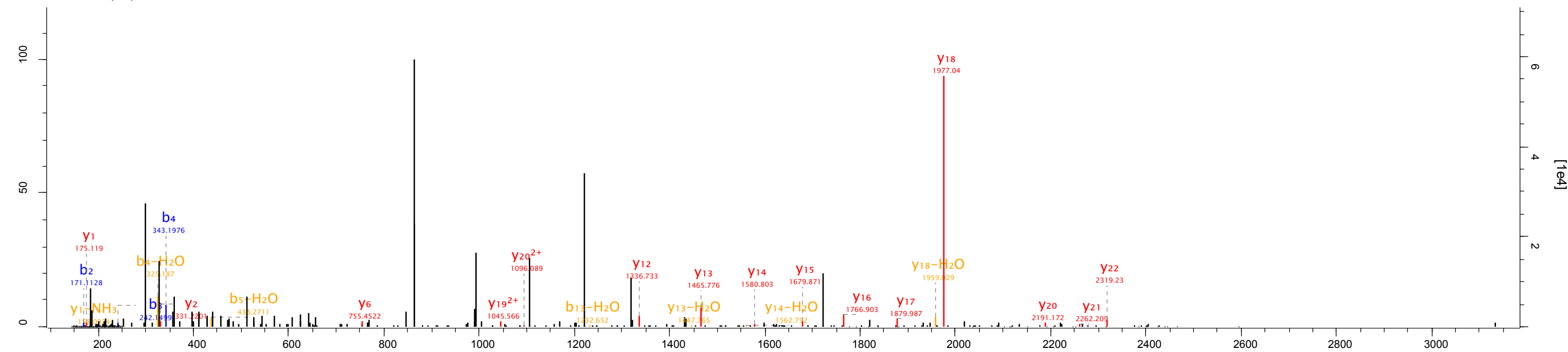


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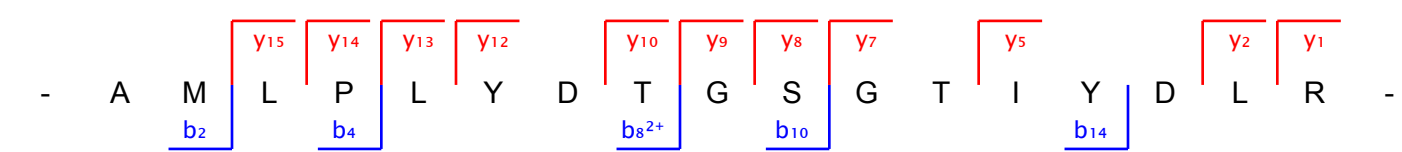
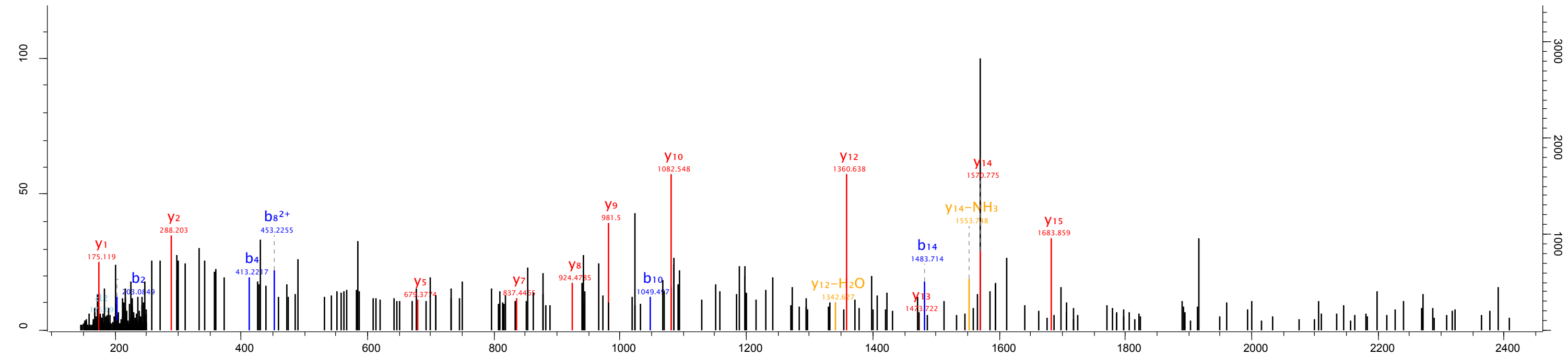


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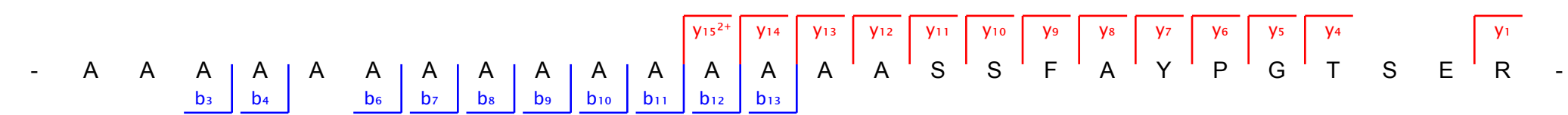
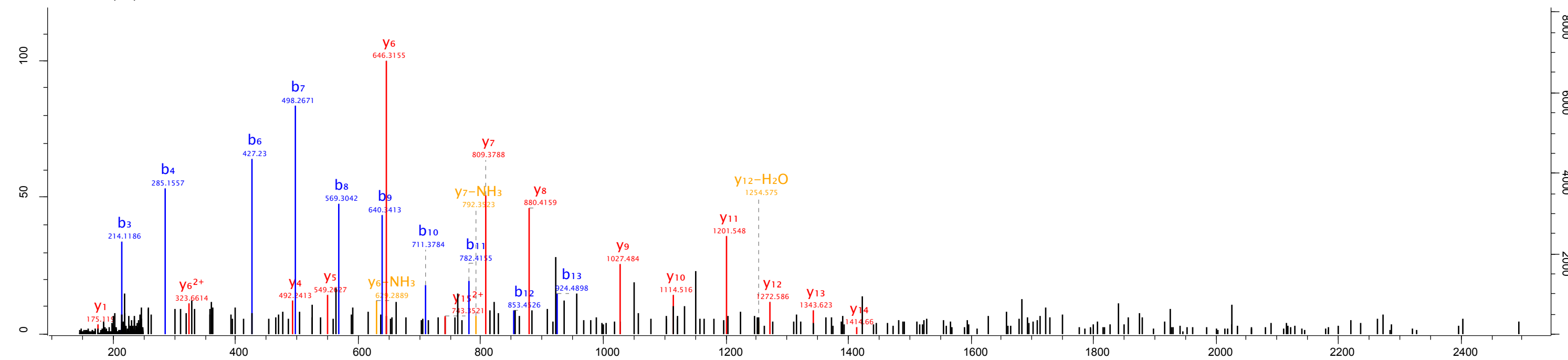


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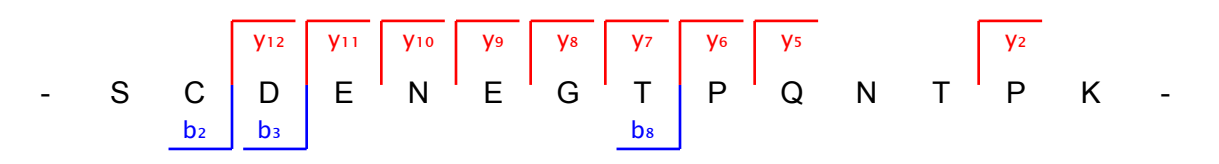
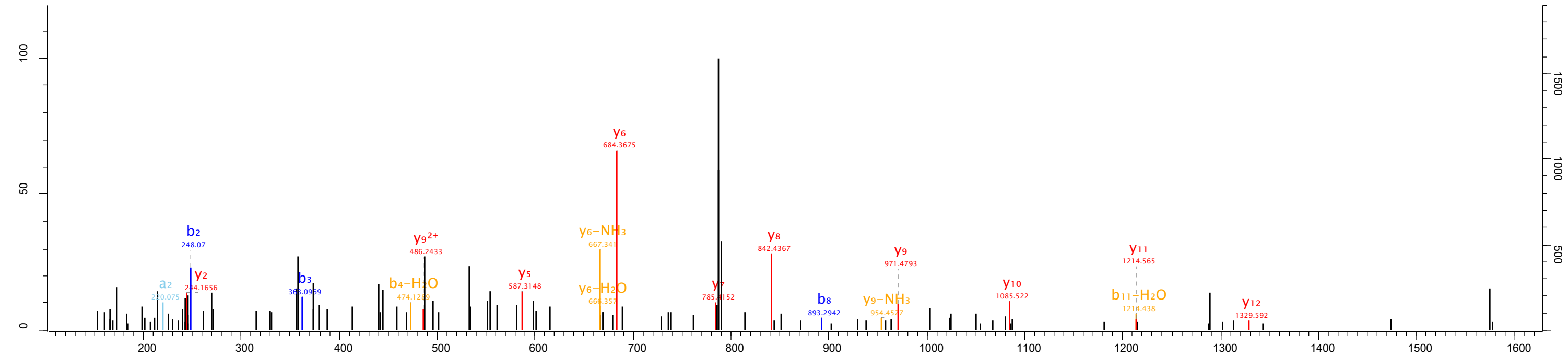
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Scan Method Score m/z Gene names
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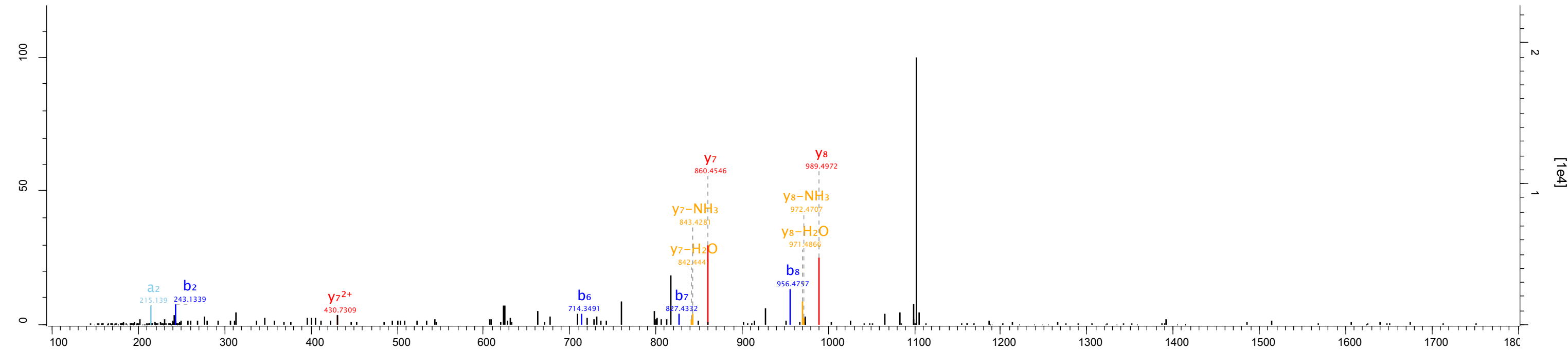
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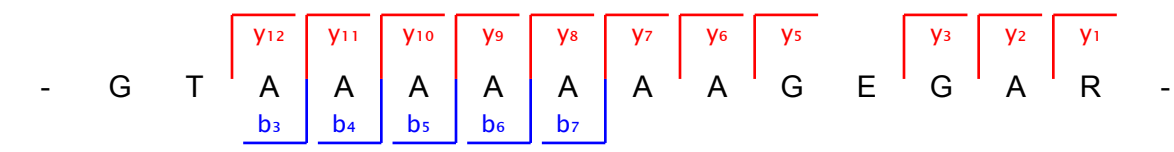
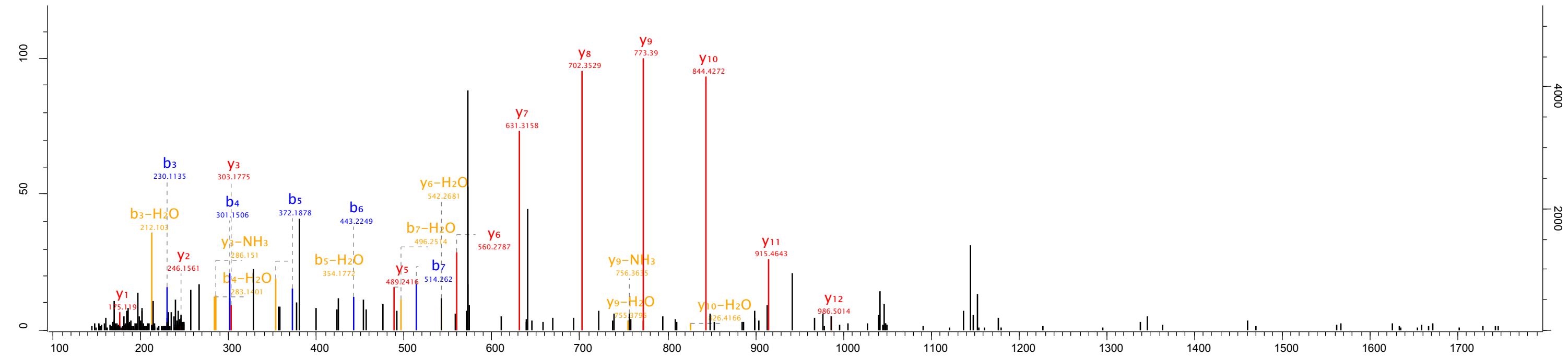


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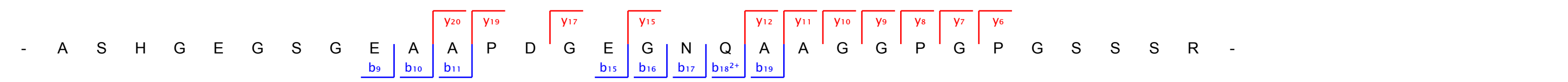
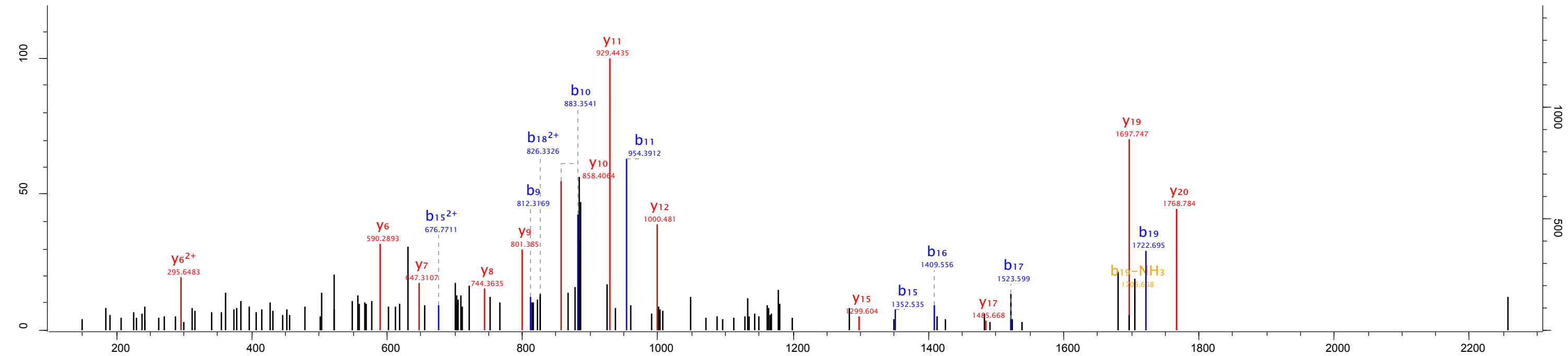


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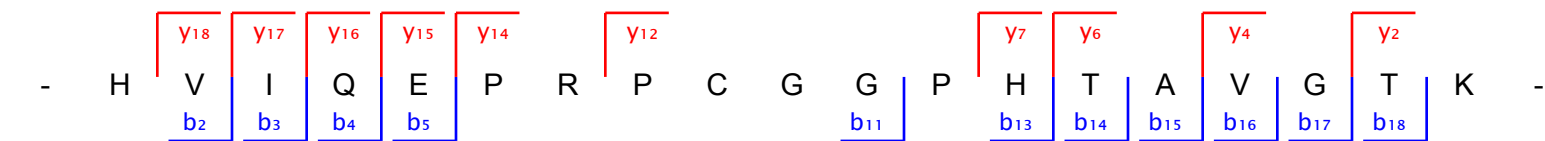
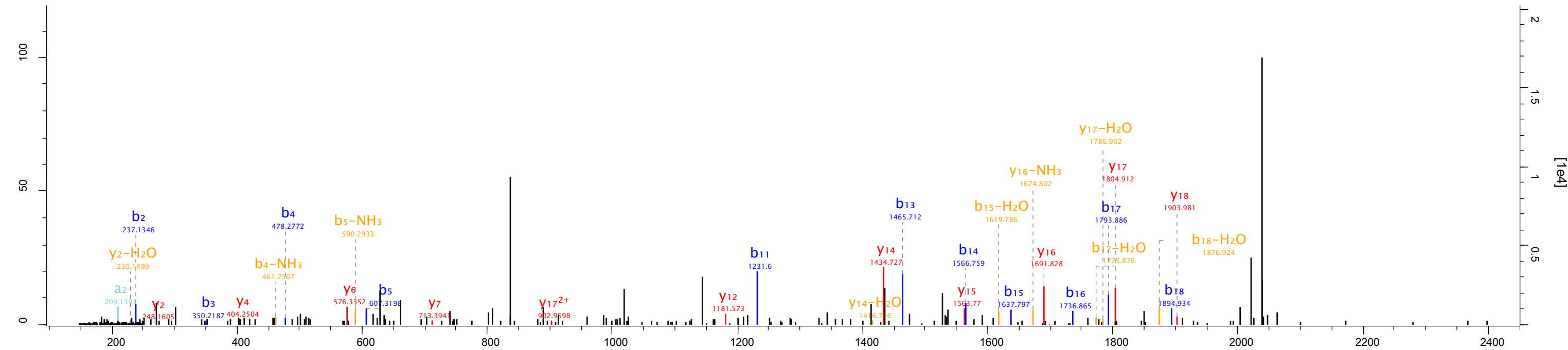


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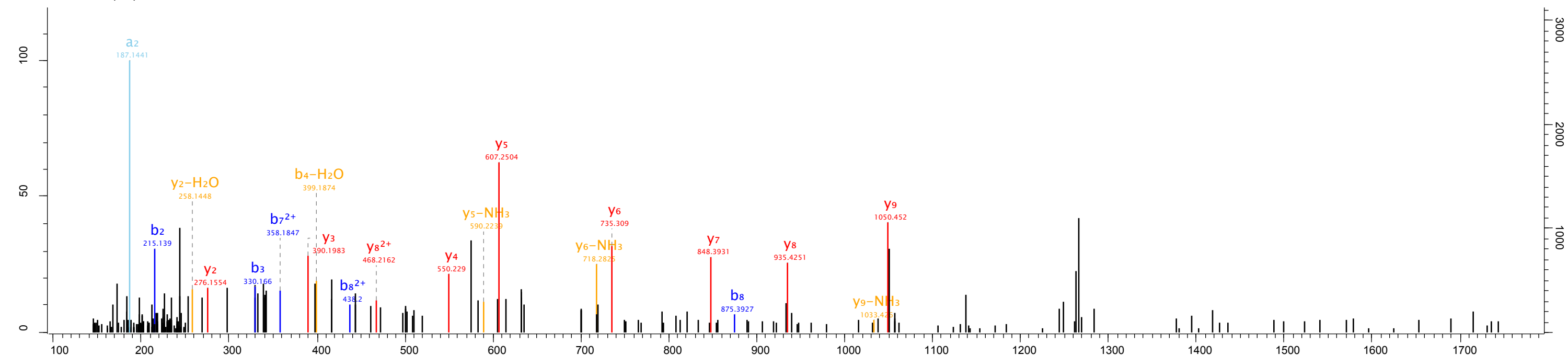
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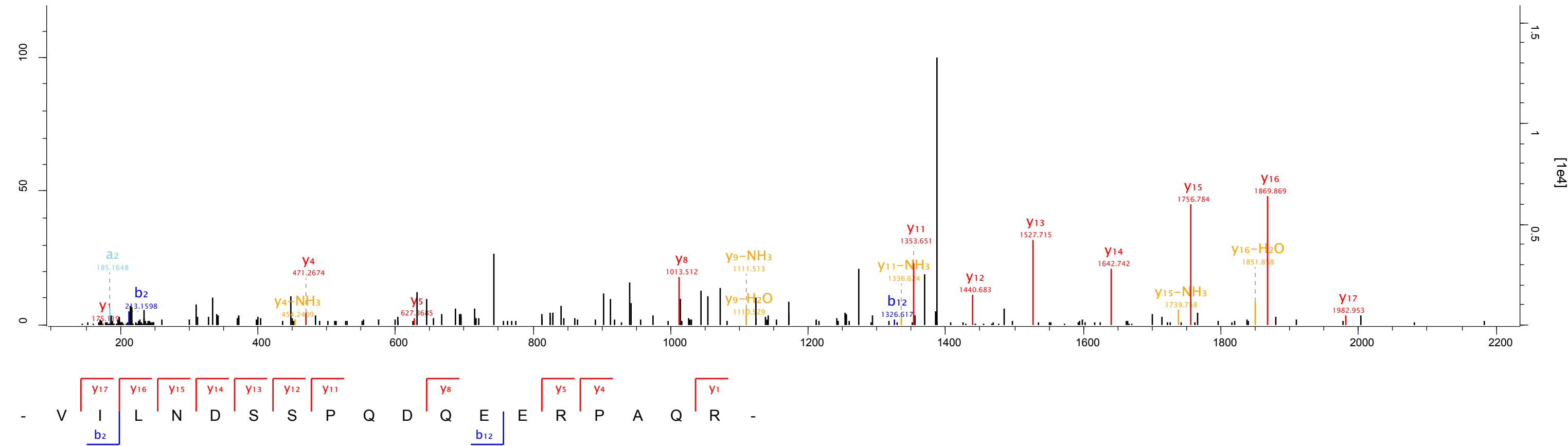


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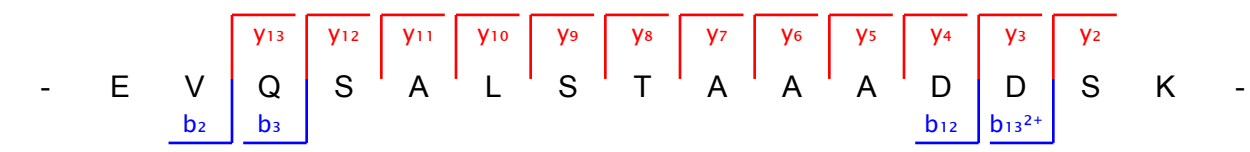
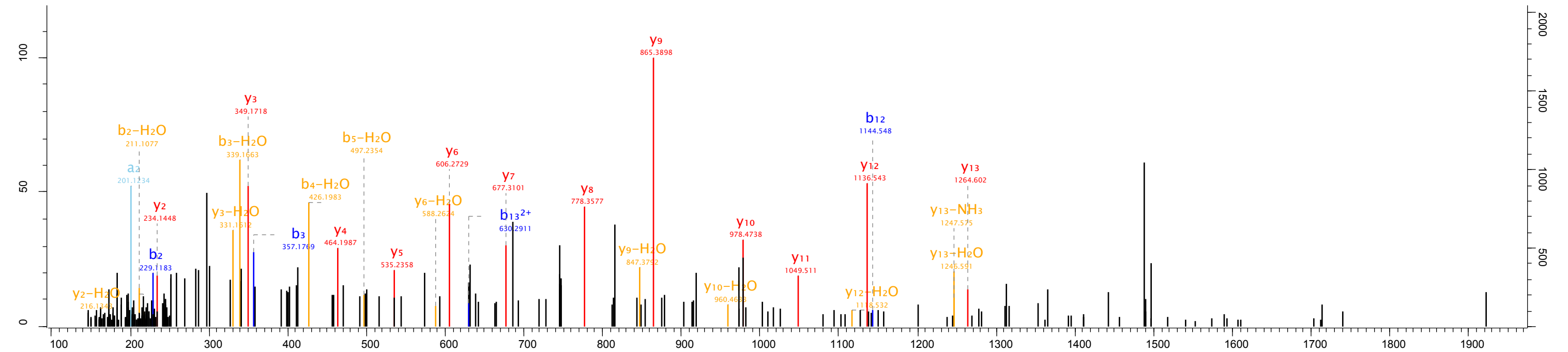
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- b₂ (L), b₃ (LD)
- y₂ (E), y₃ (EN), y₄ (CGN), y₅ (G), y₆ (Q), y₇ (SL), y₈ (SD), y₉ (LD)

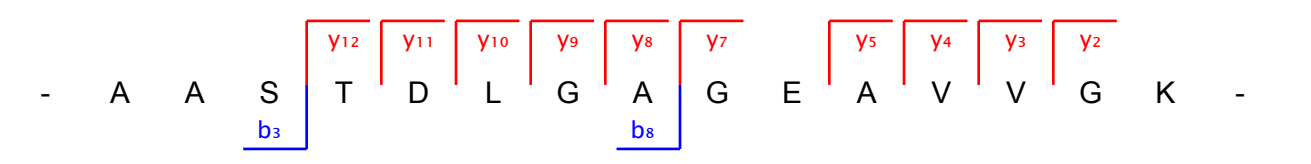
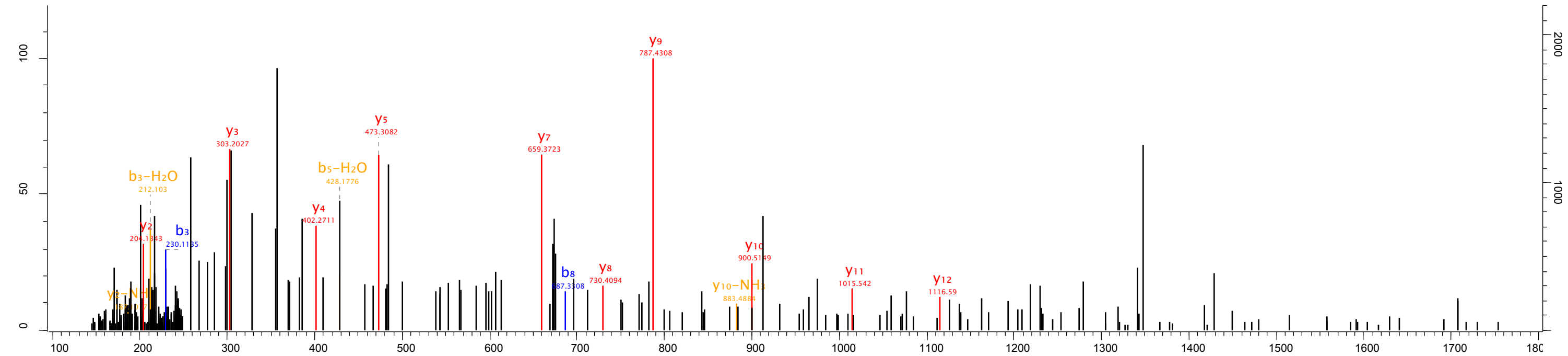
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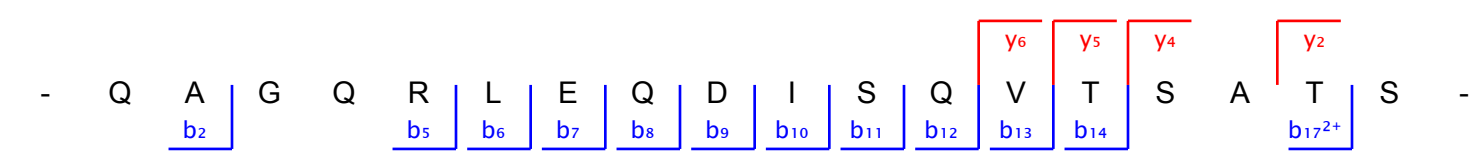
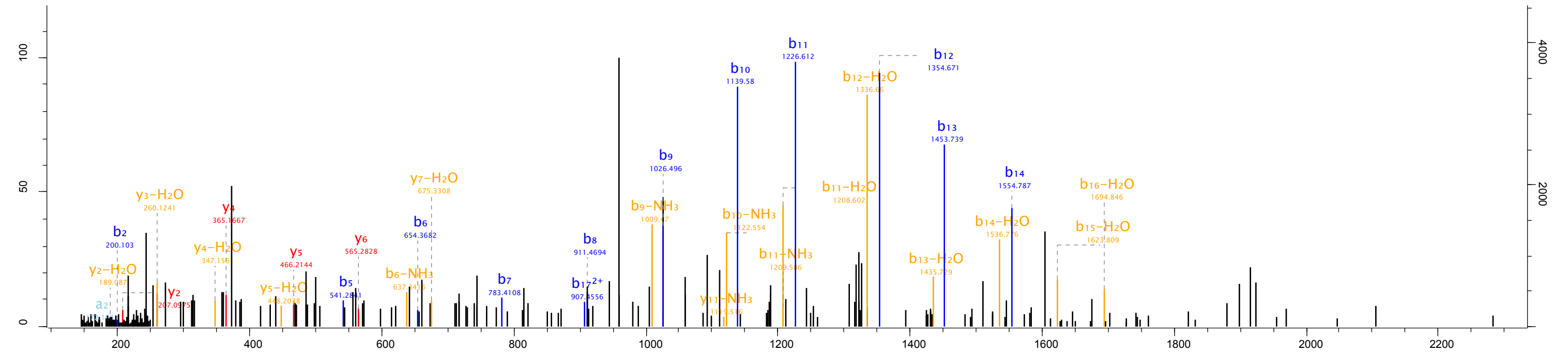
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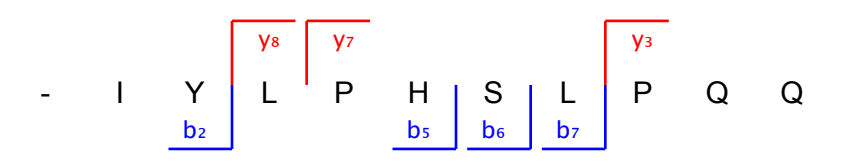
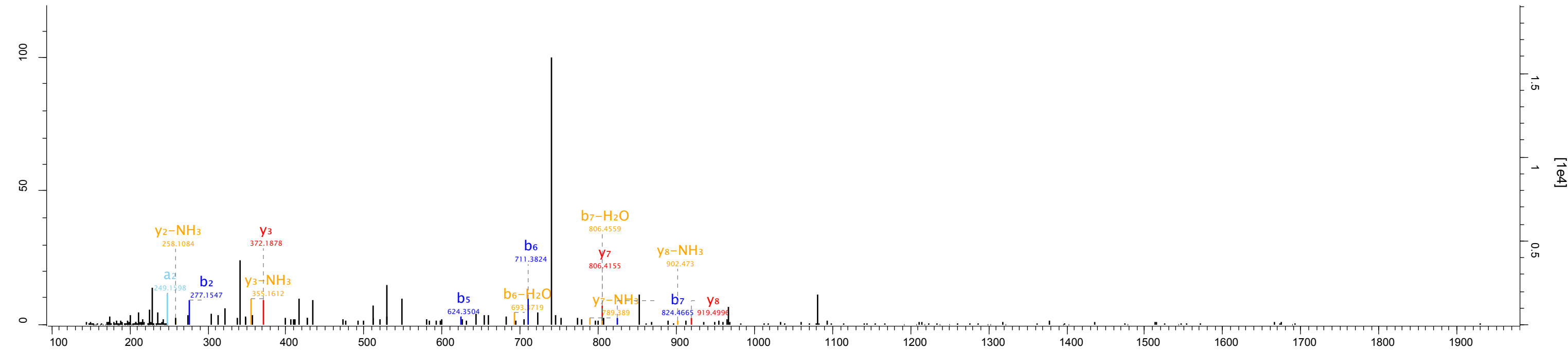


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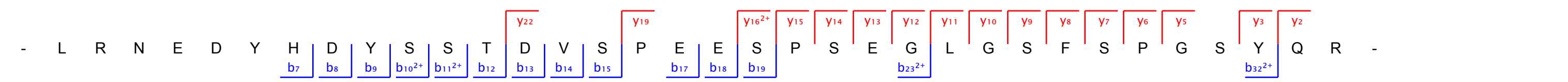
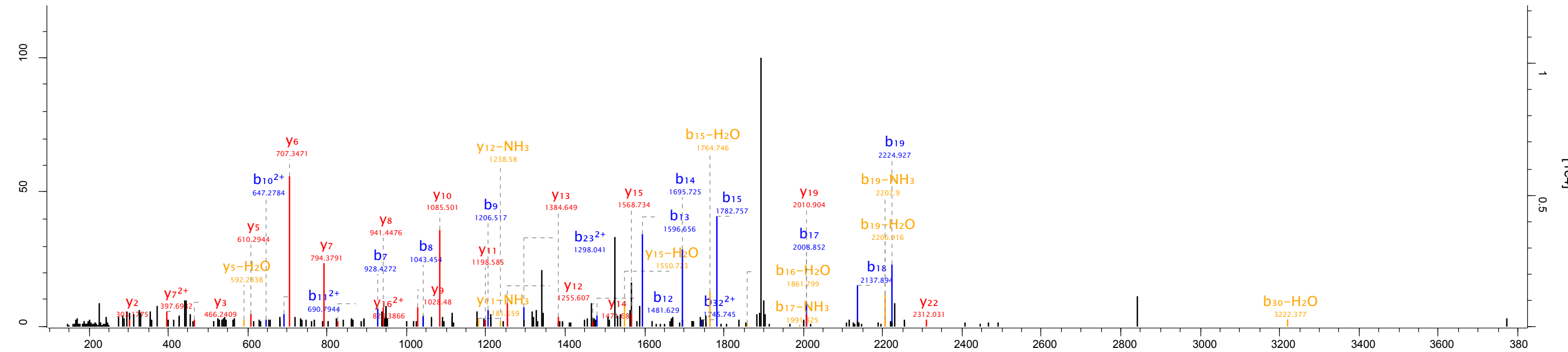


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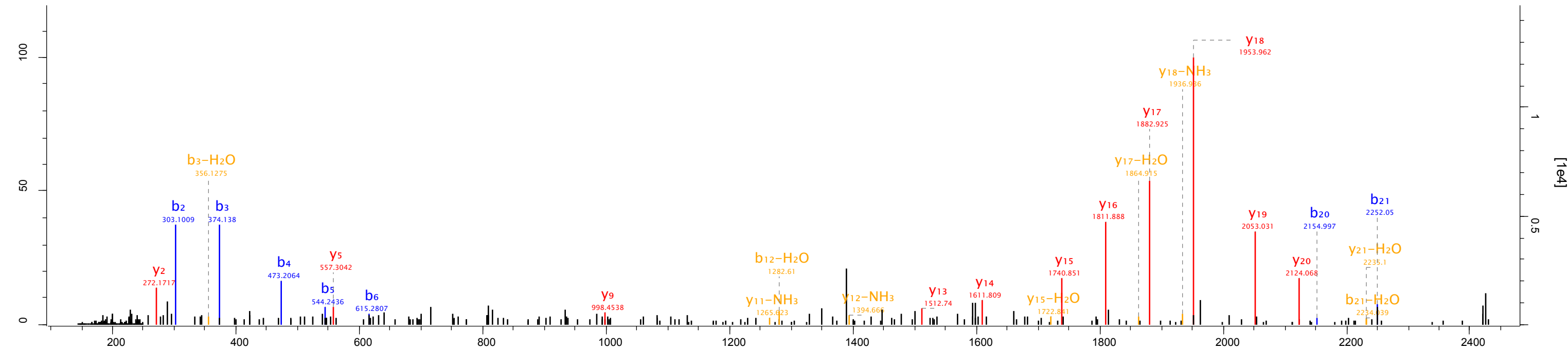
Scan 40040 Method TOF; CID Score 76.22 m/z 598.32 Gene names Mtatp8;mt-Atp8



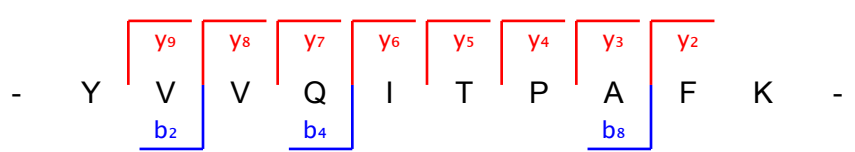
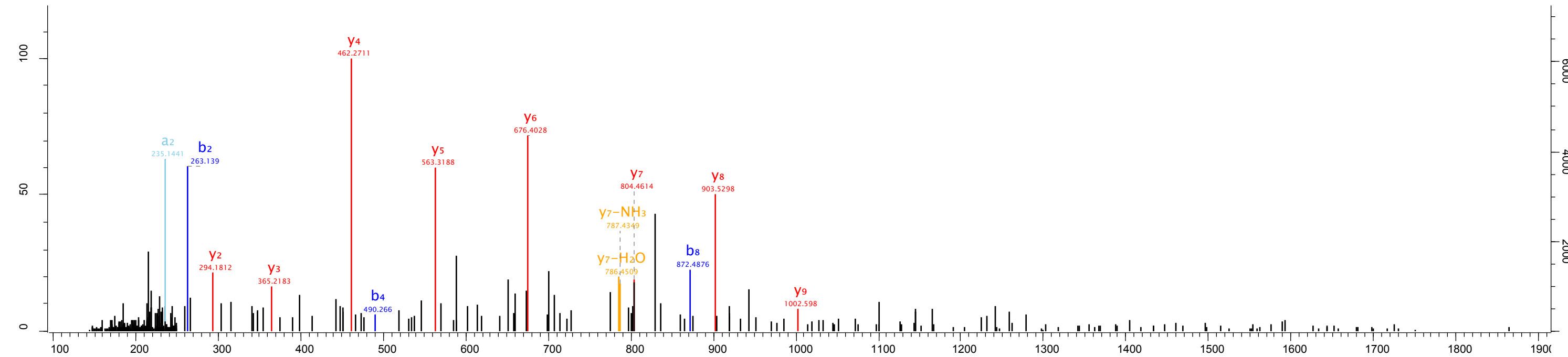
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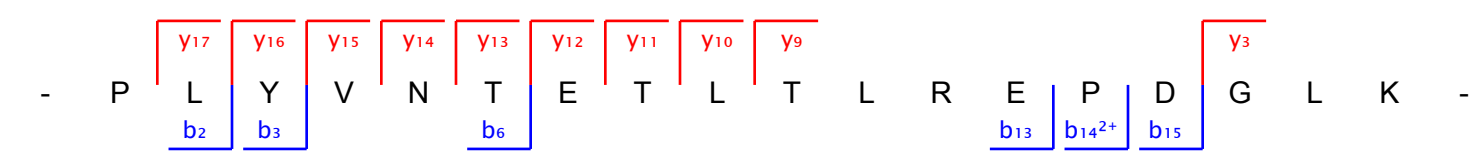
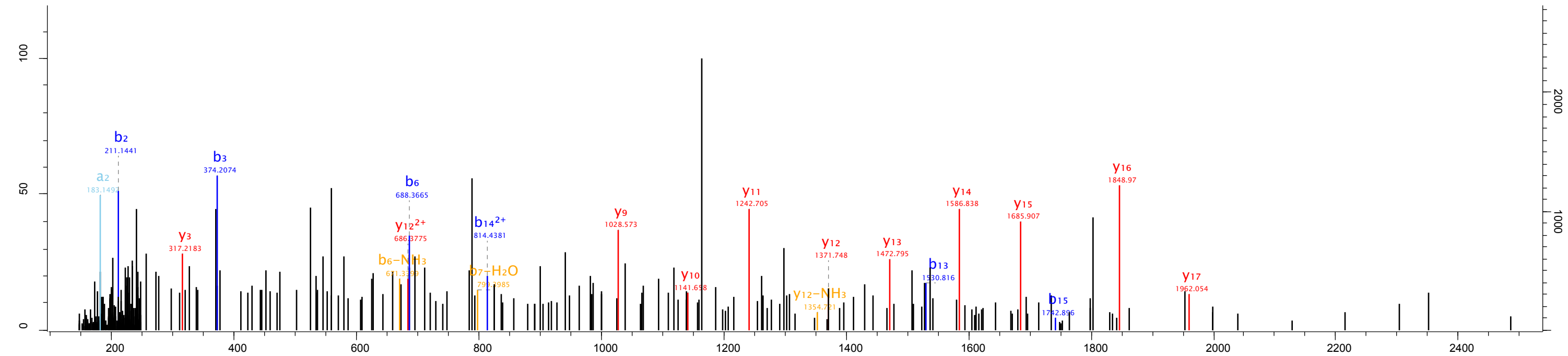
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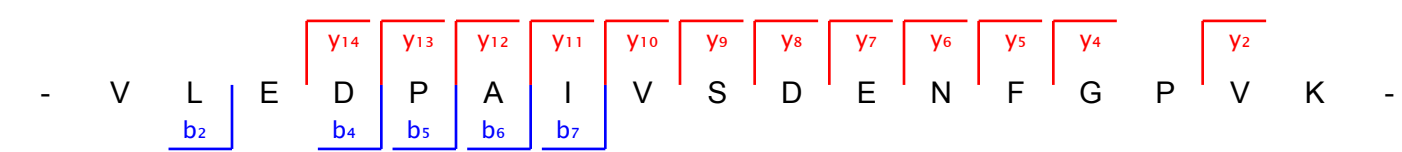
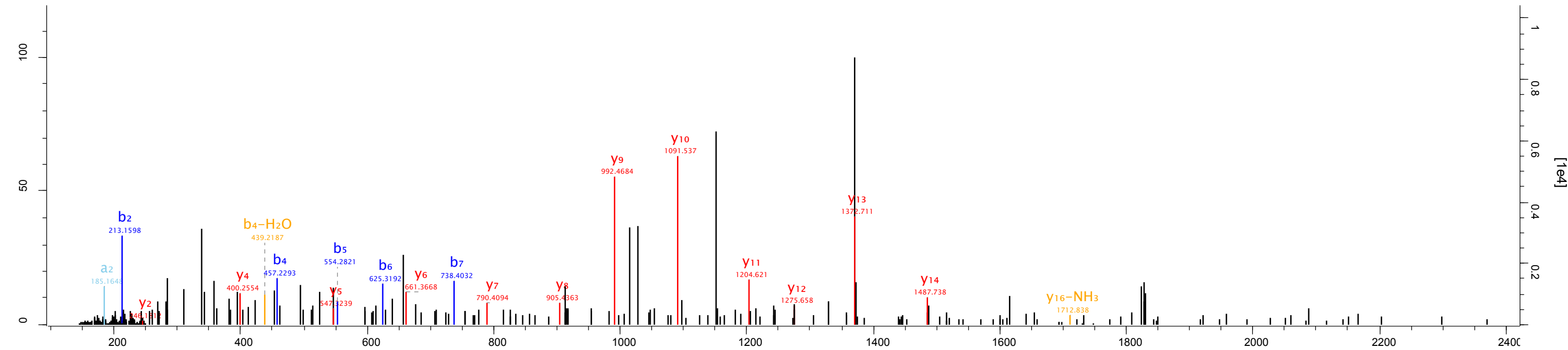
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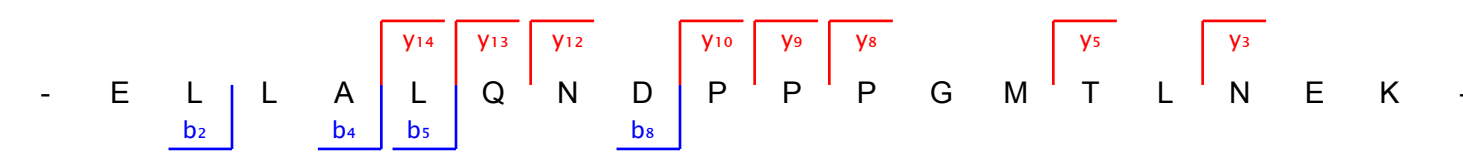
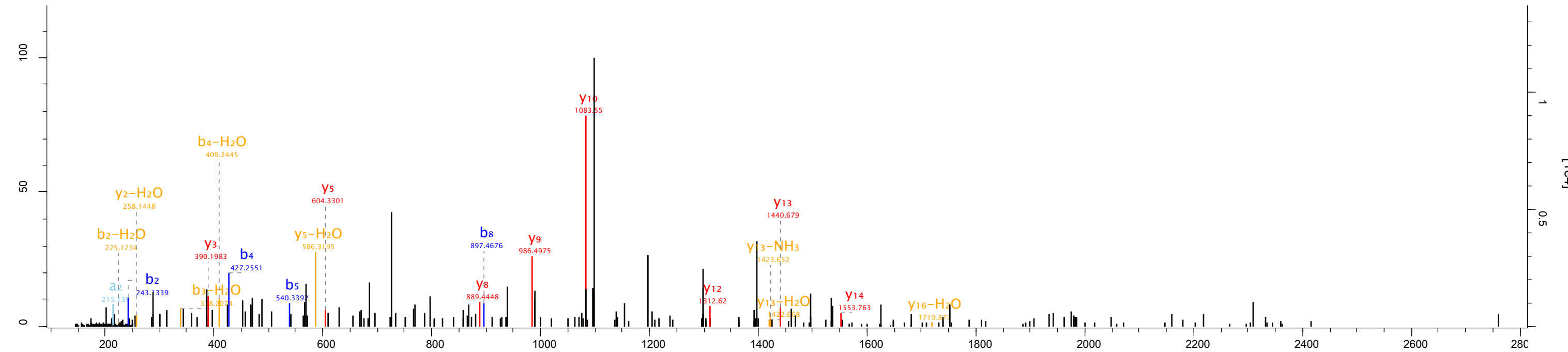
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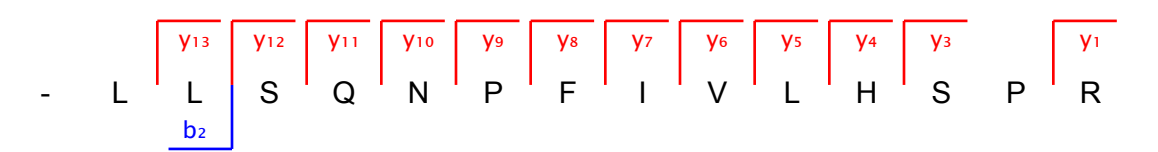
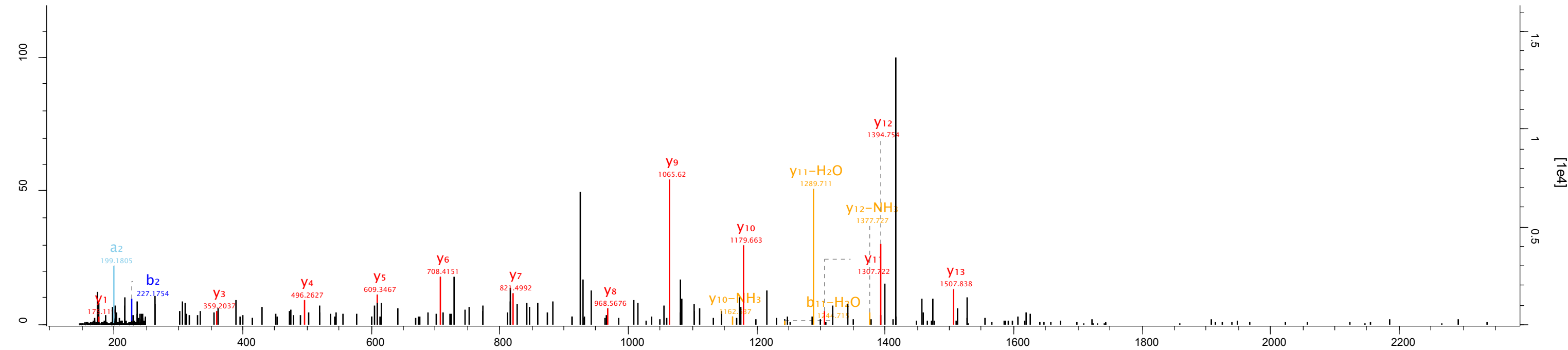
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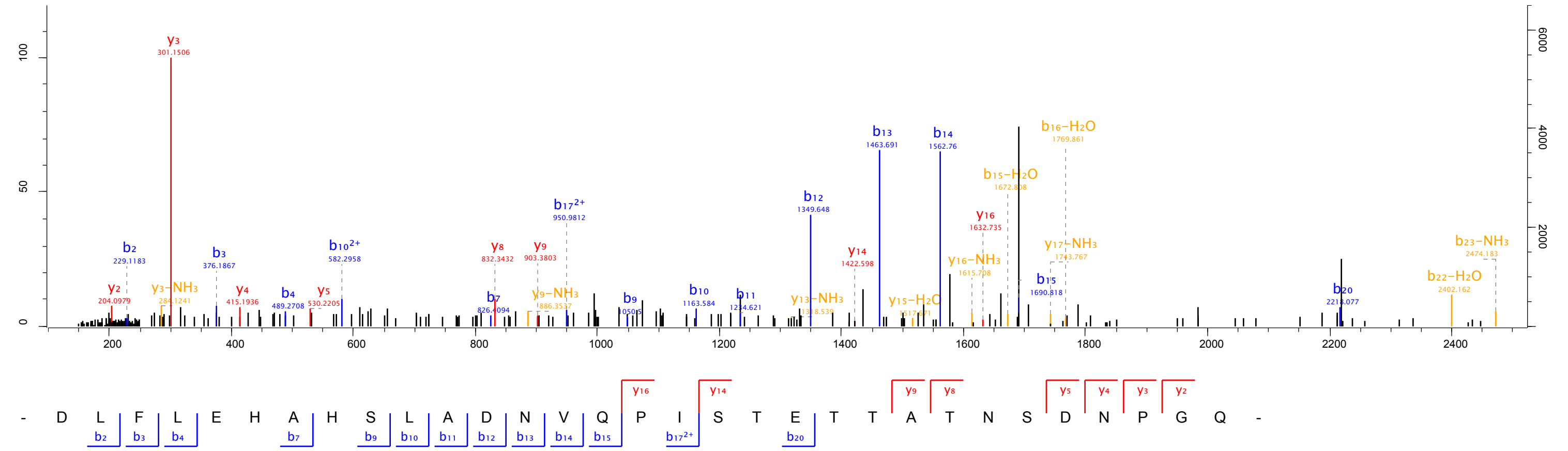


Raw file: 20150307_NSC1_Top_opt_F1_01_1678
 Scan: 52349 Method: TOF; CID Score: 55.44 m/z: 991.5 Gene names: Ube2w

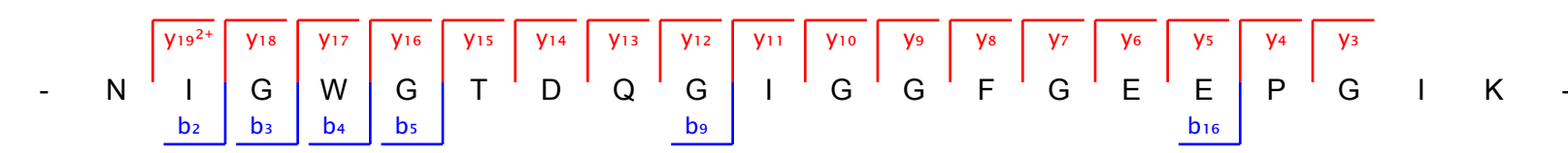
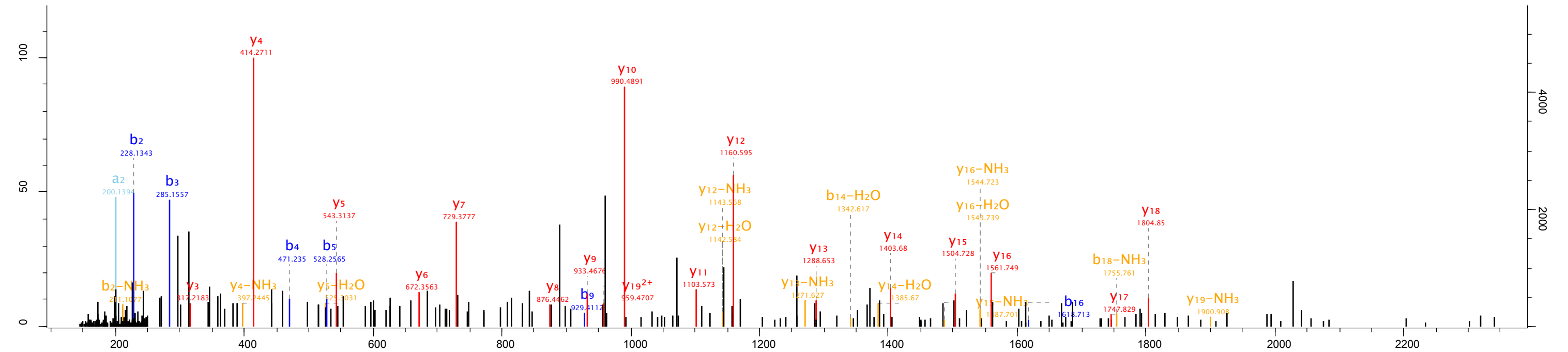


Raw file 20150307_NSC1_Top_opt_F1_01_1678 Scan 52580 Method TOF; CID Score 62.36 m/z 541.3 Gene names Mterf2

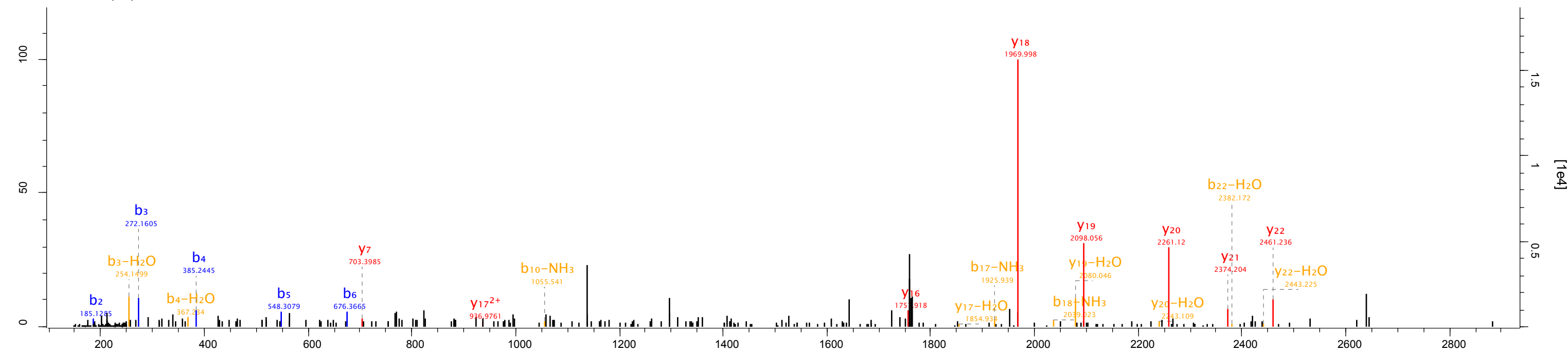




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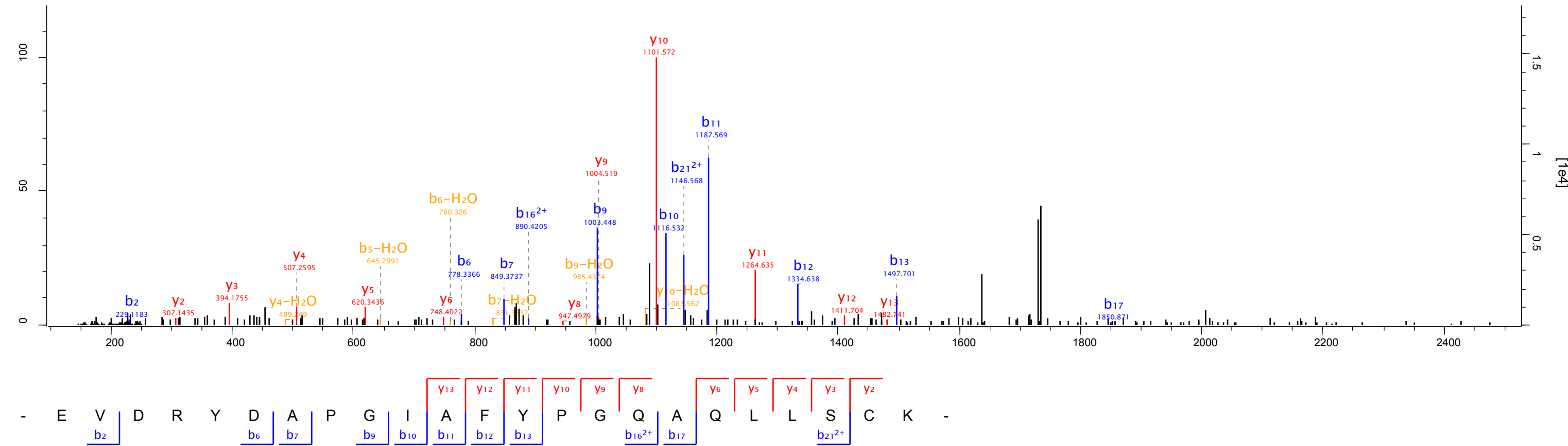


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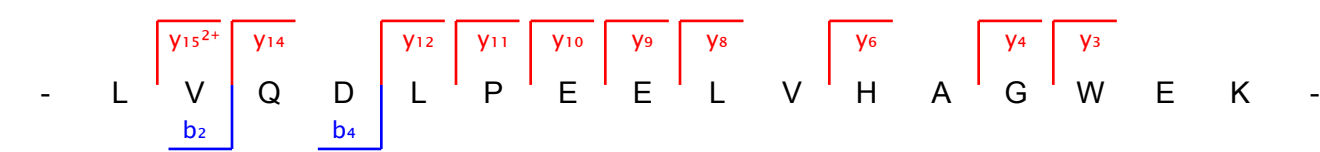
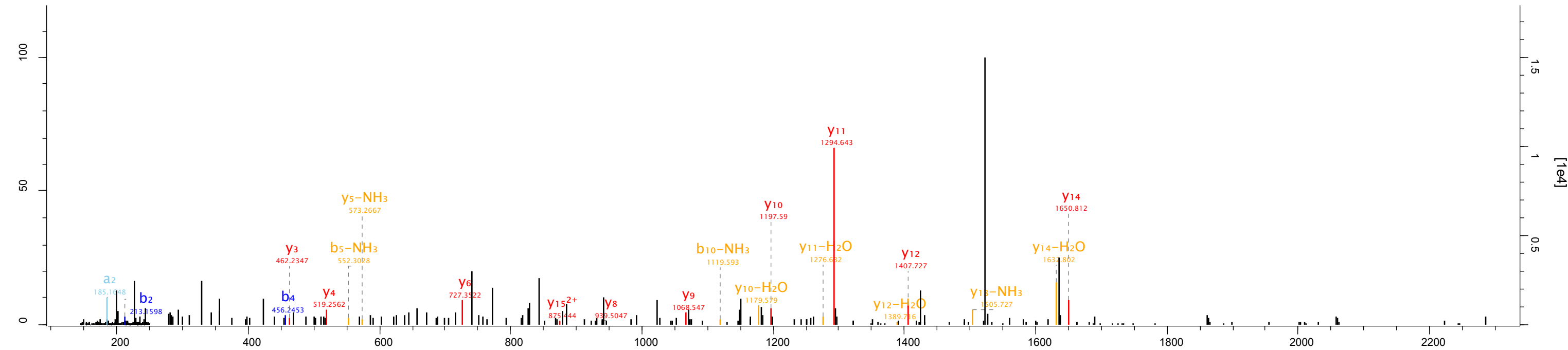


- L A S L Y Q P D L A S R P W T Q D I E G A S V K -

Fragmentation mapping:
b2: A-S
b3: S-L
b4: L-Y
b5: Y-Q
b6: Q-P
y7: D-I
y16: L-E
y17²⁺: D-E
y18: P-I
y19: Q-L
y20: Y-L
y21: L-S
y22: S-A

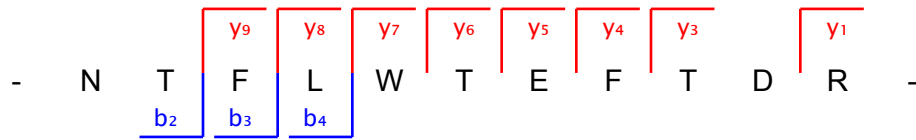
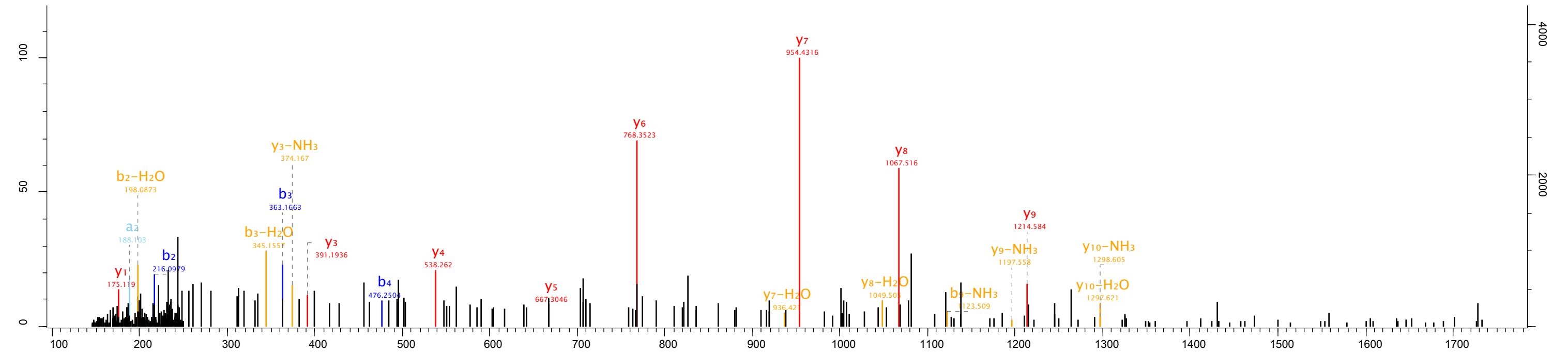


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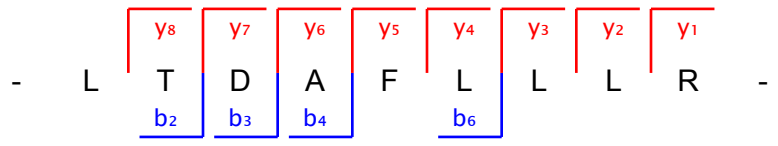
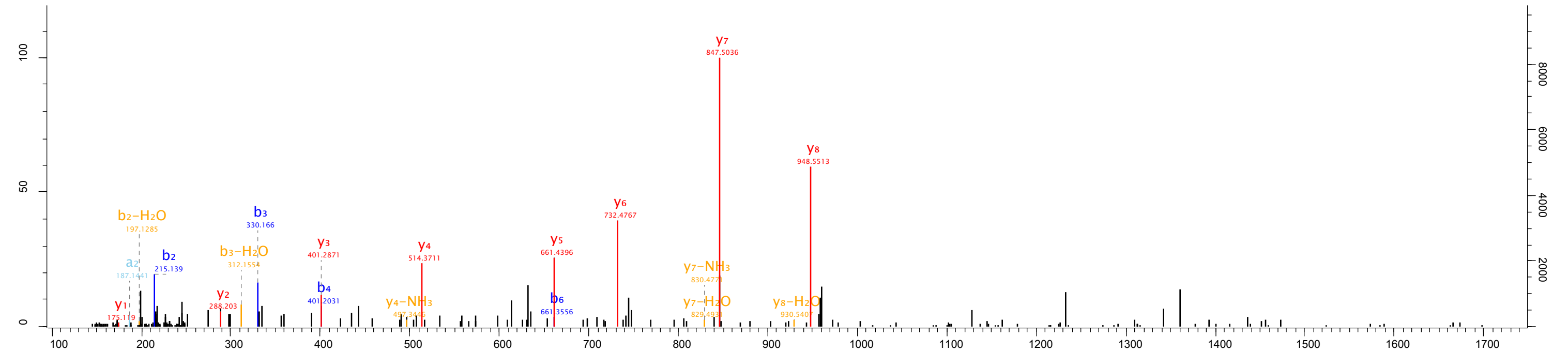


Raw file
20150307_NSC1_Top_opt_F1_01_1678

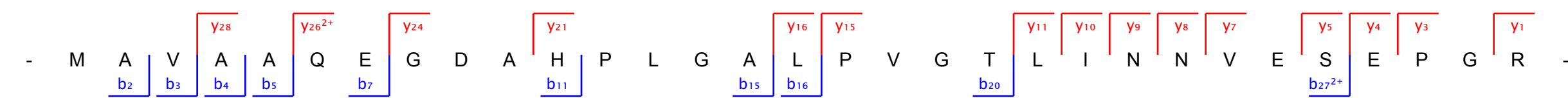
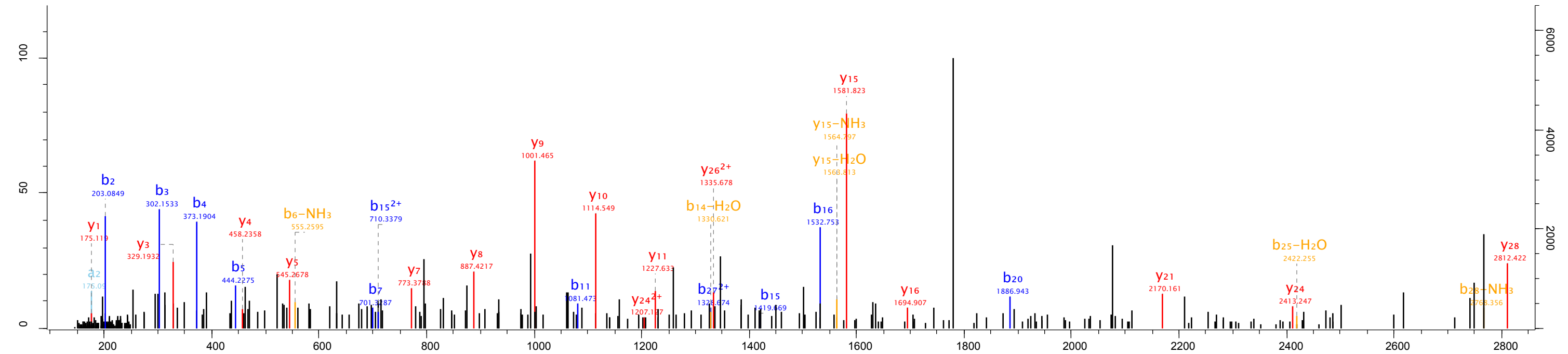
Scan 61347 Method TOF; CID Score 68.68 m/z 715.34 Gene names Tmem55b



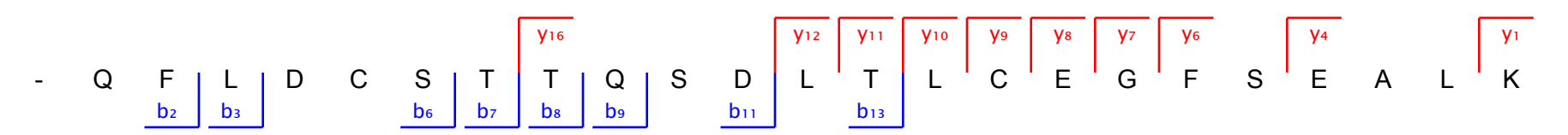
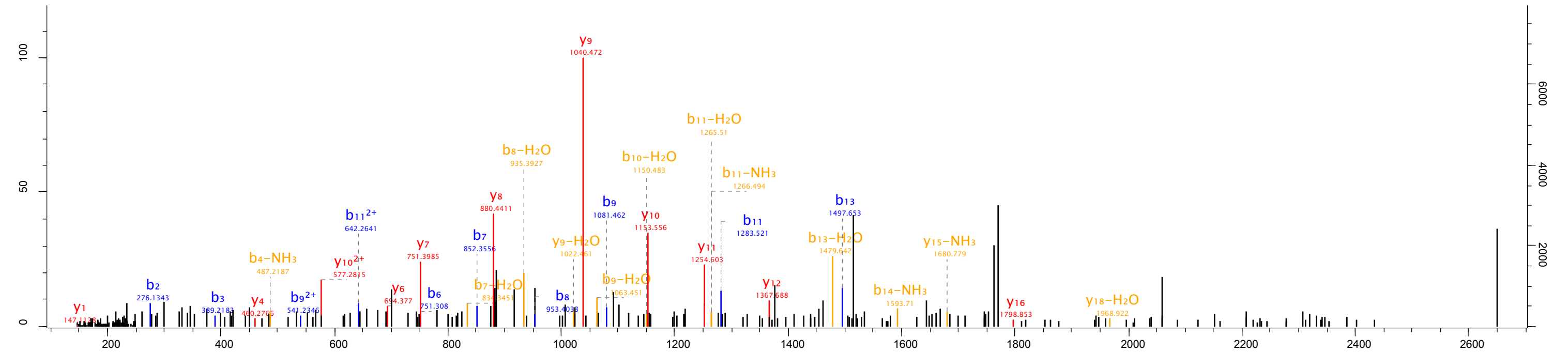
Raw file 20150307_NSC1_Top_opt_F1_01_1678 Scan 61742 Method TOF; CID Score 83.65 m/z 531.32 Gene names Stx16



Raw file 20150307_NSC1_Top_opt_F1_01_1678 Scan 62123 Method TOF; CID Score 75.44 m/z 1038.86 Gene names Mrpl2

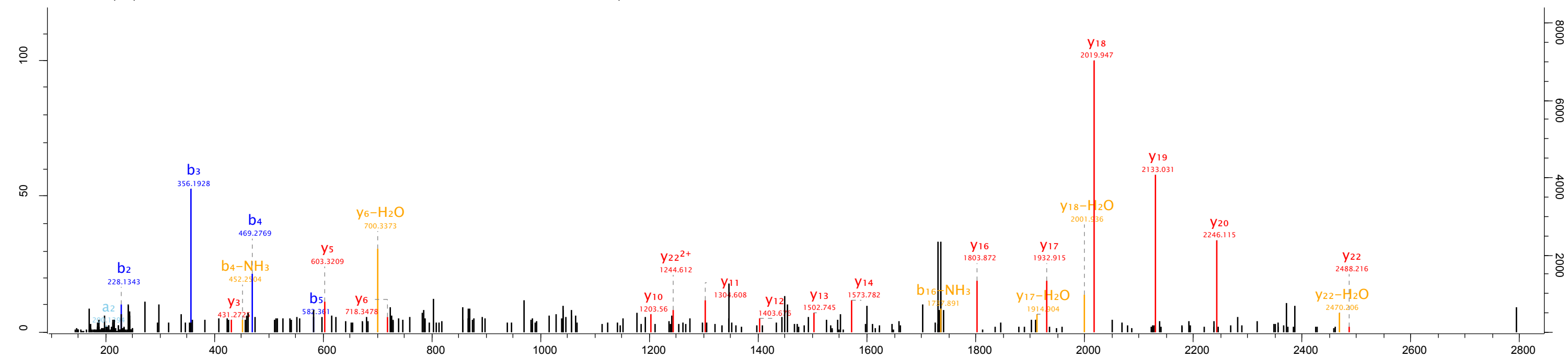


Raw file 20150307_NSC1_Top_opt_F1_01_1678 Scan 62249 Method TOF; CID Score 63.38 m/z 884.4 Gene names Chchd10



Raw file
20150307_NSC1_Top_opt_F1_01_1678

Scan 66028 Method TOF; CID Score 78.98 m/z 868.1 Gene names Xpr1

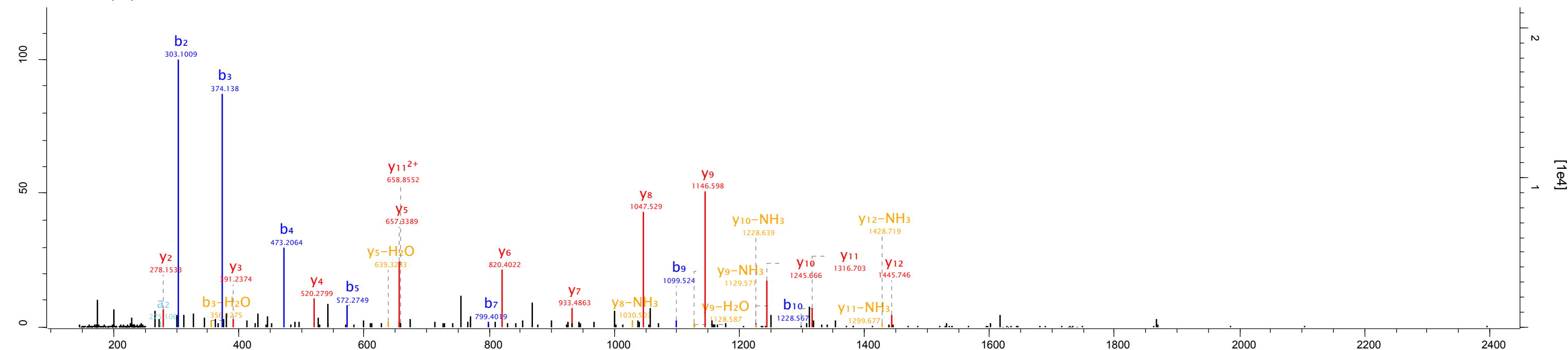


- I N Q L I S E T E A V V T N E L E D G D R Q K -

Fragmentation mapping:
b2: N
b3: Q
b4: L
b5: I
y3: I
y5: E
y6: V
y10: N
y11: T
y12: V
y13: V
y14: A
y16: T
y17: S
y18: I
y19: L
y20: Q
y22: D

Raw file
20150307_NSC1_Top_opt_F1_01_1678

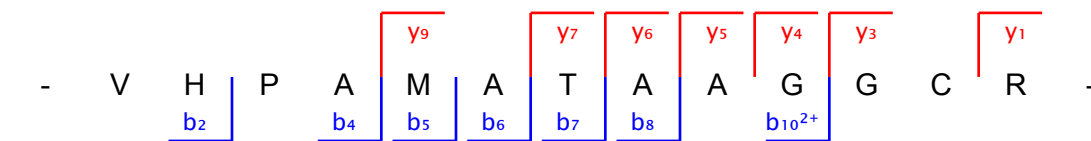
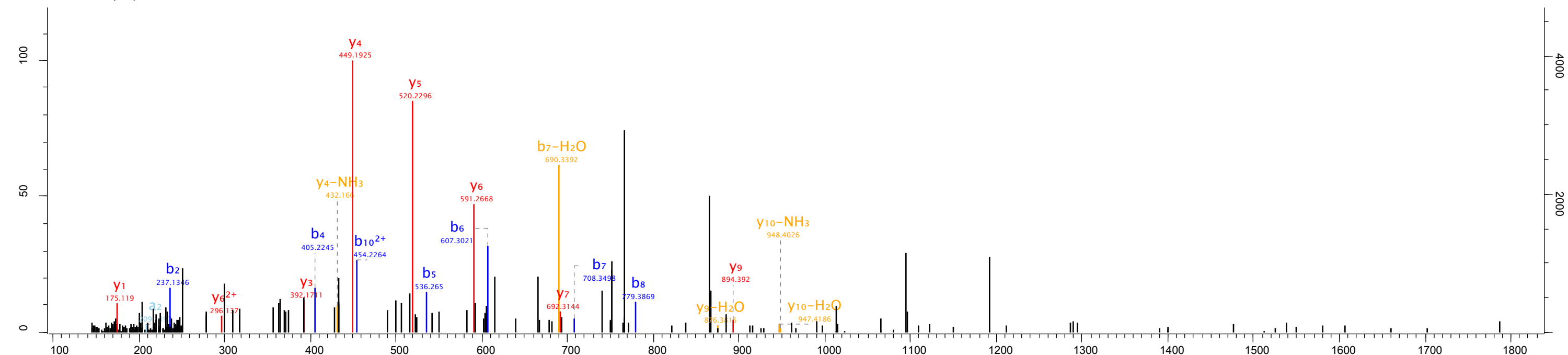
Scan 69983 Method TOF; CID Score 108.66 m/z 809.9 Gene names Elovl1



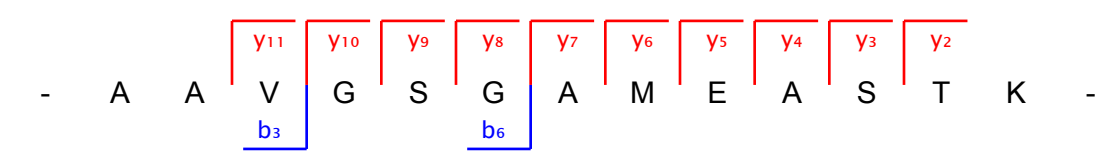
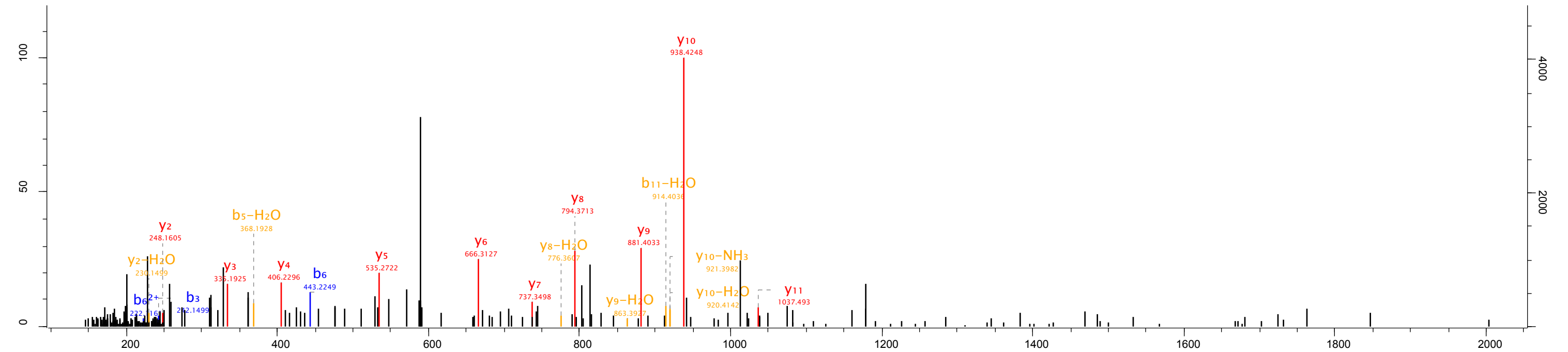
ac
- M E A V V N L Y H E L M K -

Fragmentation scheme diagram showing amino acid sequence: M E A V V N L Y H E L M K. The sequence is divided into segments by brackets, with b-ions (blue) and y-ions (red) labeled above and below the segments. The b-ions are labeled b₂ through b₁₀, and the y-ions are labeled y₂ through y₁₂.

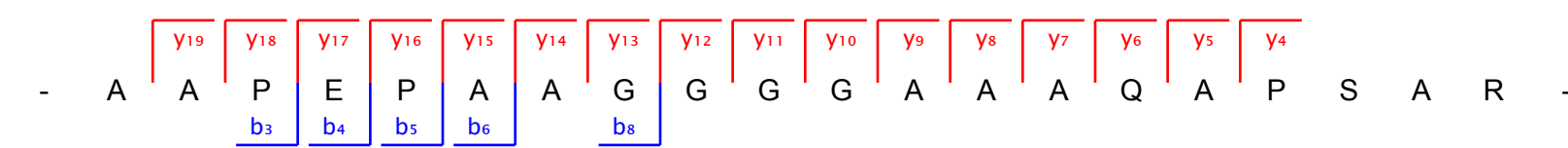
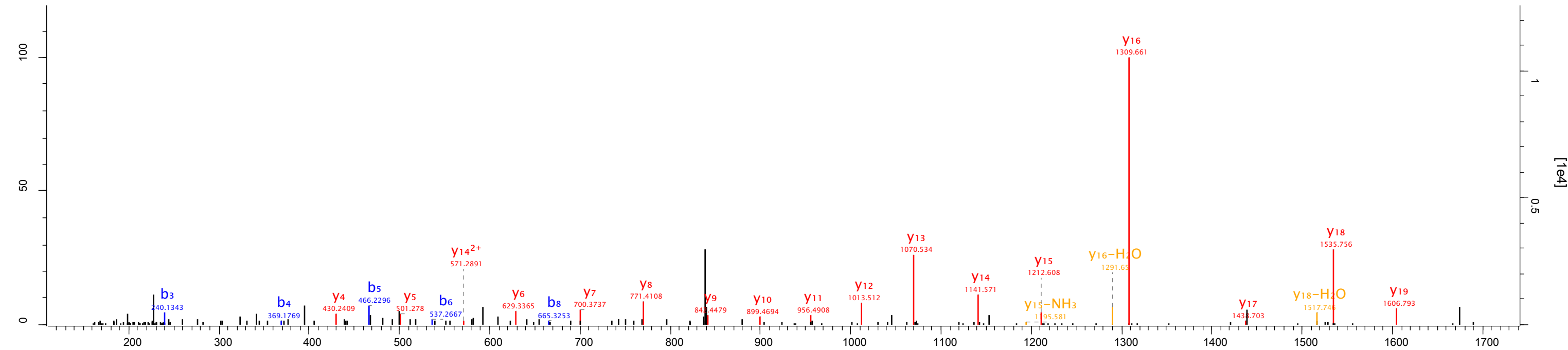
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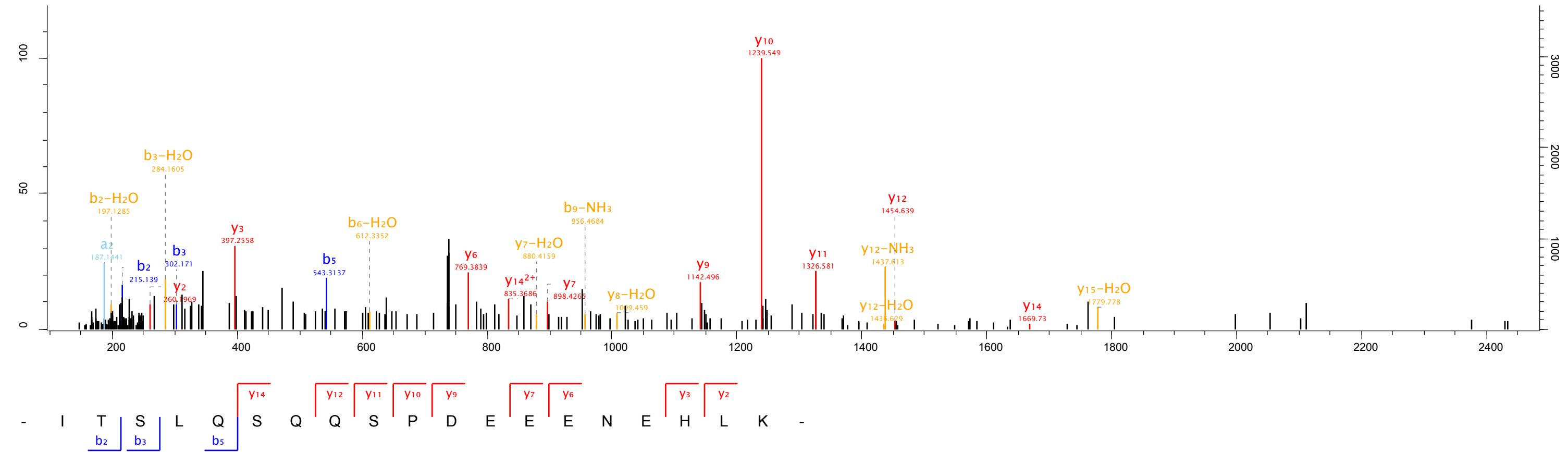


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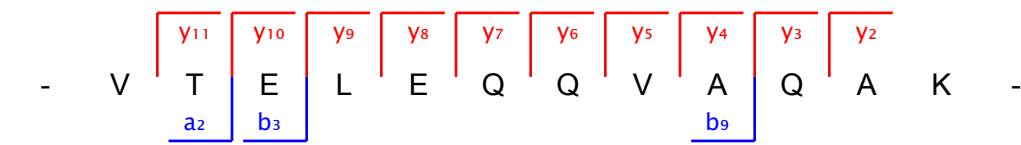
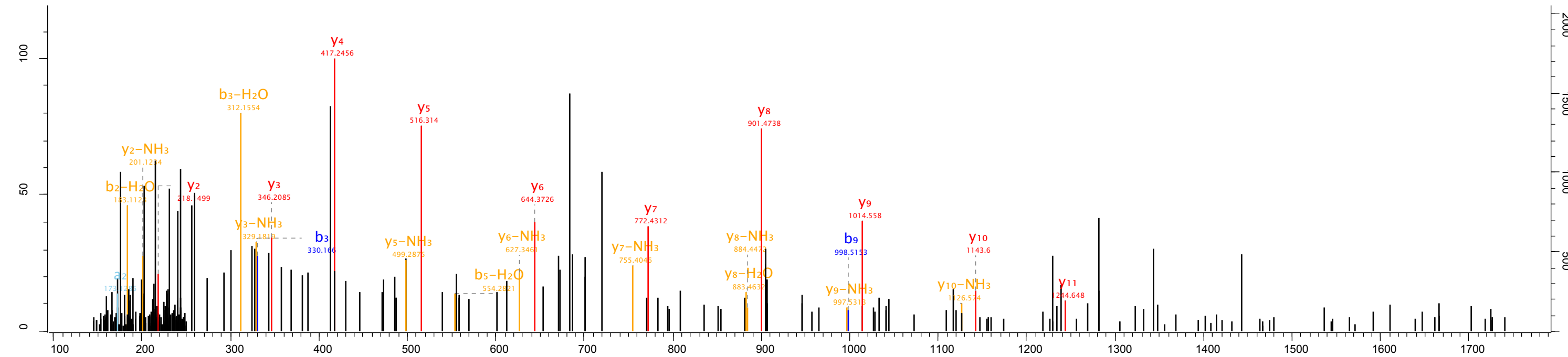


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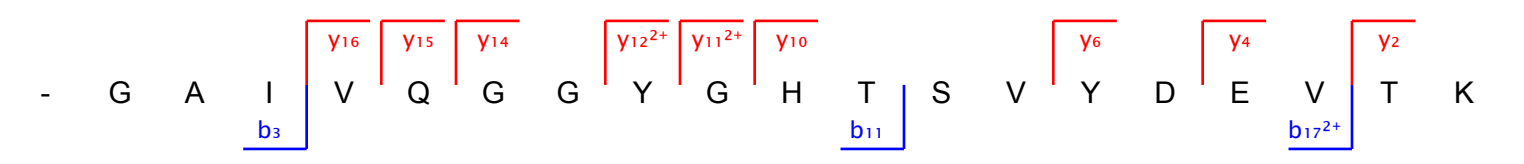
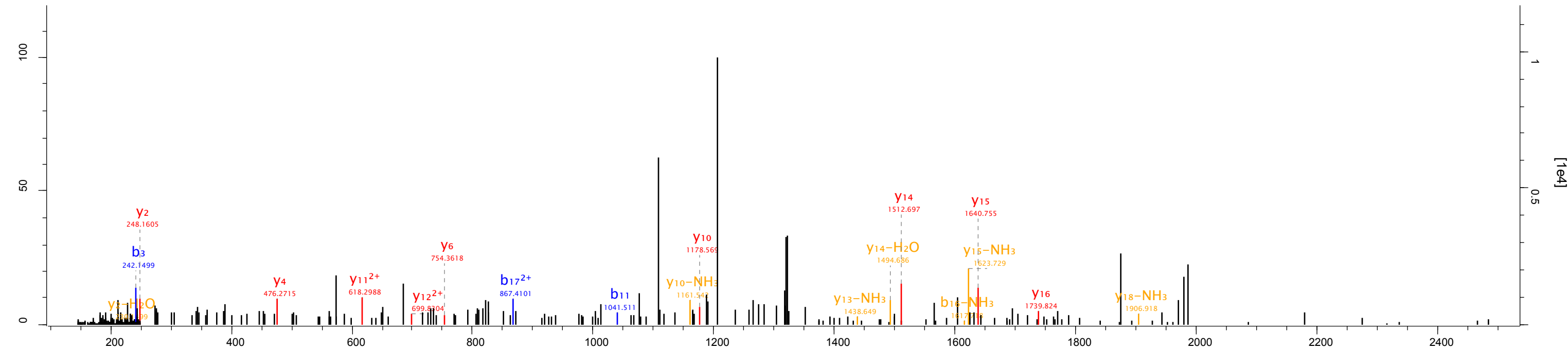


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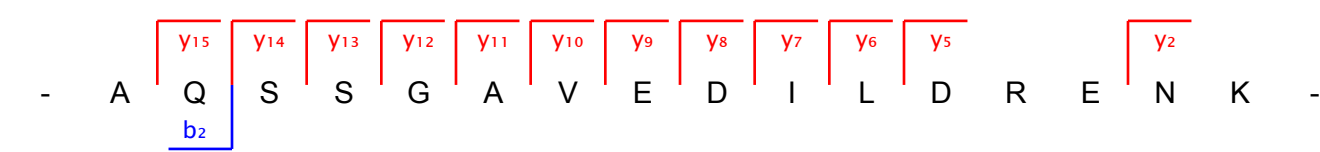
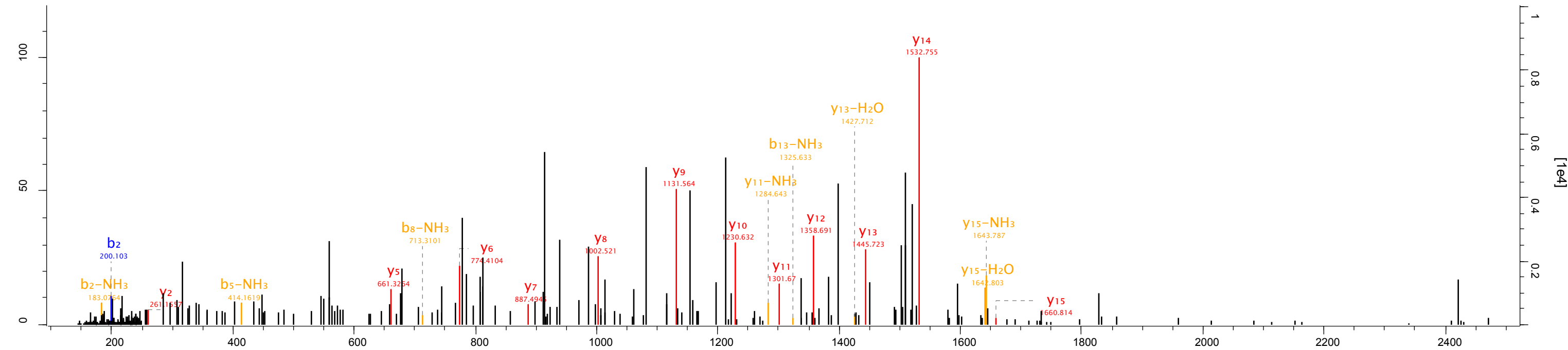


Raw file
20150307_NSC1_Top_opt_F1_01_1685

Scan 31535 Method TOF; CID Score 43.95 m/z 661.32 Gene names Atrnl1

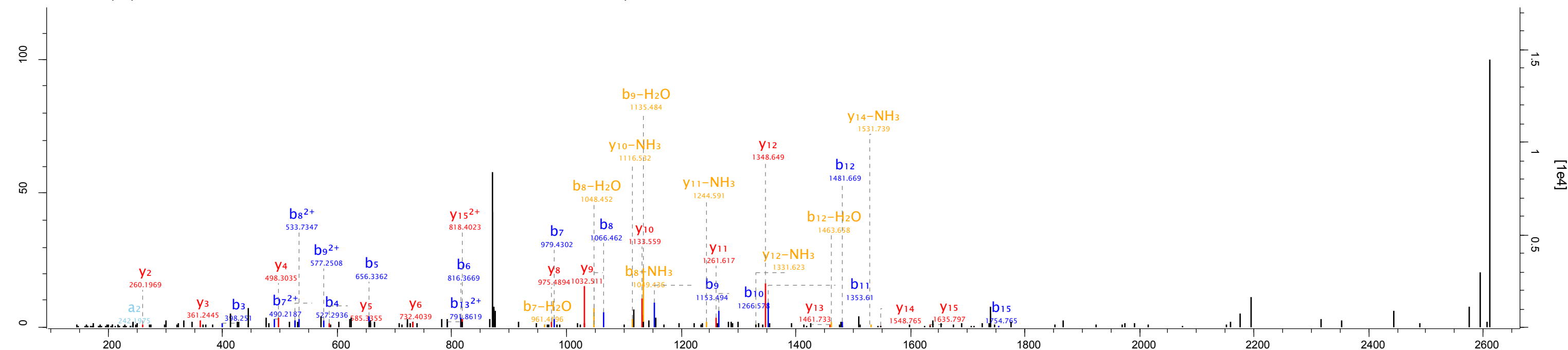


Raw file 20150307_NSC1_Top_opt_F1_01_1685 Scan 32424 Method TOF; CID Score 58.98 m/z 577.95 Gene names Bet11



Raw file
20150307_NSC1_Top_opt_F1_01_1685

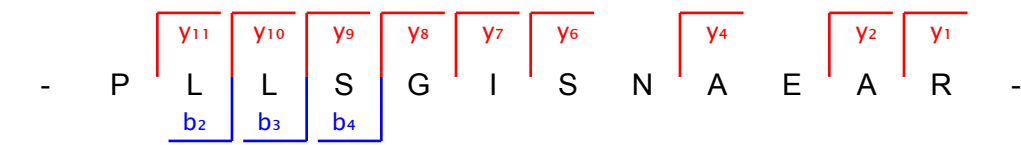
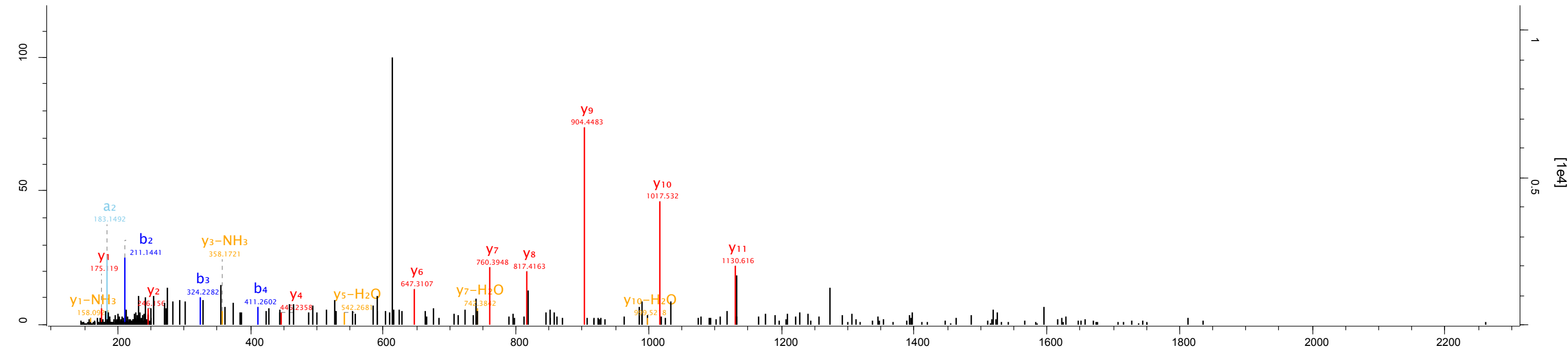
Scan 34103 Method TOF; CID Score 91.48 m/z 872.41 Gene names Scyl3



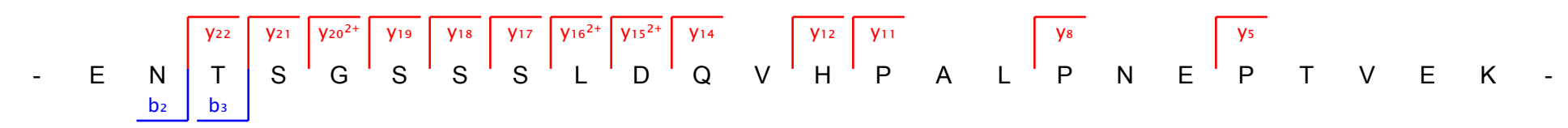
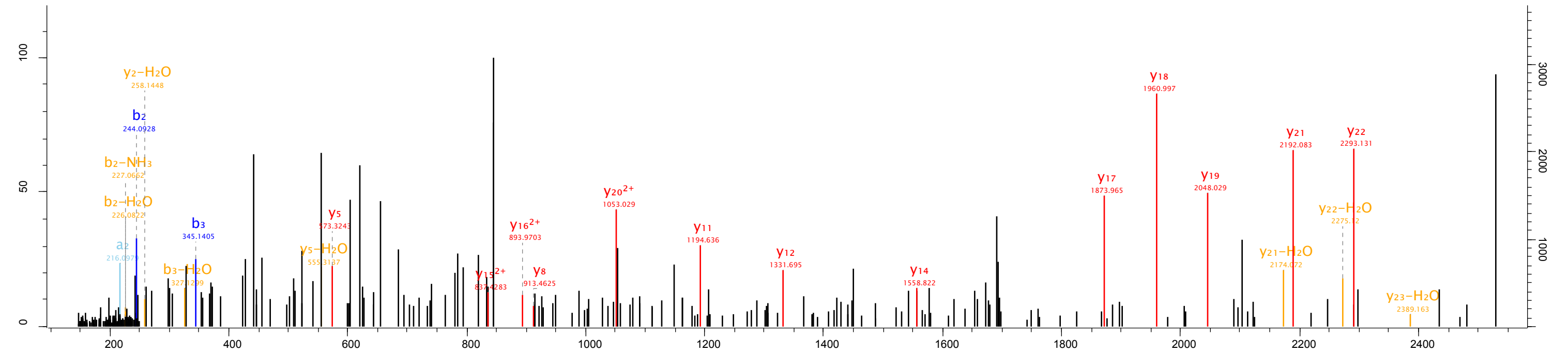
- R I Q E E C Y S S L S Q T G D Q F S H T I K -

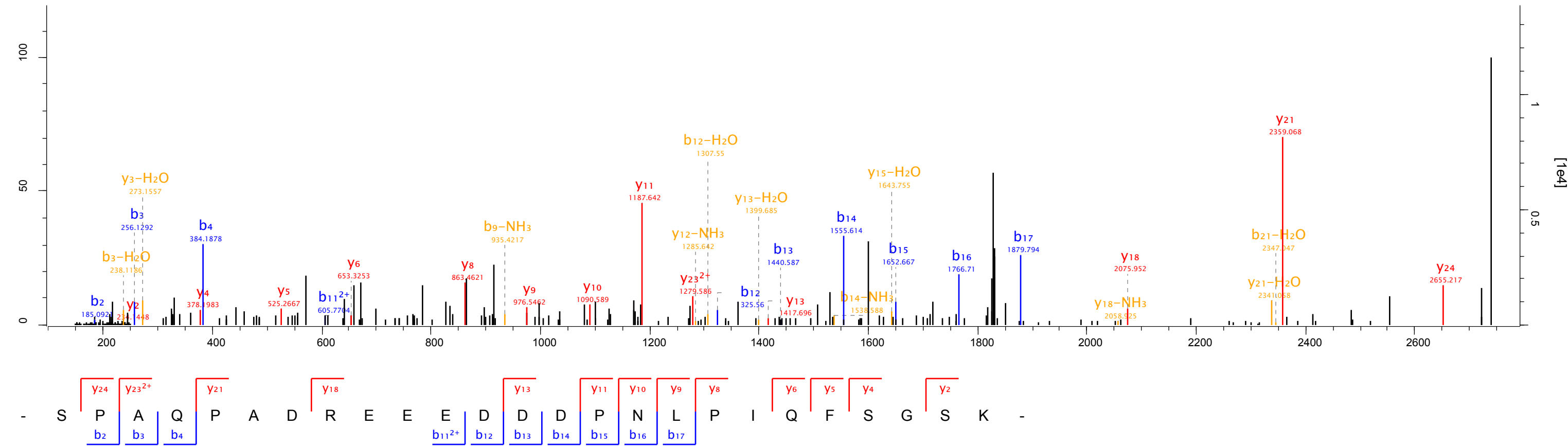
Fragmentation mapping:
a₂ (I), b₃ (Q), b₄ (E), b₅ (E), b₆ (C), b₇ (Y), b₈ (S), b₉ (S), b₁₀ (L), b₁₁ (S), b₁₂ (Q), b₁₃²⁺ (T), b₁₅ (D), y₂ (I), y₃ (T), y₄ (H), y₅ (S), y₆ (F), y₈ (D), y₉ (G), y₁₀ (T), y₁₁ (Q), y₁₂ (S), y₁₃ (L), y₁₄ (S), y₁₅ (S)

Raw file 20150307_NSC1_Top_opt_F1_01_1685 Scan 35132 Method TOF; CID Score 53.45 m/z 614.34 Gene names Adarb1

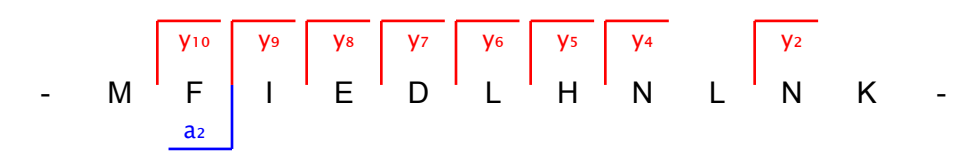
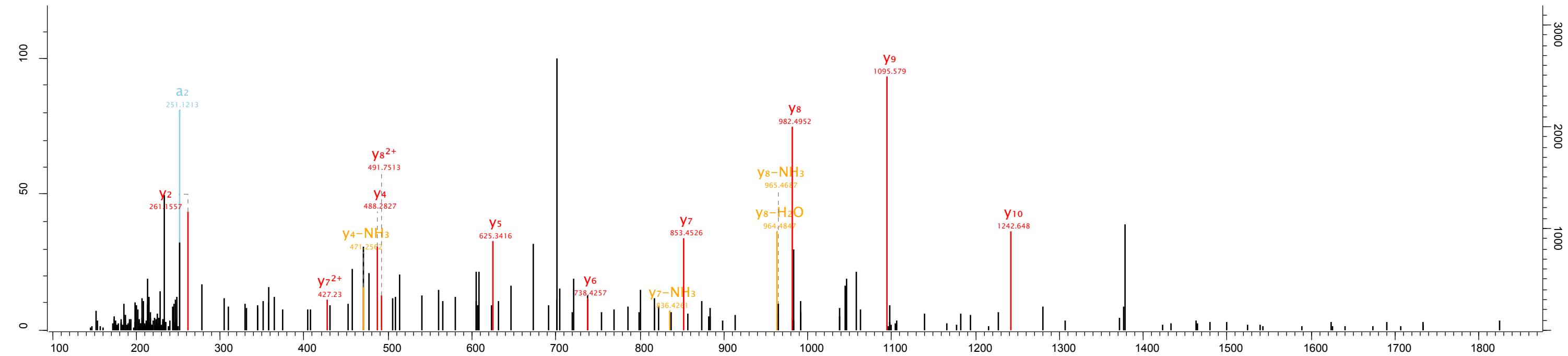


Raw file: 20150307_NSC1_Top_opt_F1_01_1685
 Scan: 35978 Method: TOF; CID Score: 52.9 m/z: 846.4 Gene names: Pja2

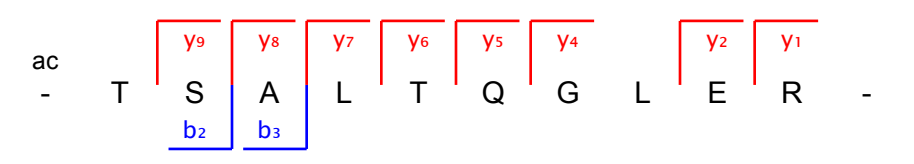
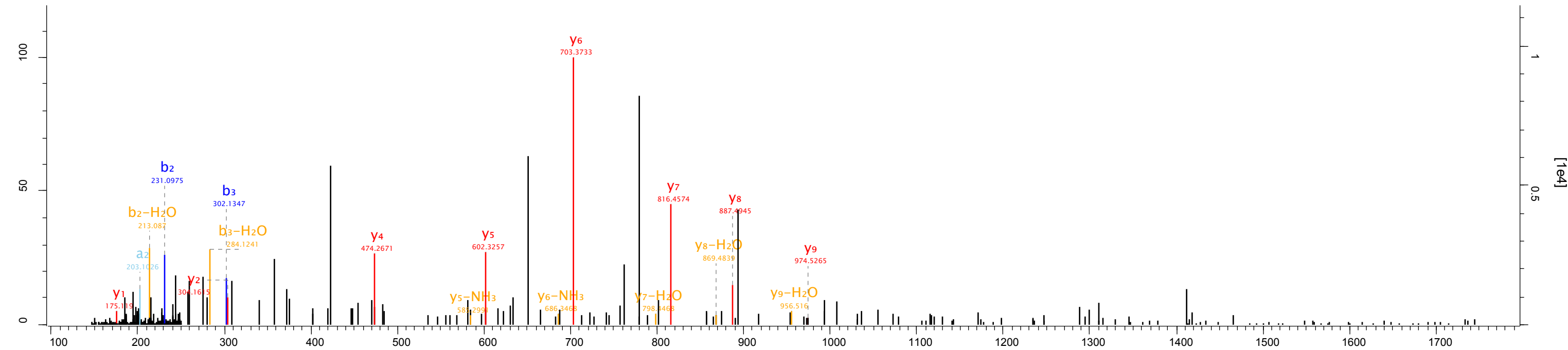




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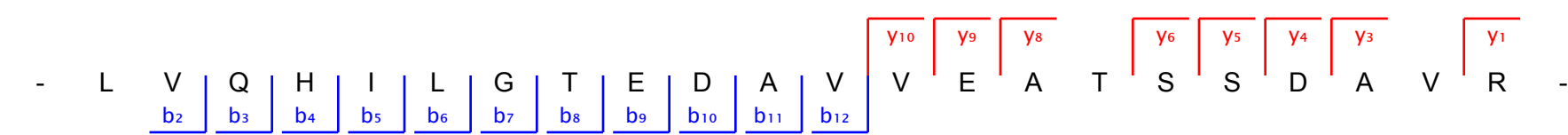
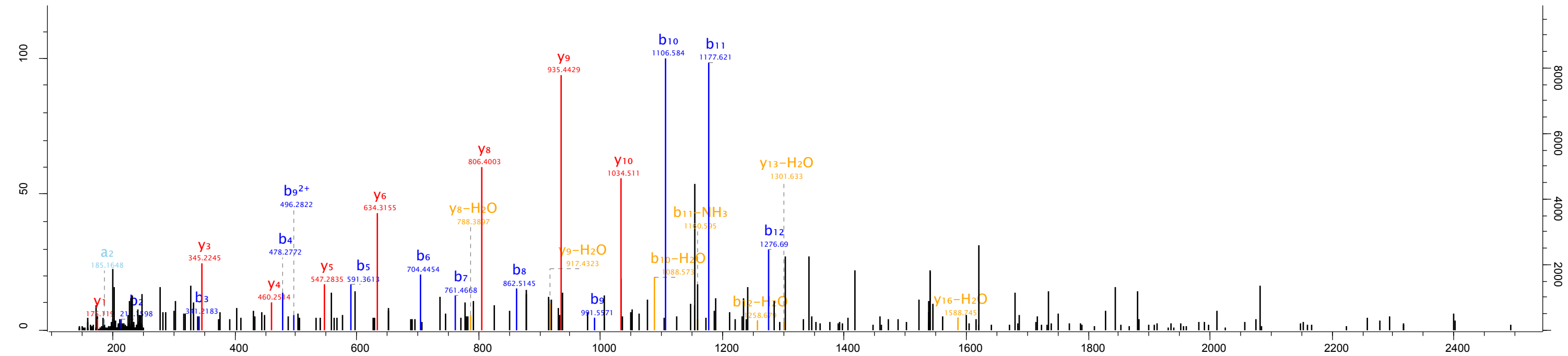


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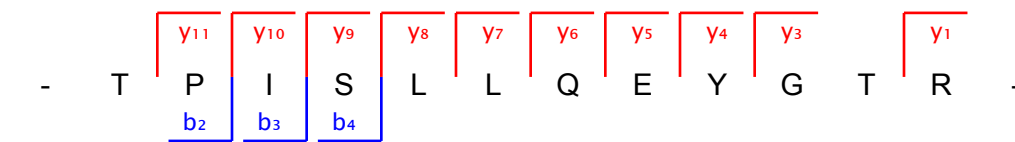
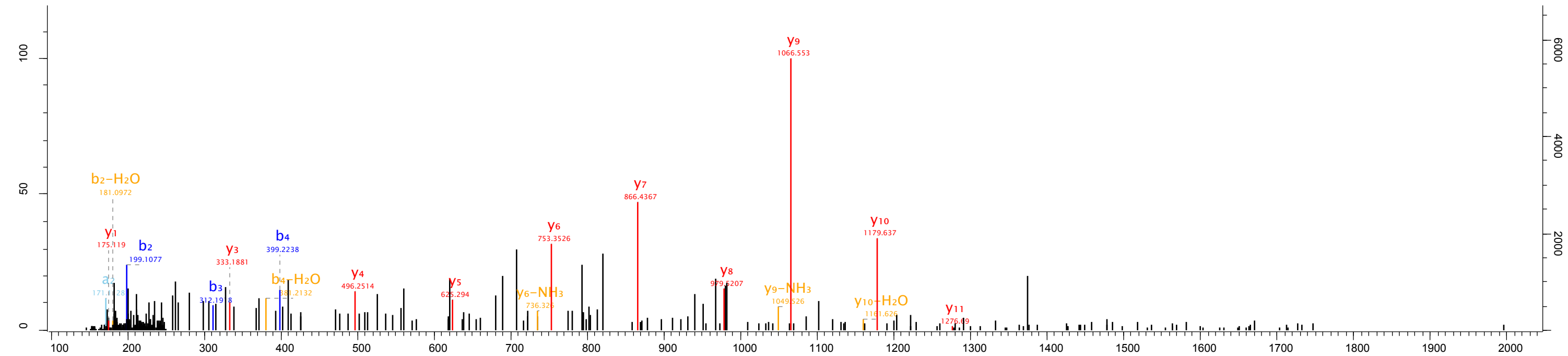


Raw file
20150307_NSC1_Top_opt_F1_01_1685

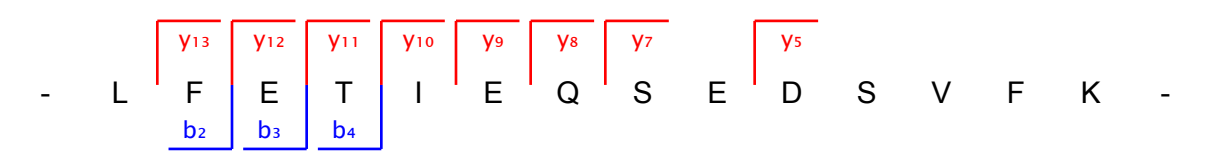
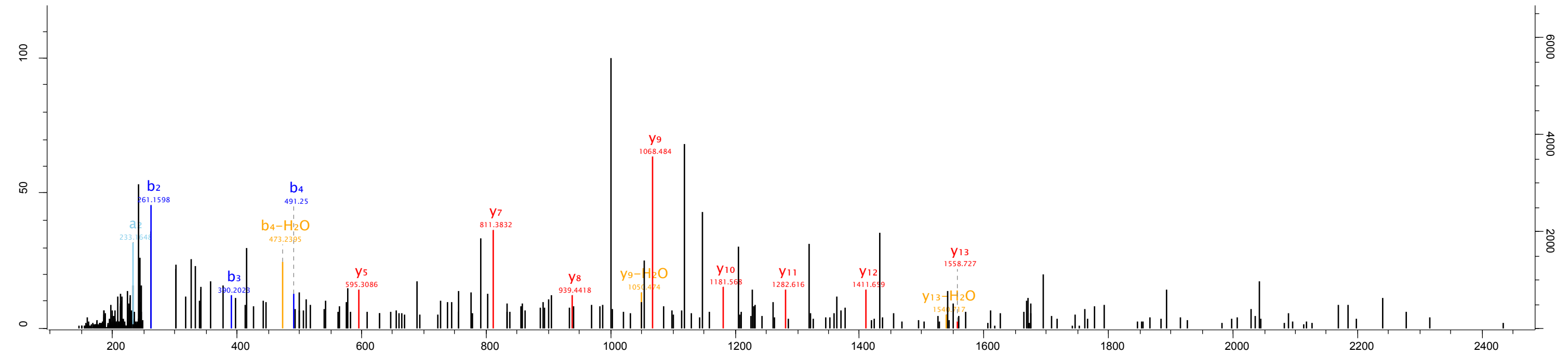
Scan 44871 Method TOF; CID Score 54.56 m/z 771.07 Gene names Aagab



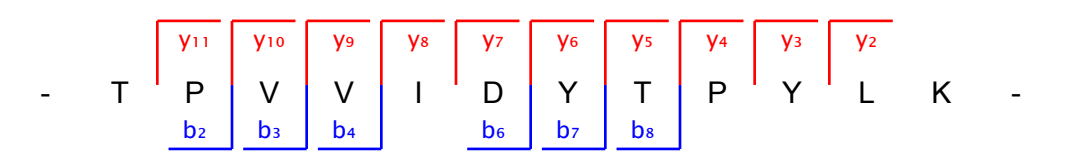
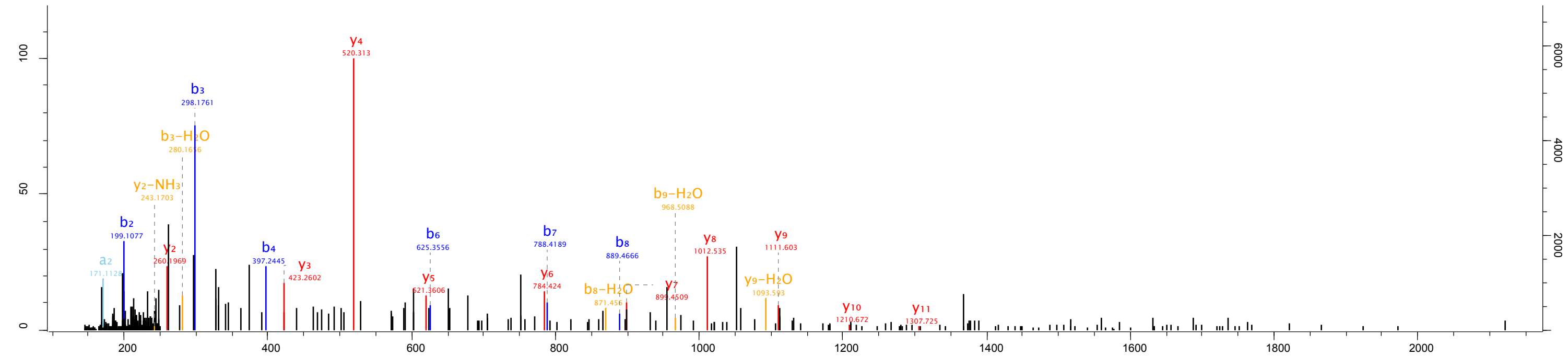
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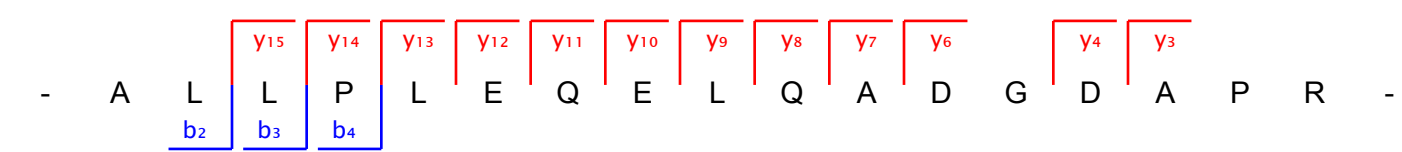
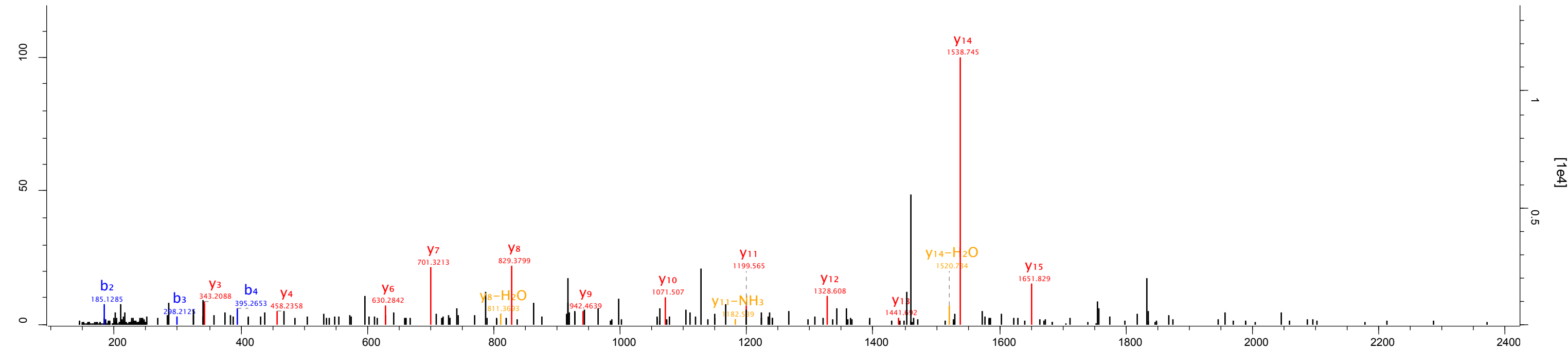
Raw file 20150307_NSC1_Top_opt_F1_01_1685 Scan 52937 Method TOF; CID Score 54.09 m/z 836.4 Gene names Tfb2m;Gm1818



Raw file: 20150307_NSC1_Top_opt_F1_01_1685
 Scan: 53359 Method: TOF; CID Score: 83.2 m/z: 705.39 Gene names: Rundc3a

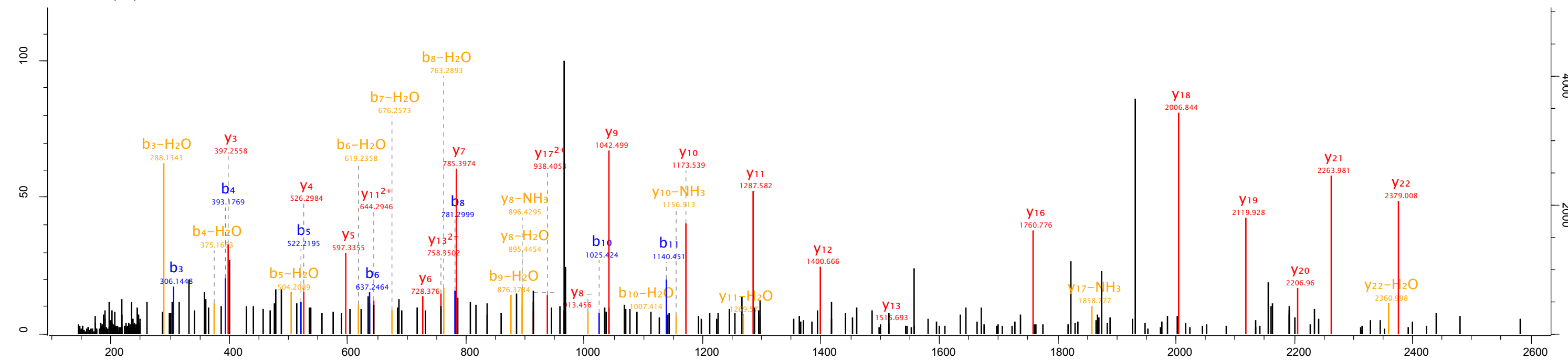


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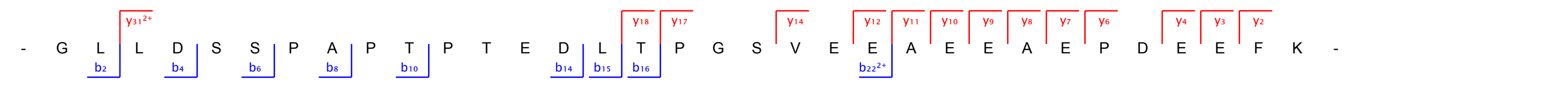
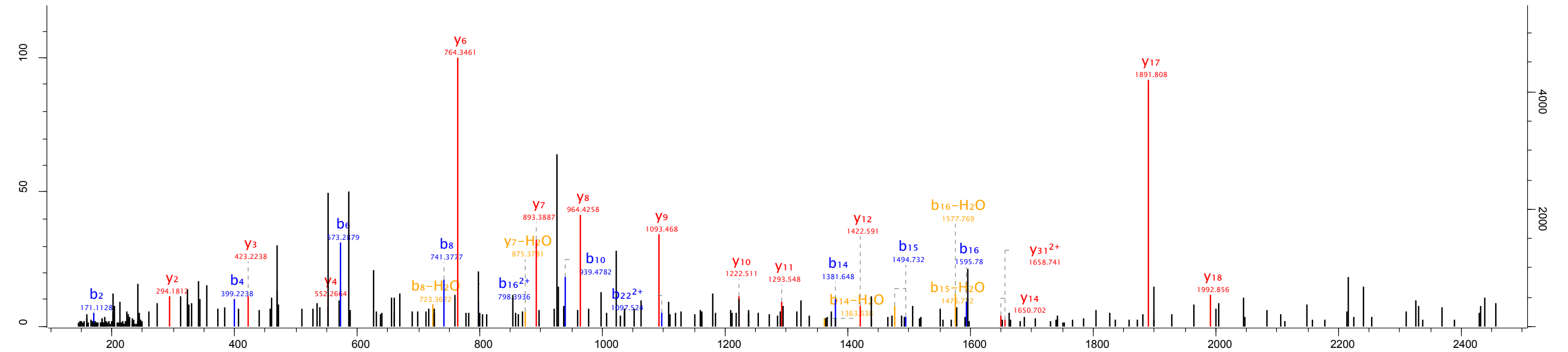


Raw file
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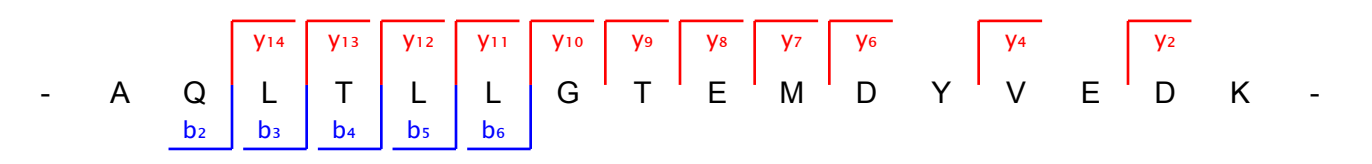
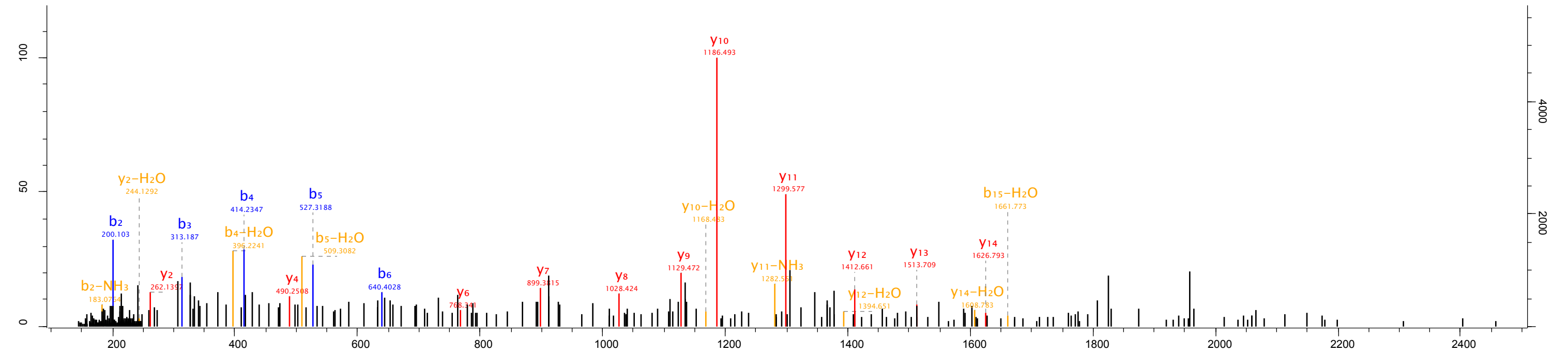
Scan 57125 Method TOF; CID Score 112.26 m/z 967.74 Gene names Tmem208



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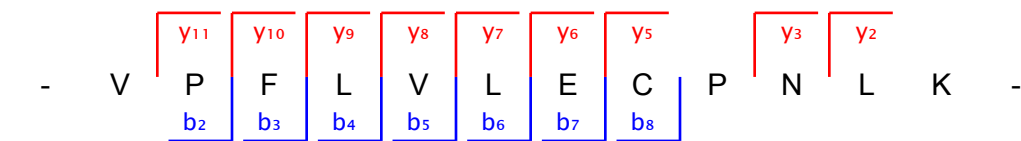
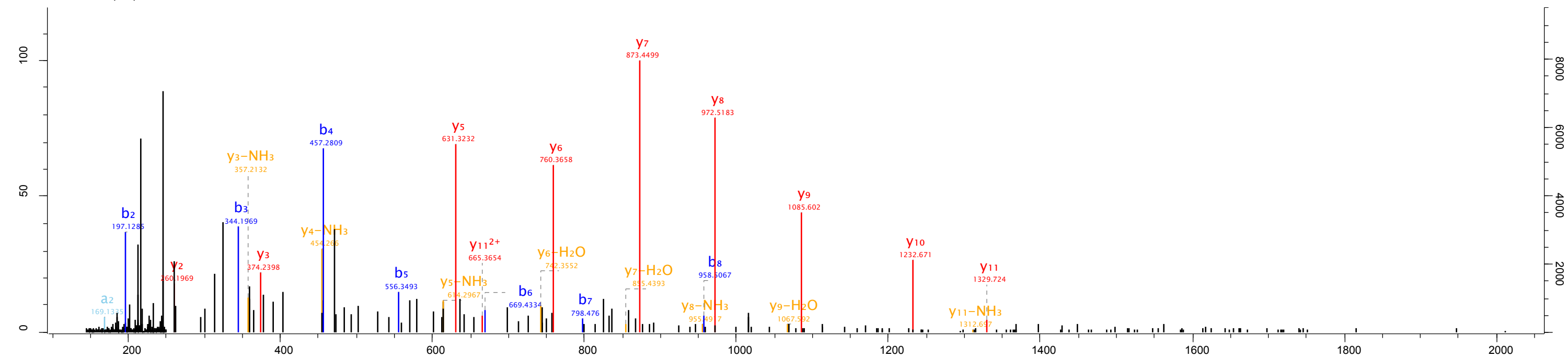


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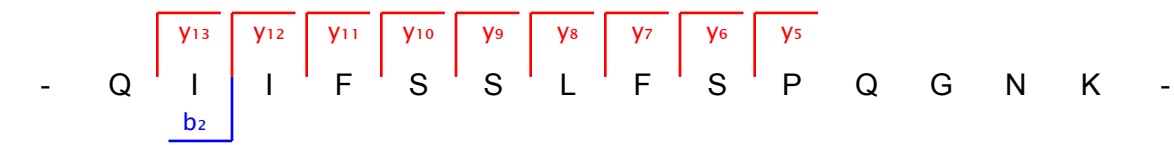
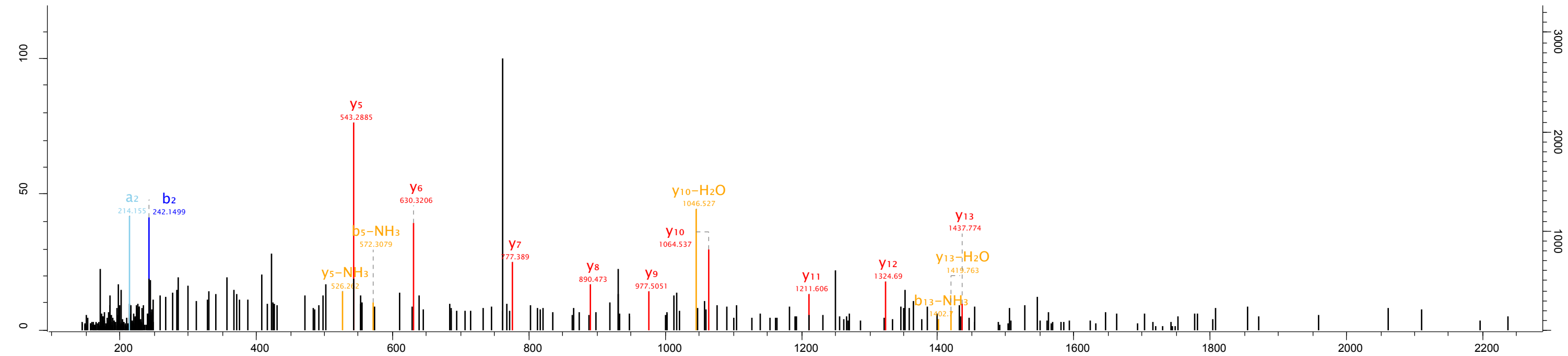


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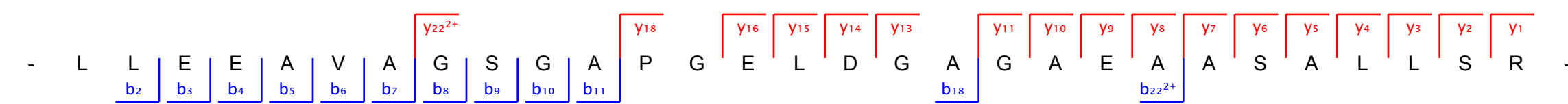
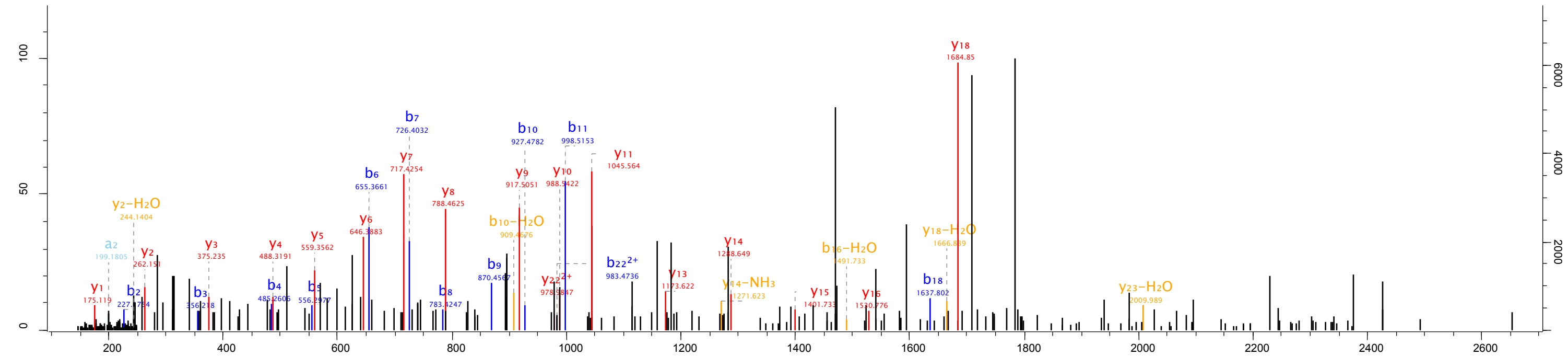
Scan 61453 Method TOF; CID Score 120.86 m/z 714.89 Gene names Ostc



Raw file 20150307_NSC1_Top_opt_F1_01_1685 Scan 61809 Method TOF; CID Score 62.29 m/z 783.41

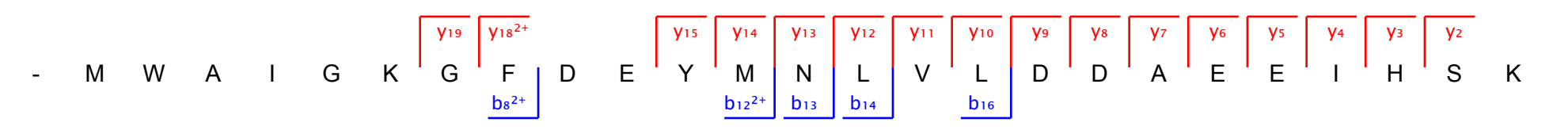
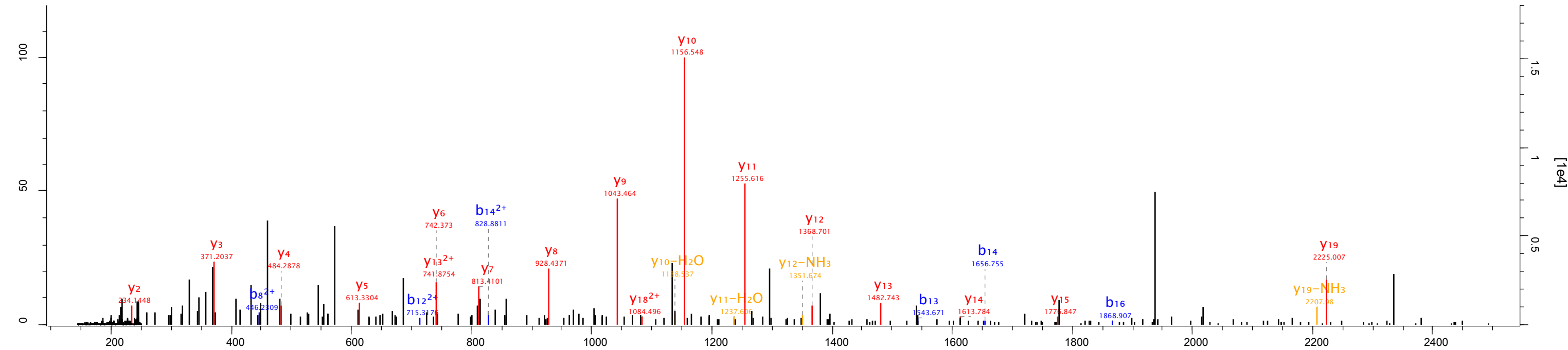


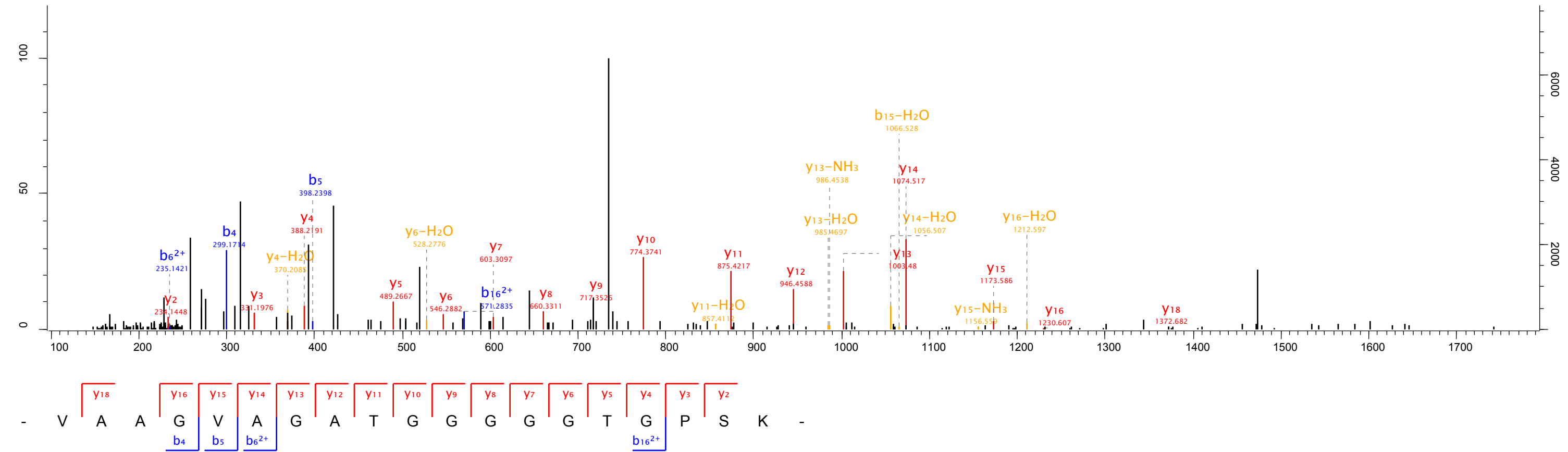
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Raw file
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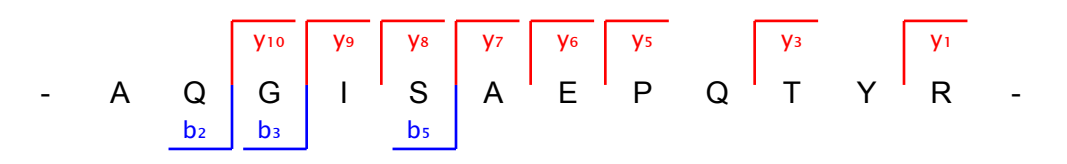
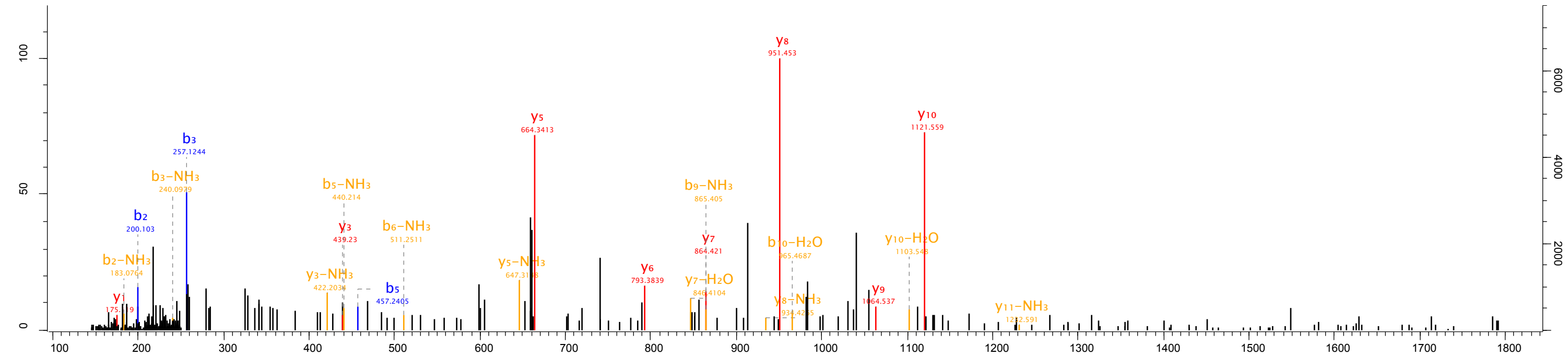
Scan 69185 Method TOF; CID Score 63.7 m/z 971.12 Gene names Snrpe



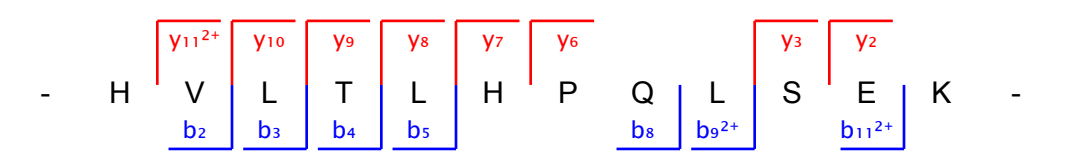
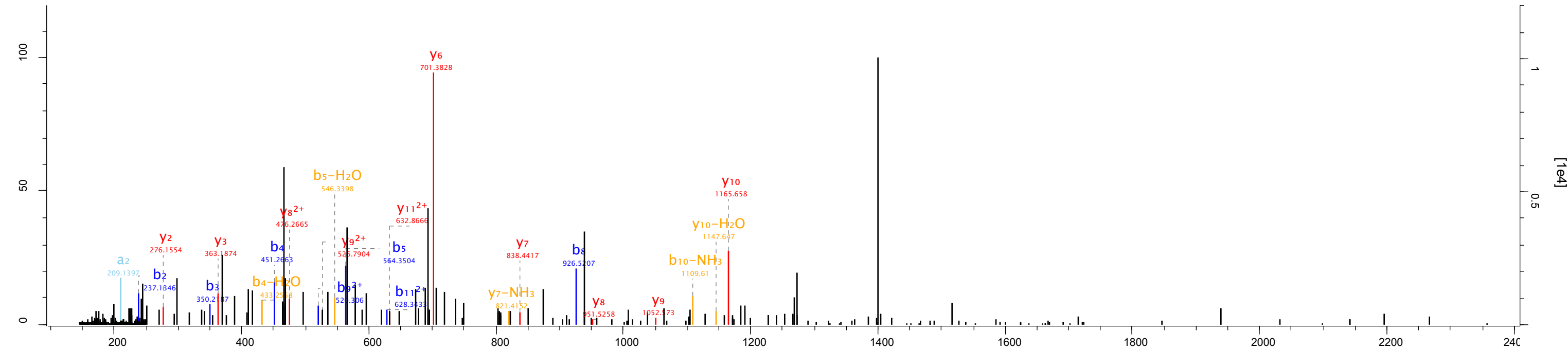


Raw file
20150307_NSC2_Top_opt_F2_01_1688

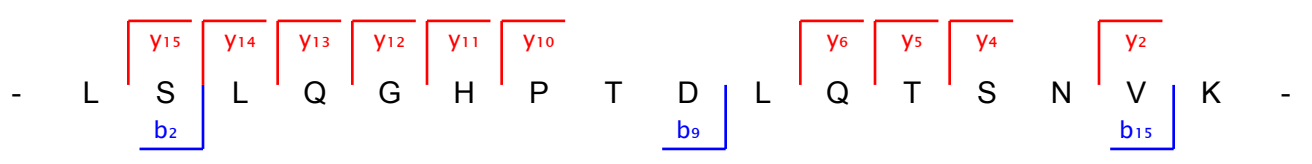
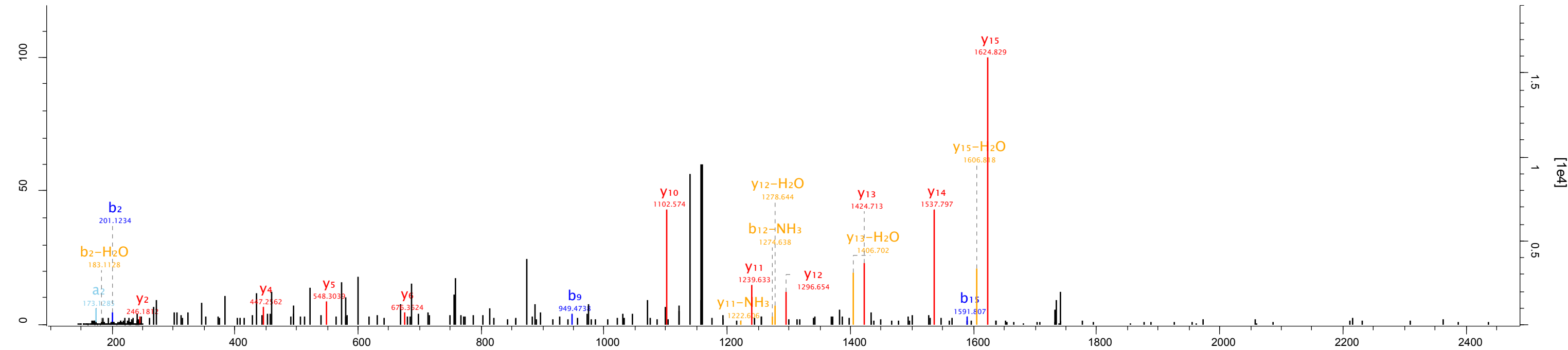
Scan 20810
Method TOF; CID
Score 69.03
m/z 660.82
Gene names Prkg1

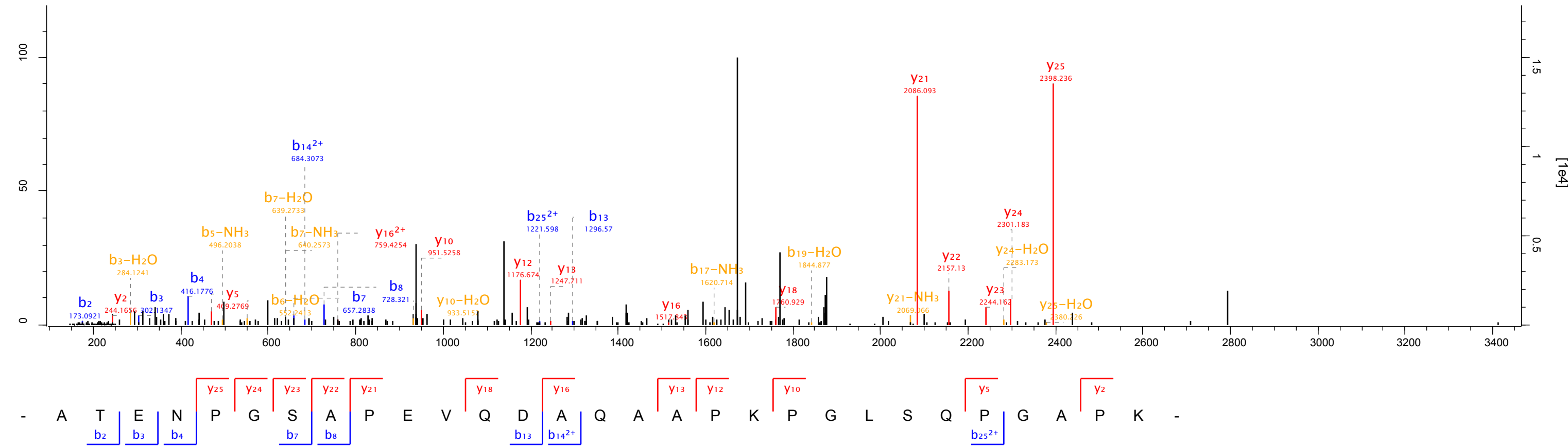


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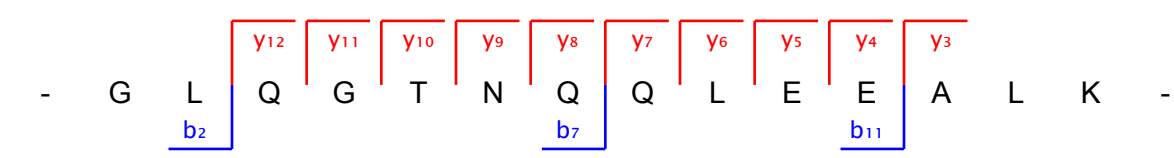
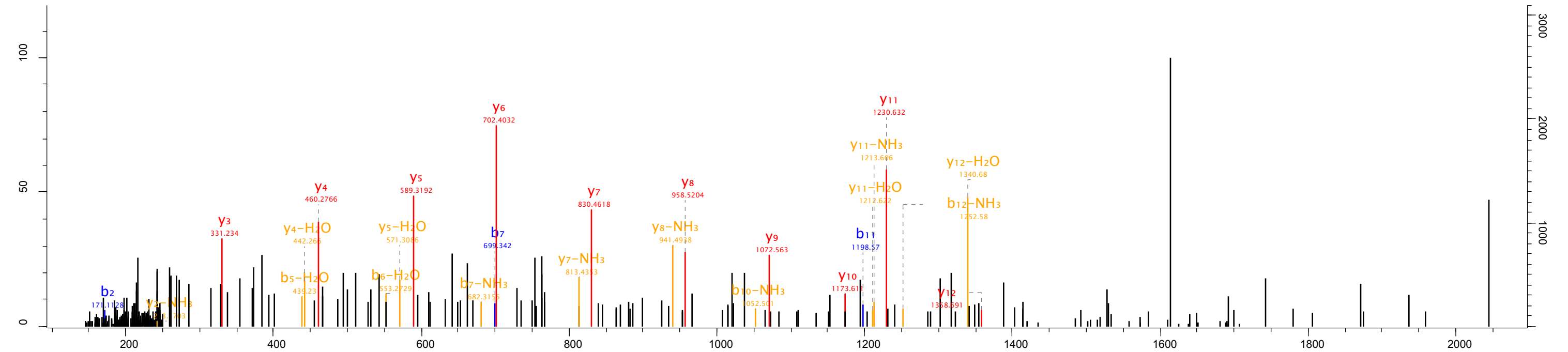


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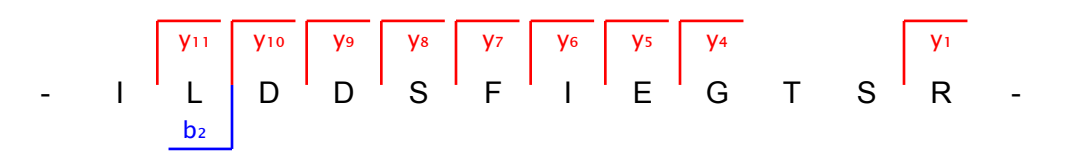
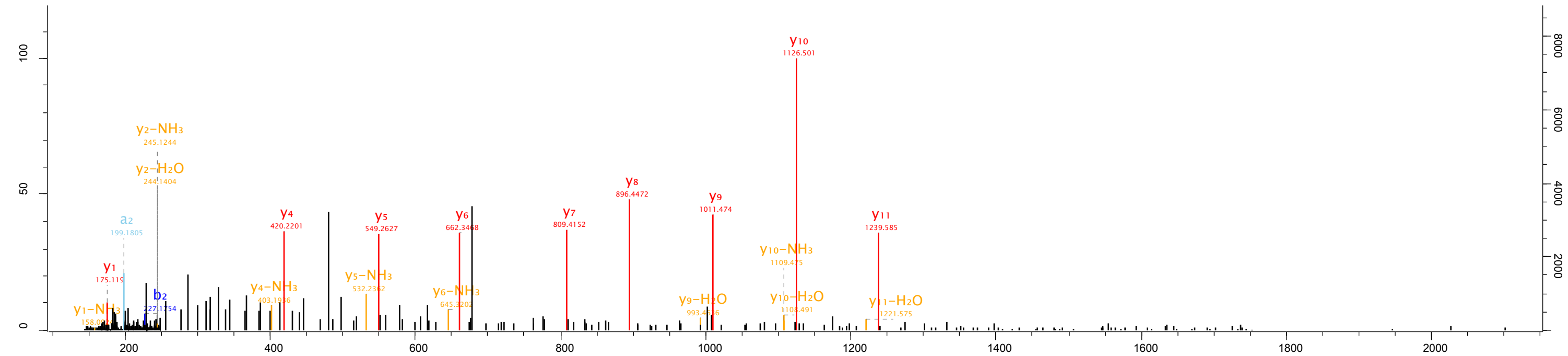


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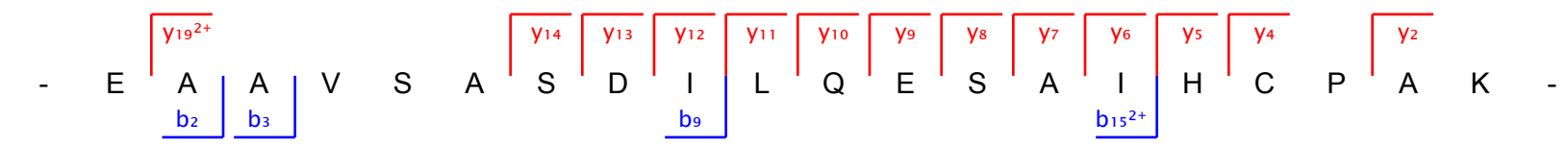
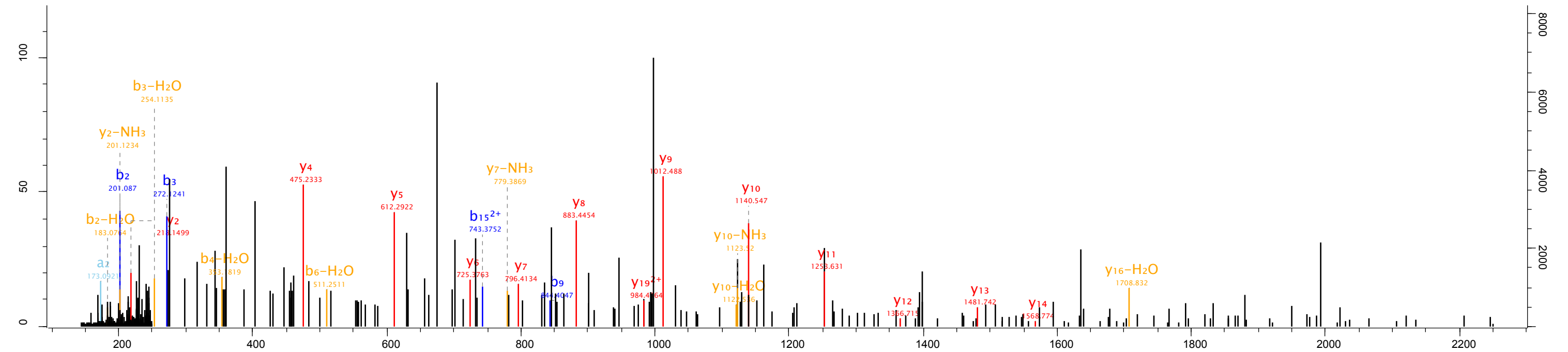


Raw file
20150307_NSC2_Top_opt_F2_01_1688

Scan 44883 Method TOF; CID Score 100.93 m/z 676.83 Gene names Zdhhc6

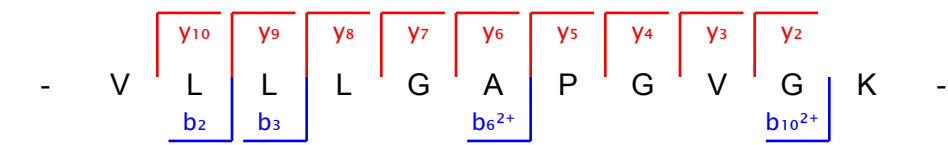
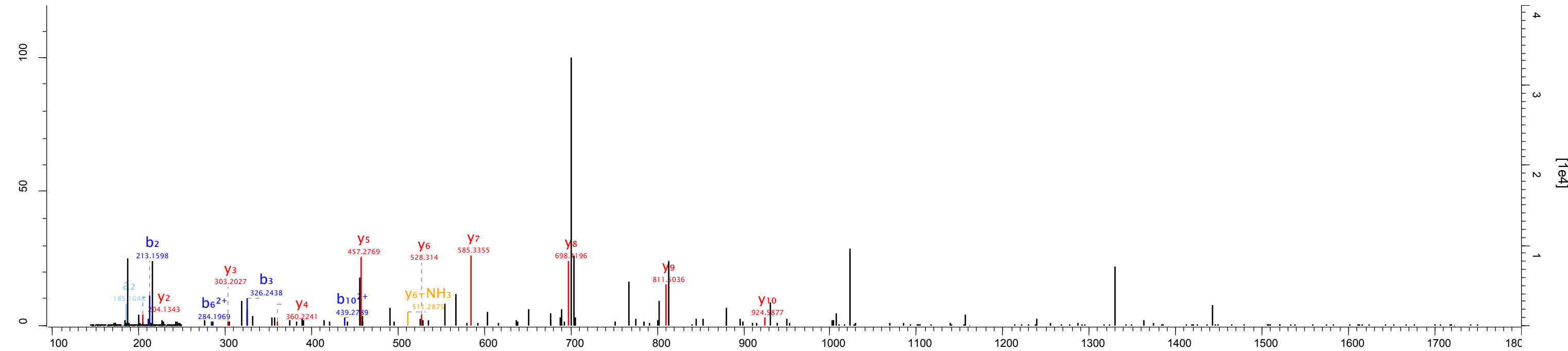


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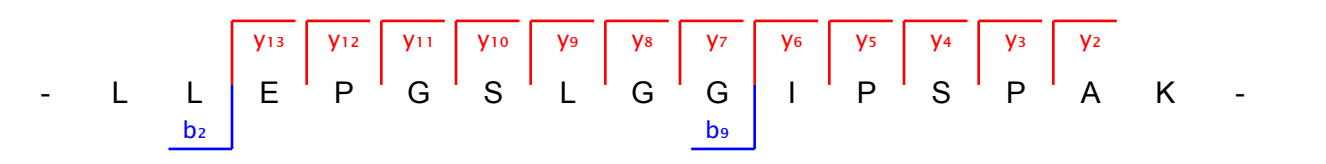
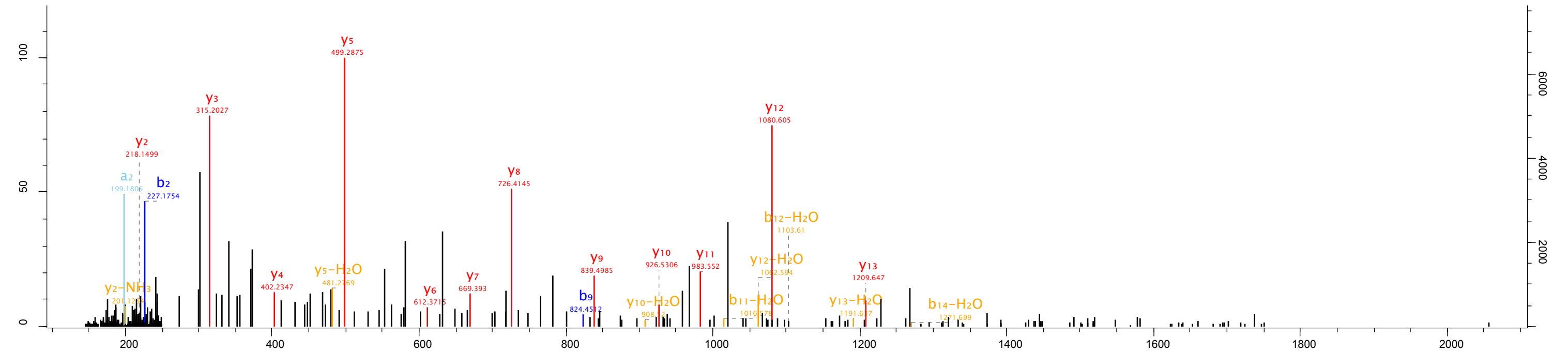


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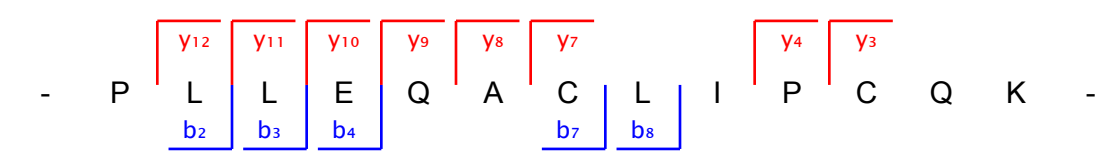
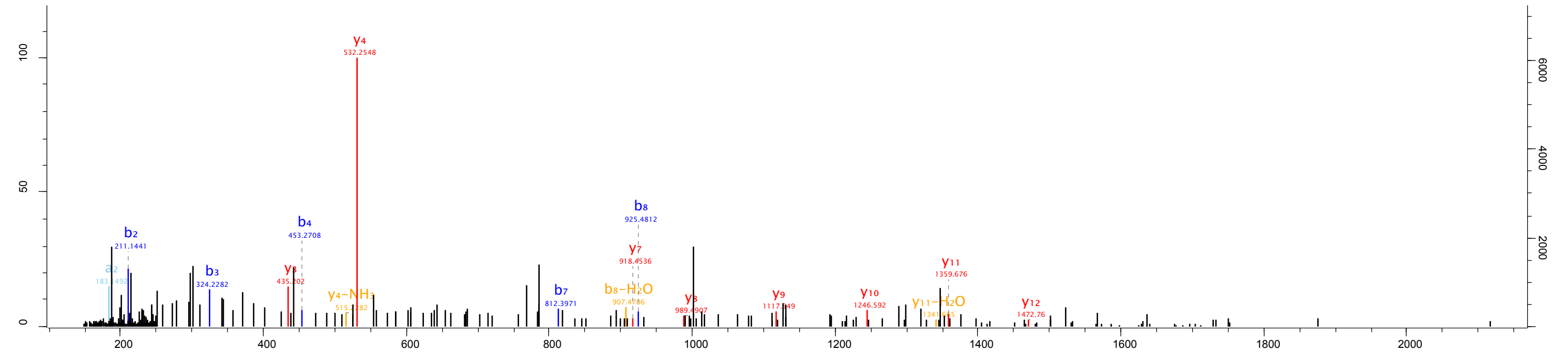
Scan 48560 Method TOF; CID Score 65.72 m/z 512.33 Gene names Rrad



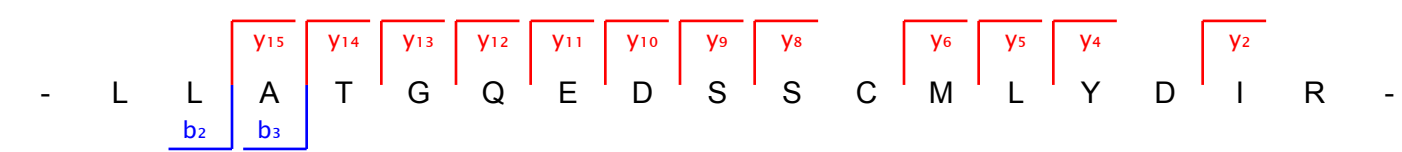
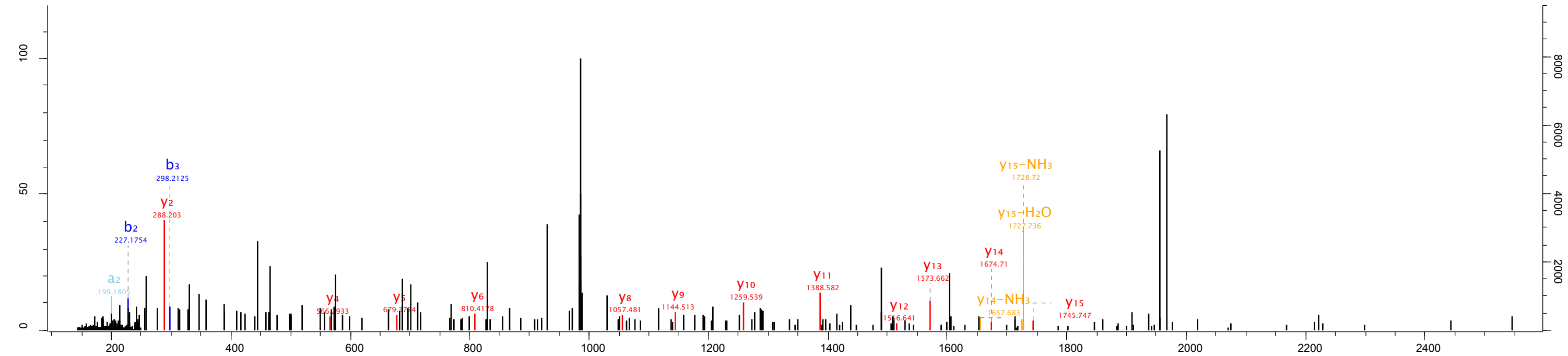
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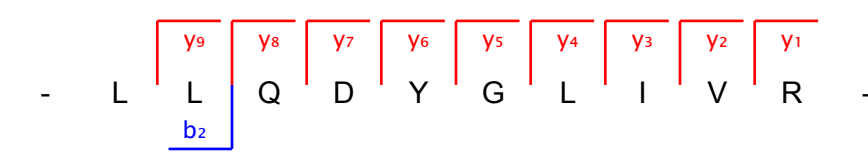
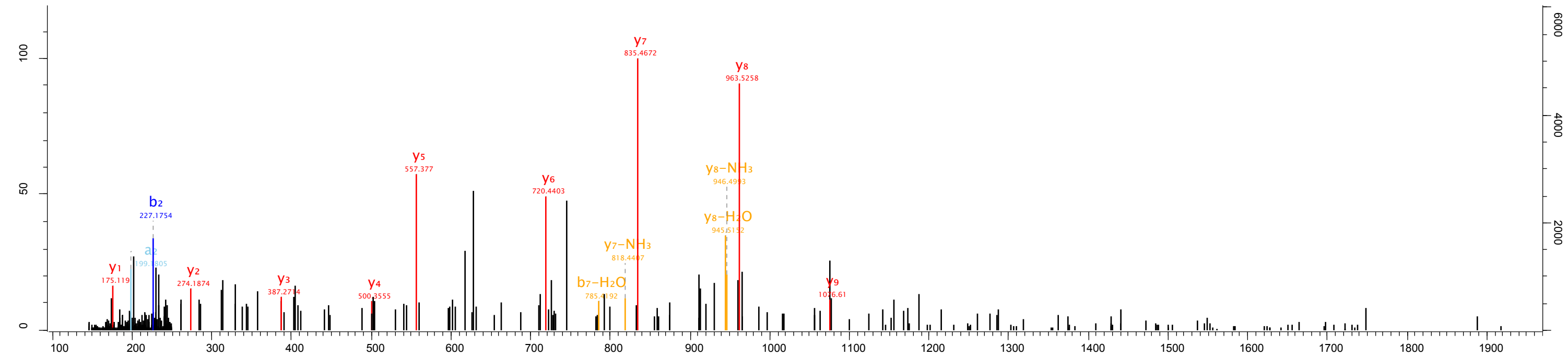
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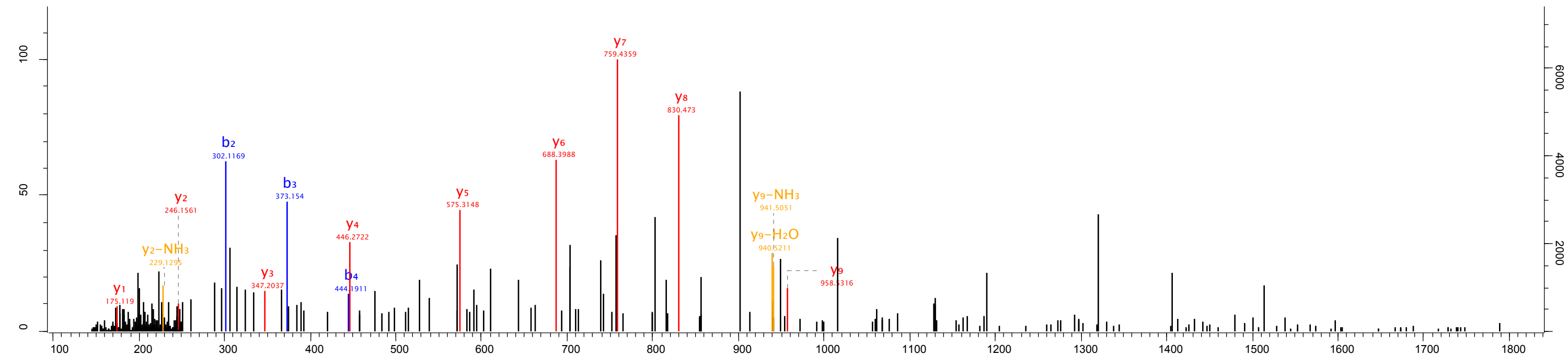


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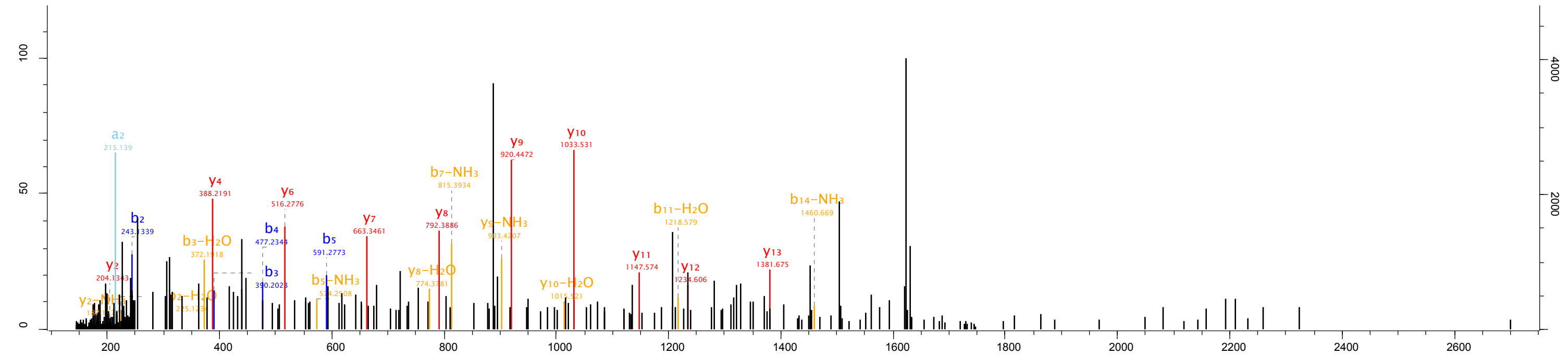




ac
- M Q A A L E V T A R -

Fragmentation scheme diagram showing amino acid sequence M Q A A L E V T A R - with b and y ions indicated by brackets above and below the sequence.

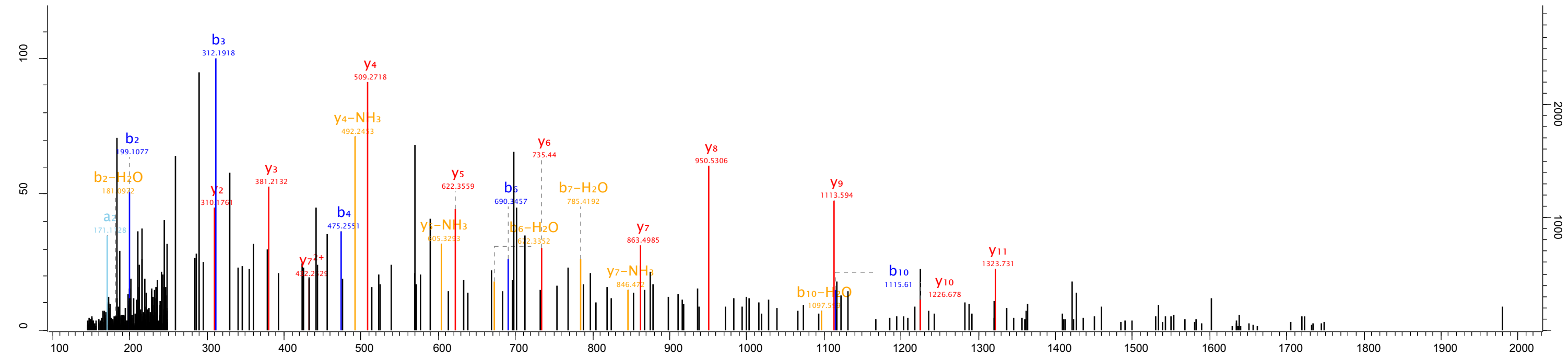
- Red brackets above the sequence indicate y ions: y9 (M-Q), y8 (Q-A), y7 (A-A), y6 (A-L), y5 (L-E), y4 (E-V), y3 (V-T), y2 (T-A), y1 (A-R).
- Blue brackets below the sequence indicate b ions: b2 (Q-A), b3 (A-A), b4 (A-L).



- E L F S N L Q E F A G P S G K -

b2 b3 b4 b5 y13 y12 y11 y10 y9 y8 y7 y6 y4 y2

Raw file 20150307_NSC2_Top_opt_F2_01_1688 Scan 58928 Method TOF; CID Score 96.82 m/z 713.39 Gene names Med27



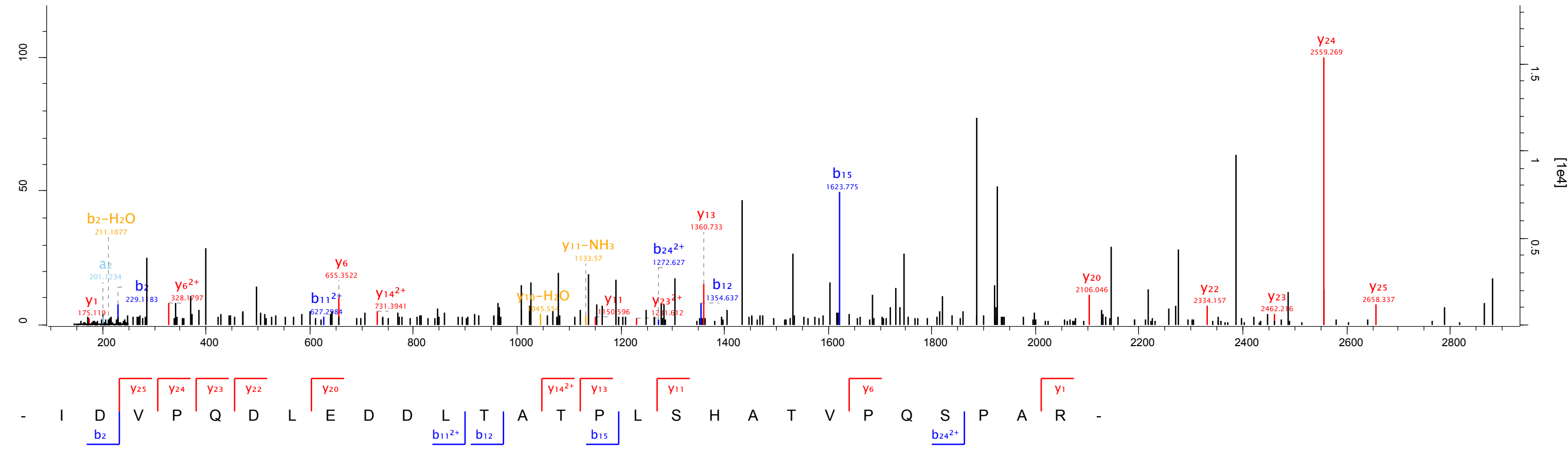
- T P L Y S Q L L Q A Y K -

Fragmentation mapping (b and y ions):

- b₂ (P), b₃ (L), b₄ (Y), b₆ (Q), b₁₀ (A)
- y₂ (Y), y₃ (S), y₄ (Q), y₅ (L), y₆ (L), y₇ (Q), y₈ (S), y₉ (Y), y₁₀ (L), y₁₁ (P)

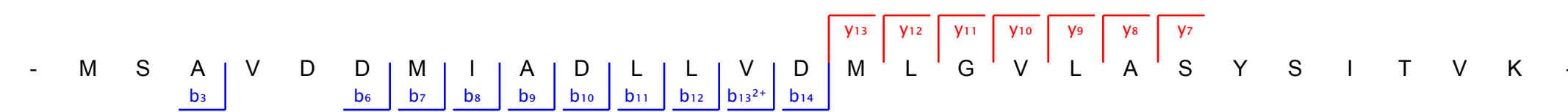
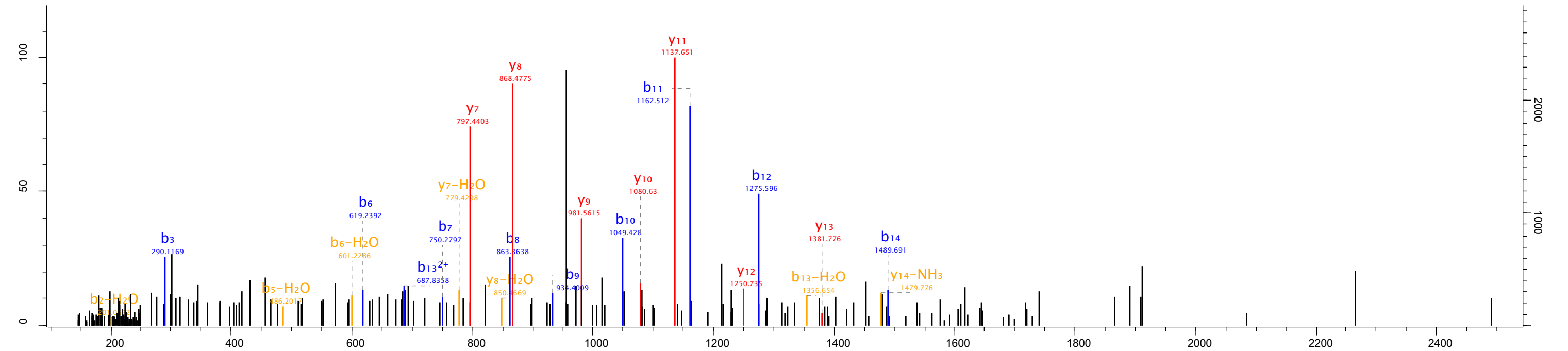
Raw file
20150307_NSC2_Top_opt_F2_01_1688

Scan 70592 Method TOF; CID Score 30.7 m/z 963.48 Gene names Snrk



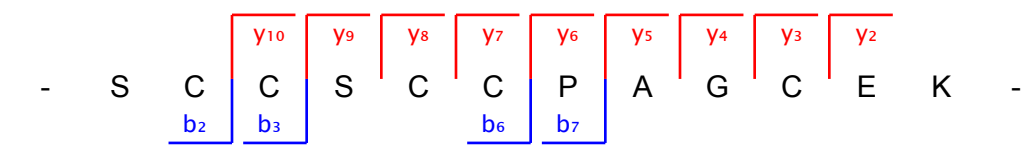
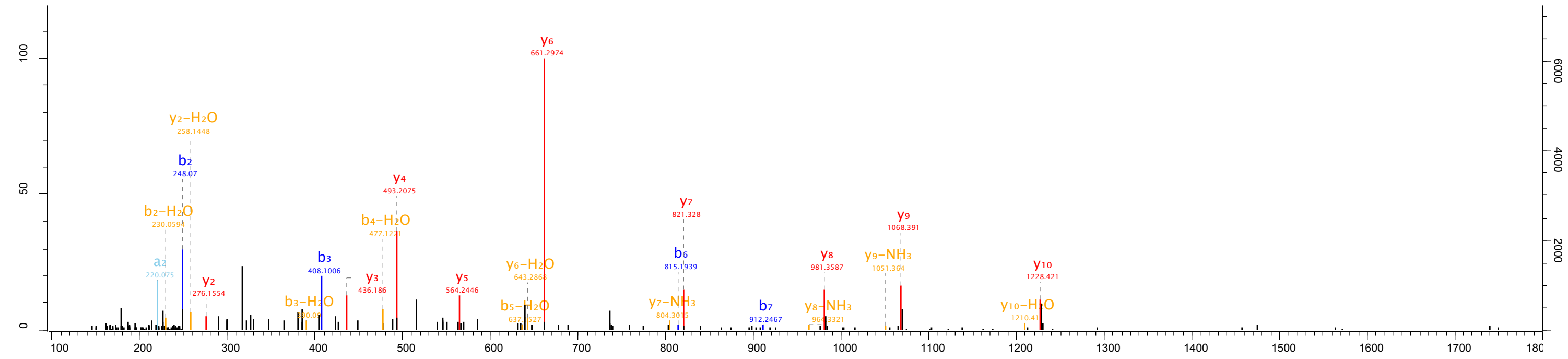
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Scan 76458 Method TOF; CID Score 53.48 m/z 957.48 Gene names Nbea

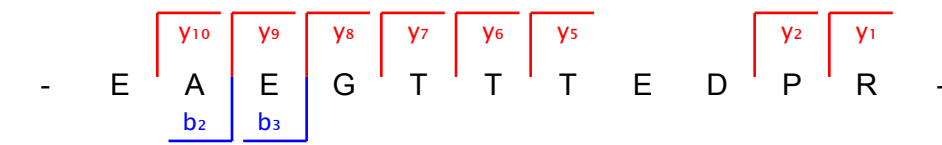
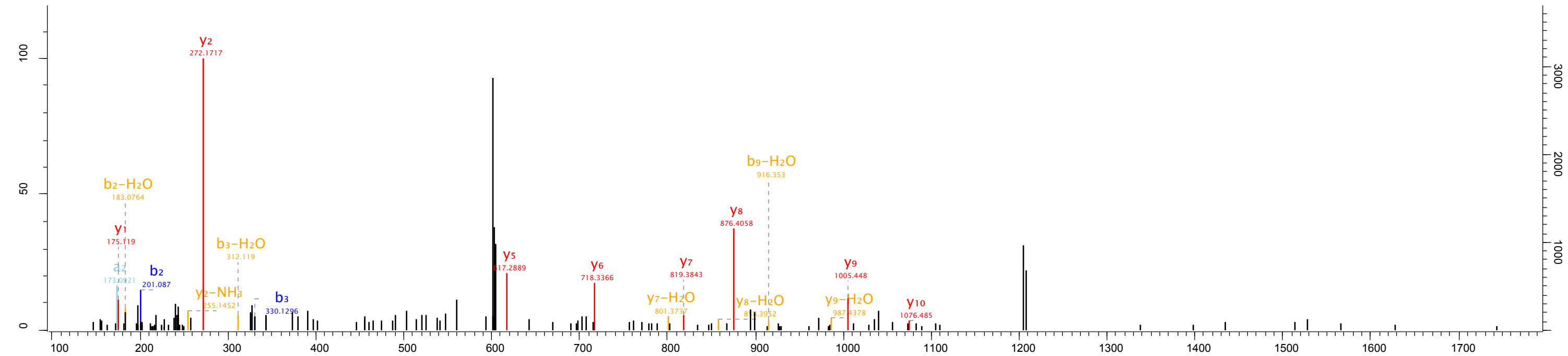


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20150307_NSC3_Top_opt_F3_01_1682

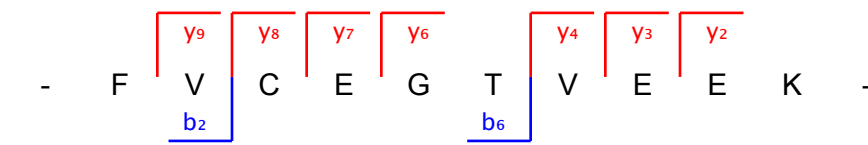
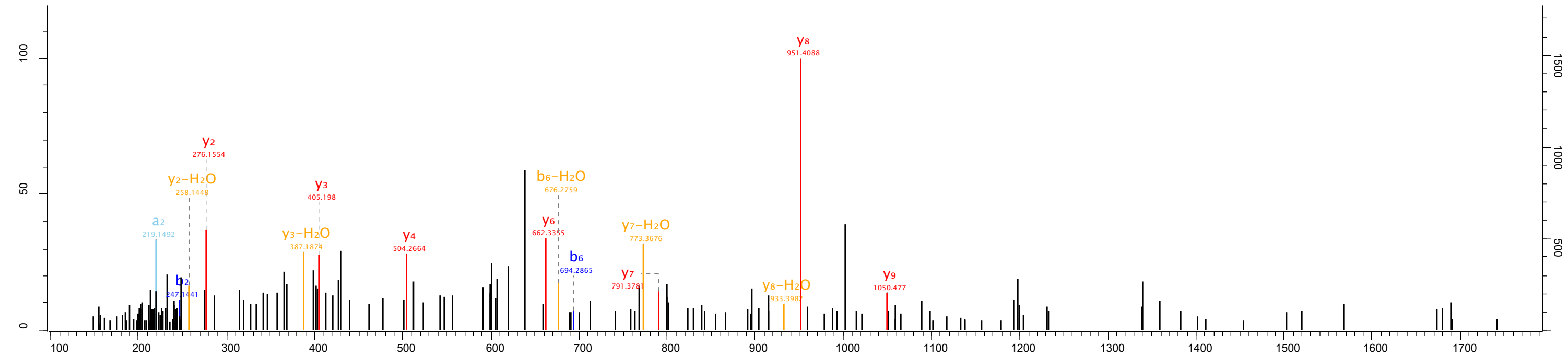
Scan 5024 Method TOF; CID Score 125.54 m/z 738.24 Gene names Mt3



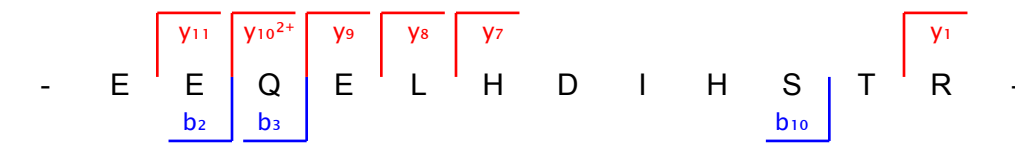
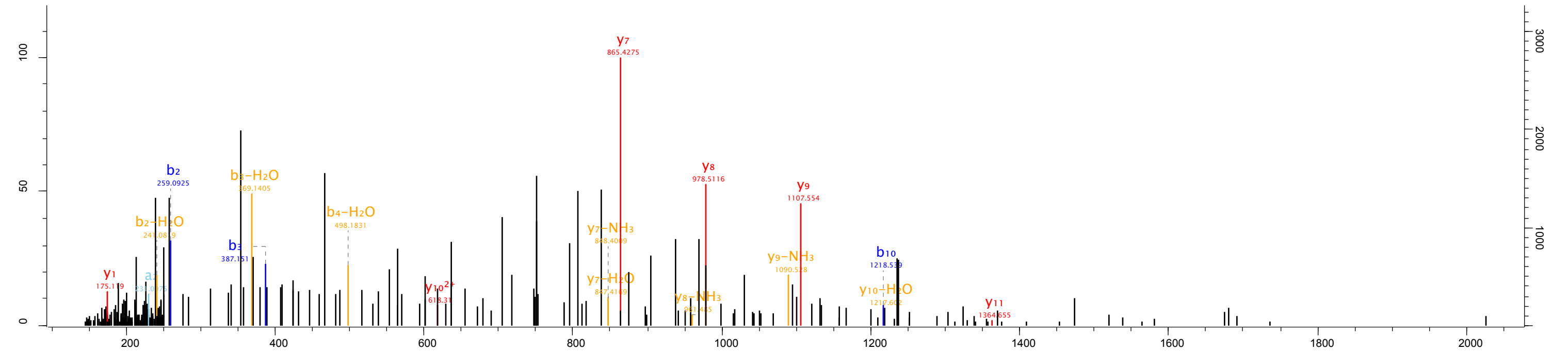
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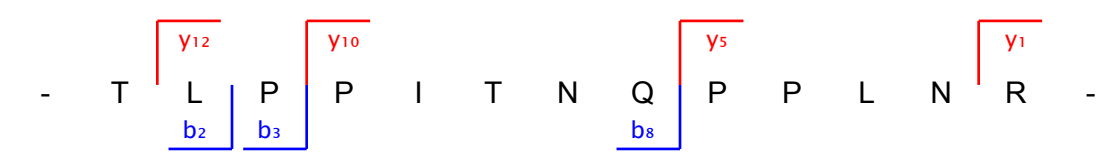
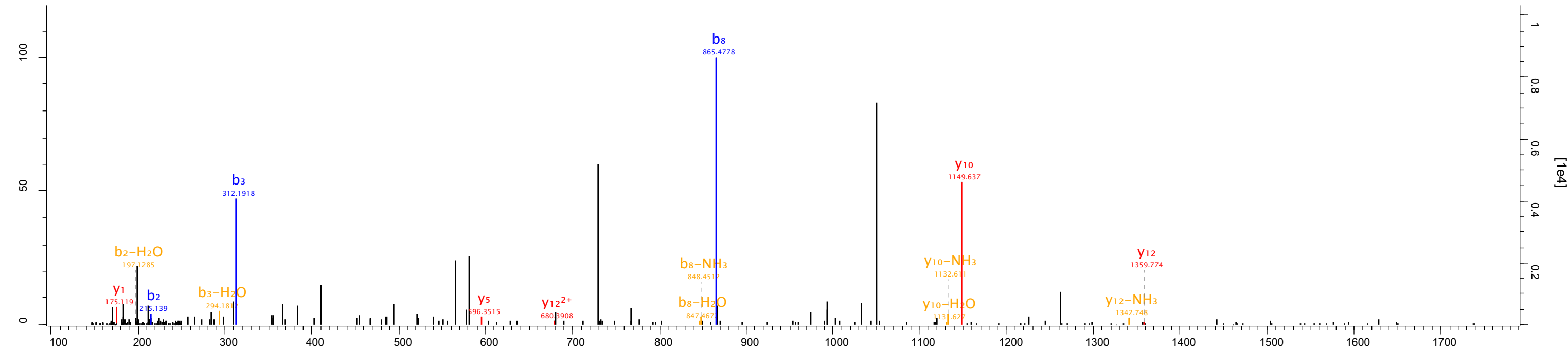
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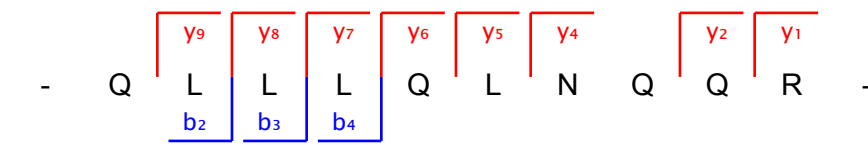
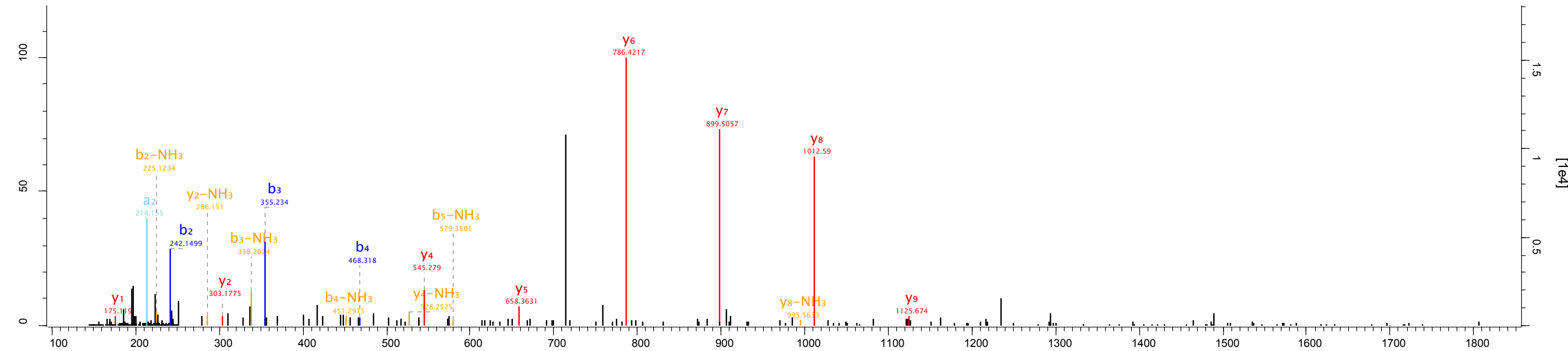


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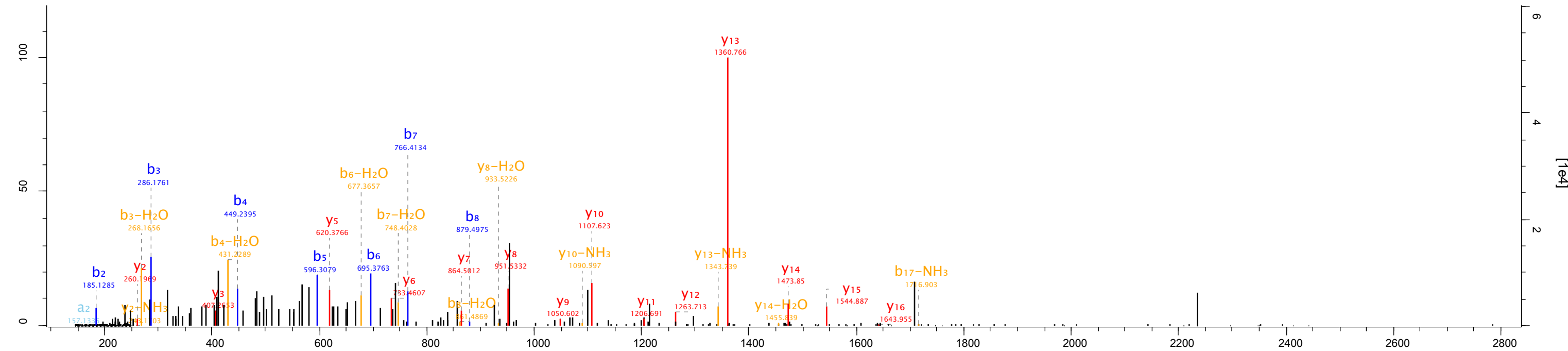
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20150307_NSC3_Top_opt_F3_01_1682

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Raw file
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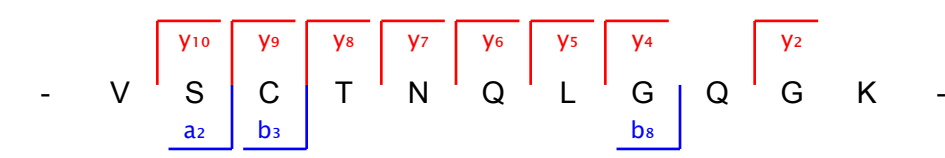
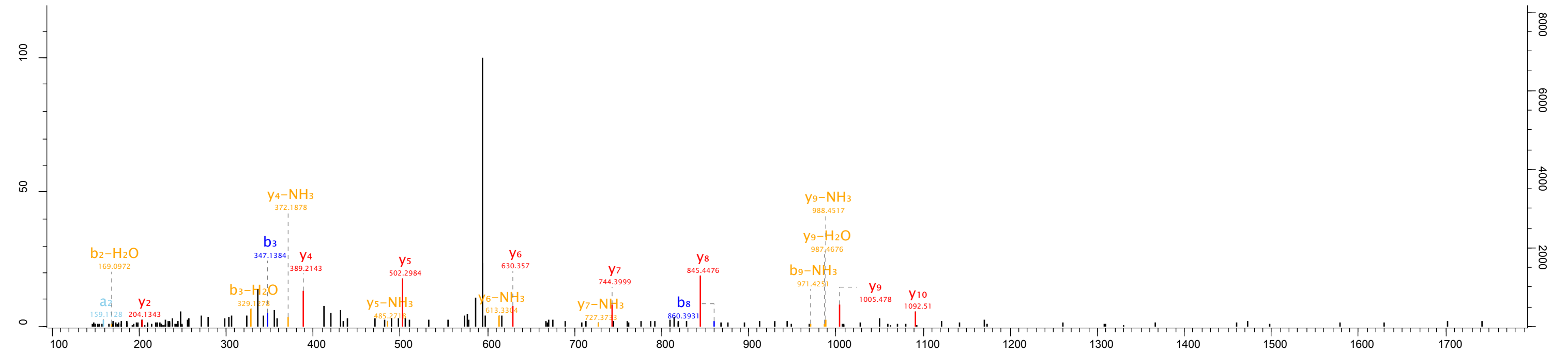
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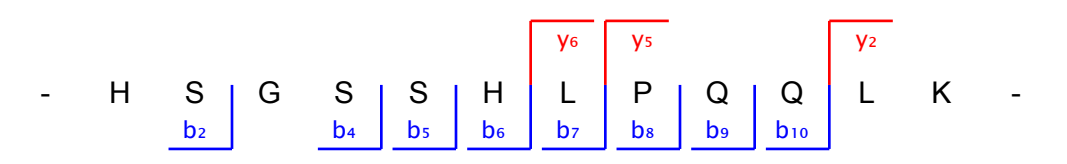
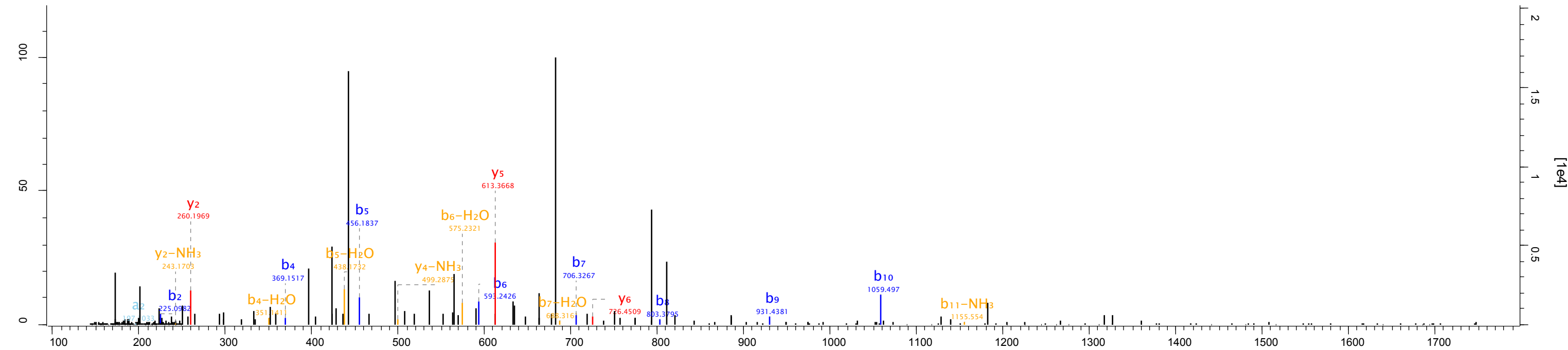
- A L T Y F V A L P G V G V S M L N V F L K -

b2 b3 b4 b5 b6 b7 b8 y16 y15 y14 y13 y12 y11 y10 y9 y8 y7 y6 y5 y3 y2

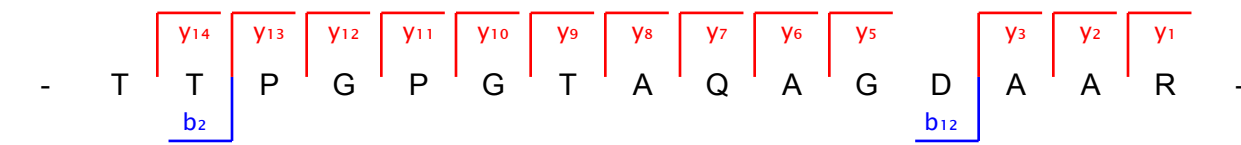
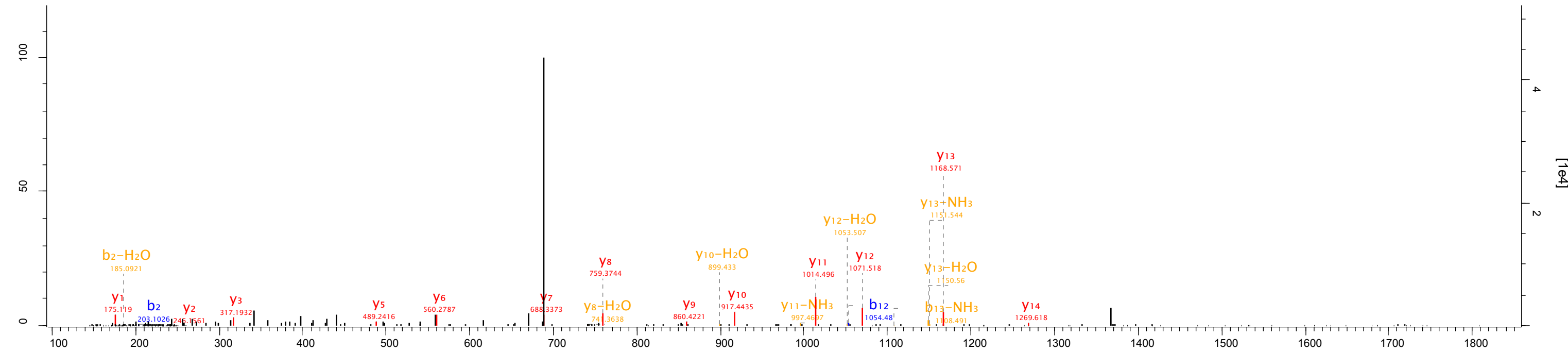
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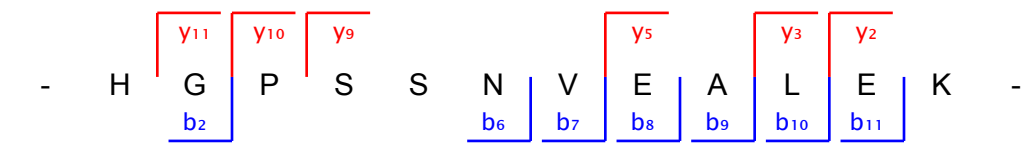
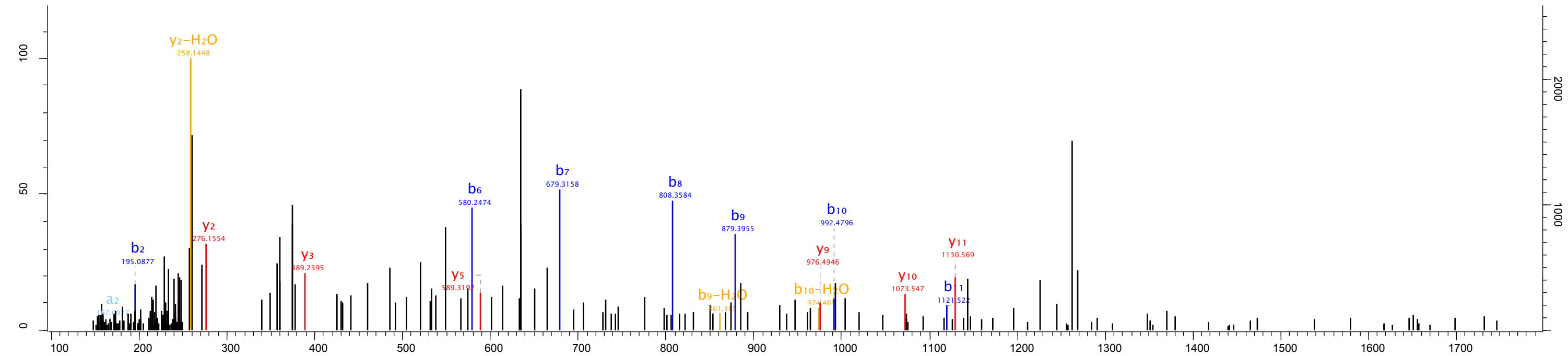
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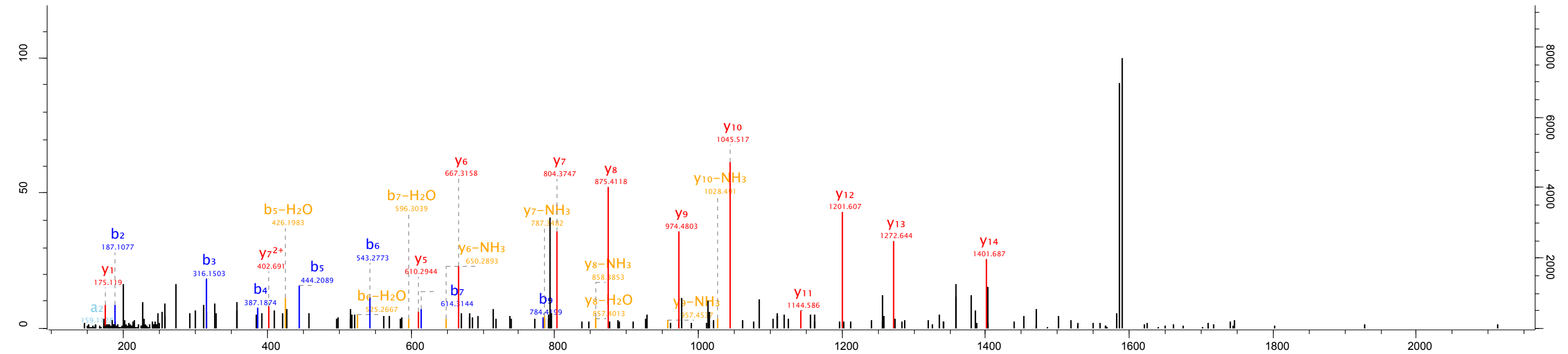
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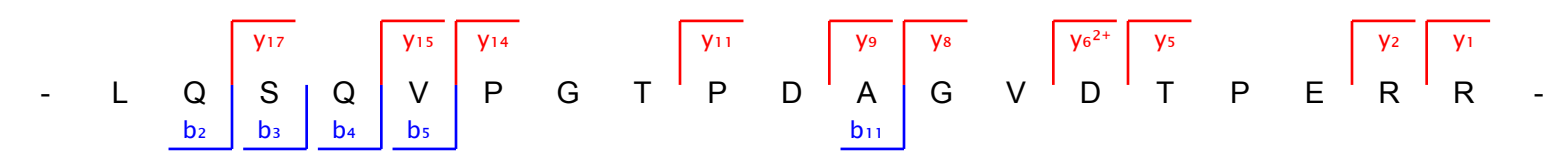
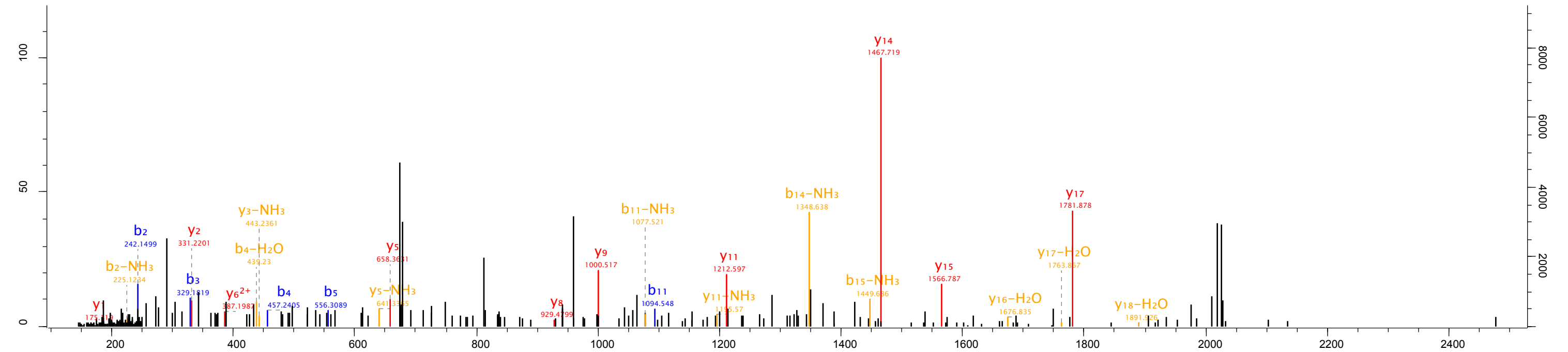


- S V E A G V A V A H G T Y G N R -

Fragmentation mapping:
 Blue boxes (b1-b9) indicate b-ion fragments: b2 (V-E), b3 (E-A), b4 (A-G), b5 (G-V), b6 (V-A), b7 (A-V), b9 (A-H).
 Red boxes (y1-y14) indicate y-ion fragments: y1 (R), y5 (T-G), y6 (G-H), y7 (H-A), y8 (A-V), y9 (V-A), y10 (A-G), y11 (G-V), y12 (V-A), y13 (A-G), y14 (E-A).

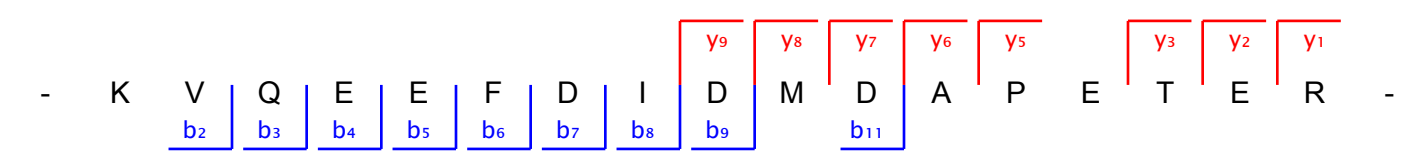
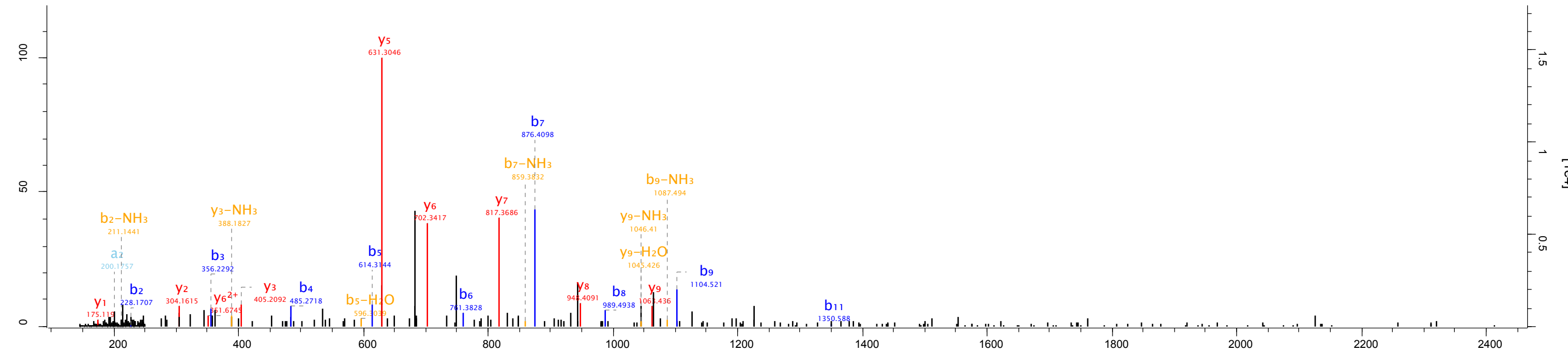
Raw file
20150307_NSC3_Top_opt_F3_01_1691

Scan 25670 Method TOF; CID Score 54.51 m/z 675.34 Gene names Zgpat

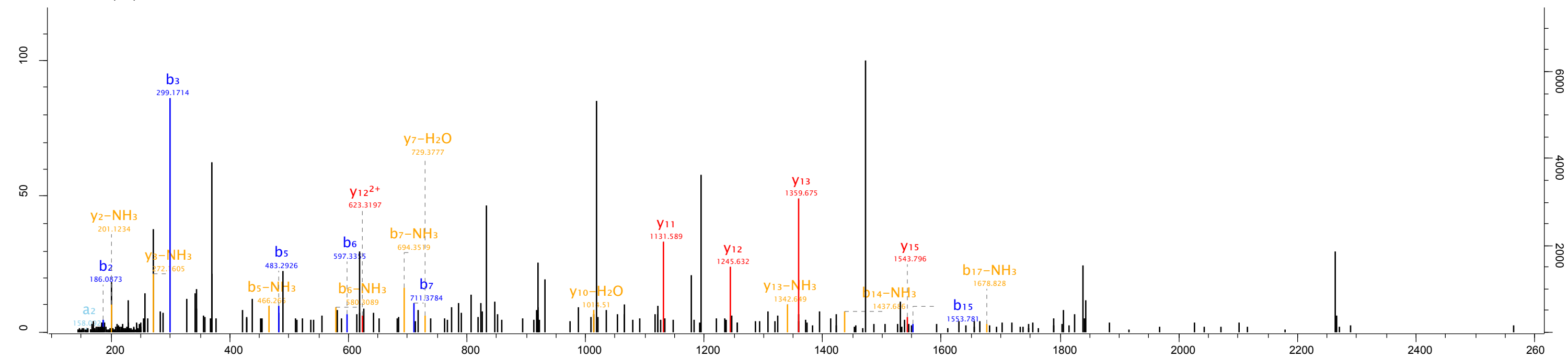


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Scan 40929 Method TOF; CID Score 47.09 m/z 685.32 Gene names Pcp4;Igsf5

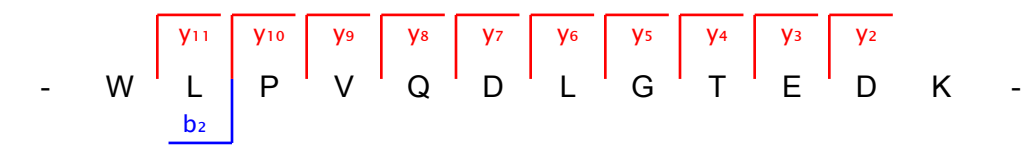
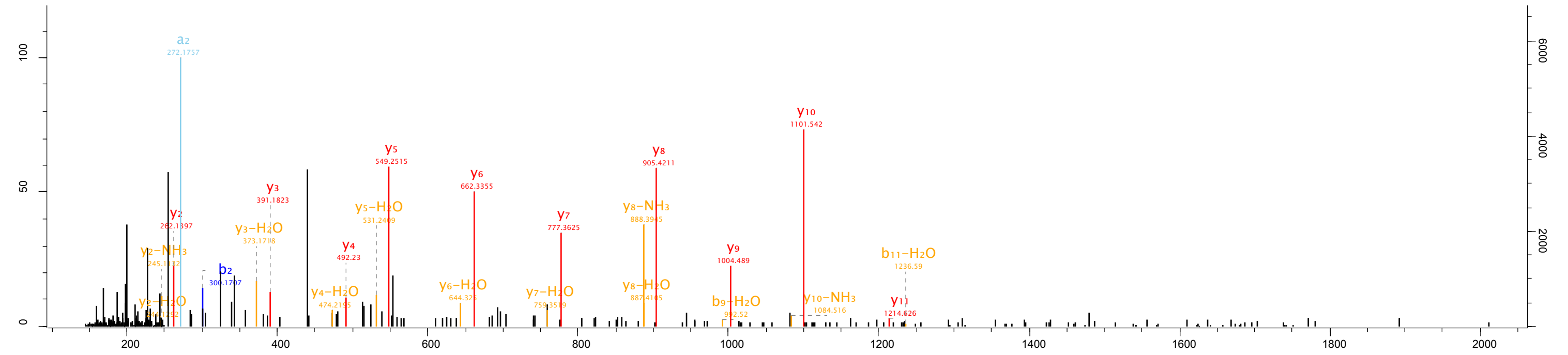


Raw file 20150307_NSC3_Top_opt_F3_01_1691 Scan 47062 Method TOF; CID Score 45 m/z 921.98 Gene names Stab2

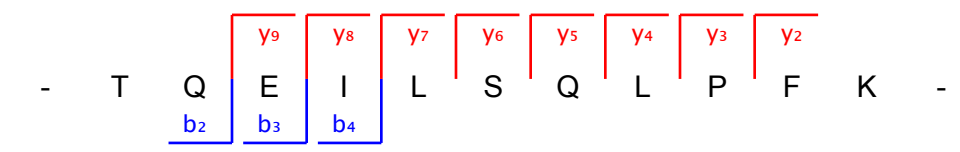
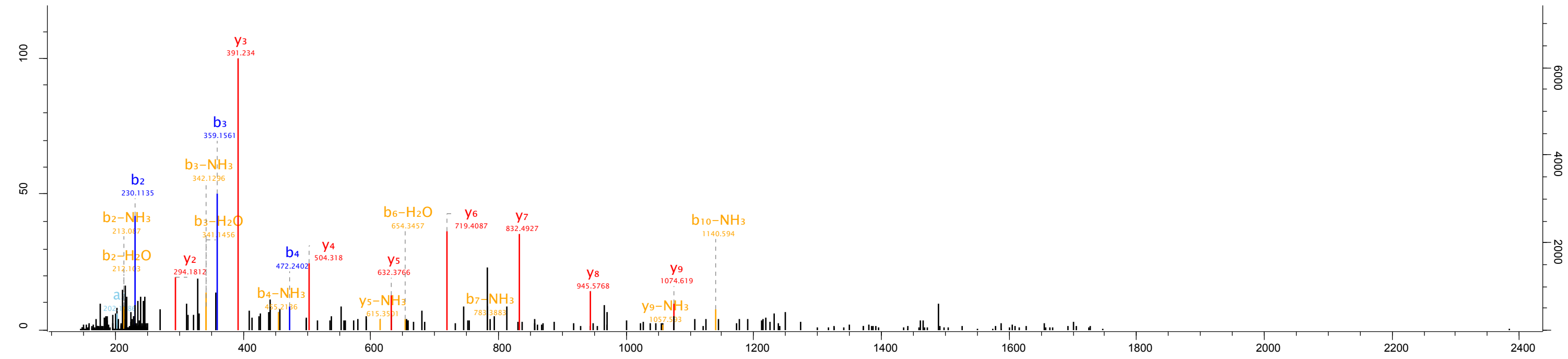


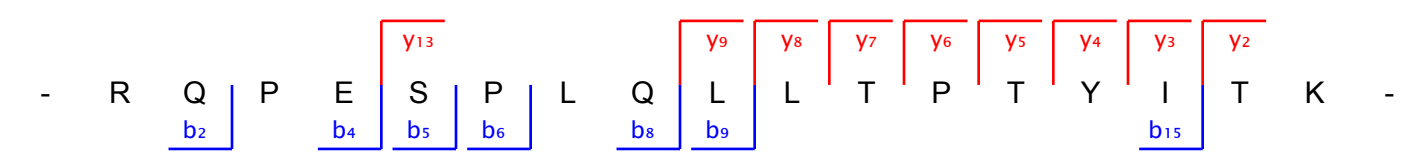
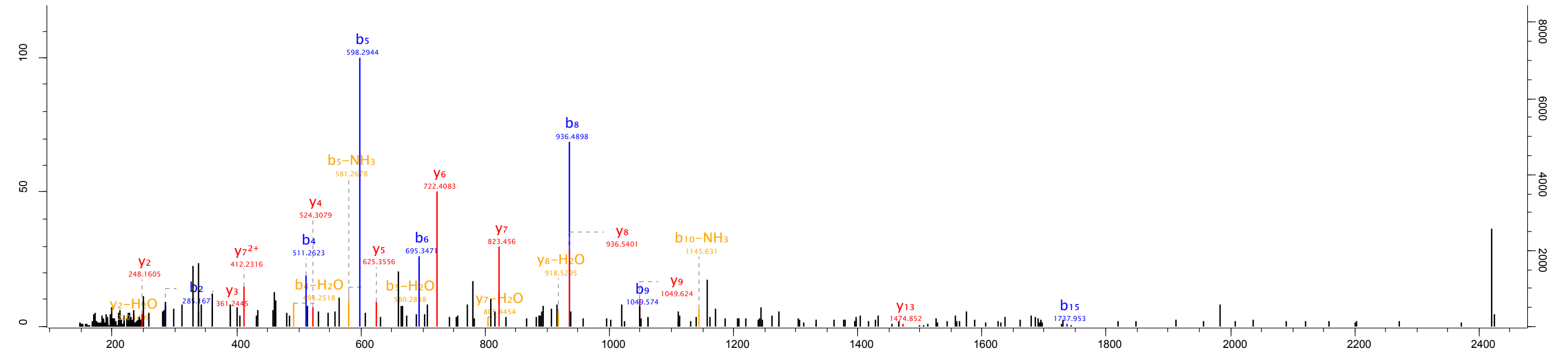
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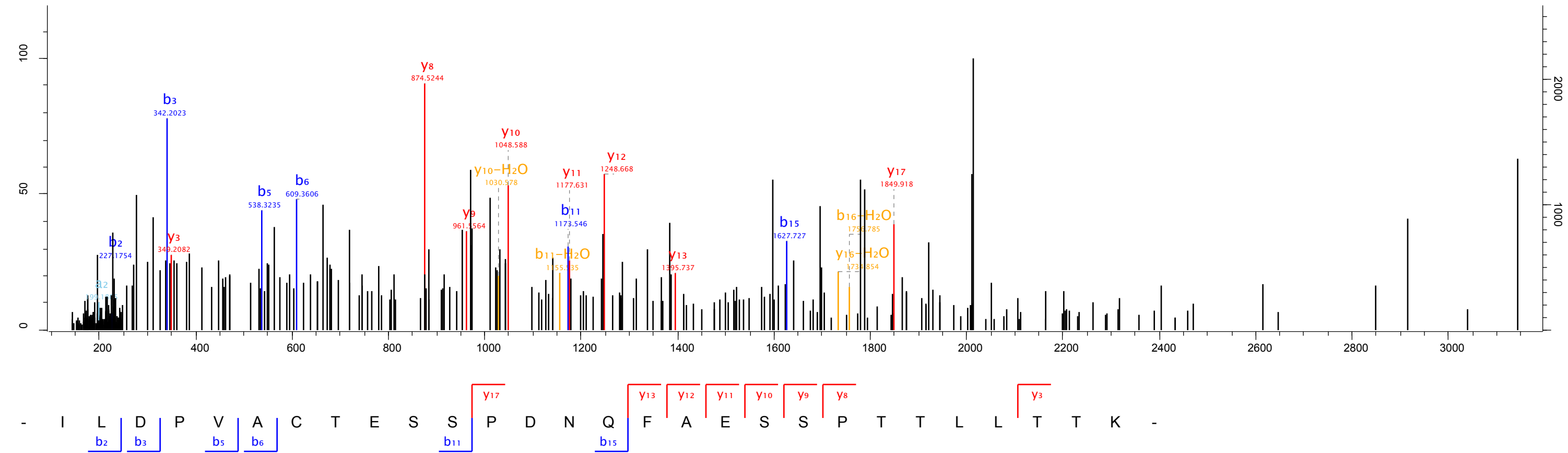
Scan 48875 Method TOF; CID Score 117.79 m/z 700.85 Gene names Spcs1

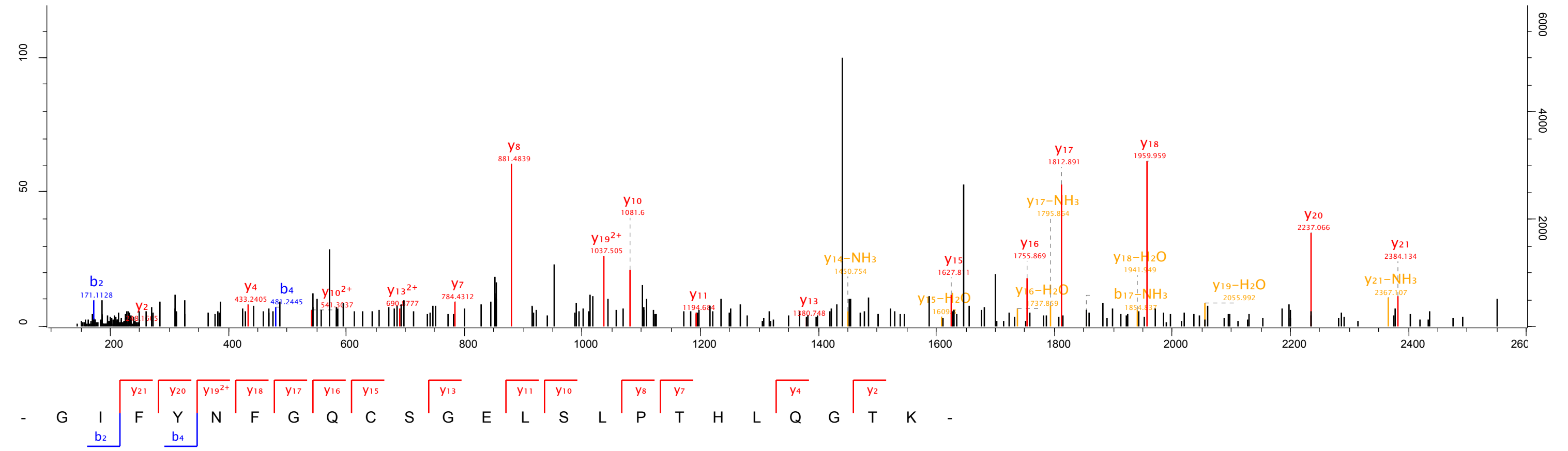


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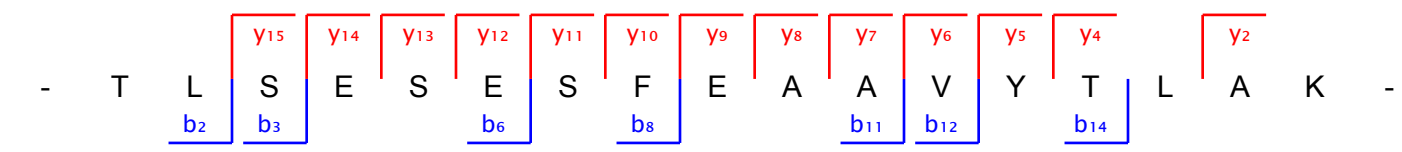
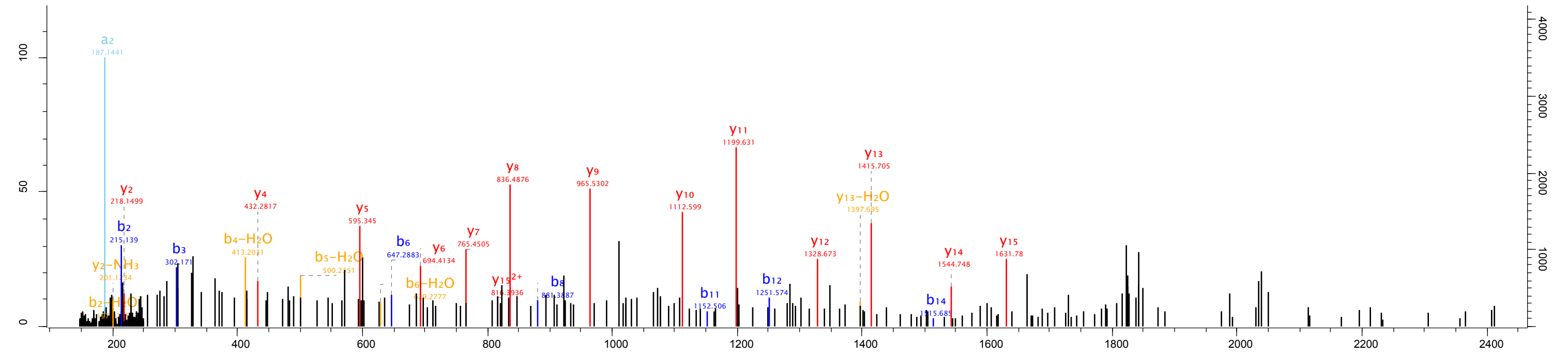






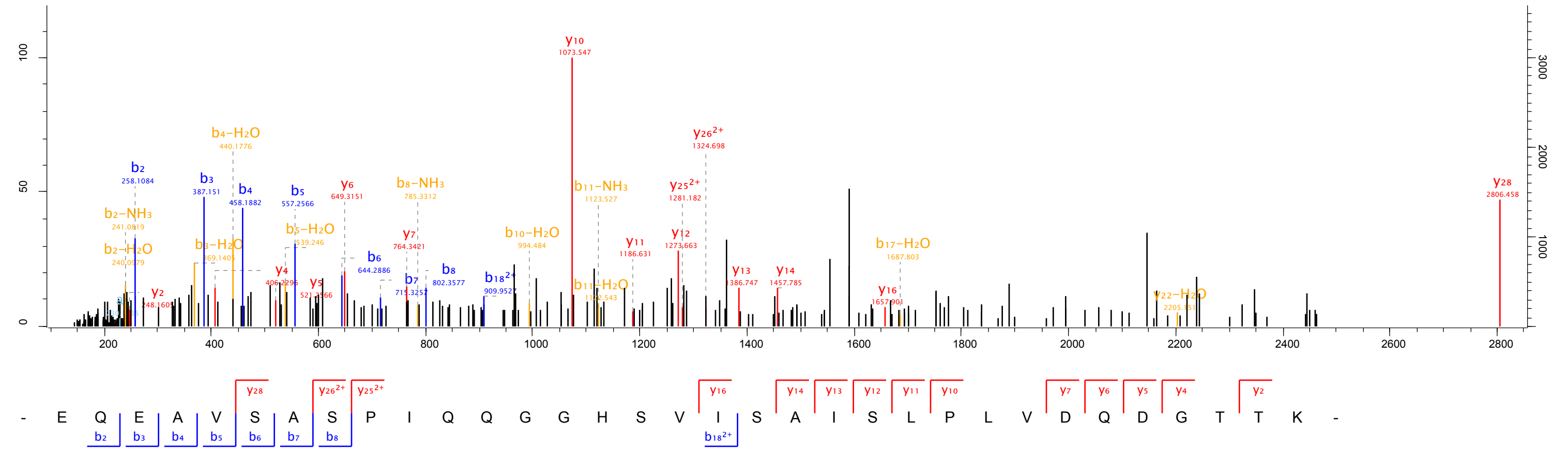
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Scan 62835 Method TOF; CID Score 73.92 m/z 923.45 Gene names Naaa

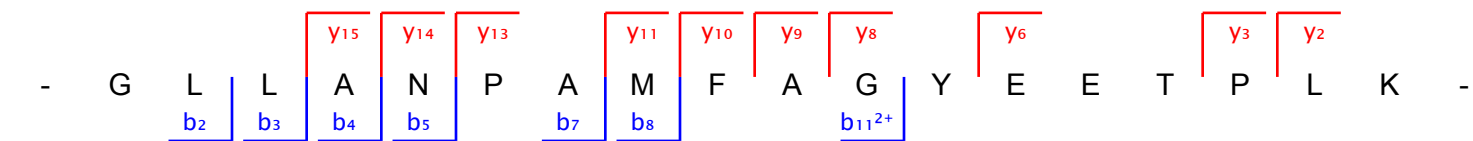
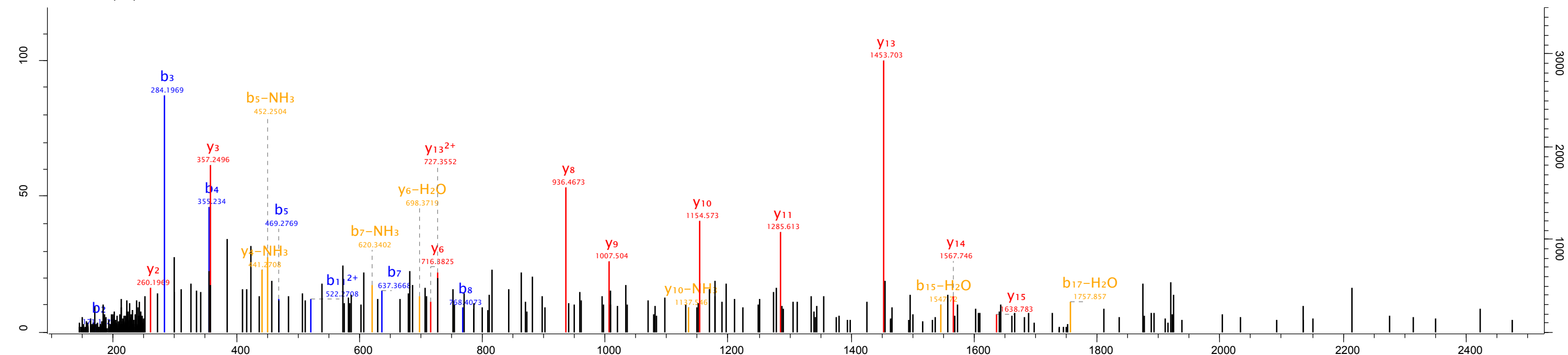


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Scan 63973 Method TOF; CID Score 47.59 m/z 1121.9 Gene names Zeb1

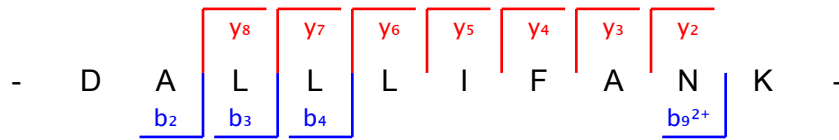
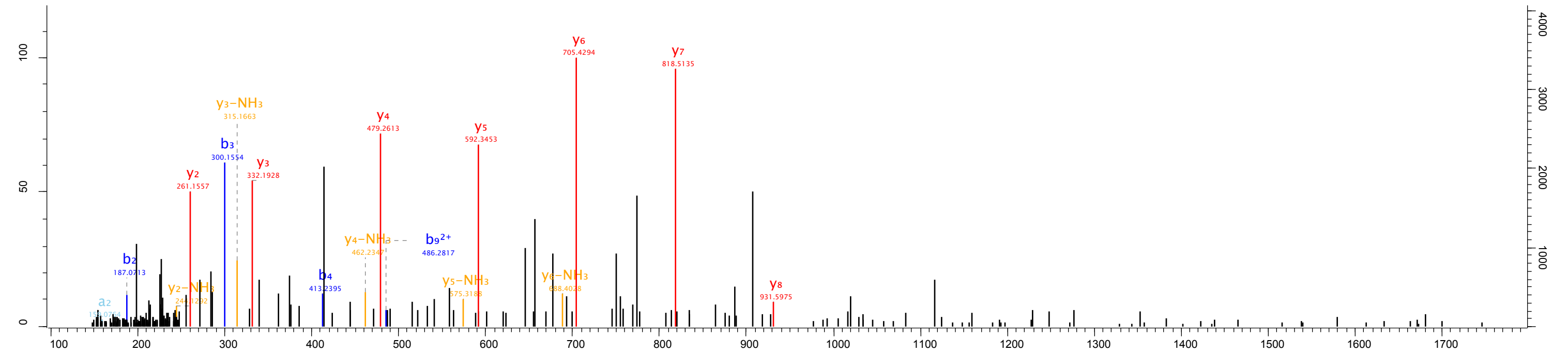


Raw file 20150307_NSC3_Top_opt_F3_01_1691 Scan 65141 Method TOF; CID Score 51.09 m/z 961.48 Gene names Dus4l



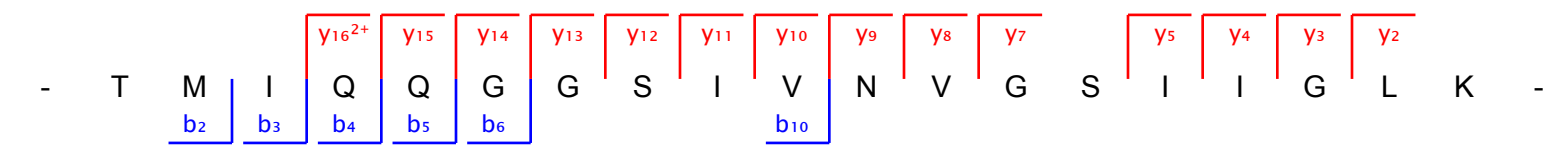
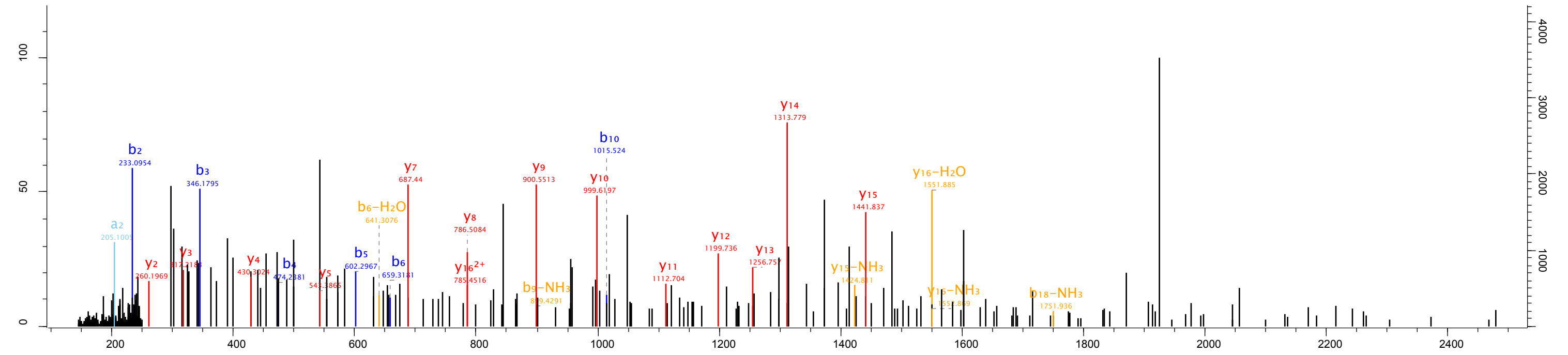
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Scan 65496 Method TOF; CID Score 90.91 m/z 559.33 Gene names Trim23

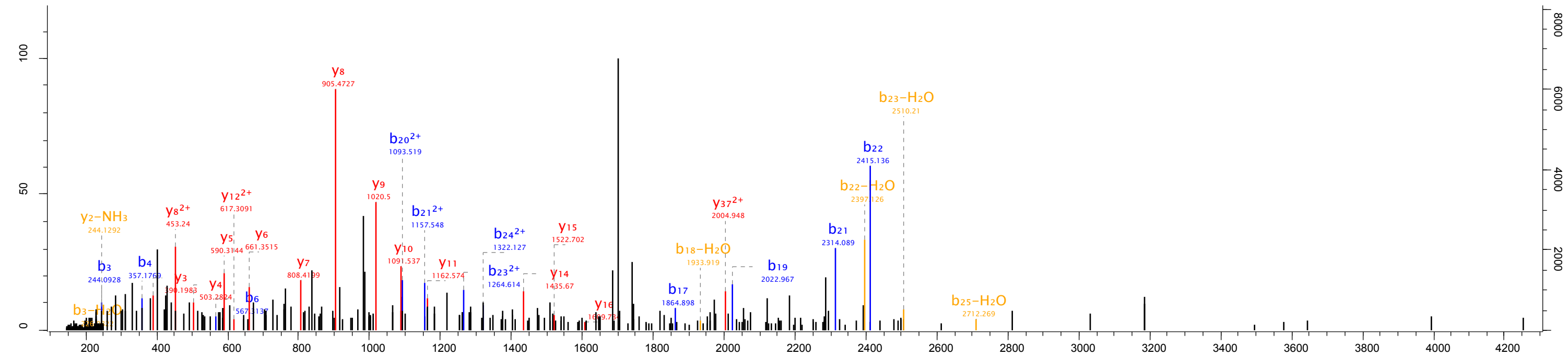


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20150307_NSC3_Top_opt_F3_01_1691

Scan 67746 Method TOF; CID Score 53.03 m/z 958.03 Gene names Cbr4



Raw file 20150307_NSC3_Top_opt_F3_01_1691 Scan 67877 Method TOF; CID Score 53.89 m/z 1064.49 Gene names Agtrap



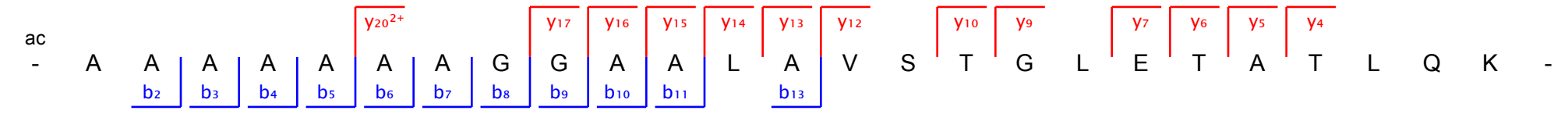
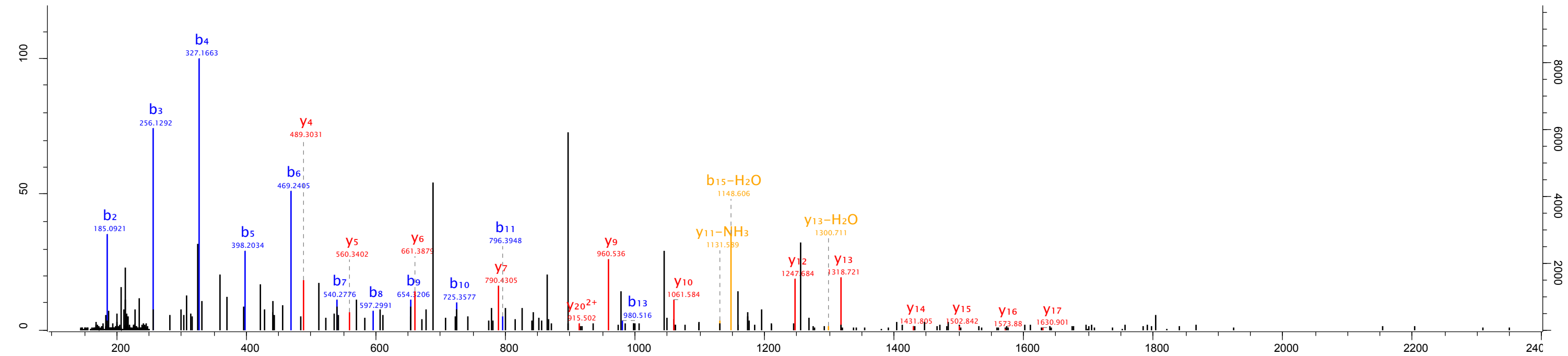
- G G E L P L R P D F F G P S Q E H S A Y Q T I D S S S D A A A D P F A S L E

b₃ b₄ b₆ b₁₇ b₁₉ b₂₀²⁺ b₂₁ b₂₂ b₂₃²⁺ b₂₄²⁺ y₃ y₄ y₅ y₆ y₇ y₈ y₉ y₁₀ y₁₁ y₁₂²⁺ y₁₄ y₁₅ y₁₆

N K -

Raw file
20150307_NSC3_Top_opt_F3_01_1691

Scan: 70975
Method: TOF; CID
Score: 52.46
m/z: 743.4
Gene names: Mzt2



Raw file: 20150307_NSC3_Top_opt_F3_01_1691
 Scan: 71540 Method: TOF; CID Score: 183.7 m/z: 989.49 Gene names: G6pc3

